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Soros et al.(10) **Pub. No.: US 2019/0062448 A1**(43) **Pub. Date: Feb. 28, 2019**(54) **ANTI-CD39 ANTIBODIES, COMPOSITIONS
COMPRISING ANTI-CD39 ANTIBODIES AND
METHODS OF USING ANTI-CD39
ANTIBODIES****Publication Classification**(51) **Int. Cl.**
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CPC **C07K 16/2896** (2013.01); **G01N 33/566**
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2317/24 (2013.01); **C07K 2317/31** (2013.01);
C07K 2317/92 (2013.01); **C07K 2317/76**
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CA (US); **Paul Fredrick Widboom**,
Lebanon, NH (US); **Joseph Robert**
Warfield, Lebanon, NH (US)(21) Appl. No.: **16/049,736**(22) Filed: **Jul. 30, 2018****Related U.S. Application Data**(60) Provisional application No. 62/539,527, filed on Jul.
31, 2017.(57) **ABSTRACT**Provided herein are antibodies that selectively bind to CD39
and its isoforms and homologs, and compositions compris-
ing the antibodies. Also provided are methods of using the
antibodies, such as therapeutic and diagnostic methods.**Specification includes a Sequence Listing.**

Clone ID	K _D (M)	kon (M ⁻¹ s ⁻¹)	koff (s ⁻¹)	Clone ID	K _D (M)	kon (M ⁻¹ s ⁻¹)	koff (s ⁻¹)
27535	PF	PF	PF	29872	1.13E-08	1.75E+05	2.02E-03
27536	1.14E-07	6.59E+04	7.51E-03	31393	6.72E-10	2.98E+05	2.00E-04
27549	4.05E-08	1.93E+04	7.82E-04	31414	1.01E-08	4.31E+05	4.37E-03
27550	1.43E-07	4.44E+05	6.33E-02	31415	1.63E-08	2.27E+05	3.71E-03
27568	1.73E-07	2.72E+05	4.70E-02	31418	1.30E-08	3.14E+05	4.06E-03
27571	1.64E-08	6.39E+05	1.05E-02	31421	1.88E-08	2.81E+05	5.26E-03
27575	PF	PF	PF	31429	2.39E-08	4.73E+05	1.13E-02
27577	4.09E-07	8.93E+05	3.65E-01	31430	1.01E-08	3.26E+05	3.28E-03
27579	1.67E-07	9.55E+05	1.60E-01	31431	1.60E-08	1.73E+05	2.76E-03
27587	3.37E-08	2.11E+05	7.11E-03	31432	1.07E-09	2.68E+05	2.86E-04
27588	5.49E-08	1.17E+05	6.44E-03	31436	9.24E-10	2.63E+05	2.43E-04
27589	1.91E-07	2.02E+05	3.85E-02	31437	5.58E-10	3.82E+05	2.13E-04
27590	1.31E-07	1.76E+05	2.30E-02	31861	1.16E-09	2.46E+05	2.86E-04
27596	3.11E-08	1.72E+06	5.33E-02	31873	9.22E-10	3.11E+05	2.86E-04
27597	3.35E-07	2.73E+05	9.14E-02	31891	1.34E-09	4.53E+05	6.09E-04
28337	1.27E-08	1.43E+05	1.80E-03	31895	1.81E-09	4.63E+05	8.39E-04
28347	9.05E-09	9.01E+05	8.15E-03	31896	9.05E-09	9.01E+05	8.15E-03
29851	1.23E-09	3.13E+05	3.85E-04	31901	1.28E-10	1.03E+06	1.32E-04
29852	2.66E-10	5.03E+05	1.34E-04	31905	7.31E-11	1.52E+06	1.11E-04
29857	7.60E-10	3.02E+05	2.29E-04	31915	8.11E-10	3.53E+05	2.86E-04
29871	2.44E-07	2.73E+05	6.66E-02	A1	1.92E-09	1.66E+05	3.18E-04

FIG. 1

Clone ID	K ₀ (M)	kon (M ⁻¹ s ⁻¹)	koff (s ⁻¹)	Clone ID	K ₀ (M)	kon (M ⁻¹ s ⁻¹)	koff (s ⁻¹)
27535	PF	PF	PF	29872	1.13E-08	1.75E+05	2.02E-03
27536	1.14E-07	6.59E+04	7.51E-03	31393	6.72E-10	2.98E+05	2.00E-04
27549	4.05E-08	1.93E+04	7.82E-04	31414	1.01E-08	4.31E+05	4.37E-03
27550	1.43E-07	4.44E+05	6.33E-02	31415	1.63E-08	2.27E+05	3.71E-03
27568	1.73E-07	2.72E+05	4.70E-02	31418	1.30E-08	3.14E+05	4.06E-03
27571	1.64E-08	6.39E+05	1.05E-02	31421	1.88E-08	2.81E+05	5.26E-03
27575	PF	PF	PF	31429	2.39E-08	4.73E+05	1.13E-02
27577	4.09E-07	8.93E+05	3.65E-01	31430	1.01E-08	3.26E+05	3.28E-03
27579	1.67E-07	9.55E+05	1.60E-01	31431	1.60E-08	1.73E+05	2.76E-03
27587	3.37E-08	2.11E+05	7.11E-03	31432	1.07E-09	2.68E+05	2.86E-04
27588	5.49E-08	1.17E+05	6.44E-03	31436	9.24E-10	2.63E+05	2.43E-04
27589	1.91E-07	2.02E+05	3.85E-02	31437	5.58E-10	3.82E+05	2.13E-04
27590	1.31E-07	1.76E+05	2.30E-02	31861	1.16E-09	2.46E+05	2.86E-04
27596	3.11E-08	1.72E+06	5.33E-02	31873	9.22E-10	3.11E+05	2.86E-04
27597	3.35E-07	2.73E+05	9.14E-02	31891	1.34E-09	4.53E+05	6.09E-04
28337	1.27E-08	1.43E+05	1.80E-03	31895	1.81E-09	4.63E+05	8.39E-04
28347	9.05E-09	9.01E+05	8.15E-03	31896	9.05E-09	9.01E+05	8.15E-03
29851	1.23E-09	3.13E+05	3.85E-04	31901	1.28E-10	1.03E+06	1.32E-04
29852	2.66E-10	5.03E+05	1.34E-04	31905	7.31E-11	1.52E+06	1.11E-04
29857	7.60E-10	3.02E+05	2.29E-04	31915	8.11E-10	3.53E+05	2.86E-04
29871	2.44E-07	2.73E+05	6.66E-02	A1	1.92E-09	1.66E+05	3.18E-04

FIGS. 2 A-B

A.

Clone Name	Human CD39 Inhibition Assay Cell Titer Glo Average Response (RLU)
27536	7489
27549	16867
27550	5574
27568	5727
27571	6823
27575	2598
27577	3596
27579	6471
27587	8733
27588	11166
27589	6580
27590	5680
27596	3929
27597	8889
Isotype Control	375

B.

Clone Name	Human CD39 Inhibition Assay Cell Titer Glo Average Response (RLU)
28337	9399
28347	9083
27535	4890
Isotype Control	857

FIGS. 2 C-E

C.

Clone Name	Human CD39 Inhibition Assay Cell Titer Glo Average Response (RLU)
28337	11768
27549	15648
28347	11182
29851	11554
29852	11980
29857	11637
27571	8543
27579	8878
29871	8708
29872	8372
BY40va	415
no IgG	979

D.

Clone Name	Human CD39 Inhibition Assay Cell Titer Glo Average Response (RLU)
27571	10885
31393	12105
27579	8035
29872	8368
31414	10254
31415	10289
31418	9447
31421	7263
31429	11441
31430	8380
31431	9993
28347	13306
31436	14157
31437	13509
31393	12105
Isotype Control	38

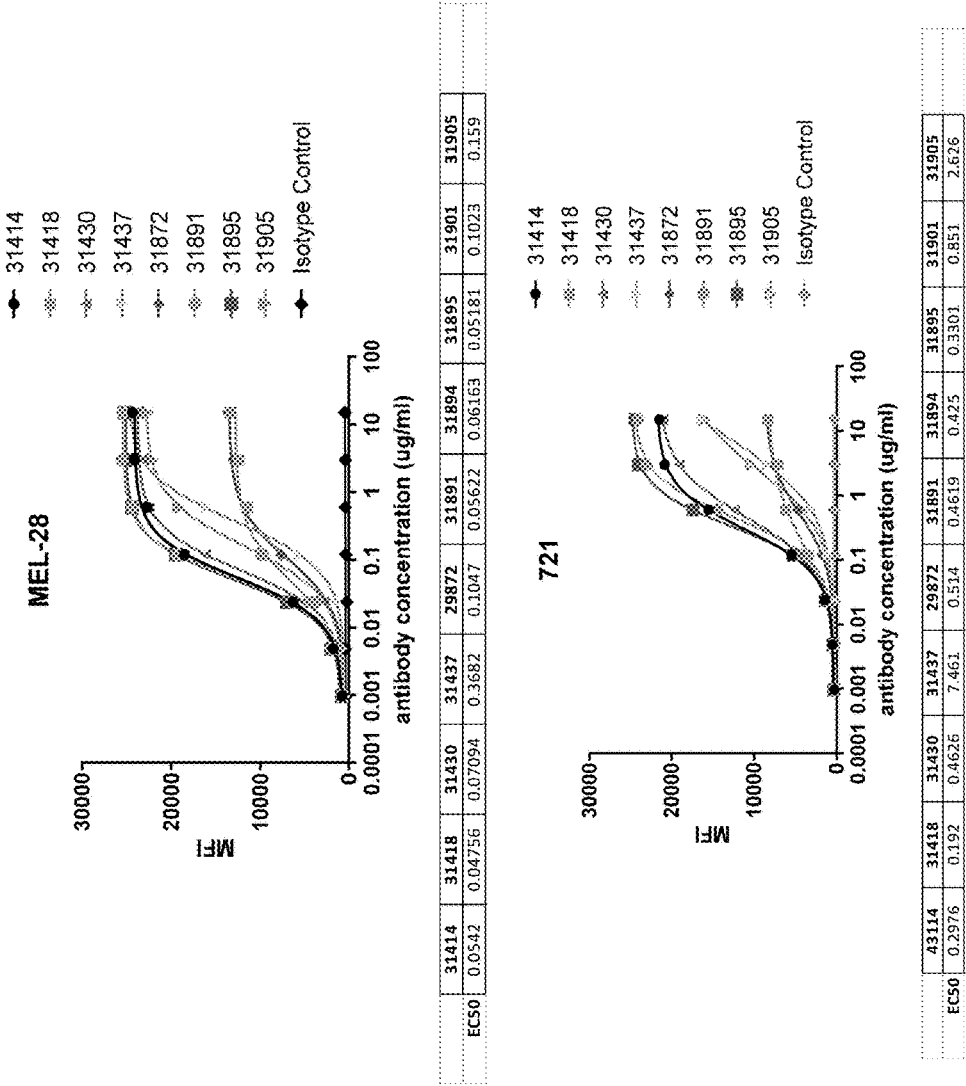
E.

Clone Name	Human CD39 Inhibition Assay Cell Titer Glo Average Response (RLU)
27571	14303
31861	17866
31873	16645
27579	8575
31414	11375
31891	13470
31895	12828
28347	18736
31432	18610
31896	11911
31901	14798
31905	20329
31915	15694
Isotype Control	44
BY40va	11

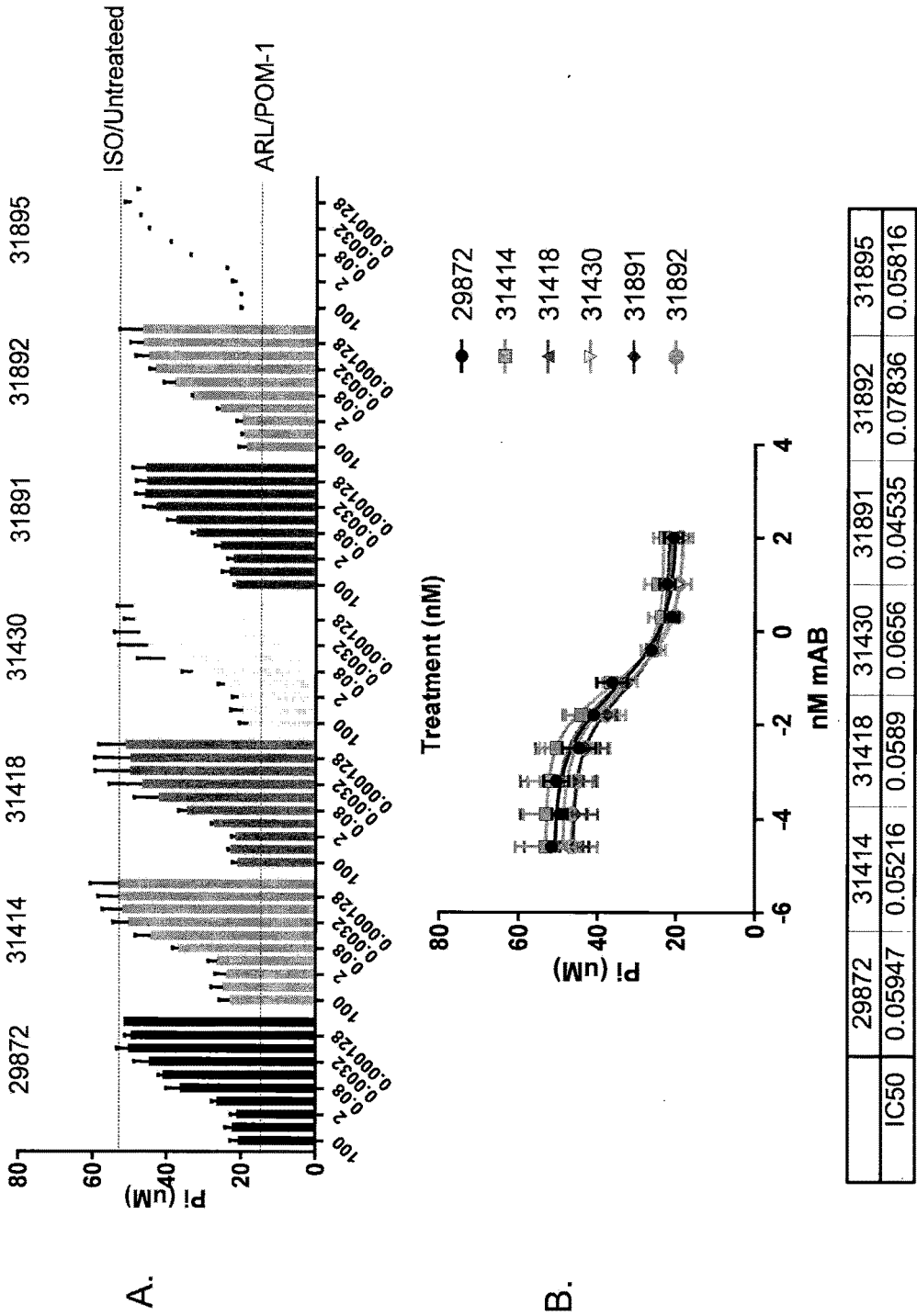
FIG. 2F

Clone Number	Cell Binding (FOB)		Clone Number	Cell Binding (FOB)	
	hCD39-CHO	cCD39-CHO		hCD39-CHO	cCD39-CHO
27535	301	738	31393	1064	2955
27536	89	113	31414	1236	3568
27549	822	566	31415	1168	3365
27550	2,033	2870	31418	1077	3183
27568	267	260	31421	1075	3053
27571	1,405	1607	31429	1291	3800
27575	2	128	31430	1222	3573
27577	390	339	31431	1235	3533
27579	1,953	2667	31432	1167	5697
27587	1,450	1403	31436	1317	3568
27588	10	14	31437	1292	3643
27589	311	531	31861	1432	5477
27590	33	44	31873	1321	5083
27596	252	257	31891	1026	4651
27597	799	908	31895	1042	4493
28337	4	17	31896	1042	4539
28347	1,020	1340	31901	1113	4662
29851	129	398	31905	1077	4937
29852	337	1418	31915	1087	4578
29857	224	1145	A1	796-2191	2426-3054
29871	451	3350	BY40va	1292	3867
29872	1454	4191	isotype Control	1	1

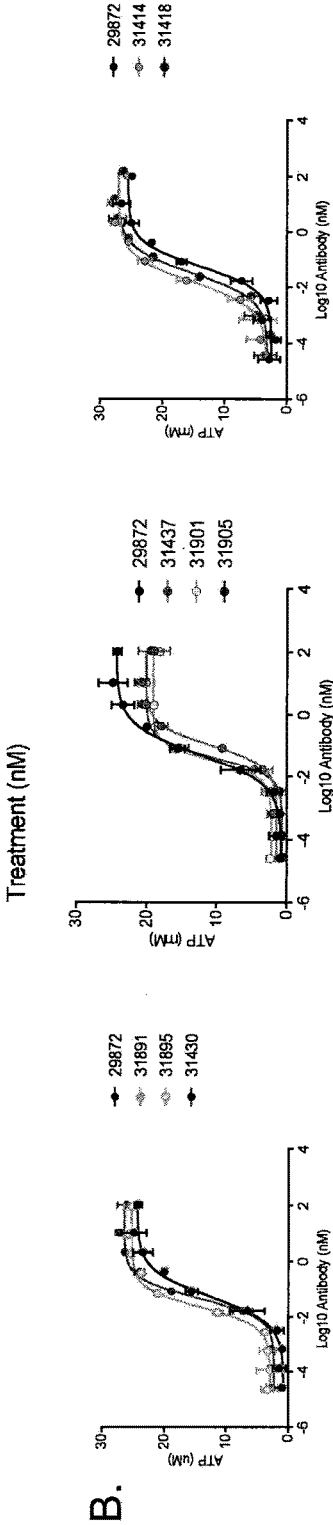
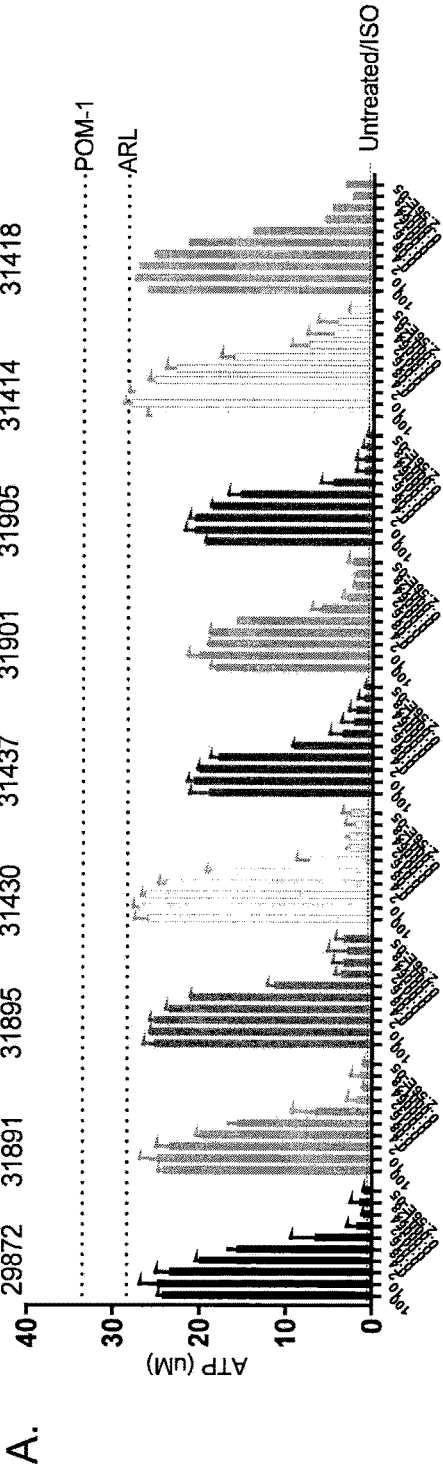
FIG. 3



FIGS. 4 A-B

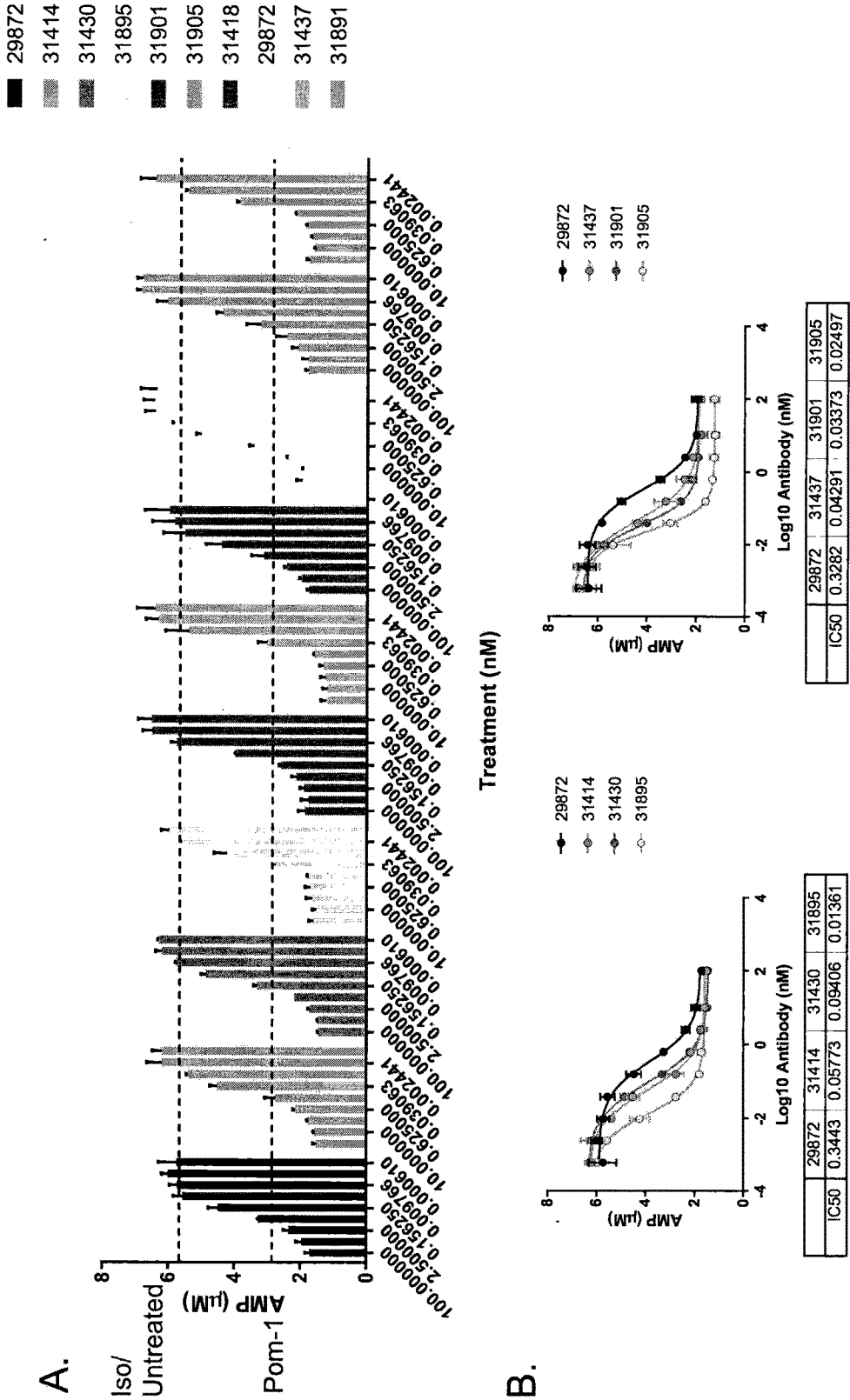


FIGS. 5 A-B



	29872	31891	31895	31430	31437	31901	31905	31414	31418
IC50	0.05357	0.05644	0.02219	0.0467	0.1036	0.03386	0.04161	0.01511	0.03103

FIGS. 6 A-B



FIGS. 7 A-B

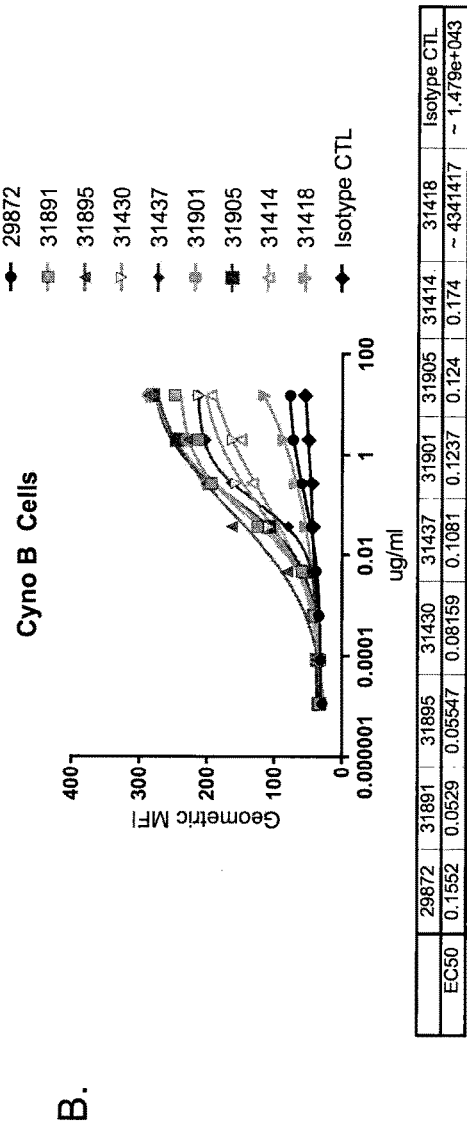
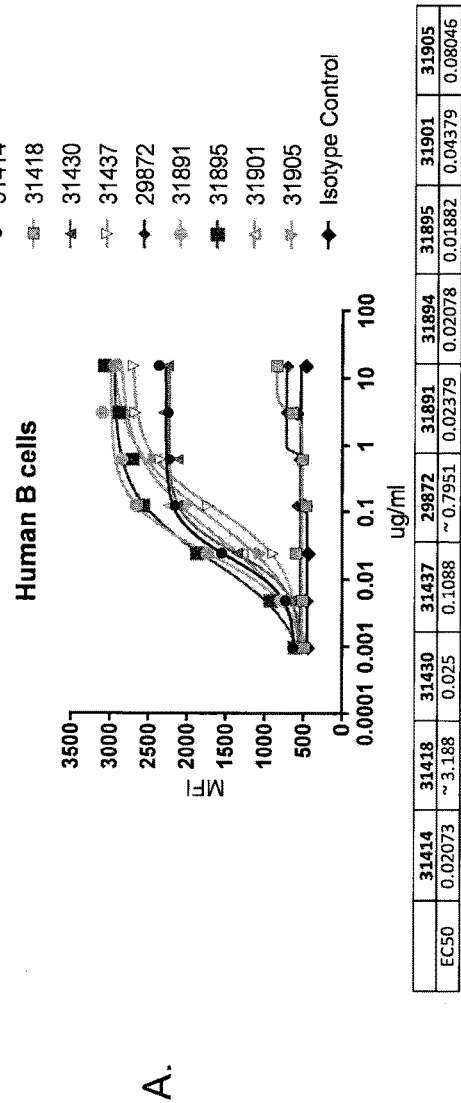


FIG. 8

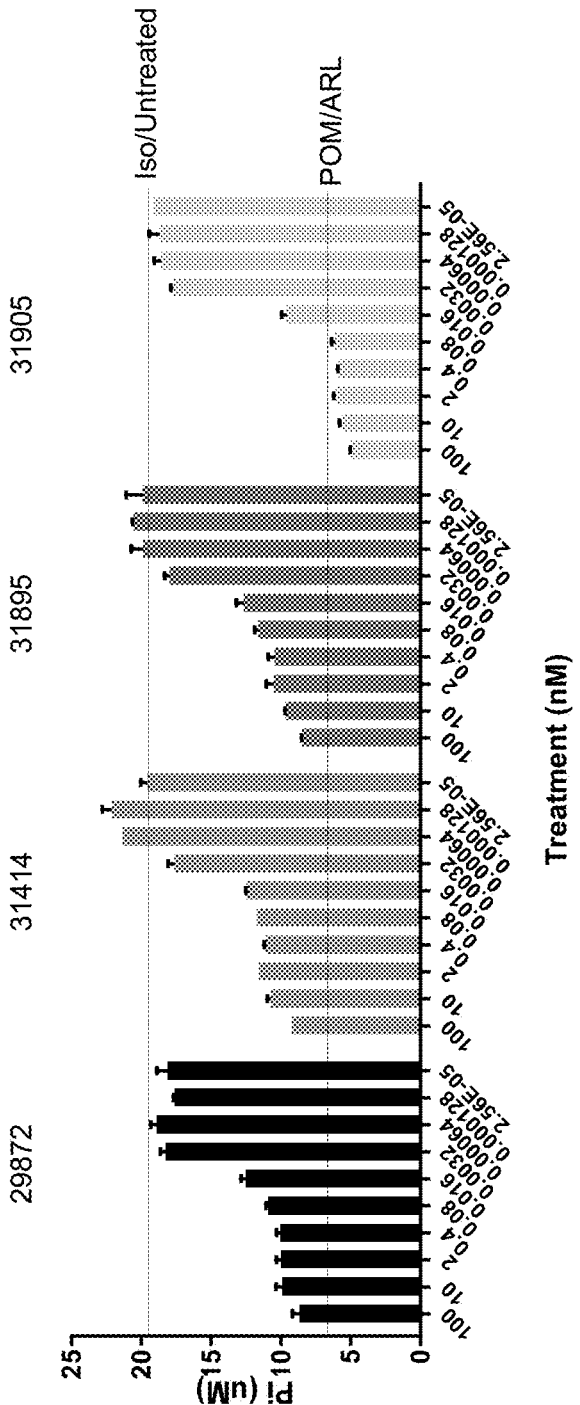


FIG. 9

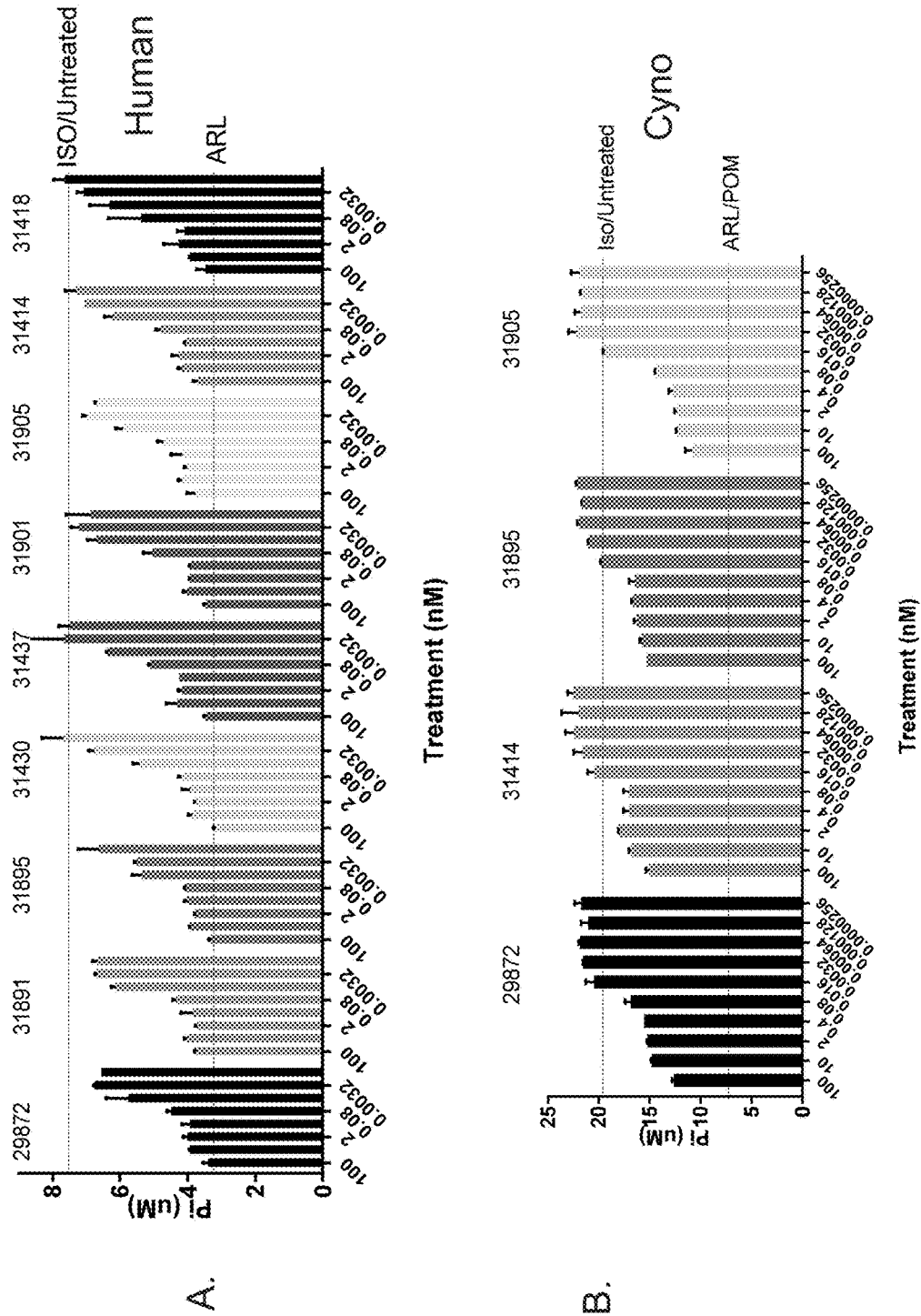
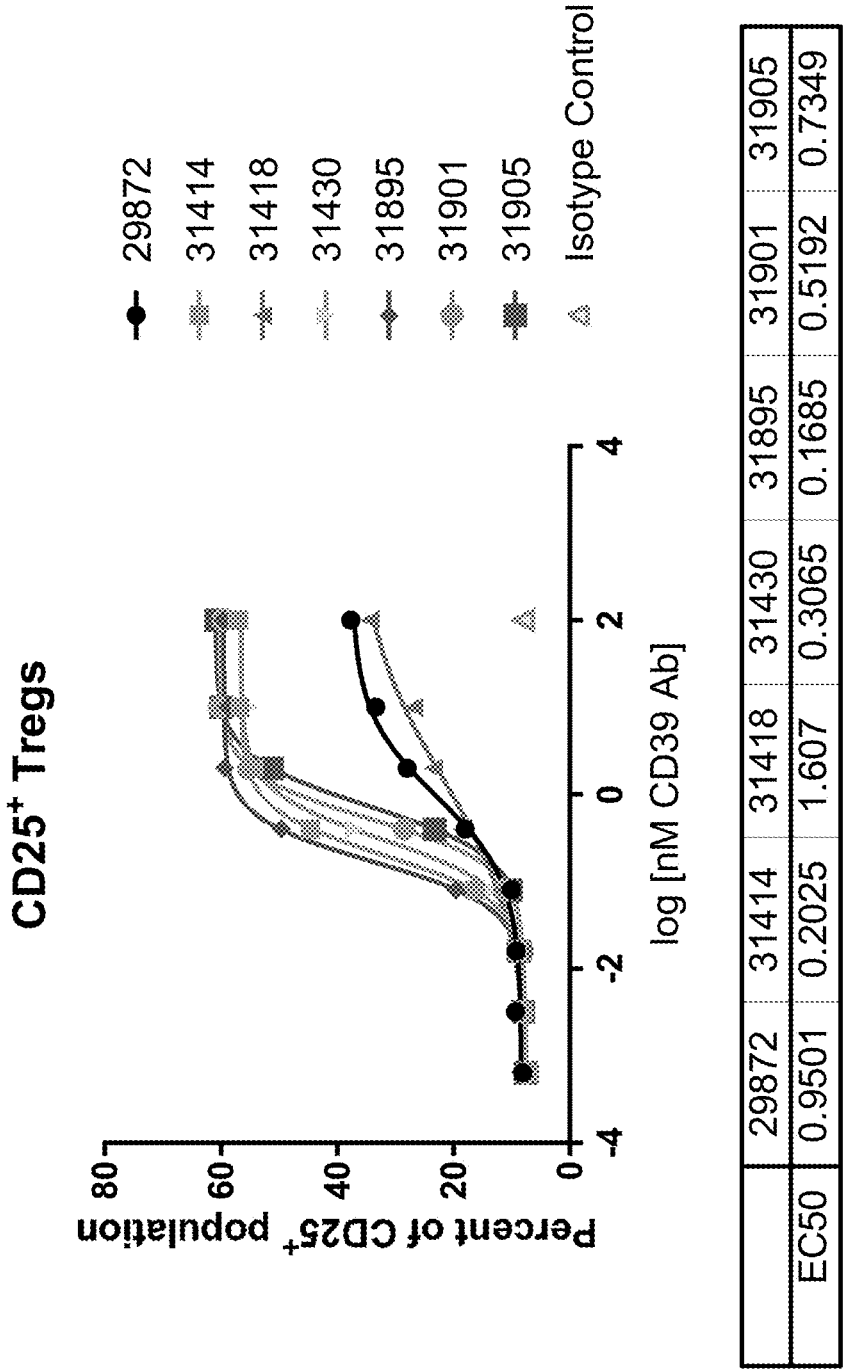


FIG. 10



7
 7
 8
 9
 9

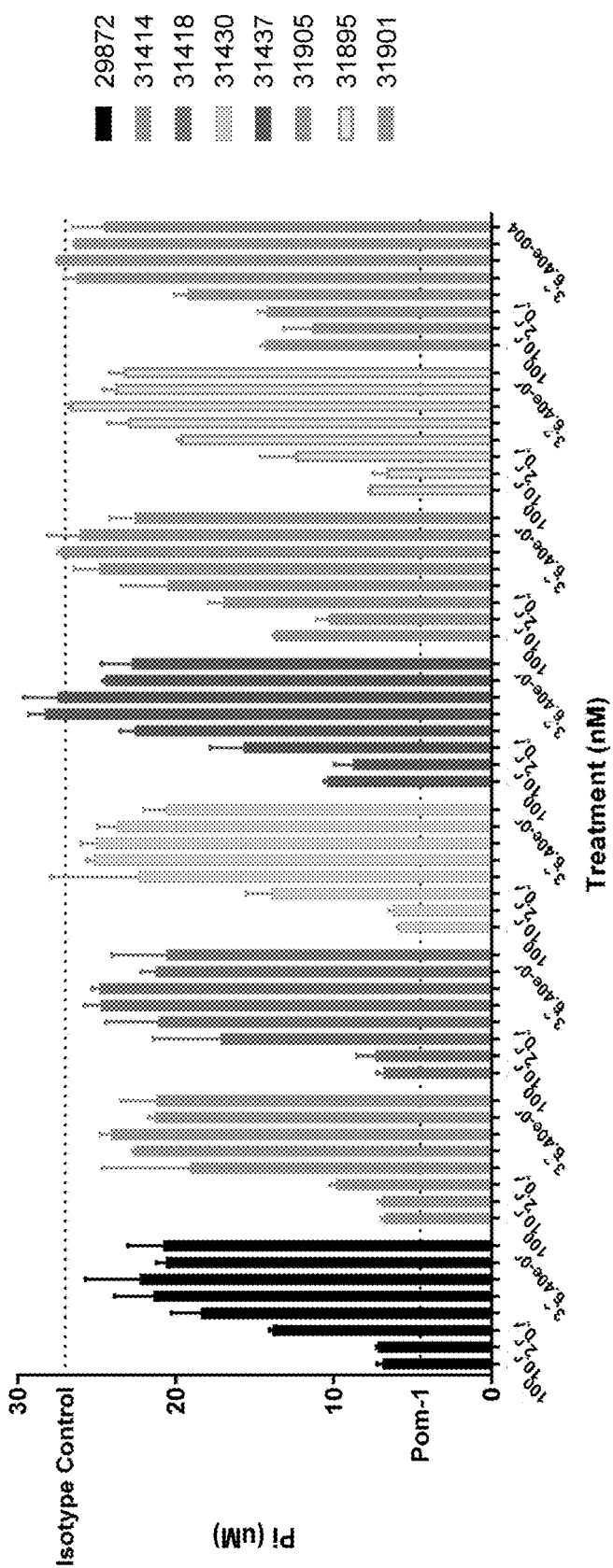
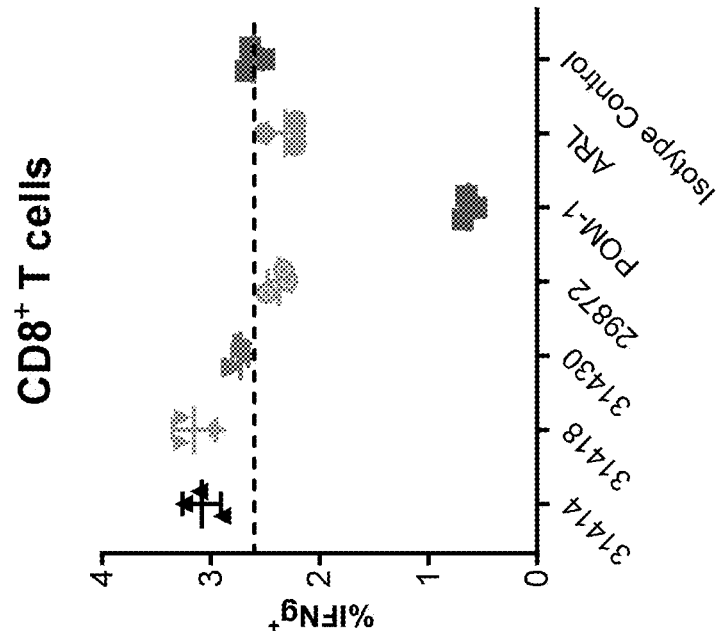


FIG. 12



FIGS. 13 A-B

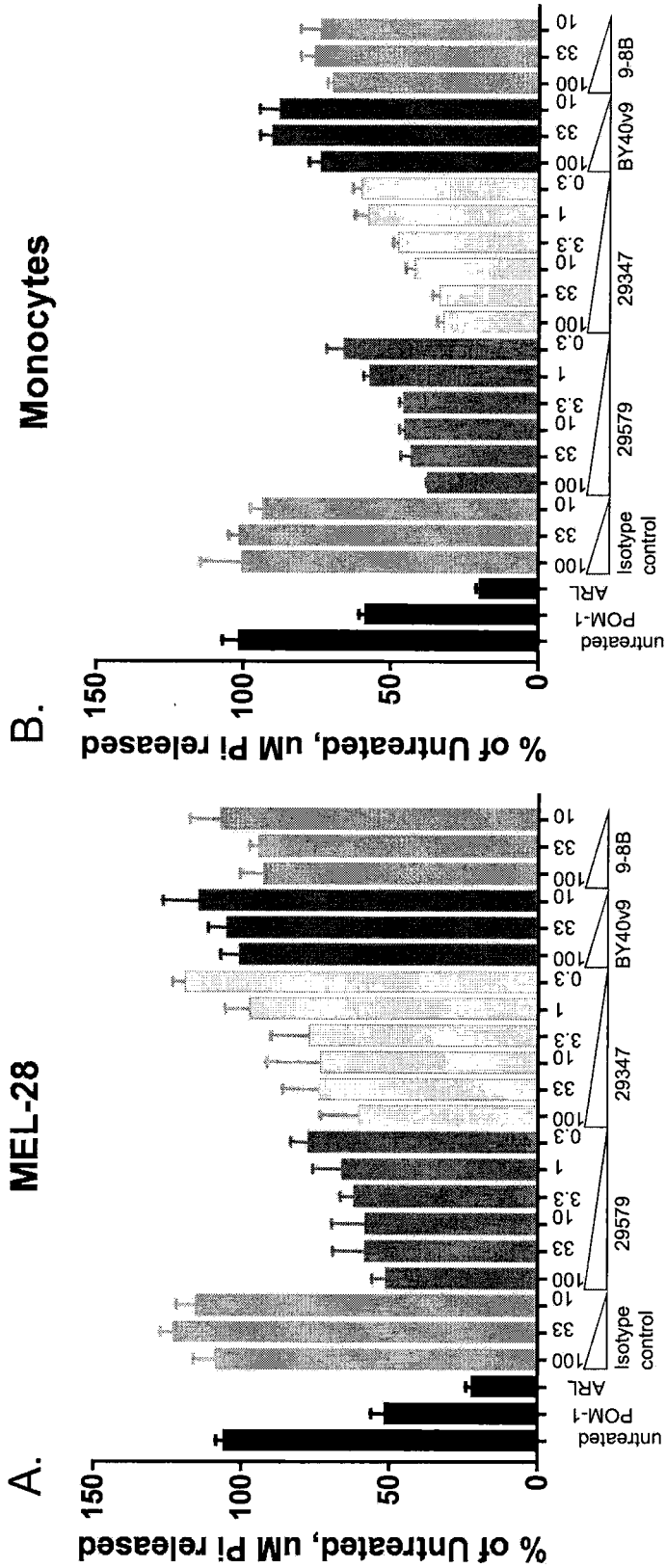


FIG. 14A

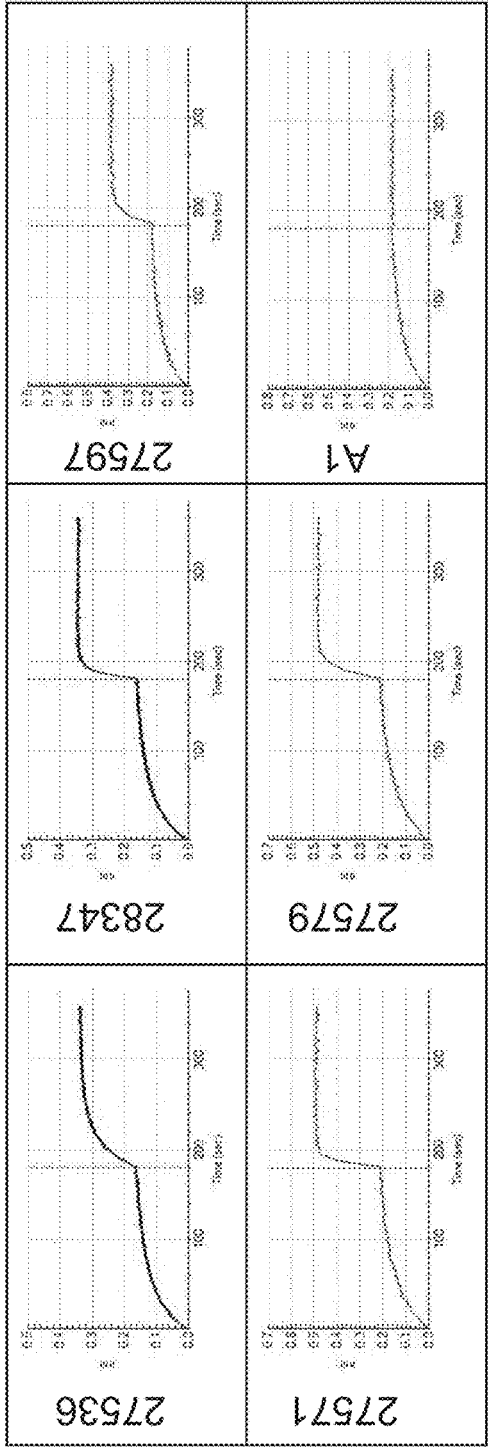
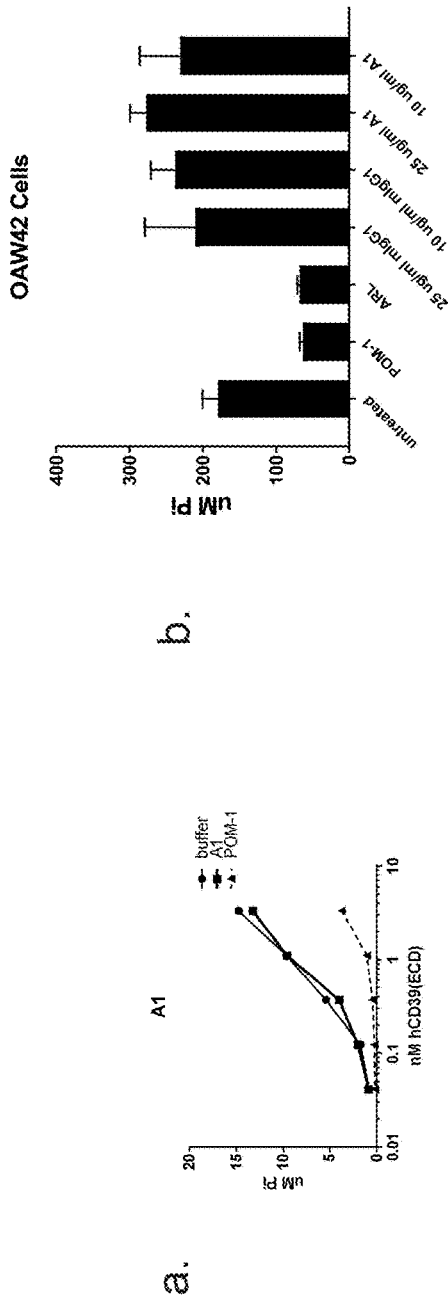


FIG. 14B

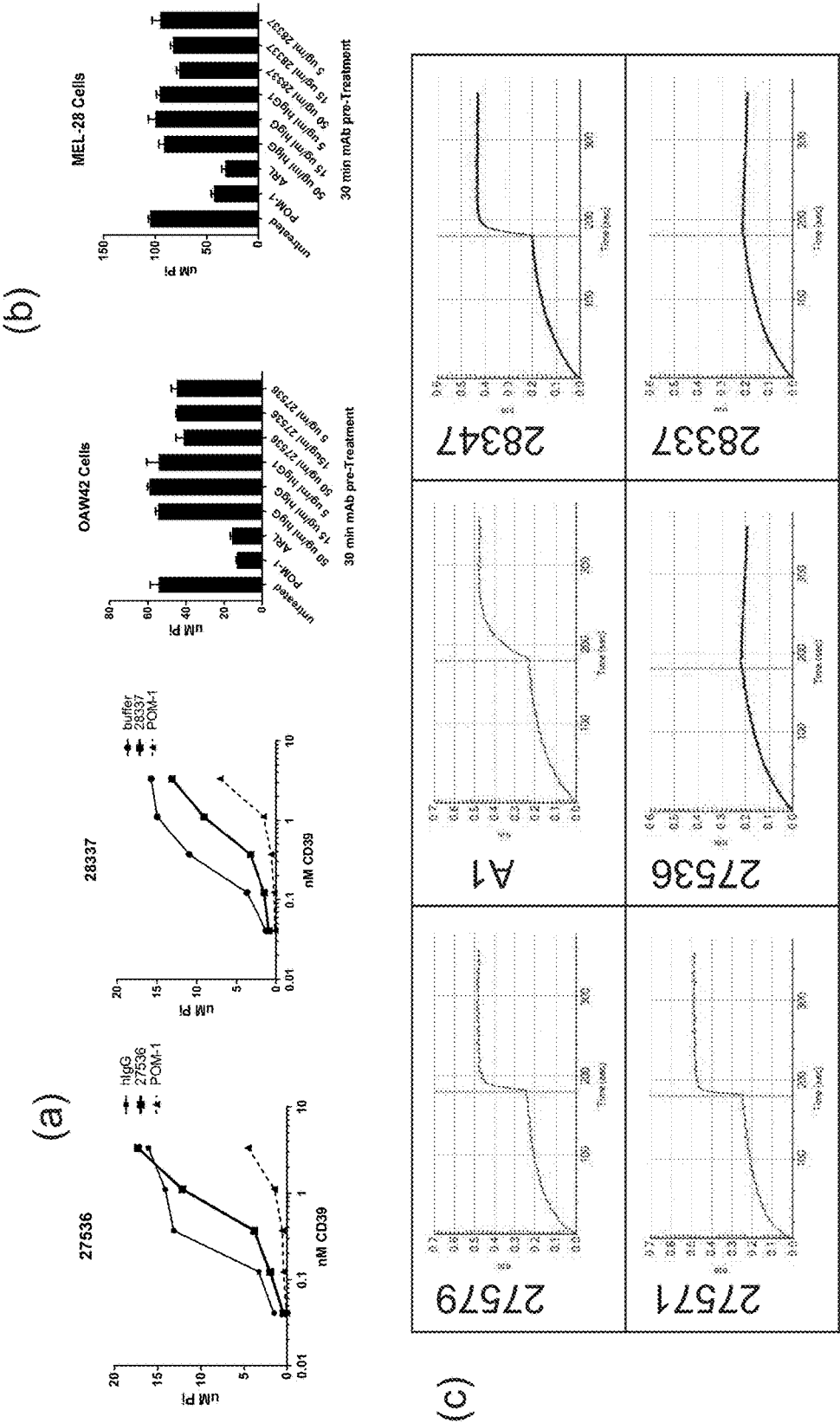


FIG. 14C

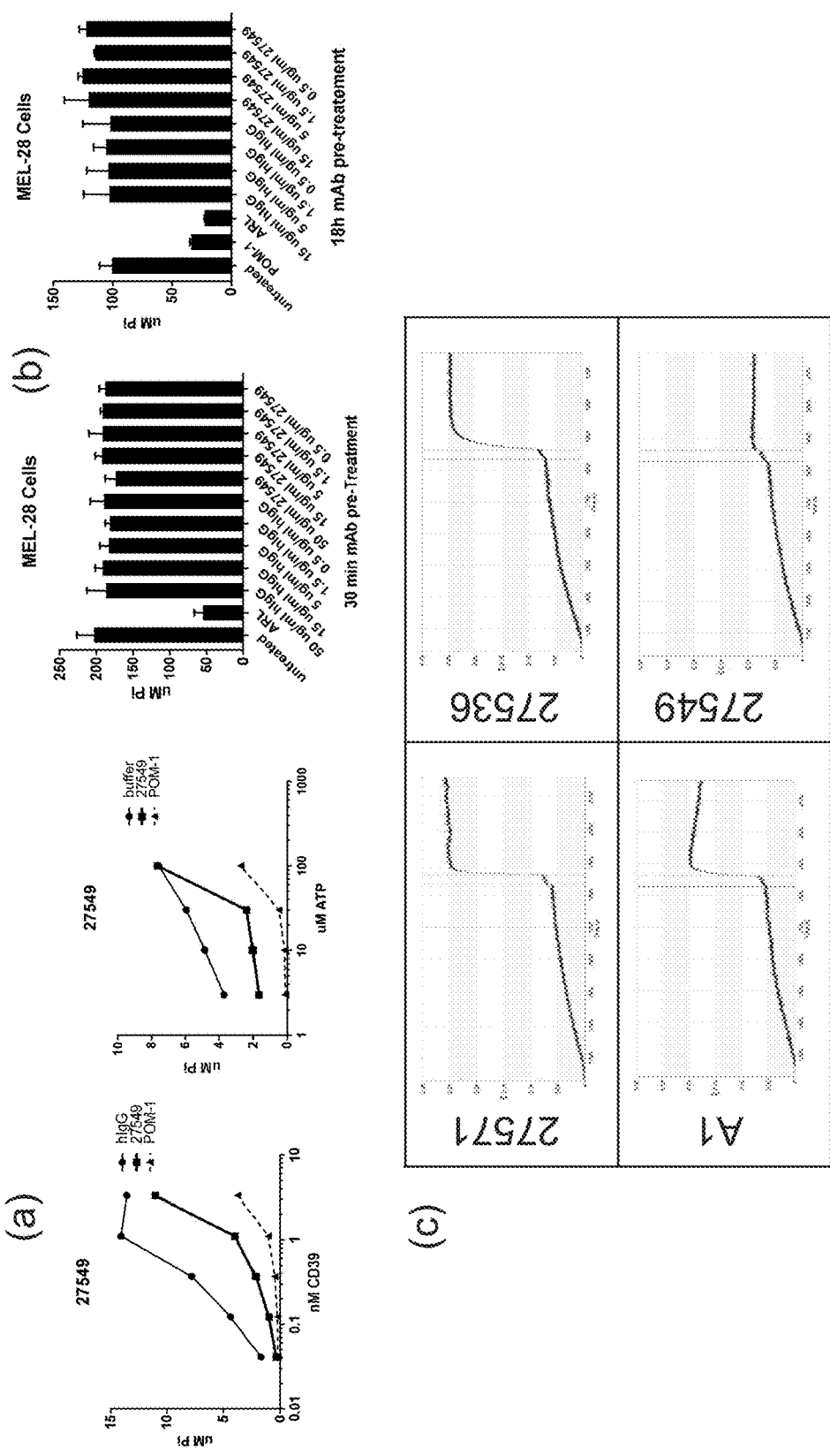


FIG.14E

Table 1.

Chimera #	FASTA Residue Number from Species of Origin in Chimera			Mouse amino acid sequence ⁴	mAb binding to human-mouse CD39 chimeras					
	Human ¹	Mouse ²	Human ³		31895 31414 31418	31873	31901 31905	BY40v9	9-8B	A1 498403 [#]
1	M1-E110	L111-Q123	T124-V510	L ₁₁₁ STELIPTSKHHQ	yes	yes	yes	yes	yes	yes
2	M1-E142	Q143-S158	Y159-V510	Q ₁₄₃ SADEVLA ⁴ AVSTSLKS	NO	NO	NO	yes	yes	yes
3	M1-G187	R188-K204	Q206-V510	R ₁₈₈ FTQEQSWLSLSDSOK	yes	yes	yes	yes	yes	yes
4	M1-S274	G274-V277	L278-V510	G ₂₇₈ GV	yes	yes	yes	yes	yes	NO
5	M1-E306	K306-E322	Q324-V510	K ₃₀₆ KLPFDQFRIGTG ⁴ DYE	yes	yes	yes	yes	yes	yes
6	M1-M367	D367-I378	S378-V510	D ₃₆₇ FFKKVAKNSVI	yes	yes	yes	yes	yes	yes
7	M1-C390	S392-S404	V404-V510	S ₃₉₂ KSWEEKTSYPS	yes	yes	yes	yes	yes	yes
8	M1-H428	N428-N447	A448-V510	N ₄₂₈ FTDSSWEQIHFMGKIK DSN	yes	yes	yes	yes	yes	yes

FIG. 14E

Table 2.

# Chimera	FASTA Residue Number from Species of Origin in Chimera			Mouse and Human amino acid sequences*	mAb binding to human-mouse CD39 chimeras				
	Human	Mouse	Human		31895 31414 31418	3187 3	3190 1 3190 5	BY40v9	9-8B
2	M1-E142	Q143-S158	Y159-V510	Q ₁₄₃ SADEVLA _{AV} STSLKS	NO	NO	NO	yes	yes
9	M1-E142 Y159-V510	Q143-L149 A151-S158	D150	Q ₁₄₃ SADEVL _D AVSTSLKS	YES	NO	NO	yes	yes
10	M1-E142 Y159-V510	Q143-V152 R154-S158	E153	Q ₁₄₃ SADEVLA _{AV} E STSLKS	YES	NO	NO	yes	yes
WT	M1-V510			V ₉₅ QKVNEIGI E ₁₄₃ LADRVLDVVERSKSN	yes	yes	yes	yes	yes
11	M1-V98 E100-V510	D99		V ₉₅ QKV D EIGI	yes	yes	yes	yes	yes
12	M1-E153 S155-V510	T154		E ₁₄₃ LADRVLDVVE T SKSN	yes	yes	yes	yes	yes
13	M1-V98 E100-E153 S155-V510	D99 T154		V ₉₅ QKV D EIGI E ₁₄₃ LADRVLDVVE T SKSN	yes	NO	NO	yes	yes
14	M1-V152 S155-V510	S153 T154		E ₁₄₃ LADRVLDV ST SKSN	yes	NO	NO	yes	yes

FIG. 14F

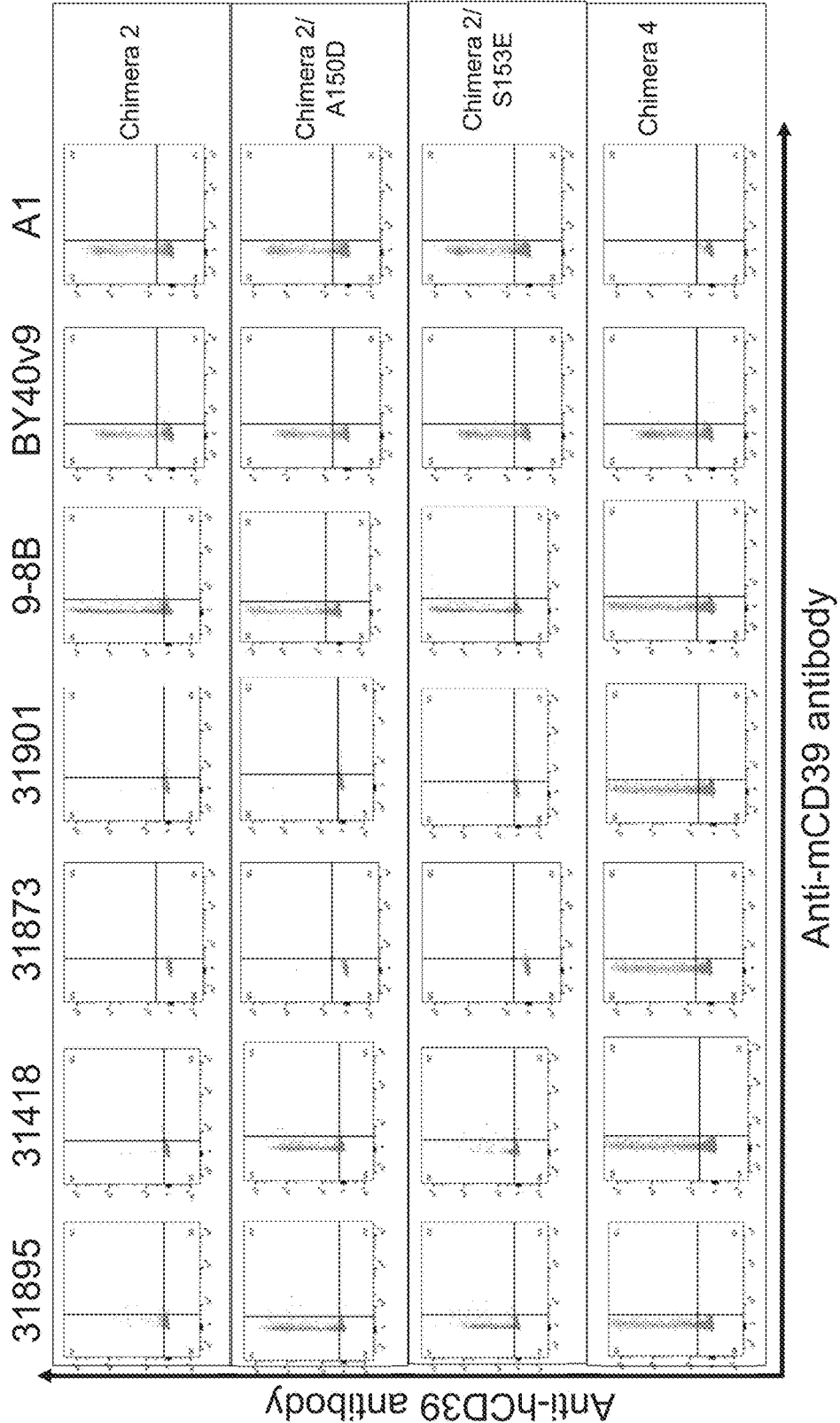
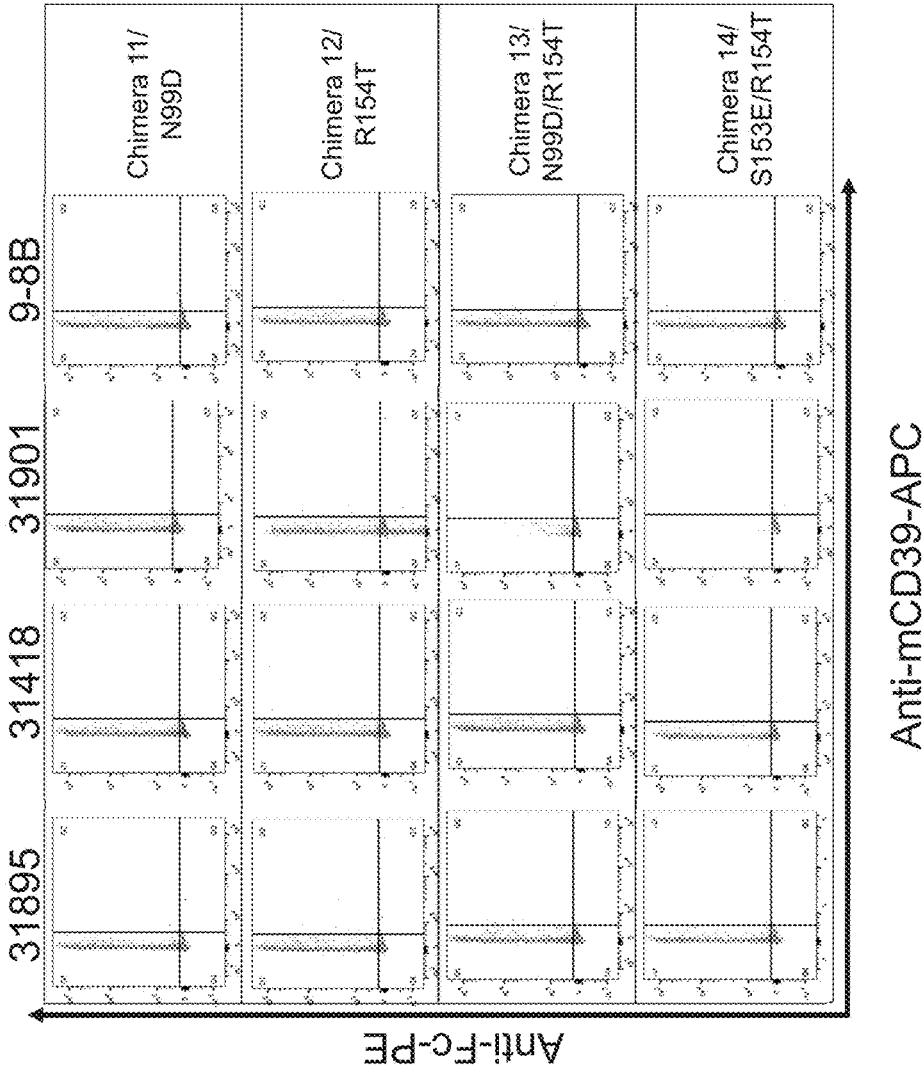


FIG. 14G



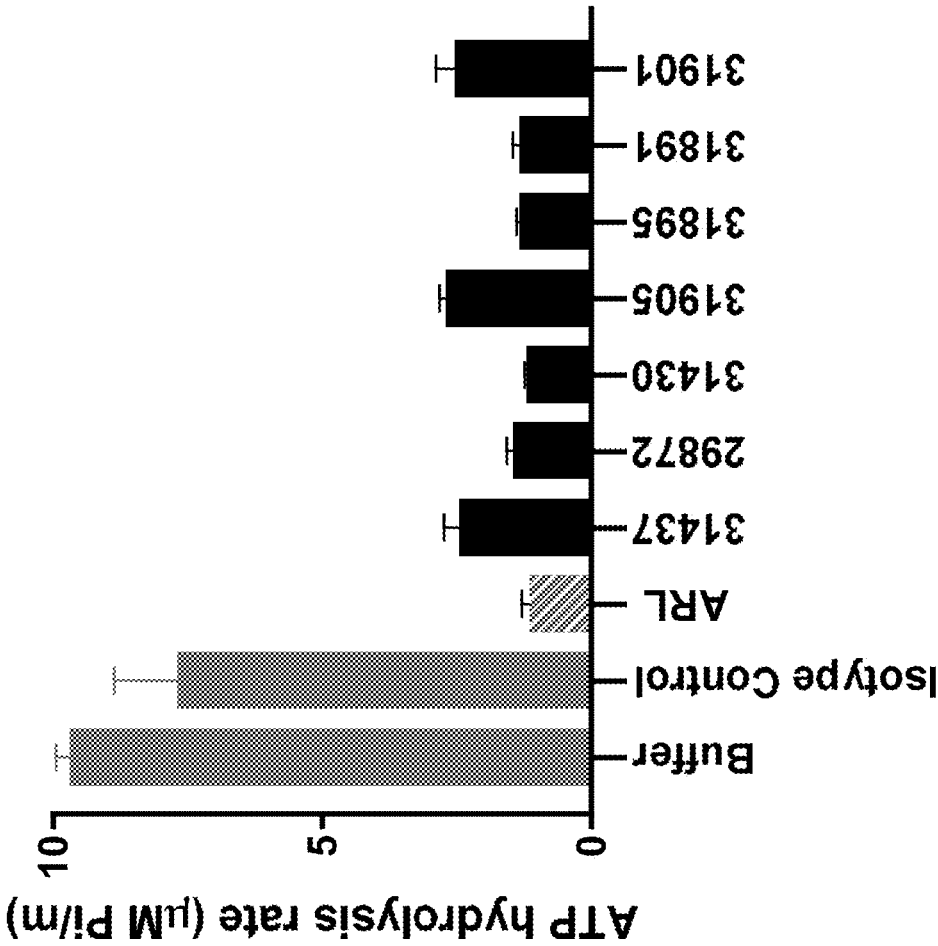


FIG. 15

FIG. 16A

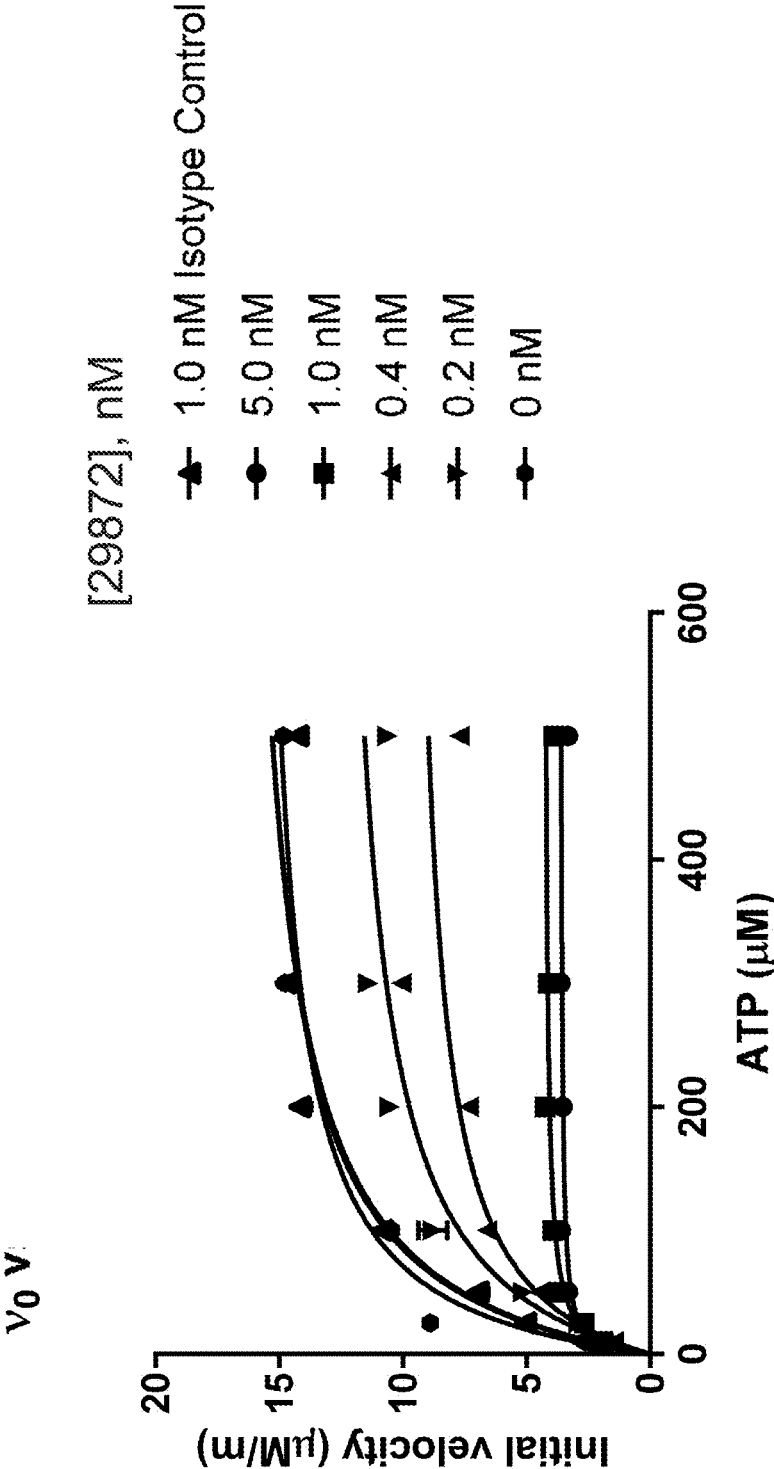


FIG. 16B

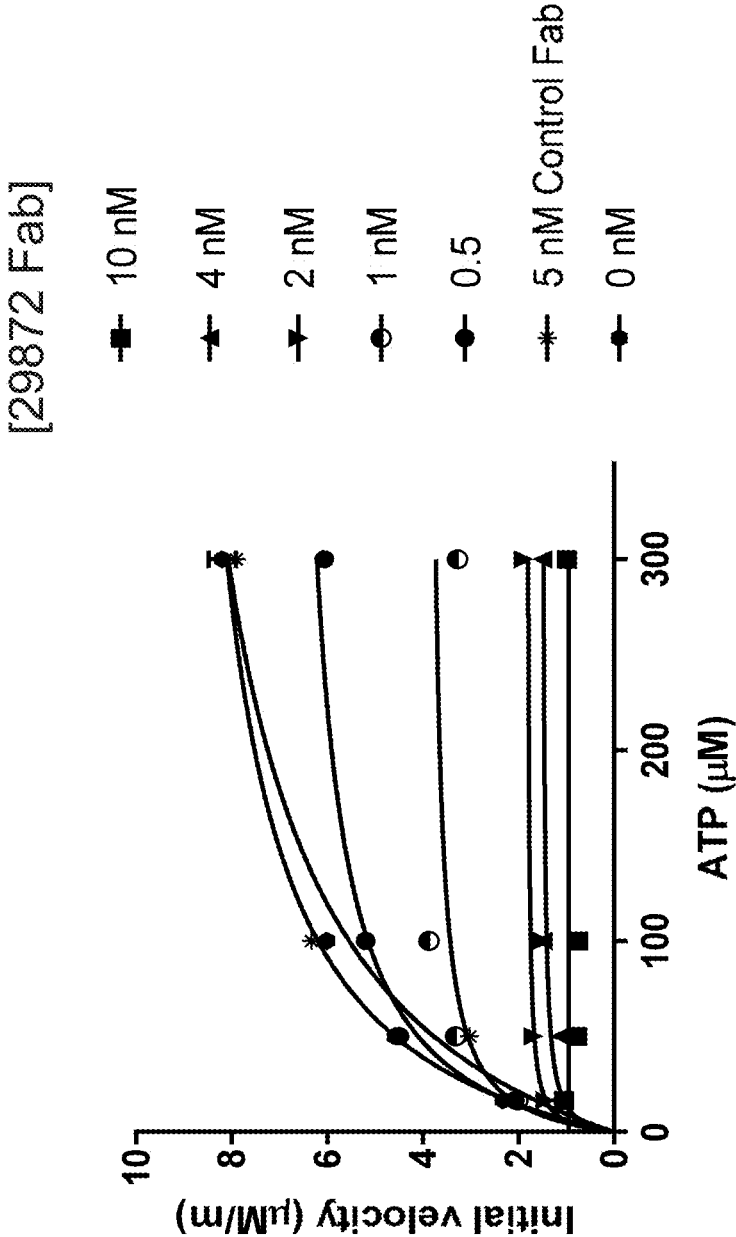


FIG. 17

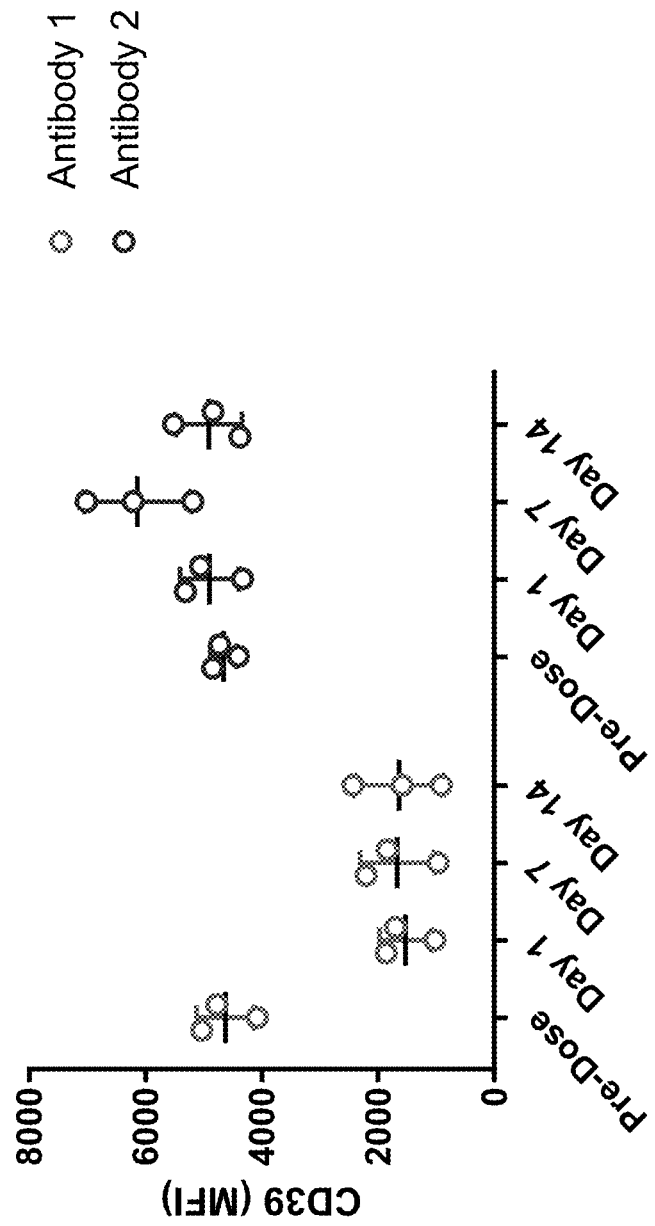


FIG. 18

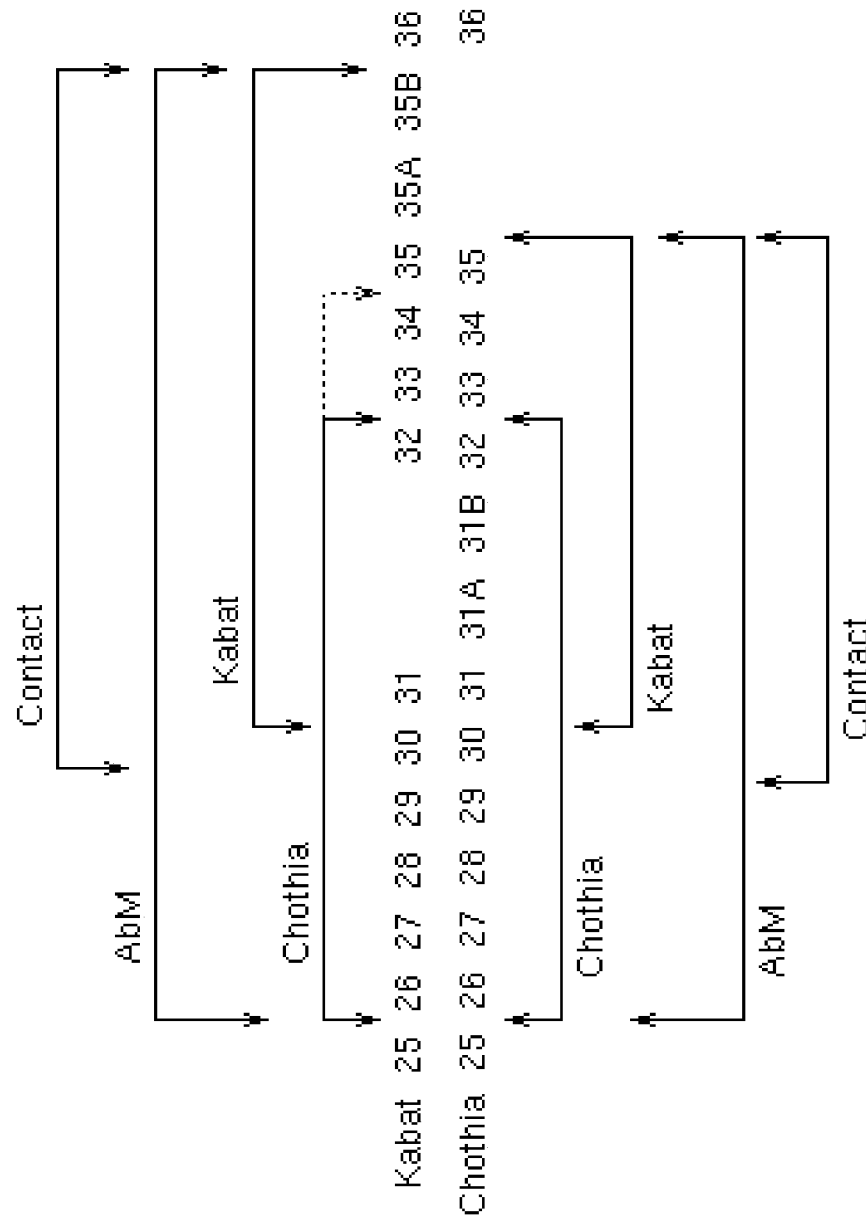


FIG. 19

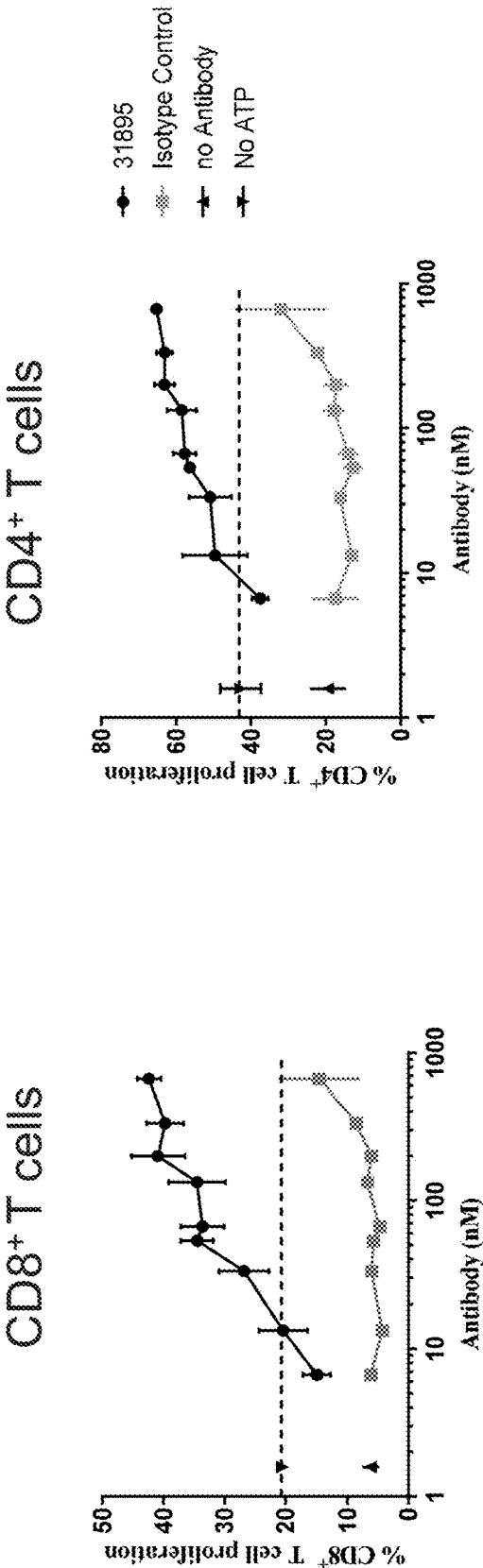
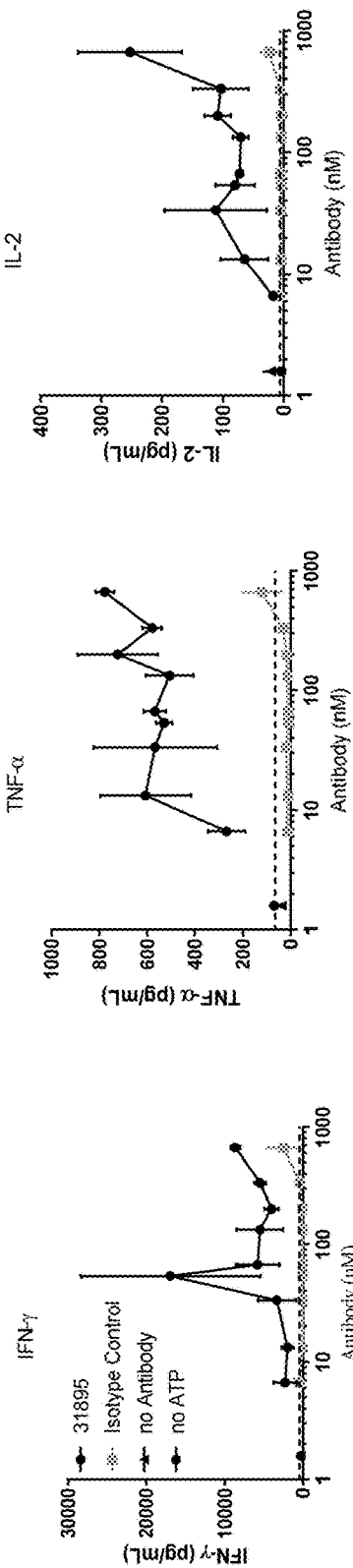


FIG. 20

A.

Exogenous ATP Added



B.

No Exogenous ATP Added

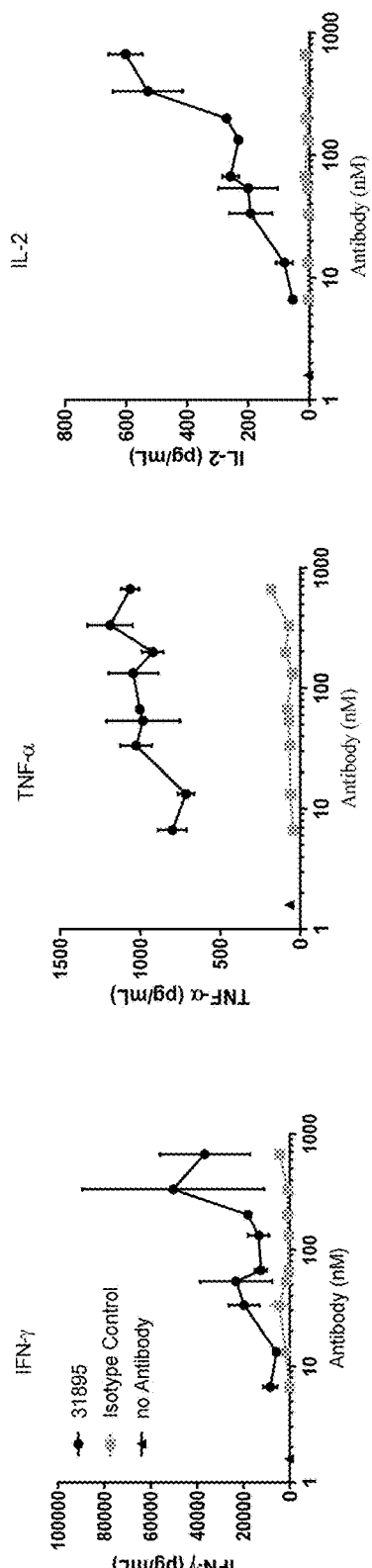


FIG. 21

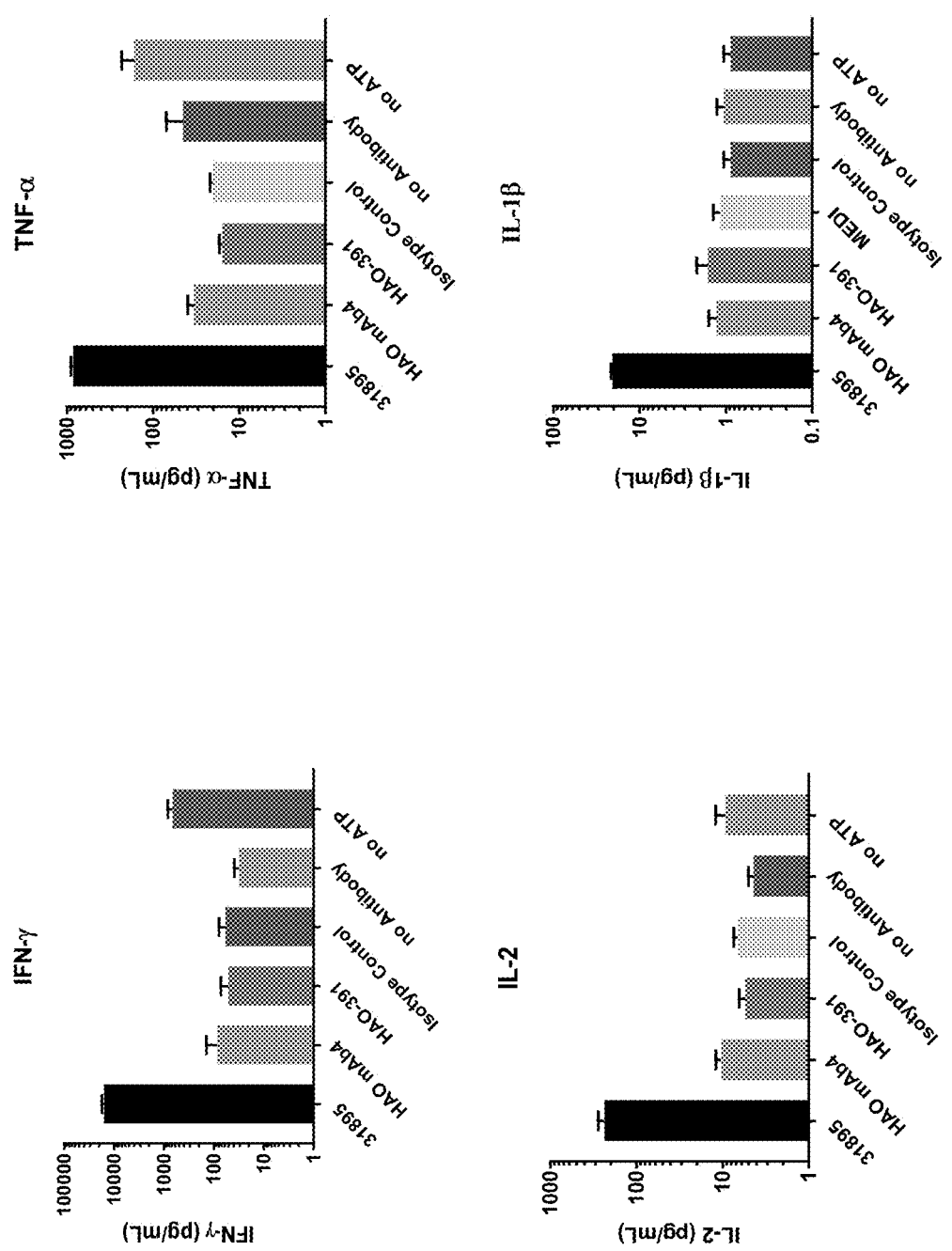
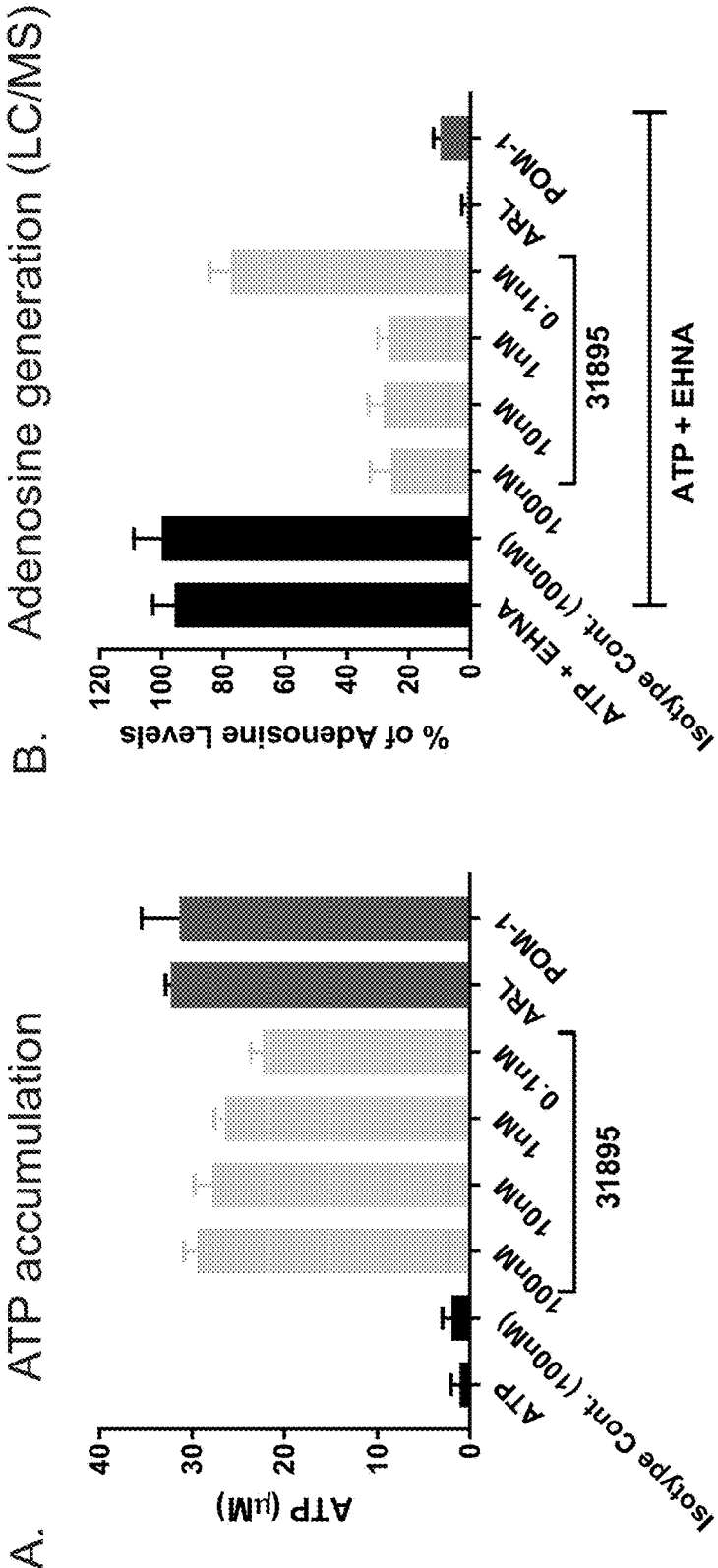


FIG. 22



ANTI-CD39 ANTIBODIES, COMPOSITIONS COMPRISING ANTI-CD39 ANTIBODIES AND METHODS OF USING ANTI-CD39 ANTIBODIES

RELATED APPLICATION

[0001] This application claims priority to U.S. provisional application No. 62/539,527, filed Jul. 31, 2017, which is incorporated by reference herein in its entirety.

FIELD

[0002] Provided herein are antibodies with binding specificity for CD39 and compositions comprising the antibodies, including pharmaceutical compositions, diagnostic compositions and kits. Also provided are methods of using anti-CD39 antibodies for therapeutic and diagnostic purposes.

BACKGROUND

[0003] CD39 is an integral membrane protein that phosphohydrolyzes ATP to yield ADP and AMP. Human CD39 is a 510-amino acid protein with seven potential N-linked glycosylation sites, 11 cysteine residues, and two transmembrane regions. Structurally, it is characterized by two transmembrane domains, a small cytoplasmic domain comprising the NH₂- and COOH-terminal segments, and a large extracellular hydrophobic domain consisting of five highly conserved domains, known as apyrase conserved regions (ACR) 1-5, which are pivotal for the catabolic activity of the enzyme. CD39 becomes catalytically active upon its localization on the cell surface, and its glycosylation is important for protein folding, membrane targeting, and enzyme activity.

[0004] CD39 is constitutively expressed in spleen, thymus, lung, and placenta and in these tissues it is associated primarily with endothelial cells and immune cell populations, such as B cells, natural killer (NK) cells, dendritic cells, Langerhans cells, monocytes, macrophages, mesangial cells, neutrophils, and regulatory T cells (Tregs). Given that CD39, along with other enzymes, degrades ATP, ADP, and AMP to adenosine, CD39 can be viewed as an immunological switch that shifts ATP-driven pro-inflammatory immune cell activity toward an anti-inflammatory state mediated by adenosine.

[0005] Within a neoplastic milieu, cancer and immune cells can closely interact to generate an immunosuppressive environment by releasing immunomodulatory factors, which support neoplastic growth. The expression of CD39 is increased in many solid tumors (for example, colorectal cancer, head and neck cancer, pancreatic cancer (Kunzli et al., *Am J Physiol*, 2006, 292: 223-230), bladder cancer, brain cancer, breast cancer, gastric cancer, hepatocellular carcinoma, lung cancer, non-small cell lung cancer (Li et al., *Oncoimmunology*, 2017, 6: 6), chronic lymphocytic leukemia (Pulte et al., *Clin Lymphoma Myeloma Leuk*, 2011, 11(4): 367-372) and lymphoma, melanoma (Dzhandzhugazyan et al., *FEBS Letters*, 1998, 430: 227-230), ovarian cancer, and prostate cancer, among others) suggesting this enzyme is involved in the development and progression of malignancies. Modulators of CD39 may provide potential therapies for these types of cancers.

[0006] Interactions between tumor cells and their microenvironment are important for tumorigenesis. CD39 can participate in tumor immunoevasion by inhibiting the

activation, clonal expansion, and homing of tumor-specific T cells, impairing tumor cell killing by effector T lymphocytes. In addition to these immunoregulatory roles, CD39 can contribute directly to the modulation of cancer cell growth, differentiation, invasion, migration, metastasis, and angiogenesis. CD39 is important for both the initiation of angiogenesis and the progression of neovascularization. CD39 on vasculature mediates the angiogenic process in mouse models of melanoma, lung, and liver malignancy.

[0007] Modulators of CD39 activity may also provide potential therapeutics for the treatment of CD39 conditions including, but not limited to, autoimmune diseases and infections. In particular, modulators of CD39 activity may provide potential therapeutics for diseases such as, for example, without limitation, Celiac disease (Cook et al., *American Academy of Allergy, Asthma & Immunology*, 2017, Article in Press), colitis (Longhi et al., *JCI Insight*, 2017, 2(9)), thrombotic disease (Marcus et al., *Journal of Pharmacology and Experimental Therapeutics*, 2003, 305, 1: 9-16), HIV infection (zur Wiesch et al., *Journal of Virology*, 2011, February: 1287-1297), HBV infection, HCV infection, and inflammatory bowel disease (Friedman et al. *PNAS*, 2009, 106, 39: 16788-16793) and Crohn's disease (Bai et al., *J Immunol*, 2014, 3366-3377).

SUMMARY

[0008] Provided herein are antibodies that selectively bind CD39. In some embodiments, the antibodies bind human CD39. In some embodiments, the antibodies also bind homologs of human CD39.

[0009] In some embodiments, the antibodies comprise at least one CDR sequence defined by a consensus sequence provided in this disclosure. In some embodiments, the antibodies comprise an illustrative CDR, V_H, or V_L sequence provided in this disclosure, heavy chain or light chain provided in the disclosure, or a variant thereof. In some aspects, the variant is a variant with one or more conservative amino acid substitutions.

[0010] Also provided are compositions and kits comprising the antibodies. In some embodiments, the compositions are pharmaceutical compositions. Any suitable pharmaceutical composition may be used. In some embodiments, the pharmaceutical composition is a composition for parenteral administration.

[0011] This disclosure also provides methods of using the anti-CD39 antibodies provided herein. In some embodiments, the method is a method of treatment. In some embodiments, the method is a diagnostic method. In some embodiments, the method is an analytical method. In some embodiments, the method is a method of purifying and/or quantifying CD39.

[0012] In some embodiments, the antibodies are used to treat a disease or condition. In some aspects, the disease or condition is selected from a cancer, autoimmune disease, and infection.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] FIG. 1 provides a table showing monovalent affinity of anti-huCD39 antibodies to recombinant human CD39 extracellular domain. The table provides binding kinetics of anti-CD39 antibodies interacting with soluble recombinant human CD39 (ENTDP1) extracellular domain (ECD) by biolayer interferometry (ForteBio Octet). Anti-CD39 anti-

bodies were captured on an anti-human Fc sensor and exposed to recombinant human CD39 ECD at concentration ranging from 10-300 nanomolar. The kinetic data was globally fit with a simple 1:1 Langmuir binding model to yield on-rate (k_{on}) and off-rate (k_{off}) values. The equilibrium dissociation constants (K_D) were calculated from the k_{on} and k_{off} values.

[0014] FIGS. 2 A-E show inhibition of enzymatic catabolism of ATP and ADP to Pi by human CD39 extracellular domain (ECD). Recombinant human CD39 at a final concentration of either 10 nanomolar (A-D) or 5 nanomolar (E) was incubated with anti-CD39 IgGs at a final concentration of either 1 micromolar (A-D) or 0.25 micromolar (E) in 25 mM Tris, 5 mM $CaCl_2$, pH 7.5 at room temperature for 2 hours. ATP (500 micromolar) was added to the reaction and incubated at 37° C. for 60 minutes. Residual ATP levels in the reaction were measured using the Cell Titer-Glo assay. Data values are the average of two replicates.

[0015] FIG. 2 F shows antibodies that bind to CHO cells expressing human or cyno CD39.

[0016] FIG. 3 shows evaluation of antibody binding to MEL-28 (A) and 721 (B) cells. Anti-CD39 antibodies (each antibody clone number indicated in the figure) were titrated from 15 to 0.001 μ g/ml. EC_{50} s were calculated using GraphPad Prism Software. The figure represents three independent experiments.

[0017] FIGS. 4 A-B provide evaluation of antibody driven inhibition of ATP hydrolysis of CD39 on MEL-28 cells in a short term ATP assay. FIG. 4A shows the results when anti-CD39 antibodies were compared to the non-specific small molecule inhibitors POM-1 and ARL. Inhibition is determined by decreased phosphate release (Pi). Data is representative of at least 10 independent experiments. Anti-CD39 antibodies (each antibody clone number is indicated in the figure) were titrated from 15 to 0.001 μ g/ml. IC_{50} values were calculated using GraphPad Prism Software, as can be seen in FIG. 4B. Three independent experiments were performed.

[0018] FIGS. 5 A-B provide an illustration of quantification when MEL-28 cells are treated with CD39 enzymatic inhibitors. FIG. 5A shows evaluation of ATP levels after incubating MEL-28 cells with a dose titration of anti-CD39 antibodies that inhibit enzymatic activity. FIG. 5B provides IC_{50} values calculated using GraphPad Prism. At least three independent experiments were performed.

[0019] FIGS. 6 A-B show that antibodies were evaluated for inhibiting CD39 enzymatic activity overnight to MEL-28 cells. FIG. 6A shows anti-CD39 antibodies (each number represents a unique clone indicated in the figure) were titrated from 100 nM to 0.000610 nM. FIG. 6B provide IC_{50} values calculated using GraphPad Prism Software. Three independent experiments are represented.

[0020] FIGS. 7 A-B show results of testing of antibodies for binding to CD39 on human and cyno primary B cells. In FIG. 7A, anti-CD39 antibodies were titrated on purified B cells from healthy donor and detected with anti-human IgG-PE secondary antibody. EC_{50} was calculated using GraphPad Prism software. In FIG. 7B, anti-CD39 antibodies were titrated on cyno PBMCs and detected using a-human IgG PE secondary antibody. B cells were gated using FlowJo software and EC_{50} s were calculated using GraphPad Prism.

[0021] FIG. 8 sets forth antibodies that were evaluated for inhibition of CD39 activity on primary human B cells.

Anti-CD39 antibodies (each unique antibody clone number indicated in the figure) were titrated from 100 to 0.00013 nM.

[0022] FIG. 9 provides evaluation of inhibition of CD39 activity on primary human (a) and cyno (b) monocytes. Anti-CD39 antibodies (each number represents a unique antibody clone number as indicated in the figure) were titrated from 100 to 0.00013 nM and incubated with monocytes in presence of ATP. Phosphate release by CD39 processing of ATP was quantified using Malachite Green assay.

[0023] FIG. 10 shows binding of anti-CD39 antibodies on purified human $CD4^+CD25^+CD127^{dim}$ Treg cells by FACS. Anti-CD39 antibodies were titrated on purified Treg from healthy donor and detected with anti-human IgG secondary antibody. EC_{50} s were calculated using GraphPad Prism software.

[0024] FIG. 11 shows results for antibody ability to inhibit primary Treg CD39 activity. $CD24^+CD25^+CD127^{dim}$ m T regulatory cells were incubated with serially diluted anti-CD39 antibodies and tested for ATPase activity after addition of exogenous ATP. Free phosphate (Pi) was used as a readout of CD39 activity.

[0025] FIG. 12 shows treatment with anti-CD39 antibodies increase the percent of IFN gamma producing $CD8^+$ T cells that respond to CMV peptides in an antigen recall response assay.

[0026] FIGS. 13 A-B show evaluation of antibodies for inhibition of CD39 activity on MEL-28 (FIG. 13A) and human monocytes (FIG. 13B) as compared to the anti-CD39 antibodies generated based on Innate/Orega (BY-40v9) and Igenica (9-8B) and variants thereof. Anti-CD39 antibodies were titrated as indicated and incubated in presence of ATP. Phosphate release by CD39 processing of ATP was quantified using Malachite Green assay.

[0027] FIGS. 14 A-G provides examples of antibodies. FIG. 14A provides examples of antibodies that bind soluble recombinant CD39 ECD and cellular CD39 but do not inhibit ATPase activity and do not compete with cellular inhibitors for binding to ECD inhibitors. FIG. 14B provides examples of antibodies that have limited ability to inhibit the ATPase activity of both soluble recombinant and cellular CD39 and bin separately from other cellular CD39 inhibitors. FIG. 14C provides example of antibodies that inhibit the ATPase activity of soluble recombinant CD39 ECD but do not inhibit cellular CD39 and bin separately from other CD39 ECD inhibitors. FIG. 14D provides examples of antibodies that inhibit the ATPase activity of ECD and cellular CD39 and bin separately from other CD39 ECD and/or cellular inhibitors. FIG. 14E provides examples of inhibitory antibodies that make distinct contacts with CD39. FIG. 14E has two tables, Table 1 and Table 2. Table 1 provides examples of inhibitory antibodies that make distinct contacts with CD39. Table 2 provides examples of inhibitory antibodies that bind critical yet distinct contacts residues with CD39. FIG. 14F and FIG. 14G provide FACS plotting highlighting the importance of certain human CD39 residues.

[0028] FIG. 15 shows that anti-CD39 antibodies inhibit CD39 by 75-90%. Anti-CD39 antibodies (100 nanomolar), isotype control antibody (100 nanomolar), or ARL (200 micromolar) were incubated with MEL-28 cells endogenously expressing human CD39 for 2 hours. ATP was then added and the rate of ATP hydrolysis to Pi by CD39 was

monitored using the EnzChek kinetic Pi detection assay. The initial enzyme velocity, v_0 , was determined from the linear region of Pi vs. time curve over the first 15 minutes post-ATP addition. Each value is the mean of 3 replicates.

[0029] FIGS. 16A-B shows that the CD39 inhibitor 29872 is not a competitive inhibitor due to suppression of V_{max} suppression.

[0030] FIG. 17 shows that anti-CD39 antibodies can induce internalization of CD39 on cyno monocytes.

[0031] FIG. 18 provides a comparison of the Kabat and Chothia numbering systems for CDR-H1. Adapted from Martin A. C. R. (2010). Protein Sequence and Structure Analysis of Antibody Variable Domains. In R. Kontermann & S. Dübel (Eds.), *Antibody Engineering* vol. 2 (pp. 33-51). Springer-Verlag, Berlin Heidelberg.

[0032] FIG. 19 shows an anti-CD39 antibody increases proliferation of stimulated CD4⁺ and CD8⁺ T cells.

[0033] FIG. 20 shows anti-CD39 antibody increases stimulated PBMC secretion of INF- γ , TNF- α and IL-2.

[0034] FIG. 21 shows anti-CD39 antibody increases stimulated PBMC secretion of INF- γ , TNF- α , IL-2 and IL-1 β .

[0035] FIG. 22 shows CD39 inhibition leads to accumulation of ATP and blocks generation of adenosine.

DETAILED DESCRIPTION

1. Definitions

[0036] Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodologies by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 2nd ed. (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

[0037] As used herein, the singular forms “a,” “an,” and “the” include the plural referents unless the context clearly indicates otherwise.

[0038] The term “about” indicates and encompasses an indicated value and a range above and below that value. In certain embodiments, the term “about” indicates the designated value $\pm 10\%$, $\pm 5\%$, or $\pm 1\%$. In certain embodiments, the term “about” indicates the designated value $\pm$ one standard deviation of that value.

[0039] The term “combinations thereof” includes every possible combination of elements to which the term refers.

[0040] The terms “CD39” and “CD39 antigen” and “Cluster of Differentiation 39” are used interchangeably herein. CD39 is also known as also known as ectonucleoside triphosphate diphosphohydrolase-1 (gene: ENTPD1; protein: NTPDase1, See www.ncbi.nlm.nih.gov/gene/953). CD39 has also been referred to as ATPDase and SPG64.

Each of the terms set forth may be used interchangeably. Unless specified otherwise, the terms include any variants, isoforms and species homologs of human CD39 that are naturally expressed by cells, or that are expressed by cells transfected with a CD39 gene. In some embodiments, CD39 proteins include murine CD39. In some embodiments, CD39 proteins include cynomolgus CD39.

[0041] The term “immunoglobulin” refers to a class of structurally related proteins generally comprising two pairs of polypeptide chains: one pair of light (L) chains and one pair of heavy (H) chains. In an “intact immunoglobulin,” all four of these chains are interconnected by disulfide bonds. The structure of immunoglobulins has been well characterized. See, e.g., Paul, *Fundamental Immunology* 7th ed., Ch. 5 (2013) Lippincott Williams & Wilkins, Philadelphia, Pa. Briefly, each heavy chain typically comprises a heavy chain variable region (V_H) and a heavy chain constant region (C_H). The heavy chain constant region typically comprises three domains, C_{H1} , C_{H2} , and C_{H3} . Each light chain typically comprises a light chain variable region (V_L) and a light chain constant region. The light chain constant region typically comprises one domain, abbreviated C_L .

[0042] The term “antibody” describes a type of immunoglobulin molecule and is used herein in its broadest sense. An antibody specifically includes intact antibodies (e.g., intact immunoglobulins), and antibody fragments. Antibodies comprise at least one antigen-binding domain. One example of an antigen-binding domain is an antigen binding domain formed by a V_H - V_L dimer. A “CD39 antibody,” “anti-CD39 antibody,” “CD39 Ab,” “CD39-specific antibody” or “anti-CD39 Ab” is an antibody, as described herein, which binds specifically to the antigen CD39. In some embodiments, the antibody binds the extracellular domain of CD39.

[0043] The V_H and V_L regions may be further subdivided into regions of hypervariability (“hypervariable regions (HVRs);” also called “complementarity determining regions” (CDRs)) interspersed with regions that are more conserved. The more conserved regions are called framework regions (FRs). Each V_H and V_L generally comprises three CDRs and four FRs, arranged in the following order (from N-terminus to C-terminus): FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4. The CDRs are involved in antigen binding, and confer antigen specificity and binding affinity to the antibody. See Kabat et al., *Sequences of Proteins of Immunological Interest* 5th ed. (1991) Public Health Service, National Institutes of Health, Bethesda, Md., incorporated by reference in its entirety.

[0044] The light chain from any vertebrate species can be assigned to one of two types, called kappa and lambda, based on the sequence of the constant domain.

[0045] The heavy chain from any vertebrate species can be assigned to one of five different classes (or isotypes): IgA, IgD, IgE, IgG, and IgM. These classes are also designated α , δ , ϵ , γ , and μ , respectively. The IgG and IgA classes are further divided into subclasses on the basis of differences in sequence and function. Humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0046] The amino acid sequence boundaries of a CDR can be determined by one of skill in the art using any of a number of known numbering schemes, including those described by Kabat et al., supra (“Kabat” numbering scheme); Al-Lazikani et al., 1997, *J. Mol. Biol.*, 273:927-948 (“Chothia” numbering scheme); MacCallum et al.,

1996, *J. Mol. Biol.* 262:732-745 (“Contact” numbering scheme); Lefranc et al., *Dev. Comp. Immunol.*, 2003, 27:55-77 (“IMGT” numbering scheme); and Honegge and Plückthun, *J. Mol. Biol.*, 2001, 309:657-70 (“AHO” numbering scheme), each of which is incorporated by reference in its entirety.

[0047] Table 1 provides the positions of CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3 as identified by the Kabat and Chothia schemes. For CDR-H1, residue numbering is provided using both the Kabat and Chothia numbering schemes. FIG. 1 provides a comparison of the Kabat and Chothia numbering schemes for CDR-H1. See Martin (2010), supra.

[0048] Unless otherwise specified, the numbering scheme used for identification of a particular CDR herein is the Kabat/Chothia numbering scheme. Where the residues encompassed by these two numbering schemes diverge, the numbering scheme is specified as either Kabat or Chothia.

TABLE 1

Residues in CDRs according to Kabat and Chothia numbering schemes.		
CDR	Kabat	Chothia
L1	L24-L34	L24-L34
L2	L50-L56	L50-L56
L3	L89-L97	L89-L97
H1 (Kabat Numbering)	H31-H35B	H26-H32 or H34*
H1 (Chothia Numbering)	H31-H35	H26-H32
H2	H50-H65	H52-H56
H3	H95-H102	H95-H102

*The C-terminus of CDR-H1, when numbered using the Kabat numbering convention, varies between H32 and H34, depending on the length of the CDR, as illustrated in FIG. 1.

[0049] The “EU numbering scheme” is generally used when referring to a residue in an antibody heavy chain constant region (e.g., as reported in Kabat et al., supra). Unless stated otherwise, the EU numbering scheme is used to refer to residues in antibody heavy chain constant regions described herein.

[0050] An “antibody fragment” comprises a portion of an intact antibody, such as the antigen binding or variable region of an intact antibody. Antibody fragments include, for example, Fv fragments, Fab fragments, F(ab')₂ fragments, Fab' fragments, scFv (sFv) fragments, and scFv-Fc fragments.

[0051] “Fv” fragments comprise a non-covalently-linked dimer of one heavy chain variable domain and one light chain variable domain.

[0052] “Fab” fragments comprise, in addition to the heavy and light chain variable domains, the constant domain of the light chain and the first constant domain (C_{H1}) of the heavy chain. Fab fragments may be generated, for example, by papain digestion of a full-length antibody.

[0053] “F(ab')₂” fragments contain two Fab' fragments joined, near the hinge region, by disulfide bonds. F(ab')₂ fragments may be generated, for example, by pepsin digestion of an intact antibody. The F(ab') fragments can be dissociated, for example, by treatment with β-mercaptoethanol.

[0054] “Single-chain Fv” or “sFv” or “scFv” antibody fragments comprise a V_H domain and a V_L domain in a single polypeptide chain. The V_H and V_L are generally linked by a peptide linker. See Plückthun A. (1994). Antibodies from *Escherichia coli*. In Rosenberg M. & Moore G.

P. (Eds.), *The Pharmacology of Monoclonal Antibodies* vol. 113 (pp. 269-315). Springer-Verlag, New York, incorporated by reference in its entirety. “scFv-Fc” fragments comprise an scFv attached to an Fc domain. For example, an Fc domain may be attached to the C-terminal of the scFv. The Fc domain may follow the V_H or V_L, depending on the orientation of the variable domains in the scFv (i.e., V_H-V_L or V_L-V_H). Any suitable Fc domain known in the art or described herein may be used.

[0055] The term “monoclonal antibody” refers to an antibody from a population of substantially homogeneous antibodies. A population of substantially homogeneous antibodies comprises antibodies that are substantially similar and that bind the same epitope(s), except for variants that may normally arise during production of the monoclonal antibody. Such variants are generally present in only minor amounts. A monoclonal antibody is typically obtained by a process that includes the selection of a single antibody from a plurality of antibodies. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, yeast clones, bacterial clones, or other recombinant DNA clones. The selected antibody can be further altered, for example, to improve affinity for the target (“affinity maturation”), to humanize the antibody, to improve its production in cell culture, and/or to reduce its immunogenicity in a subject.

[0056] The term “chimeric antibody” refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[0057] “Humanized” forms of non-human antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. A humanized antibody is generally a human immunoglobulin (recipient antibody) in which residues from one or more CDRs are replaced by residues from one or more CDRs of a non-human antibody (donor antibody). The donor antibody can be any suitable non-human antibody, such as a mouse, rat, rabbit, chicken, or non-human primate antibody having a desired specificity, affinity, or biological effect. In some instances, selected framework region residues of the recipient antibody are replaced by the corresponding framework region residues from the donor antibody. Humanized antibodies may also comprise residues that are not found in either the recipient antibody or the donor antibody. Such modifications may be made to further refine antibody function. For further details, see Jones et al., *Nature*, 1986, 321:522-525; Riechmann et al., *Nature*, 1988, 332:323-329; and Presta, *Curr. Op. Struct. Biol.*, 1992, 2:593-596, each of which is incorporated by reference in its entirety.

[0058] A “human antibody” is one which possesses an amino acid sequence corresponding to that of an antibody produced by a human or a human cell, or derived from a non-human source that utilizes a human antibody repertoire or human antibody-encoding sequences (e.g., obtained from human sources or designed de novo). Human antibodies specifically exclude humanized antibodies.

[0059] An “isolated antibody” is one that has been separated and/or recovered from a component of its natural environment. Components of the natural environment may include enzymes, hormones, and other proteinaceous or nonproteinaceous materials. In some embodiments, an iso-

lated antibody is purified to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence, for example by use of a spinning cup sequenator. In some embodiments, an isolated antibody is purified to homogeneity by gel electrophoresis (e.g., SDS-PAGE) under reducing or nonreducing conditions, with detection by Coomassie blue or silver stain. An isolated antibody includes an antibody in situ within recombinant cells, since at least one component of the antibody's natural environment is not present. In some aspects, an isolated antibody is prepared by at least one purification step.

[0060] In some embodiments, an isolated antibody is purified to at least 80%, 85%, 90%, 95%, or 99% by weight. In some embodiments, an isolated antibody is provided as a solution comprising at least 85%, 90%, 95%, 98%, 99% to 100% by weight of an antibody, the remainder of the weight comprising the weight of other solutes dissolved in the solvent.

[0061] "Affinity" refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (e.g., an antibody) and its binding partner (e.g., an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity, which reflects a 1:1 interaction between members of a binding pair (e.g., antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured by common methods known in the art, including those described herein. Affinity can be determined, for example, using surface plasmon resonance (SPR) technology, such as a Biacore® instrument.

[0062] With regard to the binding of an antibody to a target molecule, the terms "specific binding," "specifically binds to," "specific for," "selectively binds," and "selective for" a particular antigen (e.g., a polypeptide target) or an epitope on a particular antigen mean binding that is measurably different from a non-specific or non-selective interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule. Specific binding can also be determined by competition with a control molecule that is similar to the target, such as an excess of non-labeled target. In that case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by the excess non-labeled target.

[0063] The term " k_d " (sec^{-1}), as used herein, refers to the dissociation rate constant of a particular antibody-antigen interaction. This value is also referred to as the k_{off} value.

[0064] The term " k_a " ($\text{M}^{-1}\times\text{sec}^{-1}$), as used herein, refers to the association rate constant of a particular antibody-antigen interaction. This value is also referred to as the k_{on} value.

[0065] The term " K_D " (M), as used herein, refers to the dissociation equilibrium constant of a particular antibody-antigen interaction. $K_D=k_d/k_a$.

[0066] The term " K_A " (M^{-1}), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction. $K_A=k_a/k_d$.

[0067] An "affinity matured" antibody is one with one or more alterations in one or more CDRs or FRs that result in an improvement in the affinity of the antibody for its antigen, compared to a parent antibody which does not possess the alteration(s). In one embodiment, an affinity matured antibody has nanomolar or picomolar affinity for the target

antigen. Affinity matured antibodies may be produced using a variety of methods known in the art. For example, Marks et al. (*Bio/Technology*, 1992, 10:779-783, incorporated by reference in its entirety) describes affinity maturation by V_H and V_L domain shuffling. Random mutagenesis of CDR and/or framework residues is described by, for example, Barbas et al. (*Proc. Nat. Acad. Sci. U.S.A.*, 1994, 91:3809-3813); Schier et al., *Gene*, 1995, 169:147-155; Yelton et al., *J. Immunol.*, 1995, 155:1994-2004; Jackson et al., *J. Immunol.*, 1995, 154:3310-3319; and Hawkins et al., *J. Mol. Biol.*, 1992, 226:889-896, each of which is incorporated by reference in its entirety.

[0068] When used herein in the context of two or more antibodies, the term "competes with" or "cross-competes with" indicates that the two or more antibodies compete for binding to an antigen (e.g., CD39). In one exemplary assay, CD39 is coated on a plate and allowed to bind a first antibody, after which a second, labeled antibody is added. If the presence of the first antibody reduces binding of the second antibody, then the antibodies compete. The term "competes with" also includes combinations of antibodies where one antibody reduces binding of another antibody, but where no competition is observed when the antibodies are added in the reverse order. However, in some embodiments, the first and second antibodies inhibit binding of each other, regardless of the order in which they are added. In some embodiments, one antibody reduces binding of another antibody to its antigen by at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%.

[0069] The term "epitope" means a portion of an antigen capable of specific binding to an antibody. Epitopes frequently consist of surface-accessible amino acid residues and/or sugar side chains and may have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents. An epitope may comprise amino acid residues that are directly involved in the binding, and other amino acid residues, which are not directly involved in the binding. The epitope to which an antibody binds can be determined using known techniques for epitope determination such as, for example, testing for antibody binding to CD39 variants with different point-mutations.

[0070] Percent "identity" between a polypeptide sequence and a reference sequence is defined as the percentage of amino acid residues in the polypeptide sequence that are identical to the amino acid residues in the reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, MEGALIGN (DNASTAR), CLUSTALW, or CLUSTAL OMEGA software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0071] A "conservative substitution" or a "conservative amino acid substitution," refers to the substitution of one or more amino acids with one or more chemically or functionally similar amino acids. Conservative substitution tables

providing similar amino acids are well known in the art. Polypeptide sequences having such substitutions are known as “conservatively modified variants.” Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles. By way of example, the following groups of amino acids are considered conservative substitutions for one another.

Acidic Residues	D and E
Basic Residues	K, R, and H
Hydrophilic Uncharged Residues	S, T, N, and Q
Aliphatic Uncharged Residues	G, A, V, L, and I
Non-polar Uncharged Residues	C, M, and P
Aromatic Residues	F, Y, and W
Alcohol Group-Containing Residues	S and T
Aliphatic Residues	I, L, V, and M
Cycloalkenyl-associated Residues	F, H, W, and Y
Hydrophobic Residues	A, C, F, G, H, I, L, M, R, T, V, W, and Y
Negatively Charged Residues	D and E
Polar Residues	C, D, E, H, K, N, Q, R, S, and T
Positively Charged Residues	H, K, and R
Small Residues	A, C, D, G, N, P, S, T, and V
Very Small Residues	A, G, and S
Residues Involved in Turn Formation	A, C, D, E, G, H, K, N, Q, R, S, P, and T
Flexible Residues	Q, T, K, S, G, P, D, E, and R
Group 1	A, S, and T
Group 2	D and E
Group 3	N and Q
Group 4	R and K
Group 5	I, L, and M
Group 6	F, Y, and W
Group A	A and G
Group B	D and E
Group C	N and Q
Group D	R, K, and H
Group E	I, L, M, V
Group F	F, Y, and W
Group G	S and T
Group H	C and M

Additional conservative substitutions may be found, for example, in Creighton, *Proteins: Structures and Molecular Properties* 2nd ed. (1993) W. H. Freeman & Co., New York, N.Y. An antibody generated by making one or more conservative substitutions of amino acid residues in a parent antibody is referred to as a “conservatively modified variant.”

[0072] The term “amino acid” refers to the twenty common naturally occurring amino acids. Naturally occurring amino acids include alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C); glutamic acid (Glu; E), glutamine (Gln; Q), Glycine (Gly; G); histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V).

[0073] “Treating” or “treatment” of any disease or disorder refers, in certain embodiments, to ameliorating a disease or disorder that exists in a subject. In another embodiment, “treating” or “treatment” includes ameliorating at least one physical parameter, which may be indiscernible by the subject. In yet another embodiment, “treating” or “treatment” includes modulating the disease or disorder, either physically (e.g., stabilization of a discernible symptom) or physiologically (e.g., stabilization of a physical parameter)

or both. In yet another embodiment, “treating” or “treatment” includes delaying or preventing the onset of the disease or disorder.

[0074] As used herein, the term “therapeutically effective amount” or “effective amount” refers to an amount of an antibody or composition that when administered to a subject is effective to treat a disease or disorder.

[0075] As used herein, the term “subject” means a mammalian subject. Exemplary subjects include, but are not limited to humans, monkeys, dogs, cats, mice, rats, cows, horses, camels, avians, goats, and sheep. In certain embodiments, the subject is a human. In some embodiments, the subject has cancer, an autoimmune disease or condition, and/or an infection that can be treated with an antibody provided herein. In some embodiments, the subject is a human that is suspected to have cancer, an autoimmune disease or condition, and/or an infection.

2. Antibodies

[0076] Provided herein are antibodies that selectively bind human CD39, as well as the nucleic acids that encode the antibodies. In some aspects, the antibody selectively binds to the extracellular domain of human CD39.

[0077] In some embodiments, the antibody binds to homologs of human CD39. In some aspects, the antibody binds to a homolog of human CD39 from a species selected from monkeys, mice, dogs, cats, rats, cows, horses, goats, and sheep. In some aspects, the homolog is a cynomolgus monkey homolog. In some aspects, the homolog is a murine homolog.

[0078] In some embodiments, the antibody has one or more CDRs having particular lengths, in terms of the number of amino acid residues. In some embodiments, the Chothia CDR-H1 of the antibody is 6, 7, 8, or 9 residues in length. In some embodiments, the Kabat CDR-H1 of the antibody is 4, 5, 6, or 7 residues in length. In some embodiments, the Chothia CDR-H2 of the antibody is 5, 6, or 7 residues in length. In some embodiments, the Kabat CDR-H2 of the antibody is 15, 16, 17, or 18 residues in length. In some embodiments, the Kabat/Chothia CDR-H3 of the antibody is 5, 6, 7, 8, 9, 10, 11, or 12 residues in length.

[0079] In some aspects, the Kabat/Chothia CDR-L1 of the antibody is 9, 10, 11, 12, 13, 14, 15, or 16 residues in length. In some aspects, the Kabat/Chothia CDR-L2 of the antibody is 6, 7, or 8 residues in length. In some aspects, the Kabat/Chothia CDR-L3 of the antibody is 8, 9, 10, 11, or 12 residues in length.

[0080] In some embodiments, the antibody comprises a light chain. In some aspects, the light chain is a kappa light chain. In some aspects, the light chain is a lambda light chain.

[0081] In some embodiments, the antibody comprises a heavy chain. In some aspects, the heavy chain is an IgA. In some aspects, the heavy chain is an IgD. In some aspects, the heavy chain is an IgE. In some aspects, the heavy chain is an IgG. In some aspects, the heavy chain is an IgM. In some aspects, the heavy chain is an IgG1. In some aspects, the heavy chain is an IgG2. In some aspects, the heavy chain is an IgG3. In some aspects, the heavy chain is an IgG4. In some aspects, the heavy chain is an IgA1. In some aspects, the heavy chain is an IgA2.

[0082] In some embodiments, the antibody is an antibody fragment. In some aspects, the antibody fragment is an Fv

fragment. In some aspects, the antibody fragment is a Fab fragment. In some aspects, the antibody fragment is a F(ab')₂ fragment. In some aspects, the antibody fragment is a Fab' fragment. In some aspects, the antibody fragment is an scFv (sFv) fragment. In some aspects, the antibody fragment is an scFv-Fc fragment.

[0083] In some embodiments, the antibody is a monoclonal antibody. In some embodiments, the antibody is a polyclonal antibody.

[0084] In some embodiments, the antibody is a chimeric antibody. In some embodiments, the antibody is a humanized antibody. In some embodiments, the antibody is a human antibody.

[0085] In some embodiments, the antibody is an affinity matured antibody. In some aspects, the antibody is an affinity matured antibody derived from an illustrative sequence provided in this disclosure.

[0086] In some aspects, the antibody inhibits conversion by CD39 of ATP to ADP and/or ADP to AMP. In some aspects, the antibody decreases the levels of phosphate, ADP, AMP, and/or adenosine and/or increases the levels of ATP.

[0087] In some embodiments, the antibody increases proliferation of stimulated CD4⁺ and CD8⁺ T cells. In some embodiments, the antibody increases stimulated PBMC secretion of INF- γ , TNF- α , IL-2, and/or IL-1 β .

[0088] In some embodiments, the antibody increases a T effector cell function. In some embodiments, the antibody decreases the number of regulatory T cells in tissues or in circulation. In some embodiments, the antibody suppresses a regulatory or T cell activity. In some embodiments, the antibody increase B cell function. In some embodiments, the antibody increases antigen presenting cell function. In some embodiments, the antibody decreases or prevents activation of phospho antigen specific T cells selected from MAIT cells and gamma delta T cells.

[0089] In some aspects, the decrease is about or less than a 10% decrease, about or less than a 20% decrease, about or less than a 30% decrease, about or less than a 40% decrease, about or less than a 50% decrease, about or less than a 60% decrease, about or less than a 70% decrease, about or less than an 80% decrease, about or less than a 90% decrease, or about a complete decrease. In some aspects, the increase is about or greater than a 10% increase, about or greater than a 20% increase, about or greater than a 30% increase, about or greater than a 40% increase, about or greater than a 50% increase, about or greater than a 60% increase, about or greater than a 70% increase, about or greater than an 80% increase, about or greater than a 90% increase, or a complete increase.

[0090] Given that CD39 degrades ATP and ADP to adenosine, CD39 can be viewed as an immunological switch that shifts ATP-driven pro-inflammatory immune cell activity toward an anti-inflammatory state mediated by adenosine. CD39 has a role in regulating the function of several immune cell types, including lymphocytes, neutrophils, monocytes/macrophages, dendritic cells, and endothelial cells and shifting the switch can have a significant impact on disease. For example, the generation of adenosine via CD39 is recognized as a major mechanism of regulatory T cell (Treg) immunosuppressive function.

[0091] The antibodies provided herein may be useful for the treatment of a variety of diseases and conditions, including cancers, autoimmune diseases, and infections. In some

embodiments, the antibody inhibits CD39 function on tumor cells. In some embodiments, the antibody inhibits angiogenesis.

[0092] The frequency of CD39⁺ Tregs and the expression on the cell surface is increased in some human cancers, and the importance of CD39⁺ Tregs in promoting tumor growth and metastasis has been demonstrated using several in vivo models. Immunohistochemical staining of normal and tumor tissues has revealed that CD39 expression is significantly higher in several types of human cancer than in normal tissues. In cancer specimens, CD39 is expressed by infiltrating lymphocytes, the tumor stroma, and/or tumor cells. CD39 in cancer cells displays ATPase activity and generates adenosine. CD39⁺ cancer cells inhibited the proliferation of CD4 and CD8 T cells and the generation of cytotoxic effector CD8 T cells (CTL) in a CD39- and adenosine-dependent manner.

2.1. CDR-H3 Sequences

[0093] In some embodiments, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 82-109. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 82. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 83. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 84. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 85. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 86. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 87. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 88. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 89. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 90. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 91. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 92. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 93. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 94. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 95. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 96. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 97. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 98. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 99. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or

consisting essentially of SEQ ID NO: 100. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 101. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 102. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 103. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 104. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 105. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 106. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 107. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 108. In some aspects, the antibody comprises a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 109.

[0094] In some aspects, the CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-H3 sequence provided in this disclosure. In some aspects, the CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-H3 sequences provided in this disclosure. In some aspects, the CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

2.2. V_H Sequences Comprising Illustrative CDRs

[0095] In some embodiments, the antibody comprises a V_H sequence comprising one or more CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative CDR-H sequences provided in this disclosure, and variants thereof.

2.2.1. V_H Sequences Comprising Illustrative Kabat CDRs

[0096] In some embodiments, the antibody comprises a V_H sequence comprising one or more Kabat CDR-H sequences comprising, consisting of, or consisting essentially of one or more illustrative Kabat CDR-H sequences provided in this disclosure, and variants thereof.

2.2.1.1. Kabat CDR-H3

[0097] In some embodiments, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOS: 82-109. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 82. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 83. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 84. In some aspects, the antibody comprises a V_H

[illegible]

CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 107. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 108. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 109.

2.2.1.2. Kabat CDR-H2

[illegible]

consisting essentially of SEQ ID NO: 80. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 81.

2.2.1.3. Kabat CDR-H1

[illegible]

[0100] In some embodiments, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 82-109, and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 63-81. In some aspects, the Kabat CDR-H3 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some aspects, the Kabat CDR-H3 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOs: 179-218.

[0101] In some embodiments, the antibody comprises a V_H sequence comprising a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 82-109, and a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 25-45. In some aspects, the Kabat CDR-H3 sequence and the Kabat CDR-H1 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some aspects, the Kabat CDR-H3 and Kabat CDR-H1 are both from a single illustrative V_H sequence selected from SEQ ID NOs: 179-218.

[0102] In some embodiments, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 25-45 and a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 63-81. In some aspects, the Kabat CDR-H1 sequence and the Kabat CDR-H2 sequence are both from a single illustrative V_H sequence provided in this disclosure. For example, in some aspects, the Kabat CDR-H1 and Kabat CDR-H2 are both from a single illustrative V_H sequence selected from SEQ ID NOs: 179-218.

[0103] In some embodiments, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 25-45, a Kabat CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 63-81, and a Kabat CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 82-109. In some aspects, the Kabat CDR-H1 sequence, Kabat CDR-H2 sequence, and Kabat CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some aspects, the Kabat CDR-

[illegible]

2.2.1.8. Variants of V_H Sequences Comprising Illustrative Kabat CDRs

[10106] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Kabat CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

[0107] In some aspects, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H3 sequence provided in this disclosure. In some aspects, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H3 sequences provided in this disclosure. In some aspects, the Kabat CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0108] In some aspects, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H2 sequence provided in this disclosure. In some aspects, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H2 sequences provided in this disclosure. In some aspects, the Kabat CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[10109] In some aspects, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Kabat CDR-H1 sequence provided in this disclosure. In some aspects, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Kabat CDR-H1 sequences provided in this disclosure. In some aspects, the Kabat CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Kabat CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

2.2.2.1. Chothia CDR-H3

[illegible]

99. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 100. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 101. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 102. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 103. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 104. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 105. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 106. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 107. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 108. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 109.

2.2.2.2. Chothia CDR-H2

[0112] In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 46-62. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 46. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 47. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 48. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 49. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 50. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 51. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 52. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 53. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 54. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of SEQ

[0117] In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 1-24, a Chothia CDR-H2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 46-62, and a Chothia CDR-H3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 82-109. In some aspects, the Chothia CDR-H1 sequence, Chothia CDR-H2 sequence, and Chothia CDR-H3 sequence are all from a single illustrative V_H sequence provided in this disclosure. For example, in some aspects, the Chothia CDR-H1, Chothia CDR-H2, and Chothia CDR-H3 are all from a single illustrative V_H sequence selected from SEQ ID NOs: 179-218.

[0118] In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 47, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 83. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 1, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 84. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 47, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 85. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 3, a Chothia CDR-H2 sequence comprising SEQ ID NO: 47, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 86. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 4, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 2, a Chothia CDR-H2 sequence comprising SEQ ID NO: 46, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 5, a Chothia CDR-H2 sequence comprising SEQ ID NO: 49, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 82. In some embodiments, the antibody comprises a V_H sequence

[illegible]

[illegible]

[0120] In some embodiments, the V_H sequences provided herein comprise a variant of an illustrative Chothia CDR-H3, CDR-H2, and/or CDR-H1 sequence provided in this disclosure.

with any of the illustrative Chothia CDR-H3 sequences provided in this disclosure. In some aspects, the Chothia CDR-H3 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0122] In some aspects, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H2 sequence provided in this disclosure. In some aspects, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H2 sequences provided in this disclosure. In some aspects, the Chothia CDR-H2 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0123] In some aspects, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a variant of an illustrative Chothia CDR-H1 sequence provided in this disclosure. In some aspects, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative Chothia CDR-H1 sequences provided in this disclosure. In some aspects, the Chothia CDR-H1 sequence comprises, consists of, or consists essentially of any of the illustrative Chothia CDR-H1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0124] In some embodiments, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 179-218. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 179. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 180. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 181. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 182. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 183. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 184. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 185. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 186. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 187. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 188. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 189. In some aspects, the antibody comprises a V_H sequence comprising, consisting of, or consisting essentially of

[0125] In some embodiments, the V_H sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_H sequence provided in this disclosure.

[0126] In some aspects, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some aspects, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.5% identity with any of the illustrative V_H sequences provided in this disclosure.

[0127] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0128] In some embodiments, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 141-166. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 141. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 142. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 143. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 144. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 145. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 146. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 147. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 148. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 149. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 150. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 151. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 152. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 153. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 154. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 155. In some aspects, the antibody comprises a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 156. In some aspects, the antibody com-

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2.5.2. CDR-L2

[0132] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 125-140. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L2 sequence comprising, consisting of, or consisting essentially of SEQ

[0131] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 141-166. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 141. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 142. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 143. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 144. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 145. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, con-

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2.5.3. CDR-L1

[10133] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 110-124. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 110. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 111. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 112. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 113. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 114. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 115. In

some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 116. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 117. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 118. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 119. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 120. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 121. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 122. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 123. In some aspects, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 124.

2.5.4. CDR-L3+CDR-L2

[0134] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 141-166 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 125-140. In some aspects, the CDR-L3 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some aspects, the CDR-L3 and CDR-L2 are both from a single illustrative V_L sequence selected from SEQ ID NOs: 219-248.

2.5.5. CDR-L3+CDR-L1

[0135] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L3 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 141-166 and a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 110-124. In some aspects, the CDR-L3 sequence and the CDR-L1 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some aspects, the CDR-L3 and CDR-L1 are both from a single illustrative V_L sequence selected from SEQ ID NOs: 219-248.

2.5.6. CDR-L1+CDR-L2

[0136] In some embodiments, the antibody comprises a V_L sequence comprising a CDR-L1 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 110-124 and a CDR-L2 sequence comprising, consisting of, or consisting essentially of a sequence selected from SEQ ID NOs: 125-140. In some aspects, the CDR-L1 sequence and the CDR-L2 sequence are both from a single illustrative V_L sequence provided in this disclosure. For example, in some aspects, the CDR-L1

[0139] In some aspects, the antibody comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 128, and a CDR-L3 sequence SEQ ID NO: 144. In some aspects, the antibody comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence comprising SEQ ID NO: 144. In some aspects, the antibody comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 126, and a CDR-L3 sequence comprising sequence selected from SEQ ID NO: 144. In some aspects, the antibody comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 116, a CDR-L2 sequence comprising SEQ ID NO: 131, and a CDR-L3 sequence comprising SEQ ID NO: 150. In some aspects, the antibody comprises a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 117, a CDR-L2 sequence comprising SEQ ID NO: 134, and a CDR-L3 sequence comprising SEQ ID NO: 150.

[0140] In some embodiments, the V_L sequences provided herein comprise a variant of an illustrative CDR-L3, CDR-L2, and/or CDR-L1 sequence provided in this disclosure.

[0141] In some aspects, the CDR-L3 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L3 sequence provided in this disclosure. In some aspects, the CDR-L3 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L3 sequences provided in this disclosure. In some aspects, the CDR-L3 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L3 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0142] In some aspects, the CDR-L2 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L2 sequence provided in this disclosure. In some aspects, the CDR-L2 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L2 sequences provided in this disclosure. In some aspects, the CDR-L2 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L2 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0143] In some aspects, the CDR-L1 sequence comprises, consists of, or consists essentially of a variant of an illustrative CDR-L1 sequence provided in this disclosure. In some aspects, the CDR-L1 sequence comprises, consists of, or consists essentially of a sequence having at least 70%, 75%, 80%, 85%, 90%, or 95% identity with any of the illustrative CDR-L1 sequences provided in this disclosure. In some aspects, the CDR-L1 sequence comprises, consists of, or consists essentially of any of the illustrative CDR-L1 sequences provided in this disclosure, with 1, 2, or 3 amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

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comprising, consisting of, or consisting essentially of SEQ ID NO: 240. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 241. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 242. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 243. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 244. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 245. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 246. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 247. In some aspects, the antibody comprises a V_L sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 248.

2.6.1. Variants of V_L Sequences

[0145] In some embodiments, the V_L sequences provided herein comprise, consist of, or consist essentially of a variant of an illustrative V_L sequence provided in this disclosure.

[0146] In some aspects, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some aspects, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[0147] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

2.7. Pairs

2.7.1. CDR-H3-CDR-L3 Pairs

[0148] In some embodiments, the antibody comprises a CDR-H3 sequence and a CDR-L3 sequence. In some aspects, the CDR-H3 sequence is part of a V_H and the CDR-L3 sequence is part of a V_L .

[0149] In some aspects, the CDR-H3 sequence is a CDR-H3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOs: 82-109, and the CDR-L3 sequence is a CDR-L3 sequence comprising, consisting of, or consisting essentially of SEQ ID NOs: 141-166.

[0150] In some aspects, the CDR-H3 sequence is SEQ ID NO: 82 and the CDR-L3 sequence is selected from SEQ ID NOs: 141-166. In some aspects, the CDR-L3 sequence is SEQ ID NO: 141. In some aspects, the CDR-L3 sequence is SEQ ID NO: 142. In some aspects, the CDR-L3 sequence is SEQ ID NO: 143. In some aspects, the CDR-L3 sequence is SEQ ID NO: 144. In some aspects, the CDR-L3 sequence is SEQ ID NO: 145. In some aspects, the CDR-L3 sequence is SEQ ID NO: 146. In some aspects, the CDR-L3 sequence is SEQ ID NO: 147. In some aspects, the CDR-L3 sequence is

SEQ ID NO: 148. In some aspects, the CDR-L3 sequence is SEQ ID NO: 149. In some aspects, the CDR-L3 sequence is SEQ ID NO: 150. In some aspects, the CDR-L3 sequence is SEQ ID NO: 151. In some aspects, the CDR-L3 sequence is SEQ ID NO: 152. In some aspects, the CDR-L3 sequence is SEQ ID NO: 153. In some aspects, the CDR-L3 sequence is SEQ ID NO: 154. In some aspects, the CDR-L3 sequence is SEQ ID NO: 155. In some aspects, the CDR-L3 sequence is SEQ ID NO: 156. In some aspects, the CDR-L3 sequence is SEQ ID NO: 157. In some aspects, the CDR-L3 sequence is SEQ ID NO: 158. In some aspects, the CDR-L3 sequence is SEQ ID NO: 159. In some aspects, the CDR-L3 sequence is SEQ ID NO: 160. In some aspects, the CDR-L3 sequence is SEQ ID NO: 161. In some aspects, the CDR-L3 sequence is SEQ ID NO: 162. In some aspects, the CDR-L3 sequence is SEQ ID NO: 163. In some aspects, the CDR-L3 sequence is SEQ ID NO: 164. In some aspects, the CDR-L3 sequence is SEQ ID NO: 165. In some aspects, the CDR-L3 sequence is SEQ ID NO: 166.

[0151] In some aspects, the CDR-H3 sequence is SEQ ID NO: 83 and the CDR-L3 sequence is selected from SEQ ID NOs: 141-166. In some aspects, the CDR-L3 sequence is SEQ ID NO: 141. In some aspects, the CDR-L3 sequence is SEQ ID NO: 142. In some aspects, the CDR-L3 sequence is SEQ ID NO: 143. In some aspects, the CDR-L3 sequence is SEQ ID NO: 144. In some aspects, the CDR-L3 sequence is SEQ ID NO: 145. In some aspects, the CDR-L3 sequence is SEQ ID NO: 146. In some aspects, the CDR-L3 sequence is SEQ ID NO: 147. In some aspects, the CDR-L3 sequence is SEQ ID NO: 148. In some aspects, the CDR-L3 sequence is SEQ ID NO: 149. In some aspects, the CDR-L3 sequence is SEQ ID NO: 150. In some aspects, the CDR-L3 sequence is SEQ ID NO: 151. In some aspects, the CDR-L3 sequence is SEQ ID NO: 152. In some aspects, the CDR-L3 sequence is SEQ ID NO: 153. In some aspects, the CDR-L3 sequence is SEQ ID NO: 154. In some aspects, the CDR-L3 sequence is SEQ ID NO: 155. In some aspects, the CDR-L3 sequence is SEQ ID NO: 156. In some aspects, the CDR-L3 sequence is SEQ ID NO: 157. In some aspects, the CDR-L3 sequence is SEQ ID NO: 158. In some aspects, the CDR-L3 sequence is SEQ ID NO: 159. In some aspects, the CDR-L3 sequence is SEQ ID NO: 160. In some aspects, the CDR-L3 sequence is SEQ ID NO: 161. In some aspects, the CDR-L3 sequence is SEQ ID NO: 162. In some aspects, the CDR-L3 sequence is SEQ ID NO: 163. In some aspects, the CDR-L3 sequence is SEQ ID NO: 164. In some aspects, the CDR-L3 sequence is SEQ ID NO: 165. In some aspects, the CDR-L3 sequence is SEQ ID NO: 166.

[0152] In some aspects, the CDR-H3 sequence is SEQ ID NO: 84 and the CDR-L3 sequence is selected from SEQ ID NOs: 141-166. In some aspects, the CDR-L3 sequence is SEQ ID NO: 141. In some aspects, the CDR-L3 sequence is SEQ ID NO: 142. In some aspects, the CDR-L3 sequence is SEQ ID NO: 143. In some aspects, the CDR-L3 sequence is SEQ ID NO: 144. In some aspects, the CDR-L3 sequence is SEQ ID NO: 145. In some aspects, the CDR-L3 sequence is SEQ ID NO: 146. In some aspects, the CDR-L3 sequence is SEQ ID NO: 147. In some aspects, the CDR-L3 sequence is SEQ ID NO: 148. In some aspects, the CDR-L3 sequence is SEQ ID NO: 149. In some aspects, the CDR-L3 sequence is SEQ ID NO: 150. In some aspects, the CDR-L3 sequence is SEQ ID NO: 151. In some aspects, the CDR-L3 sequence is SEQ ID NO: 152. In some aspects, the CDR-L3 sequence is SEQ ID NO: 153. In some aspects, the CDR-L3 sequence is

[0181] In some embodiments, the antibody comprises a V_H sequence and a V_L sequence.

aspects, the V_L sequence is SEQ ID NO: 238. In some aspects, the V_L sequence is SEQ ID NO: 239. In some aspects, the V_L sequence is SEQ ID NO: 240. In some aspects, the V_L sequence is SEQ ID NO: 241. In some aspects, the V_L sequence is SEQ ID NO: 242. In some aspects, the V_L sequence is SEQ ID NO: 243. In some aspects, the V_L sequence is SEQ ID NO: 244. In some aspects, the V_L sequence is SEQ ID NO: 245. In some aspects, the V_L sequence is SEQ ID NO: 246. In some aspects, the V_L sequence is SEQ ID NO: 247. In some aspects, the V_L sequence is SEQ ID NO: 248.

[0185] In some aspects, the V_H sequence is SEQ ID NO: 181 and the V_L sequence is selected from SEQ ID NOs: 219-248. In some aspects, the V_L sequence is SEQ ID NO: 219. In some aspects, the V_L sequence is SEQ ID NO: 220. In some aspects, the V_L sequence is SEQ ID NO: 221. In some aspects, the V_L sequence is SEQ ID NO: 222. In some aspects, the V_L sequence is SEQ ID NO: 223. In some aspects, the V_L sequence is SEQ ID NO: 224. In some aspects, the V_L sequence is SEQ ID NO: 225. In some aspects, the V_L sequence is SEQ ID NO: 226. In some aspects, the V_L sequence is SEQ ID NO: 227. In some aspects, the V_L sequence is SEQ ID NO: 228. In some aspects, the V_L sequence is SEQ ID NO: 229. In some aspects, the V_L sequence is SEQ ID NO: 230. In some aspects, the V_L sequence is SEQ ID NO: 231. In some aspects, the V_L sequence is SEQ ID NO: 232. In some aspects, the V_L sequence is SEQ ID NO: 233. In some aspects, the V_L sequence is SEQ ID NO: 234. In some aspects, the V_L sequence is SEQ ID NO: 235. In some aspects, the V_L sequence is SEQ ID NO: 236. In some aspects, the V_L sequence is SEQ ID NO: 237. In some aspects, the V_L sequence is SEQ ID NO: 238. In some aspects, the V_L sequence is SEQ ID NO: 239. In some aspects, the V_L sequence is SEQ ID NO: 240. In some aspects, the V_L sequence is SEQ ID NO: 241. In some aspects, the V_L sequence is SEQ ID NO: 242. In some aspects, the V_L sequence is SEQ ID NO: 243. In some aspects, the V_L sequence is SEQ ID NO: 244. In some aspects, the V_L sequence is SEQ ID NO: 245. In some aspects, the V_L sequence is SEQ ID NO: 246. In some aspects, the V_L sequence is SEQ ID NO: 247. In some aspects, the V_L sequence is SEQ ID NO: 248.

[0186] In some aspects, the V_H sequence is SEQ ID NO: 182 and the V_L sequence is selected from SEQ ID NOs: 219-248. In some aspects, the V_L sequence is SEQ ID NO: 219. In some aspects, the V_L sequence is SEQ ID NO: 220. In some aspects, the V_L sequence is SEQ ID NO: 221. In some aspects, the V_L sequence is SEQ ID NO: 222. In some aspects, the V_L sequence is SEQ ID NO: 223. In some aspects, the V_L sequence is SEQ ID NO: 224. In some aspects, the V_L sequence is SEQ ID NO: 225. In some aspects, the V_L sequence is SEQ ID NO: 226. In some aspects, the V_L sequence is SEQ ID NO: 227. In some aspects, the V_L sequence is SEQ ID NO: 228. In some aspects, the V_L sequence is SEQ ID NO: 229. In some aspects, the V_L sequence is SEQ ID NO: 230. In some aspects, the V_L sequence is SEQ ID NO: 231. In some aspects, the V_L sequence is SEQ ID NO: 232. In some aspects, the V_L sequence is SEQ ID NO: 233. In some aspects, the V_L sequence is SEQ ID NO: 234. In some aspects, the V_L sequence is SEQ ID NO: 235. In some aspects, the V_L sequence is SEQ ID NO: 236. In some aspects, the V_L sequence is SEQ ID NO: 237. In some

aspects, the V_L sequence is SEQ ID NO: 238. In some aspects, the V_L sequence is SEQ ID NO: 239. In some aspects, the V_L sequence is SEQ ID NO: 240. In some aspects, the V_L sequence is SEQ ID NO: 241. In some aspects, the V_L sequence is SEQ ID NO: 242. In some aspects, the V_L sequence is SEQ ID NO: 243. In some aspects, the V_L sequence is SEQ ID NO: 244. In some aspects, the V_L sequence is SEQ ID NO: 245. In some aspects, the V_L sequence is SEQ ID NO: 246. In some aspects, the V_L sequence is SEQ ID NO: 247. In some aspects, the V_L sequence is SEQ ID NO: 248.

2.7.3. CDR-H1+CDR-112+CDR-113+CDR-L1+CDR-L2+CDR-L3

[0223] In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 63, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 82 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 141. In some aspects, the antibody comprises a V_L sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 83 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 111, a CDR-L2 sequence comprising SEQ ID NO: 126, and a CDR-L3 sequence SEQ ID NO: 142. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 27, a Kabat CDR-H2 sequence comprising SEQ ID NO: 65, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 84 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 141. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 85 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 141. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 64, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 86 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 127, and a CDR-L3 sequence SEQ ID NO: 142. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 25, a Kabat CDR-H2 sequence comprising SEQ ID NO: 66, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 82 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 141. In some aspects, the antibody comprises a V_H sequence comprising a Kabat CDR-H1 sequence comprising SEQ ID NO: 26, a Kabat CDR-H2 sequence comprising SEQ ID NO: 65, and a Kabat CDR-H3 sequence comprising SEQ ID NO: 82 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 110, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 143. In some aspects, the antibody comprises a V_L

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[illegible]

[illegible]

sequence SEQ ID NO: 154. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 22, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 99 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 120, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 155. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 22, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 100 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 156. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 101 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 157. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 59, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 102 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 122, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 158. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 103 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 159. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 23, a Chothia CDR-H2 sequence comprising SEQ ID NO: 60, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 104 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 118, a CDR-L2 sequence comprising SEQ ID NO: 135, and a CDR-L3 sequence SEQ ID NO: 160. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 103 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 139, and a CDR-L3 sequence SEQ ID NO: 161. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 105 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 123, a CDR-L2 sequence comprising SEQ ID NO: 140, and a CDR-L3 sequence SEQ ID NO: 162. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 106 and a VL sequence comprising a CDR-L1 sequence comprising SEQ

ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 138, and a CDR-L3 sequence SEQ ID NO: 163. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 51, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 107 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 121, a CDR-L2 sequence comprising SEQ ID NO: 139, and a CDR-L3 sequence SEQ ID NO: 164. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 61, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 108 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 120, a CDR-L2 sequence comprising SEQ ID NO: 137, and a CDR-L3 sequence SEQ ID NO: 165. In some aspects, the antibody comprises a V_H sequence comprising a Chothia CDR-H1 sequence comprising SEQ ID NO: 17, a Chothia CDR-H2 sequence comprising SEQ ID NO: 62, and a Chothia CDR-H3 sequence comprising SEQ ID NO: 109 and a VL sequence comprising a CDR-L1 sequence comprising SEQ ID NO: 124, a CDR-L2 sequence comprising SEQ ID NO: 125, and a CDR-L3 sequence SEQ ID NO: 166.

2.7.3.1. Variants of V_H - V_L Pairs

[0225] In some embodiments, the V_H - V_L pairs provided herein comprise a variant of an illustrative V_H and/or V_L sequence provided in this disclosure.

[0226] In some aspects, the V_H sequence comprises, consists of, or consists essentially of a variant of an illustrative V_H sequence provided in this disclosure. In some aspects, the V_H sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.1% identity with any of the illustrative V_H sequences provided in this disclosure.

[0227] In some embodiments, the V_H sequence comprises, consists of, or consists essentially of any of the illustrative V_H sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

[0228] In some aspects, the V_L sequence comprises, consists of, or consists essentially of a variant of an illustrative V_L sequence provided in this disclosure. In some aspects, the V_L sequence comprises, consists of, or consists essentially of a sequence having at least 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 99.05% identity with any of the illustrative V_L sequences provided in this disclosure.

[0229] In some embodiments, the V_L sequence comprises, consists of, or consists essentially of any of the illustrative V_L sequences provided in this disclosure, 20 or fewer, 19 or fewer, 18 or fewer, 17 or fewer, 16 or fewer, 15 or fewer, 14 or fewer, 13 or fewer, 12 or fewer, 11 or fewer, 10 or fewer, 9 or fewer, 8 or fewer, 7 or fewer, 6 or fewer, 5 or fewer, 4 or fewer, 3 or fewer, 2 or fewer, or 1 or fewer amino acid substitutions. In some aspects, the amino acid substitutions are conservative amino acid substitutions.

2.7.4 HC+LC

[0230] In some embodiments, the antibody comprises or consists of one or more heavy chains consisting of an HC

sequence and one or more light chains consisting of an LC sequence. In some embodiments, the antibody comprises or consists of two identical heavy chains consisting of an HC sequence and two identical light chains consisting of an LC sequence.

[0231] In some embodiments, the HC sequence is an HC sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, or SEQ ID NO: 297 and the LC sequence is a LC sequence comprising, consisting of, or consisting essentially of SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, or SEQ ID NO: 298. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, or SEQ ID NO: 297 and the LC sequence is an LC sequence consisting of SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, or SEQ ID NO: 298.

[0232] In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 255 and the LC sequence is an LC sequence consisting of SEQ ID NO: 256. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 257 and the LC sequence is an LC sequence consisting of SEQ ID NO: 258. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 259 and the LC sequence is an LC sequence consisting of SEQ ID NO: 260. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 261 and the LC sequence is an LC sequence consisting of SEQ ID NO: 262. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 263 and the LC sequence is an LC sequence consisting of SEQ ID NO: 264. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 265 and the LC sequence is an LC sequence consisting of SEQ ID NO: 266. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 267 and the LC sequence is an LC sequence consisting of SEQ ID NO: 268. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 269 and the LC sequence is an LC sequence consisting of SEQ ID NO: 270. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 271 and the LC sequence is an LC sequence consisting of

SEQ ID NO: 272. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 273 and the LC sequence is an LC sequence consisting of SEQ ID NO: 274. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 275 and the LC sequence is an LC sequence consisting of SEQ ID NO: 276. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 277 and the LC sequence is an LC sequence consisting of SEQ ID NO: 278. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 279 and the LC sequence is an LC sequence consisting of SEQ ID NO: 280. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 281 and the LC sequence is an LC sequence consisting of SEQ ID NO: 282. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 283 and the LC sequence is an LC sequence consisting of SEQ ID NO: 284. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 285 and the LC sequence is an LC sequence consisting of SEQ ID NO: 286. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 287 and the LC sequence is an LC sequence consisting of SEQ ID NO: 288. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 289 and the LC sequence is an LC sequence consisting of SEQ ID NO: 290. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 291 and the LC sequence is an LC sequence consisting of SEQ ID NO: 292. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 293 and the LC sequence is an LC sequence consisting of SEQ ID NO: 294. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 295 and the LC sequence is an LC sequence consisting of SEQ ID NO: 296. In some embodiments, the HC sequence is an HC sequence consisting of SEQ ID NO: 297 and the LC sequence is an LC sequence consisting of SEQ ID NO: 298.

2.8. Consensus Sequences

[0233] In some embodiments, provided herein are anti-CD39 antibodies comprising one or more sequences defined by consensus sequences. Each consensus sequence is based, at least in part, on one or more alignments of two or more useful anti-CD39 CDR sequences provided in this disclosure. Based on such alignments, a person of skill in the art would recognize that different amino acid residues may be useful in certain positions of the CDRs. Accordingly, each consensus sequence encompasses two or more useful anti-CD39 CDR sequences.

2.8.1. CDR-113 Consensus Sequences

[0234] In some embodiments, the antibody comprises a CDR-H3 sequence defined by the consensus sequence G-K-R-E-G-G-T-E-Y-L-R- y_{12} (SEQ ID NOS: 82-86), where y_{12} is H, K, S, N, or V.

[0235] In some aspects, y_{12} is H. In some aspects, y_{12} is K. In some aspects, y_{12} is S. In some aspects, y_{12} is N. In some aspects, y_{12} is V.

[0236] In some embodiments, the antibody comprises a CDR-H3 sequence defined by the consensus sequence E-S-G- Φ_4 -Y-R-D-H-R-L- Φ_{11} -V (SEQ ID NOS: 94-96), where Φ_4 is G or T and Φ_{11} is D or G.

[0237] In some aspects, Φ_4 is G when Φ_{11} is D or G. In some aspects, Φ_{11} is D when Φ_4 is G or T.

[0238] In some aspects, ψ_4 is G and Φ_{11} is D. In some aspects, Φ_4 is T and Φ_{11} is D. In some aspects, Φ_4 is G and Φ_{11} is G.

[0239] In some embodiments, the antibody comprises a CDR-H3 sequence defined by the consensus sequence G-G-A-K-Y-A- $\mathcal{O}_7$ - $\mathcal{O}_8$ - $\mathcal{O}_9$ -G-M-D-V (SEQ ID NOS: 87-93), where $\mathcal{O}_7$ is S, V, G, or R; $\mathcal{O}_8$ is T, Q, K, G, or R; and $\mathcal{O}_9$ is Y, H, L, or W.

[0240] In some aspects, $\mathcal{O}_7$ is S when $\mathcal{O}_8$ is T, Q, or K and $\mathcal{O}_9$ is Y, H, L, or W. In some aspects, $\mathcal{O}_8$ is T when $\mathcal{O}_7$ is S or R and $\mathcal{O}_9$ is Y or H. In some aspects, $\mathcal{O}_9$ is Y when $\mathcal{O}_7$ is S, V, G, or R and $\mathcal{O}_8$ is T, G, or R.

[0241] In some aspects, $\mathcal{O}_7$ is S when $\mathcal{O}_8$ is T and $\mathcal{O}_9$ is Y. In some aspects, $\mathcal{O}_7$ is S when $\mathcal{O}_8$ is T and $\mathcal{O}_9$ is H. In some aspects, $\mathcal{O}_7$ is S when $\mathcal{O}_8$ is Q and $\mathcal{O}_9$ is L. In some aspects, $\mathcal{O}_7$ is S when $\mathcal{O}_8$ is K and $\mathcal{O}_9$ is W. In some aspects, $\mathcal{O}_7$ is V when $\mathcal{O}_8$ is G and $\mathcal{O}_9$ is Y. In some aspects, $\mathcal{O}_7$ is G when $\mathcal{O}_8$ is R and $\mathcal{O}_9$ is Y. In some aspects, $\mathcal{O}_7$ is R when $\mathcal{O}_8$ is T and $\mathcal{O}_9$ is Y.

2.8.2. Chothia CDR-H2 Consensus Sequences

[0242] In some embodiments, the antibody comprises a Chothia CDR-H2 sequence defined by the consensus sequence N-P- ϵ_5 - ϵ_6 -G-S-T (SEQ ID NOS: 46-48), where ϵ_5 is L, R, or S and ϵ_6 is G or V.

[0243] In some aspects, when ϵ_5 is S, ϵ_6 is G or V. In some aspects, when ϵ_6 is G, ϵ_5 is S, L, or R.

[0244] In some aspects, when ϵ_5 is L, ϵ_6 is G. In some aspects, when ϵ_5 is S, ϵ_6 is G. In some aspects, when ϵ_5 is S, ϵ_6 is V. In some aspects, when ϵ_5 is R, ϵ_6 is G.

[0245] In some embodiments, the antibody comprises a Chothia CDR-H2 sequence defined by the consensus sequence α_3 - α_4 - α_5 - α_6 -G-T-A (SEQ ID NOS: 51-54), where α_3 is I or L or is absent; α_4 is P or is absent; and α_5 is I, G, or R; and α_6 is A, F, or G.

[0246] In some aspects, when α_3 is I, α_4 is P; α_5 is I or R; and α_6 is F or G. In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is A or G. In some aspects, when α_4 is P, α_3 is I or L; α_5 is I or R; and α_6 is A, F, or G. In some aspects, when α_5 is I, α_3 is I or L; α_4 is P; and α_6 is A, F, or G. In some aspects, when α_6 is F, α_3 is I or is absent; α_4 is P or is absent; and α_5 is I or G. In some aspects, when α_6 is G, α_3 is I or L; α_4 is P; and α_5 is I or R.

[0247] In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is A. In some aspects, when α_3 is I, α_4 is P; α_5 is I; and α_6 is F. In some aspects, when α_3 is absent, α_4 is absent; α_5 is G; and α_6 is F. In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is G. In some aspects, when α_3 is I, α_4 is P; α_5 is R; and α_6 is G.

[0248] In some embodiments, the antibody comprises a Chothia CDR-H2 sequence defined by the consensus sequence I-P- β_5 - β_6 -G- β_8 -A (SEQ ID NOS: 56-60), where β_5 is I, E, S, or T; β_6 is F, I, or S; and β_8 is I or T.

[0249] In some aspects, when β_5 is I, β_6 is F or S and β_8 is T. In some aspects, when β_6 is F, β_5 is E, I, or T and β_8 is I or T. In some aspects, when β_8 is T, β_5 is I, S, or T and β_6 is F, I, or S.

[0250] In some aspects, when β_5 is I, β_6 is F and β_8 is T. In some aspects, when β_5 is E, β_6 is F and β_8 is I. In some aspects, when β_5 is S, β_6 is I and β_8 is T. In some aspects, when β_5 is I, β_6 is S and β_8 is T. In some aspects, when β_5 is T, β_6 is S and β_8 is T.

2.8.3. Chothia CDR-H1 Consensus Sequences

[0251] In some embodiments, the antibody comprises a Chothia CDR-H1 sequence defined by the consensus sequence G-Y-T-F- Ω_5 -S-Y (SEQ ID NOS: 1-2 and 4-6), where Ω_5 is T, K, Q, F, or V.

[0252] In some aspects, Ω_5 is T. In some aspects, Ω_5 is K. In some aspects, Ω_5 is Q. In some aspects, Ω_5 is F. In some aspects, Ω_5 is V.

[0253] In some embodiments, the antibody comprises a Chothia CDR-H1 sequence defined by the consensus sequence G-G-T-F- ν_5 - ν_6 -Y (SEQ ID NOS: 17-22 and 24), where ν_5 is S, G, or E and ν_6 is S, K, R, or S.

[0254] In some aspects, ν_5 is S when ν_6 is S or K. In some aspects, ν_6 is S when ν_5 is S or E.

[0255] In some aspects, ν_5 is S when ν_6 is S. In some embodiments, ν_5 is S when ν_6 is K. In some aspects, ν_5 is G when ν_6 is R. In some aspects ν_5 is E when ν_6 is S.

[0256] In some embodiments, the antibody comprises a Chothia CDR-H1 sequence defined by the consensus sequence G-G-T-F- κ_5 - κ_6 - κ_7 (SEQ ID NOS: 7-16), where κ_5 is S, Q, P, or A; κ_6 is S, K, H, L, A, or W; and κ_7 is Y, L, T, N, or M.

[0257] In some aspects, when κ_5 is S, κ_6 is S, K, H, L, A, or W and κ_7 is Y, L, T, or M. In some aspects, when κ_6 is S, κ_5 is S, Q, P, or A and κ_7 is Y, L, or N. In some aspects, when κ_7 is L, κ_5 is S, Q, or A and κ_6 is S, K, L, or W.

[0258] In some aspects, when κ_5 is S, κ_6 is S and κ_7 is Y. In some aspects, when κ_5 is S, is S and κ_7 is L. In some aspects, when κ_5 is S, κ_6 is K and κ_7 is L. In some aspects, when κ_5 is S, κ_6 is H and κ_7 is T. In some aspects, when κ_5 is S, κ_6 is L and κ_7 is L. In some aspects, when κ_5 is Q, κ_6 is S and κ_7 is L. In some aspects, when κ_5 is P, κ_6 is S and κ_7 is N. In some aspects, when κ_5 is S, κ_6 is A and κ_7 is M. In some aspects, when κ_5 is A, κ_6 is S and κ_7 is L. In some aspects, when κ_5 is S, κ_6 is W and κ_7 is L.

2.8.4. Kabat CDR-H2 Consensus Sequences

[0259] In some embodiments, the antibody comprises a Kabat CDR-H2 sequence defined by the consensus sequence ϵ_1 -I-N-P- ϵ_5 - ϵ_6 -G-S-T- ϵ_{10} -Y-A-Q-K-F-Q-G (SEQ ID NOS: 63-66 and 68), where ϵ_1 is K, S, R, or V; ϵ_5 is L, R, or S; ϵ_6 is G or V; and ϵ_{10} is S or W.

[0260] In some aspects, when ϵ_1 is V; ϵ_5 is L or S; ϵ_6 is G; and ϵ_{10} is S. In some aspects, when ϵ_1 is R; ϵ_5 is S; ϵ_6 is V or G; and ϵ_{10} is W. In some aspects, when ϵ_5 is S; ϵ_1 is R or V; ϵ_6 is G or V; and ϵ_{10} is S or W. In some aspects, when ϵ_6 is G; ϵ_1 is R or V; ϵ_5 is S; and ϵ_{10} is S or W. In some aspects, when ϵ_{10} is S; ϵ_1 is V or S; ϵ_5 is L, R, or S; and ϵ_6 is G. In some aspects, when ϵ_{10} is W; ϵ_1 is K or R; ϵ_5 is S; and ϵ_6 is G or V.

[0261] In some aspects, when ϵ_1 is V; ϵ_5 is L; ϵ_6 is G; and ϵ_{10} is S. In some aspects, when ϵ_1 is V; ϵ_5 is S; ϵ_6 is G; and ϵ_{10} is S. In some aspects, when ϵ_1 is R; ϵ_5 is S; ϵ_6 is V; and ϵ_{10} is W. In some aspects, when ϵ_1 is R; ϵ_5 is S; ϵ_6 is G; and ϵ_{10} is W. In some aspects, when ϵ_1 is K; ϵ_5 is S; ϵ_6 is G; and ϵ_{10} is W. In some aspects, when ϵ_1 is S; ϵ_5 is R; ϵ_6 is G; and ϵ_{10} is S.

[0262] In some embodiments, the antibody comprises a Kabat CDR-H2 sequence defined by the consensus sequence G-I- α_3 - α_4 - α_5 - α_6 -G-T-A-N-Y-A-Q-K-F-Q-G (SEQ ID NOS: 69-72), where α_3 is I or L or is absent; α_4 is P or is absent; and α_5 is I, G, or R; and α_6 is A, F, or G.

[0263] In some aspects, when α_3 is I, α_4 is P; as is I or R; and α_6 is F or G. In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is A or G. In some aspects, when α_4 is P, α_3 is I or L; as is I or R; and α_6 is A, F, or G. In some aspects, when as, is I, α_3 is I or L; α_4 is P; and α_6 is A, F, or G. In some aspects, when α_6 is F, α_3 is I or is absent; α_4 is P or is absent; and α_5 is I or G. In some aspects, when α_6 is G, α_3 is I or L; α_4 is P; and α_5 is I or R.

[0264] In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is A. In some aspects, when α_3 is I, α_4 is P; α_5 is I; and α_6 is F. In some aspects, when α_3 is absent, α_4 is absent; as is G; and α_6 is F. In some aspects, when α_3 is L, α_4 is P; α_5 is I; and α_6 is G. In some aspects, when α_3 is I, α_4 is P; as is R; and α_6 is G.

[0265] In some embodiments, the antibody comprises a Kabat CDR-H2 sequence defined by the consensus sequence β_1 -I-P- β_5 - β_6 -G- β_8 -A-N-Y-A-Q-K-F-G-Q (SEQ ID NOS: 74 and 76-79) where β_1 is S or G; β_5 is I, E, S, or T; β_6 is F, I, or S; and β_8 is I or T.

[0266] In some aspects, when β_1 is S, β_5 is E, I, or S; β_6 is I or F; and β_8 is I or T. In some aspects, when β_1 is G, β_5 is I or T; β_6 is F or S; and β_8 is T. In some aspects, when β_5 is I, β_1 is G or S; β_6 is F or S; and β_8 is T. In some aspects, when β_6 is F, β_1 is G or S; β_5 is E, I, or T; and β_8 is I or T. In some aspects, when β_8 is T, β_1 is G or S; β_5 is I, S, or T; and β_6 is F, I, or S.

[0267] In some aspects, when β_1 is S, β_5 is I; β_5 is F; and β_8 is T. In some aspects, when β_1 is S, β_5 is E; β_5 is F; and β_8 is I. In some aspects, when β_1 is S, β_5 is S; β_5 is I; and β_8 is T. In some aspects, when β_1 is G, β_5 is I; β_5 is F; and β_8 is T. In some aspects, when β_1 is G, β_5 is I; β_5 is S; and β_8 is T. In some aspects, when β_1 is G, β_5 is T; β_5 is F; and β_8 is I or T.

2.8.5. Kabat CDR-H1 Consensus Sequences

[0268] In some embodiments, the antibody comprises a Kabat CDR-H1 sequence defined by the consensus sequence S-Y- Δ_3 -M- Δ_5 (SEQ ID NOS: 25-29 and 44-45), where Δ_3 is E, F, Q, or Y and Δ_5 is H or Y.

[0269] In some aspects, when Δ_3 is Y, Δ_5 is H or Y. In some aspects, when Δ_5 is H, Δ_3 is E, F, Q, or Y.

[0270] In some aspects, Δ_3 is Y when Δ_5 is H. In some aspects, Δ_3 is Y when Δ_5 is Y. In some aspects, Δ_3 is E when Δ_5 is H. In some aspects, Δ_3 is Q when Δ_5 is H. In some aspects, Δ_3 is F when Δ_5 is H.

[0271] In some embodiments, the antibody comprises a Kabat CDR-H1 sequence defined by the consensus sequence θ_1 - θ_2 - θ_3 -I-S (SEQ ID NOS: 30-37), where θ_1 is A, H, K, L, S, or W; θ_2 is L, M, N, or T; and θ_3 is A or P.

[0272] In some aspects, when θ_1 is S, θ_2 is L or N and θ_3 is A or P. In some aspects, when θ_2 is L, θ_1 is K, L, S, or W and θ_3 is A or P. In some aspects, when θ_3 is A, θ_1 is A, H, K, L, S, or W and θ_2 is L, M, N, or T.

[0273] In some aspects, θ_1 is S, when θ_2 is L and θ_3 is A. In some aspects, θ_1 is K, when θ_2 is L and θ_3 is A. In some aspects, θ_1 is H when θ_2 is T and θ_3 is A. In some aspects, θ_1 is S when θ_2 is L and θ_3 is P. In some aspects, θ_1 is L when θ_2 is L and θ_3 is A. In some aspects, θ_1 is S when θ_2 is N and θ_3 is A. In some aspects, θ_1 is A when θ_2 is M and θ_3 is A. In some aspects, θ_1 is W when θ_2 is L and θ_3 is A.

[0274] In some embodiments, the antibody comprises a Kabat CDR-H1 sequence defined by the consensus sequence η_1 -Y- η_3 -I-S (SEQ ID NOS: 38-41), where η_1 is S, K, N, or R and η_3 is A or G.

[0275] In some aspects, η_1 is S where η_3 is A or G. In some aspects, η_3 is A where η_1 is N or S. In some aspects, η_3 is G where η_1 is K, R, or S.

[0276] In some aspects, when η_1 is S, η_3 is A. In some aspects, when η_1 is S, η_3 is G. In some aspects, when η_1 is K, η_3 is G. In some aspects, when η_1 is R, η_3 is G. In some aspects, when η_1 is N, η_3 is A.

2.8.6. CDR-L3 Consensus Sequences

[0277] In some embodiments, the antibody comprises a CDR-L3 sequence defined by the consensus sequence Q-Q-Y- π_4 - π_5 - π_6 - π_7 -T (SEQ ID NOS: 141-147), where π_4 is G, H, or Y; π_5 is S, N, F, G, or R; π_6 is S, Y, A, G, or R; and π_7 is P, I, or L.

[0278] In some aspects, π_4 is H when π_5 is S, N, G, or R; π_6 is Y, A, G, or R; and π_7 is I or L. In some aspects, π_5 is S, when π_4 is G or H; π_6 is S, Y, or A; and π_7 is P, I or L. In some aspects, π_6 is Y, when π_4 is H or Y; π_5 is S or F; and π_7 is I. In some aspects, π_6 is A when π_4 is H; π_5 is N or S; and π_7 is I or L. In some aspects, π_7 is I when π_4 is H or Y; π_5 is S, N, F, G, or R; and π_6 is Y, A, G, or R.

[0279] In some aspects, π_4 is G when π_5 is S; π_6 is S; and π_7 is P. In some aspects, π_4 is H when π_5 is S; π_6 is Y; and π_7 is I. In some aspects, π_4 is H when π_5 is N; π_6 is I; and π_7 is A. In some aspects, π_4 is Y when π_5 is F; π_6 is Y; and π_7 is I. In some aspects, π_4 is H when π_5 is S; π_6 is A; and π_7 is L. In some aspects, π_4 is H when π_5 is G; π_6 is G; and π_7 is I. In some aspects, π_4 is H when π_5 is R; π_6 is R; and π_7 is I.

[0280] In some embodiments, the antibody comprises a CDR-L3 sequence defined by consensus sequence Q-Q- λ_3 - λ_4 - λ_5 - λ_6 -P-T (SEQ ID NOS: 148-150), where λ_3 is R, F, H, S, L, D, Y, or V; λ_4 is S, V, T, G, L, Y, or N; λ_5 is N, L, F, K, or V; and λ_6 is W, F, Y, or L.

[0281] In some aspects, λ_3 is R, when λ_4 is S or N; λ_5 is N or F; and λ_6 is W or Y. In some aspects, λ_3 is H when λ_4 is V or T; λ_5 is N or V; and λ_6 is F or W. In some aspects, λ_3 is S when λ_4 is V or Y; λ_5 is F; and λ_6 is W or L. In some aspects, λ_4 is V when λ_3 is F, H, S, or D; λ_5 is L, N, or F; and λ_6 is W or F. In some aspects, λ_4 is T when λ_3 is L or H; λ_5 is K or V; and λ_6 is W. In some aspects, λ_5 is N when λ_3 is R, H, or V; λ_4 is S, V, or L; and λ_6 is W, F, or Y. In some aspects, λ_5 is L when λ_3 is F, D, or Y; λ_4 is V or G; and λ_6 is W or F. In some aspects, λ_5 is F when λ_3 is S or R; λ_4 is V, Y, or N; and λ_6 is W, L, or Y. In some aspects, λ_6 is W when λ_3 is R, F, S, L, D, or H; λ_4 is S, V, or T; and λ_5 is N, L, F, K, or V. In some aspects, λ_6 is F when λ_3 is H or Y; λ_4 is V or G; and λ_5 is N or L. In some aspects, λ_6 is Y when λ_3 is V or R; λ_4 is L or N; and λ_5 is N or F.

[0282] In some aspects, λ_3 is R when λ_4 is S; λ_5 is N; and λ_6 is W. In some aspects, λ_3 is F when λ_4 is V; λ_5 is L; and λ_6 is W. In some aspects, λ_3 is H when λ_4 is V; λ_5 is N; and λ_6 is F. In some aspects, λ_3 is S when λ_4 is V; λ_5 is F; and λ_6 is W. In some aspects, λ_3 is L when λ_4 is T; λ_5 is K; and λ_6 is W. In some aspects, λ_3 is D when λ_4 is V; λ_5 is L; and λ_6 is W. In some aspects, λ_3 is Y when λ_4 is G; λ_5 is L; and λ_6 is F. In some aspects, λ_3 is H when λ_4 is T; λ_5 is V; and λ_6 is W. In some aspects, λ_3 is V when λ_4 is L; λ_5 is N; and λ_6 is Y. In some aspects, λ_3 is S when λ_4 is Y; λ_5 is F; and λ_6 is L. In some aspects, λ_3 is R when λ_4 is N; λ_5 is F; and λ_6 is Y.

[0283] In some embodiments, the antibody comprises a CDR-L3 sequence defined by the consensus sequence Q-Q-Y- ρ_3 - ρ_4 -W-P-L-T (SEQ ID NOS: 151 and 152), where ρ_3 is N or L and ρ_4 is N or L.

[0284] In some aspects, ρ_3 is N when ρ_4 is L. In some aspects, ρ_3 is L when ρ_4 is L.

[0285] In some embodiments, the antibody comprises a CDR-L3 sequence defined by the consensus sequence Q-Q- ω_3 - ω_4 - ω_5 - ω_6 -P- ω_8 -T (SEQ ID NOS: 153-156), where ω_3 is Y or F; ω_4 is Y or W; ω_5 is S, L, T, or F; ω_6 is T, Y, or F; and ω_8 is L or P.

[0286] In some aspects, ω_3 is Y when ω_4 is Y or W; ω_5 is S, L, or T; ω_6 is T or Y; and ω_8 is L. In some aspects, ω_4 is Y when ω_3 is Y or F; ω_5 is S, L, or F; ω_6 is T or Y; and ω_8 is L or P. In some aspects, ω_6 is Y when ω_3 is Y; ω_4 is Y or W; ω_5 is L or T; and ω_6 is L. In some aspects, ω_8 is L when ω_3 is Y; ω_4 is Y or W; ω_5 is S, L, or T; and ω_6 is T or Y.

[0287] In some aspects, ω_3 is Y when ω_4 is Y; ω_5 is S; ω_6 is T; and ω_8 is L. In some aspects, ω_3 is Y when ω_4 is Y; ω_5 is L; ω_6 is Y; and ω_8 is L. In some aspects, ω_3 is Y when ω_4 is W; ω_5 is T; ω_6 is Y; and ω_8 is L. In some aspects, ω_3 is F when ω_4 is Y; ω_5 is F; ω_6 is F; and ω_8 is P.

2.8.7. CDR-L2 Consensus Sequences

[0288] In some embodiments, the antibody comprises a CDR-L2 sequence defined by the consensus sequence ψ_1 -A-S- ψ_4 -R- ψ_6 - ψ_7 (SEQ ID NOS: 125-136), where ψ_1 is G or Y; ψ_4 is S or N; ψ_6 is A or H; and ψ_7 is T, Y, or N.

[0289] In some aspects, ψ_1 is G when ψ_4 is S or N; ψ_6 is A or H; and ψ_7 is T or N. In some aspects, ψ_1 is Y when ψ_4 is S or N; ψ_6 is A; and ψ_7 is Y or T. In some aspects, ψ_4 is S when ψ_1 is G or Y; ψ_6 is A; and ψ_7 is T, Y, or N. In some aspects, ψ_4 is N when ψ_1 is G or Y; ψ_6 is H or A; and ψ_7 is T. In some aspects, ψ_6 is A when ψ_1 is G or Y; ψ_4 is S or N; and ψ_7 is T, Y, or N. In some aspects, ψ_7 is T when ψ_1 is G or Y; ψ_4 is S or N; and ψ_6 is A or H.

[0290] In some aspects, ψ_1 is G when ψ_4 is S; ψ_6 is A; and ψ_7 is T. In some aspects, ψ_1 is G when ψ_4 is N; ψ_6 is H; and ψ_7 is T. In some aspects, ψ_1 is Y when ψ_4 is S; ψ_6 is A; and ψ_7 is Y. In some aspects, ψ_1 is G when ψ_4 is S; ψ_6 is A; and ψ_7 is N. In some aspects, ψ_1 is Y when ψ_4 is N; ψ_6 is A; and ψ_7 is T.

[0291] In some embodiments, the antibody comprises a CDR-L2 sequence defined by the consensus sequence D-A-S- χ_4 -R-A-T (SEQ ID NOS: 138 and 139), where χ_4 is N or K.

[0292] In some aspects, χ_4 is N. In some aspects, χ_4 is K.

[0293] In some embodiments, the antibody comprises a CDR-L2 sequence defined by the consensus sequence W-A-S-T-R- σ_6 -S (SEQ ID NOS: 131 and 133-134), where σ_6 is A, E, or Q.

[0294] In some aspects, σ_6 is A. In some aspects, σ_6 is E. In some aspects, σ_6 is Q.

2.8.8. CDR-L1 Consensus Sequences

[0295] In some embodiments, the antibody comprises a CDR-L1 sequence defined by the consensus sequence ϕ_1 -A-S- ϕ_4 - ϕ_5 -V- ϕ_7 - ϕ_8 - ϕ_9 -Y-L-A (SEQ ID NOS: 1101-114), where ϕ_1 is E, K, or R; ϕ_4 is Q or E; ϕ_5 is S or Y; ϕ_7 is S or A; ϕ_8 is S or Y; and ϕ_9 is D or S.

[0296] In some aspects, ϕ_1 is R when ϕ_4 is Q or E; ϕ_5 is S or Y; ϕ_7 is S or A; ϕ_8 is S or Y; and ϕ_9 is S or D. In some aspects, ϕ_4 is E when ϕ_1 is K or R; ϕ_5 is S; ϕ_7 is S; ϕ_8 is S;

and ϕ_9 is S. In some aspects, ϕ_4 is Q when ϕ_1 is E or R; ϕ_5 is S or Y; ϕ_7 is S or A; ϕ_8 is S or Y; and ϕ_9 is S or D. In some aspects, ϕ_5 is S when ϕ_1 is E, K, or R; ϕ_4 is E or Q; ϕ_7 is S or A; ϕ_8 is S or Y; and ϕ_9 is S or D. In some aspects, ϕ_7 is S when ϕ_1 is E, K, or R; ϕ_4 is E or Q; ϕ_5 is S or Y; ϕ_8 is S or Y; and ϕ_9 is S or D. In some aspects, ϕ_8 is S when ϕ_1 is K or R; ϕ_4 is E or Q; ϕ_5 is S or S; ϕ_7 is A or S; and ϕ_9 is S or D. In some aspects, ϕ_8 is R when ϕ_1 is E or R; ϕ_4 is Q; ϕ_5 is S; ϕ_7 is S; and ϕ_9 is S. In some aspects, ϕ_9 is S when ϕ_1 is E, K, or R; ϕ_4 is E or Q; ϕ_5 is S or Y; ϕ_7 is A or S; and ϕ_8 is S or Y.

[0297] In some aspects, ϕ_1 is K when ϕ_4 is E; ϕ_5 is S; ϕ_7 is S; ϕ_8 is S; and ϕ_9 is S. In some aspects, ϕ_1 is E, when ϕ_4 is Q; ϕ_5 is S; ϕ_7 is S; ϕ_8 is Y; and ϕ_9 is S. In some aspects, ϕ_1 is R when ϕ_4 is Q; ϕ_5 is S; ϕ_7 is S; ϕ_8 is S; and ϕ_9 is D. In some aspects, ϕ_1 is R when ϕ_4 is Q; ϕ_5 is S; ϕ_7 is S; ϕ_8 is S; and ϕ_9 is S. In some aspects, ϕ_1 is R when ϕ_4 is Q; ϕ_5 is S; ϕ_7 is A; ϕ_8 is S; and ϕ_9 is S. In some aspects, ϕ_1 is R when ϕ_4 is Q; ϕ_5 is S; ϕ_7 is S; ϕ_8 is Y; and ϕ_9 is S. In some aspects, ϕ_1 is R when ϕ_4 is E; ϕ_5 is S; ϕ_7 is S; ϕ_8 is S; and ϕ_9 is S. In some aspects, ϕ_1 is R when ϕ_4 is Q; ϕ_5 is Y; ϕ_7 is S; ϕ_8 is S; and ϕ_9 is S.

[0298] In some embodiments, the antibody comprises a CDR-L1 sequence defined by the consensus sequence $\bar{\phi}_1$ -A-S-Q- $\bar{\phi}_5$ - $\bar{\phi}_6$ - $\bar{\phi}_7$ - $\bar{\phi}_8$ - $\bar{\phi}_9$ -L- $\bar{\phi}_{11}$ (SEQ ID NOS: 118 and 120-123), where $\bar{\phi}_1$ is Q or R; $\bar{\phi}_5$ is D or S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is G or S; $\bar{\phi}_8$ is N, R, or S; $\bar{\phi}_9$ is N, Y, or W; and $\bar{\phi}_{11}$ is A or N.

[0299] In some aspects, when $\bar{\phi}_1$ is R, $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is G or S; $\bar{\phi}_8$ is R or S; $\bar{\phi}_9$ is N, Y, or W; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_5$ is S, $\bar{\phi}_1$ is R; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is G or S; $\bar{\phi}_8$ is R or S; $\bar{\phi}_9$ is N, Y, or W; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_6$ is I, $\bar{\phi}_1$ is Q or R; $\bar{\phi}_5$ is D or S; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is N or S; $\bar{\phi}_9$ is Y or W; and $\bar{\phi}_{11}$ is A or N. In some aspects, when $\bar{\phi}_6$ is V, $\bar{\phi}_1$ is R; $\bar{\phi}_5$ is S; $\bar{\phi}_7$ is G or S; $\bar{\phi}_8$ is R or S; $\bar{\phi}_9$ is N or W; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_7$ is S, $\bar{\phi}_1$ is Q or R; $\bar{\phi}_5$ is D or S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_8$ is N, S, or R; $\bar{\phi}_9$ is Y or W; and $\bar{\phi}_{11}$ is A or N. In some aspects, when $\bar{\phi}_8$ is S, $\bar{\phi}_1$ is R; $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is S; $\bar{\phi}_9$ is N, Y, or W; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_9$ is Y, $\bar{\phi}_1$ is Q or R; $\bar{\phi}_5$ is D or S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is N, S, or R; and $\bar{\phi}_{11}$ is A or N. In some aspects, when $\bar{\phi}_{11}$ is A, $\bar{\phi}_1$ is R; $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is S or G; $\bar{\phi}_8$ is S, or R; and $\bar{\phi}_9$ is N, W, or Y.

[0300] In some aspects, when $\bar{\phi}_1$ is R, $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is V; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is S; $\bar{\phi}_9$ is Y; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_1$ is Q, $\bar{\phi}_5$ is D; $\bar{\phi}_6$ is I; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is N; $\bar{\phi}_9$ is Y; and $\bar{\phi}_{11}$ is N. In some aspects, when $\bar{\phi}_1$ is R, $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is V; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is R; $\bar{\phi}_9$ is Y; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_1$ is R, $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is V; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is S; $\bar{\phi}_9$ is N; and $\bar{\phi}_{11}$ is A. In some aspects, when $\bar{\phi}_1$ is R, $\bar{\phi}_5$ is S; $\bar{\phi}_6$ is I; $\bar{\phi}_7$ is S; $\bar{\phi}_8$ is S; $\bar{\phi}_9$ is W; and $\bar{\phi}_{11}$ is A.

[0301] In some embodiments, the antibody comprises a CDR-L1 sequence defined by the consensus sequence K-S-S- Γ_4 -S-V-L- Γ_8 -S- Γ_{10} -N-N-K-N-Y-L-A (SEQ ID NOS: 115-117), where Γ_4 is Q, R or K; Γ_8 is F or Y; and Γ_{10} is S or N.

[0302] In some aspects, Γ_4 is Q when Γ_8 is F or Y and Γ_{10} is S. In some aspects, Γ_8 is F when Γ_4 is Q or R and Γ_{10} is S. In some aspects, Γ_8 is Y when Γ_4 is K or Q and Γ_{10} is S or N. In some aspects, Γ_{10} is S when Γ_4 is R or Q and Γ_8 is F or Y.

[0303] In some aspects, Γ_4 is Q when Γ_8 is Y and Γ_{10} is S. In some aspects, Γ_4 is K when Γ_8 is Y and Γ_{10} is N. In some

aspects, Γ_4 is Q when Γ_8 is F and Γ_{10} is S. In some aspects, Γ_4 is R when Γ_8 is F and Γ_{10} is S.

3. Germline

[0304] In some embodiments, the antibody that specifically binds CD39 is an antibody comprising a variable region that is encoded by a particular germline gene, or a variant thereof. The illustrative antibodies provided herein comprise variable regions that are encoded by the heavy chain variable region germline genes VH1-46, VH1-69, 1-69, and VH1-46, or variants thereof; and the light chain variable region germline genes VK3-20, VK3-11, VK4-01, VK3, and VK3-15, or variants thereof. One of skill in the art would recognize that the CDR sequences provided herein may also be useful when combined with variable regions encoded by other variable region germline genes, or variants thereof. In particular, the CDR sequences provided herein may be useful when combined with variable regions encoded by variable region germline genes, or variants thereof, that are structurally similar to the variable region germline genes recited above. For example, in some embodiments, a CDR-H sequence provided herein may be combined with a variable region encoded by a variable region germline gene selected from the VH1 or VH3 family, or a variant thereof. In some embodiments, a CDR-L sequence provided herein may be combined with a variable region encoded by a variable region germline gene selected from the VL3, Vk1, Vk3, and Vk4 families, or a variant thereof.

4. Affinity

[0305] In some embodiments, the affinity of the antibody for CD39, as indicated by K_D , is less than about 10^{-5} M, less than about 10^{-6} M, less than about 10^{-7} M, less than about 10^{-8} M, less than about 10^{-9} M, less than about 10^{-10} M, less than about 10^{-11} M, or less than about 10^{-12} M. In some embodiments, the affinity of the antibody is between about 10^{-7} M and 10^{-11} M. In some embodiments, the affinity of the antibody is between about 10^{-7} M and 10^{-10} M. In some embodiments, the affinity of the antibody is between about 10^{-7} M and 10^{-9} M. In some embodiments, the affinity of the antibody is between about 10^{-7} M and 10^{-8} M. In some embodiments, the affinity of the antibody is between about 10^{-8} M and 10^{-11} M. In some embodiments, the affinity of the antibody is between about 10^{-8} M and 10^{-10} M. In some embodiments, the affinity of the antibody is between about 10^{-9} M and 10^{-11} M. In some embodiments, the affinity of the antibody is between about 10^{-10} M and 10^{-11} M.

[0306] In some embodiments, the affinity of the antibody for human CD39 is between about 4.09×10^{-7} M and 7.31×10^{-11} M. In some embodiment, the affinity of the antibody for human CD39 is about 1.14×10^{-7} M, about 1.31×10^{-7} M, about 1.67×10^{-7} M, about 1.43×10^{-7} M, about 1.30×10^{-8} M, about 1.27×10^{-8} M, about 1.13×10^{-8} M, about 1.60×10^{-8} M, about 1.34×10^{-9} M, about 1.16×10^{-9} M, about 7.31×10^{-11} M, about 7.60×10^{-10} M, about 2.66×10^{-10} M, about 9.22×10^{-10} M, about 6.72×10^{-10} M, about 9.24×10^{-10} M, about 5.58×10^{-10} M, about 5.48×10^{-8} M, about 3.37×10^{-8} M, about 3.11×10^{-8} M, about 1.88×10^{-8} M, about 1.63×10^{-8} M, about 1.64×10^{-8} M, about 1.01×10^{-8} M, about 2.44×10^{-7} M, about 4.09×10^{-7} M, about 3.35×10^{-8} M, about 1.91×10^{-8} M, about 1.73×10^{-8} M, or about 2.39×10^{-8} M.

[0307] In some embodiments the antibody has a k_{on} when associating with human CD39 of between about 1.93×10^4 $M^{-1} \times sec^{-1}$ and about 1.72×10^6 $M^{-1} \times sec^{-1}$. In some embodiments the antibody has a k_d when associating with human CD39 of about 6.59×10^4 $M^{-1} \times sec^{-1}$, about 1.93×10^4 $M^{-1} \times sec^{-1}$, about 4.44×10^5 $M^{-1} \times sec^{-1}$, about 2.72×10^5 $M^{-1} \times sec^{-1}$, about 6.39×10^5 $M^{-1} \times sec^{-1}$, about 8.93×10^5 $M^{-1} \times sec^{-1}$, about 9.55×10^5 $M^{-1} \times sec^{-1}$, about 2.11×10^5 $M^{-1} \times sec^{-1}$, about 1.17×10^5 $M^{-1} \times sec^{-1}$, about 2.02×10^5 $M^{-1} \times sec^{-1}$, about 1.76×10^5 $M^{-1} \times sec^{-1}$, about 1.72×10^5 $M^{-1} \times sec^{-1}$, about 2.73×10^5 $M^{-1} \times sec^{-1}$, about 1.43×10^5 $M^{-1} \times sec^{-1}$, about 9.01×10^5 $M^{-1} \times sec^{-1}$, about 3.13×10^5 $M^{-1} \times sec^{-1}$, about 5.03×10^5 $M^{-1} \times sec^{-1}$, about 3.02×10^5 $M^{-1} \times sec^{-1}$, about 2.73×10^5 $M^{-1} \times sec^{-1}$, about 1.78×10^5 $M^{-1} \times sec^{-1}$, about 2.98×10^5 $M^{-1} \times sec^{-1}$, about 4.31×10^5 $M^{-1} \times sec^{-1}$, about 2.27×10^5 $M^{-1} \times sec^{-1}$, about 3.14×10^5 $M^{-1} \times sec^{-1}$, about 2.81×10^5 $M^{-1} \times sec^{-1}$, about 4.73×10^5 $M^{-1} \times sec^{-1}$, about 3.26×10^5 $M^{-1} \times sec^{-1}$, about 1.73×10^5 $M^{-1} \times sec^{-1}$, about 2.68×10^5 $M^{-1} \times sec^{-1}$, about 2.63×10^5 $M^{-1} \times sec^{-1}$, about 3.82×10^5 $M^{-1} \times sec^{-1}$, about 2.46×10^5 $M^{-1} \times sec^{-1}$, about 3.11×10^5 $M^{-1} \times sec^{-1}$, about 4.53×10^5 $M^{-1} \times sec^{-1}$, about 4.63×10^5 $M^{-1} \times sec^{-1}$, about 9.01×10^5 $M^{-1} \times sec^{-1}$, about 1.03×10^6 $M^{-1} \times sec^{-1}$, about 1.52×10^6 $M^{-1} \times sec^{-1}$, or about 3.53×10^5 $M^{-1} \times sec^{-1}$.

[0308] In some embodiments the antibody has a k_{off} of about 7.51×10^{-3} sec^{-1} , about 6.33×10^{-2} sec^{-1} , about 4.70×10^{-2} sec^{-1} , about 7.82×10^{-4} sec^{-1} , about 4.70×10^{-2} sec^{-1} , about 1.05×10^{-2} sec^{-1} , about 3.65×10^{-1} sec^{-1} , about 1.60×10^{-1} sec^{-1} , about 7.11×10^{-3} sec^{-1} , about 6.44×10^{-3} sec^{-1} , about 3.85×10^{-2} sec^{-1} , about 2.30×10^{-2} sec^{-1} , about 5.33×10^{-2} sec^{-1} , about 9.14×10^{-2} sec^{-1} , about 1.80×10^{-3} sec^{-1} , about 8.15×10^{-3} sec^{-1} , about 3.85×10^{-4} sec^{-1} , about 1.34×10^{-4} sec^{-1} , about 2.29×10^{-4} sec^{-1} , about 4.37×10^{-3} sec^{-1} , about 3.71×10^{-3} sec^{-1} , about 4.06×10^{-3} sec^{-1} , about 6.66×10^{-2} sec^{-1} , about 2.02×10^{-3} sec^{-1} , about 2.00×10^{-4} sec^{-1} , about 5.26×10^{-3} sec^{-1} , about 1.13×10^{-2} sec^{-1} , about 3.28×10^{-3} sec^{-1} , about 2.76×10^{-3} sec^{-1} , about 2.86×10^{-4} sec^{-1} , about 2.43×10^{-4} sec^{-1} , about 2.13×10^{-4} sec^{-1} , about 6.09×10^{-4} sec^{-1} , about 8.39×10^{-4} sec^{-1} , about 8.15×10^{-3} sec^{-1} , about 1.32×10^{-4} sec^{-1} , about 1.11×10^{-4} sec^{-1} , about 2.43×10^{-4} sec^{-1} , about 2.13×10^{-4} sec^{-1} , about 6.09×10^{-4} sec^{-1} , about 8.15×10^{-3} sec^{-1} , about 1.32×10^{-4} sec^{-1} , or about 1.11×10^{-4} sec^{-1} .

[0309] In some aspects, the K_D , k_a , and k_d are determined at 25° C. In some embodiments, the K_D , k_a , and k_d are determined by surface plasmon resonance. In some embodiments, the K_D , k_a , and k_d are determined according to the methods described in the examples.

5. Inhibition of CD39

[0310] In some aspects, the antibody decreases affinity of CD39 to its substrate. In some aspects, the antibody inhibits CD39 function on tumor cells. In some aspects, the antibody inhibits or impedes the release of ADP or AMP from CD39. In some aspects, the antibody inhibits or impedes CD39 processivity.

[0311] In some aspects, the antibody binds CD39 but does not inhibit ATPase. In some aspects, the antibody binds CD39 and inhibits extracellular CD39 activity but not cellular ATPase activity. In some aspects, the antibody binds both the extracellular domain of CD39 and cellular CD39 and can inhibit both the extracellular domain of CD39 and

cellular CD39. In some aspects, the antibodies do not compete with A1 and/or others in binding to the extracellular domain.

6. CD39 Assays

[0312] In some embodiments, the antibody binds to an epitope of CD39. In some aspects, CD39 has a sequence identical to the amino acid sequence set forth in SEQ ID NO: 249. In some aspects, the epitope has an amino acid sequence that is identical to the amino acid sequence set forth in SEQ ID NO: 249. In some aspects, the epitope is in an extracellular domain of CD39. In some aspects, the extracellular domain corresponds to all or at least a portion of amino acids 38-478 of SEQ ID NO: 249. In some aspects, the epitope has an amino acid sequence that is 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% identical to the sequence set forth in SEQ ID NO: 249 or all or a portion of the extracellular domain. In some aspects, the epitope has a sequence that is identical or corresponds to residues 143-158 and/or residues 274-277 of SEQ ID NO: 249. In some aspects, the epitope is in the region of E143 to N158 on the human CD39 polypeptide having the sequence set forth in SEQ ID NO: 249. In some aspects, the epitope has a sequence that has a 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95% identity to residues 143-158 or 274-277 of the sequence set forth in SEQ ID NO: 249. In some aspects, the epitope has 1, 2, 3, 4, 5, 6, 7, 8, or 9 substitutions from residues 143-158 of the sequence set forth in SEQ ID NO: 249. In some aspects, the epitope has 1, 2 or 3 substitutions from residues 274-277 of SEQ ID NO: 249. In some aspects, the antibody makes contact with any of the residues set forth in FIG. 14E, Table 1. In some aspects, the antibody makes contact with any of the residues set forth in FIG. 14E, Table 2. In some aspects, the antibody binds to D150, E153, and/or R154 or to N99 and none, one, two, or three of D150, E153, and R154 or to any of the above alone or in combination.

[0313] In some aspects, the antibody competes with 1, 2, 3, 4, or 5 of antibodies 27536, 27571, 28347, 27579, or 27597 as set forth in FIG. 14A. In some aspects, the antibody competes with 1, 2, 3, 4, or 5 antibodies 27536, 27571, 28347, 27579, or 27597 as set forth in FIG. 14A. In some aspects, the antibody competes with 1, 2, or 3 of antibodies 25571, 27536, or 27549 as set forth in FIG. 14C. In some aspects, the antibody competes with 1, 2, or 3 of antibodies 25571, 27536, or 27549 set forth in FIG. 14C.

[0314] In some aspects, the antibody inhibits conversion by CD39 of ATP to ADP and/or ADP to AMP. In some aspects, the antibody inhibits platelet aggregation. In some aspects, the antibody decreases or prevents activation of phospho antigen specific T cells selected from MAIT cells and $\gamma\delta$ T cells. In some aspects, the antibody inhibits angiogenesis. In some aspects, the antibody decreases levels of phosphate, ADP, AMP, and/or adenosine and/or increasing levels of ATP. In some aspects, the antibody increases T effector cell function. In some aspects, the antibody decreases the number of regulatory T cells in tissues or in circulation. In some aspects, the antibody decreases the regulatory T cells or regulatory T cell activity. In some aspects, the antibody increases B cell function. In some aspects, the antibody increases antigen presenting cell function. In some aspects, the antibody inhibits processing of at least one of phospho-antigen from phosphorylated isoprenoid, phosphorylated vitamin B metabolite, and/or phosphorylated riboflavin.

[0315] In some aspects, the antibody has limited ability to limit ATPase of the soluble or extracellular domain. In some aspects, the antibody has limited ability to inhibit ATPase of the cellular and/or extracellular domain of CD39.

7. Glycosylation Variants

[0316] In certain embodiments, an antibody may be altered to increase, decrease or eliminate the extent to which it is glycosylated. Glycosylation of polypeptides is typically either "N-linked" or "O-linked."

[0317] "N-linked" glycosylation refers to the attachment of a carbohydrate moiety to the side chain of an asparagine residue. The tripeptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tripeptide sequences in a polypeptide creates a potential glycosylation site.

[0318] "O-linked" glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0319] Addition or deletion of N-linked glycosylation sites to the antibody may be accomplished by altering the amino acid sequence such that one or more of the above-described tripeptide sequences is created or removed. Addition or deletion of O-linked glycosylation sites may be accomplished by addition, deletion, or substitution of one or more serine or threonine residues in or to (as the case may be) the sequence of an antibody.

[0320] In certain embodiments, the antibody is glycosylated. In certain embodiments, the antibody is deglycosylated. Carbohydrates may be removed by standard techniques. In certain embodiments, the antibody is aglycosylated, for instance by expression in a system that does not glycosylate.

8. Fc Variants

[0321] In certain embodiments, amino acid modifications may be introduced into the Fc region of an antibody provided herein to generate an Fc region variant. In certain embodiments, the Fc region variant possesses some, but not all, effector functions. Such antibodies may be useful, for example, in applications in which the half-life of the antibody in vivo is important, yet certain effector functions are unnecessary or deleterious. Examples of effector functions include complement-dependent cytotoxicity (CDC) and antibody-directed complement-mediated cytotoxicity (ADCC). Numerous substitutions or deletions with altered effector function are known in the art.

[0322] An alteration in in CDC and/or ADCC activity can be confirmed using in vitro and/or in vivo assays. For example, Fc receptor (FcR) binding assays can be conducted to measure Fc γ R binding. The primary cells for mediating ADCC, NK cells, express Fc γ RIII only, whereas monocytes express Fc γ RI, Fc γ RII and Fc γ RIII. FcR expression on hematopoietic cells is summarized in Ravetch and Kinet, *Ann. Rev. Immunol.*, 1991, 9:457-492.

[0323] Non-limiting examples of in vitro assays to assess ADCC activity of a molecule of interest are provided in U.S. Pat. Nos. 5,500,362 and 5,821,337; Hellstrom et al., *Proc.*

Natl. Acad. Sci. U.S.A., 1986, 83:7059-7063; Hellstrom et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1985, 82:1499-1502; and Bruggemann et al., *J. Exp. Med.*, 1987, 166:1351-1361. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed in vivo, using an animal model such as that disclosed in Clynes et al. *Proc. Natl. Acad. Sci. U.S.A.*, 1998, 95:652-656.

[0324] C1q binding assays may also be carried out to confirm that the antibody is unable to bind C1q and hence lacks CDC activity. Examples of C1q binding assays include those described in WO 2006/029879 and WO 2005/100402.

[0325] Complement activation assays include those described, for example, in Gazzano-Santoro et al., *J. Immunol. Methods*, 1996, 202:163-171; Cragg et al., *Blood*, 2003, 101:1045-1052; and Cragg and Glennie, *Blood*, 2004, 103:2738-2743.

[0326] FcRn binding and in vivo clearance (half-life determination) can also be measured, for example, using the methods described in Petkova et al., *Intl. Immunol.*, 2006, 18:1759-1769.

9. Preparation of Antibodies

9.1. Antigen Preparation

[0327] The CD39 antigen to be used for production of antibodies may be intact CD39 or a fragment of CD39. The intact CD39, or fragment of CD39, may be in the form of an isolated protein or expressed by a cell. Other forms of CD39 useful for generating antibodies will be apparent to those skilled in the art.

9.2. Monoclonal Antibodies

[0328] Monoclonal antibodies may be obtained, for example, using the hybridoma method first described by Kohler et al., *Nature*, 1975, 256:495-497, and/or by recombinant DNA methods (see e.g., U.S. Pat. No. 4,816,567). Monoclonal antibodies may also be obtained, for example, using phage or yeast-based libraries. See e.g., U.S. Pat. Nos. 8,258,082 and 8,691,730.

[0329] In the hybridoma method, a mouse or other appropriate host animal is immunized to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized in vitro. Lymphocytes are then fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell. See Goding J. W., *Monoclonal Antibodies: Principles and Practice* 3rd ed. (1986) Academic Press, San Diego, Calif.

[0330] The hybridoma cells are seeded and grown in a suitable culture medium that contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

[0331] Useful myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive media

conditions, such as the presence or absence of HAT medium. Among these, preferred myeloma cell lines are murine myeloma lines, such as those derived from MOP-21 and MC-11 mouse tumors (available from the Salk Institute Cell Distribution Center, San Diego, Calif.), and SP-2 or X63-Ag8-653 cells (available from the American Type Culture Collection, Rockville, Md.). Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies. See e.g., Kozbor, *J. Immunol.*, 1984, 133:3001.

[0332] After the identification of hybridoma cells that produce antibodies of the desired specificity, affinity, and/or biological activity, selected clones may be subcloned by limiting dilution procedures and grown by standard methods. See Goding, *supra*. Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown in vivo as ascites tumors in an animal.

[0333] DNA encoding the monoclonal antibodies may be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies). Thus, the hybridoma cells can serve as a useful source of DNA encoding antibodies with the desired properties. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as bacteria (e.g., *E. coli*), yeast (e.g., *Saccharomyces* or *Pichia* sp.), COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce antibody, to produce the monoclonal antibodies.

9.3. Humanized Antibodies

[0334] Humanized antibodies may be generated by replacing most, or all, of the structural portions of a monoclonal antibody with corresponding human antibody sequences. Consequently, a hybrid molecule is generated in which only the antigen-specific variable, or CDR, is composed of non-human sequence. Methods to obtain humanized antibodies include those described in, for example, Winter and Milstein, *Nature*, 1991, 349:293-299; Rader et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1998, 95:8910-8915; Steinberger et al., *J. Biol. Chem.*, 2000, 275:36073-36078; Queen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1989, 86:10029-10033; and U.S. Pat. Nos. 5,585,089, 5,693,761, 5,693,762, and 6,180,370.

9.4. Human Antibodies

[0335] Human antibodies can be generated by a variety of techniques known in the art, for example by using transgenic animals (e.g., humanized mice). See, e.g., Jakobovits et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1993, 90:2551; Jakobovits et al., *Nature*, 1993, 362:255-258; Bruggemann et al., *Year in Immuno.*, 1993, 7:33; and U.S. Pat. Nos. 5,591,669, 5,589,369 and 5,545,807. Human antibodies can also be derived from phage-display libraries (see e.g., Hoogenboom et al., *J. Mol. Biol.*, 1991, 227:381-388; Marks et al., *J. Mol. Biol.*, 1991, 222:581-597; and U.S. Pat. Nos. 5,565,332 and 5,573,905). Human antibodies may also be generated by in vitro activated B cells (see e.g., U.S. Pat. Nos. 5,567,610 and 5,229,275). Human antibodies may also be derived from yeast-based libraries (see e.g., U.S. Pat. No. 8,691,730).

10. Vectors, Host Cells, and Recombinant Methods

[0336] The invention also provides isolated nucleic acids encoding anti-CD39 antibodies, vectors and host cells comprising the nucleic acids, and recombinant techniques for the production of the antibodies.

[0337] For recombinant production of the antibody, the nucleic acid encoding it may be isolated and inserted into a replicable vector for further cloning (i.e., amplification of the DNA) or expression. In some aspects, the nucleic acid may be produced by homologous recombination, for example as described in U.S. Pat. No. 5,204,244.

[0338] Many different vectors are known in the art. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence, for example as described in U.S. Pat. No. 5,534,615.

[0339] Illustrative examples of suitable host cells are provided below. these host cells are not meant to be limiting.

[0340] Suitable host cells include any prokaryotic (e.g., bacterial), lower eukaryotic (e.g., yeast), or higher eukaryotic (e.g., mammalian) cells. Suitable prokaryotes include eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *Escherichia* (*E. coli*), *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella* (*S. typhimurium*), *Serratia* (*S. marcescens*), *Shigella*, *Bacilli* (*B. subtilis* and *B. licheniformis*), *Pseudomonas* (*P. aeruginosa*), and *Streptomyces*. One useful *E. coli* cloning host is *E. coli* 294, although other strains such as *E. coli* B, *E. coli* X1776, and *E. coli* W3110 are suitable.

[0341] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are also suitable cloning or expression hosts for anti-CD39 antibody-encoding vectors. *Saccharomyces cerevisiae*, or common baker's yeast, is a commonly used lower eukaryotic host microorganism. However, a number of other genera, species, and strains are available and useful, such as *Schizosaccharomyces pombe*, *Kluyveromyces* (*K. lactis*, *K. fragilis*, *K. bulgaricus*, *K. wickerhamii*, *K. waltii*, *K. drosophilae*, *K. thermotolerans*, and *K. marxianus*), *Yarrowia*, *Pichia pastoris*, *Candida* (*C. albicans*), *Trichoderma reesii*, *Neurospora crassa*, *Schwannomyces* (*S. occidentalis*), and filamentous fungi such as, for example *Penicillium*, *Tolypocladium*, and *Aspergillus* (*A. nidulans* and *A. niger*).

[0342] Useful mammalian host cells include COS-7 cells, HEK293 cells; baby hamster kidney (BHK) cells; Chinese hamster ovary (CHO); mouse sertoli cells; African green monkey kidney cells (VERO-76), and the like.

[0343] The host cells used to produce the anti-CD39 antibody of this invention may be cultured in a variety of media. Commercially available media such as, for example, Ham's F10, Minimal Essential Medium (MEM), RPMI-1640, and Dulbecco's Modified Eagle's Medium (DMEM) are suitable for culturing the host cells. In addition, any of the media described in Ham et al., *Meth. Enz.*, 1979, 58:44; Barnes et al., *Anal. Biochem.*, 1980, 102:255; and U.S. Pat. Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, and 5,122,469, or WO 90/03430 and WO 87/00195 may be used.

[0344] Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics, trace elements (defined as inorganic

compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art.

[0345] The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[0346] When using recombinant techniques, the antibody can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, is removed, for example, by centrifugation or ultrafiltration. For example, Carter et al. (*Bio/Technology*, 1992, 10:163-167) describes a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 minutes. Cell debris can be removed by centrifugation.

[0347] In some embodiments, the antibody is produced in a cell-free system. In some aspects, the cell-free system is an in vitro transcription and translation system as described in Yin et al., *mAbs*, 2012, 4:217-225, incorporated by reference in its entirety. In some aspects, the cell-free system utilizes a cell-free extract from a eukaryotic cell or from a prokaryotic cell. In some aspects, the prokaryotic cell is *E. coli*. Cell-free expression of the antibody may be useful, for example, where the antibody accumulates in a cell as an insoluble aggregate, or where yields from periplasmic expression are low.

[0348] Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon® or Millipore® Pellicon® ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

[0349] The antibody composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being a particularly useful purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the antibody. Protein A can be used to purify antibodies that are based on human $\gamma 1$, $\gamma 2$, or $\gamma 4$ heavy chains (Lindmark et al., *J. Immunol. Meth.*, 1983, 62:1-13). Protein G is useful for all mouse isotypes and for human $\gamma 3$ (Guss et al., *EMBO J.*, 1986, 5:1567-1575).

[0350] The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody comprises a C_{H3} domain, the BakerBond ABX® resin is useful for purification.

[0351] Other techniques for protein purification, such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin Sepharos®, chromatofocusing,

SDS-PAGE, and ammonium sulfate precipitation are also available, and can be applied by one of skill in the art.

[0352] Following any preliminary purification step(s), the mixture comprising the antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5 to about 4.5, generally performed at low salt concentrations (e.g., from about 0 to about 0.25 M salt).

11. Pharmaceutical Compositions and Methods of Administration

[0353] Any of the antibodies provided herein can be provided in any appropriate pharmaceutical composition and be administered by any suitable route of administration. Suitable routes of administration include, but are not limited to, the inhalation, intraarterial, intradermal, intramuscular, intraperitoneal, intravenous, nasal, parenteral, pulmonary, and subcutaneous routes.

[0354] The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the *Handbook of Pharmaceutical Excipients*, Rowe et al. (Eds.) 6th Ed. (2009), incorporated by reference in its entirety.

[0355] In some embodiments, the pharmaceutical composition comprises an anti-foaming agent. Any suitable anti-foaming agent may be used. In some aspects, the anti-foaming agent is selected from an alcohol, an ether, an oil, a wax, a silicone, a surfactant, and combinations thereof. In some aspects, the anti-foaming agent is selected from a mineral oil, a vegetable oil, ethylene bis stearamide, a paraffin wax, an ester wax, a fatty alcohol wax, a long chain fatty alcohol, a fatty acid soap, a fatty acid ester, a silicon glycol, a fluorosilicone, a polyethylene glycol-polypropylene glycol copolymer, polydimethylsiloxane-silicon dioxide, ether, octyl alcohol, capryl alcohol, sorbitan trioleate, ethyl alcohol, 2-ethyl-hexanol, dimethicone, oleyl alcohol, simethicone, and combinations thereof.

[0356] In some embodiments, the pharmaceutical composition comprises a cosolvent. Illustrative examples of cosolvents include ethanol, poly(ethylene) glycol, butylene glycol, dimethylacetamide, glycerin, and propylene glycol.

[0357] In some embodiments, the pharmaceutical composition comprises a buffer. Illustrative examples of buffers include acetate, borate, carbonate, lactate, malate, phosphate, citrate, hydroxide, diethanolamine, monoethanolamine, glycine, methionine, guar gum, and monosodium glutamate.

[0358] In some embodiments, the pharmaceutical composition comprises a carrier or filler. Illustrative examples of carriers or fillers include lactose, maltodextrin, mannitol, sorbitol, chitosan, stearic acid, xanthan gum, and guar gum.

[0359] In some embodiments, the pharmaceutical composition comprises a surfactant. Illustrative examples of surfactants include d-alpha tocopherol, benzalkonium chloride, benzethonium chloride, cetrimide, cetylpyridinium chloride, docusate sodium, glyceryl behenate, glyceryl monooleate, lauric acid, macrogol 15 hydroxystearate, myristyl alcohol, phospholipids, polyoxyethylene alkyl ethers, polyoxyethylene sorbitan fatty acid esters, polyoxyethylene stearates,

polyoxylglycerides, sodium lauryl sulfate, sorbitan esters, and vitamin E polyethylene(glycol) succinate.

[0360] In some embodiments, the pharmaceutical composition comprises an anti-caking agent. Illustrative examples of anti-caking agents include calcium phosphate (tribasic), hydroxymethyl cellulose, hydroxypropyl cellulose, and magnesium oxide.

[0361] Other excipients that may be used with the pharmaceutical compositions include, for example, albumin, antioxidants, antibacterial agents, antifungal agents, bioabsorbable polymers, chelating agents, controlled release agents, diluents, dispersing agents, dissolution enhancers, emulsifying agents, gelling agents, ointment bases, penetration enhancers, preservatives, solubilizing agents, solvents, stabilizing agents, and sugars. Specific examples of each of these agents are described, for example, in the *Handbook of Pharmaceutical Excipients*, Rowe et al. (Eds.) 6th Ed. (2009), The Pharmaceutical Press, incorporated by reference in its entirety.

[0362] In some embodiments, the pharmaceutical composition comprises a solvent. In some aspects, the solvent is saline solution, such as a sterile isotonic saline solution or dextrose solution. In some aspects, the solvent is water for injection.

[0363] In some embodiments, the pharmaceutical compositions are in a particulate form, such as a microparticle or a nanoparticle. Microparticles and nanoparticles may be formed from any suitable material, such as a polymer or a lipid. In some aspects, the microparticles or nanoparticles are micelles, liposomes, or polymersomes. In certain embodiments, a composition provided herein is a pharmaceutical composition or a single unit dosage form. Pharmaceutical compositions and single unit dosage forms provided herein comprise a prophylactically or therapeutically effective amount of one or more prophylactic or therapeutic antibodies.

[0364] Further encompassed herein are anhydrous pharmaceutical compositions and dosage forms comprising an antibody, since water can facilitate the degradation of some antibodies.

[0365] Anhydrous pharmaceutical compositions and dosage forms provided herein can be prepared using anhydrous or low moisture containing ingredients and low moisture or low humidity conditions. Pharmaceutical compositions and dosage forms that comprise lactose and at least one active ingredient that comprises a primary or secondary amine can be anhydrous if substantial contact with moisture and/or humidity during manufacturing, packaging, and/or storage is expected.

[0366] An anhydrous pharmaceutical composition should be prepared and stored such that its anhydrous nature is maintained. Accordingly, anhydrous compositions can be packaged using materials known to prevent exposure to water such that they can be included in suitable formulary kits. Examples of suitable packaging include, but are not limited to, hermetically sealed foils, plastics, unit dose containers (e.g., vials), blister packs, and strip packs.

11.1. Parenteral Dosage Forms

[0367] In certain embodiments, provided are parenteral dosage forms. Parenteral dosage forms can be administered to subjects by various routes including, but not limited to, subcutaneous, intravenous (including bolus injection), intramuscular, and intraarterial. Because their administration

typically bypasses subjects' natural defenses against contaminants, parenteral dosage forms are typically, sterile or capable of being sterilized prior to administration to a subject. Examples of parenteral dosage forms include, but are not limited to, solutions ready for injection, dry products ready to be dissolved or suspended in a pharmaceutically acceptable vehicle for injection, suspensions ready for injection, and emulsions.

[0368] Suitable vehicles that can be used to provide parenteral dosage forms are well known to those skilled in the art. Examples include, but are not limited to: Water for Injection USP; aqueous vehicles such as, but not limited to, Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, and Lactated Ringer's Injection; water miscible vehicles such as, but not limited to, ethyl alcohol, polyethylene glycol, and polypropylene glycol; and non-aqueous vehicles such as, but not limited to, corn oil, cottonseed oil, peanut oil, sesame oil, ethyl oleate, isopropyl myristate, and benzyl benzoate.

[0369] Excipients that increase the solubility of one or more of the antibodies disclosed herein can also be incorporated into the parenteral dosage forms.

11.2. Dosage and Unit Dosage Forms

[0370] In human therapeutics, the doctor will determine the posology which he considers most appropriate according to a preventive or curative treatment and according to the age, weight, condition and other factors specific to the subject to be treated.

[0371] The amount of the antibody or composition which will be effective in the prevention or treatment of a disorder or one or more symptoms thereof will vary with the nature and severity of the disease or condition, and the route by which the antibody is administered. The frequency and dosage will also vary according to factors specific for each subject depending on the specific therapy (e.g., therapeutic or prophylactic agents) administered, the severity of the disorder, disease, or condition, the route of administration, as well as age, body, weight, response, and the past medical history of the subject. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

[0372] In certain embodiments, exemplary doses of a composition include milligram or microgram amounts of the antibody per kilogram of subject or sample weight (e.g., about 10 micrograms per kilogram to about 50 milligrams per kilogram, about 100 micrograms per kilogram to about 25 milligrams per kilogram, or about 100 microgram per kilogram to about 10 milligrams per kilogram). In certain embodiment, the dosage of the antibody provided herein, based on weight of the antibody, administered to prevent, treat, manage, or ameliorate a disorder, or one or more symptoms thereof in a subject is 0.1 mg/kg, 1 mg/kg, 2 mg/kg, 3 mg/kg, 4 mg/kg, 5 mg/kg, 6 mg/kg, 10 mg/kg, or 15 mg/kg or more of a subject's body weight. In another embodiment, the dosage of the composition or a composition provided herein administered to prevent, treat, manage, or ameliorate a disorder, or one or more symptoms thereof in a subject is 0.1 mg to 200 mg, 0.1 mg to 100 mg, 0.1 mg to 50 mg, 0.1 mg to 25 mg, 0.1 mg to 20 mg, 0.1 mg to 15 mg, 0.1 mg to 10 mg, 0.1 mg to 7.5 mg, 0.1 mg to 5 mg, 0.1 to 2.5 mg, 0.25 mg to 20 mg, 0.25 to 15 mg, 0.25 to 12 mg, 0.25 to 10 mg, 0.25 mg to 7.5 mg, 0.25 mg to 5 mg, 0.25 mg to 2.5 mg, 0.5 mg to 20 mg, 0.5 to 15 mg, 0.5 to 12 mg, 0.5

to 10 mg, 0.5 mg to 7.5 mg, 0.5 mg to 5 mg, 0.5 mg to 2.5 mg, 1 mg to 20 mg, 1 mg to 15 mg, 1 mg to 12 mg, 1 mg to 10 mg, 1 mg to 7.5 mg, 1 mg to 5 mg, or 1 mg to 2.5 mg.

[0373] The dose can be administered according to a suitable schedule, for example, once, two times, three times, or for times weekly. It may be necessary to use dosages of the antibody outside the ranges disclosed herein in some cases, as will be apparent to those of ordinary skill in the art. Furthermore, it is noted that the clinician or treating physician will know how and when to interrupt, adjust, or terminate therapy in conjunction with subject response.

[0374] Different therapeutically effective amounts may be applicable for different diseases and conditions, as will be readily known by those of ordinary skill in the art. Similarly, amounts sufficient to prevent, manage, treat or ameliorate such disorders, but insufficient to cause, or sufficient to reduce, adverse effects associated with the antibodies provided herein are also encompassed by the herein described dosage amounts and dose frequency schedules. Further, when a subject is administered multiple dosages of a composition provided herein, not all of the dosages need be the same. For example, the dosage administered to the subject may be increased to improve the prophylactic or therapeutic effect of the composition or it may be decreased to reduce one or more side effects that a particular subject is experiencing.

[0375] In certain embodiments, treatment or prevention can be initiated with one or more loading doses of an antibody or composition provided herein followed by one or more maintenance doses.

[0376] In certain embodiments, a dose of an antibody or composition provided herein can be administered to achieve a steady-state concentration of the antibody in blood or serum of the subject. The steady-state concentration can be determined by measurement according to techniques available to those of skill or can be based on the physical characteristics of the subject such as height, weight and age.

[0377] In certain embodiments, administration of the same composition may be repeated and the administrations may be separated by at least 1 day, 2 days, 3 days, 5 days, 10 days, 15 days, 30 days, 45 days, 2 months, 75 days, 3 months, or 6 months. In other embodiments, administration of the same prophylactic or therapeutic agent may be repeated and the administration may be separated by at least 1 day, 2 days, 3 days, 5 days, 10 days, 15 days, 30 days, 45 days, 2 months, 75 days, 3 months, or 6 months.

12. Therapeutic Applications

[0378] For therapeutic applications, the antibodies of the invention are administered to a mammal, generally a human, in a pharmaceutically acceptable dosage form such as those known in the art and those discussed above. For example, the antibodies of the invention may be administered to a human intravenously as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intra-cerebrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, or intratumoral routes. The antibodies also are suitably administered by peritumoral, intralesional, or perilesional routes, to exert local as well as systemic therapeutic effects. The intraperitoneal route may be particularly useful, for example, in the treatment of ovarian tumors.

[0379] The antibodies provided herein may be useful for the treatment of any disease or condition involving CD39, such as cancer, autoimmune disease, and infection.

[0380] Any suitable cancer may be treated with the antibodies provided herein. Illustrative suitable cancers include, for example, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, anal cancer, appendix cancer, astrocytoma, basal cell carcinoma, brain tumor, bile duct cancer, bladder cancer, bone cancer, breast cancer, bronchial tumor, Burkitt Lymphoma, carcinoma of unknown primary origin, cardiac tumor, cervical cancer, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasm, colon cancer, colorectal cancer, craniopharyngioma, cutaneous T-cell lymphoma, ductal carcinoma, embryonal tumor, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, fibrous histiocytoma, Ewing sarcoma, eye cancer, germ cell tumor, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumor, gestational trophoblastic disease, glioma, head and neck cancer, hairy cell leukemia, hepatocellular cancer, histiocytosis, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumor, Kaposi sarcoma, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lobular carcinoma in situ, lung cancer, lymphoma, macroglobulinemia, malignant fibrous histiocytoma, melanoma, Merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer with occult primary, midline tract carcinoma involving NUT gene, mouth cancer, multiple endocrine neoplasia syndrome, multiple myeloma, mycosis fungoides, myelodysplastic syndrome, myelodysplastic/myeloproliferative neoplasm, nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oropharyngeal cancer, osteosarcoma, ovarian cancer, pancreatic cancer, papillomatosis, paraganglioma, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytomas, pituitary tumor, pleuropulmonary blastoma, primary central nervous system lymphoma, prostate cancer, rectal cancer, renal cell cancer, renal pelvis and ureter cancer, retinoblastoma, rhabdoid tumor, salivary gland cancer, Sezary syndrome, skin cancer, small cell lung cancer, small intestine cancer, soft tissue sarcoma, spinal cord tumor, stomach cancer, T-cell lymphoma, teratoid tumor, testicular cancer, throat cancer, thymoma and thymic carcinoma, thyroid cancer, urethral cancer, uterine cancer, vaginal cancer, vulvar cancer, and Wilms tumor.

[0381] Any suitable autoimmune disease may be treated with the antibodies provided herein. Illustrative suitable autoimmune diseases, or diseases with an autoimmune component, include, for example, acute disseminated encephalomyelitis (ADEM), acute necrotizing hemorrhagic leukoencephalitis, Addison's disease, agammaglobulinemia, alopecia areata, amyloidosis, ankylosing spondylitis, anti-GBM/anti-TBM nephritis, antiphospholipid syndrome (APS), autoimmune angioedema, autoimmune aplastic anemia, autoimmune dysautonomia, autoimmune hepatitis, autoimmune hyperlipidemia, autoimmune immunodeficiency, autoimmune inner ear disease (AIED), autoimmune myocarditis, autoimmune oophoritis, autoimmune pancreatitis, autoimmune retinopathy, autoimmune thrombocytopenic purpura (ATP), autoimmune thyroid disease, autoimmune urticarial, axonal & neuronal neuropathies, Balo disease, Behcet's disease, bullous pemphigoid, cardiomyopathy, Castleman disease, Celiac disease, Chagas disease, chronic fatigue syndrome, chronic inflammatory demyeli-

nating polyneuropathy (CIDP), chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss syndrome, cicatricial pemphigoid/benign mucosal pemphigoid, Crohn's disease, Cogans syndrome, cold agglutinin disease, colitis, congenital heart block, coxsackie myocarditis, CREST disease, essential mixed cryoglobulinemia, demyelinating neuropathies, dermatitis herpetiformis, dermatomyositis, Devic's disease (neuromyelitis optica), discoid lupus, Dressler's syndrome, endometriosis, eosinophilic esophagitis, eosinophilic fasciitis, erythema nodosum, experimental allergic encephalomyelitis, Evans syndrome, fibromyalgia, fibrosing alveolitis, giant cell arteritis (temporal arteritis), giant cell myocarditis, glomerulonephritis, Goodpasture's syndrome, granulomatosis with polyangiitis (GPA) (formerly called Wegener's Granulomatosis), Graves' disease, Guillain-Barre syndrome, Hashimoto's encephalitis, Hashimoto's thyroiditis, hemolytic anemia, Henoch-Schönlein purpura, herpes gestationis, hypogammaglobulinemia, idiopathic thrombocytopenic purpura (ITP), IgA nephropathy, IgG4-related sclerosing disease, immunoregulatory lipoproteins, inclusion body myositis, inflammatory bowel disease, interstitial cystitis, juvenile arthritis, juvenile diabetes (Type 1 diabetes), juvenile myositis, Kawasaki syndrome, Lambert-Eaton syndrome, leukocytoclastic vasculitis, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA disease (LAD), lupus (SLE), Lyme disease (chronic), Meniere's disease, microscopic polyangiitis, mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-Habermann disease, multiple sclerosis, myasthenia gravis, myositis, narcolepsy, neuromyelitis optica (Devic's), neutropenia, ocular cicatricial pemphigoid, optic neuritis, palindromic rheumatism, PANDAS (Pediatric Autoimmune Neuropsychiatric Disorders Associated with *Streptococcus*), paraneoplastic cerebellar degeneration, paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, Parsonnage-Turner syndrome, pars planitis (peripheral uveitis), pemphigus, peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia, POEMS syndrome, polyarteritis nodosa, type I, II, & III autoimmune polyglandular syndromes, polymyalgia rheumatic, polymyositis, postmyocardial infarction syndrome, postpericardiotomy syndrome, progesterone dermatitis, primary biliary cirrhosis, primary sclerosing cholangitis, psoriasis, psoriatic arthritis, idiopathic pulmonary fibrosis, pyoderma gangrenosum, pure red cell aplasia, Raynaud's phenomenon, reactive arthritis, reflex sympathetic dystrophy, Reiter's syndrome, relapsing polychondritis, restless legs syndrome, retroperitoneal fibrosis, rheumatic fever, rheumatoid arthritis, sarcoidosis, Schmidt syndrome, scleritis, scleroderma, Sjogren's syndrome, sperm & testicular autoimmunity, stiff person syndrome, subacute bacterial endocarditis (SBE), Susac's syndrome, sympathetic ophthalmia, Takayasu's arteritis, temporal arteritis/giant cell arteritis, thrombotic disease, thrombocytopenic purpura (TTP), Tolosa-Hunt syndrome, transverse myelitis, type 1 diabetes, ulcerative colitis, undifferentiated connective tissue disease (UCTD), uveitis, vasculitis, vesiculobullous dermatosis, vitiligo, and Wegener's granulomatosis (now termed Granulomatosis with Polyangiitis (GPA)).

[0382] Any suitable infection may be treated with the antibodies provided herein. Illustrative suitable infections include, for example, hepatitis A virus, hepatitis B virus, hepatitis C virus (HCV), human immunodeficiency virus (HIV), and other viral infections.

13. Diagnostic Applications

[0383] In some embodiments, the antibodies provided herein are used in diagnostic applications. For example, an anti-CD39 antibody may be useful in assays for CD39 protein. In some aspects, the antibody can be used to detect the expression of CD39 in various cells and tissues. These assays may be useful, for example, evaluating cancer and autoimmune disease.

[0384] In some diagnostic applications, the antibody may be labeled with a detectable moiety. Suitable detectable moieties include, but are not limited to radioisotopes, fluorescent labels, and enzyme-substrate labels. In another embodiment of the invention, the anti-CD39 antibody need not be labeled, and the presence thereof can be detected using a labeled antibody which specifically binds to the anti-CD39 antibody.

14. Affinity Purification Reagents

[0385] The antibodies of the invention may be used as affinity purification agents. In this process, the antibodies may be immobilized on a solid phase such as a resin or filter paper, using methods well known in the art. The immobilized antibody is contacted with a sample containing the CD39 protein (or fragment thereof) to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the CD39 protein, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent, such as glycine buffer, pH 5.0, that will release the CD39 protein from the antibody.

15. Kits

[0386] In some embodiments, an anti-CD39 antibody provided herein is provided in the form of a kit, i.e., a packaged combination of reagents in predetermined amounts with instructions for performing a procedure. In some embodiments, the procedure is a diagnostic assay. In other embodiments, the procedure is a therapeutic procedure.

[0387] In some embodiments, the kit further comprises a solvent for the reconstitution of the anti-CD39 antibody. In some embodiments, the anti-CD39 antibody is provided in the form of a pharmaceutical composition.

EXAMPLES

Example 1: Selection of CD39 Antigen-Binding Proteins

[0388] CD39 ABPs were selected from a synthetic library of human antibodies presented on the surface of yeast cells in IgG format, as generally described, e.g., in WO2009036379; WO2010105256; WO2012009568; and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670 (each incorporated by reference in its entirety), and more specifically as provided below. The sequences and characteristics of the ABPs isolated from the recombinant library are provided in Table S.

[0389] Eight naïve human synthetic yeast libraries each of $\sim 10^9$ diversity were propagated as described in WO2009036379; WO2010105256; WO2012009568; and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670; each incorporated by reference in its entirety. For the first two rounds of selection, a magnetic bead sorting technique utilizing the Miltenyi MACS® system was performed, as

described in Siegel et al., J. Immunol. Meth., 2004, 286: 141-153. The following rounds of selection were performed using flow cytometry based sorting. For all round of selection, the antigen was biotinylated human CD39 extracellular domain (hereinafter “ECD”), and decreasing concentrations of antigen were used in each subsequent round of selection. In addition to selection on antigen, some rounds of selection were employed in order to reduce the number of non-specific binders utilizing soluble membrane proteins from CHO cells (see WO2014179363 and Xu et al., Protein Eng. Des. Sel., 2013, 26:663-670, each incorporated by reference in its entirety). After the final round of sorting, yeast were plated and individual colonies were picked for characterization and for nomination of clones for affinity maturation.

[0390] Antibody variable domains of interest were synthesized, with codon optimization to maximize transient expression in host cells. The variable regions were cloned in to expression vectors containing human immunoglobulin constant domains and their sequence confirmed. Antibody heavy and light chain vector pairings were transfected into Expi293 cells using the Expifectamine system (Invitrogen). Transient cultures were harvested on day 4 and clarified cell culture supernatant IgG titer was estimated using Bio-Layer Interferometry (BLI) using Octet (ForteBio) alongside standards. Antibodies were subsequently purified on a Protein A column and eluted using low pH glycine. Purified antibody samples were then buffer-exchanged or dialyzed into downstream assay-compatible buffers.

[0391] Antibody purity was assessed by running samples on SDS-PAGE and on an analytical size exclusion chromatography column.

[0392] Light Chain Shuffling: Heavy chain plasmids were extracted from naïve outputs (described herein) and transformed into a pre-made naïve light chain library with a diversity of 10^6 . Selections were performed as described above with one round of MACS sorting and three rounds of FACS sorting using decreasing amounts of biotinylated ECD antigen for respective rounds. Selected individual heavy chains from the primary discovery process were also independently transformed into separate pre-made light chain libraries with a diversity of 10^6 and selections performed as described above with one round of MACS sorting and three rounds of FACS sorting using decreasing amount of biotinylated ECD antigen for respective rounds.

Example 2: Affinity Maturation

[0393] Optimization of naïve clones was carried out utilizing three maturation strategies; diversification of CDR-H1 and CDR-H2; diversification of CDR-H3; diversification of CDR-L1, L2 and L3; shuffling of diversified heavy and light chains.

[0394] CDR-H1 and CDR-H2 Selection: The CDR-H3s from clones selected from each of the light chain batch diversification, light chain diversification, and naïve discovery efforts were independently recombined into premade libraries with CDR-H1 and CDR-H2 variants of a diversity of $>10^8$ and selections were performed using ECD antigen. Affinity pressures were applied by using decreasing concentrations of antigen.

[0395] CDR-H3 Selection: Clones obtained from the CDR-H1 and CDR-H2 selection procedure were subject to additional rounds of affinity maturation via walking dimer mutagenesis of the heavy chain. Selections were performed

using ECD as antigen generally as described above but with the addition of employing FACS sorting for all selection rounds.

[0396] CDR-L1, L2, L3 Selection: Clones obtained from the CDR-H1 and CDR-H2 selection procedure were subject to additional rounds of affinity maturation via mutagenesis of the light chain. The CDR-L1 and CDR-L2 diversity derived from a pre-made library while CDR-L3 diversity derived from walking dimer mutagenesis. Selections were performed using ECD as antigen generally as described above but with the addition of employing FACS sorting for all selection rounds, with one round of MACS followed by three rounds of FACS in the CDR-L1, L2, L3 process described here.

[0397] Diversified Heavy Chain and Light Chain Shuffling: Outputs from heavy chain diversification and light diversification described above were recombined and selections were performed using ECD as antigen generally as described above but with the addition of employing FACS sorting for all selection rounds.

Example 3: Monovalent Affinity of Anti-hCD39 Antibodies to Recombinant CD39 Extracellular Domain

[0398] Binding kinetics were measured using the Octet Red96 system (ForteBio) at 25° C. in running buffer (1× Pall ForteBio Kinetics Buffer diluted into PBS or Tris pH 7.4). In brief, 1.25 mg/ml of unlabeled anti-hCD39 antibodies were immobilized onto anti-human Fc sensors. After a short baseline step in running buffer, the sensors were exposed to varying concentrations (10-300 nM) of rhCD39-ECD-His (R&D Systems) for the association step. Dissociation of the complex was monitored upon exposure of the sensors to running buffer once again. Data was processed using ForteBio Octet software with baseline subtraction, global fit and 1:1 binding model to obtain association and dissociation rates. K_D was calculated from the ratio of k_d to k_a .

[0399] Data shown in FIG. 1 had $R^2 > 0.980$. PF=poor fit. The association and dissociation time course data was globally fit with a simple 1:1 Langmuir binding model to yield on-rate (k_{on}) and off-rate (k_{off}) values. The equilibrium dissociation constants (K_D) were calculated from the k_{on} and k_{off} values. The k_{on} values ranged from $1.93E+04$ to $1.72E+06 \text{ M}^{-1}\text{s}^{-1}$ and the off rate values ranged from $3.65E-01$ to $1.11E-04 \text{ s}^{-1}$. The K_D values ranged from $4.09E-07$ to $7.31E-011$ molar indicating that all of the antibodies bound with moderate or high affinity to human CD39 ECD.

[0400] The paralog specificity of the anti-CD39 antibodies was assessed by biolayer interferometry using soluble recombinant human ENTDP2 and soluble recombinant human ENTDP3 (both from R&D Systems). ENTDP2 and ENTDP3 are enzymes with functions similar to CD39. None of the antibodies exhibited detectable binding to ENTDP2 or ENTDP3 (data not shown). Thus all of the antibodies exhibit specific binding to human CD39.

Example 4: Inhibition of Recombinant Human CD39 Extracellular Domain

[0401] The inhibition of recombinant human CD39 ECD by anti-CD39 antibodies was measured as follows. Recombinant human CD39/ENTDP1 (4397-EN from R&D systems), (either 5 or 10 nM final concentration) was combined

with anti-CD39 IgGs (0.25 or 1 micromolar final concentration) in 25 mM Tris, 5 mM CaCl_2 , pH 7.5 in a 96-well plate and incubated at room temperature for 2 hrs. ATP (Sigma A1852-1VL) was then added to a final concentration of 500 micromolar and incubated at 37° C. for 60 minutes. The plate was then placed at room temperature and CellTiter-Glo Luminescent Cell Viability Assay solution was added to each well of the assay plate, mixed and read on a microplate reader using “CellTiter-Glo luminescent” preset. Control reactions consisting of negative control IgG, IgG only (no ATP), ATP only (no CD39) were run using the same method. Data values are the average of 2 replicates.

[0402] Inhibition of human CD39 ECD enzymatic activity by anti-CD39 antibodies was determined by measuring ATP levels using the CellTiter-Glo assay (FIGS. 2 A-E). The enzymatic catabolism of ATP by CD39 ECD was observed in the presence of an isotype control antibody or no IgG with average RLU values ranging from 38 to 857. All of the anti-CD39 antibodies showed marked inhibition ATP catabolism by CD39, having much higher average RLU values than the isotype control antibody (average RLU values range from 4890 to 20329). In contrast, Benchmark antibody BY40va did not show significant inhibition of CC39 ECD in this assay having RLU values similar to the isotype control antibody (average RLU values 11 and 415).

Example 5: Antibodies Bind to CHO Cells Expressing Human and Cyno CD39

[0403] Binding of anti-CD39 IgGs to Chinese Hamster Ovary K1 (CHO) CD39 cells. 100 nanomolar IgGs (each antibody is indicated as a unique clone number in the FIG.) were incubated at 25° C. for 30 minutes on ice in phosphate buffered saline (PBS) with parental CHO cells or CHO cells engineered to express either human or cynomolgus macaque (*Macaca fascicularis*) CD39 (CHO CD39 cells). Cells were then washed with ice cold PBS and incubated with a fluorescently labeled goat-anti-human IgG for 20 minutes on ice. Cells were washed and resuspended in ice cold PBS prior to analysis by flow cytometry. Fold over background binding levels represent the ratio of median fluorescence intensity (MFI) values for anti-CD39 antibodies binding to CHO CD39 to MFI values for anti-CD39 antibodies binding to the parental CHO cells.

[0404] The anti-CD39 antibodies bound to CHO cells expressing cellular human CD39 (CHO CD39 cells) and did not exhibit significant binding to parental CHO cells (FIGS. 2F-J). The binding of these antibodies to CHO CD39 cells ranged from 10 to 2033-fold over background. Antibodies 28337 and 27575 did not show significant binding to CHO CD39 cells (only 2 to 4-fold over background) (FIGS. 2F-J) indicating that these antibodies do not have low affinity for the cellular form of human CD39.

[0405] The ortholog specificity of the anti-CD39 antibodies was assessed with flow cytometry using CHO cells engineered to express either cynomolgus macaque or mouse CD39. The anti-CD39 antibodies bound to cynomolgus macaque CD39 to a similar extent as human CD39 (FIGS. 2 F-J). None of the anti-CD39 antibodies showed detectable binding to mouse CD39. Thus, the anti-CD39 antibodies are cross reactive to cynomolgus macaque CD39 but not to mouse CD39.

Example 6: Binding of Antibodies to Cell Surface
CD39 in MEL-28 or 721 Cells and Antibodies that
Inhibit CD39 on MEL-28 Cells a Short Term
ATPase Assay

[0406] Cells were incubated with serially diluted anti-CD39 antibodies for 30 minutes at 4 degrees C. Cells were washed 3 times in FACS buffer (PS, 2% FBS, and 2 mM EDTA) and next incubated with secondary antibody (goat anti-human IgG Southern Biotech) at 1:100 for 30 minutes at 4 degrees C. Cells were washed, resuspended in FACS buffer, and analyzed for binding by flow cytometry analysis on BD Celesta.

[0407] 3.5×10^4 MEL-28 cells/well were washed with Tris buffer and incubated with serially diluted (100-0.00013 nM) antibody for 30 minutes at 37 degrees C. 50 μ M ATP was added to each well and incubated with cells for 15 minutes. The supernatants were collected and analyzed in Malachite Green Assay (R&D) according to manufacturer's protocol. Phosphate released from CD39 processing of ATP was used as a readout of enzyme activity. Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar), non-specific small molecule inhibitors of CD39, were used as positive controls at 100 μ M.

[0408] All antibodies bound to endogenously expressed CD39 on both cell lines with similar affinity with EC50 ranges from 0.05-0.28 μ g/ml on MEL-28 (see FIG. 3 A) and with EC50 ranges of 0.2-7.5 μ g/ml on 721.22 cell line (see FIG. 3B). Maximum signal (MFI) differed between antibodies tested even when EC50 values were similar (FIGS. 3A-B).

[0409] After confirmation of cellular binding, anti-CD39 antibodies were evaluated for inhibition of ATPase activity on MEL-28 cell in short term 30 minute Malachite Green phosphate readout assay. Isotype control was used to establish maximum possible signal from ATP processing in MEL-28 cells-50 μ M ATP addition to cells typically resulted in 55-60 μ M phosphate signal in this assay (see FIGS. 4 A-B). Anti-CD39 antibodies inhibited ATPase activity in MEL-28 cells by 60-80% at the highest concentration of antibodies tested (100 nM)—this level of inhibition was similar to non-specific ATPase inhibitors ARL and POM1 (see FIG. 4 A). IC50 values for anti-CD39 antibodies in MEL-28 malachite green assay were all in sub-nanomolar range (see FIG. 4 B).

Example 7: ATP Preservation Quantified when
MEL-28 Cells are Treated with CD39 Enzymatic
Inhibitors

[0410] 3.5×10^4 MEL-28 cells were plated overnight at 37 degrees C. Cells were washed with Tris assay buffer to remove phosphate. 100 nM titrated down to 0.005 pM of monoclonal antibodies were incubated with cells for 30 minutes at 37 degrees C. 50 μ M ATP was added and incubated for 15 minutes. Supernates were harvested and frozen. Supernates were thawed and evaluated for ATP using the EnzyLight (EnzyLight ATP Assay Kit, BioAssay Systems). Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar) used at a concentration of 100 μ M are non-specific small molecule inhibitors of CD39 as positive controls.

[0411] ATP was almost undetectable after 30 minutes post ATP addition to the cells in untreated and/or isotype treated samples (see FIG. 5 A) while all of the anti-CD39 antibodies

tested prevented processing of ATP in dose dependent manner (see FIGS. 5 A-B). Most of the anti-CD39 antibodies tested in this assay prevented ATP processing by CD39 to a similar extent as ARL (see FIG. 5 A). IC50s of anti-CD39 antibodies in ATP preservation assay ranged from 0.02-0.1 nM. Overall potency of antibodies in this assay was consistent with what was observed in Malachite Green phosphate readout assay.

Example 8: Antibodies Inhibit CD39 Activity on
MEL-28 in an Overnight Assay

[0412] 3.5×10^4 MEL-28 cells/well were plated and incubated with antibodies overnight at 37 degrees C. Cells were washed to remove FBS. Cells next were pre-treated with antibodies in X-VIVO 15 FBS free media overnight at 37 degrees C. ATP was then spiked in at 50 μ M for 15 minutes. Supernatants were collected and analyzed using AMP-Glo kit according to manufacturer's instructions (Promega). Palivizumab was used as an isotype control and POM-1 (Alpha Aesar), a non-specific small molecule inhibitor of CD39, was used as positive control at 100 μ M.

[0413] Anti-CD39 antibodies tested in overnight AMPGlo assay in MEL-28 cells demonstrated sustained inhibition of ATPase activity as indicated by decreased AMP levels present in the supernatants (see FIG. 6 A). Inhibition of CD39 activity by antibodies was equivalent to or more potent compared to POM-1 treatment. The data is consistent with results obtained in CD39 short-term Malachite Green assay in MEL-28 (see FIG. 4). Antibodies tested in an overnight assay had IC50 values in an AMPGlo CD39 inhibition assay ranging from 0.01 to 0.3 nM. (see FIG. 6 B)

Example 9: Anti-CD 39 Antibodies Bind to
Primary Human and Cyno B Cells

[0414] B cells were isolated from human donor leukopak using EasySep B cell isolation kit (STEMCELL Technologies). Cyno monocytes were purified from fresh cyno blood using NHP CD14 positive selection kit (Miltenyi) and flow through was collected and stained with CD4, CD8, CD20, CD16, and CD3 antibodies (BD). Human B cells or cyno cells were incubated with serially diluted anti-CD39 antibodies (15 μ g/ml 7.5 fold serial dilution, 8-point) for 30 minutes at 4 degrees C. Cell were washed 3 times in FACS buffer (PS, 2% FBS, and 2 mM EDTA) and incubated with secondary antibody (mouse anti-human IgG southern biotech) at 1:100 for 30 minutes at 4 degrees C. Cells were washed 2 times in FACS buffer and resuspended in FACS buffer and analyzed on BD Celesta.

[0415] Detection of antibody binding is as described in FIGS. 7 A-B where B cells were incubated with serially diluted antibodies and detected using a fluorescently tagged antibody and analyzed by flow cytometry. The results are shown in FIGS. 7 A-B and appear to indicate that the antibodies bind specifically to both human and cyno B cells with EC50s that range from 0.02 μ g/ml to 3.18 μ g/ml (human) and 0.03 μ g/ml to 0.17 μ g/ml (cyno). Similar binding was observed on human tumor cells lines (FIG. 3) where subset of the antibodies had a low maximal MFI and a subset had a high MFI to both the human and cyno B cells.

Example 10: Antibodies Inhibit CD39 Activity on
Human B Cells

[0416] B cells were isolated from human leukopak using EasySep B cell isolation kit (STEMCELL Technologies).

5×10^4 B cells/well were washed with Tris buffer and incubated with serially diluted (100-0.00013 nM) antibodies for 30 minutes at 37 degrees C. 50 μ M ATP was added to each well and incubated with cells for 2 hrs. The supernatants were collected and analyzed in Malachite Green Assay (R&D) according to manufacturer's protocol. Phosphate released from CD39 processing of ATP was used as a readout of enzyme activity. Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar), non-specific small molecule inhibitors of CD39, were used as positive controls at 100 μ M.

[0417] The antibodies were demonstrated to bind to primary human and cyno B cells (see FIGS. 7 A-B) and the next step was to evaluate the inhibition of ATP hydrolysis by detection of free phosphate (Pi) using a malachite green assay. The results are shown in FIG. 8 and indicate the anti-CD39 antibodies inhibit the enzymatic inhibition/dephosphorylation of ATP by primary human B cells. The ability of the antibodies to inhibit enzymatic activity was comparable regardless of high vs. low max MFI detected in the binding to human B cells (FIGS. 7 A-B).

Example 11: Anti-CD39 Antibodies Inhibit ATPase Activity on Human and Cyno Monocytes

[0418] Human monocytes were purified from leukopak using EasySep Human monocytes isolation kit (STEMCELL). Cyno monocytes were isolated from whole cyno blood using NHP CD14 positive selection kit (Miltenyi). Monocytes at 5×10^4 cells/well were washed with Tris buffer and incubated with serially diluted (100-0.00013 nM) anti-CD39 antibodies for 30 minutes at 37 C. 50 μ M ATP was added to the cells for 15 minutes at 37 C and supernatants were harvested and analyzed in Malachite Green Assay (R&D) for phosphate levels. Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar), non-specific small molecule inhibitors of CD39, were used as positive controls at 100 μ M.

[0419] CD39 expression has been detected on human leukocytes with the highest expression detected on monocytes (Thromb Res. 2007; 121(3):309-17). Because of this information, it was important to evaluate the ability of the anti-CD39 antibodies to inhibit ATPase activity on the cell surface. As demonstrated in FIGS. 7 A-B, anti-CD39 antibodies bind to both human and cyno B cells. It is appropriate to evaluate the inhibition of enzymatic activity on human and cyno monocytes. The results indicate that all the antibodies are able to inhibit ATPase activity of CD39 on human and cyno monocytes with similar potencies.

Example 12: Anti-CD39 Antibodies Bind to Primary Human TRegs and Inhibit CD39 Enzymatic Activity

[0420] Treg cells were isolated from human donor leukopak using CD4⁺CD25⁺CD127^{dim} regulatory T cell isolation kit II (Miltenyi). Human Treg cells were incubated with serially diluted anti-CD39 antibodies (100 nM-0.00064 nM) for 30 minutes at 4 degrees C. Cells were washed 3 times in FACS buffer (PS, 2% FBS, and 2 mM EDTA) and incubated with secondary antibody (mouse anti-human IgG southern biotech) at 1:100 for 30 minutes at 4 degrees C. Cells were washed 2 times in FACS buffer, resuspended in FACS buffer and analyzed on BD Fortessa.

[0421] CD4⁺CD25⁺CD127^{dim} human Treg cells were washed 3 $\times$ with Tris buffer. Cells were incubated with anti-CD39 antibodies (100 nM-0.00064 nM) for 30 minutes at 37 C. The cells were spiked with 50 μ M ATP and supernatants were collected after 15 minutes incubation at 37 C. Supernatants were analyzed for phosphate levels in Malachite Green Assay kit (R&D). Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar), non-specific small molecule inhibitors of CD39, were used as positive controls at 100 μ M.

[0422] CD39 had been shown to be expressed on human regulatory T cells (Treg) and important for their suppressive function by hydrolysis of ATP to immune suppressive adenosine. (Blood. 2007 Aug. 15; 110(4):1225-32, *Cellular & Molecular Immunology* (2017) 14, 521-528; doi:10.1038/cmi.2016.30). In order to determine whether the anti-CD39 antibodies were capable of inhibiting CD39 enzymatic activity, it was important to evaluate the binding to human Tregs. Tregs were isolated from human PBMCs and the Tregs were purified and the anti-bodies were evaluated for binding by flow cytometry. The result indicate that the anti-CD39 antibodies bind to human Tregs (FIG. 10). Of note, both the high maximum MFI and low MFI profiles were observed similar to the human B cell staining (see FIG. 8). The ability of the antibodies to inhibit the ATPase activity on human Tregs was also evaluated. All the antibodies inhibit Treg CD39 enzymatic activity (see FIG. 11) equally well regardless of the maximal MFI staining observed.

Example 13: Anti-CD39 Antibodies Increase CD8⁺ T Cell Response in a CMV Recall Response Assay

[0423] Frozen PBMCs are thawed and resuspended at 3×10^6 /ml and cultured in presence of CMV peptides (Miltenyi, Peptivator CMV pp65) for 3 days in complete (10% FBS) media at 37 degrees C. T cells were then purified (STEMCELL, EasyStep) and rested for 24 hours at 37 degrees C. APCs were generated by depleting CD2 positive cells (STEMCELL, Easystep) from PBMCs from the same donor and plated at 5×10^4 /well overnight at 37 degrees C. The following day 5×10^4 rested T cells were added to the APCs. Antibodies were added at 25 μ g/ml plus 100 μ M ATP+1 μ M EHNA and Golgi plug/stop with CMV peptides and incubated at 37 degrees C. for 5 hours. T cells were stained and analyzed for intracellular IFN gamma on a Fortessa (Becton Dickinson) flow cytometer.

[0424] Adenosine has been shown to inhibit T cell activation. (Int J Oncol. 2008 March; 32(3):527-35). As the rate-limiting enzyme in ATP/ADP-AMP-adenosine pathway, inhibiting CD39 would diminish the levels of immune suppressive adenosine and increase immune activating ATP resulting in enhanced T cell activity. In order to evaluate the role of anti-CD39 antibodies inhibiting ATP/ADP-AMP hydrolysis, preventing the generation of adenosine which could result in an increased T cell response, a CMV recall assay was used. PBMCs were cultured in the presence of a pool of CMV peptides for 3 days and then the T cells were purified cultured with autologous PBMC plus CMV peptides and ATP+EHNA. After 5 hours the T cells were evaluated for the production of IFN gamma. The results indicate that some of the anti-CD39 antibodies were able to increase CD8⁺ T cells activity in a CMV recall responses assay. This demonstrates that inhibiting the enzymatic activity of CD39 prevents the generation of adenosine and preserves ATP levels and allowing for a robust T cell response to a

peptide:MHC complex. In addition, not all antibodies that bind to CD39 and inhibit cell surface enzymatic activity are capable of increasing T cell response and the specific interaction of the antibody to CD39 is important.

Example 14: Evaluation of Antibodies for Inhibition of CD39 Activity on Mel-28 and Human Monocytes

[0425] 3.5×10^4 MEL-28 cells/well were incubated with 100 nM down to 0.32 pM of monoclonal antibodies for 30 minutes. 50 μ M ATP was added and incubated for 15 minutes. Supernate was evaluated for free phosphate (Pi) using the Malachite Green Phosphate Detection Kit (R&D Systems cat#DY996). Palivizumab was used as an isotype control and ARL (Tocris) and POM-1 (Alpha Aesar) used at a concentration of 100 μ M as non-specific small molecule inhibitors of CD39 as positive controls. Cyno monocytes were isolated from whole cyno blood using NHP CD14 positive selection kit (Miltenyi). Monocytes at 5×10^4 cells/well were washed with Tris buffer and incubated as described above.

[0426] When comparing anti-CD39 antibodies for enzymatic inhibition in short term assays, differences were observed. Some were able to block the release of free phosphate (Pi) measured in a malachite green assay and others demonstrated very little activity. For example, BY40v9 and 9-8B have little to no enzymatic inhibition at concentrations of 100 nM using both the MEL-28 cell or primary human monocyte compared to other anti-CD39 antibodies (e.g., 29579 and 28347) that are able to inhibit ATPase activity at low nM concentrations.

[0427] 9-8B was produced as described in US 2017/0335007 A1, using SEQ ID Nos. 22 and 23, as hIgG4. BY40v9 is an engineered variant of the antibody BY40 described in WO 2009/095478 A1 SEQ ID Nos. 1 and 5. We tried to express BY40 as described as a human IgG4 but repeated attempts failed. The VH described in SEQ No. 1 appears to be missing several N-terminal residues compared to germline VH's, so we engineered in the missing residues with closest germline sequence from IMGT (<http://imgt.org/>), resulting in BY40-v9, which expressed and was determined to specifically bind rhCD39-ECD and cellular ECD.

Example 15: Design of Chimera and Region of Distinct Binding

[0428] (a) Examples of Antibodies that Bind Soluble Recombinant CD39 ECD and Cellular CD39 but do not Inhibit ATPase Activity and do not Compete with Cellular Inhibitors for Binding to ECD Inhibitors

[0429] 0.04-3.3 nM rhCD39-ECD (R&D Systems) was incubated with buffer, 50 μ g/ml antibody or 100 μ M POM-1 (Alpha Aesar) for 1 hr at 37° C. in assay buffer (25 mM Tris pH 7.5, 5 mM CaCl_2) at which point ATP (Sigma) was spiked in to a final concentration of 10 μ M, and the reaction further incubated for 30 min 37° C. Production of free phosphate (Pi) was subsequently measured using Malachite Green Phosphate Detection kit (R&D Systems).

[0430] Indicated cells were incubated in assay buffer with 10-25 μ g/ml antibody, 100 μ M POM-1 or 100 μ M ARL for 30 min at 37° C. 5% CO_2 . ATP was added to a final concentration of 50 μ M and the incubation continued for 15 min. Supernatant was evaluated for free phosphate (Pi) using the Malachite Green Phosphate Detection kit. Palivi-

zumab is used as an isotype control and POM-1 and ARL are non-specific small molecule inhibitors of CD39.

[0431] A1 antibody was immobilized onto an Anti-Mouse IgG Fc Capture (AMC) biosensor (ForteBio). Association of hCD39-ECD was then monitored for 180 seconds via Bio-Layer Interferometry (BLI) using the Octet system (ForteBio), at which point the biosensor was dipped into competitor antibody and monitored for another 180 seconds. Association of the second antibody was recorded as an upward shift in the interference pattern and indicates that the antibodies bind to different epitopes on CD39. No change in the interference pattern indicated that A1 blocks the second antibody from binding to CD39.

[0432] Although A1 does bind hCD39 ECD (FIG. 1), it does not inhibit its ATPase activity. Although A1 does bind cellular CD39 (FIG. 2), it does not appreciably directly inhibit the ATPase activity of CD39 expressed on OAW42. Capture of hCD39 ECD by A1 blocks subsequent binding by A1 (FIG. 14A, bottom right hand sensorgram), but does not block binding of inhibitory antibodies such as 27536, 27571, 27579, 27597, or 38347.

[0433] The commercially available A1 antibody represents a group of anti-human CD39 monoclonal antibodies that do not directly inhibit the ATPase activity of CD39 and do not bin with any of the other anti-CD39 antibodies described here. More than 30 antibodies were discovered that do not inhibit ECD ATPase activity, do not inhibit cellular CD39 ATPase activity, but do compete with A1 for binding to ECD. These antibodies may be considered to bin with anti-hCD39 antibody A1.

(b) Example of Antibodies that have Limited Ability to Inhibit the ATPase Activity of Both Soluble Recombinant and Cellular CD39 and Bin Separately from Other Cellular CD39 Inhibitors

[0434] The methods are the same as set forth above except that instead of A1, the representative antibody was immobilized using anti-human IgG Fc Capture (AHC) biosensor.

[0435] Anti-hCD39 antibodies exemplified by 27536 and 28337 represent a group of antibodies that bind both soluble ECD and cellular CD39 and have the ability to inhibit their ATPase activity yet do not compete with other inhibitors for CD39 binding. Both 27536 and 28337 are able to inhibit the hydrolysis of ATP by hCD39 ECD compared to isotype or buffer controls as shown by μ M Pi, as described herein (top left panel). 27536 and 28337 inhibit the hydrolysis of CD39 expressed on MEL-28 and OAW42 cells, as shown, compared to isotype control. Antibodies 27536 and 28337 represent a distinct bin group of anti-hCD39 inhibitory antibodies since they are blocked from binding CD39 ECD by another bin member that does not block other inhibitory antibodies such as 27571, 27579, 27597, or 38347 (see insert (c) at the bottom of FIG. 14B).

(c) Example of Antibodies that Inhibit the ATPase Activity of Soluble Recombinant CD39ECD but do not Inhibit Cellular CD39 and Bin Separately from Other CD39 ECD Inhibitors

[0436] The methods are as provided above, with the addition of experimental design where inhibition of 0.37 nM CD39 by 50 μ g/ml antibody was challenged by ATP concentrations of 3-100 μ M. Also, an 18 hour incubation was used with the antibody or isotype control. Finally, an additional 30 second baseline dip in buffer between antigen capture and dipping into a second competitor antibody for 300 seconds was used.

[0437] Anti-hCD39 antibodies exemplified by 27549 represent a group of antibodies that can bind ECD and cellular CD39 but can only inhibit ECD ATPase activity and not cellular CD39 ATPase activity. As can be seen in FIG. 14C (top left), 27549 is able to inhibit the hydrolysis of ATP by hCD39 ECD compared to isotype or buffer controls. Also from FIG. 14C (top right), 27549 is unable to inhibit the hydrolysis of CD39 expressed on MEL-28 cells compared to isotype control. Antibodies 27536 and 28337 represent a distinct bin group of anti-hCD39 inhibitory antibodies since they are blocked from binding CD39 ECD by another bin member that does not block other inhibitory antibodies such as 27571, 27579, 27597, or 38347 (see FIG. 14C, bottom).

[0438] Antibody 27549 represents a group of anti-human CD39 monoclonal antibodies that directly inhibit the ATPase activity of sol CD39 ECD yet does inhibit cellular CD39 despite being able to bind to CD39 expressed on cells (FIG. 2). It does not compete with A1 or with any of the other inhibitory anti-CD39 antibodies described here for binding to ECD, so 27549 represents another bin of anti-hCD39 antibodies (see FIG. 14C).

(d) Example of Antibodies that Inhibit the ATPase Activity of ECD and Cellular CD39 and Bin Separately from Other CD39 ECD and/or Cellular Inhibitors

[0439] The methods are as provided above.

[0440] Antibodies 27571, 27579 and 28347 represent a group of anti-human CD39 antibodies that directly inhibit the ATPase activity of soluble CD39 ECD and inhibit cellular CD39 and yet do not compete with A1, cellular inhibitors 27536 or 28337, or ECD inhibitor 27549 (FIGS. 14A-C) for binding to ECD. 27571, 27579, and 28347 are able to inhibit the hydrolysis of ATP by hCD39 ECD compared to isotype or buffer controls (see FIG. 14D, left). 27571, 27579, and 28347 also inhibit the hydrolysis of CD39 expressed on MEL-28 cells compared to isotype control (see FIG. 14D, right). These cellular inhibitors represent another bin of anti-hCD39 antibodies (see FIG. 14D).

(e) Examples of Inhibitory Antibodies that Make Distinct Contacts with CD39

[0441] Chimeras were generated by replacing human CD39 with mouse CD39 sequence in mammalian expression vectors. The chimeras were expressed in CHO cells and the ability of anti-human CD39 antibodies to bind the chimeras tested via FACS. In brief, cells were washed and blocked in FACS buffer (PBS/2% FBS) for 30 min on ice. They were then incubated with 15 µg/ml anti-human CD39 antibodies diluted in FACS buffer×1 h on ice. After 2 washes, cells were incubated with fluorescently labeled anti-human Fc antibodies, anti-mouse Fc antibodies, or anti-mCD39 antibody (R&D Systems 495826) diluted in FACS buffer per manufacturers' instructions×30 min on ice. After 2 washes, cells were resuspended in FACS buffer and analyzed on BD Fortessa. Data was processed with FlowJo. Positive binding was scored as "yes" and lack of binding was scored as "NO" and examples of FACS plots used to generate this table are in FIGS. 14.F and 14.G.

[0442] Chimeras formed between human and mouse CD39 distinguish regions critical for antibody contact that are unique to inhibitory antibodies such as 31414, 31895, 31873, 31901, 31905, reference antibodies such as BY40v9 and 9-8B, and commercial antibodies such as A1 and 498403. Columns 1 and 3 describe the human CD39

sequences flanking the mouse CD39 sequence described in column 2. Column 4 lists the exact mouse amino sequence in the chimera.

[0443] The antibodies described thus far have no/minimal cross-reactivity to mouse CD39, which shares 78% percent identity with human CD39 in the extracellular domain. Chimeras were therefore made between human and mouse CD39 in order to identify those region(s) critical to antibody recognition and binding. To that end, 8 chimeras were generated with the sequence swaps chosen based on sequence diversity between human and mouse CD39 and potential for surface exposure based on rat ENTPD1 and rat ENTPD2 crystal structures. Thus, these 8 chimeras do not comprehensively interrogate all potential contact residues. All tested antibodies were able to bind Chimeras #1,3,5,6,7, and 8, suggesting that these chimeras maintained overall global structural integrity. A1 and 498403 lost the ability to bind Chimera #4, indicating that residues critical to their contact with human CD39 had been lost. A1, 498403, BY40v9 and 9-8B were able to bind Chimera #2, suggesting that this chimera maintained overall global structural integrity. In contrast, inhibitory antibodies 31414, 31895, 31901, 31905, and 31873 were able to bind all chimeras but Chimera #2. Thus, Chimera #2 has lost residues critical to making contacts with these antibodies and therefore E143-N158 constitute part or all of the human CD39 epitope for these antibodies. Notably, these antibodies belong to the bin group exemplified by 27571, 27579 and 28347 in FIG. 14D, i.e. they do not bin with anti-CD39 antibody bin groups represented by antibodies A1, 27536, or 27549.

[0444] Chimeras were generated by mutagenesis of Chimera #2 or WT hCD39 expression vectors. Residues for mutagenesis were chosen based on divergence between human and mouse CD39. The chimeras were expressed in CHO cells and the ability of anti-human CD39 antibodies to bind the chimeras tested via FACS, as described in FIG. 14E. Table 2. Positive binding was scored as "Yes" and lack of binding was scored as "No" and examples of FACS plots used to generate this table are in FIGS. 14.F and 14.G.

[0445] Specific residues critical for antibody contact can distinguish inhibitory antibodies 31414, 31418, and 31895 from 31901, 31905, and 31873. Individual amino acids in the mouse sequence of human-mouse Chimera #2, when reverted back to the respective human residue (resulting in Chimera #9,10), restore the ability of antibodies 31895, 31414, 31418 to bind to CD39 but not the ability of 31901, 31905, or 31873 to bind CD39. Mutation of individual residues in the context of otherwise fully human CD39 (Chimeras #11,12) did not impair the binding ability of any of the tested antibodies. Co-mutation of two human residues to the cognate mouse residues (Chimeras #13,14) did not impair binding by antibodies 31414, 31418 or 31895. In stark contrast, antibodies 31901, 31905, and 31873 completely lost their ability to bind Chimeras #13 and 14. The ability of indicated antibodies to bind a given chimera was determined by FACS. In particular, FIG. 14F and FIG. 14G show representative FACS plots used to populate this table and FIG. 14G shows the importance of human CD39 residues N99, R154, and/or S153 in recognition by antibodies represented by 31901, 31905, and 31873.

[0446] As demonstrated in FIG. 14E, Table 1, inhibitory antibodies 31414, 31418, 31895, 31901, 31905 and 31873 can be distinguished from other monoclonal anti-CD39 antibodies based on their inability to recognize Chimera #2.

In Table 2, these antibodies are further distinguished by the gain or loss of the ability to bind specific point mutants of hCD39 or Chimera #2. Thus, these antibodies, while binding the same general region of human CD39, form distinct contacts with different critical residues in hCD39. Since these antibodies share the requirement for residues E143-N158, they may share some common contact residues yet can be differentiated based on the demonstrated unique points of contact.

(f) FACS Plots Highlighting the Importance of Human CD39 Residue D150 and/or E153 in Recognition of Antibodies Represented by 31414, 31418, and 31895 and FACS Plots Highlighting the Importance of Human CD39 Residues N99, R154, and/or E153 in Recognition by Antibodies Represented by 31901, 31905, and 31873

[0447] The methods are as provided above for the examples of inhibitory antibodies that make distinct contacts with CD39.

[0448] The ability of indicated antibodies to bind to a given chimera was determined by FACS.

[0449] While antibodies 31414, 31418, 31895, 31873, 31901, and 31905 all share a common requirement for human CD39 residues E143-N158, these antibodies make different critical contacts with residues within and outside of this region. Thus, antibodies, which belong to the bin group represented, by antibodies 27571, 27579, and 28347 (FIG. 14.D) can be further distinguished into at least two more groups based on sensitivity to distinct residues. There are at least 5 bin groups: (1) A1-like antibodies that compete each other for ECD binding yet do not inhibit ECD activity, but do not compete with antibodies in bin groups 2, 3, 4, or 5 for ECD binding and make critical contacts with N275-1277 as evidenced by loss of binding to Chimera #4; (2) 27536/28337-like antibodies that compete each other for ECD binding and can inhibit both ECD and cellular CD39 ATPase activity, but do not compete with antibodies in bin groups 1, 3, 4 or 5 for ECD binding; (3) 27549-like antibodies that compete each other for ECD binding and can inhibit CD39 ECD but not cellular CD39, and do not compete with antibodies in bin groups 1, 2, 4 or 5 for ECD binding; (4) 31414/31418/31895-like antibodies that make critical contacts with E143-N158 in cellular CD39 including (but not limited to) D150 and E153, inhibit the ATPase activity of both ECD and cellular CD39, compete with each other for ECD binding, but do not compete with antibodies in bins 1, 2 or 3 for ECD binding; and (5) 31873/31901/31905-like antibodies that make critical contacts with E143-N158 in cellular CD39 including (but not limited to) E153 and R154, as well as a sensitivity to residue N99, inhibit the ATPase activity of both ECD and cellular CD39, compete with each other for ECD binding, but do not compete with antibodies in bins 1, 2, or 3 for ECD binding. Thus, there are anti-human CD39 antibodies that can be distinguished based on their affinity for ECD, affinity for cells, ability to inhibit ECD ATPase activity, ability to inhibit cellular ATPase activity, and points of contact with CD39. For example, 27549 binds both ECD (FIG. 1) and cells well (FIG. 2) yet can only inhibit ECD ATPase activity. 27579 binds ECD weakly but is a potent cellular CD39 inhibitor.

Example 16: Anti-CD39 Antibodies are Reversible Allosteric, not Competitive, Inhibitors Due to V_{max} Suppression of V_{max}

[0450] Anti-CD39 antibodies or isotype control antibody (100 nanomolar final concentration) were incubated with

MEL-28 cells (35,000 MEL-28 cells/well) endogenously expressing human CD39 at 37° C. for 20 minutes in the presence of EnzChek reagents (PNP & MESG). Immediately following the addition of ATP (final concentrations ranging from 0-450 micromolar), the rate of ATP hydrolysis to free phosphate (Pi) by CD39 was monitored over time at Abs360 nm using SpectraMax i3x plate reader. The initial enzyme velocity, v_0 , was determined from the linear region of Pi vs. time curve for each ATP concentration. The plot of v_0 vs. [ATP] was curve fit using non-linear regression of the Michaelis-Menten kinetic model.

[0451] The ATP hydrolysis rate by CD39 expressed on MEL-28 cells can be markedly reduced by the anti-CD39 antibodies (see FIG. 15). The ATP hydrolysis rate in the presence of the anti-CD39 antibodies ranges from 1.2 to 2.7 micromolar Pi per minute, which is much less than the ATP hydrolysis rate observed in the presence of an isotype control antibody (7.7 micromolar Pi per minute) and similar in magnitude to the pan ATPase inhibitor ARL (1.2 micromolar Pi per minute).

[0452] The plot of initial velocity versus ATP concentration for multiple concentrations of the anti-CD39 antibody 29872 indicates that the mechanism of inhibition of this IgG antibody is not competitive (see FIG. 16 A.). The reduction in initial velocity is constant for ATP concentrations above 100 micromolar (100, 200, 300 and 500 micromolar) in the presence of 5 nanomolar 29872. 29872 could be a non-competitive inhibitor, an un-competitive inhibitor, or a mixed inhibitor of CD39 (having properties of both non-competitive and un-competitive inhibition). The monovalent Fab form of anti-CD39 antibody 29872 showed a very similar inhibition profile (see FIG. 16 B), indicating that the CD39 inhibition activity of 29872 is not dependent on the bivalent structure of the IgG and the potential properties that could result from IgG bivalency such as CD39 crosslinking.

[0453] Many of the other anti-CD39 antibodies tested in this assay showed a similar profile for CD39 enzymatic inhibition (data not shown), indicating that they also may be non-competitive inhibitors, un-competitive inhibitors, or mixed inhibitors of CD39. The mechanism of enzymatic inhibition of these antibodies suggests that they retain their full inhibition of CD39 enzymatic inhibition at high ATP concentrations. The anti-CD39 antibodies appear to be reversible inhibitors.

Example 17: Anti-CD39 can Induce Internalization of CD39 on Cyno Monocytes

[0454] Anti-CD39 antibodies were injected into cynomolgus monkeys to test for ability to downregulate CD39 on cell surface of cyno monocytes. CD39 internalization was assessed by FACS of whole blood samples collected pre-dose, Day 1, Day 7, and Day 14 after antibody treatment. Non-competing anti-CD39-PE antibody (clone A1) was used to measure CD39 levels on CD14+ gated monocytes. Data is shown as MFI of A1-PE on gated cyno monocytes in FIG. 17.

[0455] Cynomolgus monkeys were injected with anti-CD39 antibodies at 10 mg/kg. Blood samples were collected prior to injection and on Day 1, Day 7, and Day 14 after treatment. For each time-point, 50 uL of cynomolgus whole blood was incubated with 30 uL of staining buffer (PBS, 2% FBS, 2 mM EDTA, 3% mouse serum, 5% goat serum) containing CD14 and CD20 antibodies (eBioscience) and an Fc blocking reagent (BD) for 30 minutes at 4 C. CD39

antibody (clone eBioA1, eBioscience) was added to the sample and incubated for an additional 40 minutes at 4 degrees C. Following incubation, the samples were treated with ACK lysis buffer (ThermoFisher) for 10 minutes at room temperature to lyse red blood cells. Samples were washed several times with staining buffer and fixed with 1% PFA (Sigma) before acquisition on a BD Fortessa X-20 flow cytometer. Total CD39 receptor expression on CD14 positive monocytes was determined by mean fluorescence intensity.

[0456] CD39 was highly expressed on cyno monocytes prior to antibody treatment in all blood samples tested (pre-dose). Anti-CD39 antibodies tested in vivo had distinct internalization profiles where antibody 1 treatment led to downregulation of CD39 on cell surface of monocytes and antibody 2 had no effect on overall CD39 levels. Apparent decrease of CD39 levels after antibody 1 treatment was not due to A1 antibody competing with antibody 1 for binding to CD39 as the epitopes for A1 and antibody 1 are distinct from each other.

Example 18: Anti-CD39 Antibody Increases Stimulated Human CD4⁺ and CD8⁺ T Cell in the Presence of Exogenous ATP

[0457] Anti-CD3+anti-CD28 stimulated PBMCs were treated with anti-CD39 antibody 31895 or isotype control in the presence of 50 μM ATP for 96 hours. Proliferation of CD4⁺ and CD8⁺ T cells was measured by Cell Trace Violet by flow cytometry.

[0458] FIG. 19 shows that anti-CD39 antibody increases proliferation of stimulated human CD4⁺ and CD8⁺ T cell in the presence of exogenous ATP. The left side shows CD8⁺ T cells, with the x-axis showing antibody (nM) and the y-axis showing % CD8⁺ T cell proliferation. The right side shows CD4⁺ T cells, with the x-axis showing antibody (nM) and the y-axis showing % CD4⁺ T cell proliferation. The inset to the right shows symbols for the respective antibodies and controls.

Example 19: Anti-CD39 Antibody Increase Stimulated PBMC Secretion of INF-γ, TNF-α and IL-2

[0459] Human PBMCs were treated with anti-CD3+anti-CD28 and incubated with anti-CD39 antibody 31895 or isotype control in presence (B) or absence (A) of exogenous ATP (50 μM). Supernatants were harvested after 96 hours and cytokines were measured using a Meso Scale Discovery human cytokine kit.

[0460] FIG. 20 shows anti-CD39 antibody 31895 increases cytokine secretion by anti-CD3+anti-CD28 acti-

vated PBMC in absence (A) or presence (B) of exogenous ATP in a dose dependent manner. The top row shows results with exogenous ATP added and the bottom row shows results with no exogenous ATP added. The x-axis shows antibody (nM) and the y-axis shows secretion of INF-γ, TNF-α and IL-2, respectively.

Example 20: Anti-CD39 Antibody Increases Stimulated PBMC Secretion of INF-γ, TNF-α, IL-2 and IL-1β

[0461] Human PBMCs were stimulated with anti-CD3+anti-CD28 and incubated with anti-CD39 antibodies 31895, HAO-391 (See, SEQ ID 10/SEQ ID 11 from WO 2017/089334), HAO mAb4 (See SEQ ID 12/SEQ ID 13 from WO2017157948) or isotype control at a fixed concentration of 50 μg/ml in presence of ATP. Supernatants were harvested after 96 hours and analyzed by Meso Scale Discovery human cytokine kit.

[0462] FIG. 21 shows anti-CD39 antibody 31895 increased cytokine release by activated PBMCs to a higher degree compared to anti-CD39 antibodies HAO-391 (VL SEQ ID No. 10; VH SEQ ID No. 11 from WO 2017/089334) and HAO mAb4 (VL SEQ ID No. 12; VH SEQ ID No. 13 from WO2017157948). The x-axis indicates the antibody and/or conditions and the y-axis shows INF-γ, TNF-α, IL-2 and IL-1β, respectively.

Example 21: Anti-39 Antibody 31895 Increase Extracellular ATP Accumulation and Reduces Adenosine Generation by CD39⁺CD73⁺SK-MEL-28 Cells

[0463] SK-MEL-28 cells were treated with 31895, isotype control, or small molecule inhibitors (EHNA, ARL, or POM-1) for 1 hour and 50 μM ATP was added for 15 min prior to harvesting of the supernatants. The supernatants were analyzed for ATP levels using AmpGlo Kit (A) and for adenosine levels using LC/MS analysis (B). % Adenosine levels were normalized to isotype control (100%) and SK-MEL-28 CD39 KO cells (0%).

[0464] The results are shown in FIG. 22. The left graph shows ATP accumulation and the right graph shows adenosine generation (LC/MC). The x-axis for each graph shows conditions. The y-axis for the left graph shows ATP (μM) and the y-axis for the right graph shows % of adenosine levels.

Example S: Sequences

[0465] Table S provides sequences referred to herein.

TABLE S			
Sequences.			
SEQ ID NO: Region	Scheme/Clone	Sequence	
1 CDR-H1	Chothia	GYTFTSY	
2 CDR-H1	Chothia	GYTFKSY	
3 CDR-H1	Chothia	GYIFKSY	
4 CDR-H1	Chothia	GYTFQSY	

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
5 CDR-H1	Chothia	GYTFFSY	
6 CDR-H1	Chothia	GYTFVSY	
7 CDR-H1	Chothia	GGTFSSLAIS	
8 CDR-H1	Chothia	GGTFSKLAIS	
9 CDR-H1	Chothia	GGTFSSH	
10 CDR-H1	Chothia	GGTFSSL	
11 CDR-H1	Chothia	GGTFSL	
12 CDR-H1	Chothia	GGTFQSL	
13 CDR-H1	Chothia	GGTFPSN	
14 CDR-H1	Chothia	GGTFSAM	
15 CDR-H1	Chothia	GGTFASL	
16 CDR-H1	Chothia	GGTFSWL	
17 CDR-H1	Chothia	GGTFSSY	
18 CDR-H1	Chothia	GGTFGSY	
19 CDR-H1	Chothia	GGTFSKY	
20 CDR-H1	Chothia	GGTFGRY	
21 CDR-H1	Chothia	GGTFESY	
22 CDR-H1	Chothia	GGTFSNY	
23 CDR-H1	Chothia	GGAFSSY	
24 CDR-H1	Chothia	GFTFSSY	
25 CDR-H1	Kabat	SYMH	
26 CDR-H1	Kabat	SYEMH	
27 CDR-H1	Kabat	SYQMH	
28 CDR-H1	Kabat	SYMY	
29 CDR-H1	Kabat	SYFMH	
30 CDR-H1	Kabat	SLAIS	
31 CDR-H1	Kabat	KLAIS	
32 CDR-H1	Kabat	HTAIS	
33 CDR-H1	Kabat	SLPIS	
34 CDR-H1	Kabat	LLAIS	
35 CDR-H1	Kabat	SNAIS	
36 CDR-H1	Kabat	AMAI	
37 CDR-H1	Kabat	WLAIS	
38 CDR-H1	Kabat	SYAIS	
39 CDR-H1	Kabat	SYGIS	
40 CDR-H1	Kabat	KYGIS	

TABLE S-continued

Sequences.			
SEQ ID NO:	Region	Scheme/ Clone	Sequence
41	CDR-H1	Kabat	NYAIS
42	CDR-H1	Kabat	SYATS
43	CDR-H1	Kabat	SYAIG
44	CDR-H1	Kabat	SYSMN
45	CDR-H1	Kabat	SYGMN
46	CDR-H2	Chothia	NPSGGST
47	CDR-H2	Chothia	NPSVGS
48	CDR-H2	Chothia	NPSGGS
49	CDR-H2	Chothia	NPLGGG
50	CDR-H2	Chothia	NPRGGS
51	CDR-H2	Chothia	IPIFGT
52	CDR-H2	Chothia	GFGT
53	CDR-H2	Chothia	LPIGGT
54	CDR-H2	Chothia	LPIAGT
55	CDR-H2	Chothia	LPIFGE
56	CDR-H2	Chothia	IPRGGT
57	CDR-H2	Chothia	IPEFGI
58	CDR-H2	Chothia	IPSIGT
59	CDR-H2	Chothia	IPISGT
60	CDR-H2	Chothia	IPTFGT
61	CDR-H2	Chothia	SSSSSY
62	CDR-H2	Chothia	WYDGSN
63	CDR-H2	Kabat	VINPSGGSTSYAQKFQG
64	CDR-H2	Kabat	RINPSVGSTWYAQKFQG
65	CDR-H2	Kabat	RINPSGGSTWYAQKFQG
66	CDR-H2	Kabat	KINPSGGSTWYAQKFQG
67	CDR-H2	Kabat	VINPLGGGTSYAQKFQG
68	CDR-H2	Kabat	SINPRGGSTSYAQKFQG
69	CDR-H2	Kabat	GIIPIFGTANYAQKFQG
70	CDR-H2	Kabat	GI--GFGTANYAQKFQG
71	CDR-H2	Kabat	GILPIGGTANYAQKFQG
72	CDR-H2	Kabat	GILPIAGTANYAQKFQG
73	CDR-H2	Kabat	GILPIFGEANYAQKFQG
74	CDR-H2	Kabat	GIIPRGGTANYAQKFQG
75	CDR-H2	Kabat	SIIPIFGTANYAQKFRG
76	CDR-H2	Kabat	SIPEFGIANY AQKFQG

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
77 CDR-H2	Kabat	SIIPIFGTANYAQKFQG	
78 CDR-H2	Kabat	GIIPISGTANYAQEFQG	
79 CDR-H2	Kabat	GIIPTFGTANYAQKFQG	
80 CDR-H2	Kabat	SISSSSSYIYADSVKG	
81 CDR-H2	Kabat	VIWYDGSNKYYADSVKG	
82 CDR-H3		GKREGGTEYLRH	
83 CDR-H3		GKREGGTEYLRK	
84 CDR-H3		GKREGGTEYLRN	
85 CDR-H3		GKREGGTEYLRV	
86 CDR-H3		GGAKYASTYGM DV	
87 CDR-H3		GGAKYASTHGM DV	
88 CDR-H3		GGAKYASQLGM DV	
89 CDR-H3		GGAKYASKWGM DV	
90 CDR-H3		GGAKYAVGYGM DV	
91 CDR-H3		GGAKYAGRYGM DV	
92 CDR-H3		GGAKYARTYGM DV	
93 CDR-H3		ESGGYRDHRLDV	
94 CDR-H3		ESGTYRDHRLDV	
95 CDR-H3		ESGGYRDHRLGV	
96 CDR-H3		DFTDYSSGYSSGWTY	
97 CDR-H3		DTLYSSGAYYGYNV	
98 CDR-H3		AKRGYDSYGGVYFDY	
99 CDR-H3		GPTVTATTSIGTHNWFD P	
100 CDR-H3		EGRGYDSSRYKFWFDPWGQGLVTVSS	
101 CDR-H3		DGGGYRHHYFDL	
102 CDR-H3		ESGGYRDHKL DV	
103 CDR-H3		DGGGYQH HYFDL	
104 CDR-H3		DSGYHRHYS DY	
105 CDR-H3		DPLGIRKHWFD P	
106 CDR-H3		DTPRWRYHYFDY	
107 CDR-H3		ERRGSLALGM DV	
108 CDR-H3		DLGGYSYGEPIYYYGM DV	
109 CDR-H3		RASQSVSSSYLA	
110 CDR-L1		RASQSVASSYLA	
111 CDR-L1		EASQSVSYSYLA	
112 CDR-L1			

TABLE S-continued

Sequences.		
SEQ ID NO: Region	Scheme/ Clone	Sequence
113 CDR-L1		KASESVSSSYLA
114 CDR-L1		RASQYVSSSYLA
115 CDR-L1		KSSQSVLFSSNNKNYLA
116 CDR-L1		KSSRSVLFSSNNKNYLA
117 CDR-L1		KSSKSVLYSNNKNYLA
118 CDR-L1		RASQSVGSNLA
119 CDR-L1		KSSQSVLYSSNNKNYLA
120 CDR-L1		QASQDISNYLN
121 CDR-L1		RASQSVSSSYLA
122 CDR-L1		RASQSVSRYLE
123 CDR-L1		RASQSISSWLA
124 CDR-L1		RASQSVSSDYLA
125 CDR-L2		GASSRAT
126 CDR-L2		GASNRHT
127 CDR-L2		YASSRAY
128 CDR-L2		GASSRAN
129 CDR-L2		YASSRAT
130 CDR-L2		YASNRAT
131 CDR-L2		WASTRES
132 CDR-L2		WASSRES
133 CDR-L2		WASTRQS
134 CDR-L2		WASTRAS
135 CDR-L2		GASTRAT
136 CDR-L2		GASTRAS
137 CDR-L2		DASNLET
138 CDR-L2		DASNRAT
139 CDR-L2		DASKRAT
140 CDR-L2		KASSLES
141 CDR-L3		QQYHSYIT
142 CDR-L3		QQYHNAIT
143 CDR-L3		QQYFYFIT
144 CDR-L3		QQYHSALT
145 CDR-L3		QQYHGGIT
146 CDR-L3		QQYHRRIT
147 CDR-L3		QQYHSGIT
148 CDR-L3		QQYYLYPLT

TABLE S-continued

Sequences.			
SEQ ID NO:	Region	Scheme/ Clone	Sequence
149	CDR-L3		QQYWTYPLT
150	CDR-L3		QQYLLYPLT
151	CDR-L3		QQYLIWPLT
152	CDR-L3		QQYLLWPLT
153	CDR-L3		QQFYFFPPT
154	CDR-L3		QQAYTFPPT
155	CDR-L3		QQYIFPPT
156	CDR-L3		QQRNFYPPT
157	CDR-L3		QQFVLWPRT
158	CDR-L3		QQHVNFPPLT
159	CDR-L3		QQSVFWPIT
160	CDR-L3		QQLTKWPLT
161	CDR-L3		QQDVLWPLT
162	CDR-L3		QQYGLFPIT
163	CDR-L3		QQHTVWPIT
164	CDR-L3		QQVLNYPLT
165	CDR-L3		QQSYFLPPT
166	CDR-L3		QQAHSFPYT
167	Leader for scFv, scFv-Fc	Leader	MKYLLPTAAAGLLLLAAQPAMA
168	Linker for scFv, scFv-Fc	Linker	GGGGSGGGSGGGGS
169	C-Term Tag for scFv, scFv-Fc	C-Term Tag	GPGGQHSHHHH
170	C-Term Tag for scFv, scFv-Fc	C-Term Tag	PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK
171	scFv	29872	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KEPGASVKVCKAPGYTFTSYMHWRQAPGQG LEWMGVINPSGGSTSYAQKFQGRVIMIRDTS TVYMESSLRSEDTAVYYCARGKREGGTEYLRH WGQGTLVTVSSGGGSGGGSGGGGSEIVLTQS PGTSLSPGERATLSCRASQSVSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYHSYITFGGGTKVEI KGPGGQHSHHHH
172	scFv	31895	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KKPGASVKVCKASGYTFKSYEMHWVRQAPGQG LEWMGRINPSVGTWYAQKFQGRVTMTDRDTS TVYMESSLRSEDTAVYYCARGKREGGTEYLRK WGQGTLVTVSSGGGSGGGSGGGGSEIVLTQS PGTSLSPGERATLSCRASQSVASSYLAWYQQK PGQAPRLLIYGASNRHTGIPDRFSGSGSGTDFT LIISRLEPEDFAVYYCQQYHNAITFGGGTKVEI K GPGGQHSHHHH

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
173 scFv	31414	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KKPASVKVSCASGYTFKSYEMHWVRQAPGQG LEWMGRINPSVGSTWYAQKFQGRVTMTDSTST TVYMELSSLRSEDTAVYYCARGKREGGTEYLRN WGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQS PGTLSLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYHSYITFGGGTKVEI KGPGGQHSHHHH	
174 scFv	31905	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KKPASVKVSCASGGTFPSNAISWVRQAPGQG LEWMGGIGFGTANYAQKFQGRVTITADESTSTA YMELSSLRSEDTAVYYCARGGAKYARTYGMVW GQGTTLTVSSGGGSGGGGSGGGSDIVMTQSP DSLAVSLGERATINCKSSKSVLYSNMKNYLAW YQQKPGQPPKLLIYWASTRQSGVPDRFSGSGSG TDFTLTISLQAEDVAVYYCQYLLYPLTFGGG TKVEIKGPGGQHSHHHH	
175 scFv-Fc	29872	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KEPGASVKVSCAPGYTFTSYMHWVRQAPGQG LEWMGVINPSGGSTSYAQKFQGRVIMIRDSTST TVYMELSSLRSEDTAVYYCARGKREGGTEYLRH WGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQS PGTLSLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYHSYITFGGGTKVEI KPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG K	
176 scFv-Fc	31895	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KKPASVKVSCASGYTFKSYEMHWVRQAPGQG LEWMGRINPSVGSTWYAQKFQGRVTMTDSTST TVYMELSSLRSEDTAVYYCARGKREGGTEYLRK WGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQS PGTLSLSPGERATLSCRASQSVASSYLAWYQQK PGQAPRLLIYGASNRHTGIPDRFSGSGSGTDFT LIISRLEPEDFAVYYCQQYHNAITFGGGTKVEI KPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG K	
177 scFv-Fc	31414	MKYLLPTAAAGLLLLAAQPAMAQVQLVQSGAEV KKPASVKVSCASGYTFKSYEMHWVRQAPGQG LEWMGRINPSVGSTWYAQKFQGRVTMTDSTST TVYMELSSLRSEDTAVYYCARGKREGGTEYLRN WGQGTLVTVSSGGGSGGGGSGGGGSEIVLTQS PGTLSLSPGERATLSCRASQSVSSSYLAWYQQK PGQAPRLLIYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYHSYITFGGGTKVEI KPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK DTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPI EKTISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPG K	

TABLE S-continued

Sequences.			
SEQ ID NO.: Region	Scheme/ Clone	Sequence	
178 scFv-Fc	31905	MKYLLPTAAAGLLLLAAQPAMAVQLVQSGAEV KKPSSSVKVSCKASGGTFPSNAISWVRQAPGQG LEWMGGIGFGTANYAQKFQGRVITADESTSTA YMELSSLRSEDTAVYYCARGGAKYARTYGMVW GGGTTTVSSGGGGSGGGSGGGSDIVMTQSP DSLAVSLGERATINCKSSKSVLYSNNKNYLAW YQQKPGQPPKLLIWASTRQSGVPDRFSGSGSG TDFLTITSSSLQAEDVAVYYCQYLLYPLTFGGG TKVEIKPKSCDKTHTCPPCPAPELLGGPSVFLF PPKPKDTLMISRIPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL HQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPVLDSGGSFFLYS KLTVDKSRWQQGNVFSQVMHEALHNHYTQKSL SLSPGK	
179 VH	27579	QVQLVQSGAEVKEPGASVKVSCKAPGYTFTSY MHWVRQAPGQGLEWMGVINPSGGSTSYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
180 VH	31895	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
181 VH	31415	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYQ MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
182 VH	31414	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
183 VH	31891	QVQLVQSGAEVKKPGASVKVSCKASGYIFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
184 VH	29871	QVQLVQSGAEVKKPGASVKVSCKASGYTFQSY MHWVRQAPGQGLEWMGKINPSGGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
185 VH	31418	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
186 VH	31431	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYQ MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
187 VH	31421	QVQLVQSGAEVKKPGASVKVSCKASGYTFPSY MYWVRQAPGQGLEWMGVINPLGGSTSYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
188 VH	31429	QVQLVQSGAEVKKPGASVKVSCKASGYTFVSYF MHWVRQAPGQGLEWMGSINPRGGSTSYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	
189 VH	29872	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQ RVIMIRDTSTSTVYMESSLRSEDTAVYYCARG KREGGTEYLRHWGQGLTVTVSS	

TABLE S-continued

Sequences.			
SEQ ID NO.: Region	Scheme/ Clone	Sequence	
190 VH	28347	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLA ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQ RVTITADESTNTAYMELSSLRSEDTAVYYCARG GAKYASTYGMDEVWGQGTITVTVSS	
191 VH	31896	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLA ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQGRV TITADESASTAYMELSSLRSEDTAVYYCARGGA KYASTHGMDVWGQGTITVTVSS	
192 VH	31432	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSHTA ISWVRQAPGQGLEWMGGI LPIGGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYASQLGMDVWGQGTITVTVSS	
193 VH	31915	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLP ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDTAVYYCARGGA KYASKWGMDEVWGQGTITVTVSS	
194 VH	31436	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLA ISWVRQAPGQGLEWMGGI LPIAGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYAVGYGMDEVWGQGTITVTVSS	
195 VH	31437	QVQLVQSGAEVKKPGASVKVSCKASGGTFQSLA ISWVRQAPGQGLEWMGGI LPIGGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYAGRYGMDEVWGQGTITVTVSS	
196 VH	31905	QVQLVQSGAEVKKPGSSVKVSCKASGGTFPSNA ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDTAVYYCARGGA KYARTYGMDEVWGQGTITVTVSS	
197 VH	31901	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLP ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDTAVYYCARGGA KYAGRYGMDEVWGQGTITVTVSS	
198 VH	29852	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSAMA ISWVRQAPGQGLEWMGGI LPIAGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYASTYGMDEVWGQGTITVTVSS	
199 VH	29851	QVQLVQSGAEVKKPGSSVKVSCKASGGTFASLA ISWVRQAPGQGLEWMGGI LPIFGEANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYASTYGMDEVWGQGTITVTVSS	
200 VH	29857	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSLA ISWVRQAPGQGLEWMGGI IPRGGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARG GAKYASTYGMDEVWGQGTITVTVSS	
201 VH	27571	QVQLVQSGAEVKKPGSSVKASCKASGGTFSSYA ISWVRQAPGQGLEWMGSI IPIFGTANYAQKFRG RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGGYRDHRLDVWGQGTMTVTVSS	
202 VH	31861	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYG ISWVRQAPGQGLEWMGSI IPEFGIANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGTYRDHRLDVWGQGTMTVTVSS	
203 VH	31873	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYG ISWVRQAPGQGLEWMGSI IPEFGIANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGGYRDHRLGVWGQGTMTVTVSS	
204 VH	31393	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYG ISWVRQAPGQGLEWMGSI IPEFGIANYAQKFQ	

TABLE S-continued

Sequences.		
SEQ ID NO.: Region	Scheme/ Clone	Sequence
		RVTITADESTSTTYMELSSLRSED TAVYYCARE SGGYRDHRLDVWGQGTMTVTVSS
205 VH	27534	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD FTDYSSGYSSGWTYWGQGT LVTVSS
206 VH	27536	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSNYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD TLYSSGAYYGYNVWGQGTMTVTVSS
207 VH	27588	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSNYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARA KRGYDSYGGVYFDYWGQGT LVTVSS
208 VH	27590	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSNYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARG PTVTATTSTIGTHNWFDPWGQGT LVTVSS
209 VH	27597	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARE GRGYDSSRYKFWFDPWGQGT LVTVSS
210 VH	27575	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA TSWVRQAPGGGLEWMGGI IPISGTANYAQEFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD GGGYRHHYFDLWGRGT LVTVSS
211 VH	27568	QVQLVQSGAEVKKPGSSVKVPCKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCAGE SGGYRDHKLDVWGQGT VTVTVSS
212 VH	27577	QVQLVQSGAEVKKPGSSVKVSKASGGAFSSYA IGWVRQAPGGGLEWMGGI IPTFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD GGGYQHYYFDLWGRGT LVTVSS
213 VH	27587	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARE SGGYRDHKLDVWGQGTMTVTVSS
214 VH	27589	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD SGYHRHYSYDWGQGT LVTVSS
215 VH	27596	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD PLGIRKHWFDPPWGQGT LVTVSS
216 VH	27535	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGGLEWMGGI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSED TAVYYCARD TPRWRYHYFDYWGQGT LVTVSS
217 VH	27550	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYS MNWVRQAPGKGLEWVSSISSSSYIYYADSVKG RFTISRDNAKNSLYLQMNSLRAED TAVYYCARE RRGSLALGMDVWGQGT LVTVSS
218 VH	27549	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYG MNWVRQAPGKGLEWVAVIWDGSNKYYADSVKG RFTISRDN SKNTLYLQMNSLRAED TAVYYCARD LGGYSYGEPIYYYGMDVWGQGT TTVTVSS

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
219 VL	27579	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHSYITFG GGTKVEIK	
220 VL	31895	EIVLIQSPGILSLSPGERATLSCRASQSVASSY LAWYQQKPGQAPRLLIYGASNRHTGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHNAITFG GGTKVEIK	
221 VL	31891	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYASSRAYGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHNAITFG GGTKVEIK	
222 VL	31418	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYFYITFG GGTKVEIK	
223 VL	31430	EIVLIQSPGILSLSPGERATLSCEASQSVSYSY LAWYQQKPGQAPRLLIYGASSRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHSALTFG GGTKVEIK	
224 VL	31431	EIVLIQSPGILSLSPGERATLSCRASQSVASSY LAWYQQKPGQAPRLLIYGASNRHTGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHGGITFG GGTKVEIK	
225 VL	31421	EIVLIQSPGILSLSPGERATLSCKASESVSSSY LAWYQQKPGQAPRLLIYASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHRRITFG GGTKVEIK	
226 VL	31429	EIVLIQSPGILSLSPGERATLSCRASQYVSSSY LAWYQQKPGQAPRLLIYASNRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHSGITFG GGTKVEIK	
227 VL	28347	DIVMTQSPDSLAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASTRESGVDP RFSGSGSGTDFTLTISSLQAEDVAVYYCQYYL YPLTFGGGTKVEIK	
228 VL	31896	DIVMTQSPDSLAVSLGERATINCKSSRSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASTRESGVDP RFSGSGSGTDFTLTISSLQAEDVAVYYCQYWT YPLTFGGGTKVEIK	
229 VL	31915	DIVMTQSPDSLAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASSRESGVDP RFSGSGSGTDFTLTISSLQAEDVAVYYCQYWT YPLTFGGGTKVEIK	
230 VL	31905	DIVMTQSPDSLAVSLGERATINCKSSKSVLYSN NNKNYLAWYQQKPGQPPKLLIYWASTRQSGVPD RFSGSGSGTDFTLTISSLQAEDVAVYYCQYLL YPLTFGGGTKVEIK	
231 VL	31901	GIVMTQSPDSLAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASTRASGVDP RFSGSGSGTDFTLTISSLQAEDVAVYYCQYYL YPLTFGGGTKVEIK	
232 VL	27571	EIVMTQSPATLSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQYLIWPLTFG GGTKVEIK	

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
233 VL	31861	EIVMTQSPATLSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISLQSEDFAVYYCQQYLLWPLTFG GGTKVEIK	
234 VL	31873	EIVMTQSPATLSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISLQSEDFAVYYCQQYLLWPLTFG GGTKVEIK	
235 VL	28337	DIVMTQSPDSLAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASTRESGVPD RFGSGSGTDFTLTISLQAEDVAVYYCQQFYF YPPTFGGGTKVEIK	
236 VL	27536	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSS NNKNYLAWYQQKPGQPPKLLIYWASTRESGVPD RFGSGSGTDFTLTISLQAEDVAVYYCQQAYT FPPTFGGGTKVEIK	
237 VL	27588	DIQMTQSPSSLSASVGDRTITCQASQDISNYL NWYQQKPGKAPKLLIYDASNLETGVPSTRFSGSG SGTDFTLTISLQPEDIATYYCQQYIIPPTFG GGTKVEIK	
238 VL	27590	EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRTGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQRNFYPTFG GGTKVEIK	
239 VL	27597	EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRTGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQFVLWPTFG GGTKVEIK	
240 VL	27575	EIVLTQSPATLSLSPGERATLSCRASQSVSRYL AWYQQKPGQAPRLLIYDASNRTGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQHVNPLTFG GGTKVEIK	
241 VL	27568	EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRTGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQSVFWPITFG GGTKVEIK	
242 VL	27577	EIVMTQSPATLSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISLQSEDFAVYYCQQLTKWPLTFG GGTKVEIK	
243 VL	27587	EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASKRATGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQDVLPPLTFG GGTKVEIK	
244 VL	27589	DIQMTQSPSTLSASVGDRTITCRASQSISSWL AWYQQKPGKAPKLLIYKASLESQVPSRFGSGSG SGTEFTLTISLQPDFFATYYCQQYGLFPITFG GGTKVEIK	
245 VL	27596	EIVMTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRTGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQHTVWPITFG GGTKVEIK	
246 VL	27535	EIVLTQSPATLSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASKRATGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQVLNPLTFG GGTKVEIK	

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
247 VL	27550	DIQMTQSPSSLSASVGDRTITCQASQDISNYL NWYQQKPGKAPKLLIYDASNLETGVPSRFSGSG SGTDFTFTISSLPEDIATYYCQQSYFLPPTFG GGTKVEIK	
248 VL	27549	EIVLIQSPGILSLSPGERATLSCRASQSVSSDY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQAHSSPYTF GGGTKVEIK	
249	hCD39	MEDTKESNVKTFCSKNILAILGFSSIIAVIAL AVGLTQNKALPENVKYGI VLDAGSSHTSLYIYK WPAEKENDTG VVHQVEECRVKGPISKFVQKVN EIGIYLTDCMERAREV IPRSQHQETPVYLGATA GMRLLRMESEELADRVLDVVERSLSNYPDFQGG ARIITGQEEGAYGWITINYL LGKFSQKTRWFSI VPYETNNQETFGALDLGGASTQVTFVPQNQTIE SPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQ KLAKDIQVASNEILRDP CFHPGYKKVNVSDLY KTPCTKRFEMTLPPQQFEIQIGNYQQCHQSIL ELFNTSYCPYSQCAFNGIFLPLQGDGFAFSAF YFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE IKTSYAGVKEKYLSEYCFSGTYILSLLQGYHF TADSWEHIHF IGKIQGS DAGWTLGYMLNLNMI PAEQPLSTPLSHSTYVFLMVLFSLVLTVAIIG LLIFHKPSYFWKDMV	
250	mCD39	MEDIKDSKVKRFCSKNIL IILGFTSILAVIALI AVGLTQNKPLPENVKYGI VLDAGSSHTNLYIYK WPAEKENDTG VVQQLEECQVKGPGISKYAQKTD EIGAYLAECMELSTELIPTS KHHQTPVYLGATA GMRLLRMESEQSAD EVLAAVSTSLKSYPPDFQGG AKIITGQEEGAYGWITINYL LGRFTQEQSWSL ISDSQKQETFGALDLGGASTQITFVPQNSTIES PENSLQFRLYGEDYTVYTHSFLCYGKDQALWQK LAKDIQVSSGGVLKDP CFNPGYEKVVNVSELYG TPCTKRFEKKLPFDQFRIQGTGDYEQCHQSILE LFNNSHCPYSQCAFNGVFLPPLHGSFGAFSAFY FVMDFFKKVAKNSVISQEKMTETIKNFCSKSWE ETKTSYPSVKEKYLSEYCFSGAYILSLLQGYNF TDSWEQIHFMGKIKDSNAGWTLGYMLNLNMI PAEQPLSPPLPHSTYIGLMVLFSLLLVAVAITG LFIYSKPSYFWKEAV	
251	Macaca fascicularis cCD39	MLFDSILSTVGLSKLVS VVSSPAAALS KSNVKT FCSKNILAILGFSSIIAVIAL LAVGLTQNKALP ENIKYGI VLDAGSSHTSLYIYK WPAEKENDTG VHQVEECRVKGPISKYVQK VNEIGIYLTDCME RAREV IPRSQHQETPVYLGATAGMRLLRMESEE LADRVLDVVERSLSNYPDFQGGARIITGQEEGA YGWITINYL LGKFSQKTRWFSI VPYETNNQET GALDLGGASTQITFVPQNQTIESPDNALQFRLY GKDYNVYTHSFLCYGKDQALWQKLAKDIQVASN EILRDP CFHPGYKKVNVSDLYKTPCTKRFEMT LPPQQFEIQIGNYQQCHQS VLELFNTSYCPYS QCAFNGIFLPLQGDGFAFSAFYFVMNFLNLT SEKVSQEKVTEMMKKFCSQPWEEIKTSYAGVKEK YLSEYCFSGTYILSLLQGYHFTADSWEHIHFI GKIQGS DAGWTLGYMLNLNMI PAEQPLSTPLS HSTYVFLMVLFSLVLVIVAIIGLLIFHKPSYFW KDMV	
252	hCD39 ECD	TQNKALPENVKYGI VLDAGSSHTSLYIYK WPAE KENDTG VVHQVEECRVKGPISKFVQK VNEIGI YLTDCMERAREV IPRSQHQETPVYLGATAGMRL LRMESEELADRVLDVVERSLSNYPDFQGGARI ITGQEEGAYGWITINYL LGKFSQKTRWFSI VPYE TNNQETFGALDLGGASTQVTFVPQNQTIESPDN ALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK DIQVASNEILRDP CFHPGYKKVNVSDLYKTPC TKRFEMTLPPQQFEIQIGNYQQCHQSILELFN	

TABLE S-continued

Sequences.		
SEQ ID NO: Region	Scheme/ Clone	Sequence
		TSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVM KFLNLTSEKVSQEKVTEMMKKFCAQPWEEKTS YAGVKEKYLSEYCFSGTYILSLLQGYHFTADS WEHIHFIGIKQGSAGWTLGYMLNLTNMI PAEQ PLSTPLSHSTYVFLMVLFSLVLTVAIIGLLIF HKPSYFWKDMV
253	mCD39 ECD	TQNKPLPENVKYGI VLDAGSSHTNLYIYKWP AE KENDTGVVQQLEECQVKPGISKYAQKTDEIGA YLAECMELSTELIPTSKHHQTPVYLGATAGMRL LRMESEQSADEVLAAVSTSLKSYPDFQGA KII TGQEEGAYGWITINYLGRFTQEQSWLSLISDS QKQETFGALDLGGASTQITFVPQNSTIESPENS LQFRLYGEDYTVYTHSFLCYGKDQALWQKLAKD IQVSSGGVLKDCPNPGYEKVVNVSELYGTPCT KRFEKKLPFDQFRIQGTGDYEQCHQSILELFNN SHCPYSQCAFNGVFLPPLHGSFGAFSAFYFVMD FFKKVAKNSVISQEKMTETKNFCSKSWEETKT SYPSVKEKYLSEYCFSGAYILSLLQGYNFTDSS WEQIHFMGKIKDSNAGWTLGYMLNLTNMI PAEQ PLSPPLPHSTYI GLMVLFSLLLVAVAITGLFIY SKPSYFWKEAV
254	cCD39 ECD	TQNKALPENIKYGI VLDAGSSHTSLYIYKWP AE KENDTGVVHQVEECRVKPGISKYVQKVNEIGI YLTDCMERAREV IPRSQHETPVYLGATAGMRL LRMESEELADRVLDVVERSLSNYPDFQGA RII TGQEEGAYGWITINYLKGFSQKTRWFSIVPYE TNNQETFGALDLGGASTQITFVPQNQTTESPDN ALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAK DIQVASNEILRDCPFHPGYKKVVNVSDLYKTPC TKRFEMTLPFQQFEIQIGNYQQCHQSVLELFN TSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVM NFLNLTSEKVSQEKVTEMMKKFCSQPWEEKTS YAGVKEKYLSEYCFSGTYILSLLQGYHFTADS WEHIHFIGIKQGSAGWTLGYMLNLTNMI PAEQ PLSTPLSHSTYVFLMVLFSLVLTVAIIGLLIF HKPSYFWKDMV
255 HC	31895	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQG RVIMIRDTSTSTVYMESSLRSED TAVVYCARG KREGGTEYLRKWGGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSKVHTFPFAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPCCP APEFLGGPSVFLFPPKPKDILMISRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTI SKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYSDIAVEWESNGQPENNYKTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
256 LC	31895	EIVLIQSPGILSLSPGERATLSCRASQSVASSY LAWYQQKPGQAPRLLIYGASNRHTGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHNAITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSSTYLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
257 HC	31415	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYQ MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQG RVIMIRDTSTSTVYMESSLRSED TAVVYCARG KREGGTEYLRSWGGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSKVHTFPFAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPCCP APEFLGGPSVFLFPPKPKDILMISRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP

TABLE S-continued

Sequences.		
SEQ ID NO.: Region	Scheme/ Clone	Sequence
		SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
258 LC	31415	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHSYITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
259 HC	31891	QVQLVQSGAEVKKPGASVKVSCKASGYIFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQ RVIMIRDSTSTVYMELSLRSEDFAVYYCARG KREGGTEYLRHWGQGTLTVTSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDILMISRTPEVICV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
260 LC	31891	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYASSRAYGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHNAITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
261 HC	31418	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQ RVIMIRDSTSTVYMELSLRSEDFAVYYCARG KREGGTEYLRHWGQGTLTVTSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDILMISRTPEVICV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
262 LC	31418	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYFYITFG GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
263 HC	31430	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSGGSTWYAQKFQ RVIMIRDSTSTVYMELSLRSEDFAVYYCARG KREGGTEYLRHWGQGTLTVTSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDILMISRTPEVICV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ

TABLE S-continued

Sequences.		
SEQ ID NO.: Region	Scheme/ Clone	Sequence
		VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGSGFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
264 LC	31430	EIVLIQSPGILSLSPGERATLSCEASQSVSY LAWYQQKPGQAPRLLIYGASSRANGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQYHSALTFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKSTYLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
265 HC	31915	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSLP ISWVRQAPGGGLEWMGGIGFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDVAVYCARGGA KYASKWGMVWGQGTITVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDILMISRIPEVICVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTIKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSGFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLGK
266 LC	31915	DIVMTQSPDLSAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASSRESGVDP RFSGSGSGTDFTLTISLQAEDVAVYCCQYWT YPLTFGGGTKEIKRTVAAPSVFI FPPSDEQLK SGTASVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
267 HC	31905	QVQLVQSGAEVKKPGSSVKVSKASGGTFPSNA ISWVRQAPGGGLEWMGGIGFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDVAVYCARGGA KYARTYGMVWGQGTIVIVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDILMISRIPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTIKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSGFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLGK
268 LC	31905	DIVMTQSPDLSAVSLGERATINCKSSKSVLYSN NNKNYLAWYQQKPGQPPKLLIYWASTRQSGVDP RFSGSGSGTDFTLTISLQAEDVAVYCCQYLL YPLTFGGGTKEIKRTVAAPSVFI FPPSDEQLK SGTASVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKSTYLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC
269 HC	31901	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSLP ISWVRQAPGGGLEWMGGIGFGTANYAQKFQGRV TITADESTSTAYMELSSLRSEDVAVYCARGGA KYAGRYGMVWGQGTIVIVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDILMISRIPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTIKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSGFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLGK

TABLE S-continued

Sequences.			
SEQ ID NO: Region	Scheme/ Clone	Sequence	
270 LC	31901	GIVMTQSPDLSLAVSLGERATINCKSSQSVLFSS NNKNYLAWYQQKPGQPPKLLIYWASTRASGVDP RFGSGSGTDFTLTISSLQAEDVAVYYCQYYL YPLTFGGGTKEIKRTVAAPSVFIFPPSDEQLK SGTASVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSSTLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	
271 HC	31861	QVQLVQSGAEVKKPGSSVKVCSKASGGTFGSYG ISWVRQAPGGGLEWMGSI IPEFGIANYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGTYRDHRLDVWGQGTMTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLDSGGSFPLYSRITVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK	
272 LC	31861	EIVMTQSPAILSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQYLLWPLTFG GGTKEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSSTLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC	
273 HC	31873	QVQLVQSGAEVKKPGSSVKVCSKASGGTFESYG ISWVRQAPGGGLEWMGSI IPEFGIANYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGGYRDHRLGVWGQGTMTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLDSGGSFPLYSRITVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK	
274 LC	31873	EIVMTQSPAILSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRASGIPARFSGSG SGTEFTLTISSLQSEDFAVYYCQYLLWPLTFG GGTKEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSSTLSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC	
275 HC	31393	QVQLVQSGAEVKKPGSSVKVCSKASGGTFESYG ISWVRQAPGGGLEWMGSI IPEFGIANYAQKFQG RVTITADESTSTYTMELSSLRSEDTAVYYCARE SGGYRDHRLDVWGQGTMTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYPSDIAVEWESNGQPENNYKTP PVLDSGGSFPLYSRITVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK	
276 LC	31393	EIVMTQSPAILSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG	

TABLE S-continued

Sequences.		
SEQ ID NO.: Region	Scheme/ Clone	Sequence
		SGTEFTLTISLQSEDFAVYYCQQYLLWPLTFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
277 HC	27597	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGGQGLEWMGSI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARE GRGYDSSRYKFWFDPWGQGTLVTVSSASTKGP SVFPLAPCSRSTSESTAALGCLVKDYFPEPVT SWNSGALTSQVHTFPAVLQSSGLYSLSSVTVTP SSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPP CPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV NKGLPSSI EKTISKAKGQPREPQVYTLPPSQEE MTKNQVSLTCLVKGFPYSDIAVEWESNGQPENN YKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLGLK
278 LC	27597	EIVLTQSPAILSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQFVLWPRTFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
279 HC	27575	QVQLVQSGAEVKEPGSSVKVSKASGGTFSSYA TSWVRQAPGGQGLEWMGGI IPISGTANYAQEFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARD GGGYRHHYFDLWGRGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVICV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYSDIAVEWESNGQPENNYKTT PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK
280 LC	27575	EIVLTQSPAILSLSPGERATLSCRASQSVSRYL AWYQQKPGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQHVNFPLTFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
281 HC	27568	QVQLVQSGAEVKKPGSSVKVPCKASGGTFSSYA ISWVRQAPGGQGLEWMGSI IPIFGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCAGE SGGYRDHKLVDVWGQGTVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVICV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFPYSDIAVEWESNGQPENNYKTT PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK
282 LC	27568	EIVLTQSPAILSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRATGIPARFSGSG SGTDFTLTISLLEPEDFAVYYCQQSVFWPITFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE

TABLE S-continued

Sequences.		
SEQ ID NO: Region	Scheme/ Clone	Sequence
		QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
283 HC	27577	QVQLVQSGAEVKKPGSSVKVSCASGGAFSSYA IGWVRQAPGGGLEWMGGIIPFTGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARD GGGYQHHPDLWGRGTLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSKVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVICVV VDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGDSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK
284 LC	27577	EIVMTQSPAILSVSPGERATLSCRASQSVGSNL AWYQQKPGQAPRLLIYGASTRATGIPARFSGSG SGTEFTLTISLQSEDFAVYCCQLTKWPLTFG GGTKVEIKRTVAAPSVEIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
285 HC	27587	QVQLVQSGAEVKKPGSSVKVSCASGGTFSSYA ISWVRQAPGGGLEWMGSIIPFTGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARE SGGYRDHKLVDWGQGTMTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSKVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCP APEFLGGPSVFLFPPKPKDTLMISRTPEVICVV VDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGDSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLK
286 LC	27587	EIVLTQSPAILSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASKRATGIPARFSGSG SGTDFTLTISLQEPEDFAVYCCQDVLWPLTFG GGTKVEIKRTVAAPSVEIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC
287 HC	27589	QVQLVQSGAEVKKPGSSVKVSCASGGTFSSYA ISWVRQAPGGGLEWMGGIIPFTGTANYAQKFQ RVTITADESTSTAYMELSSLRSEDTAVYYCARD SGYHRHYSYDWGQGTMTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEFLGGPSVFLFPPKPKDTLMISRIPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTP VLDSDGDSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLK
288 LC	27589	DIQMTQSPSTLSASVGDRTITCRASQSISSWL AWYQQKPGKAPKLLIYKASSLESGVPSRFSGSG SGTEFTLTISLQPDFAFYCCQYGLFPITFG GGTKVEIKRTVAAPSVEIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC

TABLE S-continued

Sequences.			
SEQ ID NO.: Region	Scheme/ Clone	Sequence	
289 HC	27596	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCARD PLGIRKHWFDPWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK	
290 LC	27596	EIVMTQSPAILSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASNRATGI PARFSGSG SGTDFTLTISLLEPEDFAVYYCQOHTVWPITFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC	
291 HC	27535	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYA ISWVRQAPGQGLEWMGGI IPIFGTANYAQKFQG RVTITADESTSTAYMELSSLRSEDTAVYYCARD TPRWRVHYFDYWGGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK	
292 LC	27535	EIVLTQSPAILSLSPGERATLSCRASQSVSSYL AWYQQKPGQAPRLLIYDASKRATGI PARFSGSG SGTDFTLTISLLEPEDFAVYYCQQLNYPITFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC	
293 HC	27550	EVQLVESGGGLVLPKGGSLRLSCAASGFTFSSYS MNWVRQAPGKGLEWVSSISSSSYIYYADSVKG RFTISRDNKNSLYLQMNSLRAEDTAVYYCARE RRGSLALGMDVWGQGT LVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDTLMI SRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTP PVLDSGGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK	
294 LC	27550	DIQMTQSPSSLSASVGRVTITCQASQDISNYL NWYQQKPGKAPKLLIYDASNLETGVPSRFSGSG SGTDFTFITISLQPEDIAITYCQQSYFLPPTFG GGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC	
295 HC	27549	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYG MNWVRQAPGKGLEWVAVIYDGSNKYYADSVKG RFTISRDNKNTLYLQMNSLRAEDTAVYYCARD	

TABLE S-continued

Sequences.		
SEQ ID NO: Region	Scheme/ Clone	Sequence
		LGGYSYGEPIYYYYGMDVWQGGTTVTVSSASTK GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYG PPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTI SKAKGQPREPQVYITLPPSQ EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSLRTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGLGK
296 LC	27549	EIVLIQSPGILSLSPGERATLSCRASQSVSSDY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQAHSYPYTF GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDYSLSSSTLTLSKADYEKHKVYACEVT HQGLSSPVTKSFNRGEC
297 HC	31414	QVQLVQSGAEVKKPGASVKVSCKASGYTFKSYE MHWVRQAPGQGLEWMGRINPSVGSTWYAQKFQG RVIMIRDSTSTVYMELSSLRSEDTAVYYCARG KREGGTEYLRNWQGTLLVTVSSASTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGLVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVESKYGPCCPPCP APEFLGGPSVFLFPPKPKDILMISRTPEVICVV VDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQF NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLP SSIEKTISKAKGQPREPQVYITLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSGDSFFLYSLRTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLGLGK
298 LC	31414	EIVLIQSPGILSLSPGERATLSCRASQSVSSSY LAWYQQKPGQAPRLLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYHSYITFG GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDYSLSSSTLTLSKADYEKHKVYACEVTH QGLSSPVTKSFNRGEC

EQUIVALENTS

[0466] The disclosure set forth above may encompass multiple distinct inventions with independent utility. Although each of these inventions has been disclosed in its preferred form(s), the specific embodiments thereof as disclosed and illustrated herein are not to be considered in a limiting sense, because numerous variations are possible. The subject matter of the inventions includes all novel and nonobvious combinations and subcombinations of the various elements, features, functions, and/or properties dis-

closed herein. The following claims particularly point out certain combinations and subcombinations regarded as novel and nonobvious. Inventions embodied in other combinations and subcombinations of features, functions, elements, and/or properties may be claimed in this application, in applications claiming priority from this application, or in related applications. Such claims, whether directed to a different invention or to the same invention, and whether broader, narrower, equal, or different in scope in comparison to the original claims, also are regarded as included within the subject matter of the inventions of the present disclosure.

SEQUENCE LISTING

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1 5

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Gly Gly Thr Phe Ser Ala Met
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Gly Gly Thr Phe Ala Ser Leu
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Gly Gly Thr Phe Ser Trp Leu
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Gly Gly Thr Phe Ser Ser Tyr
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Gly Gly Thr Phe Gly Ser Tyr
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Gly Gly Thr Phe Ser Lys Tyr
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Gly Gly Thr Phe Gly Arg Tyr
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Gly Gly Thr Phe Glu Ser Tyr
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Gly Gly Thr Phe Ser Asn Tyr
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Gly Gly Ala Phe Ser Ser Tyr
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Gly Phe Thr Phe Ser Ser Tyr
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Ser Tyr Tyr Met His
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Ser Tyr Glu Met His
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Ser Tyr Gln Met His
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Ser Tyr Tyr Met Tyr
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Ser Tyr Phe Met His
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Ser Leu Ala Ile Ser
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<400> SEQUENCE: 31

Lys Leu Ala Ile Ser
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<210> SEQ ID NO 32
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<400> SEQUENCE: 32

His Thr Ala Ile Ser
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<210> SEQ ID NO 33
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Ser Leu Pro Ile Ser
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<210> SEQ ID NO 34
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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 34

Leu Leu Ala Ile Ser
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<210> SEQ ID NO 35
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<400> SEQUENCE: 35

Ser Asn Ala Ile Ser
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<210> SEQ ID NO 36
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Ala Met Ala Ile Ser
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<210> SEQ ID NO 37

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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 37

Trp Leu Ala Ile Ser
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<210> SEQ ID NO 38

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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

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Ser Tyr Ala Ile Ser
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<210> SEQ ID NO 39

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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 39

Ser Tyr Gly Ile Ser
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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 40

Lys Tyr Gly Ile Ser
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<210> SEQ ID NO 41

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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

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Asn Tyr Ala Ile Ser
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<210> SEQ ID NO 42

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<212> TYPE: PRT

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<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

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Ser Tyr Ala Thr Ser
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Ser Tyr Ala Ile Gly
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<210> SEQ ID NO 44

<211> LENGTH: 5

<212> TYPE: PRT

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 44

Ser Tyr Ser Met Asn
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<210> SEQ ID NO 45

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<212> TYPE: PRT

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H1, Kabat

<400> SEQUENCE: 45

Ser Tyr Gly Met Asn
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<210> SEQ ID NO 46

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

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Asn Pro Ser Gly Gly Ser Thr
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<212> TYPE: PRT

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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 47

Asn Pro Ser Val Gly Ser
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<210> SEQ ID NO 48

<211> LENGTH: 6

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 48

Asn Pro Ser Gly Gly Ser
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<210> SEQ ID NO 49
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 49

Asn Pro Leu Gly Gly Gly
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<210> SEQ ID NO 50
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 50

Asn Pro Arg Gly Gly Ser
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<210> SEQ ID NO 51
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 51

Ile Pro Ile Phe Gly Thr
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<210> SEQ ID NO 52
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<400> SEQUENCE: 52

Gly Phe Gly Thr
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<210> SEQ ID NO 53
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 53

Leu Pro Ile Gly Gly Thr
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<210> SEQ ID NO 54

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<400> SEQUENCE: 54

Leu Pro Ile Ala Gly Thr
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<210> SEQ ID NO 55
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

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Leu Pro Ile Phe Gly Glu
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<400> SEQUENCE: 56

Ile Pro Arg Gly Gly Thr
1 5

<210> SEQ ID NO 57
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 57

Ile Pro Glu Phe Gly Ile
1 5

<210> SEQ ID NO 58
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<212> TYPE: PRT
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 58

Ile Pro Ser Ile Gly Thr
1 5

<210> SEQ ID NO 59
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<400> SEQUENCE: 59

Ile Pro Ile Ser Gly Thr
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<210> SEQ ID NO 60
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 60

Ile Pro Thr Phe Gly Thr
1 5

<210> SEQ ID NO 61
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 61

Ser Ser Ser Ser Ser Tyr
1 5

<210> SEQ ID NO 62
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<212> TYPE: PRT
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Chothia

<400> SEQUENCE: 62

Trp Tyr Asp Gly Ser Asn
1 5

<210> SEQ ID NO 63
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 63

Val Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
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Gly

<210> SEQ ID NO 64
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 64

Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 65
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

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<400> SEQUENCE: 65

Arg Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 66

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<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 66

Lys Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 67

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<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 67

Val Ile Asn Pro Leu Gly Gly Gly Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 68

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 68

Ser Ile Asn Pro Arg Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 69

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 69

Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 70

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

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<400> SEQUENCE: 70

Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly
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<210> SEQ ID NO 71

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 71

Gly Ile Leu Pro Ile Gly Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 72

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 72

Gly Ile Leu Pro Ile Ala Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 73

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 73

Gly Ile Leu Pro Ile Phe Gly Glu Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 74

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 74

Gly Ile Ile Pro Arg Gly Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 75

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 75

Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Arg

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Gly

<210> SEQ ID NO 76
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 76

Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 77
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 77

Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 78
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 78

Gly Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Glu Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 79
<211> LENGTH: 17
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<400> SEQUENCE: 79

Gly Ile Ile Pro Thr Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> SEQ ID NO 80
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 80

Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

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Gly

<210> SEQ ID NO 81
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H2, Kabat

<400> SEQUENCE: 81

Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> SEQ ID NO 82
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 82

Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His
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<210> SEQ ID NO 83
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 83

Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Lys
1 5 10

<210> SEQ ID NO 84
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 84

Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Ser
1 5 10

<210> SEQ ID NO 85
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 85

Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Asn
1 5 10

<210> SEQ ID NO 86
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 86

Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Val
1 5 10

<210> SEQ ID NO 87

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 87

Gly Gly Ala Lys Tyr Ala Ser Thr Tyr Gly Met Asp Val
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<210> SEQ ID NO 88

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 88

Gly Gly Ala Lys Tyr Ala Ser Thr His Gly Met Asp Val
1 5 10

<210> SEQ ID NO 89

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 89

Gly Gly Ala Lys Tyr Ala Ser Gln Leu Gly Met Asp Val
1 5 10

<210> SEQ ID NO 90

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 90

Gly Gly Ala Lys Tyr Ala Ser Lys Trp Gly Met Asp Val
1 5 10

<210> SEQ ID NO 91

<211> LENGTH: 13

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 91

Gly Gly Ala Lys Tyr Ala Val Gly Tyr Gly Met Asp Val
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<210> SEQ ID NO 92

<211> LENGTH: 13

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 92

Gly Gly Ala Lys Tyr Ala Gly Arg Tyr Gly Met Asp Val
1 5 10

<210> SEQ ID NO 93
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 93

Gly Gly Ala Lys Tyr Ala Arg Thr Tyr Gly Met Asp Val
1 5 10

<210> SEQ ID NO 94
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 94

Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Asp Val
1 5 10

<210> SEQ ID NO 95
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 95

Glu Ser Gly Thr Tyr Arg Asp His Arg Leu Asp Val
1 5 10

<210> SEQ ID NO 96
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 96

Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Gly Val
1 5 10

<210> SEQ ID NO 97
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 97

Asp Phe Thr Asp Tyr Ser Ser Gly Tyr Ser Ser Gly Trp Thr Tyr
1 5 10 15

<210> SEQ ID NO 98

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<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 98

Asp Thr Leu Tyr Ser Ser Gly Ala Tyr Tyr Gly Tyr Asn Val
1 5 10

<210> SEQ ID NO 99
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 99

Ala Lys Arg Gly Tyr Asp Ser Tyr Gly Gly Val Tyr Phe Asp Tyr
1 5 10 15

<210> SEQ ID NO 100
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 100

Gly Pro Thr Val Thr Ala Thr Thr Ser Ile Gly Thr His Asn Trp Phe
1 5 10 15

Asp Pro

<210> SEQ ID NO 101
<211> LENGTH: 28
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 101

Glu Gly Arg Gly Tyr Asp Ser Ser Arg Tyr Tyr Lys Phe Trp Phe Asp
1 5 10 15

Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
20 25

<210> SEQ ID NO 102
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 102

Asp Gly Gly Gly Tyr Arg His His Tyr Phe Asp Leu
1 5 10

<210> SEQ ID NO 103
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-H3

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<400> SEQUENCE: 103

Glu Ser Gly Gly Tyr Arg Asp His Lys Leu Asp Val
1 5 10

<210> SEQ ID NO 104

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 104

Asp Gly Gly Gly Tyr Gln His His Tyr Phe Asp Leu
1 5 10

<210> SEQ ID NO 105

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 105

Asp Ser Gly Tyr His Arg His Tyr Ser Asp Tyr
1 5 10

<210> SEQ ID NO 106

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 106

Asp Pro Leu Gly Ile Arg Lys His Trp Phe Asp Pro
1 5 10

<210> SEQ ID NO 107

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 107

Asp Thr Pro Arg Trp Arg Tyr His Tyr Phe Asp Tyr
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<210> SEQ ID NO 108

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 108

Glu Arg Arg Gly Ser Leu Ala Leu Gly Met Asp Val
1 5 10

<210> SEQ ID NO 109

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic: CDR-H3

<400> SEQUENCE: 109

Asp Leu Gly Gly Tyr Ser Tyr Gly Glu Pro Tyr Tyr Tyr Tyr Gly
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Met Asp Val

<210> SEQ ID NO 110

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 110

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> SEQ ID NO 111

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 111

Arg Ala Ser Gln Ser Val Ala Ser Ser Tyr Leu Ala
1 5 10

<210> SEQ ID NO 112

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 112

Glu Ala Ser Gln Ser Val Ser Tyr Ser Tyr Leu Ala
1 5 10

<210> SEQ ID NO 113

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 113

Lys Ala Ser Glu Ser Val Ser Ser Ser Tyr Leu Ala
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<210> SEQ ID NO 114

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 114

Arg Ala Ser Gln Tyr Val Ser Ser Ser Tyr Leu Ala
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<210> SEQ ID NO 115

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<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 115

Lys Ser Ser Gln Ser Val Leu Phe Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> SEQ ID NO 116
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 116

Lys Ser Ser Arg Ser Val Leu Phe Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> SEQ ID NO 117
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 117

Lys Ser Ser Lys Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> SEQ ID NO 118
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 118

Arg Ala Ser Gln Ser Val Gly Ser Asn Leu Ala
1 5 10

<210> SEQ ID NO 119
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 119

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> SEQ ID NO 120
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 120

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
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<210> SEQ ID NO 121

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 121

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> SEQ ID NO 122

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 122

Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Ala
1 5 10

<210> SEQ ID NO 123

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 123

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> SEQ ID NO 124

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L1

<400> SEQUENCE: 124

Arg Ala Ser Gln Ser Val Ser Ser Asp Tyr Leu Ala
1 5 10

<210> SEQ ID NO 125

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 125

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> SEQ ID NO 126

<211> LENGTH: 7

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 126

Gly Ala Ser Asn Arg His Thr
1 5

<210> SEQ ID NO 127
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 127

Tyr Ala Ser Ser Arg Ala Tyr
1 5

<210> SEQ ID NO 128
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 128

Gly Ala Ser Ser Arg Ala Asn
1 5

<210> SEQ ID NO 129
<211> LENGTH: 7
<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 129

Tyr Ala Ser Ser Arg Ala Thr
1 5

<210> SEQ ID NO 130
<211> LENGTH: 7
<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 130

Tyr Ala Ser Asn Arg Ala Thr
1 5

<210> SEQ ID NO 131
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 131

Trp Ala Ser Thr Arg Glu Ser
1 5

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<210> SEQ ID NO 132
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 132

Trp Ala Ser Ser Arg Glu Ser
1 5

<210> SEQ ID NO 133
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 133

Trp Ala Ser Thr Arg Gln Ser
1 5

<210> SEQ ID NO 134
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<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 134

Trp Ala Ser Thr Arg Ala Ser
1 5

<210> SEQ ID NO 135
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 135

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> SEQ ID NO 136
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 136

Gly Ala Ser Thr Arg Ala Ser
1 5

<210> SEQ ID NO 137
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<212> TYPE: PRT
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<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 137

Asp Ala Ser Asn Leu Glu Thr
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<210> SEQ ID NO 138
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<212> TYPE: PRT
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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 138

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> SEQ ID NO 139
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 139

Asp Ala Ser Lys Arg Ala Thr
1 5

<210> SEQ ID NO 140
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L2

<400> SEQUENCE: 140

Lys Ala Ser Ser Leu Glu Ser
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<210> SEQ ID NO 141
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 141

Gln Gln Tyr His Ser Tyr Ile Thr
1 5

<210> SEQ ID NO 142
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 142

Gln Gln Tyr His Asn Ala Ile Thr
1 5

<210> SEQ ID NO 143
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 143

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Gln Gln Tyr Tyr Phe Tyr Ile Thr
1 5

<210> SEQ ID NO 144
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 144

Gln Gln Tyr His Ser Ala Leu Thr
1 5

<210> SEQ ID NO 145
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 145

Gln Gln Tyr His Gly Gly Ile Thr
1 5

<210> SEQ ID NO 146
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 146

Gln Gln Tyr His Arg Arg Ile Thr
1 5

<210> SEQ ID NO 147
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 147

Gln Gln Tyr His Ser Gly Ile Thr
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<210> SEQ ID NO 148
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 148

Gln Gln Tyr Tyr Leu Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 149
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

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<400> SEQUENCE: 149

Gln Gln Tyr Trp Thr Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 150

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 150

Gln Gln Tyr Leu Leu Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 151

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 151

Gln Gln Tyr Leu Ile Trp Pro Leu Thr
1 5

<210> SEQ ID NO 152

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 152

Gln Gln Tyr Leu Leu Trp Pro Leu Thr
1 5

<210> SEQ ID NO 153

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 153

Gln Gln Phe Tyr Phe Phe Pro Pro Thr
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<210> SEQ ID NO 154

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 154

Gln Gln Ala Tyr Thr Phe Pro Pro Thr
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<210> SEQ ID NO 155

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 155

Gln Gln Tyr Tyr Ile Phe Pro Pro Thr
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<210> SEQ ID NO 156

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 156

Gln Gln Arg Asn Phe Tyr Pro Pro Thr
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<210> SEQ ID NO 157

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 157

Gln Gln Phe Val Leu Trp Pro Arg Thr
1 5

<210> SEQ ID NO 158

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 158

Gln Gln His Val Asn Phe Pro Leu Thr
1 5

<210> SEQ ID NO 159

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 159

Gln Gln Ser Val Phe Trp Pro Ile Thr
1 5

<210> SEQ ID NO 160

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 160

Gln Gln Leu Thr Lys Trp Pro Leu Thr
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<210> SEQ ID NO 161

<211> LENGTH: 9

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 161

Gln Gln Asp Val Leu Trp Pro Leu Thr
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<210> SEQ ID NO 162
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 162

Gln Gln Tyr Gly Leu Phe Pro Ile Thr
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<210> SEQ ID NO 163
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 163

Gln Gln His Thr Val Trp Pro Ile Thr
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<210> SEQ ID NO 164
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 164

Gln Gln Val Leu Asn Tyr Pro Leu Thr
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<210> SEQ ID NO 165
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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 165

Gln Gln Ser Tyr Phe Leu Pro Pro Thr
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<210> SEQ ID NO 166
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: CDR-L3

<400> SEQUENCE: 166

Gln Gln Ala His Ser Ser Pro Tyr Thr
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<210> SEQ ID NO 167

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<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Leader for scFV, scFv-Fc, Leader

<400> SEQUENCE: 167

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala
20

<210> SEQ ID NO 168
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: Linker for scFV, scFV-FC, Linker

<400> SEQUENCE: 168

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> SEQ ID NO 169
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-Term Tag for scFV, scFV-FC, C-Term Tag

<400> SEQUENCE: 169

Gly Pro Gly Gly Gln His His His His His His
1 5 10

<210> SEQ ID NO 170
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: C-Term Tag for scFv, scFV-FC, C-Term Tag

<400> SEQUENCE: 170

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
1 5 10 15

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
20 25 30

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
35 40 45

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
50 55 60

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
65 70 75 80

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
85 90 95

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
100 105 110

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
115 120 125

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Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys
130						135					140				
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
145					150					155					160
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
			165						170					175	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
			180					185					190		
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
	195						200					205			
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
210					215						220				
Leu	Ser	Leu	Ser	Pro	Gly	Lys									
225					230										

<210> SEQ ID NO 171

<211> LENGTH: 276

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: scFv, 29872

<400> SEQUENCE: 171

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Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu
			20					25					30		
Val	Lys	Glu	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Pro	Gly
		35				40					45				
Tyr	Thr	Phe	Thr	Ser	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly
	50					55					60				
Gln	Gly	Leu	Glu	Trp	Met	Gly	Val	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr
65				70					75					80	
Ser	Tyr	Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr
			85					90					95		
Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp
			100				105					110			
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu
	115					120					125				
Tyr	Leu	Arg	His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly
	130				135						140				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile
145				150					155					160	
Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg
			165					170					175		
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Tyr	Leu
		180						185					190		
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
		195				200						205			
Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
210					215					220					
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu
225					230					235				240	

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Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Ile Thr Phe
245 250 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Pro Gly Gly Gln His His
260 265 270

His His His His
275

<210> SEQ ID NO 172
<211> LENGTH: 276
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: scFv, 31895

<400> SEQUENCE: 172

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Thr Phe Lys Ser Tyr Glu Met His Trp Val Arg Gln Ala Pro Gly
50 55 60

Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Ser Val Gly Ser Thr
65 70 75 80

Trp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
85 90 95

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu
115 120 125

Tyr Leu Arg Lys Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser Tyr Leu
180 185 190

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
195 200 205

Gly Ala Ser Asn Arg His Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
210 215 220

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
225 230 235 240

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Asn Ala Ile Thr Phe
245 250 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Pro Gly Gly Gln His His
260 265 270

His His His His
275

<210> SEQ ID NO 173
<211> LENGTH: 276

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: scFv, 31414

<400> SEQUENCE: 173

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30
Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45
Tyr Thr Phe Lys Ser Tyr Glu Met His Trp Val Arg Gln Ala Pro Gly
50 55 60
Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Ser Val Gly Ser Thr
65 70 75 80
Trp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
85 90 95
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
100 105 110
Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu
115 120 125
Tyr Leu Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile
145 150 155 160
Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175
Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu
180 185 190
Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
195 200 205
Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
210 215 220
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
225 230 235 240
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Ile Thr Phe
245 250 255
Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Pro Gly Gly Gln His His
260 265 270
His His His His
275

<210> SEQ ID NO 174
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: scFv, 31905

<400> SEQUENCE: 174

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30

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Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 35 40 45
 Gly Thr Phe Pro Ser Asn Ala Ile Ser Trp Val Arg Gln Ala Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Met Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr
 65 70 75 80
 Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr
 85 90 95
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Arg Gly Gly Ala Lys Tyr Ala Arg Thr Tyr Gly
 115 120 125
 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
 130 135 140
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
 145 150 155 160
 Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala
 165 170 175
 Thr Ile Asn Cys Lys Ser Ser Lys Ser Val Leu Tyr Ser Asn Asn Asn
 180 185 190
 Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
 195 200 205
 Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val Pro Asp Arg
 210 215 220
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
 225 230 235 240
 Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Leu
 245 250 255
 Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Pro
 260 265 270
 Gly Gly Gln His His His His His His
 275 280

<210> SEQ ID NO 175

<211> LENGTH: 496

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: scFv-Fc, 29872

<400> SEQUENCE: 175

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
 20 25 30
 Val Lys Glu Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Pro Gly
 35 40 45
 Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly
 50 55 60
 Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Ser Gly Gly Ser Thr
 65 70 75 80
 Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
 85 90 95

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Ser	Thr	Ser	Thr	Val	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp
			100					105					110		
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu
		115					120					125			
Tyr	Leu	Arg	His	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly
	130				135						140				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Ile
145				150						155				160	
Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg
				165					170					175	
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Tyr	Leu
			180					185					190		
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
	195						200					205			
Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	210					215					220				
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu
225				230						235					240
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	His	Ser	Tyr	Ile	Thr	Phe
				245					250					255	
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Pro	Lys	Ser	Cys	Asp	Lys	Thr
			260					265					270		
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
		275					280					285			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
	290					295					300				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
305					310				315						320
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				325					330					335	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
			340					345					350		
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
		355					360					365			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
	370					375				380					
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
385					390					395					400
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			405						410					415	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
			420					425					430		
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
		435					440					445			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr								

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<210> SEQ ID NO 176
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: scFv-Fc, 31895

<400> SEQUENCE: 176

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Thr Phe Lys Ser Tyr Glu Met His Trp Val Arg Gln Ala Pro Gly
50 55 60

Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Ser Val Gly Ser Thr
65 70 75 80

Trp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
85 90 95

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu
115 120 125

Tyr Leu Arg Lys Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile
145 150 155 160

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
165 170 175

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser Tyr Leu
180 185 190

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
195 200 205

Gly Ala Ser Asn Arg His Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
210 215 220

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
225 230 235 240

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Asn Ala Ile Thr Phe
245 250 255

Gly Gly Gly Thr Lys Val Glu Ile Lys Pro Lys Ser Cys Asp Lys Thr
260 265 270

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
275 280 285

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
290 295 300

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
305 310 315 320

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
325 330 335

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
340 345 350

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Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
   355                               360               365

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
   370                               375               380

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
  385                               390               395               400

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                     405               410               415

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
                     420               425               430

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
   435                               440               445

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
   450                               455               460

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
  465                               470               475               480

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                     485               490               495

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<210> SEQ ID NO 177

<211> LENGTH: 496

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: scFv-Fc, 31414

<400> SEQUENCE: 177

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
  1                               5               10               15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
                     20               25               30

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
   35                               40               45

Tyr Thr Phe Lys Ser Tyr Glu Met His Trp Val Arg Gln Ala Pro Gly
   50                               55               60

Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Ser Val Gly Ser Thr
   65                               70               75               80

Trp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
                     85               90               95

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
   100                               105               110

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu
   115                               120               125

Tyr Leu Arg Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
   130                               135               140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Glu Ile
  145                               150               155               160

Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
                     165               170               175

Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu
   180                               185               190

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
   195                               200               205

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<210> SEQ ID NO 178
<211> LENGTH: 501
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: scFv-Fc, 31905

<400> SEQUENCE: 178

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1             5             10             15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu
                20             25             30

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
            35             40             45

Gly Thr Phe Pro Ser Asn Ala Ile Ser Trp Val Arg Gln Ala Pro Gly
            50             55             60

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Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Gly	Phe	Gly	Thr	Ala	Asn	Tyr	65	70	75	80
Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	85	90	95	
Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	100	105	110	
Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Gly	Ala	Lys	Tyr	Ala	Arg	Thr	Tyr	Gly	115	120	125	
Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	130	135	140	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	145	150	155	160
Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly	Glu	Arg	Ala	165	170	175	
Thr	Ile	Asn	Cys	Lys	Ser	Ser	Lys	Ser	Val	Leu	Tyr	Ser	Asn	Asn	Asn	180	185	190	
Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	195	200	205	
Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Gln	Ser	Gly	Val	Pro	Asp	Arg	210	215	220	
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	225	230	235	240
Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Leu	Leu	245	250	255	
Tyr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Pro	Lys	260	265	270	
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	275	280	285	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	290	295	300	
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	305	310	315	320
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	325	330	335	
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	340	345	350	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	355	360	365	
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	370	375	380	
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	385	390	395	400
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	405	410	415	
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	420	425	430	
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	435	440	445	
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	450	455	460	
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser				

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465	470	475	480
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
	485	490	495
Leu Ser Pro Gly Lys			
500			

<210> SEQ ID NO 179
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27579

<400> SEQUENCE: 179

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Glu Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Pro Gly Tyr Thr Phe Thr Ser Tyr			
20	25	30	
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Val Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe			
50	55	60	
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr			
65	70	75	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly			
100	105	110	
Gln Gly Thr Leu Val Thr Val Ser Ser			
115	120		

<210> SEQ ID NO 180
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 31895

<400> SEQUENCE: 180

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr			
20	25	30	
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe			
50	55	60	
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr			
65	70	75	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Lys Trp Gly			
100	105	110	
Gln Gly Thr Leu Val Thr Val Ser Ser			
115	120		

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<210> SEQ ID NO 181
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31415

<400> SEQUENCE: 181

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gln Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Ser Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 182
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31414

<400> SEQUENCE: 182

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr
20 25 30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Asn Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 183
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31891

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<400> SEQUENCE: 183

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Lys Ser Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Val Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 184

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 29871

<400> SEQUENCE: 184

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Gln Ser Tyr
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Lys Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 185

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 31418

<400> SEQUENCE: 185

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr
20 25 30

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Glu	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Arg	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Trp	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu	Tyr	Leu	Arg	His	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120								

<210> SEQ ID NO 186
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 31431

<400> SEQUENCE: 186

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
		20					25						30		
Gln	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Arg	Ile	Asn	Pro	Ser	Gly	Gly	Ser	Thr	Trp	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu	Tyr	Leu	Arg	His	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
		115					120								

<210> SEQ ID NO 187
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 31421

<400> SEQUENCE: 187

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Phe	Ser	Tyr
		20					25						30		
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Val	Ile	Asn	Pro	Leu	Gly	Gly	Gly	Thr	Ser	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr
65					70					75					80

-continued

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 188
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31429

<400> SEQUENCE: 188

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Val Ser Tyr
20 25 30
Phe Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Asn Pro Arg Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 189
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 29872

<400> SEQUENCE: 189

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr
20 25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser

-continued

115	120
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<210> SEQ ID NO 190
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 28347

<400> SEQUENCE: 190

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Leu	
20 25 30	
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	
50 55 60	
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr	
65 70 75 80	
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Arg Gly Gly Ala Lys Tyr Ala Ser Thr Tyr Gly Met Asp Val Trp	
100 105 110	
Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

<210> SEQ ID NO 191
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31896

<400> SEQUENCE: 191

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	
1 5 10 15	
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Lys Leu	
20 25 30	
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly	
50 55 60	
Arg Val Thr Ile Thr Ala Asp Glu Ser Ala Ser Thr Ala Tyr Met Glu	
65 70 75 80	
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg	
85 90 95	
Gly Gly Ala Lys Tyr Ala Ser Thr His Gly Met Asp Val Trp Gly Gln	
100 105 110	
Gly Thr Thr Val Thr Val Ser Ser	
115 120	

<210> SEQ ID NO 192
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic: VH, 31432

<400> SEQUENCE: 192

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser His Thr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Leu Pro Ile Gly Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Ala Lys Tyr Ala Ser Gln Leu Gly Met Asp Val Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 193

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 31915

<400> SEQUENCE: 193

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Leu
20 25 30
Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly
50 55 60
Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
65 70 75 80
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95
Gly Gly Ala Lys Tyr Ala Ser Lys Trp Gly Met Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 194

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 31436

<400> SEQUENCE: 194

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Leu Leu

-continued

20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35	40	45
Gly Gly Ile Leu Pro Ile Ala Gly Thr Ala Asn Tyr Ala Gln Lys Phe		
50	55	60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr		
65	70	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Gly Gly Ala Lys Tyr Ala Val Gly Tyr Gly Met Asp Val Trp		
100	105	110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
115	120	

<210> SEQ ID NO 195

<211> LENGTH: 122

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 31437

<400> SEQUENCE: 195

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
1	5	10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gln Ser Leu		
20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35	40	45
Gly Gly Ile Leu Pro Ile Gly Gly Thr Ala Asn Tyr Ala Gln Lys Phe		
50	55	60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr		
65	70	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Gly Gly Ala Lys Tyr Ala Gly Arg Tyr Gly Met Asp Val Trp		
100	105	110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
115	120	

<210> SEQ ID NO 196

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VH, 31905

<400> SEQUENCE: 196

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser		
1	5	10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Pro Ser Asn		
20	25	30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35	40	45
Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly		
50	55	60

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Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
65                               70                               75                               80

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                        85                               90                               95

Gly Gly Ala Lys Tyr Ala Arg Thr Tyr Gly Met Asp Val Trp Gly Gln
                100                               105                               110

Gly Thr Thr Val Thr Val Ser Ser
        115                               120

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<210> SEQ ID NO 197
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31901

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<400> SEQUENCE: 197

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1                               5                               10                               15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Leu
                20                               25                               30

Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                               40                               45

Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly
        50                               55                               60

Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu
65                               70                               75                               80

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                        85                               90                               95

Gly Gly Ala Lys Tyr Ala Gly Arg Tyr Gly Met Asp Val Trp Gly Gln
                100                               105                               110

Gly Thr Thr Val Thr Val Ser Ser
        115                               120

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<210> SEQ ID NO 198
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 29852

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<400> SEQUENCE: 198

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1                               5                               10                               15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ala Met
        20                               25                               30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                               40                               45

Gly Gly Ile Leu Pro Ile Ala Gly Thr Ala Asn Tyr Ala Gln Lys Phe
        50                               55                               60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                               70                               75                               80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                        85                               90                               95

Ala Arg Gly Gly Ala Lys Tyr Ala Ser Thr Tyr Gly Met Asp Val Trp
        100                               105                               110

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Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 199
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 29851

<400> SEQUENCE: 199

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ala Ser Leu
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Leu Pro Ile Phe Gly Glu Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Ala Lys Tyr Ala Ser Thr Tyr Gly Met Asp Val Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 200
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 29857

<400> SEQUENCE: 200

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Trp Leu
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Arg Gly Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gly Gly Ala Lys Tyr Ala Ser Thr Tyr Gly Met Asp Val Trp
100 105 110
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 201
<211> LENGTH: 121
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27571

<400> SEQUENCE: 201

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Ala Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Arg Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Thr Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Asp Val Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 202
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31861

<400> SEQUENCE: 202

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Ser Tyr
20 25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ser Gly Thr Tyr Arg Asp His Arg Leu Asp Val Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 203
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31873

<400> SEQUENCE: 203

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

-continued

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Lys Tyr
20 25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Gly Val Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 204
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 31393

<400> SEQUENCE: 204

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Glu Ser Tyr
20 25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Asp Val Trp Gly
100 105 110
Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 205
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27534

<400> SEQUENCE: 205

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe

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50	55	60
Gln Gly Arg Val Thr	Ile Thr Ala Asp Glu Ser	Thr Ser Thr Ala Tyr
65	70	75 80
Met Glu Leu Ser Ser	Leu Arg Ser Glu Asp Thr	Ala Val Tyr Tyr Cys
	85	90 95
Ala Arg Asp Phe Thr	Asp Tyr Ser Ser Gly Tyr	Ser Ser Gly Trp Thr
	100	105 110
Tyr Trp Gly Gln Gly	Thr Leu Val Thr Val Ser Ser	
	115	120

<210> SEQ ID NO 206
 <211> LENGTH: 123
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27536

<400> SEQUENCE: 206

Gln Val Gln Leu Val	Gln Ser Gly Ala Glu Val	Lys Lys Pro Gly Ser
1	5	10 15
Ser Val Lys Val Ser	Cys Lys Ala Ser Gly Gly	Thr Phe Ser Asn Tyr
	20	25 30
Ala Ile Ser Trp Val	Arg Gln Ala Pro Gly Gln	Gly Leu Glu Trp Met
	35	40 45
Gly Gly Ile Ile Pro	Ile Phe Gly Thr Ala Asn	Tyr Ala Gln Lys Phe
	50	55 60
Gln Gly Arg Val Thr	Ile Thr Ala Asp Glu Ser	Thr Ser Thr Ala Tyr
65	70	75 80
Met Glu Leu Ser Ser	Leu Arg Ser Glu Asp Thr	Ala Val Tyr Tyr Cys
	85	90 95
Ala Arg Asp Thr Leu	Tyr Ser Ser Gly Ala Tyr	Tyr Gly Tyr Asn Val
	100	105 110
Trp Gly Gln Gly Thr	Met Val Thr Val Ser Ser	
	115	120

<210> SEQ ID NO 207
 <211> LENGTH: 124
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27588

<400> SEQUENCE: 207

Gln Val Gln Leu Val	Gln Ser Gly Ala Glu Val	Lys Lys Pro Gly Ser
1	5	10 15
Ser Val Lys Val Ser	Cys Lys Ala Ser Gly Gly	Thr Phe Ser Asn Tyr
	20	25 30
Ala Ile Ser Trp Val	Arg Gln Ala Pro Gly Gln	Gly Leu Glu Trp Met
	35	40 45
Gly Gly Ile Ile Pro	Ile Phe Gly Thr Ala Asn	Tyr Ala Gln Lys Phe
	50	55 60
Gln Gly Arg Val Thr	Ile Thr Ala Asp Glu Ser	Thr Ser Thr Ala Tyr
65	70	75 80
Met Glu Leu Ser Ser	Leu Arg Ser Glu Asp Thr	Ala Val Tyr Tyr Cys
	85	90 95

-continued

Ala	Arg	Ala	Lys	Arg	Gly	Tyr	Asp	Ser	Tyr	Gly	Gly	Val	Tyr	Phe	Asp
			100					105						110	

Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115				120					

<210> SEQ ID NO 208
 <211> LENGTH: 127
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27590

<400> SEQUENCE: 208

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Asn	Tyr
		20						25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75				80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Gly	Pro	Thr	Val	Thr	Ala	Thr	Thr	Ser	Ile	Gly	Thr	His	Asn
			100					105					110		
Trp	Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
		115				120					125				

<210> SEQ ID NO 209
 <211> LENGTH: 126
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27597

<400> SEQUENCE: 209

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
		20						25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Ser	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55				60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75				80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Glu	Gly	Arg	Gly	Tyr	Asp	Ser	Ser	Arg	Tyr	Tyr	Lys	Phe	Trp
		100						105					110		
Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115				120					125				

<210> SEQ ID NO 210

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<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27575

<400> SEQUENCE: 210

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Glu Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Thr Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Glu Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Gly Gly Gly Tyr Arg His His Tyr Phe Asp Leu Trp Gly
100 105 110
Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 211
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27568

<400> SEQUENCE: 211

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Pro Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Glu Gln Gly Leu Glu Trp Met
35 40 45
Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Gly Glu Ser Gly Gly Tyr Arg Asp His Lys Leu Asp Val Trp Gly
100 105 110
Gln Gly Thr Val Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 212
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27577

<400> SEQUENCE: 212

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ala Phe Ser Ser Tyr
          20          25          30
Ala Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Gly Ile Ile Pro Thr Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
          65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Asp Gly Gly Gly Tyr Gln His His Tyr Phe Asp Leu Trp Gly
          100          105          110
Arg Gly Thr Leu Val Thr Val Ser Ser
          115          120

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<210> SEQ ID NO 213
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27587

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<400> SEQUENCE: 213

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
          65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Lys Leu Asp Val Trp Gly
          100          105          110
Gln Gly Thr Met Val Thr Val Ser Ser
          115          120

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<210> SEQ ID NO 214
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27589

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<400> SEQUENCE: 214

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45

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Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Tyr His Arg His Tyr Ser Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 215
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27596

<400> SEQUENCE: 215

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro Leu Gly Ile Arg Lys His Trp Phe Asp Pro Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 216
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VH, 27535

<400> SEQUENCE: 216

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

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85	90	95
Ala Arg Asp Thr Pro Arg Trp Arg Tyr His Tyr Phe Asp Tyr Trp Gly		
100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser		
115	120	

<210> SEQ ID NO 217
 <211> LENGTH: 121
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27550

<400> SEQUENCE: 217

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly		
1	5	10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr		
20	25	30
Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr		
65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Glu Arg Arg Gly Ser Leu Ala Leu Gly Met Asp Val Trp Gly		
100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser		
115	120	

<210> SEQ ID NO 218
 <211> LENGTH: 128
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VH, 27549

<400> SEQUENCE: 218

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg		
1	5	10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr		
20	25	30
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Asp Leu Gly Gly Tyr Ser Tyr Gly Glu Pro Tyr Tyr Tyr Tyr		
100	105	110
Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser		
115	120	125

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<210> SEQ ID NO 219
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27579

<400> SEQUENCE: 219

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Ile
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 220
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31895

<400> SEQUENCE: 220

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg His Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Asn Ala Ile
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 221
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31891

<400> SEQUENCE: 221

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Glu	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Asn	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75				80	
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	His	Ser	Ala	Leu
				85					90					95	

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Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 224
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31431

<400> SEQUENCE: 224

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Asn Arg His Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Gly Gly Ile
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 225
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31421

<400> SEQUENCE: 225

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Glu Ser Val Ser Ser
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Tyr Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Arg Arg Ile
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 226
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31429

<400> SEQUENCE: 226

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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1	5	10	15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Ser Ser Ser	20	25	30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	35	40	45
Ile Tyr Tyr Ala Ser Asn Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser	50	55	60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	65	70	75
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Ser Gly Ile	85	90	95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys	100	105	

<210> SEQ ID NO 227
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 28347

<400> SEQUENCE: 227

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	1	5	10	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser	20	25	30	
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45	
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60	
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65	70	75	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	85	90	95	
Tyr Tyr Leu Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	100	105	110	

Lys

<210> SEQ ID NO 228
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 31896

<400> SEQUENCE: 228

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	1	5	10	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Arg Ser Val Leu Phe Ser	20	25	30	
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45	
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60	
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr				

-continued

65	70	75	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln			
	85	90	95
Tyr Trp Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile			
	100	105	110

Lys

<210> SEQ ID NO 229
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 31915

<400> SEQUENCE: 229

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly			
1	5	10	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser			
	20	25	30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln			
	35	40	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ser Arg Glu Ser Gly Val			
	50	55	60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr			
65	70	75	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln			
	85	90	95
Tyr Trp Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile			
	100	105	110

Lys

<210> SEQ ID NO 230
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 31905

<400> SEQUENCE: 230

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly			
1	5	10	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Lys Ser Val Leu Tyr Ser			
	20	25	30
Asn Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln			
	35	40	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val			
	50	55	60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr			
65	70	75	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln			
	85	90	95
Tyr Leu Leu Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile			
	100	105	110

Lys

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<210> SEQ ID NO 231
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31901

<400> SEQUENCE: 231

Gly Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Leu Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> SEQ ID NO 232
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27571

<400> SEQUENCE: 232

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Ile Trp Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 233
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 31861

<400> SEQUENCE: 233

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Leu Trp Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 234
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 31873

<400> SEQUENCE: 234

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Thr Arg Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Leu Trp Pro Leu
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 235
 <211> LENGTH: 113
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: VL, 28337

<400> SEQUENCE: 235

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15
 Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser
 20 25 30
 Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln

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85	90	95
Phe Tyr Phe Tyr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile		
100	105	110

Lys

<210> SEQ ID NO 236
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27536

<400> SEQUENCE: 236

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly		
1	5	10
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser		
20	25	30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln		
35	40	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val		
50	55	60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr		
65	70	75
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln		
85	90	95
Ala Tyr Thr Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile		
100	105	110

Lys

<210> SEQ ID NO 237
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27588

<400> SEQUENCE: 237

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly		
1	5	10
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr		
20	25	30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile		
35	40	45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly		
50	55	60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro		
65	70	75
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ile Phe Pro Pro		
85	90	95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys		
100	105	

<210> SEQ ID NO 238
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VL, 27590

<400> SEQUENCE: 238

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Phe Tyr Pro Pro
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 239

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VL, 27597

<400> SEQUENCE: 239

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Val Leu Trp Pro Arg
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 240

<211> LENGTH: 107

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: VL, 27575

<400> SEQUENCE: 240

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
50						55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65				70						75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	His	Val	Asn	Phe	Pro	Leu
			85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> SEQ ID NO 241
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27568

<400> SEQUENCE: 241

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Tyr
		20						25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40						45			
Tyr	Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
50						55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65				70						75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Val	Phe	Trp	Pro	Ile
			85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> SEQ ID NO 242
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27577

<400> SEQUENCE: 242

Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly
1			5						10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Gly	Ser	Asn
		20						25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40						45			
Tyr	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
50						55				60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser
65				70						75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Leu	Thr	Lys	Trp	Pro	Leu
			85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys					
		100						105							

<210> SEQ ID NO 243

-continued

<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27587

<400> SEQUENCE: 243

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Val Leu Trp Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 244
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27589

<400> SEQUENCE: 244

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Gly Leu Phe Pro Ile
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 245
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27596

<400> SEQUENCE: 245

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
   35           40           45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
   50           55           60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
   65           70           75           80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Thr Val Trp Pro Ile
           85           90           95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100           105

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<210> SEQ ID NO 246
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27535

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<400> SEQUENCE: 246

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1           5           10           15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
      20           25           30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
   35           40           45

Tyr Asp Ala Ser Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
   50           55           60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
   65           70           75           80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Val Leu Asn Tyr Pro Leu
           85           90           95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100           105

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<210> SEQ ID NO 247
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27550

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<400> SEQUENCE: 247

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
      20           25           30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
   35           40           45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
   50           55           60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
   65           70           75           80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Leu Pro Pro
           85           90           95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100           105

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<210> SEQ ID NO 248
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: VL, 27549

<400> SEQUENCE: 248
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asp
20 25 30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ala His Ser Ser Pro
85 90 95
Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 249
<211> LENGTH: 510
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: hCD39

<400> SEQUENCE: 249
Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
1 5 10 15
Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
20 25 30
Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125
Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140
Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160
Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys

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180					185					190					
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr
	195						200					205			
Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val
	210					215					220				
Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg
	225				230					235					240
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr
			245						250					255	
Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val
		260					265						270		
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys
		275					280					285			
Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg
	290					295					300				
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly
	305				310					315					320
Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser
				325					330					335	
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro
		340						345					350		
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
		355					360					365			
Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu
	370					375					380				
Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser
	385				390					395					400
Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly
			405						410					415	
Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp
		420						425					430		
Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala
	435					440						445			
Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala
	450					455					460				
Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	Phe	Leu
	465				470					475					480
Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	Gly	Leu
			485					490						495	
Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val		
	500							505				510			

<210> SEQ ID NO 250

<211> LENGTH: 510

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: mCD39

<400> SEQUENCE: 250

Met	Glu	Asp	Ile	Lys	Asp	Ser	Lys	Val	Lys	Arg	Phe	Cys	Ser	Lys	Asn
1				5						10					15

Ile	Leu	Ile	Ile	Leu	Gly	Phe	Thr	Ser	Ile	Leu	Ala	Val	Ile	Ala	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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20						25						30					
Ile	Ala	Val	Gly	Leu	Thr	Gln	Asn	Lys	Pro	Leu	Pro	Glu	Asn	Val	Lys		
		35					40					45					
Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Asn	Leu	Tyr	Ile		
	50					55					60						
Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	Gln	Gln		
65					70					75				80			
Leu	Glu	Glu	Cys	Gln	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Tyr	Ala	Gln		
				85					90					95			
Lys	Thr	Asp	Glu	Ile	Gly	Ala	Tyr	Leu	Ala	Glu	Cys	Met	Glu	Leu	Ser		
		100						105					110				
Thr	Glu	Leu	Ile	Pro	Thr	Ser	Lys	His	His	Gln	Thr	Pro	Val	Tyr	Leu		
		115					120					125					
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Gln	Ser		
	130					135					140						
Ala	Asp	Glu	Val	Leu	Ala	Ala	Val	Ser	Thr	Ser	Leu	Lys	Ser	Tyr	Pro		
145					150					155					160		
Phe	Asp	Phe	Gln	Gly	Ala	Lys	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala		
			165						170					175			
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Arg	Phe	Thr	Gln	Glu		
			180					185					190				
Gln	Ser	Trp	Leu	Ser	Leu	Ile	Ser	Asp	Ser	Gln	Lys	Gln	Glu	Thr	Phe		
		195					200					205					
Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Ile	Thr	Phe	Val	Pro		
	210					215					220						
Gln	Asn	Ser	Thr	Ile	Glu	Ser	Pro	Glu	Asn	Ser	Leu	Gln	Phe	Arg	Leu		
225					230					235					240		
Tyr	Gly	Glu	Asp	Tyr	Thr	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly		
			245						250					255			
Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ser		
			260					265					270				
Ser	Gly	Gly	Val	Leu	Lys	Asp	Pro	Cys	Phe	Asn	Pro	Gly	Tyr	Glu	Lys		
		275					280					285					
Val	Val	Asn	Val	Ser	Glu	Leu	Tyr	Gly	Thr	Pro	Cys	Thr	Lys	Arg	Phe		
	290					295					300						
Glu	Lys	Lys	Leu	Pro	Phe	Asp	Gln	Phe	Arg	Ile	Gln	Gly	Thr	Gly	Asp		
305					310					315					320		
Tyr	Glu	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Asn	Ser	His		
			325						330					335			
Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Val	Phe	Leu	Pro	Pro	Leu		
			340					345					350				
His	Gly	Ser	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Asp	Phe		
		355						360				365					
Phe	Lys	Lys	Val	Ala	Lys	Asn	Ser	Val	Ile	Ser	Gln	Glu	Lys	Met	Thr		
	370					375					380						
Glu	Ile	Thr	Lys	Asn	Phe	Cys	Ser	Lys	Ser	Trp	Glu	Glu	Thr	Lys	Thr		
385					390					395					400		
Ser	Tyr	Pro	Ser	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser		
			405						410					415			
Gly	Ala	Tyr	Ile	Leu	Ser	Leu	Leu	Gln	Gly	Tyr	Asn	Phe	Thr	Asp	Ser		
			420					425					430				

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Ser Trp Glu Gln Ile His Phe Met Gly Lys Ile Lys Asp Ser Asn Ala
435 440 445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460
Glu Gln Pro Leu Ser Pro Pro Leu Pro His Ser Thr Tyr Ile Gly Leu
465 470 475 480
Met Val Leu Phe Ser Leu Leu Leu Val Ala Val Ala Ile Thr Gly Leu
485 490 495
Phe Ile Tyr Ser Lys Pro Ser Tyr Phe Trp Lys Glu Ala Val
500 505 510

<210> SEQ ID NO 251
<211> LENGTH: 532
<212> TYPE: PRT
<213> ORGANISM: Macaca fascicularis
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(532)
<223> OTHER INFORMATION: Macaca fascicularis cCD39

<400> SEQUENCE: 251

Met Leu Phe Asp Ser Ile Leu Ser Thr Val Gly Leu Ser Lys Leu Val
1 5 10 15
Ser Val Val Ser Ser Pro Ala Ala Ala Leu Ser Lys Ser Asn Val Lys
20 25 30
Thr Phe Cys Ser Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile
35 40 45
Ile Ala Val Ile Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala
50 55 60
Leu Pro Glu Asn Ile Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser
65 70 75 80
His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp
85 90 95
Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly
100 105 110
Ile Ser Lys Tyr Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr
115 120 125
Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln
130 135 140
Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg
145 150 155 160
Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg
165 170 175
Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr
180 185 190
Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu
195 200 205
Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu
210 215 220
Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser
225 230 235 240
Thr Gln Ile Thr Phe Val Pro Gln Asn Gln Thr Thr Glu Ser Pro Asp
245 250 255

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Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr
    260                265                270

His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu
    275                280                285

Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys
    290                295                300

Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys
    305                310                315                320

Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe
    325                330                335

Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Val Leu
    340                345                350

Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn
    355                360                365

Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala
    370                375                380

Phe Tyr Phe Val Met Asn Phe Leu Asn Leu Thr Ser Glu Lys Val Ser
    385                390                395                400

Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys Ser Gln Pro Trp
    405                410                415

Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser
    420                425                430

Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly
    435                440                445

Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys
    450                455                460

Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu
    465                470                475                480

Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His
    485                490                495

Ser Thr Tyr Val Phe Leu Met Val Leu Phe Ser Leu Val Leu Val Ile
    500                505                510

Val Ala Ile Ile Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp
    515                520                525

Lys Asp Met Val
    530

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<210> SEQ ID NO 252

<211> LENGTH: 473

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: hCD39 ECD

<400> SEQUENCE: 252

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Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1          5          10          15

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
    20          25          30

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
    35          40          45

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
    50          55          60

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Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro
65					70					75				80	
Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly
			85						90					95	
Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu
		100						105					110		
Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly
	115						120					125			
Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr
130					135						140				
Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser
145					150					155					160
Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp
				165					170					175	
Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr
			180					185					190		
Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp
		195					200					205			
Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala
210						215					220				
Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile
225					230					235					240
Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val
				245					250					255	
Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu
		260						265					270		
Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys
		275					280					285			
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser
290						295					300				
Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe
305					310					315					320
Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr
				325					330					335	
Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	Lys	Lys	Phe
			340					345					350		
Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys
		355					360					365			
Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser
370						375					380				
Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	Glu	His	Ile
385					390					395					400
His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	Thr	Leu	Gly
			405					410						415	
Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala	Glu	Gln	Pro	Leu	Ser
		420						425					430		
Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	Phe	Leu	Met	Val	Leu	Phe	Ser
		435					440					445			
Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	Gly	Leu	Leu	Ile	Phe	His	Lys
450						455					460				
Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val							

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465 470

<210> SEQ ID NO 253
<211> LENGTH: 473
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: mCD39 ECD

<400> SEQUENCE: 253

Thr Gln Asn Lys Pro Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
1 5 10 15

Asp Ala Gly Ser Ser His Thr Asn Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30

Glu Lys Glu Asn Asp Thr Gly Val Val Gln Gln Leu Glu Glu Cys Gln
35 40 45

Val Lys Gly Pro Gly Ile Ser Lys Tyr Ala Gln Lys Thr Asp Glu Ile
50 55 60

Gly Ala Tyr Leu Ala Glu Cys Met Glu Leu Ser Thr Glu Leu Ile Pro
65 70 75 80

Thr Ser Lys His His Gln Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95

Met Arg Leu Leu Arg Met Glu Ser Glu Gln Ser Ala Asp Glu Val Leu
100 105 110

Ala Ala Val Ser Thr Ser Leu Lys Ser Tyr Pro Phe Asp Phe Gln Gly
115 120 125

Ala Lys Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140

Ile Asn Tyr Leu Leu Gly Arg Phe Thr Gln Glu Gln Ser Trp Leu Ser
145 150 155 160

Leu Ile Ser Asp Ser Gln Lys Gln Glu Thr Phe Gly Ala Leu Asp Leu
165 170 175

Gly Gly Ala Ser Thr Gln Ile Thr Phe Val Pro Gln Asn Ser Thr Ile
180 185 190

Glu Ser Pro Glu Asn Ser Leu Gln Phe Arg Leu Tyr Gly Glu Asp Tyr
195 200 205

Thr Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
210 215 220

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ser Ser Gly Gly Val Leu
225 230 235 240

Lys Asp Pro Cys Phe Asn Pro Gly Tyr Glu Lys Val Val Asn Val Ser
245 250 255

Glu Leu Tyr Gly Thr Pro Cys Thr Lys Arg Phe Glu Lys Lys Leu Pro
260 265 270

Phe Asp Gln Phe Arg Ile Gln Gly Thr Gly Asp Tyr Glu Gln Cys His
275 280 285

Gln Ser Ile Leu Glu Leu Phe Asn Asn Ser His Cys Pro Tyr Ser Gln
290 295 300

Cys Ala Phe Asn Gly Val Phe Leu Pro Pro Leu His Gly Ser Phe Gly
305 310 315 320

Ala Phe Ser Ala Phe Tyr Phe Val Met Asp Phe Phe Lys Lys Val Ala
325 330 335

Lys Asn Ser Val Ile Ser Gln Glu Lys Met Thr Glu Ile Thr Lys Asn

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340	345	350
Phe Cys Ser Lys Ser Trp Glu Glu Thr Lys Thr Ser Tyr Pro Ser Val		
355	360	365
Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Ala Tyr Ile Leu		
370	375	380
Ser Leu Leu Gln Gly Tyr Asn Phe Thr Asp Ser Ser Trp Glu Gln Ile		
385	390	395
His Phe Met Gly Lys Ile Lys Asp Ser Asn Ala Gly Trp Thr Leu Gly		
405	410	415
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser		
420	425	430
Pro Pro Leu Pro His Ser Thr Tyr Ile Gly Leu Met Val Leu Phe Ser		
435	440	445
Leu Leu Leu Val Ala Val Ala Ile Thr Gly Leu Phe Ile Tyr Ser Lys		
450	455	460
Pro Ser Tyr Phe Trp Lys Glu Ala Val		
465	470	

<210> SEQ ID NO 254
 <211> LENGTH: 473
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: cCD39 ECD

<400> SEQUENCE: 254

Thr Gln Asn Lys Ala Leu Pro Glu Asn Ile Lys Tyr Gly Ile Val Leu
1 5 10 15
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
20 25 30
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
35 40 45
Val Lys Gly Pro Gly Ile Ser Lys Tyr Val Gln Lys Val Asn Glu Ile
50 55 60
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
65 70 75 80
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
85 90 95
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
100 105 110
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
115 120 125
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
130 135 140
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
145 150 155 160
Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
165 170 175
Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe Val Pro Gln Asn Gln Thr
180 185 190
Thr Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
195 200 205
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala

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210	215	220
Leu Trp Gln Lys Leu Ala	Lys Asp Ile Gln Val Ala Ser Asn Glu Ile	
225	230	235 240
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val		
	245	250 255
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu		
	260	265 270
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys		
	275	280 285
His Gln Ser Val Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser		
	290	295 300
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe		
305	310	315 320
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Asn Phe Leu Asn Leu Thr		
	325	330 335
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe		
	340	345 350
Cys Ser Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys		
	355	360 365
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser		
	370	375 380
Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile		
385	390	395 400
His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly		
	405	410 415
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser		
	420	425 430
Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu Met Val Leu Phe Ser		
	435	440 445
Leu Val Leu Val Ile Val Ala Ile Ile Gly Leu Leu Ile Phe His Lys		
	450	455 460
Pro Ser Tyr Phe Trp Lys Asp Met Val		
465	470	

<210> SEQ ID NO 255

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31895

<400> SEQUENCE: 255

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
1	5	10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr		
	20	25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
	35	40 45
Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe		
	50	55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr		
65	70	75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		

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85				90				95							
Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu	Tyr	Leu	Arg	Lys	Trp	Gly
		100						105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
		130				135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
		145			150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			165						170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180						185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
	210				215					220					
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
	225				230				235					240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
			245						250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
		260						265					270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280				285				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290				295					300					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
	305				310				315					320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
			325					330						335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
		340						345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370				375					380					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
	385				390				395					400	
Ser	Asp	Gly	Ser	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	
			405					410					415		
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
		420						425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 256

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 31895

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<400> SEQUENCE: 256

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Asn Arg His Thr Gly Ile Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Asn Ala Ile
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> SEQ ID NO 257

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31415

<400> SEQUENCE: 257

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gln Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Arg Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Ser Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

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115					120					125					
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
130					135					140					
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				180					185					190	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
				195					200					205	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
				210					215					220	
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
				225					230					235	240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				260					265					270	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				275					280					285	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
				290					295					300	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
				305					310					315	320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				340					345					350	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
				355					360					365	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
				370					375					380	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
				385					390					395	400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				420					425					430	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
				435					440					445	

<210> SEQ ID NO 258

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 31415

<400> SEQUENCE: 258

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5				10						15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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20				25				30							
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35						40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75					80
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	His	Ser	Tyr	Ile
			85						90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
		100						105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145					150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			165						170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		180						185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
	195						200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
	210														

<210> SEQ ID NO 259

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31891

<400> SEQUENCE: 259

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Lys	Ser	Tyr
		20						25					30		
Glu	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Arg	Ile	Asn	Pro	Ser	Val	Gly	Ser	Thr	Trp	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Thr	Ser	Thr	Val	Tyr
65				70					75						80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Gly	Lys	Arg	Glu	Gly	Gly	Thr	Glu	Tyr	Leu	Arg	Val	Trp	Gly
		100					105						110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	115						120					125			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val

145	150							155							160		
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
				165					170					175			
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
				180					185					190			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His		
				195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly		
				210					215					220			
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser		
				225					230					235			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
				245					250					255			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro		
				260					265					270			
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
				275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val		
				290					295					300			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
				305					310					315			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr		
				325					330					335			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
				340					345					350			
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
				355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
				370					375					380			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
				385					390					395			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser		
				405					410					415			
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
				420					425					430			
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
				435					440					445			

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<210> SEQ ID NO 260
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: LC, 31891
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<400> SEQUENCE: 260

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Tyr	Ala	Ser	Ser	Arg	Ala	Tyr	Gly	Ile	Pro	Asp	Arg	Phe	Ser

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50	55	60
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu		
65	70	75 80
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr His Asn Ala Ile		
	85	90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
	100	105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
	115	120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
	130	135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
	145	150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
	165	170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
	180	185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
	195	200 205
Phe Asn Arg Gly Glu Cys		
210		

<210> SEQ ID NO 261

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31418

<400> SEQUENCE: 261

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
1	5	10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr		
	20	25 30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
	35	40 45
Gly Arg Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe		
	50	55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr		
	65	70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90 95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly		
	100	105 110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
	115	120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala		
	130	135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
	145	150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
	165	170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		

-continued

180					185					190					
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
	195						200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
210					215					220					
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235				240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260						265				270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			275					280					285		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
290						295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315				320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
370						375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395				400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 262

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 31418

<400> SEQUENCE: 262

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
		50				55					60				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75				80	
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Phe	Tyr	Ile

-continued

85	90	95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
100	105	110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Cys		
210		

<210> SEQ ID NO 263

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31430

<400> SEQUENCE: 263

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala		
1	5	10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Lys Ser Tyr		
20	25	30
Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35	40	45
Gly Arg Ile Asn Pro Ser Gly Gly Ser Thr Trp Tyr Ala Gln Lys Phe		
50	55	60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr		
65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg His Trp Gly		
100	105	110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
115	120	125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala		
130	135	140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
145	150	155
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
165	170	175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
180	185	190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His		
195	200	205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly		

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210					215					220					
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235				240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				260					265					270	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				275					280					285	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
				290					295					300	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315				320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				340					345					350	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
				355					360					365	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
				370					375					380	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395				400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				420					425					430	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
				435					440					445	
<210> SEQ ID NO 264															
<211> LENGTH: 214															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: Synthetic: LC, 31430															
<400> SEQUENCE: 264															
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Glu	Ala	Ser	Gln	Ser	Val	Ser	Tyr	Ser
				20					25					30	
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
				35					40					45	
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Asn	Gly	Ile	Pro	Asp	Arg	Phe	Ser
				50					55					60	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu
65					70					75				80	
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	His	Ser	Ala	Leu
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
				100					105					110	
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly

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115					120					125					
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
130						135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145					150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
				165					170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
			180					185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
210															

<210> SEQ ID NO 265

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31915

<400> SEQUENCE: 265

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Leu
			20					25					30		
Pro	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Gly	Ile	Gly	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	Gln	Gly
	50					55					60				
Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu
	65				70					75					80
Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
			85						90					95	
Gly	Gly	Ala	Lys	Tyr	Ala	Ser	Lys	Trp	Gly	Met	Asp	Val	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
	145				150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165						170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
	225				230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr

245																250						255					
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu												
			260				265						270														
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys												
			275				280						285														
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser												
			290				295						300														
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys												
305						310						315			320												
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile												
			325						330						335												
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro												
			340						345						350												
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu												
			355						360						365												
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn												
			370						375						380												
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser												
385						390						395			400												
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg												
			405						410						415												
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu												
			420						425						430												
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys													
			435						440						445												
<210> SEQ ID NO 266																											
<211> LENGTH: 220																											
<212> TYPE: PRT																											
<213> ORGANISM: Artificial Sequence																											
<220> FEATURE:																											
<223> OTHER INFORMATION: Synthetic: LC, 31915																											
<400> SEQUENCE: 266																											
Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly												
1				5				10						15													
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Phe	Ser												
			20						25						30												
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln												
			35			40						45															
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ser	Arg	Glu	Ser	Gly	Val												
			50			55						60															
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr												
65						70						75			80												
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln												
			85						90						95												
Tyr	Trp	Thr	Tyr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile												
			100						105						110												
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp												
			115						120						125												
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn												
			130			135						140															
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu												

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145	150	155	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp	165	170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr	180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser	195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	210	215	220

<210> SEQ ID NO 267
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 31905

 <400> SEQUENCE: 267

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Pro Ser Asn	20	25	30	
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	35	40	45	
Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly	50	55	60	
Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu	65	70	75	80
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg	85	90	95	
Gly Gly Ala Lys Tyr Ala Arg Thr Tyr Gly Met Asp Val Trp Gly Gln	100	105	110	
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val	115	120	125	
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala	130	135	140	
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser	145	150	155	160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val	165	170	175	
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro	180	185	190	
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys	195	200	205	
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro	210	215	220	
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val	225	230	235	240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	245	250	255	
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu	260	265	270	
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys				

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275					280					285					
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
290						295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345						350	
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
			355				360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385				390						395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405					410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435					440					445			
<210> SEQ ID NO 268															
<211> LENGTH: 220															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: Synthetic: LC, 31905															
<400> SEQUENCE: 268															
Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Lys	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Asn	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
			35				40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Gln	Ser	Gly	Val
			50			55					60				
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
			65			70					75			80	
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
			85					90					95		
Tyr	Leu	Leu	Tyr	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile
			100					105					110		
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
			115				120					125			
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
			130			135					140				
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
			145			150					155			160	
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
			165					170					175		
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr

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180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
210	215	220

<210> SEQ ID NO 269
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 31901
 <400> SEQUENCE: 269

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser		
1	5	10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Leu		
20	25	30
Pro Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35	40	45
Gly Gly Ile Gly Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly		
50	55	60
Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu		
65	70	75
Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg		
85	90	95
Gly Gly Ala Lys Tyr Ala Gly Arg Tyr Gly Met Asp Val Trp Gly Gln		
100	105	110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val		
115	120	125
Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala		
130	135	140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser		
145	150	155
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val		
165	170	175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro		
180	185	190
Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys		
195	200	205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro		
210	215	220
Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val		
225	230	235
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr		
245	250	255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu		
260	265	270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys		
275	280	285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser		
290	295	300
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		

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305	310	315	320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile			
	325	330	335
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro			
	340	345	350
Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu			
	355	360	365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn			
	370	375	380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser			
	385	390	395
Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg			
	405	410	415
Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu			
	420	425	430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys			
	435	440	445

<210> SEQ ID NO 270
 <211> LENGTH: 220
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: LC, 31901

<400> SEQUENCE: 270

Gly Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1	15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Phe Ser	
20	30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35	45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Ala Ser Gly Val	
50	60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85	95
Tyr Tyr Leu Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
100	110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp	
115	125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn	
130	140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu	
145	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp	
165	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr	
180	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser	
195	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	

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210	215	220
<210> SEQ ID NO 271		
<211> LENGTH: 448		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic: HC, 31861		
<400> SEQUENCE: 271		
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser		
1	5	10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Gly Ser Tyr		
	20	25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
	35	40 45
Gly Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe		
	50	55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr		
	65	70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90 95
Ala Arg Glu Ser Gly Thr Tyr Arg Asp His Arg Leu Asp Val Trp Gly		
	100	105 110
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
	115	120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala		
	130	135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
	145	150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
	165	170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
	180	185 190
Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His		
	195	200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly		
	210	215 220
Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser		
	225	230 235 240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
	245	250 255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro		
	260	265 270
Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
	275	280 285
Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val		
	290	295 300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
	305	310 315 320
Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr		
	325	330 335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		

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340	345	350
Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys		
355	360	365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
370	375	380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
385	390	400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser		
405	410	415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
420	425	430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
435	440	445

<210> SEQ ID NO 272

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 31861

<400> SEQUENCE: 272

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly		
1	5	10
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn		
20	25	30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile		
35	40	45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly		
50	55	60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser		
65	70	75
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Leu Trp Pro Leu		
85	90	95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
100	105	110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Cys		
210		

<210> SEQ ID NO 273

<211> LENGTH: 448

<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 31873

<400> SEQUENCE: 273

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Lys Tyr
 20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Ser Ile Ile Pro Glu Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Arg Leu Gly Val Trp Gly
 100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
 325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 340 345 350

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

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370					375					380					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				420					425					430	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 274
 <211> LENGTH: 214
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: LC, 31873

<400> SEQUENCE: 274

Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Gly	Ser	Asn
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40						45			
Tyr	Gly	Ala	Ser	Thr	Arg	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
	50				55					60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser
	65			70					75					80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Leu	Leu	Trp	Pro	Leu
			85					90						95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
		100						105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115				120						125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130				135						140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
	145			150						155				160	
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			165					170						175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		180				185						190			
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195				200						205			
Phe	Asn	Arg	Gly	Glu	Cys										
			210												

<210> SEQ ID NO 275
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 31393

<400> SEQUENCE: 275

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Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	1	5	10	15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Glu	Ser	Tyr	20	25	30	
Gly	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	35	40	45	
Gly	Ser	Ile	Ile	Pro	Glu	Phe	Gly	Ile	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	50	55	60	
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Thr	Tyr	65	70	75	80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Glu	Ser	Gly	Gly	Tyr	Arg	Asp	His	Arg	Leu	Asp	Val	Trp	Gly	100	105	110	
Gln	Gly	Thr	Met	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	115	120	125	
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	130	135	140	
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	145	150	155	160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	165	170	175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	180	185	190	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	195	200	205	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	210	215	220	
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	225	230	235	240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	245	250	255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	260	265	270	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	275	280	285	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	290	295	300	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	305	310	315	320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	325	330	335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	340	345	350	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	355	360	365	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	370	375	380	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	385	390	395	400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser				

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405	410	415
Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
420	425	430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys		
435	440	445

<210> SEQ ID NO 276
 <211> LENGTH: 214
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: LC, 31393

<400> SEQUENCE: 276

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly		
1	5	10
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Asn		
20	25	30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile		
35	40	45
Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly		
50	55	60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser		
65	70	75
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Leu Leu Trp Pro Leu		
85	90	95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
100	105	110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Cys		
210		

<210> SEQ ID NO 277
 <211> LENGTH: 453
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 27597

<400> SEQUENCE: 277

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser		
1	5	10
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr		
20	25	30

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Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Ser	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Glu	Gly	Arg	Gly	Tyr	Asp	Ser	Ser	Arg	Tyr	Tyr	Lys	Phe	Trp
			100					105					110		
Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser
		115					120					125			
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr
	130					135					140				
Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
145					150					155					160
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
				165					170					175	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
		180						185					190		
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr
		195					200					205			
Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val
	210					215					220				
Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe
225					230					235					240
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
				245					250					255	
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		260						265					270		
Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
		275					280					285			
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser
	290					295					300				
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
305					310					315					320
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser
			325						330					335	
Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
		340						345					350		
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln
		355					360					365			
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
	370					375					380				
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
				390						395					400
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu
				405				410						415	
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser
			420					425					430		
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser

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435	440	445
Leu Ser Leu Gly Lys		
450		
 <210> SEQ ID NO 278		
<211> LENGTH: 214		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic: LC, 27597		
 <400> SEQUENCE: 278		
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly		
1 5 10 15		
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr		
20 25 30		
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile		
35 40 45		
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly		
50 55 60		
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro		
65 70 75 80		
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Val Leu Trp Pro Arg		
85 90 95		
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala		
100 105 110		
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115 120 125		
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130 135 140		
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145 150 155 160		
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165 170 175		
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180 185 190		
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195 200 205		
Phe Asn Arg Gly Glu Cys		
210		
 <210> SEQ ID NO 279		
<211> LENGTH: 448		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Synthetic: HC, 27575		
 <400> SEQUENCE: 279		
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Glu Pro Gly Ser		
1 5 10 15		
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr		
20 25 30		
Ala Thr Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met		
35 40 45		

Gly 50	Ile	Ile	Pro	Ile	Ser 55	Gly	Thr	Ala	Asn	Tyr 60	Ala	Gln	Glu	Phe	
Gln 65	Gly	Arg	Val	Thr	Ile 70	Thr	Ala	Asp	Glu	Ser 75	Thr	Ser	Thr	Ala	Tyr 80
Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr 95	Cys
Ala	Arg	Asp	Gly 100	Gly	Gly	Tyr	Arg	His 105	His	Tyr	Phe	Asp	Leu 110	Trp	Gly
Arg	Gly	Thr	Leu	Val	Thr	Val	Ser 120	Ser	Ala	Ser	Thr	Lys 125	Gly	Pro	Ser
Val	Phe	Pro	Leu	Ala	Pro	Cys 135	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
Ala 145	Leu	Gly	Cys	Leu	Val 150	Lys	Asp	Tyr	Phe	Pro 155	Glu	Pro	Val	Thr	Val
Ser	Trp	Asn	Ser	Gly 165	Ala	Leu	Thr	Ser	Gly 170	Val	His	Thr	Phe	Pro 175	Ala
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr 185	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys 200	Thr	Tyr	Thr	Cys	Asn 205	Val	Asp	His
Lys	Pro	Ser	Asn	Thr	Lys	Val 215	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
Pro 225	Pro	Cys	Pro	Pro	Cys 230	Pro	Ala	Pro	Glu	Phe 235	Leu	Gly	Gly	Pro	Ser
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp 250	Thr	Leu	Met	Ile	Ser	Arg
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp 265	Val	Ser	Gln	Glu	Asp	Pro
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
Lys 290	Thr	Lys	Pro	Arg	Glu	Glu 295	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
Ser 305	Val	Leu	Thr	Val	Leu	His 310	Gln	Asp	Trp	Leu 315	Asn	Gly	Lys	Glu	Tyr
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro 330	Ser	Ser	Ile	Glu	Lys 335	Thr
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg 345	Glu	Pro	Gln	Val	Tyr	Thr	Leu
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys 360	Asn	Gln	Val	Ser	Leu	Thr	Cys
Leu 370	Val	Lys	Gly	Phe	Tyr	Pro 375	Ser	Asp	Ile	Ala 380	Val	Glu	Trp	Glu	Ser
Asn 385	Gly	Gln	Pro	Glu	Asn 390	Asn	Tyr	Lys	Thr	Thr 395	Pro	Pro	Val	Leu	Asp
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg 410	Leu	Thr	Val	Asp	Lys	Ser
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser 425	Cys	Ser	Val	Met	His	Glu	Ala
Leu	His	Asn	His	Tyr	Thr	Gln	Lys 440	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys

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<210> SEQ ID NO 280
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: LC, 27575

<400> SEQUENCE: 280

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Val Asn Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> SEQ ID NO 281
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: HC, 27568

<400> SEQUENCE: 281

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Pro Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Glu Gln Gly Leu Glu Trp Met
35 40 45

Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95
Ala	Gly	Glu	Ser	Gly	Gly	Tyr	Arg	Asp	His	Lys	Leu	Asp	Val	Trp	Gly	100	105	110
Gln	Gly	Thr	Val	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	115	120	125
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	130	135	140
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	145	150	155
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	165	170	175
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	180	185	190
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	195	200	205
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	210	215	220
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	225	230	235
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	245	250	255
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	260	265	270
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	275	280	285
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	290	295	300
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	305	310	315
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	325	330	335
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	340	345	350
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	355	360	365
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	370	375	380
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	385	390	395
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	405	410	415
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	420	425	430
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	435	440	445

<210> SEQ ID NO 282

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27568

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<400> SEQUENCE: 282

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Val Phe Trp Pro Ile
85 90 95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
210

<210> SEQ ID NO 283

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 27577

<400> SEQUENCE: 283

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ala Phe Ser Ser Tyr
20 25 30
Ala Ile Gly Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Thr Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Gly Gly Gly Tyr Gln His His Tyr Phe Asp Leu Trp Gly
100 105 110

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Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
	115						120					125			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			165						170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
	180							185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
	195						200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
	210					215					220				
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260						265				270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
			325						330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
			405						410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 284

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27577

<400> SEQUENCE: 284

Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly
1					5				10					15	

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<210> SEQ ID NO 285
<211> LENGTH: 448
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic: HC, 27587

<400> SEQUENCE: 285

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45
Gly Ser Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65          70          75          80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95
Ala Arg Glu Ser Gly Gly Tyr Arg Asp His Lys Leu Asp Val Trp Gly
          100          105          110
Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
          115          120          125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
          130          135          140

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Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	145	150	155	160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	165	170	175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	180	185	190	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	195	200	205	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	210	215	220	
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	225	230	235	240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	245	250	255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	260	265	270	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	275	280	285	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	290	295	300	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	305	310	315	320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	325	330	335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	340	345	350	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	355	360	365	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	370	375	380	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	385	390	395	400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	405	410	415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	420	425	430	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	435	440	445	
<210> SEQ ID NO 286																			
<211> LENGTH: 214																			
<212> TYPE: PRT																			
<213> ORGANISM: Artificial Sequence																			
<220> FEATURE:																			
<223> OTHER INFORMATION: Synthetic: LC, 27587																			
<400> SEQUENCE: 286																			
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	1	5	10	15
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Tyr	20	25	30	
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	35	40	45	

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Tyr Asp Ala Ser Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50          55          60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65          70          75          80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Val Leu Trp Pro Leu
          85          90          95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
          100          105          110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
          115          120          125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
          130          135          140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
          145          150          155          160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
          165          170          175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
          180          185          190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
          195          200          205

Phe Asn Arg Gly Glu Cys
          210

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<210> SEQ ID NO 287

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 27589

<400> SEQUENCE: 287

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1          5          10          15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
          20          25          30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
          35          40          45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
          50          55          60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
          65          70          75          80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
          85          90          95

Ala Arg Asp Ser Gly Tyr His Arg His Tyr Ser Asp Tyr Trp Gly Gln
          100          105          110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          115          120          125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
          130          135          140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
          145          150          155          160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
          165          170          175

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Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195				200					205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215				220					
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245						250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
		260						265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
			325						330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
		435				440						445			

<210> SEQ ID NO 288

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27589

<400> SEQUENCE: 288

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser	Trp
		20					25						30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35				40						45			
Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70					75					80	

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Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Leu	Phe	Pro	Ile
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
			100					105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130				135						140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
	145				150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			165						170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		180						185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
			210												

<210> SEQ ID NO 289

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: HC, 27596

<400> SEQUENCE: 289

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
		20						25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
	65				70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Asp	Pro	Leu	Gly	Ile	Arg	Lys	His	Trp	Phe	Asp	Pro	Trp	Gly
		100						105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	145				150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
			165						170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180					185						190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
			195				200					205			

Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
210					215					220					
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260					265					270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
290						295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
370						375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			
<210> SEQ ID NO 290															
<211> LENGTH: 214															
<212> TYPE: PRT															
<213> ORGANISM: Artificial Sequence															
<220> FEATURE:															
<223> OTHER INFORMATION: Synthetic: LC, 27596															
<400> SEQUENCE: 290															
Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val</			

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Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
	145				150					155					160
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			165						170					175	
Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
		180						185					190		
Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
		195					200					205			
Phe	Asn	Arg	Gly	Glu	Cys										
		210													

<210> SEQ ID NO 291
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 27535

<400> SEQUENCE: 291

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1			5						10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
		20						25					30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35						40					45			
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
	65				70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90				95		
Ala	Arg	Asp	Thr	Pro	Arg	Trp	Arg	Tyr	His	Tyr	Phe	Asp	Tyr	Trp	Gly
		100						105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	145				150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
		165							170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180						185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
	210					215					220				
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
	225				230					235					240

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Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
			260					265					270		
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
			325						330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
			405						410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 292

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27535

<400> SEQUENCE: 292

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Tyr
		20						25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40						45			
Tyr	Asp	Ala	Ser	Lys	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Val	Leu	Asn	Tyr	Pro	Leu
			85						90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
		100						105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> SEQ ID NO 293
 <211> LENGTH: 448
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 27550

<400> SEQUENCE: 293

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Arg Arg Gly Ser Leu Ala Leu Gly Met Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
 210 215 220
 Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
 260 265 270

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Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280						285		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315				320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
370						375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395				400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
		435					440					445			

<210> SEQ ID NO 294

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27550

<400> SEQUENCE: 294

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr
		20					25					30			
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
	35					40						45			
Tyr	Asp	Ala	Ser	Asn	Leu	Glu	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
50					55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70					75					80	
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Phe	Leu	Pro	Pro
		85						90					95		
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
		100						105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115				120						125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
130						135					140				
Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
145				150						155				160	
Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
			165					170						175	

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> SEQ ID NO 295
 <211> LENGTH: 455
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic: HC, 27549

<400> SEQUENCE: 295

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Leu Gly Gly Tyr Ser Tyr Gly Glu Pro Tyr Tyr Tyr Tyr
 100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 130 135 140

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 145 150 155 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 165 170 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 180 185 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 195 200 205

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
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Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
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Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
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-continued

Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
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Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys
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Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
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Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
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Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
			420					425					430		
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
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<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic: LC, 27549

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Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser
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Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ala	His	Ser	Ser	Pro
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Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
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Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu
	130					135					140				
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser
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Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
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Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val
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Gly Arg Ile Asn Pro Ser Val Gly Ser Thr Trp Tyr Ala Gln Lys Phe
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Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Gly Lys Arg Glu Gly Gly Thr Glu Tyr Leu Arg Asn Trp Gly
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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
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Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
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 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
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Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
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 260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
 290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 305 310 315 320

[illegible]

Phe Asn Arg Gly Glu Cys
210

What is claimed is:

1. An antigen binding protein that binds specifically to a human CD39 (hCD39) and is capable of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18 of the following:

- a) inhibiting binding of CD39 to ATP;
- b) inhibiting conversion by CD39 of ATP to ADP and/or ADP to AMP;
- c) decreasing affinity of CD39 for ATP or ADP;
- d) inhibiting or impeding release of ADP or AMP from CD39;
- e) impeding or inhibiting CD39 processivity;
- f) inhibiting platelet aggregation;
- g) decreasing levels of phosphate, ADP, AMP, and/or adenosine and/or increasing levels of ATP;
- h) increasing T effector cell function;
- i) decreasing the number of regulatory T cells in tissues or in circulation;
- j) suppressing regulatory T cells or regulatory T cell activity;
- k) increasing B cell function;
- l) increasing antigen presenting cell function;
- m) inhibiting CD39 function on tumor cells;
- n) inhibiting processing of at least one of phospho-antigen from phosphorylated isoprenoid, phosphorylated vitamin B metabolite, and/or phosphorylated riboflavin;
- o) decreasing or preventing activation of phospho antigen specific T cells selected from MAIT cells and $\gamma\delta$ T cells;
- p) inhibiting angiogenesis;
- q) increasing proliferation of stimulated CD4⁺ and CD8⁺ T cells;
- r) increasing stimulated PBMC Secretion of INF- γ , TNF- α , IL-2 and/or IL-1 β .

2. The antigen binding protein of claim 1, wherein the antigen binding protein has 1, 2, 3, 4, 5, 6, or 7 of the following characteristics:

- a) is a monoclonal antibody;
- b) is a human antibody, a humanized antibody, or a chimeric antibody;
- c) is a bispecific antibody, a multi-specific antibody, a diabody, or a multivalent antibody;
- d) is of the IgG1, IgG2, IgG3, IgG4, or IgM type;
- e) is an antigen-binding antibody fragment;
- f) is a Fab fragment, a Fab' fragment, a F(ab')₂ fragment, or an Fv fragment; and/or
- g) is a single chain antibody, a single domain antibody, or a nanobody.

3. A pharmaceutical composition comprising an effective amount of an antibody which binds to hCD39 and has 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16 of the following characteristics:

- a) blocks or decreases hydrolysis of ATP to ADP and/or ADP to AMP as determined by at least one of: (i) a decreased phosphate release (Pi), (ii) an increase in ATP levels, and (iii) a decrease of ADP, AMP, and/or adenosine levels;
- b) increases T effector cell activity;
- c) suppresses regulatory T cell or decreases a regulatory T cell activity;
- d) decreases number of regulatory T cells in tissues or in circulation;
- e) increases B cell function;
- f) increases antigen presenting cell function;
- g) inhibits CD39 function on tumor cells;

h) blocks or inhibits processing of at least one of phospho-antigen from a phosphorylated isoprenoid, phosphorylated vitamin B metabolite, and phosphorylated riboflavin;

- i) decreases or prevents activation of phospho antigen specific T cells selected from MAIT cells and $\gamma\delta$ T cells;
- k) inhibits angiogenesis;
- l) decreases affinity for ATP and/or ADP;
- m) inhibits release of ADP or AMP from CD39;
- n) impedes or inhibits CD39 processivity;
- o) inhibits platelet aggregation;
- p) increases proliferation of stimulated CD4⁺ and CD8⁺ T cells;
- r) increases stimulated PBMC Secretion of INF- γ , TNF- α , IL-2, and/or IL-1 β .

4. A pharmaceutical composition comprising the antigen-binding protein of claim 1 or claim 2.

5. The pharmaceutical composition of claim 4, further comprising an effective amount of at least one of the following

- a) an anti-PD-1 antibody,
- b) an anti-PD-L1 antibody,
- c) an anti-CD73 antibody,
- d) an anti-CD38 antibody,
- e) an anti-A2A receptor antibody,
- f) an anti-A2B receptor antibody,
- g) an anti-A2A/A2B dual receptor antibody, or any combination thereof, or
- h) a small molecule inhibitor,

or a combination thereof.

6. The pharmaceutical composition of claim 4 or claim 5, further comprising one or both of

- a) an antibody to an inhibitory receptor or ligand and/or
- b) an antibody to a costimulatory receptor or ligand,

or a combination thereof.

7. The pharmaceutical composition of claim 6, wherein

- (i) the inhibitory receptor or ligand is at least one of CTLA-4, PD-L2, LAG-3, Tim3, neuritin, BTLA, CECAM-1, CECAM-5, VISTA, LAIR1, CD160, 2B4, TGF-R, HHLA2, ILT2, ILT3, ILT4, HLA-G, HLA-C, and/or a Killer-cell immunoglobulin-like receptor (KIR) and/or
- (ii) the costimulatory receptor or ligand is at least one of OX40, CD2, CD27, CDS, ICAM-1, LFA-1, ICOS (CD278), 4-1BB (CD137), GITR, CD28, CD30, CD40, BAFFR, HVEM, CD7, LIGHT, NKG2C, SLAMF7, NKp80, CD160, B7-H3, and/or CD83.

8. The pharmaceutical composition of claim 7, wherein the costimulatory receptor or ligand LFA-1 further comprises an LFA-1 β -chain CD18 and/or an LFA-1 α -chain CD11a.

9. The antigen binding protein of claim 1, wherein the antigen binding protein has one or more of the following characteristics:

- a) binds to a human CD39 polypeptide or a variant thereof with a K_D of less than about 20 nM;
- b) binds to a cyno CD39 polypeptide or a variant thereof with a K_D of less than about 200 nM;
- c) binds to a murine CD39 polypeptide or a variant thereof with a K_D of less than about 200 nM; or
- d) a combination of at least 2 of a), b), and c).

10. An antigen binding protein that competes or is capable of competing for binding to human CD39 with a reference

antigen binding protein, wherein the reference antigen binding protein is the antigen binding protein of claim 1.

11. An antigen binding protein that binds to or is capable of competing for binding to human CD39 with a reference antigen binding protein, wherein the reference antigen binding protein binds to an epitope at positions 143-158 or 274-277 of SEQ ID NO: 249 on a human CD39 polypeptide, including, but not limited to, D150, E153, R154 or N99 alone or in combination with D150, E153, R154 or any combination thereof.

12. The antigen binding protein of claim 10 or claim 11, wherein the antigen binding protein and the reference antibody cross-compete or are capable of cross-competing for binding to a human CD39.

13. The antigen binding protein of claim 1, comprising a human heavy chain constant region or fragment or a variant thereof, wherein the constant region variant comprises up to 20 conservatively modified amino acid substitutions from any sequence set forth SEQ ID NOs: 179-218.

14. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain variable region (VH) and a light chain variable region (VL), VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of:

- a) a VHCDR1 having the sequence set forth in SEQ ID NOs: 1-45,
- b) a VHCDR2 having the sequence set forth in SEQ ID NOs: 46-81,
- c) a VHCDR3 having the sequence set forth in SEQ ID NOs: 82-109,
- d) a VLCDR1 having the sequence set forth in SEQ ID NOs: 110-124,
- e) a VLCDR2 having the sequence set forth in SEQ ID NOs: 125-140, and
- f) a VLCDR3 having the sequence set forth in SEQ ID NOs: 141-166.

15. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain variable region (VH) and a light chain variable region (VL), the VH comprising,

- a) a VHCDR1 having a sequence set forth in SEQ ID NOs: 1-45,
- b) a VHCDR2 having a sequence set forth in SEQ ID NOs: 46-81, and
- c) a VHCDR3 having a sequence set forth in SEQ ID NOs: 82-109; and

the VL comprising,

- a) a VLCDR1 having a sequence set forth in SEQ ID NO: 110-124,
- b) a VLCDR2 having a sequence set forth in SEQ ID NO: 125-140, and
- c) a VLCDR3 having a sequence set forth in SEQ ID NO: 141-166.

16. An isolated nucleic acid encoding an antigen binding protein according to claim 1, claim 14, or claim 15.

17. An expression vector comprising the nucleic acid according to claim 16.

18. A prokaryotic or eukaryotic host cell comprising the vector of claim 17.

19. An oncolytic virus encoding the nucleic acid of either of claim 16 or 17.

20. A method for the production of a recombinant protein comprising the steps of expressing a nucleic acid according

to claim 16 in a prokaryotic or eukaryotic host cell and recovering the protein from the cell or the cell culture supernatant.

21. A method for treatment of a subject suffering from cancer, a chronic infection, or from an inflammatory disease, comprising the step of administering to the subject a pharmaceutical composition comprising an effective amount of the antigen binding protein of claim 1 or the pharmaceutical composition of claim 3.

22. The method of claim 21, wherein the cancer is a solid cancer.

23. The method of claim 21, wherein the cancer is a hematological cancer.

24. A method for modulating immune system function in a subject in need thereof, comprising the step of contacting a population of immune cells of the subject with a pharmaceutical composition comprising an effective amount of the antigen binding protein of claim 1, under conditions such that the immune system is modulated.

25. A method for inducing or enhancing an immune response in a subject in need thereof, comprising the step of administering to the subject a pharmaceutical composition comprising an antigen binding protein, wherein the immune response is generated against a tumor antigen.

26. The method of claim 24 or claim 25, wherein the subject is a human subject.

27. The method of claim 25, wherein the antigen binding protein comprises a bispecific antibody or a complexing antigen binding protein.

28. The method of claim 27, wherein the antigen binding protein, the bispecific antibody, or the complexing antigen binding protein is administered in an amount sufficient to achieve 1, 2, 3, 4, 5, 6, or 7 of the following in the subject:

- a) reduction of CD39 ATPase activity in a target cell population;
- b) reduction of regulatory T cells suppression of activity of effector T cells;
- c) reduction of levels of regulatory T cells;
- d) activation of effector T cells;
- e) induction or enhancement of effector T cell proliferation;
- f) inhibition of tumor growth; and/or
- g) induction of tumor regression.

29. The method of claim 28, wherein the target cell population comprises T cells, B cells, monocytes, macrophages, dendritic cells, myeloid-derived suppressor cells, and/or tumor cells.

30. The method of claim 25, wherein the method further comprises one or more of the following

- a) administering chemotherapy;
- b) administering radiation therapy; and/or
- c) administering one or more additional therapeutic agents.

31. The method of claim 30, wherein the one or more additional therapeutic agents comprise one or more immunostimulatory agents.

32. The method of claim 31, wherein the one or more immunostimulatory agents comprise an antagonist to an inhibitory receptor of an immune cell.

33. The method of claim 32, wherein the inhibitory receptor is at least one of CTLA-4, PD-1, PD-L1, PD-L2, LAG-3, Tim3, neuritin, BTLA, CECAM-1, CECAM-5, VISTA, LAIR1, CD160, 2B4, TGF-R, and/or a Killer-cell immunoglobulin-like receptor (KIR).

34. The method of claim **31**, wherein the one or more immunostimulatory agents comprise an agonist of a co-stimulatory receptor of an immune cell.

35. The method of claim **34**, wherein the co-stimulatory receptor is OX40, CD2, CD27, CDS, ICAM-1, LFA-1, ICOS (CD278), 4-1BB (CD137), GITR, CD28, CD30, CD40, BAFFR, HVEM, CD7, LIGHT, NKG2C, SLAMF7, NKP80, CD160, B7-H3, or a CD83 ligand.

36. The method of claim **35**, wherein the costimulatory receptor or ligand LFA-1 further comprises an LFA-1 β -chains CD18 and/or an LFA-1 α -chain CD11a.

37. The method of claim **31**, wherein the one or more immunostimulatory agents comprise a cytokine.

38. The method of claim **37**, wherein the cytokine is at least one of IL-2, IL-5, IL-7, IL-12, IL-15, and/or IL-21.

39. The method of claim **31**, wherein the one or more immunostimulatory agents comprise an oncolytic virus.

40. The method of claim **39**, wherein the oncolytic virus is a Herpes simplex virus, a Vesicular stomatitis virus, an adenovirus, a Newcastle disease virus, a vaccinia virus, or a maraba virus.

41. The method of claim **31**, wherein the one or more immunostimulatory agents comprise a chimeric antigen engineered T cell.

42. The method of claim **31**, wherein the one or more immunostimulatory agents comprise a bi- or multispecific T cell directed antibody.

43. The method of claim **25**, wherein the one or more additional therapeutic agents comprise at least one trap for an immune suppressive agent.

44. The method of claim **43**, wherein the at least one trap for an immune suppressive agent comprises at least one of an anti-TGF- β antibody, a TGF β receptor trap, an anti-IL-10 antibody and/or anti-IL-10 receptor trap, and/or an anti-IL-35 antibody trap and/or an anti-IL-35 receptor trap.

45. The method of any one of any of claims **3-44**, wherein administration of the pharmaceutical composition results in induction or enhancement of proliferation of a T-effector cell, or modulation of I-kappaB and/or NF- κ B in the T cell, or modulation of CD39 activity in the T cell, or T cell receptor induced signaling in a T-effector cell, or a combination thereof.

46. A method of screening for a test compound comprising an antigen binding protein of claim **1** capable of inhibiting an activity of CD39, comprising the steps of:

contacting a test sample containing CD39 with a test compound;

comparing the activity of the test sample to a control sample;

whereby a decrease in the activity of CD39 in the test sample compared to the control sample identifies the compound as one that inhibits the activity of CD39.

47. The method of claim **46**, wherein the control sample comprises a sample not contacted with a test compound.

48. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain variable region (VH) and a light chain variable region (VL),

VH comprising at least one of:

a) a VHCDR1 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 1-45,

b) a VHCDR2 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 46-81, and

c) a VHCDR3 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 82-109; and

VL comprising at least one of:

a) a VLCDR1 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 110-124,

b) a VLCDR2 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 125-140, and

c) a VLCDR3 having an amino acid sequence that is at least 90% identical to the sequence set forth in SEQ ID NOs: 141-166.

49. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain variable region (VH) and a light chain variable region (VL),

VH comprising at least one of:

a) a VHCDR1 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 1-45,

b) a VHCDR2 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 46-81, and

c) a VHCDR3 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 82-109; and

VL comprising at least one of:

a) a VLCDR1 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 110-124,

b) a VLCDR2 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 125-140, and

c) a VLCDR3 having an amino acid sequence that is homologous to the sequence set forth in SEQ ID NOs: 141-166.

50. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain and a light chain, the heavy chain comprising one or more molecules having a sequence consisting of one of SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, or SEQ ID NO: 295 and the light chain comprising one or more molecules having a sequence consisting of one of SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, or SEQ ID NO: 296.

51. An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain and a light chain,

a) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 255 and the light chain comprising one or more, each molecule having a sequence consisting of SEQ ID NO: 256;

- b) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 257 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 258;
 - c) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 259 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 260;
 - d) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 261 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 262;
 - e) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 263 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 264;
 - f) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 265 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 266;
 - g) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 267 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 268;
 - h) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 269 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 270;
 - i) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 271 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 272;
 - j) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 273 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 274;
 - k) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 275 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 276;
 - l) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 277 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 278;
 - m) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 279 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 280;
 - n) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 281 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 282;
 - o) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 283 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 284;
 - p) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 285 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 286;
 - q) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 287 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 288;
 - r) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 289 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 290;
 - s) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 291 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 292;
 - t) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 293 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 294; or
 - u) the heavy chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 295 and the light chain comprising one or more molecules, each molecule having a sequence consisting of SEQ ID NO: 296.
- 52.** An isolated nucleic acid encoding an antigen binding protein according to any one of claims **48-51**.
- 53.** An isolated antibody molecule capable of binding to human CD39 (hCD39), comprising a heavy chain variable region (VH) and a light chain variable region (VL), VH and/or VL comprising 1, 2, 3, 4, 5, or 6 of:
- a) a VHCDR1 sequence comprising:
 - (i) a Kabat CDRH1 sequence defined by the consensus sequence S-Y- Δ_3 -M- Δ_5 (SEQ ID NOS: 25-29 and 44-45), where Δ_3 is E, F, Q, or Y and Δ_5 is H or Y;
 - (ii) a Kabat CDR-H1 sequence defined by the consensus sequence θ_1 - θ_2 - θ_3 -I-S (SEQ ID NOS: 30-37), where θ_1 is A, H, K, L, S, or W; θ_2 is L, M, N, or T; and θ_3 is A or P;
 - (iii) a Kabat CDR-H1 sequence defined by the consensus sequence η_1 -Y- η_3 -I-S (SEQ ID NOS: 38-41), where η_1 is S, K, N, or R and η_3 is A or G;
 - (iv) a Chothia CDR-H1 sequence defined by the consensus sequence G-Y-T-F- Ω_5 -S-Y (SEQ ID NOS: 1-2 and 4-6), where Ω_5 is T, K, Q, F, or V;
 - (v) a Chothia CDR-H1 sequence defined by the consensus sequence G-G-T-F- v_5 - v_6 -Y (SEQ ID NOS: 17-22 and 24), where v_5 is S, G, or E and v_6 is S, K, R, or S; or
 - (vi) a Chothia CDR-H1 consensus sequence defined by the consensus sequence G-G-T-F- κ_5 - κ_6 - κ_7 (SEQ ID

- NOS: 7-16), where κ_5 is S, Q, P, or A; κ_6 is S, K, H, L, A, or W; and κ_7 is Y, L, T, N, or M,
- b) a VHCDR2 sequence comprising:
- (i) a Kabat CDR-H2 sequence defined by the consensus sequence ϵ_1 -I-N-P- ϵ_5 - ϵ_6 -G-S-T- ϵ_{10} -Y-A-Q-K-F-Q-G (SEQ ID NOS: 63-66 and 68), where ϵ_1 is K, S, R, or V; ϵ_5 is L, R, or S; ϵ_6 is G or V; and ϵ_{10} is S or W;
 - (ii) a Kabat CDR-H2 sequence defined by the consensus sequence G-I- α_3 - α_4 - α_5 - α_6 -G-T-A-N-Y-A-Q-K-F-Q-G (SEQ ID NOS: 69-72), where α_3 is I or L or is absent; α_4 is P or is absent; and α_5 is I, G, or R; and α_6 is A, F, or G;
 - (iii) a Kabat CDR-H2 sequence defined by the consensus sequence β_1 -I-I-P- β_5 - β_6 -G- β_8 -A-N-Y-A-Q-K-F-G-Q (SEQ ID NOS: 74 and 76-79), where β_1 is S or G; β_5 is I, E, S, or T; β_6 is F, I, or S; and β_8 is I or T;
 - (iv) a Chothia CDR-H2 sequence defined by the consensus sequence N-P- ϵ_5 - ϵ_6 -G-S-T (SEQ ID NOS: 46-48), where ϵ_5 is L, R, or S and ϵ_6 is G or V;
 - (v) a Chothia CDR-H2 sequence defined by the consensus sequence α_3 - α_4 - α_5 - α_6 -G-T-A (SEQ ID NOS: 51-54), where α_3 is I or L or is absent; α_4 is P or is absent; and α_5 is I, G, or R; and α_6 is A, F, or G;
 - (vi) a Chothia CDR-H2 sequence defined by the consensus sequence I-P- β_5 - β_6 -G- β_8 -A (SEQ ID NOS: 56-60), where β_5 is I, E, S, or T; β_6 is F, I, or S; and β_8 is I or T,
- c) a VHCDR3 sequence comprising:
- (i) a CDR-H3 sequence defined by the consensus sequence G-K-R-E-G-G-T-E-Y-L-R- γ_{12} (SEQ ID NOS: 82-86), where γ_{12} is H, K, S, N, or V;
 - (ii) a CDR-H3 sequence defined by the consensus sequence E-S-G- Φ_4 -Y-R-D-H-R-L- Φ_{11} -V (SEQ ID NOS: 94-96), where Φ_4 is G or T and Φ_{11} is D or G; or
 - (iii) a CDR-H3 sequence defined by the consensus sequence G-G-A-K-Y-A- $\mathfrak{D}_7$ - $\mathfrak{D}_8$ - $\mathfrak{D}_9$ -G-M-D-V (SEQ ID NOS: 87-93), where $\mathfrak{D}_7$ is S, V, G, or R; $\mathfrak{D}_8$ is T, Q, K, G, or R; and $\mathfrak{D}_9$ is Y, H, L, or W,
- d) a VLCDR1 sequence comprising:
- (i) a CDR-L1 sequence defined by the consensus sequence ϕ_1 -A-S- ϕ_4 - ϕ_5 -V- ϕ_7 - ϕ_8 - ϕ_9 -Y-L-A (SEQ ID NOS: 1101-114), where ϕ_1 is E, K, or R; ϕ_4 is Q or E; ϕ_5 is S or Y; ϕ_7 is S or A; ϕ_8 is S or Y; and ϕ_9 is D or S;
 - (ii) a CDR-L1 sequence defined by the consensus sequence $\bar{\phi}_1$ -A-S-Q- $\bar{\phi}_5$ - $\bar{\phi}_6$ - $\bar{\phi}_7$ - $\bar{\phi}_8$ - $\bar{\phi}_9$ -L- $\bar{\phi}_{11}$ (SEQ ID NOS: 118 and 120-123), where $\bar{\phi}_1$ is Q or R; $\bar{\phi}_5$ is D or S; $\bar{\phi}_6$ is I or V; $\bar{\phi}_7$ is G or S; $\bar{\phi}_8$ is N, R, or S; $\bar{\phi}_9$ is N, Y, or W; and $\bar{\phi}_{11}$ is A or N; or
 - (iii) a CDR-L1 sequence defined by the consensus sequence K-S-S- Γ_4 -S-V-L- Γ_8 -S- Γ_{10} -N-N-K-N-Y-L-A (SEQ ID NOS: 115-117), where Γ_4 is Q, R or K; Γ_8 is F or Y; and Γ_{10} is S or N,
- e) a VLCDR2 sequence comprising:
- (i) a CDR-L2 sequence defined by the consensus sequence ψ_1 -A-S- ψ_4 -R- ψ_6 - ψ_7 (SEQ ID NOS: 125-136), where ψ_1 is G or Y, ψ_4 is S or N; ψ_6 is A or H; and ψ_7 is T, Y, or N;
 - (ii) a CDR-L2 sequence defined by the consensus sequence D-A-S- χ_4 -R-A-T (SEQ ID NOS: 138 and 139), where χ_4 is N or K; or
 - (iii) a CDR-L2 sequence defined by the consensus sequence W-A-S-T-R- σ_6 -S (SEQ ID NOS: 131 and 133-134), where σ_6 is A, E, or Q, and
- f) a VLCDR3 sequence comprising:
- (i) a CDR-L3 sequence defined by the consensus sequence Q-Q-Y- π_4 - π_5 - π_6 - π_7 -T (SEQ ID NOS: 141-147), where π_4 is G, H, or Y; π_5 is S, N, F, G, or R; π_6 is S, Y, A, G, or R; and π_7 is P, I, or L;
 - (ii) a CDR-L3 sequence defined by consensus sequence Q-Q- λ_3 - λ_4 - λ_5 - λ_6 -P-T (SEQ ID NOS: 148-150), where λ_3 is R, F, H, S, L, D, Y, or V; λ_4 is S, V, T, G, L, Y, or N; λ_5 is N, L, F, K, or V; and λ_6 is W, F, Y, or L;
 - (iii) a CDR-L3 sequence defined by the consensus sequence Q-Q-Y- ρ_3 - ρ_4 -W-P-L-T (SEQ ID NOS: 151 and 152), where ρ_3 is N or L and ρ_4 is N or L; or
 - (iv) a CDR-L3 sequence defined by the consensus sequence Q-Q- ω_3 - ω_4 - ω_5 - ω_6 -P- ω_8 -T (SEQ ID NOS: 153-156), where ω_3 is Y or F; ω_4 is Y or W; ω_5 is S, L, T, or F; ω_6 is T, Y, or F; and ω_8 is L or P.
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