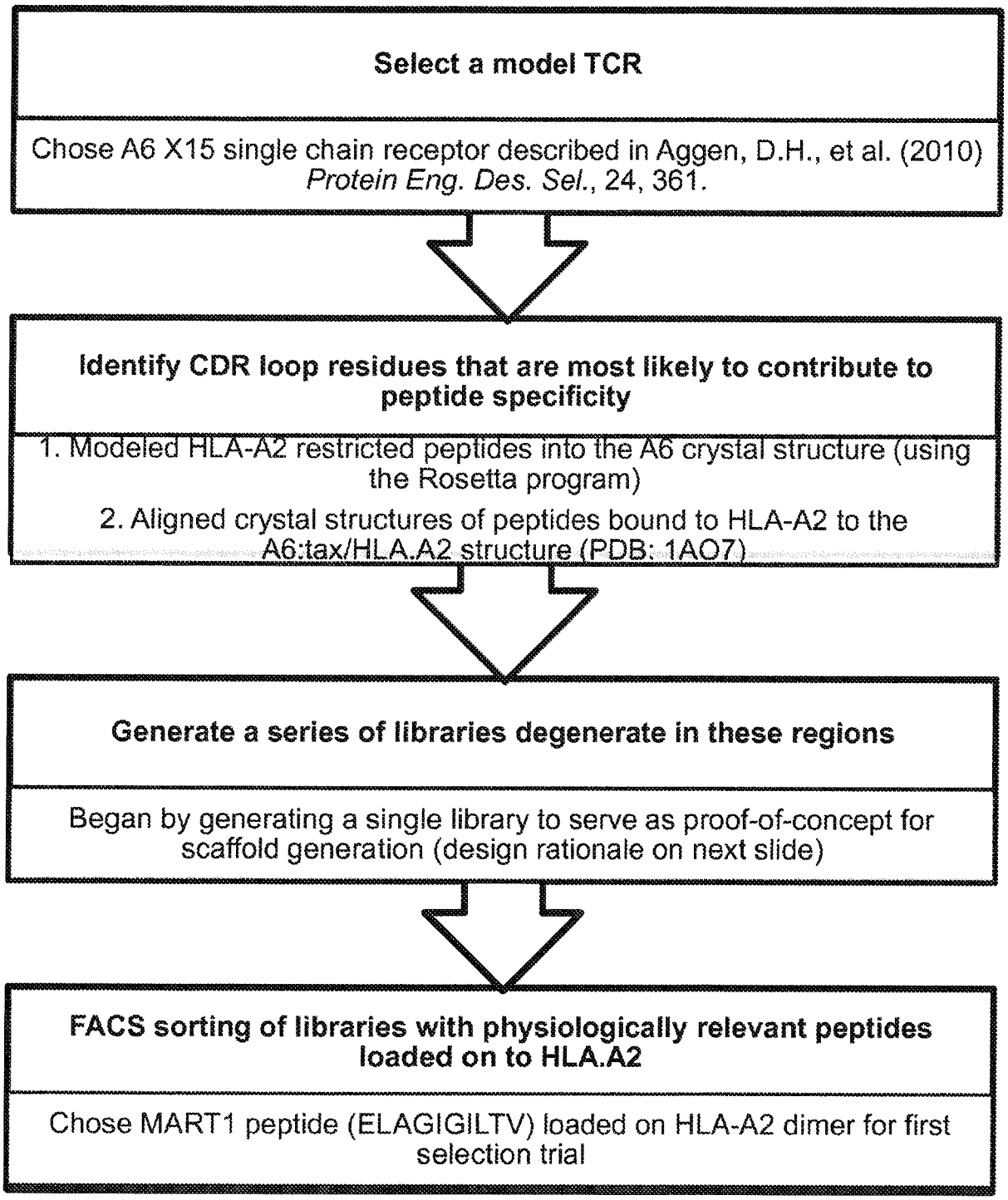

Select a model TCR
Chose A6 X15 single chain receptor described in Aggen, D.H., et al. (2010) *Protein Eng. Des. Sel.*, 24, 361.
Identify CDR loop residues that are most likely to contribute to peptide specificity
1. Modeled HLA-A2 restricted peptides into the A6 crystal structure (using the Rosetta program)
2. Aligned crystal structures of peptides bound to HLA-A2 to the A6:tax/HLA.A2 structure (PDB: 1AO7)
Generate a series of libraries degenerate in these regions
Began by generating a single library to serve as proof-of-concept for scaffold generation (design rationale on next slide)
FACS sorting of libraries with physiologically relevant peptides loaded on to HLA.A2
Chose MART1 peptide (ELAGIGILTV) loaded on HLA-A2 dimer for first selection trial

FIG. 1

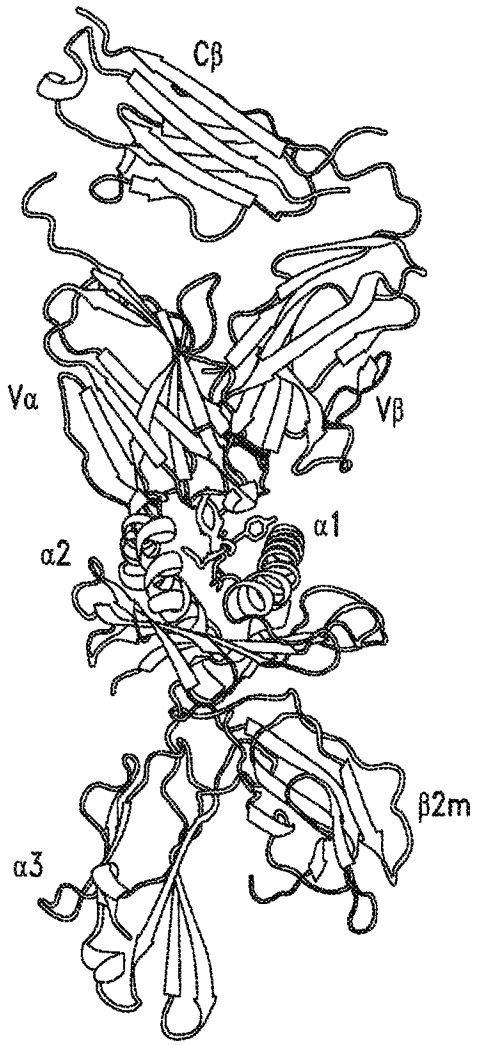


FIG. 2A

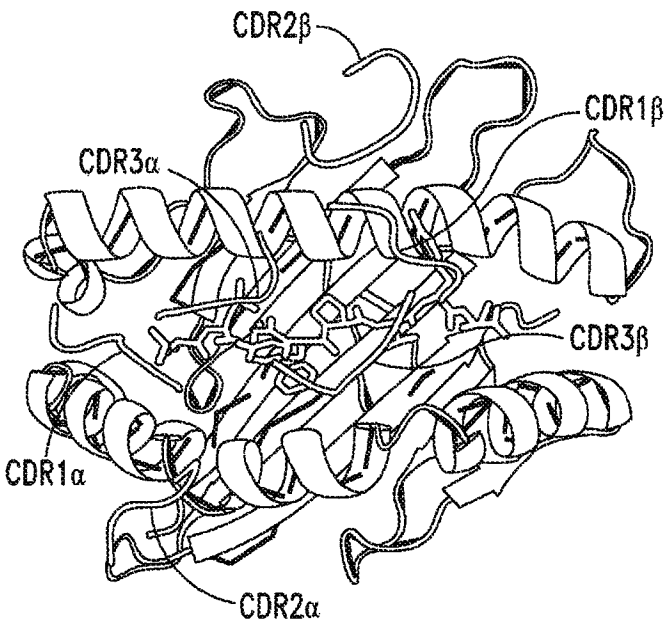


FIG. 2B

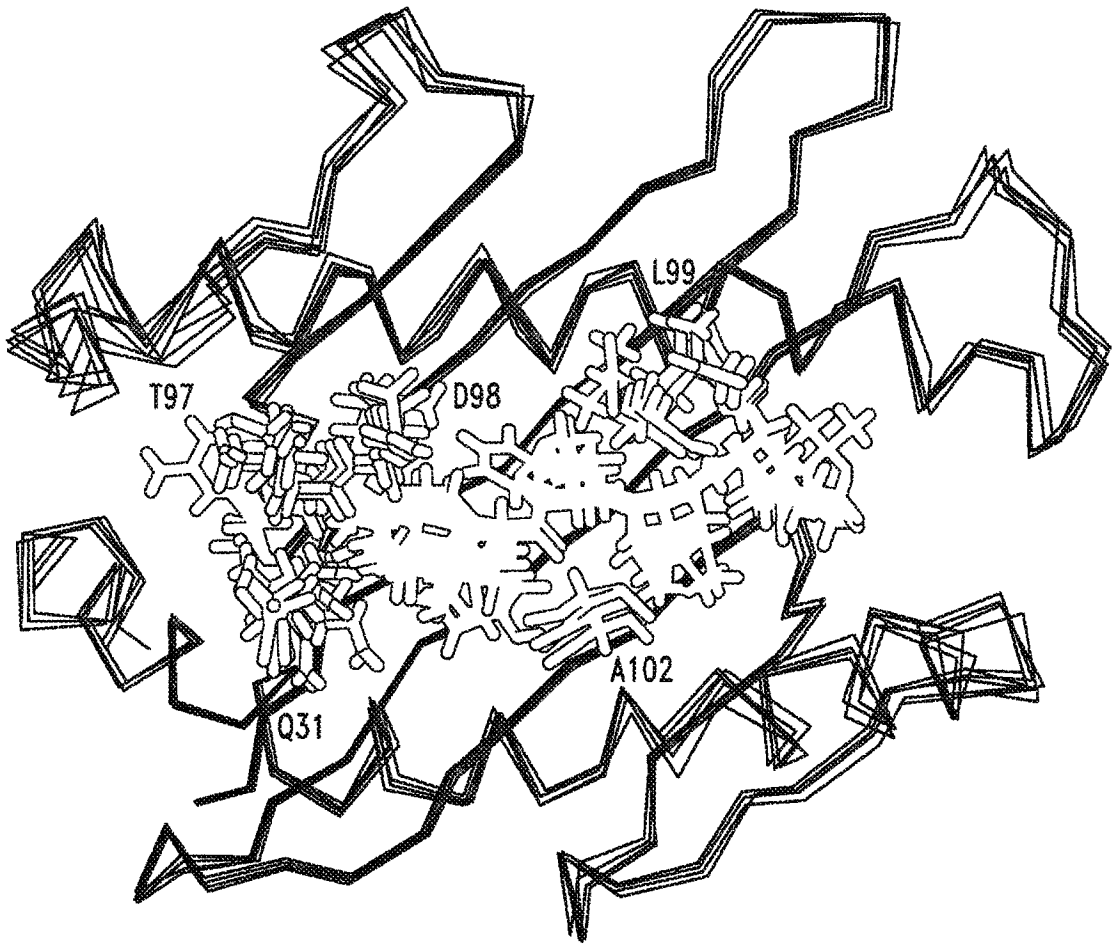


FIG. 3

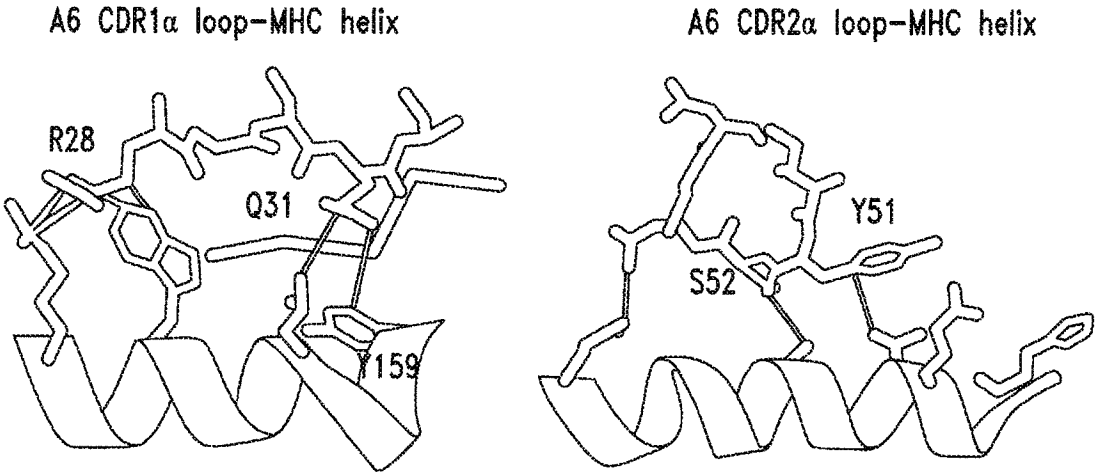

A6 CDR1α loop–MHC helix
A6 CDR2α loop–MHC helix
R28
Q31
Y159
Y51
S52

FIG. 4A

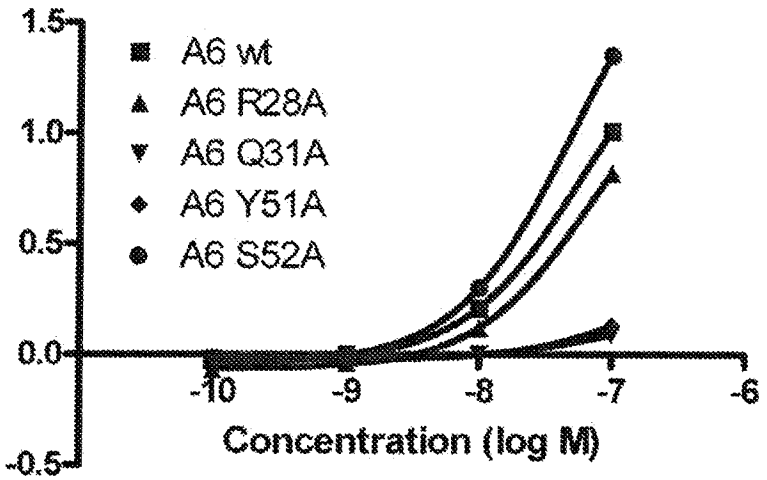

1.5
1.0
0.5
0.0
-0.5
A6 wt
A6 R28A
A6 Q31A
A6 Y51A
A6 S52A
-10
-9
-8
-7
-6
Concentration (log M)

FIG. 4B

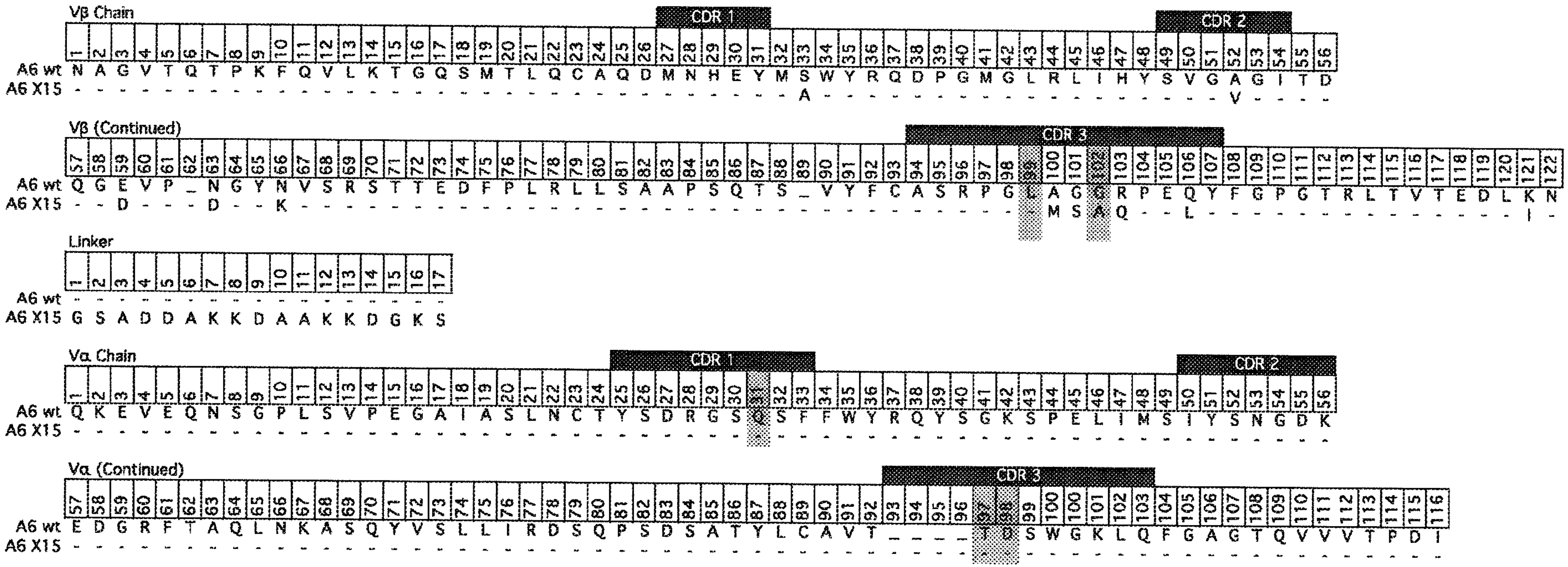

Vβ Chain
CDR 1
CDR 2
A6 wt N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D
A6 X15 - A - - - - - - - - - - - - - - - - - - V - - - -
Vβ (Continued)
CDR 3
A6 wt Q G E V P _ N G Y N V S R S T T E D F P L R L L S A A P S Q T S _ V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6 X15 - - D - - - D - - K - M S A Q - - L - - - - - - - - - - - - - - - I -
Linker
A6 wt - - - - - - - - - - - - - - - - -
A6 X15 G S A D D A K K D A A K K D G K S
Vα Chain
CDR 1
CDR 2
A6 wt Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
A6 X15 -
Vα (Continued)
CDR 3
A6 wt E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T _ _ _ _ T D S W G K L Q F G A G T Q V V V T P D I
A6 X15 -

FIG. 5

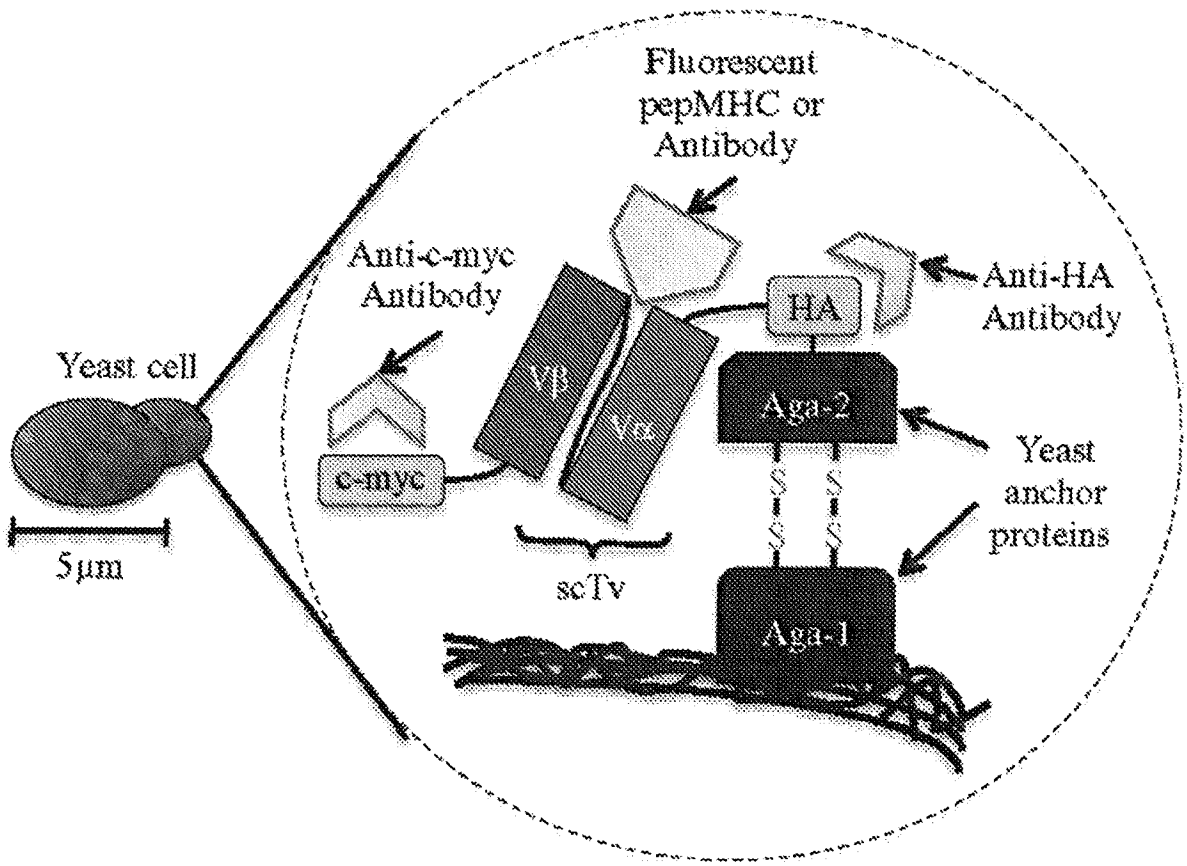

Fluorescent
pepMHC or
Antibody
Anti-c-myc
Antibody
Anti-HA
Antibody
HA
Yeast cell
Vβ
Vα
Aga-2
c-myc
Yeast
anchor
proteins
5μm
scTv
Aga-1

FIG. 6

Vβ Chain

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61
																											CDR 1																						CDR 2												
RD1 Library	N	A	G	V	T	Q	T	P	K	F	Q	V	L	K	T	G	Q	S	M	T	L	Q	C	A	Q	D	M	N	H	E	Y	M	A	W	Y	R	Q	D	P	G	M	G	L	R	L	I	H	Y	S	V	G	V	G	I	T	D	Q	G	D	V	P
Clone #1-10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vβ (Continued)

	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122
																																	CDR 3																														
RD1 Library	_	D	G	Y	K	V	S	R	S	T	T	E	D	F	P	L	R	L	L	S	A	A	P	S	Q	T	S	_	V	Y	F	C	A	S	R	P	G	X	M	S	X	Q	P	E	L	Y	F	G	P	G	T	R	L	T	V	T	E	D	L	I	N
Clone #1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	-	-	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #3						-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	-	-	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Linker

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
RD1 Library	G	S	A	D	D	A	K	K	D	A	A	K	K	D	G	K	S
Clone #1-10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vα Chain

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58
																									CDR 1																									CDR 2								
RD1 Library	Q	K	E	V	E	Q	N	S	G	P	L	S	V	P	E	G	A	I	A	S	L	N	C	T	Y	S	D	R	G	S	X	S	F	F	W	Y	R	Q	Y	S	G	K	S	P	E	L	I	M	S	I	Y	S	N	G	D	K	E	D
Clone #1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Vα (Continued)

	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117
																																			CDR 3																								
RD1 Library	G	R	F	T	A	Q	L	N	K	A	S	Q	Y	V	S	L	L	I	R	D	S	Q	P	S	D	S	A	T	Y	L	C	A	V	T	_	_	_	_	X	X	X	W	G	K	L	Q	F	G	A	G	T	Q	V	V	V	T	P	D	I
Clone #1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #6	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Clone #10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

FIG. 7

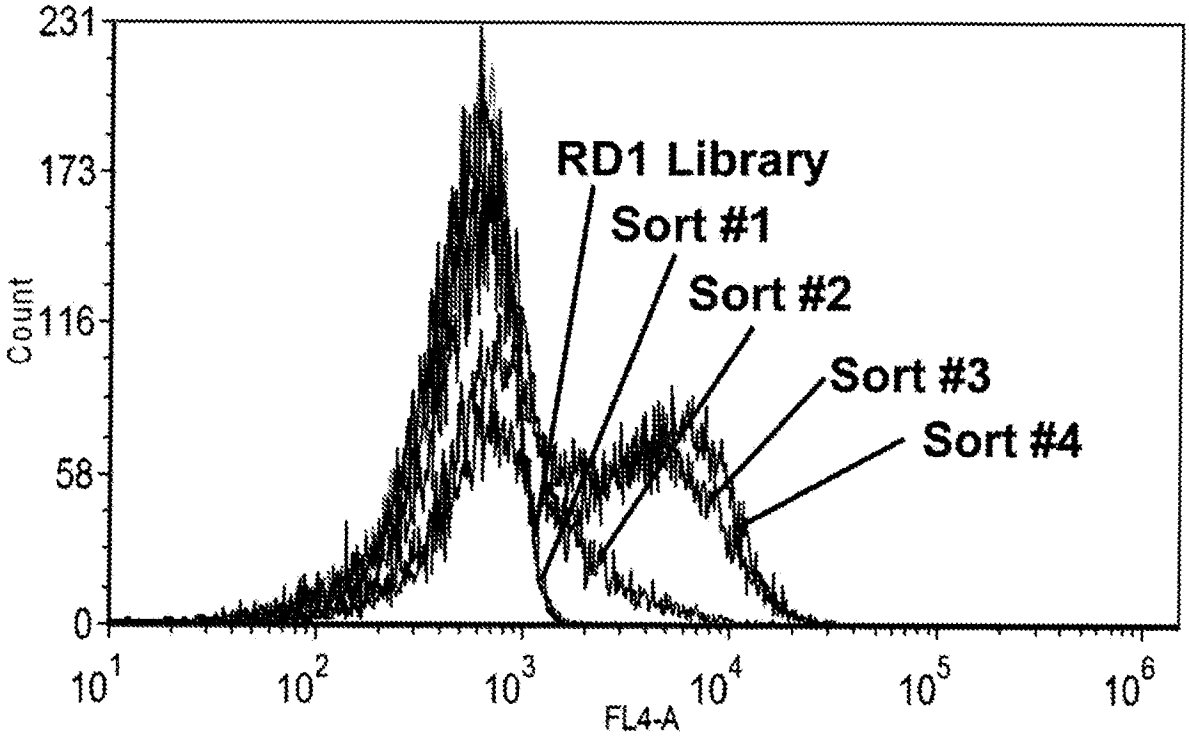

231
173
116
58
0
Count
RD1 Library
Sort #1
Sort #2
Sort #3
Sort #4
10^1
10^2
10^3
10^4
10^5
10^6
FL4-A

FIG. 8

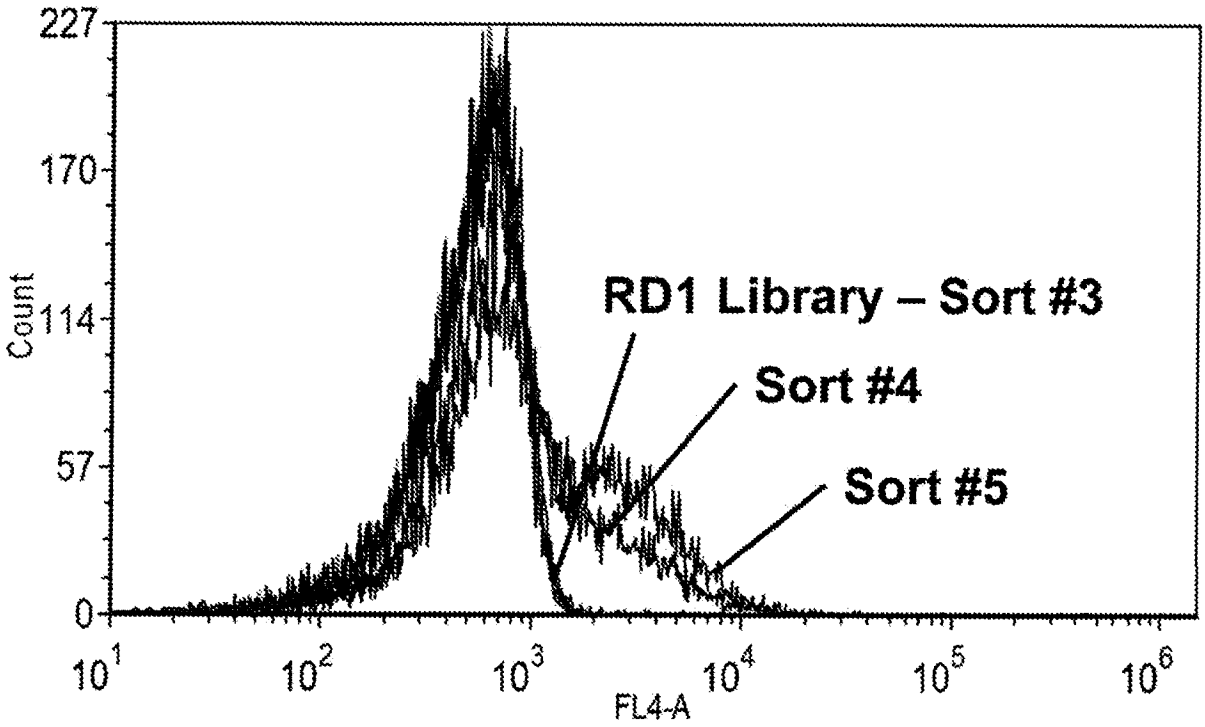

227
170
114
57
0
Count
RD1 Library – Sort #3
Sort #4
Sort #5
10^1
10^2
10^3
10^4
10^5
10^6
FL4-A

FIG. 9

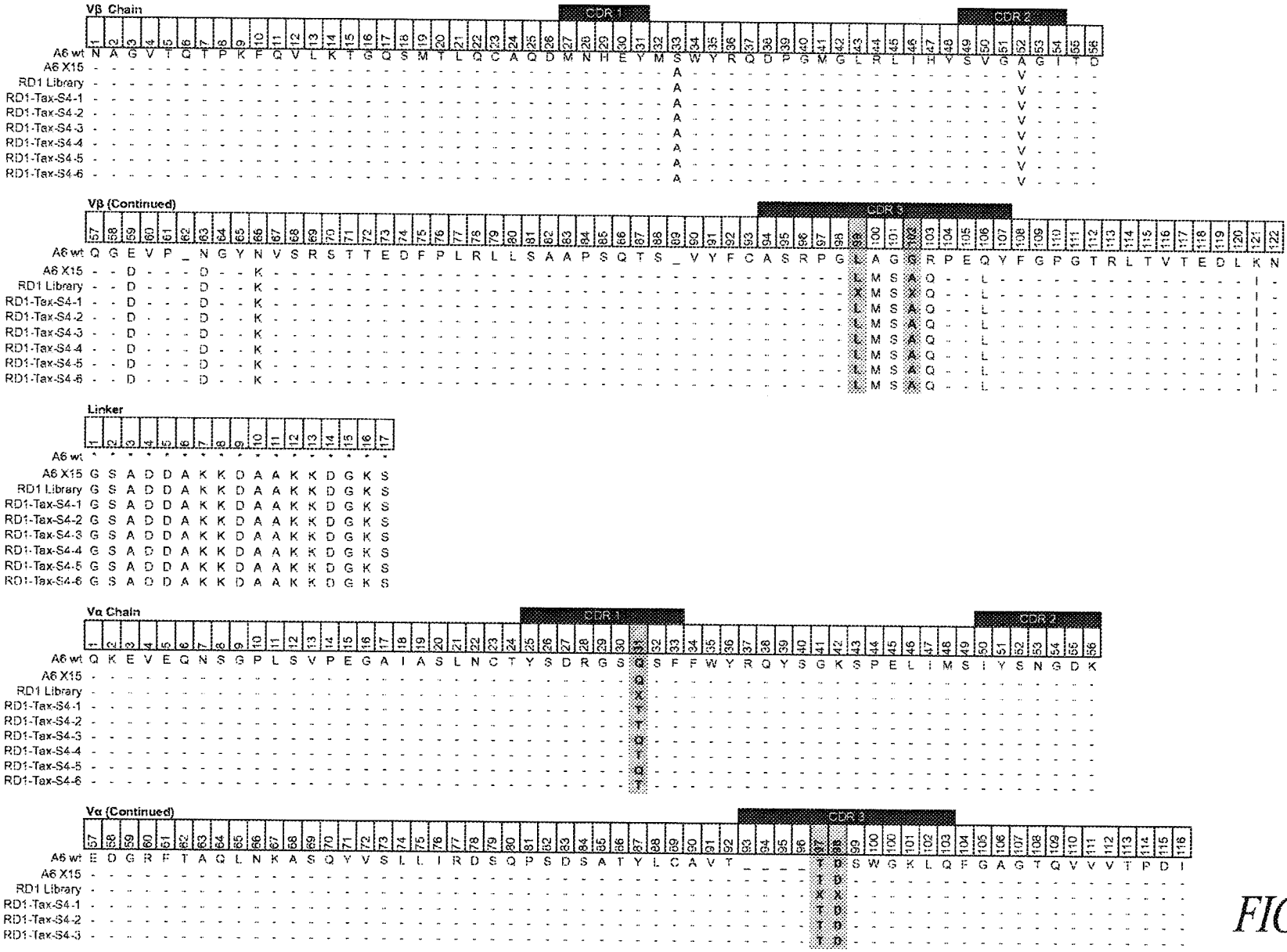

Vβ Chain
CDR 1
CDR 2
A6 wt N A G V T Q T P K I D V L K T G Q S M T L D C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D
A6 X15 A V
RD1 Library A V
RD1-Tax-S4-1 A V
RD1-Tax-S4-2 A V
RD1-Tax-S4-3 A V
RD1-Tax-S4-4 A V
RD1-Tax-S4-5 A V
RD1-Tax-S4-6 A V
Vβ (Continued)
CDR 3
A6 wt Q G E V P _ N G Y N V S R S T T E D F P L R L L S A A P S Q T S _ V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6 X15 D K L M S A Q L
RD1 Library D K X M S X Q L
RD1-Tax-S4-1 D K L M S A Q L
RD1-Tax-S4-2 D K L M S A Q L
RD1-Tax-S4-3 D K L M S A Q L
RD1-Tax-S4-4 D K L M S A Q L
RD1-Tax-S4-5 D K L M S A Q L
RD1-Tax-S4-6 D K L M S X Q L
Linker
A6 wt * * * * * * * * * * * * * * * *
A6 X15 G S A D D A K K D A A K K D G K S
RD1 Library G S A D D A K K D A A K K D G K S
RD1-Tax-S4-1 G S A D D A K K D A A K K D G K S
RD1-Tax-S4-2 G S A D D A K K D A A K K D G K S
RD1-Tax-S4-3 G S A D D A K K D A A K K D G K S
RD1-Tax-S4-4 G S A D D A K K D A A K K D G K S
RD1-Tax-S4-5 G S A D D A K K D A A K K D G K S
RD1-Tax-S4-6 G S A D D A K K D A A K K D G K S
Vα Chain
CDR 1
CDR 2
A6 wt Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
A6 X15
RD1 Library
RD1-Tax-S4-1
RD1-Tax-S4-2
RD1-Tax-S4-3
RD1-Tax-S4-4
RD1-Tax-S4-5
RD1-Tax-S4-6
Vα (Continued)
CDR 3
A6 wt E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T _ _ _ T D S W G K L Q F G A G T Q V V V T P D I
A6 X15 T D
RD1 Library X X
RD1-Tax-S4-1 T D
RD1-Tax-S4-2 T D
RD1-Tax-S4-3 T D

FIG. 10A

Position	1			2			3			4			5		
RD1 Library	N	N	S	N	N	S	N	N	S	N	N	N	N	N	S
	X			X			X			X			X		
RD1-Tax-S4-1	T	T	G	G	C	C	A	C	C	A	C	G	G	A	C
	L (3)			A (2)			T (2)			T (2)			D (1)		
RD1-Tax-S4-2	T	T	G	G	C	G	A	C	C	A	C	C	G	A	C
	L (3)			A (2)			T (2)			T (2)			D (1)		
RD1-Tax-S4-3	C	T	C	G	C	C	C	A	G	A	C	C	G	A	C
	L (3)			A (2)			Q (1)			T (2)			D (1)		
RD1-Tax-S4-4	T	T	G	G	C	G	A	C	C	A	C	C	G	A	C
	L (3)			A (2)			T (2)			T (2)			D (1)		
RD1-Tax-S4-5	C	T	C	G	C	C	C	A	G	A	C	C	G	A	C
	L (3)			A (2)			Q (1)			T (2)			D (1)		
RD1-Tax-S4-6	T	T	G	G	C	G	A	C	C	A	C	C	G	A	C
	L (3)			A (2)			T (2)			T (2)			D (1)		

FIG. 10B

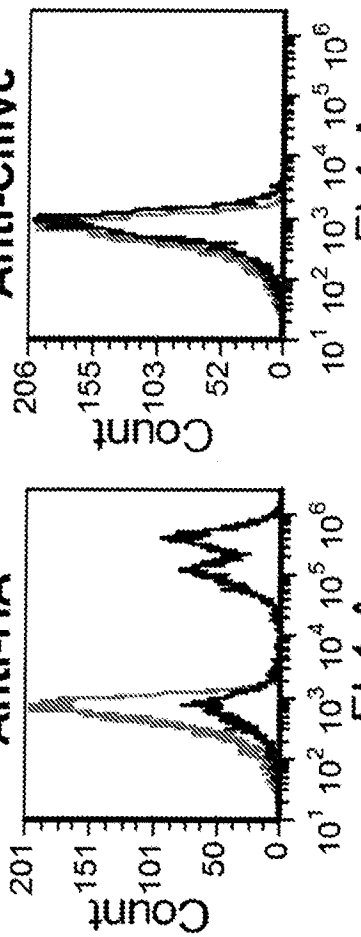


FIG. 11A

FIG. 11B

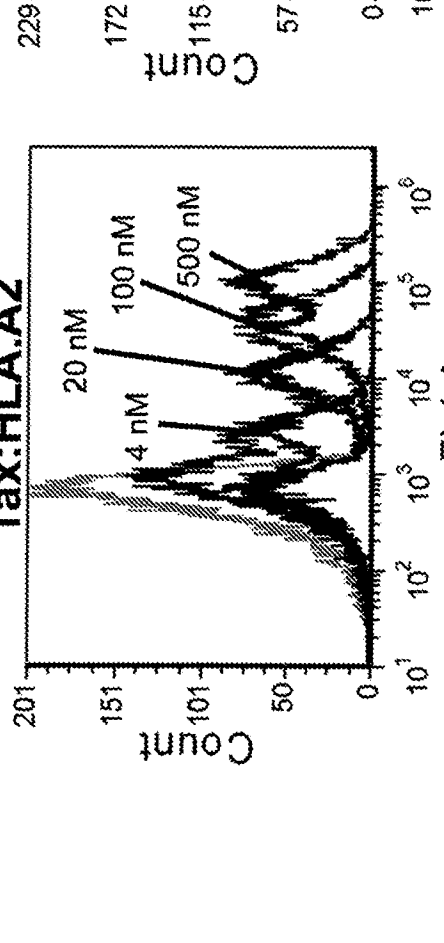


FIG. 11C

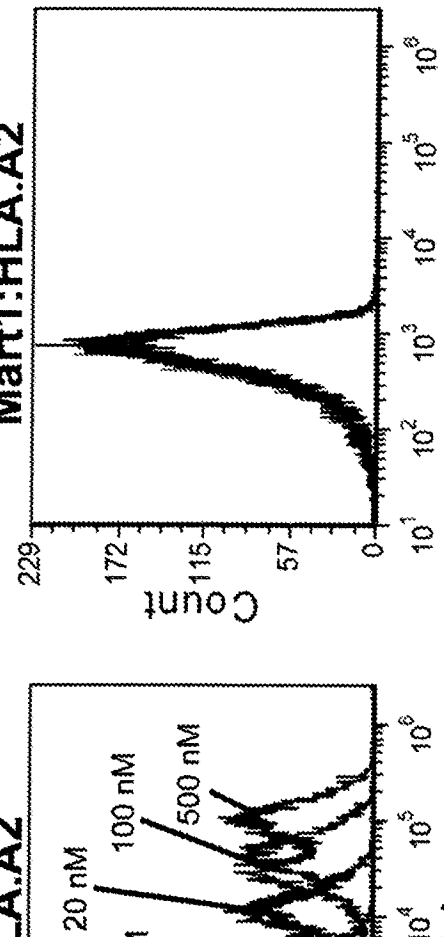


FIG. 11D

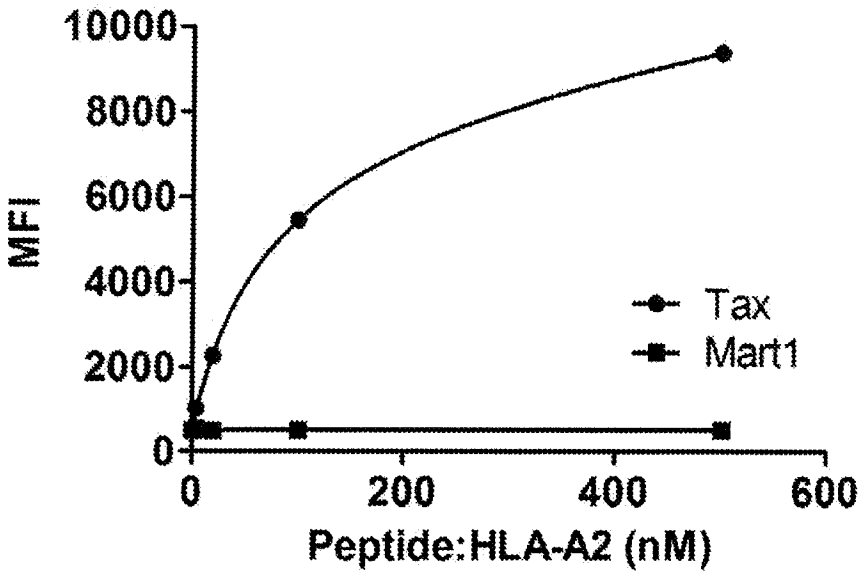

10000
8000
6000
4000
2000
0
MFI
0
200
400
600
Peptide:HLA-A2 (nM)
Tax
Mart1

FIG. 11E


Vβ Chain
CDR 1
CDR 2
A6 wt N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D
A6 X15
RD1 Library
RD1-Mart1-S5-1
RD1-Mart1-S5-2
RD1-Mart1-S5-3
RD1-Mart1-S5-4
RD1-Mart1-S5-6
Vβ (Continued)
CDR 3
A6 wt Q G E V P N G Y N V S R S T T E D F P L R L L S A A P S Q T S V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6 X15
RD1 Library
RD1-Mart1-S5-1
RD1-Mart1-S5-2
RD1-Mart1-S5-3
RD1-Mart1-S5-4
RD1-Mart1-S5-6
Linker
A6 wt
A6 X15 G S A D D A K K D A A K K D G K S
RD1 Library G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-1 G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-2 G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-3 G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-4 G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-6 G S A D D A K K D A A K K D G K S
Vα Chain
CDR 1
CDR 2
A6 wt Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
A6 X15
RD1 Library
RD1-Mart1-S5-1
RD1-Mart1-S5-2
RD1-Mart1-S5-3
RD1-Mart1-S5-4
RD1-Mart1-S5-6
Vα (Continued)
CDR 3
A6 wt E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T T D S W G K L Q F G A G T Q V V V T P D I
A6 X15
RD1 Library
RD1-Mart1-S5-1
RD1-Mart1-S5-2
RD1-Mart1-S5-3
RD1-Mart1-S5-4
RD1-Mart1-S5-6

FIG. 12A

Position	1			2			3			4			5		
RD1 Library	N	N	S	N	N	S	N	N	S	N	N	N	N	N	S
	X			X			X			X			X		
RD1-Mart1-S5-1	T	G	G	G	G	C	A	C	G	A	A	G	T	A	C
	W (1)			G (2)			T (2)			K (1)			Y (1)		
RD1-Mart1-S5-2	T	G	G	G	G	C	A	C	G	A	A	G	T	A	C
	W (1)			G (2)			T (2)			K (1)			Y (1)		
RD1-Mart1-S5-3	T	G	G	G	G	C	A	C	G	A	A	G	T	A	C
	W (1)			G (2)			T (2)			K (1)			Y (1)		
RD1-Mart1-S5-4	T	G	G	G	G	C	A	C	G	A	A	G	T	A	C
	W (1)			G (2)			T (2)			K (1)			Y (1)		
RD1-Mart1-S5-6	T	G	G	G	G	C	A	C	G	A	A	G	T	A	C
	W (1)			G (2)			T (2)			K (1)			Y (1)		

FIG. 12B

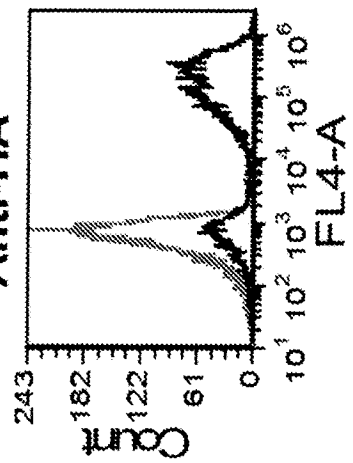


FIG. 13A

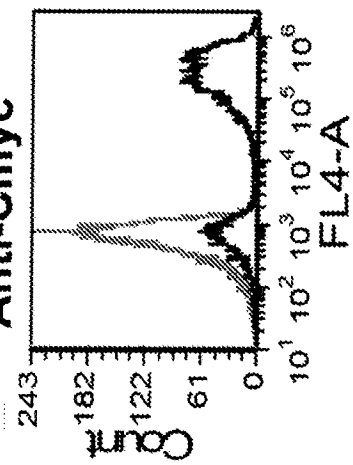


FIG. 13B

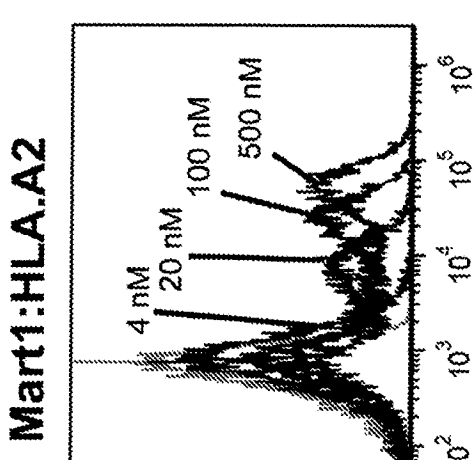


FIG. 13C

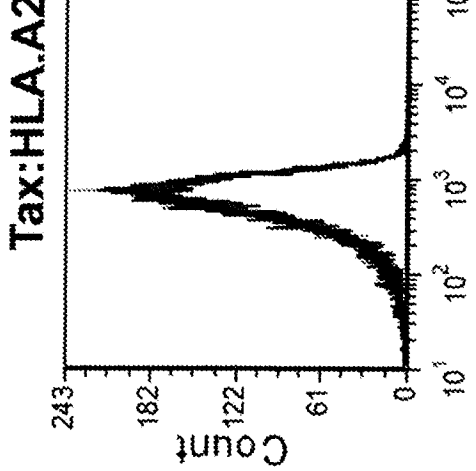


FIG. 13D

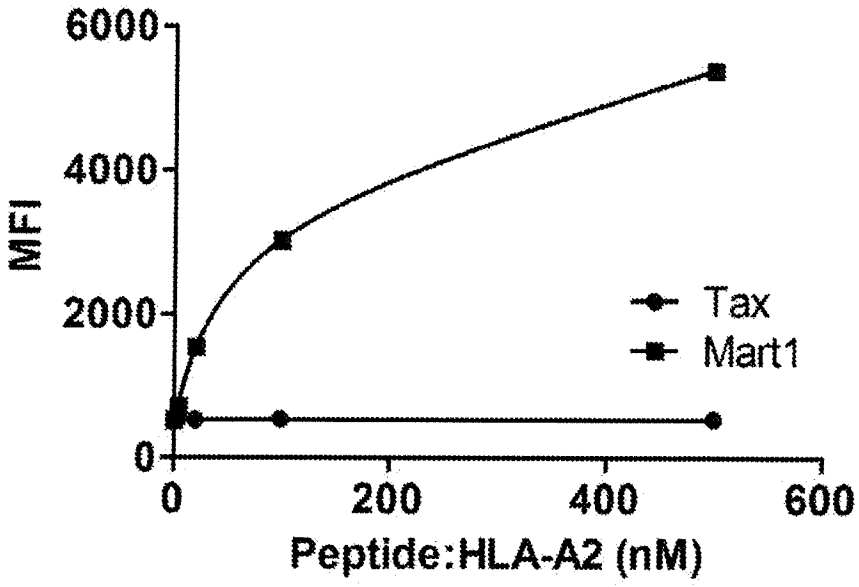


FIG. 13E

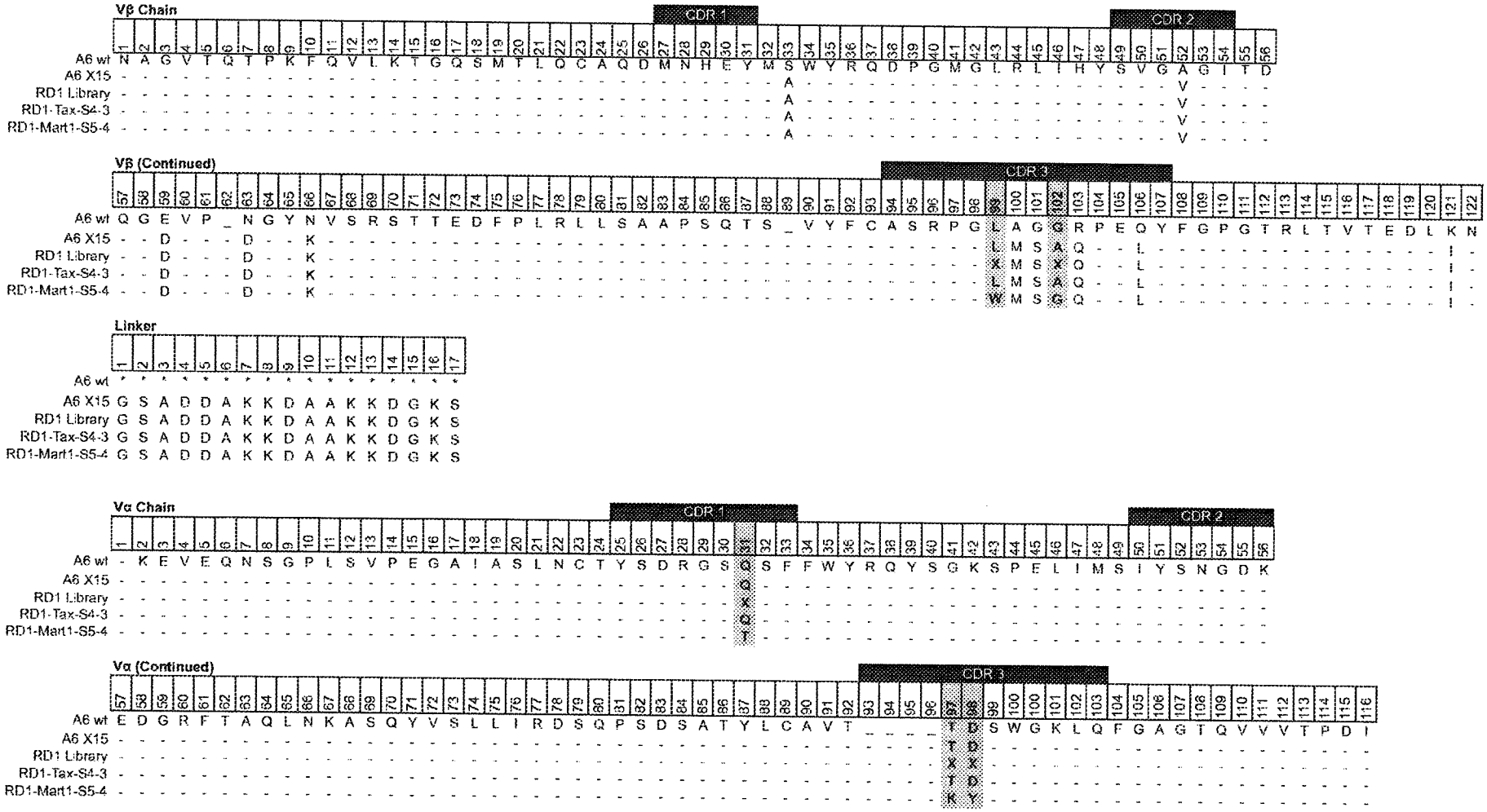

Vβ Chain
CDR 1
CDR 2
A6 wt N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D
A6 X15 A V
RD1 Library A V
RD1-Tax-S4-3 A V
RD1-Mart1-S5-4 A V
Vβ (Continued)
CDR 3
A6 wt Q G E V P _ N G Y N V S R S T T E D F P L R L L S A A P S Q T S _ V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6 X15 D D K L M S A Q L I
RD1 Library D D K X M S X Q L I
RD1-Tax-S4-3 D D K L M S A Q L I
RD1-Mart1-S5-4 D D K W M S G Q L I
Linker
A6 wt
A6 X15 G S A D D A K K D A A K K D G K S
RD1 Library G S A D D A K K D A A K K D G K S
RD1-Tax-S4-3 G S A D D A K K D A A K K D G K S
RD1-Mart1-S5-4 G S A D D A K K D A A K K D G K S
Vα Chain
CDR 1
CDR 2
A6 wt K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
A6 X15 Q
RD1 Library X
RD1-Tax-S4-3 Q
RD1-Mart1-S5-4 T
Vα (Continued)
CDR 3
A6 wt E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T _ _ _ _ T D S W G K L Q F G A G T Q V V V T P D I
A6 X15 T D
RD1 Library X X
RD1-Tax-S4-3 T D
RD1-Mart1-S5-4 K Y

FIG. 14

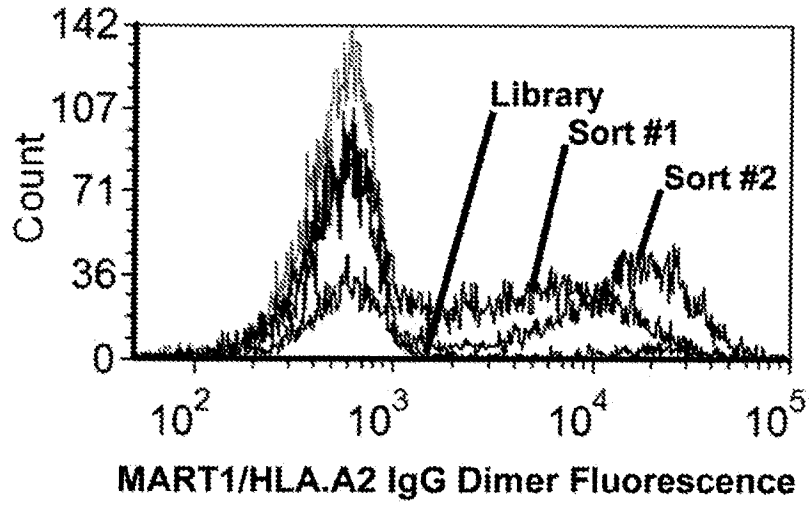


FIG. 15A

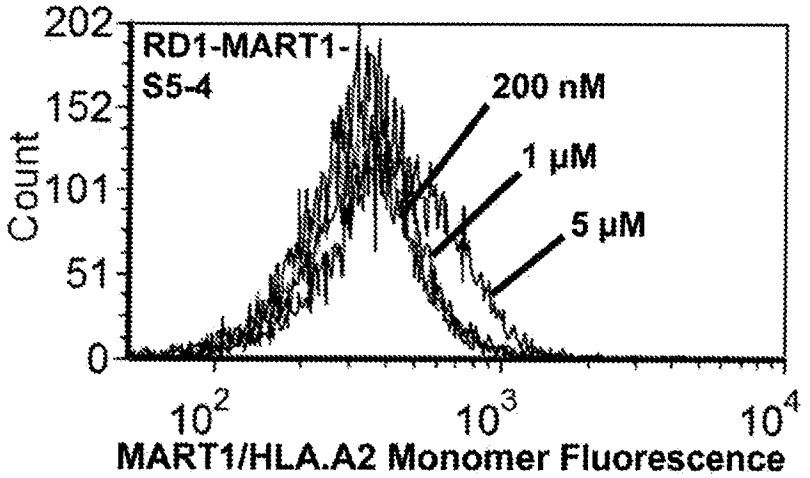


FIG. 15B

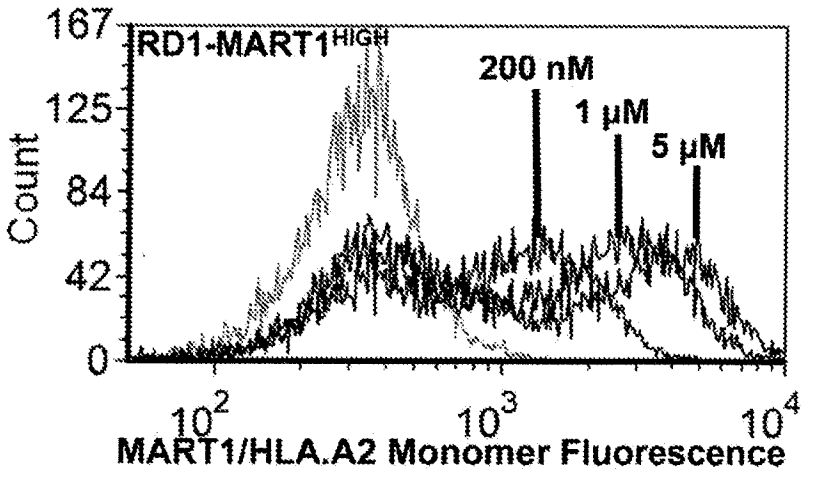


FIG. 15C

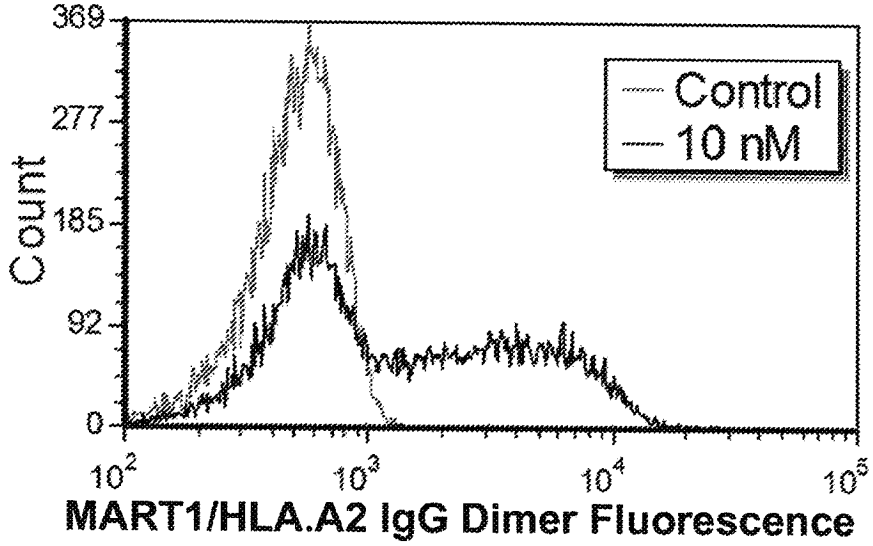


FIG. 16A

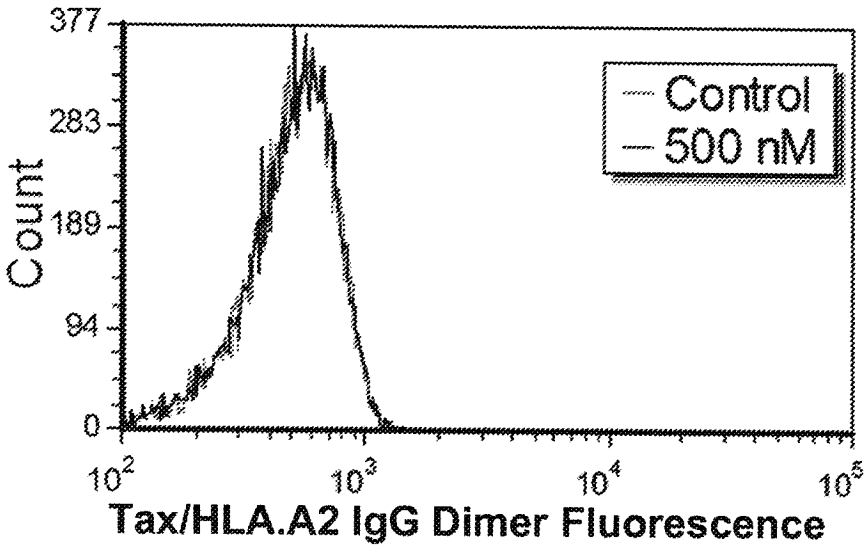


FIG. 16B

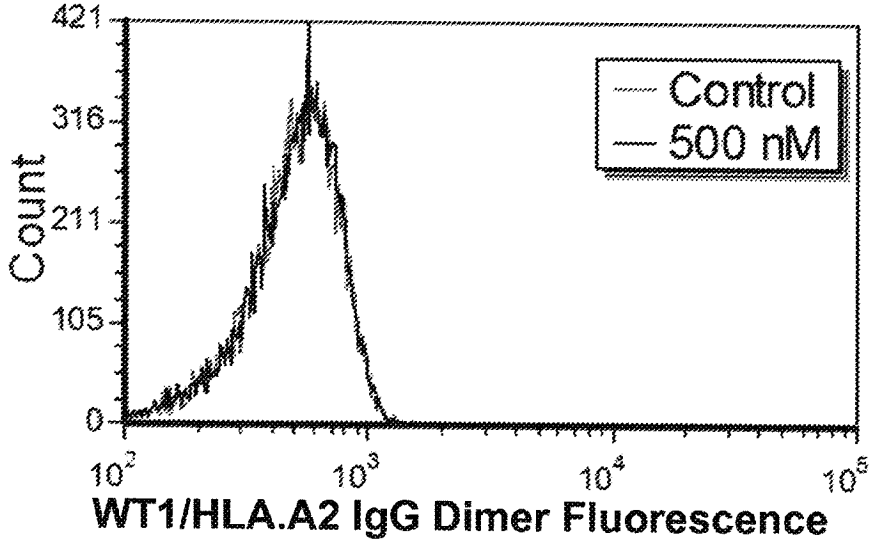


FIG. 16C

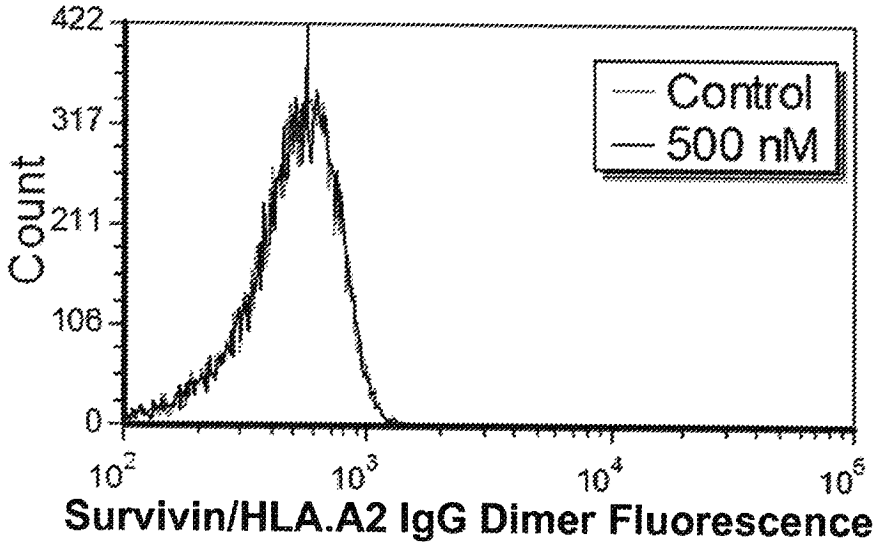


FIG. 16D

Binding and specificity of soluble RD1-MART1^{HIGH} with peptide pulsed T2 cells

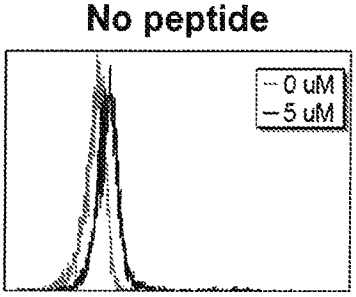


FIG. 17A

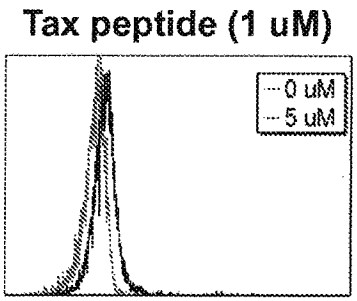


FIG. 17B

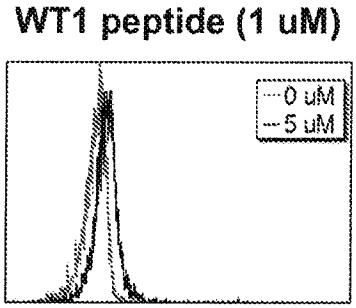


FIG. 17C

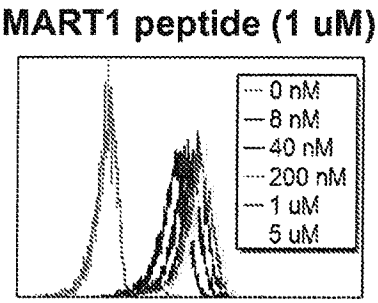


FIG. 17D

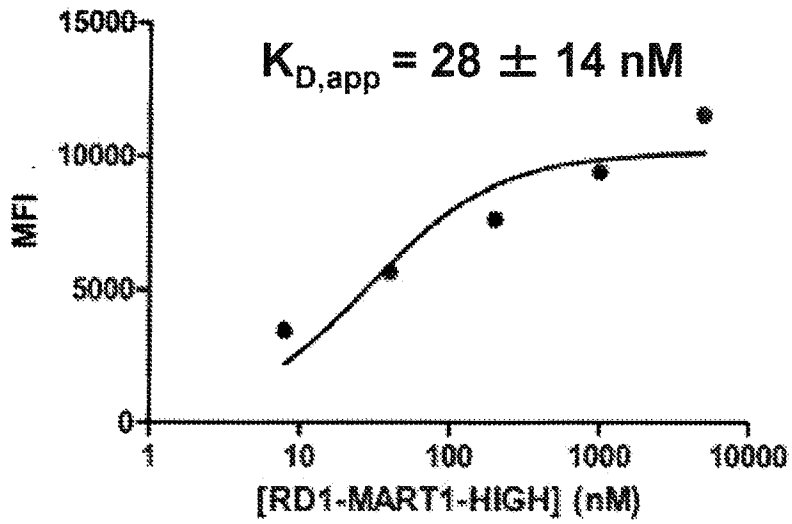


FIG. 17E

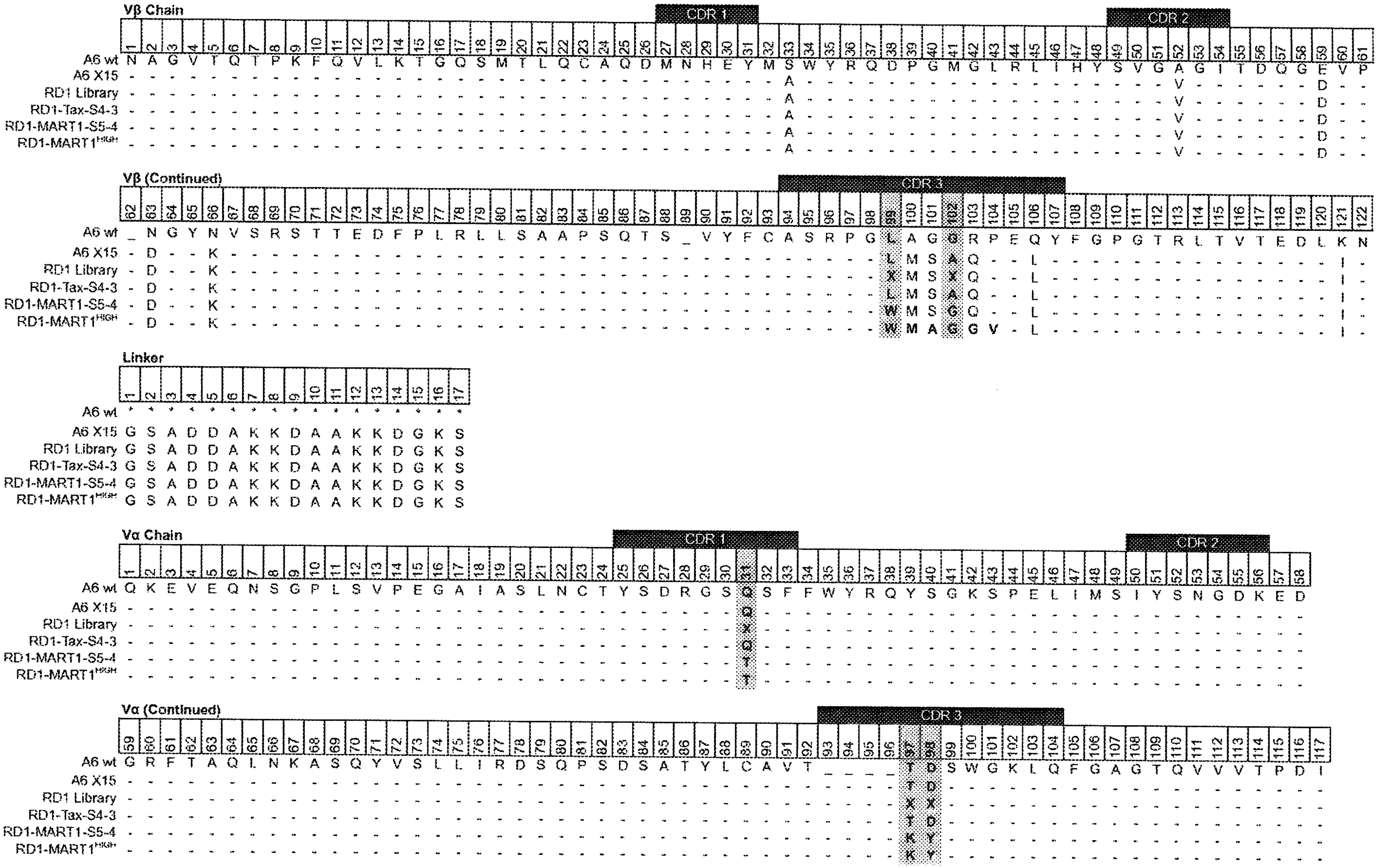

Vβ Chain
CDR 1
CDR 2
1-61
A6 wt NAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVP
A6 X15 --------------------------------A------------------V------D--
RD1 Library --------------------------------A------------------V------D--
RD1-Tax-S4-3 --------------------------------A------------------V------D--
RD1-MART1-S5-4 --------------------------------A------------------V------D--
RD1-MART1^HIGH --------------------------------A------------------V------D--
Vβ (Continued)
CDR 3
62-122
A6 wt _NGYNVSRSTTEDFPLRLLSAAPSQTS_VYFCASRPGLAGGRPEQYFGPGTRLTVTEDLKN
A6 X15 -D--K--------------------------------LMSAQ--L--------------I-
RD1 Library -D--K--------------------------------XMSXQ--L--------------I-
RD1-Tax-S4-3 -D--K--------------------------------LMSAQ--L--------------I-
RD1-MART1-S5-4 -D--K--------------------------------WMSGQ--L--------------I-
RD1-MART1^HIGH -D--K--------------------------------WMAGGV-L--------------I-
Linker
1-17
A6 wt *****************
A6 X15 GSADDAKKDAAKKDGKS
RD1 Library GSADDAKKDAAKKDGKS
RD1-Tax-S4-3 GSADDAKKDAAKKDGKS
RD1-MART1-S5-4 GSADDAKKDAAKKDGKS
RD1-MART1^HIGH GSADDAKKDAAKKDGKS
Vα Chain
CDR 1
CDR 2
1-58
A6 wt QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMSIYSNGDKED
A6 X15 ------------------------------Q---------------------------
RD1 Library ------------------------------X---------------------------
RD1-Tax-S4-3 ------------------------------Q---------------------------
RD1-MART1-S5-4 ------------------------------T---------------------------
RD1-MART1^HIGH ------------------------------T---------------------------
Vα (Continued)
CDR 3
59-117
A6 wt GRFTAQLNKASQYVSLLIRDSQPSDSATYLCAVT____TDSWGKLQFGAGTQVVVTPDI
A6 X15 --------------------------------------TD-------------------
RD1 Library --------------------------------------XX-------------------
RD1-Tax-S4-3 --------------------------------------TD-------------------
RD1-MART1-S5-4 --------------------------------------KY-------------------
RD1-MART1^HIGH --------------------------------------KY-------------------

FIG. 18

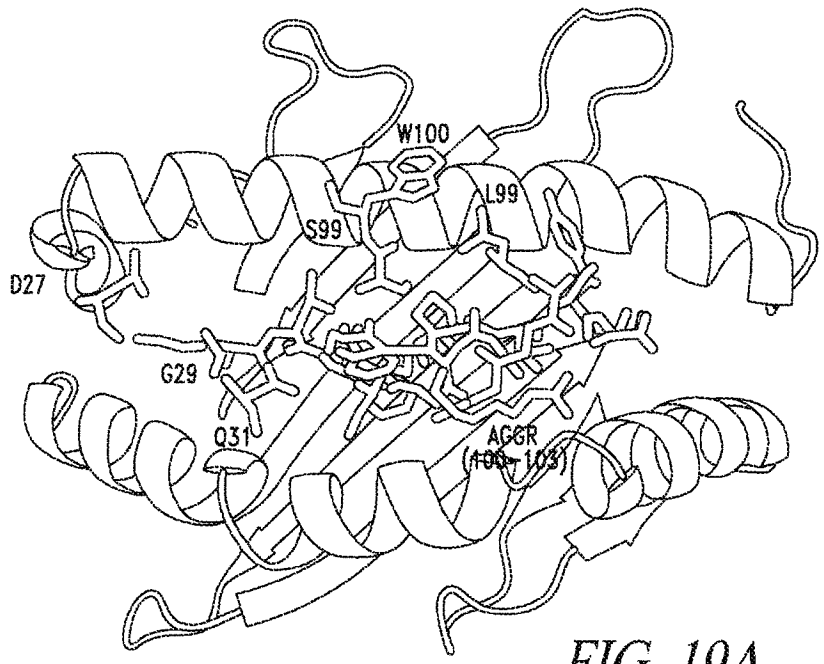


FIG. 19A

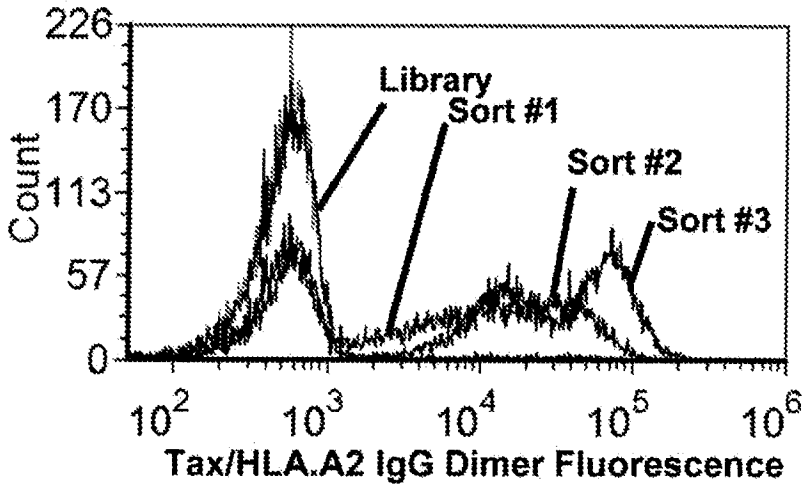


FIG. 19B

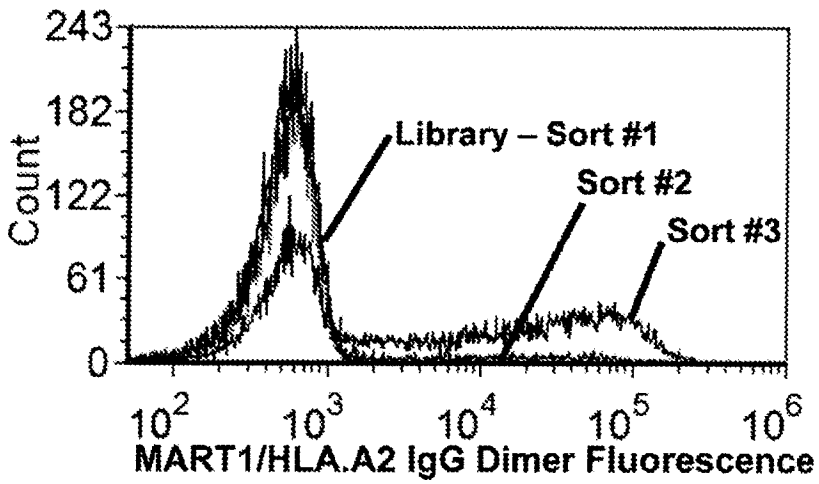


FIG. 19C

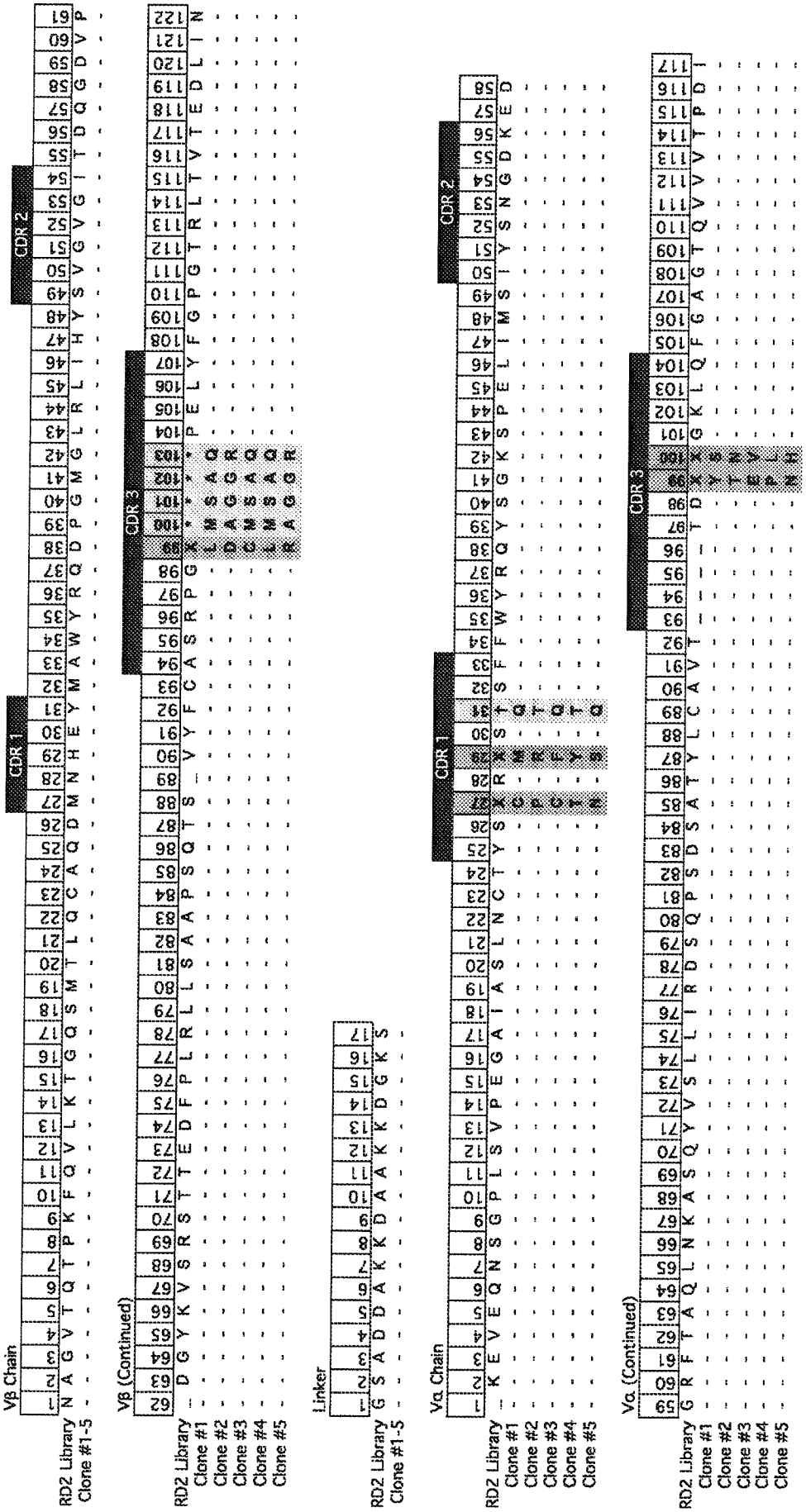

Vβ Chain
CDR 1
CDR 2
RD2 Library
Clone #1-5
Vβ (Continued)
CDR 3
Linker
Vα Chain
Vα (Continued)

FIG. 20

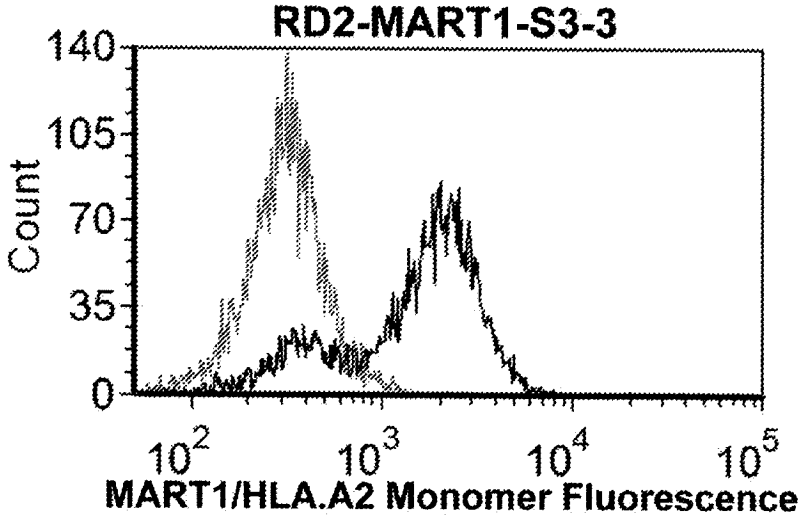


FIG. 21A

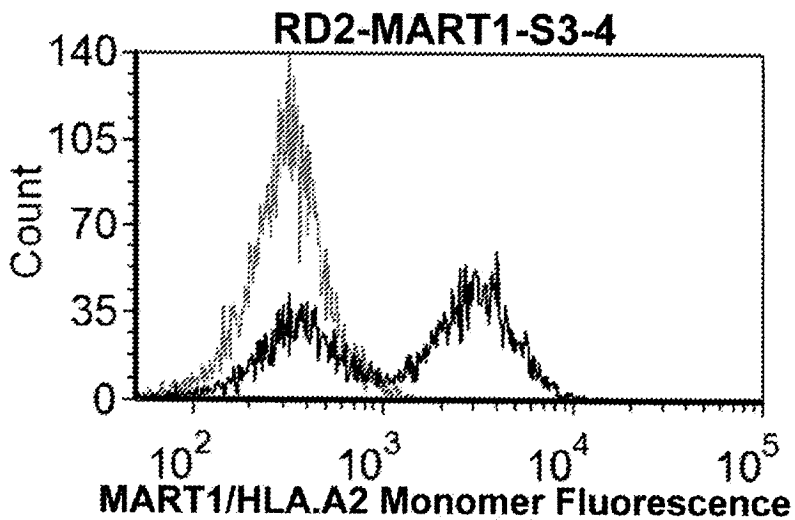


FIG. 21B

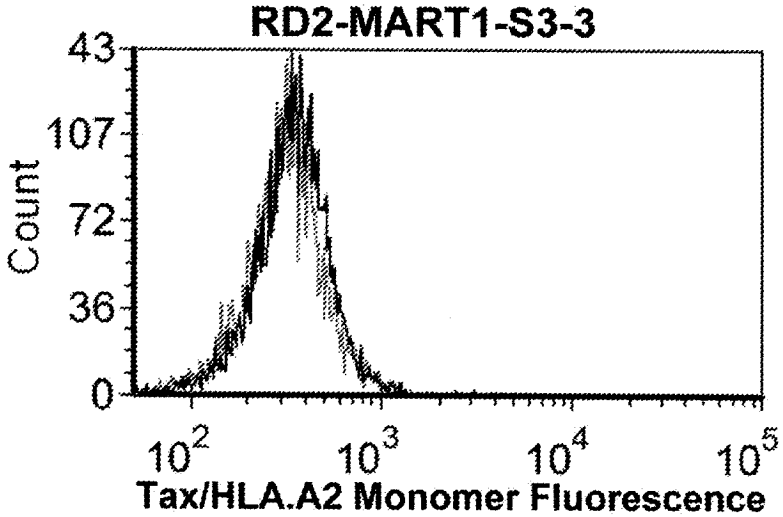


FIG. 21C

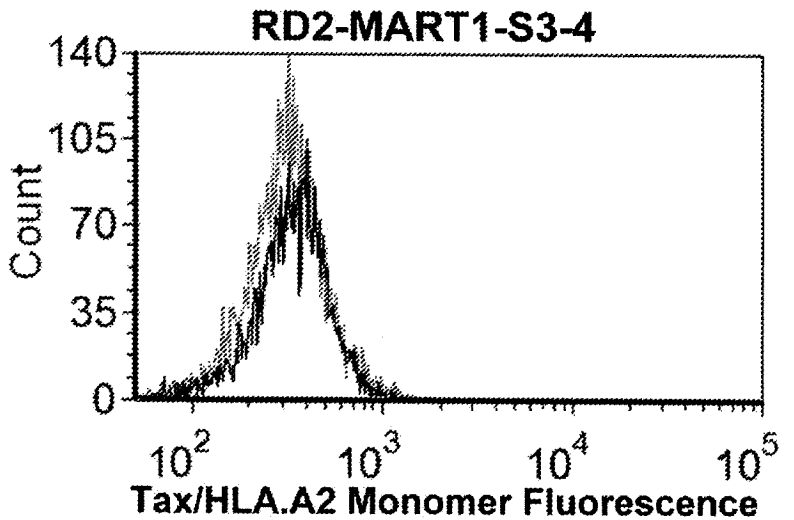


FIG. 21D

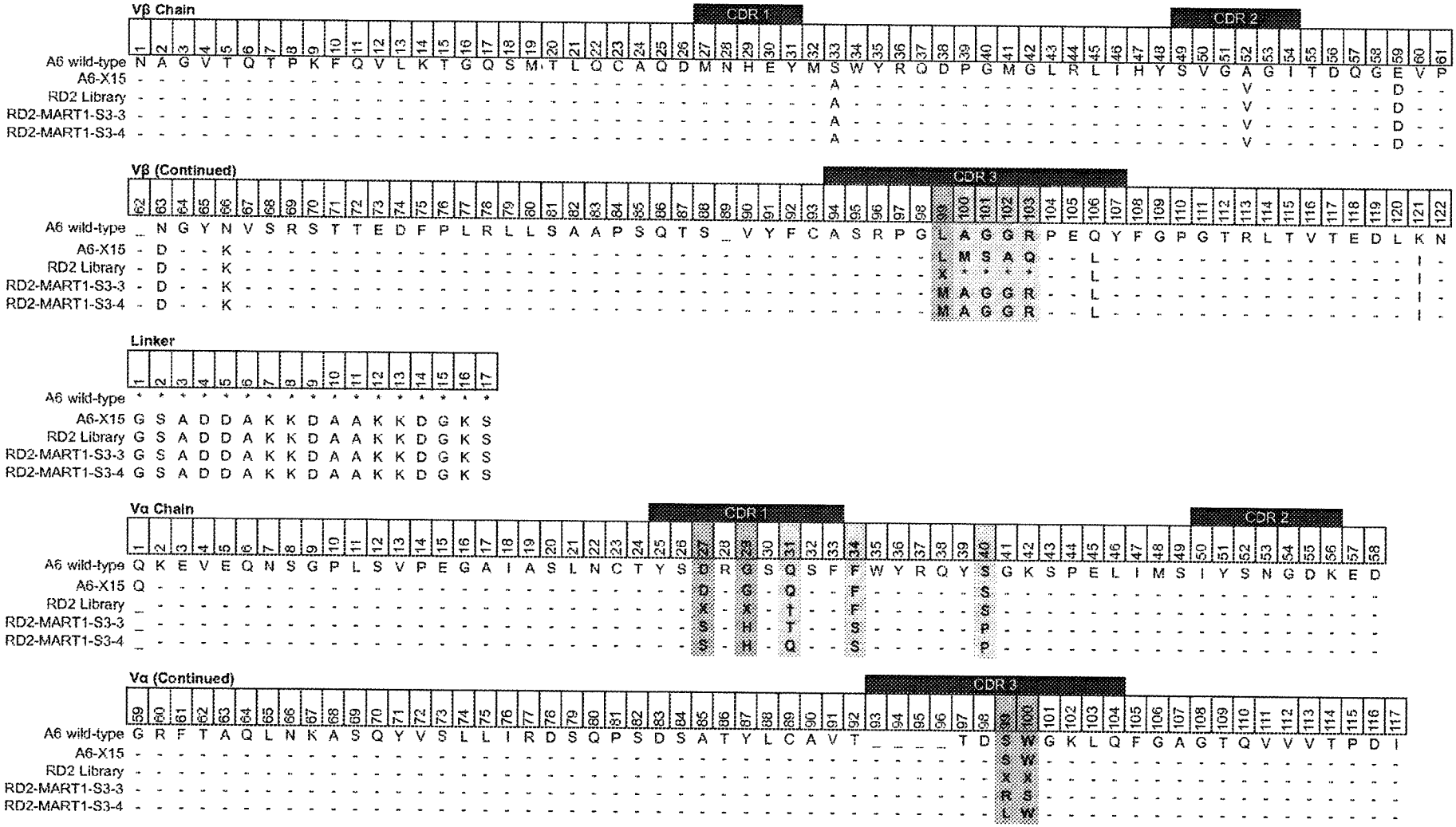

Vβ Chain
CDR 1
CDR 2
A6 wild-type N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D Q G E V P
A6-X15 A D V D
RD2 Library A V D
RD2-MART1-S3-3 A V D
RD2-MART1-S3-4 A V D
Vβ (Continued)
CDR 3
A6 wild-type N G Y N V S R S T T E D F P L R L L S A A P S Q T S V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6-X15 D K L M S A Q L I
RD2 Library D K X * * * * L I
RD2-MART1-S3-3 D K M A G G R L I
RD2-MART1-S3-4 D K M A G G R L I
Linker
A6 wild-type * * * * * * * * * * * * * * * * *
A6-X15 G S A D D A K K D A A K K D G K S
RD2 Library G S A D D A K K D A A K K D G K S
RD2-MART1-S3-3 G S A D D A K K D A A K K D G K S
RD2-MART1-S3-4 G S A D D A K K D A A K K D G K S
Vα Chain
CDR 1
CDR 2
A6 wild-type Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K E D
A6-X15 Q D G Q F S
RD2 Library X X T F S
RD2-MART1-S3-3 S H T S P
RD2-MART1-S3-4 S H Q S P
Vα (Continued)
CDR 3
A6 wild-type G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T T D S W G K L Q F G A G T Q V V V T P D I
A6-X15 S W
RD2 Library X X
RD2-MART1-S3-3 R S
RD2-MART1-S3-4 L W

FIG. 21E

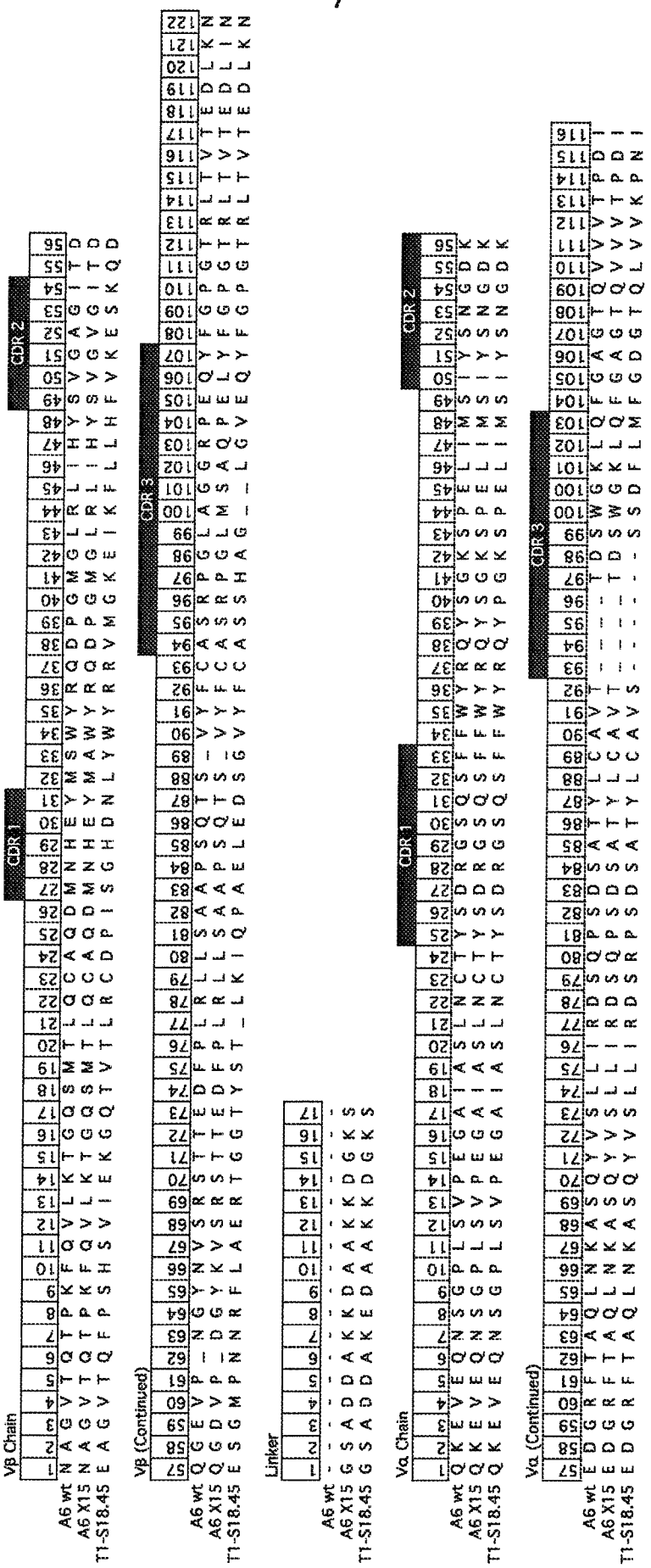

Vβ Chain
CDR 1
CDR 2
A6 wt N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q D P G M G L R L I H Y S V G A G I T D
A6 X15 N A G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M A W Y R Q D P G M G L R L I H Y S V G V G I T D
T1-S18.45 E A G V T Q F P S H S V I E K G Q T V T L R C D P I S G H D N L Y W Y R R V M G K E I K F L L H F V K E S K Q D
Vβ (Continued)
CDR 3
A6 wt Q G E V P N G Y N V S R S T T E D F P L R L L S A A P S Q T S V Y F C A S R P G L A G G R P E Q Y F G P G T R L T V T E D L K N
A6 X15 Q G D V P D G Y K V S R S T T E D F P L R L L S A A P S Q T S V Y F C A S R P G L M S A Q P E L Y F G P G T R L T V T E D L I N
T1-S18.45 E S G M P N N R F L A E R T G G T Y S T L K I Q P A E L E D S G V Y F C A S S H A G L G V E Q Y F G P G T R L T V T E D L K N
Linker
A6 wt - - - - - - - - - - - - - - - -
A6 X15 G S A D D A K K D A A K K D D G K S
T1-S18.45 G S A D D A K E D A A K K D D G K S
Vα Chain
CDR 1
CDR 2
A6 wt Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
A6 X15 Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y S G K S P E L I M S I Y S N G D K
T1-S18.45 Q K E V E Q N S G P L S V P E G A I A S L N C T Y S D R G S Q S F F W Y R Q Y P G K S P E L I M S I Y S N G D K
Vα (Continued)
CDR 3
A6 wt E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V T - - - - T D S W G K L Q F G A G T Q V V V T P D I
A6 X15 E D G R F T A Q L N K A S Q Y V S L L I R D S Q P S D S A T Y L C A V S - - - - T D S W G K L Q F G A G T Q L V V K P N I
T1-S18.45 E D G R F T A Q L N K A S Q Y V S L L I R D S R P S D S A T Y L C A V S - - - - S S D F L M F G D G T Q L V V K P N I

FIG. 22

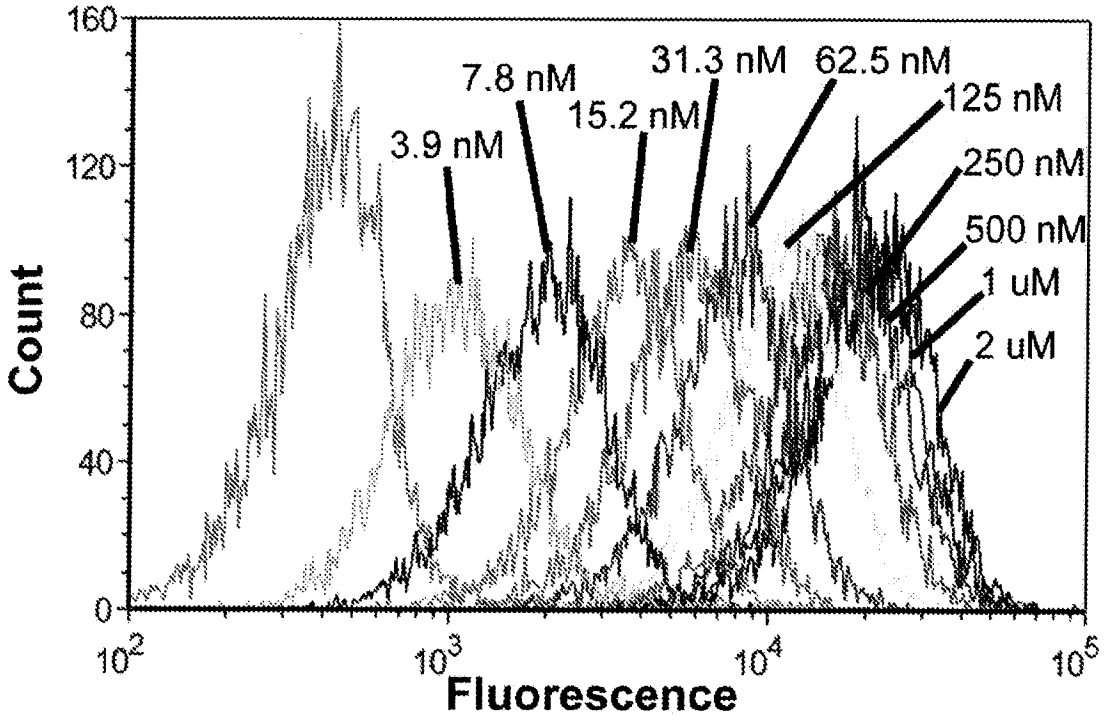


FIG. 23A

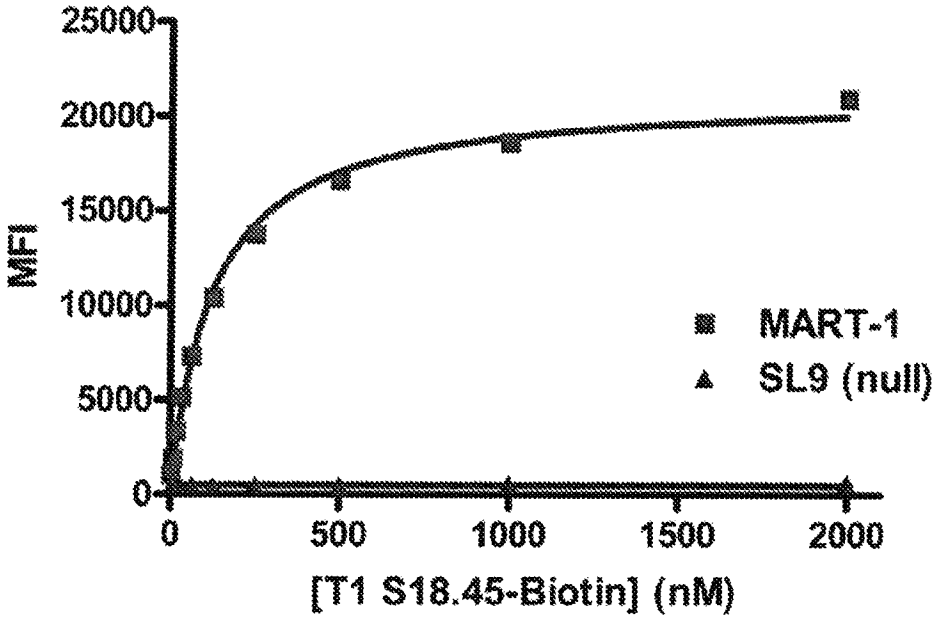


FIG. 23B

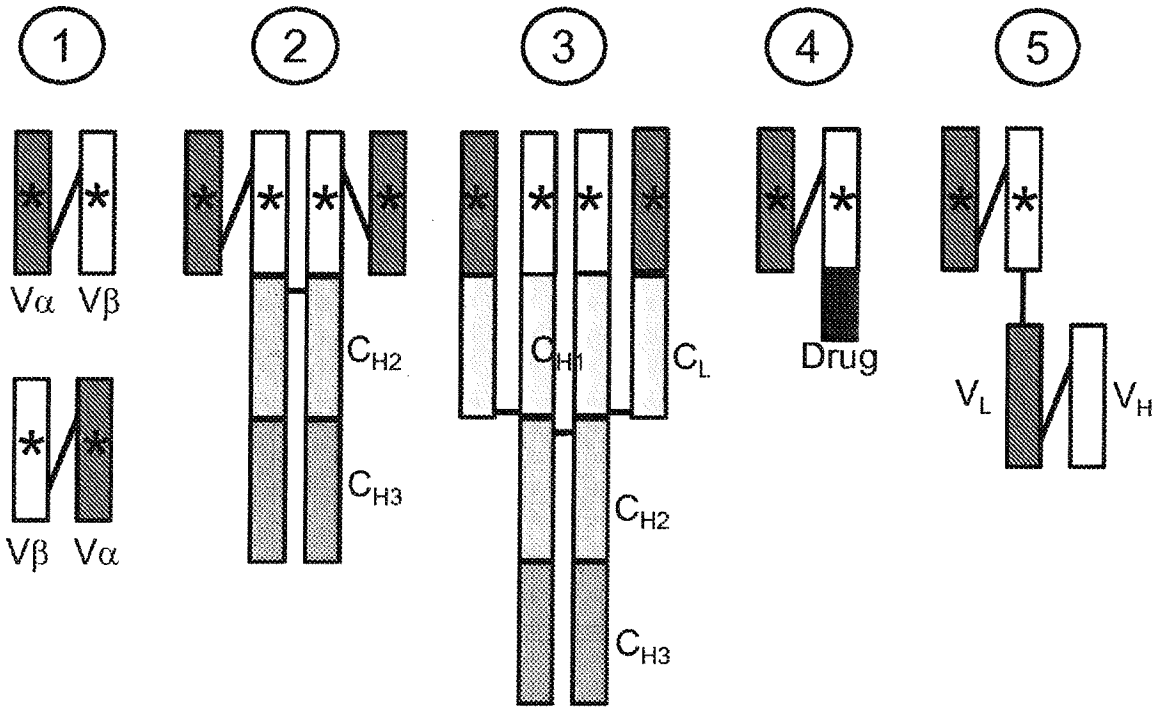


FIG. 24A

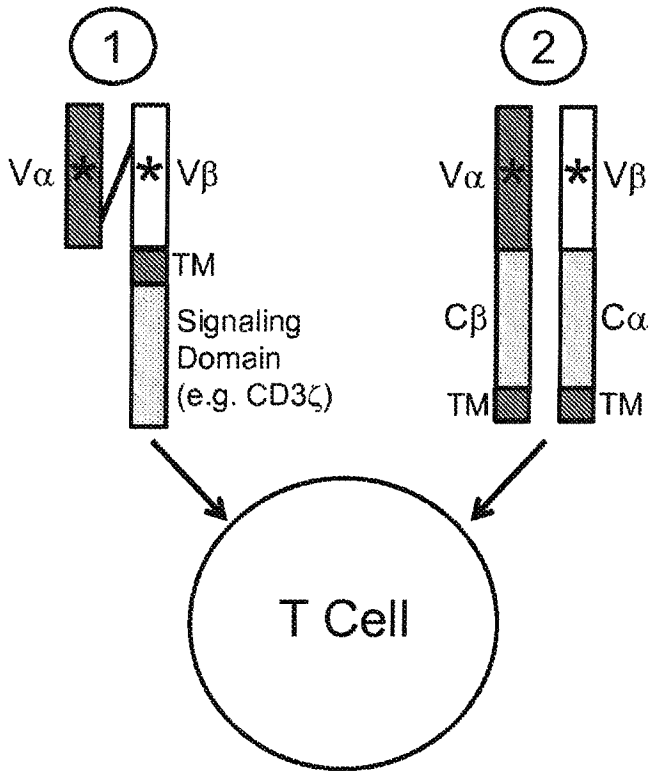


FIG. 24B

SEQUENCE LISTING

<110> The Board of Trustees of the University of Illinois

<120> ENGINEERING T-CELL RECEPTORS

<130> SG5251A

<150> US 61/676,373
<151> 2012-07-27

<160> 61

<170> PatentIn version 3.5

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<211> 113
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<213> Homo sapiens

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

Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser
20 25 30

Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
35 40 45

Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser Gln
65 70 75 80

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Thr Thr Asp Ser Trp
85 90 95

Gly Lys Leu Gln Phe Gly Ala Gly Thr Gln Val Val Val Thr Pro Asp
100 105 110

Ile

<210> 2
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

```
Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn Gly Tyr
    50                  55                  60

Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Leu Ala Gly Gly Arg Pro Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Lys Asn
        115                 120
```

<210> 3
<211> 250
<212> PRT
<213> Homo sapiens

<400> 3

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Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
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Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Leu Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140
```

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145 150 155 160

Thr Tyr Ser Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr
165 170 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
180 185 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
195 200 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
210 215 220

Leu Cys Ala Val Thr Thr Asp Ser Trp Gly Lys Leu Gln Phe Gly Ala
225 230 235 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
245 250

<210> 4
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<223> Synthesized amino acid sequence of the RD1 library

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<400> 4

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met

```
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Xaa Met Ser Xaa Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Xaa Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Xaa Xaa Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 5
<211> 9
<212> PRT
<213> Human T cell lymphotrophic virus

<400> 5

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Leu Leu Phe Gly Tyr Pro Val Tyr Val
1               5
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<210> 6
<211> 9
<212> PRT
<213> Homo sapiens

<400> 6

Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

<210> 7
<211> 10
<212> PRT
<213> Homo sapiens

<400> 7

Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Human immunodeficiency virus

<400> 8

Ser Leu Tyr Asn Thr Val Ala Thr Leu
1 5

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<400> 9

Arg Met Phe Pro Asn Ala Pro Tyr Leu
1 5

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10

Leu Thr Leu Gly Glu Phe Leu Lys Leu
1 5

<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

<400> 11

Ser Leu Leu Met Trp Ile Thr Gln Cys
1 5

<210> 12
<211> 9

<212> PRT
<213> Homo sapiens

<400> 12

Ala Leu Trp Gly Pro Asp Ala Ala Ala
1 5

<210> 13
<211> 8
<212> PRT
<213> Homo sapiens

<400> 13

Val Leu Phe Tyr Leu Gly Gln Tyr
1 5

<210> 14
<211> 9
<212> PRT
<213> Hepatitis B virus

<400> 14

Phe Leu Leu Thr Arg Ile Leu Thr Ile
1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<400> 15

Lys Thr Trp Gly Gln Tyr Trp Gln Val
1 5

<210> 16
<211> 9
<212> PRT
<213> Homo sapiens

<400> 16

Ser Thr Ala Pro Pro Val His Asn Val
1 5

<210> 17
<211> 9
<212> PRT
<213> Homo sapiens

<400> 17

Phe Leu Trp Gly Pro Arg Ala Leu Val
1 5

<210> 18
<211> 9
<212> PRT
<213> Homo sapiens

<400> 18

Lys Ile Phe Gly Ser Leu Ala Phe Leu
1 5

<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<400> 19

Leu Glu Glu Lys Lys Gly Asn Tyr Val
1 5

<210> 20
<211> 9
<212> PRT
<213> Homo sapiens

<400> 20

Tyr Leu Ser Gly Ala Asn Leu Asn Leu
1 5

<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<400> 21

Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Gly Lys
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Ser

<210> 22
<211> 250
<212> PRT
<213> Artificial Sequence

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<223> Amino acid sequence of clone from RD1 library

<400> 22

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr

50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Ile Met Ser Glu Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
100 105 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
115 120 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
130 135 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145 150 155 160

Thr Tyr Ser Asp Arg Gly Ser Ser Ser Phe Phe Trp Tyr Arg Gln Tyr
165 170 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
180 185 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
195 200 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
210 215 220

Leu Cys Ala Val Thr Pro Pro Ser Trp Gly Lys Leu Gln Phe Gly Ala
225 230 235 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
245 250

<210> 23
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 23

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

```
Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Arg Met Ser Met Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Arg Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Pro Cys Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 24
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 24

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Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15
```

```
Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Ser Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Ala Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Ile Val Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 25
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 25

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Thr Met Ser Arg Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
100 105 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
115 120 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
130 135 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145 150 155 160

Thr Tyr Ser Asp Arg Gly Ser Gly Ser Phe Phe Trp Tyr Arg Gln Tyr
165 170 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
180 185 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
195 200 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
210 215 220

Leu Cys Ala Val Thr Ser Leu Ser Trp Gly Lys Leu Gln Phe Gly Ala
225 230 235 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
245 250

<210> 26
<211> 250
<212> PRT

<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 26

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Ser Met Ser His Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Phe Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Leu His Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 27
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 27

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1 5 10 15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Ala Met Ser Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu Thr
100 105 110

Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys Asp
115 120 125

Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn Ser
130 135 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145 150 155 160

Tyr Ser Asp Arg Gly Ser Tyr Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
165 170 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
180 185 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
195 200 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
210 215 220

Cys Ala Val Thr Asn Phe Ser Trp Gly Lys Leu Gln Phe Gly Ala Gly

225 230 235 240

Thr Gln Val Val Val Thr Pro Asp Ile
245

<210> 28
<211> 250
<212> PRT
<213> Artificial Sequence

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<223> Amino acid sequence of clone from RD1 library

<400> 28

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Ser Met Ser Arg Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
100 105 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
115 120 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
130 135 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145 150 155 160

Thr Tyr Ser Asp Arg Gly Ser Ala Ser Phe Phe Trp Tyr Arg Gln Tyr
165 170 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
180 185 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
195 200 205

```
Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Arg Thr Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 29
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 29

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Arg Met Ser Gln Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Trp Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190
```

```
Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Ser Cys Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 30
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 30

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Tyr Met Ser Pro Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Asn Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175
```

```
Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Phe Leu Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 31
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD1 library

<400> 31

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Leu Met Ser Leu Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
```

145 150 155 160

Thr Tyr Ser Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr
165 170 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
180 185 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
195 200 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
210 215 220

Leu Cys Ala Val Thr Arg Ala Ser Trp Gly Lys Leu Gln Phe Gly Ala
225 230 235 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
245 250

<210> 32
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> RD1-Tax-S4-1 clone sequence

<400> 32

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
20 25 30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
35 40 45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Leu Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
100 105 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
115 120 125

```
Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Thr Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Thr Asp Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 33
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> RD1-Mart1-S5-5 clone sequence

<400> 33

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Trp Met Ser Gly Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110
```

```
Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Thr Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Lys Tyr Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 34
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> RD1-Mart1-High clone sequence

<400> 34

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95
```

```
Trp Met Ala Gly Gly Val Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn
    130                 135                 140

Ser Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys
145                 150                 155                 160

Thr Tyr Ser Asp Arg Gly Ser Thr Ser Phe Phe Trp Tyr Arg Gln Tyr
                165                 170                 175

Ser Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp
            180                 185                 190

Lys Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr
        195                 200                 205

Val Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr
    210                 215                 220

Leu Cys Ala Val Thr Lys Tyr Ser Trp Gly Lys Leu Gln Phe Gly Ala
225                 230                 235                 240

Gly Thr Gln Val Val Val Thr Pro Asp Ile
                245                 250
```

<210> 35
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Degenerate amino acid sequence for RD2 library

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa = Any amino acid

<220>
<221> MISC_FEATURE
<222> (98)..(98)
<223> Xaa = Ala or Met

<220>
<221> MISC_FEATURE
<222> (99)..(99)
<223> Xaa = Gly or Ser

<220>
<221> MISC_FEATURE
<222> (100)..(100)

<223> Xaa = Gly or Ala

<220>
<221> MISC_FEATURE
<222> (101)..(101)
<223> Xaa = Arg or Gln

<220>
<221> MISC_FEATURE
<222> (163)..(163)
<223> Xaa = Any amino acid

<220>
<221> MISC_FEATURE
<222> (165)..(165)
<223> Xaa = Any amino acid

<220>
<221> MISC_FEATURE
<222> (167)..(167)
<223> Xaa = Gln or Thr

<220>
<221> MISC_FEATURE
<222> (231)..(231)
<223> Xaa = Any amino acid

<220>
<221> MISC_FEATURE
<222> (232)..(232)
<223> Xaa = Any amino acid

<400> 35

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                  10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Xaa Xaa Xaa Xaa Xaa Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140
```

```
Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Xaa Arg Xaa Ser Xaa Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Xaa Xaa Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 36
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD2 library

<400> 36

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Leu Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125
```

```
Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Cys Arg Met Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Tyr Ser Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 37
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD2 library

<400> 37

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Asp Ala Gly Gly Arg Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
```

```
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Pro Arg Arg Ser Thr Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Thr Asn Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 38
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD2 library

<400> 38

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80
```

```
Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Cys Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Cys Arg Phe Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Glu Val Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 39
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD2 library

<400> 39

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                  10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60
```

```
Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Leu Met Ser Ala Gln Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Thr Arg Tyr Ser Thr Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Pro Leu Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 40
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of clone from RD2 library

<400> 40

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                   10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45
```

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
50 55 60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65 70 75 80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
85 90 95

Arg Ala Gly Gly Arg Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
100 105 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
115 120 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
130 135 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145 150 155 160

Tyr Ser Asn Arg Ser Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser
165 170 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
180 185 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
195 200 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
210 215 220

Cys Ala Val Thr Thr Asp Asn His Gly Lys Leu Gln Phe Gly Ala Gly
225 230 235 240

Thr Gln Val Val Val Thr Pro Asp Ile
245

<210> 41
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> RD2-Mart1-S3-3 clone sequence

<400> 41

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

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met

```
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Met Ala Gly Gly Arg Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Ser Arg His Ser Thr Ser Phe Ser Trp Tyr Arg Gln Tyr Pro
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Arg Ser Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 42
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> RD2-Mart1-S3-4 clone sequence

<400> 42

```
Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly
1               5                  10                  15

Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met
            20                  25                  30

Ala Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr
        35                  40                  45

Ser Val Gly Val Gly Ile Thr Asp Gln Gly Asp Val Pro Asp Gly Tyr
    50                  55                  60

Lys Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser
65                  70                  75                  80

Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro Gly
                85                  90                  95

Met Ala Gly Gly Arg Pro Glu Leu Tyr Phe Gly Pro Gly Thr Arg Leu
            100                 105                 110

Thr Val Thr Glu Asp Leu Ile Asn Gly Ser Ala Asp Asp Ala Lys Lys
        115                 120                 125

Asp Ala Ala Lys Lys Asp Gly Lys Ser Lys Glu Val Glu Gln Asn Ser
    130                 135                 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145                 150                 155                 160

Tyr Ser Ser Arg His Ser Gln Ser Phe Ser Trp Tyr Arg Gln Tyr Pro
                165                 170                 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
            180                 185                 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
        195                 200                 205

Ser Leu Leu Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu
    210                 215                 220

Cys Ala Val Thr Thr Asp Leu Trp Gly Lys Leu Gln Phe Gly Ala Gly
225                 230                 235                 240

Thr Gln Val Val Val Thr Pro Asp Ile
                245
```

<210> 43
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Clone T1-S18.45 amino acid sequence

<400> 43

Glu Ala Gly Val Thr Gln Phe Pro Ser His Ser Val Ile Glu Lys Gly
1 5 10 15

Gln Thr Val Thr Leu Arg Cys Asp Pro Ile Ser Gly His Asp Asn Leu
20 25 30

Tyr Trp Tyr Arg Arg Val Met Gly Lys Glu Ile Lys Phe Leu Leu His
35 40 45

Phe Val Lys Glu Ser Lys Gln Asp Glu Ser Gly Met Pro Asn Asn Arg
50 55 60

Phe Leu Ala Glu Arg Thr Gly Gly Thr Tyr Ser Thr Leu Lys Ile Gln
65 70 75 80

Pro Ala Glu Leu Glu Asp Ser Gly Val Tyr Phe Cys Ala Ser Ser His
85 90 95

Ala Gly Leu Gly Val Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
100 105 110

Val Thr Glu Asp Leu Lys Asn Gly Ser Ala Asp Asp Ala Lys Glu Asp
115 120 125

Ala Ala Lys Lys Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn Ser
130 135 140

Gly Pro Leu Ser Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr
145 150 155 160

Tyr Ser Asp Arg Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Pro
165 170 175

Gly Lys Ser Pro Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys
180 185 190

Glu Asp Gly Arg Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val
195 200 205

Ser Leu Leu Ile Arg Asp Ser Arg Pro Ser Asp Ser Ala Thr Tyr Leu
210 215 220

Cys Ala Val Ser Ser Ser Asp Phe Leu Met Phe Gly Asp Gly Thr Gln
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Leu Val Val Lys Pro Asn Ile
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<210> 50

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aatgctggtg taacacaaac gccaa 85

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tcttcttcag agatc 75

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<212> DNA
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<400> 52
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<210> 53
<211> 63
<212> DNA
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<220>
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<400> 53
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cgg 63

<210> 54
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tttggtccag gcactaga 78

<210> 55
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 55
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<210> 56
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<212> DNA
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cgg 63

<210> 57
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<220>
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aacatactgg c 71

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ggtgcgggca cccaggttgt gg 82

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tacccatacg acgttccaga ctacgctctg caggctagtg gtggtggtgg ttctggtggt 120

ggtggttctg gtggtggtgg ttctgctagc 150

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ttagctcgta caaaatacaa tatacttttc atttctccgt aaacaacatg ttttcccatg 120

taatatcctt ttctattttt cgttccgtta ccaactttac acatacttta tatagctatt 180

cacttctata cactaaaaaa ctaagacaat tttaattttg ctgcctgcca tatttcaatt 240

tgttataaat tcctataatt tatcctatta gtagctaaaa aaagatgaat gtgaatcgaa 300

tcctaagaga attgagctcc aattcgccct atagtgagtc gtatta 346