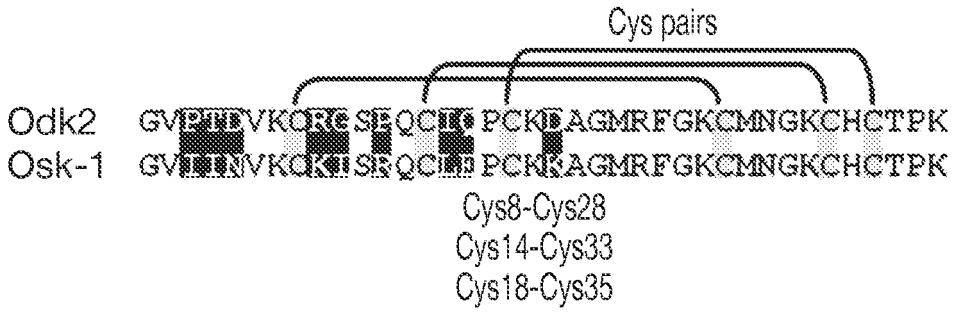


FIG. 1

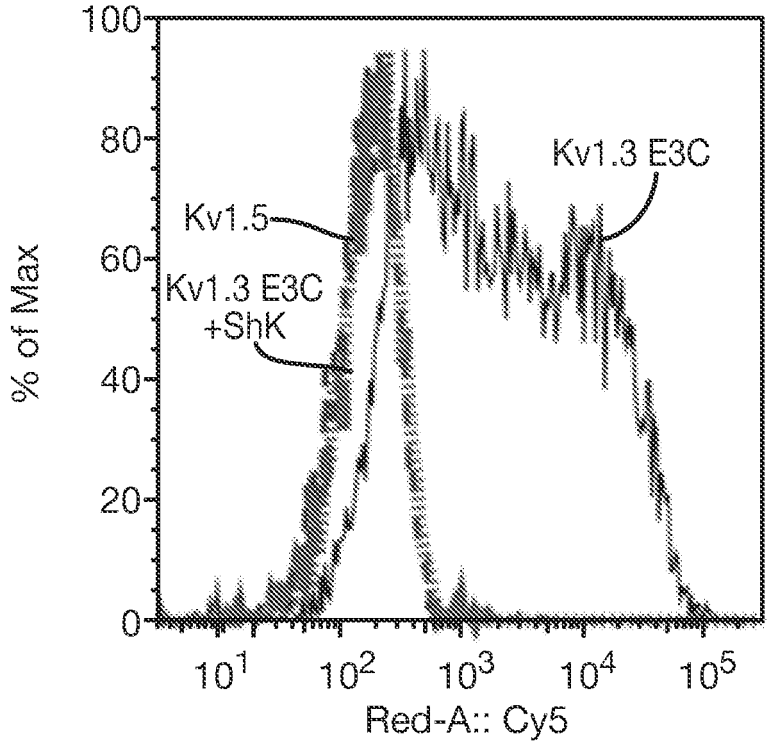

100
80
60
40
20
0
% of Max
Kv1.5
Kv1.3 E3C
+ShK
Kv1.3 E3C
10^1
10^2
10^3
10^4
10^5
Red-A:: Cy5

FIG. 2A

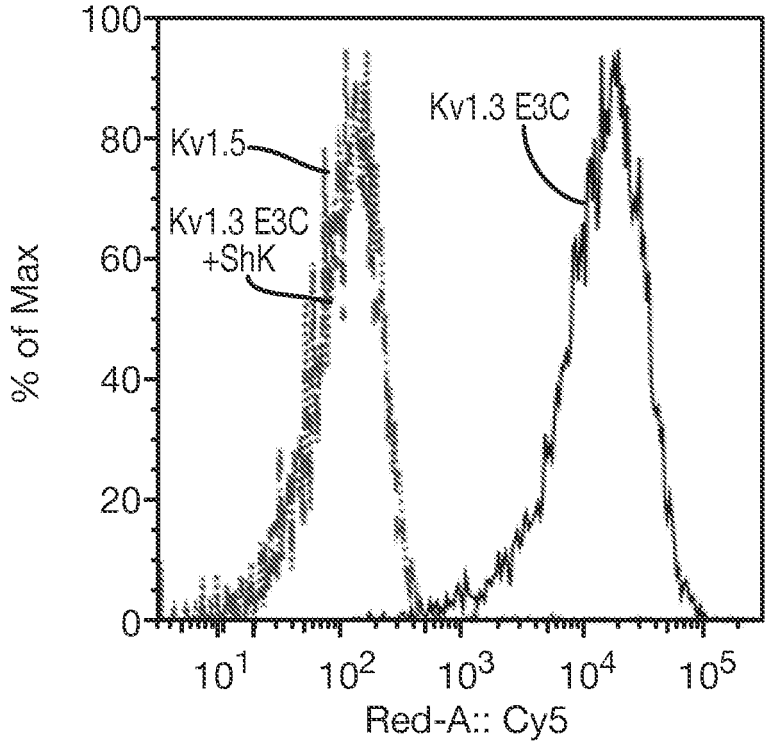

100
80
60
40
20
0
% of Max
Kv1.5
Kv1.3 E3C
+ShK
Kv1.3 E3C
10^1
10^2
10^3
10^4
10^5
Red-A:: Cy5

FIG. 2B

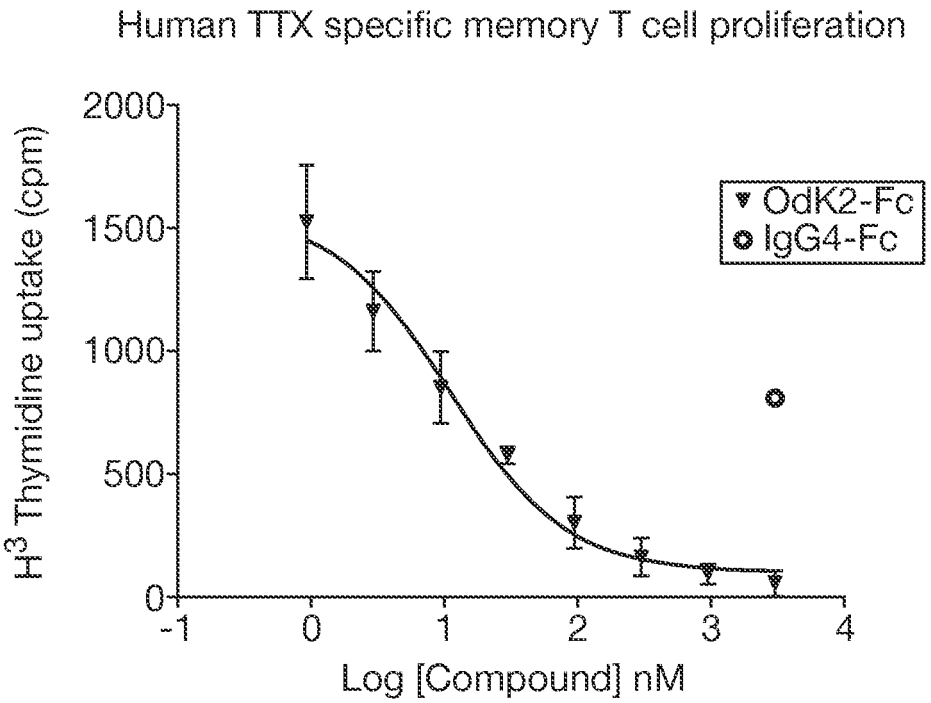

Human TTX specific memory T cell proliferation
H3 Thymidine uptake (cpm)
2000
1500
1000
500
0
-1
0
1
2
3
4
Log [Compound] nM
OdK2-Fc
IgG4-Fc

FIG. 3

Peptide ID/ clone ID	Sequence at amino acid residues																																						SEQ ID NO:
	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	
Odk2	G	V	P	T	D	V	K	C	R	G	S	P	Q	C	I	Q	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	1
Osk-1	G	V	I	I	N	V	K	C	K	I	S	R	Q	C	L	E	P	C	K	K	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	2
KV1D579	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	E	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	3
KV1D665	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	D	C	T	P	K	4
KV1D402	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	V	G	K	C	H	C	T	P	K	5
KV1D560	G	V	P	T	D	V	K	C	R	I	S	A	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	6
KV1D437	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	E	7
KV1D392	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	L	N	G	K	C	H	C	T	P	K	8
KV1D356	G	V	P	T	D	V	K	C	R	I	A	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	9
KV1D623	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	H	F	G	K	C	M	N	G	K	C	H	C	T	P	K	10
KV1D583	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	D	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	11
KV1D604	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	E	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	12
KV1D344	G	V	P	T	D	V	K	C	E	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	13
KV1D294	L	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	14
KV1D575	G	V	P	T	D	V	K	C	R	I	S	R	D	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	15
KV1D608	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	D	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	16
KV1D570	G	V	P	T	D	V	K	C	R	I	S	R	E	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	17
KV1D647	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	R	C	M	N	G	K	C	H	C	T	P	K	18
KV1D625	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	K	F	G	K	C	M	N	G	K	C	H	C	T	P	K	19
KV1D564	G	V	P	T	D	V	K	C	R	I	S	L	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	20
KV1D342	G	V	P	T	D	V	K	C	A	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	21
KV1D197	G	V	P	I	D	V	K	C	K	I	S	R	Q	C	I	E	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	22
KV1D414	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	E	C	H	C	T	P	K	23
KV1D163	G	V	P	T	D	V	K	C	K	I	S	P	Q	C	I	E	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	H	C	T	P	K	24
KV1D664	G	V	P	T	D	V	K	C	R	I	S	R	Q	C	L	K	P	C	K	D	A	G	M	R	F	G	K	C	M	N	G	K	C	V	C	T	P	K	25

FIG. 4A(1)

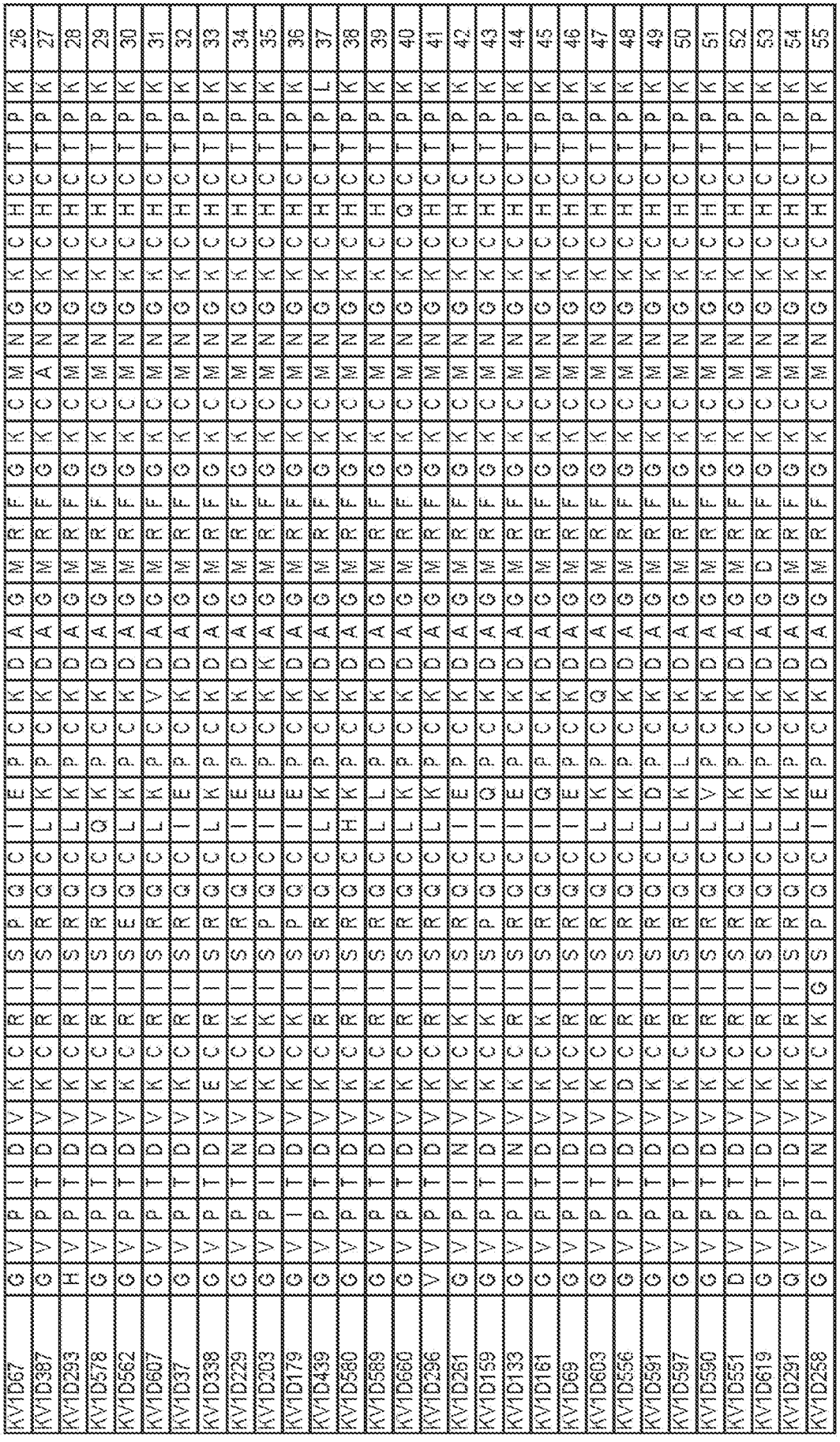

KV1D67 G V P I D V K C R I S P Q C I E P C K D A G M R F G K C M N G K C H C T P K 26
KV1D387 G V P P T D V K C R I S R Q C L K P C K D A G M R F G K C A N G K C H C T P K 27
KV1D293 H V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 28
KV1D578 G V P P T D V K C R I S R Q C Q K P C K D A G M R F G K C M N G K C H C T P K 29
KV1D562 G V P P T D V K C R I S E Q C L K P C K D A G M R F G K C M N G K C H C T P K 30
KV1D607 G V P P T D V K C R I S R Q C L W P C V D A G M R F G K C M N G W C H C T P K 31
KV1D37 G V P P T D V K C R I S R Q C I E P C K D A G M R F G K C M N G K C H C T P K 32
KV1D338 G V P P T D V E C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 33
KV1D229 G V P P T N V K C K I S R Q C I E P C K D A G M R F G K C M N G K C H C T P K 34
KV1D203 G V P P I D V K C K I S P Q C I E P C K K A G M R F G K C M N G K C H C T P K 35
KV1D179 G V P I T D V K C K I S P Q C I E P C K D A G M R F G K C M N G K C H C T P K 36
KV1D439 G V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P L 37
KV1D580 G V P P T D V K C R I S R Q C H K P C K D A G M R F G K C M N G K C H C T P K 38
KV1D589 G V P P T D V K C R I S R Q C L L P C K D A G M R F G K C M N G K C H C T P K 39
KV1D660 G V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C Q C T P K 40
KV1D256 V V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 41
KV1D261 G V P P I N V K C K I S R Q C I E P C K D A G M R F G K C M N G K C H C T P K 42
KV1D159 G V P P T D V K C K I S P Q C I Q P C K D A G M R F G K C M N G K C H C T P K 43
KV1D133 G V P P I N V K C R I S R Q C I E P C K D A G M R F G K C M N G K C H C T P K 44
KV1D161 G V P P T D V K C K I S R Q C I Q P C K D A G M R F G K C M N G K C H C T P K 45
KV1D69 G V P P I D V K C R I S R Q C I E P C K D A G M R F G K C M N G K C H C T P K 46
KV1D603 G V P P T D V K C R I S R Q C L K P C Q D A G M R F G K C M N G K C H C T P K 47
KV1D556 G V P P T D V D C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 48
KV1D591 G V P P T D V K C R I S R Q C L D P C K D A G M R F G K C M N G K C H C T P K 49
KV1D597 G V P P T D V K C R I S R Q C L K L C K D A G M R F G K C M N G K C H C T P K 50
KV1D590 G V P P T D V K C R I S R Q C L V P C K D A G M R F G K C M N G K C H C T P K 51
KV1D551 D V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 52
KV1D619 G V P P T D V K C R I I S R Q C L K P C K D A G D R F G K C M N G K C H C T P K 53
KV1D291 Q V P P T D V K C R I S R Q C L K P C K D A G M R F G K C M N G K C H C T P K 54
KV1D258 G V P P I N V K C K G S P Q C I E P C K D A G M R F G K C M N G K C H C T P K 55

FIG. 4A(2)

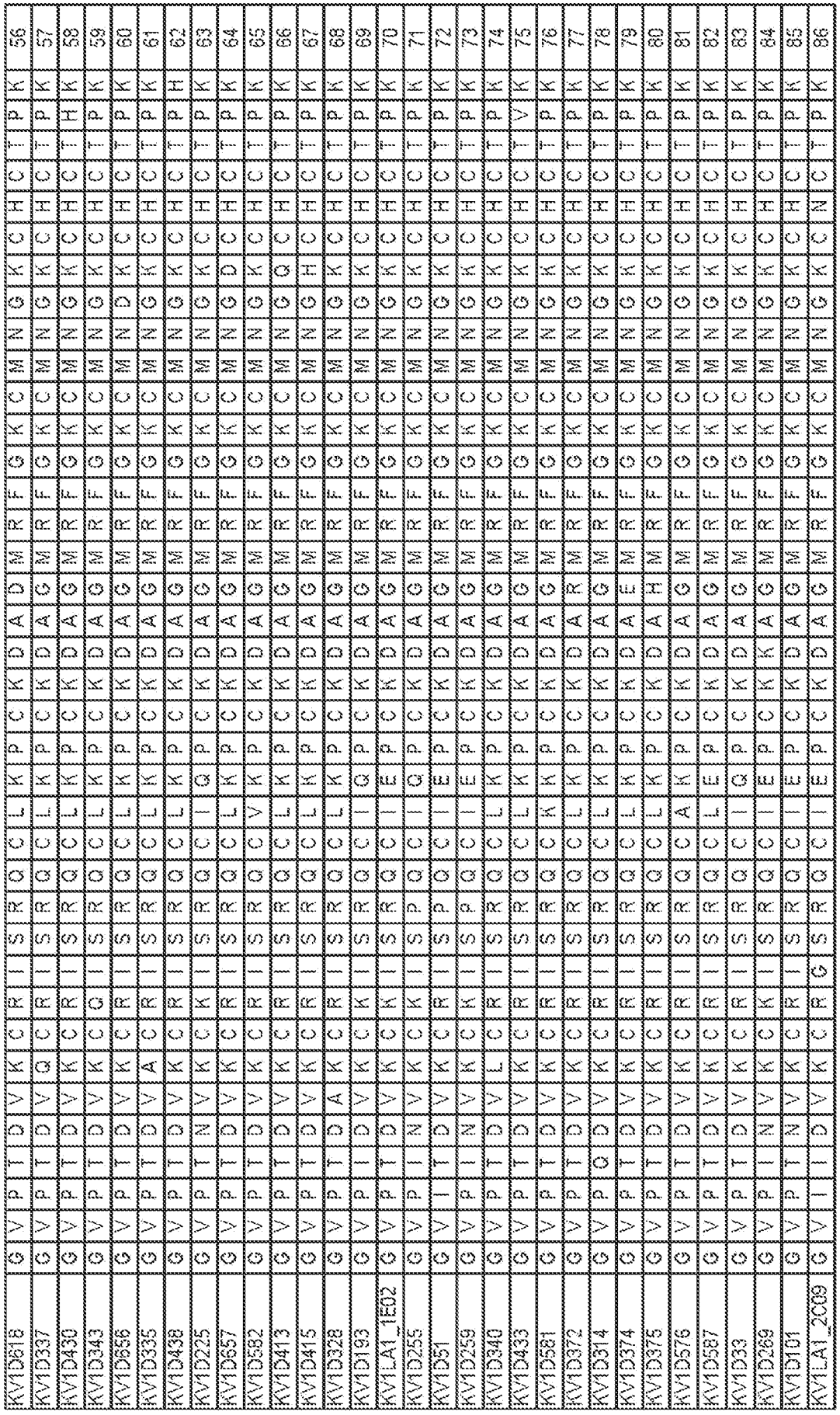


FIG. 4A(3)

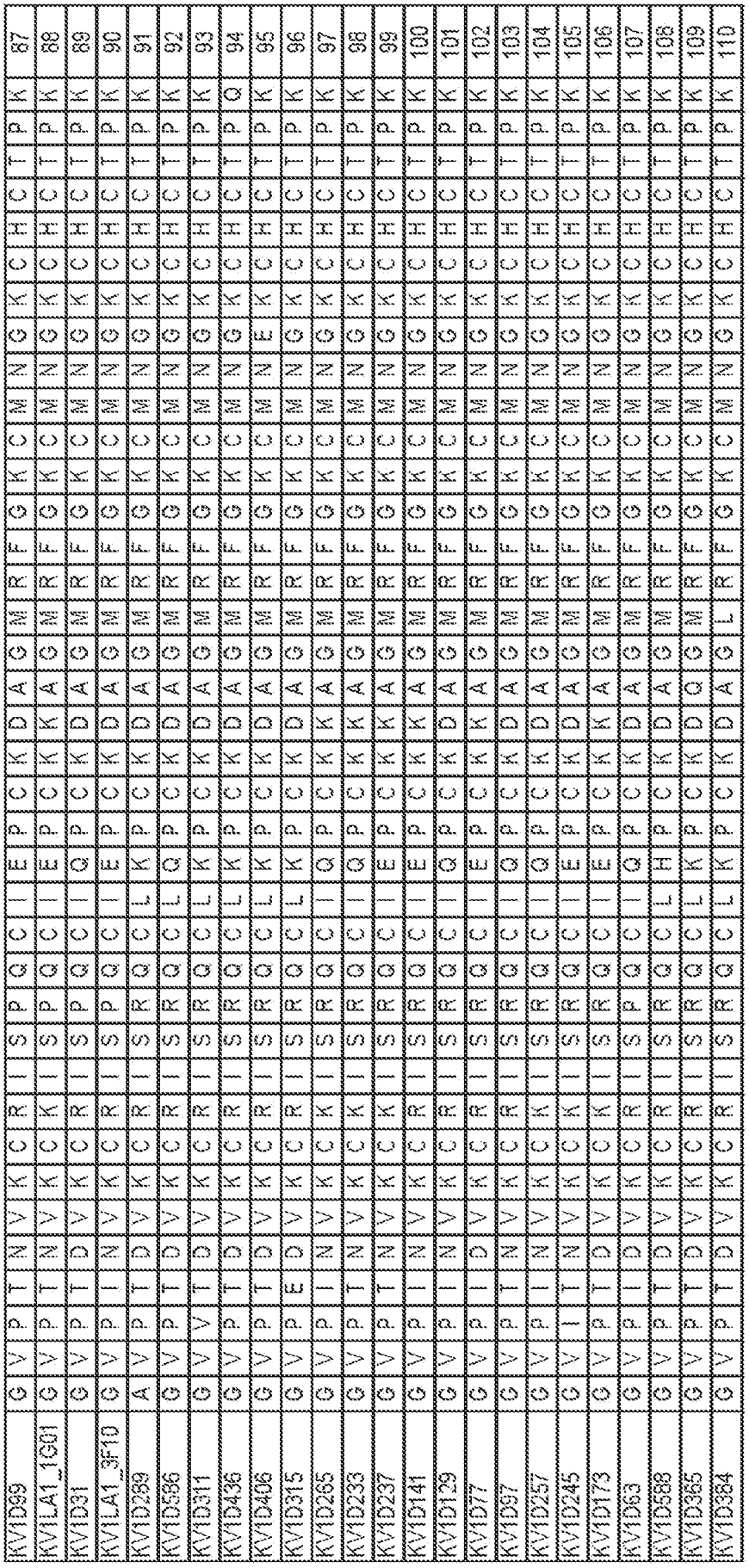


FIG. 4A(4)

Peptide ID/ clone ID	SEQ ID NO:	Library origin	Kv1.3 %Binding (of KV1C2)	Kv1.1 %Binding (of KV1C2)	Binding Selectivity*	Thallium flux IC_{50} (nM)
Odk2	1					
Osk-1	2					
KV1D579	3	KV1D26L1	319.5	4.1	77.6	0.458
KV1D665	4	KV1D26L1	151.8	8.2	18.5	0.227
KV1D402	5	KV1D26L1	226.1	29.0	7.8	2.178
KV1D560	6	KV1D26L1	379.0	55.9	6.8	0.995
KV1D437	7	KV1D26L1	232.3	36.5	6.4	1.054
KV1D392	8	KV1D26L1	359.2	59.4	6.1	1.067
KV1D356	9	KV1D26L1	418.0	77.9	5.4	0.332
KV1D623	10	KV1D26L1	88.7	17.2	5.2	2.404
KV1D583	11	KV1D26L1	245.1	51.7	4.7	1.014
KV1D604	12	KV1D26L1	213.6	48.9	4.4	1.384
KV1D344	13	KV1D26L1	199.5	47.3	4.2	1.837
KV1D294	14	KV1D26L1	358.5	86.6	4.1	0.116
KV1D575	15	KV1D26L1	364.2	93.3	3.9	0.385
KV1D608	16	KV1D26L1	200.0	54.3	3.7	0.404
KV1D570	17	KV1D26L1	321.9	95.3	3.4	0.533
KV1D647	18	KV1D26L1	83.2	27.0	3.1	0.948
KV1D625	19	KV1D26L1	190.8	62.8	3.0	0.197
KV1D564	20	KV1D26L1	235.2	77.8	3.0	1.374
KV1D342	21	KV1D26L1	263.1	87.7	3.0	0.634
KV1D197	22	KV1C2L1	162.7	55.7	2.9	#N/A
KV1D414	23	KV1D26L1	362.8	129.5	2.8	0.791
KV1D163	24	KV1C2L1	81.7	28.7	2.8	#N/A
KV1D664	25	KV1D26L1	386.5	140.3	2.8	0.110
KV1D67	26	KV1C2L1	118.0	47.0	2.5	#N/A
KV1D387	27	KV1D26L1	245.5	98.6	2.5	1.042
KV1D293	28	KV1D26L1	332.6	136.0	2.4	0.238
KV1D578	29	KV1D26L1	300.5	126.7	2.4	0.181
KV1D562	30	KV1D26L1	180.6	78.1	2.3	0.927
KV1D607	31	KV1D26L1	404.9	182.2	2.2	0.802
KV1D37	32	KV1C2L1	174.5	80.7	2.2	#N/A
KV1D338	33	KV1D26L1	274.5	125.4	2.2	0.618
KV1D229	34	KV1C2L1	171.3	82.7	2.1	#N/A
KV1D203	35	KV1C2L1	131.5	63.6	2.1	#N/A
KV1D179	36	KV1C2L1	113.0	53.2	2.1	#N/A
KV1D439	37	KV1D26L1	393.5	187.7	2.1	0.271
KV1D580	38	KV1D26L1	411.1	202.3	2.0	0.450
KV1D589	39	KV1D26L1	443.9	222.0	2.0	0.214
KV1D660	40	KV1D26L1	375.6	194.7	1.9	0.113
KV1D296	41	KV1D26	322.2	168.5	1.9	0.106
KV1D261	42	KV1C2L1	150.9	78.5	1.9	#N/A
KV1D159	43	KV1C2L1	121.5	65.1	1.9	#N/A
KV1D133	44	KV1C2L1	194.9	108.4	1.8	#N/A

FIG. 4B(1)

KV1D161	45	KV1C2L1	179.9	98.3	1.8	#N/A
KV1D69	46	KV1C2L1	161.2	88.2	1.8	#N/A
KV1D603	47	KV1D26L1	280.2	157.7	1.8	0.224
KV1D556	48	KV1D26L1	253.0	144.6	1.7	1.102
KV1D591	49	KV1D26L1	258.2	148.0	1.7	0.982
KV1D597	50	KV1D26L1	293.5	170.0	1.7	0.141
KV1D590	51	KV1D26L1	428.9	249.3	1.7	0.139
KV1D551	52	KV1D26L1	228.1	132.7	1.7	0.202
KV1D619	53	KV1D26L1	219.6	128.7	1.7	0.568
KV1D291	54	KV1D26L1	271.2	159.1	1.7	0.091
KV1D258	55	KV1C2L1	98.2	57.7	1.7	#N/A
KV1D618	56	KV1D26L1	431.9	258.6	1.7	0.622
KV1D337	57	KV1D26L1	373.0	225.5	1.7	0.334
KV1D430	58	KV1D26L1	396.6	241.2	1.6	0.698
KV1D343	59	KV1D26L1	209.0	128.3	1.6	0.332
KV1D656	60	KV1D26L1	258.1	158.5	1.6	0.314
KV1D335	61	KV1D26L1	338.3	207.9	1.6	0.325
KV1D438	62	KV1D26L1	358.1	223.0	1.6	0.650
KV1D225	63	KV1C2L1	191.7	121.3	1.6	#N/A
KV1D657	64	KV1D26L1	122.6	78.1	1.6	0.469
KV1D582	65	KV1D26L1	261.0	166.2	1.6	0.632
KV1D413	66	KV1D26L1	371.4	240.1	1.5	0.693
KV1D415	67	KV1D26L1	444.9	293.1	1.5	0.873
KV1D328	68	KV1D26L1	351.1	231.8	1.5	0.151
KV1D193	69	KV1C2L1	168.1	111.8	1.5	#N/A
KV1LA1_1E02	70	KV1C2L1	153.9	100.6	1.5	#N/A
KV1D255	71	KV1C2L1	151.6	103.8	1.5	#N/A
KV1D51	72	KV1C2L1	109.8	74.9	1.5	#N/A
KV1D259	73	KV1C2L1	108.3	73.1	1.5	#N/A
KV1D340	74	KV1D26L1	406.8	274.3	1.5	0.536
KV1D433	75	KV1D26L1	384.9	260.5	1.5	0.516
KV1D581	76	KV1D26L1	208.4	141.8	1.5	0.116
KV1D372	77	KV1D26L1	328.1	224.2	1.5	0.213
KV1D314	78	KV1D26L1	377.0	260.3	1.4	0.108
KV1D374	79	KV1D26L1	357.4	247.3	1.4	0.240
KV1D375	80	KV1D26L1	383.8	267.8	1.4	0.139
KV1D576	81	KV1D26L1	179.9	125.8	1.4	0.159
KV1D587	82	KV1D26L1	275.3	193.7	1.4	0.662
KV1D33	83	KV1C2L1	194.3	140.5	1.4	#N/A
KV1D269	84	KV1C2L1	192.5	133.3	1.4	#N/A
KV1D101	85	KV1C2L1	167.4	116.4	1.4	#N/A
KV1LA1_2C09	86	KV1C2L1	150.4	111.0	1.4	#N/A
KV1D99	87	KV1C2L1	142.6	99.0	1.4	#N/A
KV1LA1_1G01	88	KV1C2L1	134.8	95.7	1.4	#N/A
KV1D31	89	KV1C2L1	128.2	94.4	1.4	#N/A
KV1LA1_3F10	90	KV1C2L1	110.6	77.2	1.4	#N/A

FIG. 4B(2)

KV1D289	91	KV1D26L1	338.1	243.7	1.4	0.103
KV1D586	92	KV1D26L1	291.6	210.6	1.4	0.251
KV1D311	93	KV1D26L1	393.2	287.8	1.4	0.130
KV1D436	94	KV1D26L1	343.0	252.9	1.4	0.512
KV1D406	95	KV1D26L1	426.9	319.0	1.3	0.671
KV1D315	96	KV1D26L1	339.2	255.4	1.3	0.094
KV1D265	97	KV1C2L1	246.1	195.1	1.3	#N/A
KV1D233	98	KV1C2L1	246.0	194.4	1.3	#N/A
KV1D237	99	KV1C2L1	208.2	158.7	1.3	#N/A
KV1D141	100	KV1C2L1	204.4	161.1	1.3	#N/A
KV1D129	101	KV1C2L1	197.6	150.6	1.3	#N/A
KV1D77	102	KV1C2L1	195.5	150.0	1.3	#N/A
KV1D97	103	KV1C2L1	193.5	154.4	1.3	#N/A
KV1D257	104	KV1C2L1	189.0	141.5	1.3	#N/A
KV1D245	105	KV1C2L1	175.2	131.5	1.3	#N/A
KV1D173	106	KV1C2L1	164.5	131.1	1.3	#N/A
KV1D63	107	KV1C2L1	113.1	90.4	1.3	#N/A
KV1D588	108	KV1D26L1	438.7	337.8	1.3	0.536
KV1D365	109	KV1D26L1	456.8	352.0	1.3	0.326
KV1D384	110	KV1D26L1	449.1	356.9	1.3	0.536

*ratio Kv1.3 %Binding/Kv1.1 %Binding
#N/A: not done

FIG. 4B(3)

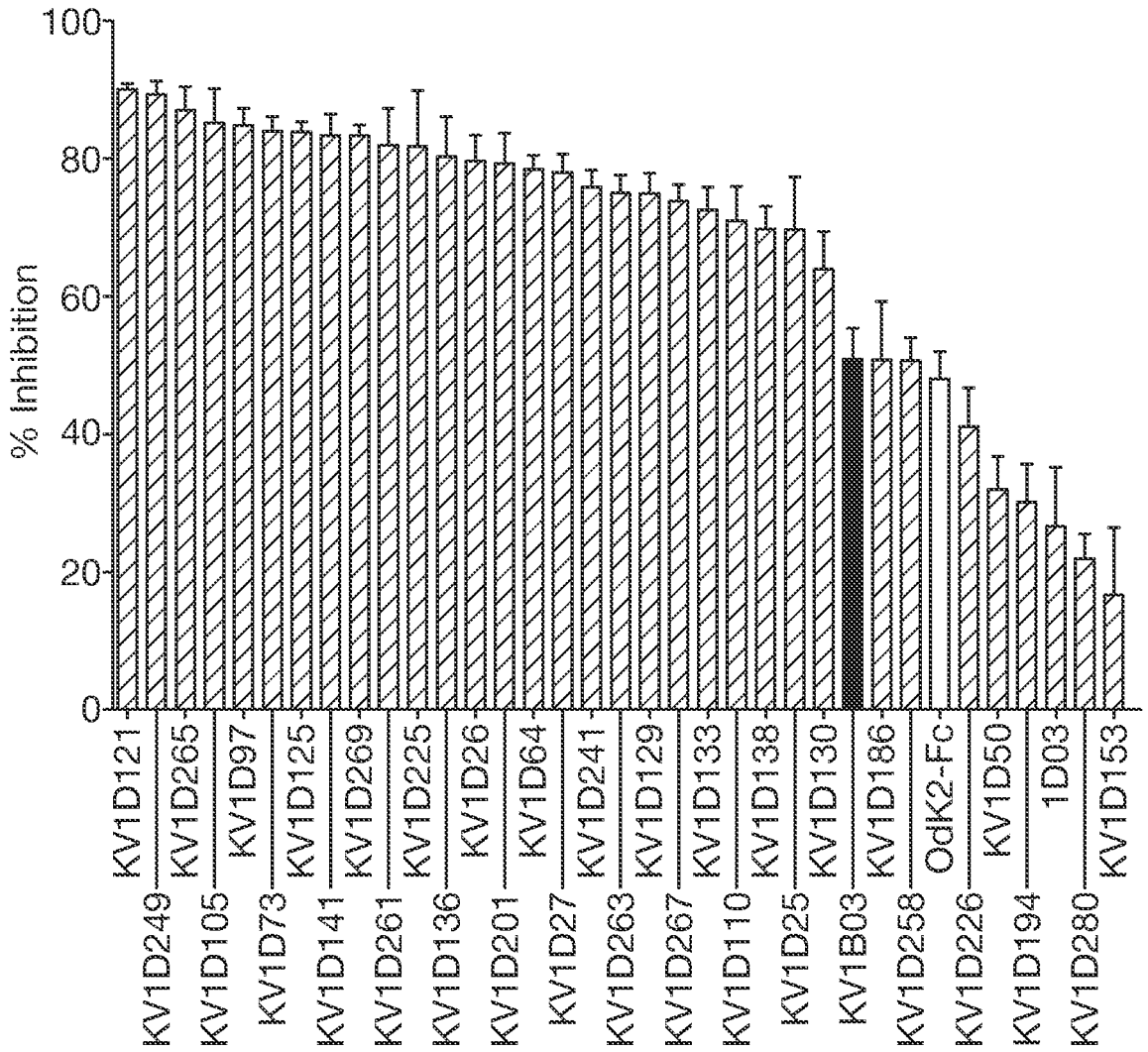

% Inhibition
100
80
60
40
20
0
KV1D121
KV1D249
KV1D265
KV1D105
KV1D97
KV1D73
KV1D125
KV1D141
KV1D269
KV1D261
KV1D225
KV1D136
KV1D26
KV1D201
KV1D64
KV1D27
KV1D241
KV1D263
KV1D129
KV1D267
KV1D133
KV1D110
KV1D138
KV1D25
KV1D130
KV1B03
KV1D186
KV1D258
OdK2-Fc
KV1D226
KV1D50
KV1D194
1D03
KV1D280
KV1D153

FIG. 5A

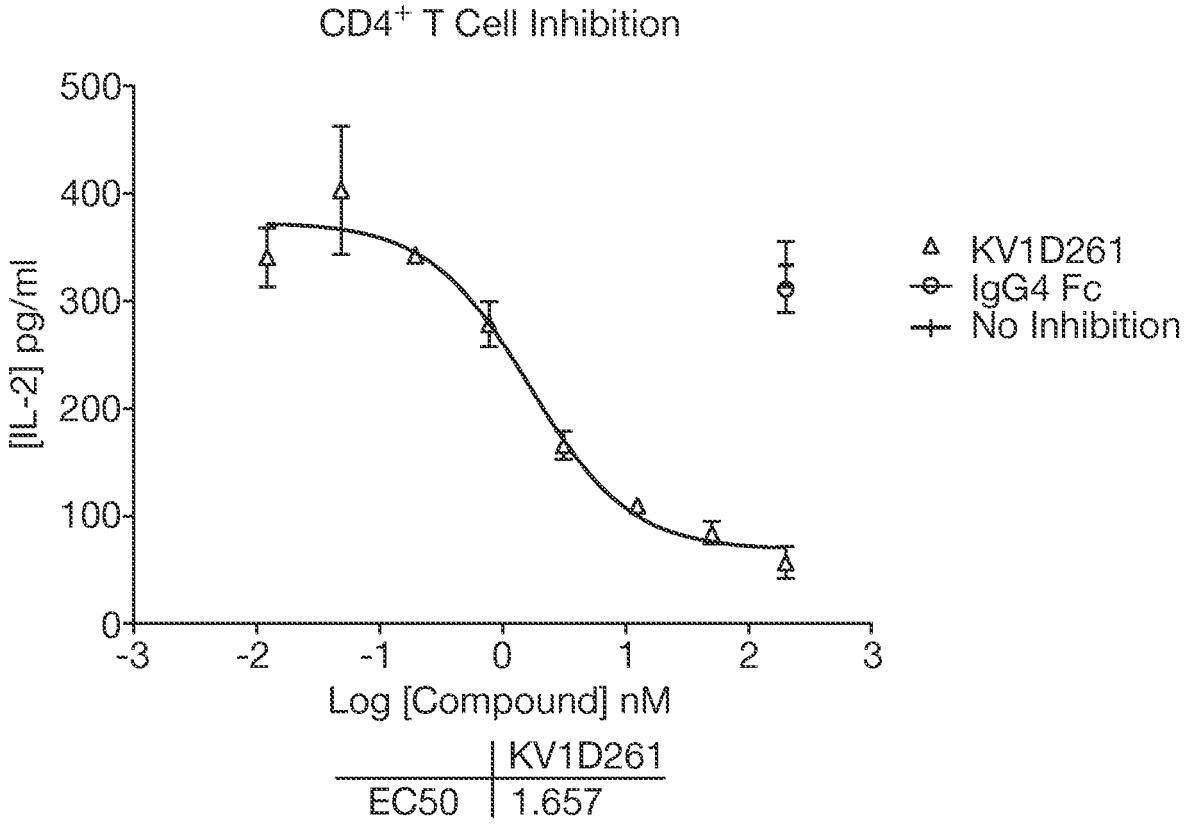
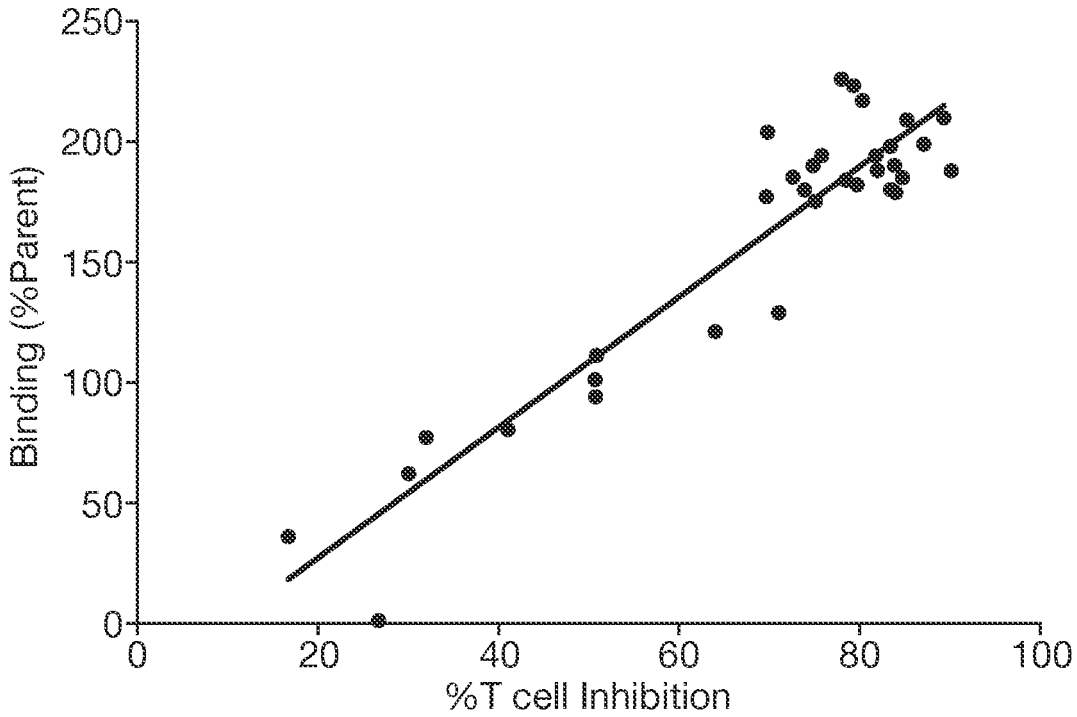

CD4+ T Cell Inhibition
[IL-2] pg/ml
500
400
300
200
100
0
-3
-2
-1
0
1
2
3
Log [Compound] nM
KV1D261
IgG4 Fc
No Inhibition
KV1D261
EC50
1.657

FIG. 5B



Number of XY Pairs	33
Pearson r	0.9339
95% confidence interval	0.8693 to 0.9671
P value (two-tailed)	< 0.0001
P value summary	***
Is the correlation significant? (alpha=0.05)	Yes
R squared	0.8722

FIG. 5C

Protein	% Binding*	Thallium flux IC_{50} (nM)	C-terminal extension		Extended peptide	
			Amino acid sequence	SEQ ID NO:	Amino acid sequence	SEQ ID NO:
KV1D819L1_55F01	367.0%	0.776	HAAG	123	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHAAG	269
KV1D819L1_94C07	153.6%	3.273	RRPT	124	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRRPT	270
KV1D819L1_94D07	132.8%	5.559	ASKP	125	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKASKP	271
KV1D819L1_74F03	128.5%	4.677	PKPQ	126	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPKPQ	272
KV1D819L1_67B04	124.5%	11.614	QDQT	127	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQDQT	273
KV1D819L1_92E05	122.1%	3.508	AHRP	128	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAHRP	274
KV1D819L1_62A05	121.5%	7.079	QPTH	129	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQPTH	275
KV1D819L1_62A06	121.1%	8.511	REQT	130	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKREQT	276
KV1D819L1_53C04	120.8%	2.851	PPKP	131	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPPKP	277
KV1D819L1_67D09	120.7%	8.710	KQGA	132	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKKQGA	278
KV1D819L1_68D08	119.4%	3.467	TRPA	133	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRPA	279
KV1D819L1_63A05	119.4%	3.273	APHK	134	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAPHK	280
KV1D819L1_62A07	119.2%	7.674	RTEH	135	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRTEH	281
KV1D819L1_67C09	118.4%	6.383	PTHT	136	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTHT	282
KV1D819L1_61A03	115.4%	4.416	RAEK	137	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRAEK	283
KV1D819L1_67C04	113.4%	5.754	PAPA	138	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPAPA	284
KV1D819L1_4B09	112.8%		SHRP	139	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKSHRP	285
KV1D819L1_4B08	112.8%		SHRP	140	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKSHRP	286
KV1D819L1_70A08	110.9%	5.821	PPTR	141	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPPTR	287
KV1D819L1_70B02	110.7%	1.603	HHTT	142	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHHTT	288
KV1D819L1_70B11	110.6%	4.677	HRPA	143	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRPA	289
KV1D819L1_74F06	109.9%	6.457	KAHP	144	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKKAHP	290
KV1D819L1_74D02	108.8%	7.161	QTTQ	145	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQTTQ	291

FIG. 6(1)

KV1D819L1_51C08	108.8%	4.217	PTPT	146	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTPT	292
KV1D819L1_70C06	108.0%	4.786	TQAP	147	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTQAP	293
KV1D819L1_13E06	106.4%	1.660	RKPH	148	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRKPH	294
KV1D819L1_53C07	106.4%	0.473	HTPP	149	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHTPP	295
KV1D819L1_69B03	105.9%	8.222	TKPP	150	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTKPP	296
KV1D819L1_71F11	105.4%	1.549	PRPT	151	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPRPT	297
KV1D819L1_74G05	105.3%	6.607	KQTA	152	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKKQTA	298
KV1D819L1_51C06	105.2%	5.012	PHTP	153	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPHTP	299
KV1D819L1_62A09	105.1%	6.683	HTPP	154	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHTPP	300
KV1D819L1_94D05	105.0%	0.380	HAKP	155	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHAKP	301
KV1D819L1_38H08	104.9%		TRRP	156	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRRP	302
KV1D819L1_45B11	103.7%	6.237	PTTP	157	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTTP	303
KV1D819L1_63C05	103.3%	3.802	RQHA	158	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRQHA	304
KV1D819L1_61D11	102.6%	1.660	PTRP	159	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTRP	305
KV1D819L1_61C05	102.3%	5.309	PAPH	160	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPAPH	306
KV1D819L1_74B07	102.2%	6.457	ADKP	161	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKADKP	307
KV1D819L1_61B08	102.2%	2.483	PHHQ	162	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPHHQ	308
KV1D819L1_35E07	102.1%	5.495	GRRT	163	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKGRRT	309
KV1D819L1_62B05	101.8%	5.495	RPDA	164	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRPDA	310
KV1D819L1_74E02	101.7%	2.065	NHRP	165	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNHRP	311
KV1D819L1_70B04	101.1%	4.732	NHQG	166	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNHQG	312
KV1D819L1_51C04	100.9%	6.095	TAPP	167	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTAPP	313
KV1D819L1_51A08	100.8%	6.457	RHPH	168	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRHPH	314
KV1D819L1_51B11	100.3%	3.162	PSRP	169	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPSRP	315
KV1D819L1_68A08	99.5%	4.786	PQHQ	170	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPQHQ	316
KV1D819L1_70D07	99.1%	2.512	PTQH	171	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTQH	317
KV1D819L1_74F07	99.0%	4.624	HTKP	172	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHTKP	318
KV1D819L1_7F10	98.8%		RKKP	173	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRKKP	319

FIG. 6(2)

KV1D819L1_13A02	98.4%	4.169	HNRP	174	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHNRP	320
KV1D819L1_62E06	98.3%	6.026	PEKP	175	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPEKP	321
KV1D819L1_74A08	98.3%	6.237	RAQT	176	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRAQT	322
KV1D819L1_51E05	97.7%	4.842	PAAT	177	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPAAT	323
KV1D819L1_62A02	97.6%	10.000	RTEQ	178	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRTEQ	324
KV1D819L1_68C11	97.4%	4.898	PPAK	179	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPPAK	325
KV1D819L1_74E03	97.3%	7.943	EPRP	180	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKEPRP	326
KV1D819L1_62B07	97.1%	6.998	TATH	181	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTATH	327
KV1D819L1_67B08	97.0%	5.370	ARPD	182	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKARPD	328
KV1D819L1_61B02	96.8%	2.754	AHPH	183	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAHPH	329
KV1D819L1_61D06	96.6%	3.981	AAPS	184	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAAPS	330
KV1D819L1_74C08	96.5%	6.095	RPRP	185	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRPRP	331
KV1D819L1_61E08	96.5%	2.951	PDKP	186	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPDKP	332
KV1D819L1_58A06	96.3%	7.079	TPHP	187	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTPHP	333
KV1D819L1_97C07	95.8%	3.548	RTRP	188	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRTRP	334
KV1D819L1_62A11	95.8%	10.471	AQQH	189	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAQQH	335
KV1D819L1_4H07	95.7%		TRRP	190	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRRP	336
KV1D819L1_4H07	95.7%		TRRP	191	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRRP	337
KV1D819L1_57B07	95.1%	1.259	RQPP	192	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRQPP	338
KV1D819L1_63D11	95.0%	5.248	RTPP	193	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRTPP	339
KV1D819L1_74G06	95.0%	10.000	EKPT	194	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKEKPT	340
KV1D819L1_68A01	94.6%	0.372	GHTA	195	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKGHTA	341
KV1D819L1_42C09	94.5%	5.309	PTKP	196	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTKP	342
KV1D819L1_61C03	94.3%	1.603	PTTP	197	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTTP	343
KV1D819L1_70A06	94.2%	6.761	TGHT	198	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTGHT	344
KV1D819L1_45E05	93.9%	3.055	GGPQ	199	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKGGPQ	345
KV1D819L1_31H11	93.7%	3.055	HRRQ	200	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRRQ	346
KV1D819L1_68A07	93.5%	4.266	HNAP	201	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHNAP	347
KV1D819L1_45E07	93.4%	4.217	PQPQ	202	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPQPQ	348

FIG. 6(3)

KV1D819L1_15B03	92.8%		NRRP	203	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNRRP	349
KV1D819L1_61C07	92.5%	3.936	QAAP	204	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQAAP	350
KV1D819L1_67E03	92.4%	3.199	QPQD	205	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQPQD	351
KV1D819L1_3B08	81.4%		ATRP	206	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKATRP	352
KV1D819L1_72E02	80.7%	0.092	NRPP	207	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNRPP	353
KV1D819L1_2A05	64.3%		RRRP	208	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRRRP	354
KV1D819L1_5D10	57.3%		AHRH	209	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAHRH	355
KV1D819L1_5H06	53.6%		AQRP	210	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAQRP	356
KV1D819L1_74G01	53.0%	4.956	TSDT	211	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTSDT	357
KV1D819L1_116E01	49.3%	2.163	RRPG	212	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRRPG	358
KV1D819L1_55B03	43.9%	0.036	QSKA	213	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQSKA	359
KV1D819L1_55E04	43.6%	0.033	AGPR	214	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAGPR	360
KV1D819L1_55E03	40.1%	0.028	RSRT	215	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRSRT	361
KV1D819L1_55H07	38.7%	0.019	RHKR	216	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRHKR	362
KV1D819L1_62F01	35.5%	0.275	NAAK	217	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNAAK	363
KV1D819L1_7F01	32.8%	10.715	APHT	218	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAPHT	364
KV1D819L1_94H02	30.8%	0.030	GGKR	219	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKGGKR	365
KV1D819L1_103H04	29.2%	4.624	RREP	220	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRREP	366
KV1D819L1_119F03	28.2%		HTRT	221	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHTRT	367
KV1D819L1_2A08	28.1%		NHRT	222	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNHRT	368
KV1D819L1_3H01	24.2%		PNRT	223	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPNRT	369
KV1D819L1_113G01	24.1%	0.025	PKTA	224	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPKTA	370
KV1D819L1_99F08	22.3%		TRRP	225	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRRP	371
KV1D819L1_3A01	22.2%		RHNT	226	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRHNT	372
KV1D819L1_93A04	20.4%	0.036	TDAR	227	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTDAR	373
KV1D819L1_102D1	19.6%	0.022	HRQQ	228	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRQQ	374
KV1D819L1_116E04	19.3%		NQRT	229	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNQRT	375
KV1D819L1_91E03	19.3%	0.039	RPRH	230	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRPRH	376

FIG. 6(4)

KV1D819L1_61G03	18.6%	0.106	HNET	231	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHNET	377
KV1D819L1_93A08	18.5%	0.040	ARNA	232	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKARNA	378
KV1D819L1_3E09	18.4%		TTRT	233	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTTRT	379
KV1D819L1_4E01	18.2%		ARRN	234	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKARRN	380
KV1D819L1_60H04	18.1%	0.022	TGRK	235	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTGRK	381
KV1D819L1_2E07	17.9%		ASDN	236	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKASDN	382
KV1D819L1_91H11	17.0%	0.009	HERT	237	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHERT	383
KV1D819L1_99F01	16.5%		TPHR	238	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTPHR	384
KV1D819L1_95H11	16.0%	0.005	RRTA	239	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRRTA	385
KV1D819L1_117E08	16.0%	0.038	NTRT	240	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNTRT	386
KV1D819L1_3A05	15.4%		PTTR	241	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTTR	387
KV1D819L1_97G04	15.2%	0.013	QRNG	242	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQRNG	388
KV1D819L1_115H04	14.1%	0.039	AHRN	243	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAHRN	389
KV1D819L1_93H05	13.5%	0.041	PRSA	244	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPRSA	390
KV1D819L1_111G03	13.3%	0.019	QRQS	245	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQRQS	391
KV1D819L1_112F01	13.3%	0.016	QRRK	246	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQRRK	392
KV1D819L1_115H08	13.2%	0.012	ARAK	247	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKARAK	393
KV1D819L1_3A03	13.2%		RTRQ	248	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRTRQ	394
KV1D819L1_96E04	12.6%	0.019	AKRD	249	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAKRD	395
KV1D819L1_60B02	12.2%	0.248	DDGA	250	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKDDGA	396
KV1D819L1_96G04	12.0%	0.013	RDKT	251	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRDKT	397
KV1D819L1_87G02	11.4%	0.004	HRRK	252	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRRK	398
KV1D819L1_4B01	11.0%		RQTR	253	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRQTR	399
KV1D819L1_61H04	8.7%	0.141	PNRD	254	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPNRD	400
KV1D819L1_54D11	8.3%	0.028	HRHK	255	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRHK	401
KV1D819L1_12C08	7.9%	0.331	HRNR	256	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKHRNR	402
KV1D819L1_87C11	7.8%	0.022	RAKR	257	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKRAKR	403
KV1D819L1_57F05	7.2%	0.021	QRTR	258	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKQRTR	404

FIG. 6(5)

KV1D819L1_54G07	5.5%	0.030	ATRH	259	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKATRH	405
KV1D819L1_13F03	5.5%	0.004	ARRS	260	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKARRS	406
KV1D819L1_71B03	5.2%	0.022	AKTR	261	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKAKTR	407
KV1D819L1_53G01	4.8%	0.065	NARQ	262	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNARQ	408
KV1D819L1_71G05	4.4%	0.031	NRQR	263	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKNRQR	409
KV1D819L1_6H05	4.2%		PTNA	264	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPTNA	410
KV1D819L1_45E01	4.1%	0.195	TRTD	265	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTRTD	411
KV1D819L1_41D01	3.6%	0.750	ADTR	266	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKADTR	412
KV1D819L1_40A01	3.3%	0.120	TSRQ	267	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKTSRQ	413
KV1D819L1_50D06	3.3%	0.015	PRNT	268	GVPINVKCKISRQCIEPCKDAGMRFGKCMNGKCHCTPKPRNT	414

*%Binding measured as % binding compared to KV1D261_26

FIG. 6(6)

Protein	Linker SEQ ID NO:	Competitive Binding Ki (nM)	Thallium Flux Kv1.3 IC_{50} (nM)	Thallium Flux Kv1.1 IC_{50} (nM)	Fold Selectivity*	C-terminal extension		T cell inhibition	
						Amino acid sequence	SEQ ID NO:	%Inhibition @1nM	IC_{50} (nM)
KV1G28.KV1W699	428	3.60	1.122	63.096	56	PKTA	224	34.5%	NT
KV1G47.KV1W718	428	2.90	0.891	89.125	100	TDAR	227	21.9%	NT
KV1G48.KV1W719	428	18.00	0.891	28.184	32	AHRN	243	32.0%	NT
KV1G11.KV1W682	116	1.94	0.794	158.489	200	HERT	237	17.5%	NT
KV1G27.KV1W698	428	2.00	0.708	50.119	71	PRNT	268	47.4%	NT
KV1G42.KV1W713	428	1.30	0.562	63.096	112	RNRE	431	21.3%	NT
KV1G29.KV1W700	428	1.30	0.562	63.096	112	ARNA	232	35.0%	NT
KV1G38.KV1W709	428	2.30	0.501	63.096	126	HRPA	143	31.0%	NT
KV1G26.KV1W697	428	0.79	0.501	31.623	63	RRTA	239	37.9%	NT
KV1G37.KV1W708	428	1.20	0.447	35.481	79	AGPR	214	36.3%	NT
KV1G43.KV1W714	428	0.75	0.447	28.184	63	NTRT	240	39.8%	NT
KV1G40.KV1W711	428	0.90	0.398	44.668	112	RRPG	212	29.2%	NT
KV1G10.KV1W681	428	0.78	0.398	39.811	100	NRPP	207	30.1%	NT
KV1G35.KV1W706	428	0.49	0.398	39.811	100	HHRQ	432	31.6%	NT
KV1G30.KV1W701	428	1.40	0.398	28.184	71	AKTR	261	29.8%	NT
KV1G31.KV1W702	428	1.10	0.355	25.119	71	RPRH	230	32.9%	NT

FIG. 7A(1)

KV1G39.KV1W710	428	0.49	0.355	17.783	50	GGKR	219	49.5%	NT
KV1G44.KV1W715	428	1.00	0.316	19.953	63	TRAK	433	37.1%	NT
KV1G36.KV1W707	428	0.32	0.282	17.783	63	NRQR	263	45.1%	NT
KV1G33.KV1W704	428	0.26	0.282	12.589	45	RHKR	216	15.1%	NT
KV1G34.KV1W705	428	0.15	0.282	10.000	35	HRRK	252	29.2%	NT
KV1G12.KV1W683	116	1.93	0.251	50.119	200	HAKP	155	23.6%	NT
KV1G13.KV1W684	116	0.61	0.251	31.623	126	NARQ	262	30.6%	NT
KV1G41.KV1W712	428	0.85	0.251	31.623	126	RTRP	188	34.8%	NT
KV1G18.KV1W689	116	0.85	0.126	39.811	316	PNRT	223	36.5%	NT
KV1G14.KV1W685	116	0.89	0.126	25.119	200	AQRP	210	38.5%	NT
KV1G19.KV1W690	116	0.59	0.063	25.119	398	TTRT	233	42.3%	NT
KV1G20.KV1W691	116	0.71	0.063	19.953	316	ATRP	206	44.4%	NT
KV1G9.KV1W680	116	0.29	0.032	15.849	501	AHRP	128	50.8%	0.61
KV1G6.KV1W677	116	0.08	0.025	7.943	316	TGRK	235	56.9%	0.21
KV1G16.KV1W687	116	0.20	0.025	7.943	316	ARRN	234	54.8%	0.26
KV1G15.KV1W686	116	0.31	0.016	10.000	631	AHRH	209	57.5%	0.37
KV1G7.KV1W678	116	0.24	0.013	10.000	794	RRRP	208	35.7%	1.43

NT = Not tested

SEQ ID NO: 116: $AS(AP)_{20}GS$

SEQ ID NO: 428: $GS(AP)_{20}AS$

*ratio $IC_{50(Kv1.1)}/IC_{50(Kv1.3)}$

FIG. 7A(2)

Compound ID	Competitive Binding Ki (nM)	T cell inhibition IC_{50} (nM)	C-terminal extension		Peptide	
			Amino acid sequence	SEQ ID NO:	Amino acid sequence	SEQ ID NO:
KV1G65.KV1W736	12.3	7.3	AHRH	209	GVPTDVKCRISRQCEKPCKDAGMRFGKCMNGKCHCTPKAHRH	415
KV1G64.KV1W735	5.95	4.4	TGRK	235	GVPTDVKCRISRQCEKPCKDAGMRFGKCMNGKCHCTPKTGRK	416
KV1G63.KV1W734	3.74	3.4	ARRN	234	GVPTDVKCRISRQCEKPCKDAGMRFGKCMNGKCHCTPKARRN	417
KV1G49.KV1W720	28.6	15.8	none		GVPTDVKCRISRQCEKPCKDAGMRFGKCMNGKCHCTPK	3

FIG. 7B

Protein ID	Fusion partner	Linker SEQ ID NO:	Peptide portion	Peptide SEQ ID NO:	Patch clamp IC_{50} (nM)			Thallium flux IC_{50} (nM)			Tcell inhibition, IC_{50} (nM)	Competitive Binding EC_{50} (nM)	Competitive Binding Ki (nM)	C-terminal extension	
					Kv1.3	Kv1.1	Selectivity**	KV1.3	KV1.1	Selectivity**				Amino acid sequence	SEQ ID NO:
KV1C2	Fc	119	OdK2	1	13	865	67	21.40	>1000	>46.7	69.9				
KV1N2	Fc	119	OsK1	2	0.3	2	7	0.03	0.10	3.2	2.8				
KV1D261	Fc	119	p261	42	0.15	85	582	0.09	17.80	198.00	1.66	7.47	0.15		
KV1D197	Fc	119	p197	22	0.3	145	483	0.10							
KV1D229	Fc	119	p229	34	0.25	70	280								
KV1D579	Fc	119	p579	3	0.14	>1000	>7143	0.14	>380	>2714	26.83	94.35	1.85		
KV1D261_34	HSA	116	p261	42	1.2	>1000	>1000	0.30	79.00	247.00	2.1	54.04	1.06		
KV1D261_23	HSA	119	p261	42	15			22.10			53.39				
KV1G49.KV1W720	HSA	116	p579	3	3			1.00	252.00	252.00	15.9	342.0	6.71		
KV1D261_26	HSA	120	p261	42				1.00	100.00	100.00	11.7	290.7	5.7		
KV1G8.KV1W677	HSA	116	p261 extended					0.025	7.943	316	0.21	4.0	0.08	TGRK	235
KV1G15.KV1W686	HSA	116	p261 extended		0.2			0.016	10.000	631	0.37	15.8	0.31	AHRH	209
KV1G16.KV1W687	HSA	116	p261 extended					0.025	7.943	316	0.26	10.0	0.20	ARRN	234
KV1G7.KV1W678	HSA	116	p261 extended					0.013	10.000	794	1.43	12.4	0.24	RRRP	208
KV1G9.KV1W680	HSA	116	p261 extended					0.032	15.849	501	0.61	14.9	0.29	AHRP	128
KV1G19.KV1W690	HSA	116	p261 extended					0.063	25.119	398	NT	30.3	0.59	TTRT	233
KV1G13.KV1W684	HSA	116	p261 extended					0.251	31.623	126	NT	31.2	0.61	NARQ	262
KV1G20.KV1W691	HSA	116	p261 extended					0.063	19.953	316	NT	36.3	0.71	ATRP	206
KV1G10.KV1W681	HSA	116	p261 extended					0.398	39.811	100	NT	39.7	0.78	NRPP	207
KV1G18.KV1W689	HSA	116	p261 extended					0.126	39.811	316	NT	43.4	0.85	PNRT	223
KV1G14.KV1W685	HSA	116	p261 extended					0.126	25.119	200	NT	45.2	0.89	AQRP	210
KV1G12.KV1W683	HSA	116	p261 extended					0.251	50.119	200	NT	98.6	1.93	HAKP	155

FIG. 8(1)

KV1G11.KV1W682	HSA	116	p261 extended					0.794	158.489	200	NT	98.9	1.94	HERT	237
KV1G26.KV1W697	HSA	116	p261 extended					0.501	31.623	63	NT	40.3	0.79	RRTA	239
KV1G27.KV1W698	HSA	116	p261 extended					0.708	50.119	71	NT	102.0	2.00	PRNT	268
KV1G28.KV1W699	HSA	116	p261 extended					1.122	63.096	56	NT	183.6	3.60	PKTA	224
KV1G29.KV1W700	HSA	116	p261 extended					0.562	63.096	112	NT	66.3	1.30	ARNA	232
KV1G30.KV1W701	HSA	116	p261 extended					0.398	28.184	71	NT	71.4	1.40	AKTR	261
KV1G31.KV1W702	HSA	116	p261 extended					0.355	25.119	71	NT	56.1	1.10	RPRH	230
KV1G33.KV1W704	HSA	116	p261 extended					0.282	12.589	45	NT	13.3	0.26	RHKR	216
KV1G34.KV1W705	HSA	116	p261 extended					0.282	10.000	35	NT	7.7	0.15	HRRK	252
KV1G35.KV1W706	HSA	116	p261 extended					0.398	39.811	100	NT	25.0	0.49	HHRQ	432
KV1G36.KV1W707	HSA	116	p261 extended					0.282	17.783	63	NT	16.3	0.32	NRQR	263
KV1G37.KV1W708	HSA	116	p261 extended					0.447	35.481	79	NT	61.2	1.20	AGPR	214
KV1G38.KV1W709	HSA	116	p261 extended					0.501	63.096	126	NT	117.3	2.30	HRPA	143
KV1G39.KV1W710	HSA	116	p261 extended					0.355	17.783	50	NT	25.0	0.49	GGKR	219
KV1G40.KV1W711	HSA	116	p261 extended					0.398	44.668	112	NT	45.9	0.90	RRPG	212
KV1G41.KV1W712	HSA	116	p261 extended					0.251	31.623	126	NT	43.4	0.85	RTRP	188
KV1G42.KV1W713	HSA	116	p261 extended					0.562	63.096	112	NT	66.3	1.30	RNRE	431
KV1G43.KV1W714	HSA	116	p261 extended					0.447	28.184	63	NT	38.3	0.75	NTRT	240
KV1G44.KV1W715	HSA	116	p261 extended					0.316	19.953	63	NT	51.0	1.00	TRAK	433
KV1G47.KV1W718	HSA	116	p261 extended					0.891	89.125	100	NT	147.9	2.90	TDAR	227
KV1G48.KV1W719	HSA	116	p261 extended					0.891	28.184	32	NT	918.0	18.00	AHRN	243
KV1G65.KV1W736	HSA	116	p579 extended					9.1	6.6	2.6	7.3	629	12.3	AHRH	209
KV1G64.KV1W735	HSA	116	p579 extended					9.2	6.7	2.4	4.4	304	5.95	TGRK	235
KV1G63.KV1W734	HSA	116	p579 extended					9.1	7.1	2.0	3.4	191	3.74	ARRN	234
KV1G49.KV1W720	HSA	116	p579 extended					1.00	252.00	252.00	15.8	1460	28.6	none	

NT= not tested

*in CHO cells

** Ratio: EC_{50}(Kv1.1)/EC_{50}(Kv1.3)

SEQ ID NO: 116: $AS(AP)_{20}GS$

SEQ ID NO: 120: $GS(G4S)_8$

SEQ ID NO: 119: $GS(G_4S)_4$

FIG. 8(2)

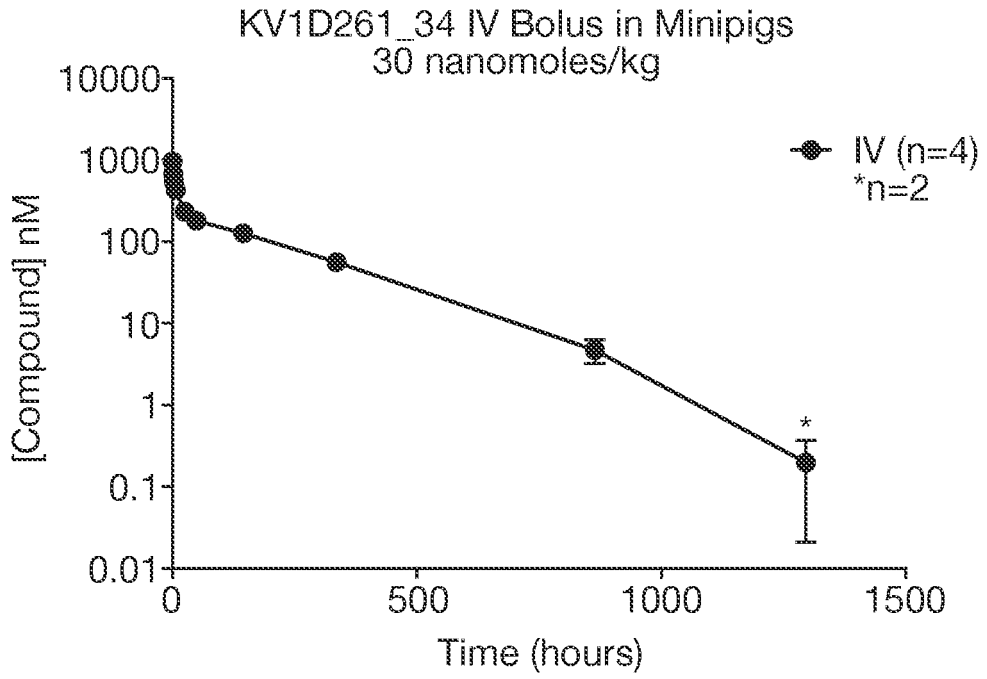

KV1D261_34 IV Bolus in Minipigs
30 nanomoles/kg
IV (n=4)
*n=2
[Compound] nM
10000
1000
100
10
1
0.1
0.01
0
500
1000
1500
Time (hours)
*

FIG. 9

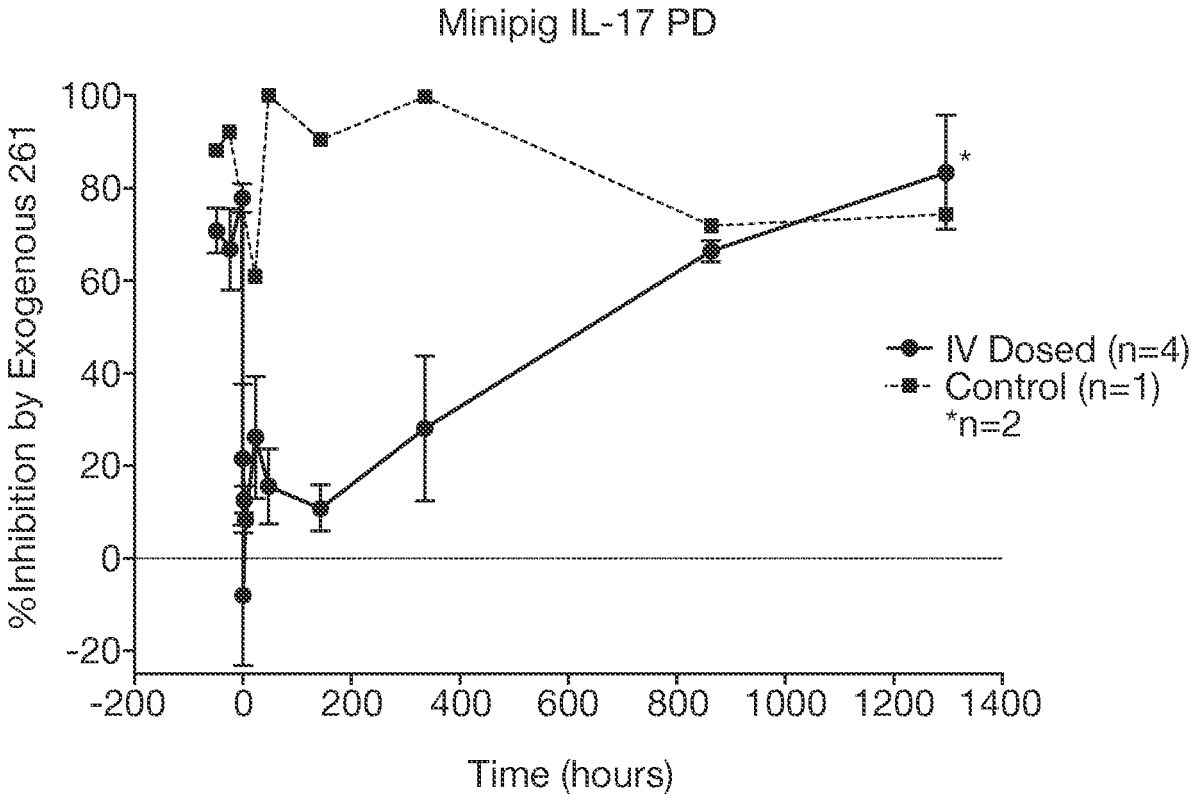

Minipig IL-17 PD
%Inhibition by Exogenous 261
100
80
60
40
20
0
-20
-200
0
200
400
600
800
1000
1200
1400
Time (hours)
IV Dosed (n=4)
Control (n=1)
*n=2
*

FIG. 10

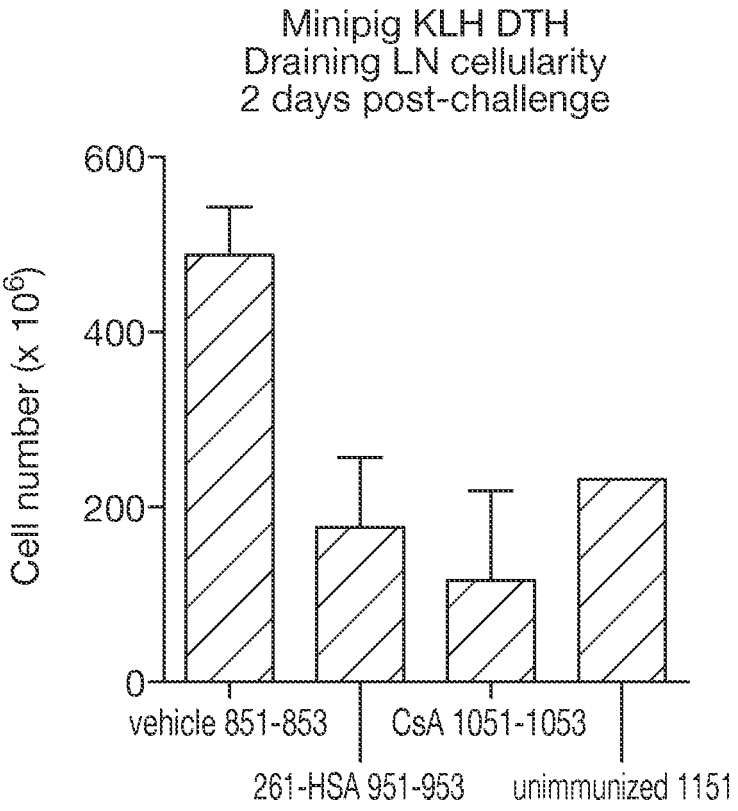

Minipig KLH DTH
Draining LN cellularity
2 days post-challenge
Cell number (x 10^6)
600
400
200
0
vehicle 851-853
CsA 1051-1053
261-HSA 951-953
unimmunized 1151

FIG. 11