

Figure 1

Hybridoma supernatants incubated on						
Clone	cells transfected with (CELISA)...		plates coated with (ELISA)...			
	IL-15 complex		IL-15 complex		free receptor IL-15Rα	
	rfu	% positive	rfu	% positive	rfu	% positive
ANTIBODY 1A6	120	12%	150	18%	93	16%
ANTIBODY 1B3	1160	120%	1629	191%	1488	258%
ANTIBODY 2D	972	98%	1280	142%	30	6%
ANTIBODY 4	1534	149%	1242	140%	97	19%
ANTIBODY 10A	1435	119%	1222	139%	57	11%
ANTIBODY 10B	1471	122%	1160	132%	72	14%
ANTIBODY 10F	1235	102%	831	95%	96	19%
ANTIBODY 13E	1435	118%	1362	167%	113	16%
ANTIBODY 5E	994	100%	810	94%	41	10%
ANTIBODY 10H	1137	119%	1752	217%	1440	316%
ANTIBODY 10F-7	43	4%	152	19%	88	19%

Figure 2A

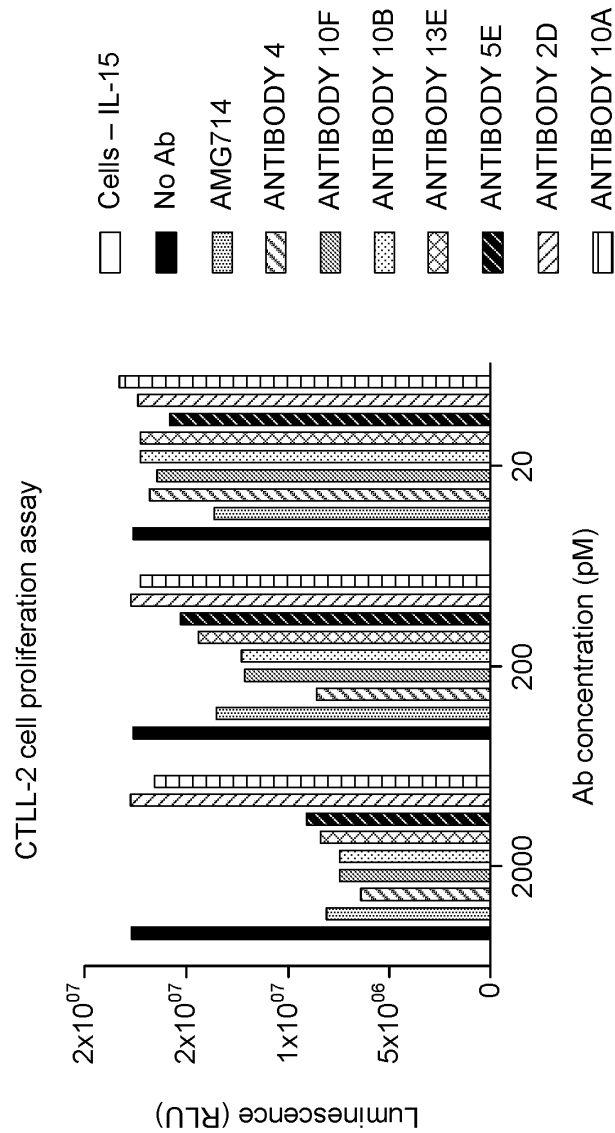


Figure 2B

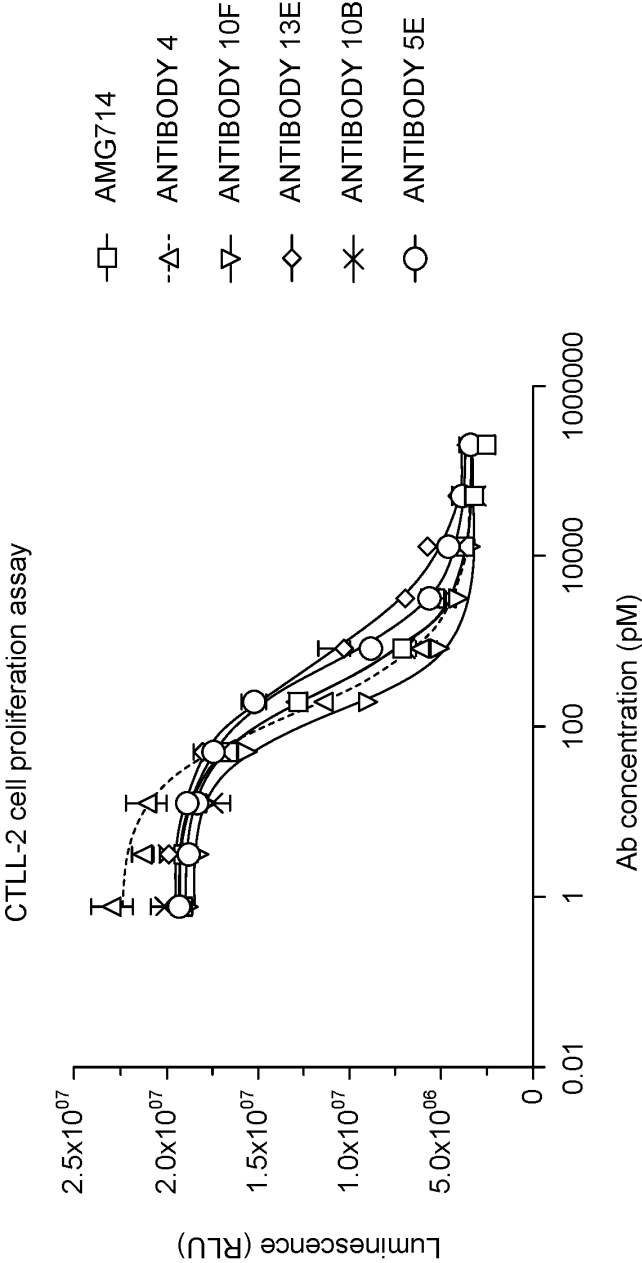


Figure 3

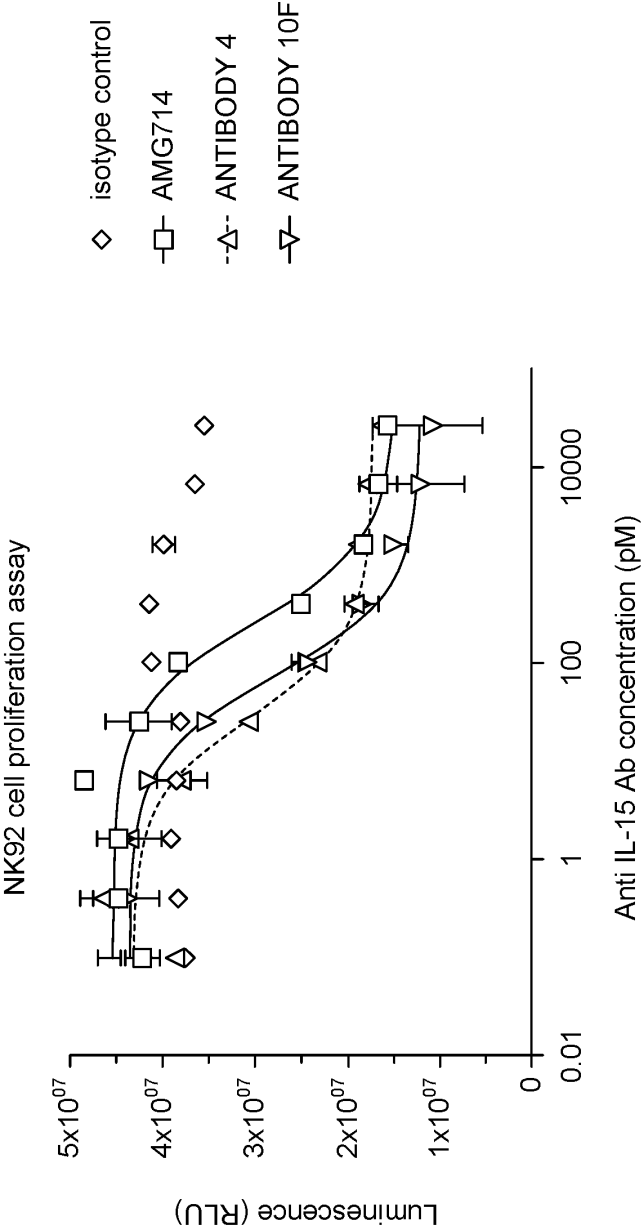


Figure 4

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_Q024A	338.1	1.35E+05	1.55E-04	1.15E-09	138.8	133.3	129.6	0.972
1	VL_Q024L	335.6	1.39E+05	1.60E-04	1.15E-09	139.5	134.5	130.6	0.971
1	VL_Q024Y	324.8	1.39E+05	1.45E-04	1.04E-09	134.3	129.4	126	0.974
1	VL_Q024W	358.3	1.36E+05	1.40E-04	1.03E-09	148.1	142.6	139	0.975
1	VL_Q024K	336.6	1.28E+05	1.65E-04	1.29E-09	134.8	128.4	124.6	0.970
1	VL_G025Q	309.3	8.36E+04	3.88E-04	4.64E-09	110.8	94.3	89.9	0.953
1	VL_G025W	387.8	7.42E+04	7.03E-03	9.47E-09	121	83.8	39.8	0.475
1	VL_G025S	370.9	8.85E+04	3.94E-04	4.45E-09	135	117.3	111.6	0.951
1	VL_G025Y	348.7	7.23E+04	3.65E-03	5.04E-08	115.4	85.9	57.3	0.667
1	VL_G025H	384.3	9.15E+04	2.90E-04	3.17E-09	140.6	123.5	118.8	0.962
1	VL_D026A	353	1.21E+05	1.65E-04	1.36E-09	139.2	131	127.4	0.973
1	VL_D026Q	417.8	1.12E+05	1.81E-04	1.61E-09	160.3	149.7	145.4	0.971
1	VL_D026S	356	1.20E+05	1.69E-04	1.41E-09	140.2	132.1	128.3	0.971
1	VL_D026W	396.7	1.15E+05	1.76E-04	1.53E-09	153.6	144.3	140.1	0.971
1	VL_D026H	366.2	1.19E+05	1.35E-04	1.13E-09	142.2	134.1	130.7	0.975
1	VL_D026K	328.7	1.15E+05	1.79E-04	1.55E-09	128.9	120.3	116.8	0.971

Figure 5

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_D026K	429.2	1.30E+05	4.78E-04	3.69E-09	175.1	167	156.9	0.940
1	VL_T027A	322.1	9.77E+04	1.94E-04	1.99E-09	118.6	106.3	103.1	0.970
1	VL_T027K	385	6.16E+04	7.42E-03	1.21E-07	111.2	70.3	31.5	0.448
1	VL_T027S	412.1	1.25E+05	6.70E-04	5.37E-09	166.8	157.1	144.7	0.921
1	VL_T027D	331.7	1.28E+05	4.64E-03	3.62E-08	131	114.7	68.6	0.598
1	VL_T027Y	329.6	9.76E+04	4.14E-03	4.24E-08	120.6	98.7	62.1	0.629
1	VL_T027H	369.9	1.09E+05	4.82E-03	4.43E-08	137.8	115.4	67.8	0.588
1	VL_L028A	347.2	6.52E+04	1.15E-03	1.76E-08	118	89.7	78.8	0.878
1	VL_L028K	345.7	1.45E+05	1.22E-03	8.45E-09	7	6.7	5.8	0.866
1	VL_L028Q	336.9	5.98E+04	2.86E-03	4.78E-08	108.5	75.3	54.7	0.726
1	VL_L028Y	403.9	5.26E+04	3.02E-04	5.75E-09	126.1	89.3	86	0.963
1	VL_L028D	376.9	1.26E+05	4.93E-04	3.93E-09	7.1	7.4	7.1	0.959
1	VL_R029A	334.2	1.46E+05	1.63E-04	1.12E-09	146	141.3	137.3	0.972
1	VL_R029K	305.7	1.38E+05	1.66E-04	1.20E-09	129.8	124.5	120.9	0.971
1	VL_R029Q	372.9	1.45E+05	1.49E-04	1.02E-09	162.3	157.6	153.6	0.975
1	VL_R029W	339.7	1.35E+05	1.59E-04	1.18E-09	141.7	135.8	132.1	0.973
1	VL_R029S	348.9	1.45E+05	1.69E-04	1.17E-09	152.6	147.9	143.7	0.972

Figure 6

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_R029L	398.9	1.42E+05	1.51E-04	1.06E-09	171.9	166.7	162.4	0.974
1	VL_R029D	384	1.40E+05	1.50E-04	1.07E-09	167.4	162.4	158.3	0.975
1	VL_R029Y	424.6	1.41E+05	1.39E-04	9.89E-10	180.3	175.3	170.8	0.974
1	VL_R029H	414	1.42E+05	1.35E-04	9.47E-10	177.9	173.3	169.1	0.976
1	VL_N030H	330.4	1.25E+05	3.05E-04	2.45E-09	134.9	127.3	121.9	0.958
1	VL_N030D	421.3	1.35E+05	6.28E-04	4.65E-09	180.2	172.5	159.5	0.925
1	VL_N030Y	357.1	1.39E+05	1.08E-03	7.80E-09	147.6	139.8	122.5	0.876
1	VL_N030W	434.1	1.14E+05	2.75E-03	2.40E-08	169	150.1	110.3	0.735
1	VL_N030S	342.8	1.42E+05	3.42E-04	2.41E-09	146.7	141.2	134.5	0.953
1	VL_N030L	305.5	1.42E+05	3.38E-03	2.38E-08	125.3	114.1	77.6	0.680
1	VL_Y031A	346.4	1.20E+05	3.21E-04	2.67E-09	7.9	7.2	7.1	0.986
1	VL_Y031K	288.3	1.06E+05	2.43E-04	2.29E-09	7.4	6.5	6.3	0.969
1	VL_Y031Q	392.9	1.36E+10	3.54E+02	2.61E-08	19.4	18.2	8.4	0.462
1	VL_Y031S	394	1.59E+05	1.87E-03	1.18E-08	10.7	10.8	9.2	0.852
1	VL_Y031L	3	8.54E+04	4.69E-04	5.49E-09	7.4	5.7	5.4	0.947
1	VL_Y031D	403.2	9.13E+04	5.59E-07	6.13E-12	7.8	7.5	7.6	1.013
1	VL_Y031H	363.6	1.49E+05	8.97E-04	6.00E-09	8.2	8	7.4	0.925

Figure 7

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_Y032A	401.9	1.05E+05	7.29E-03	6.94E-08	144	144	112.8	0.470
1	VL_Y032K	281.5	8.23E+04	1.74E-03	2.11E-08	101	101	82.6	0.821
1	VL_Y032Q	353.6	9.69E+04	4.54E-04	4.69E-09	140.3	140.3	124.6	0.945
1	VL_Y032W	364.2	1.03E+05	2.06E-04	2.00E-09	138.8	138.8	126.1	0.971
1	VL_Y032S	344.3	2.66E+05	5.85E-03	2.20E-08	15.5	15.5	15.4	0.623
1	VL_Y032L	315	1.00E+05	6.45E-04	6.43E-09	125.5	125.5	112	0.925
1	VL_Y032D	353.2	2.21E+05	3.55E-02	1.61E-07	102.1	102.1	65.5	0.153
1	VL_Y032H	298.7	1.15E+05	1.80E-04	1.56E-09	122.9	122.9	114.5	0.972
1	VL_A033L	339.6	4.58E+04	3.34E-04	7.31E-09	112.5	112.5	73	0.960
1	VL_A033D	363.2	3.60E+04	6.17E-04	1.71E-08	110.3	110.3	61.2	0.930
1	VL_A033Y	389.5	3.93E+04	8.74E-03	2.22E-07	64.5	64.5	31.4	0.411
1	VL_A033Q	375.6	3.21E+04	9.43E-04	2.94E-08	107.5	107.5	55.2	0.900
1	VL_A033W	384	1.09E+05	3.34E-04	3.06E-09	7.4	7.8	7.8	0.923
1	VL_A033H	383.4	4.35E+04	6.08E-03	1.40E-07	101.8	55.7	55.7	0.522
1	VL_A033K	353.9	1.27E+05	8.64E-04	6.82E-09	7.2	7.2	7.2	0.889
1	VL_S034A	380.3	1.36E+05	1.55E-04	1.14E-09	159.2	153.1	153.1	0.973
1	VL_S034L	361.4	7.86E+04	1.07E-04	1.36E-09	7.1	5.6	5.6	0.982

Figure 8

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_S034D	388.7	4.67E+04	8.33E-03	1.78E-07	44.9	24.2	10.3	0.426
1	VL_S034Y	351.5	8.05E+04	6.45E-07	8.01E-12	7.3	6	5.9	0.983
1	VL_S034Q	373.7	8.52E+07	6.82E-01	8.00E-09	9.8	10.3	6.7	0.650
1	VL_S034W	355.6	1.16E+05	2.17E-04	1.87E-09	7.3	6.9	6.5	0.942
1	VL_S034H	378.9	7.57E+05	1.33E-01	1.75E-07	68.3	42.3	7.3	0.173
1	VL_G025K	397.5	5.98E+04	5.25E-04	8.78E-09	125.3	93.7	88.1	0.940
1	VL_G025L	394.7	6.02E+04	4.22E-03	7.01E-08	126.9	86.3	54.6	0.633
1	VL_G025D	395.2	1.33E+05	2.31E-04	1.73E-09	165.4	158.3	152.9	0.966
1	VL_D026Y	470.1	1.18E+05	1.54E-04	1.30E-09	184.5	173.8	169.4	0.975
1	VL_T027Q	421.7	1.03E+05	2.51E-03	2.43E-08	161.2	140.1	105.7	0.754
1	VL_T027W	345.4	7.80E+04	4.75E-03	6.08E-08	121.6	90.7	53.4	0.589
1	VL_T027L	380	1.05E+05	2.35E-03	2.24E-08	150	130.6	100.3	0.768
1	VL_L028S	357.7	5.93E+04	4.48E-03	7.55E-08	114.9	76.6	46.7	0.610
1	VL_L028W	404.6	5.44E+04	5.20E-03	9.57E-08	116.3	71.4	41.9	0.587
1	VL_L028H	398.6	5.97E+04	7.56E-04	1.27E-08	134.7	99.8	91.6	0.918
1	VL_N030K	320.8	7.47E+04	1.00E-03	1.34E-08	112	90	80.2	0.891
1	VL_N030Q	379.1	1.20E+05	1.05E-03	8.71E-09	155.4	143.8	126.9	0.882

Figure 9

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
1	VL_Y031W	343.9	1.84E+05	8.74E-03	4.75E-08	145.1	126.2	48.6	0.385
1	VL_G050L	400.4	5.95E+04	8.12E-04	1.37E-08	126.1	93	84.8	0.912
1	VL_G050D	383	1.50E+05	4.97E-04	3.30E-09	169.8	164.3	154	0.937
1	VL_G050Y	368.2	8.91E+04	8.58E-04	9.62E-09	136.8	117.8	106.4	0.903
1	VL_K051A	358.7	1.48E+05	1.40E-04	9.42E-10	161.6	157	153.1	0.975
1	VL_K051L	391.7	1.40E+05	1.21E-04	8.65E-10	174.7	168.9	165.2	0.978
1	VL_K051Q	361.2	1.43E+05	1.47E-04	1.03E-09	162.8	157.3	153.3	0.975
1	VL_K051Y	312.9	1.34E+05	1.51E-04	1.12E-09	138.8	132.7	129.5	0.976
1	VL_K051S	415.3	7.08E+04	2.25E-04	3.18E-09	163.9	132.4	128.6	0.971
1	VL_K051W	447.3	1.26E+05	1.73E-04	1.38E-09	190.8	182.1	177.3	0.974
1	VL_N052A	320.3	1.34E+05	1.76E-04	1.31E-09	140.3	134.3	130.6	0.972
1	VL_N052Q	430.2	1.27E+05	1.67E-04	1.31E-09	184.9	176.8	172.2	0.974

2	VH_G026A	268.4	1.46E+05	1.85E-04	1.26E-09	107.8	104.7	101.4	0.968
2	VH_G026K	360	1.30E+05	1.78E-04	1.36E-09	145.1	139.5	135.3	0.970
2	VH_G026W	354.4	1.34E+05	1.60E-04	1.19E-09	144.8	140	136	0.971
2	VH_G026S	341.3	1.41E+05	1.66E-04	1.18E-09	143.6	139.4	135.3	0.971

Figure 10

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VH_G026L	356.7	1.43E+05	1.66E-04	1.16E-09	150.7	147.2	142.8	0.970
2	VH_G026D	363.9	1.47E+05	1.88E-04	1.28E-09	155.9	152.8	148	0.969
2	VH_G026Y	341.7	1.38E+05	1.78E-04	1.30E-09	142.1	137.2	133.1	0.970
2	VH_G026H	386.6	1.36E+05	1.85E-04	1.36E-09	160.4	155.9	151.1	0.969
2	VH_G027K	366.2	1.30E+05	1.79E-04	1.38E-09	147.4	141.7	137.3	0.969
2	VH_G027Q	318.7	1.42E+05	1.96E-04	1.38E-09	135.6	131.2	126.9	0.967
2	VH_G027W	303.4	1.38E+05	1.90E-04	1.38E-09	126.8	121.8	117.8	0.967
2	VH_G027S	371.6	1.38E+05	1.77E-04	1.28E-09	154.9	150.8	146.1	0.969
2	VH_G027L	348.8	1.47E+05	1.67E-04	1.14E-09	149.5	145.7	141.3	0.974
2	VH_G027D	314.6	1.44E+05	2.23E-04	1.55E-09	137.2	132.4	127.8	0.965
2	VH_G027Y	391.9	1.38E+05	1.82E-04	1.32E-09	164.8	160.3	155.5	0.970
2	VH_G027H	368.6	1.42E+05	1.88E-04	1.33E-09	156.3	152.4	147.6	0.969
2	VH_S028A	373.7	1.42E+05	1.63E-04	1.15E-09	158.8	155	150.5	0.971
2	VH_S028L	336.4	1.41E+05	1.85E-04	1.31E-09	142.9	137.9	133.6	0.969
2	VH_S028Y	342.1	1.39E+05	1.67E-04	1.20E-09	143.7	138.5	134.4	0.970
2	VH_S028W	341.9	1.34E+05	1.95E-04	1.46E-09	141.5	135.6	131.3	0.968
2	VH_S028H	310.9	1.39E+05	1.74E-04	1.25E-09	131.7	126.9	123.1	0.970

Figure 11

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VH_S028K	385.6	1.25E+05	1.75E-04	1.40E-09	154.2	147.9	143.6	0.971
2	VH_I029A	368.5	1.38E+05	2.26E-04	1.64E-09	154.2	150.1	144.8	0.965
2	VH_I029K	319.9	1.27E+05	2.42E-04	1.91E-09	123.3	116.8	112.4	0.962
2	VH_I029Q	338.6	1.37E+05	2.24E-04	1.64E-09	140.5	135.9	131.2	0.965
2	VH_I029W	321.1	1.35E+05	2.26E-04	1.68E-09	131.8	125.7	121.4	0.966
2	VH_I029L	371.5	1.42E+05	1.56E-04	1.10E-09	158	153.5	149.1	0.971
2	VH_I029H	351.4	1.33E+05	2.41E-04	1.82E-09	143.5	137	132	0.964
2	VH_S030A	310.2	1.43E+05	1.56E-04	1.09E-09	133.3	128.5	124.9	0.972
2	VH_S030L	328.8	1.34E+05	1.88E-04	1.40E-09	139.3	133.4	129.3	0.969
2	VH_S030D	362.3	1.45E+05	1.88E-04	1.30E-09	159	154.4	149.6	0.969
2	VH_S030Y	358	1.29E+05	1.86E-04	1.44E-09	149.2	142.6	138.3	0.970
2	VH_S030Q	367	1.41E+05	1.39E-04	9.81E-10	157.2	152.4	148.4	0.974
2	VH_S030W	376.4	1.32E+05	1.76E-04	1.33E-09	155.5	149.6	145.1	0.970
2	VH_S030H	380.5	1.41E+05	1.51E-04	1.07E-09	160.7	155.9	151.6	0.972
2	VH_S030K	343.5	1.24E+05	1.61E-04	1.30E-09	136.7	129.7	126	0.971
2	VH_S031A	349.6	1.39E+05	1.78E-04	1.28E-09	148.6	143.4	139.1	0.970
2	VH_S031L	351.2	1.32E+05	1.96E-04	1.48E-09	148.3	142	137.6	0.969

Figure 12

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VH_S031D	363.4	1.37E+05	2.79E-04	2.03E-09	158.3	152.6	146.5	0.960
2	VH_S031Y	371.5	1.35E+05	2.22E-04	1.64E-09	155.9	150.3	145.1	0.965
2	VH_S031Q	334.3	1.40E+05	1.78E-04	1.27E-09	142.5	137.3	133.2	0.970
2	VH_S031W	355.8	1.27E+05	1.75E-04	1.37E-09	142	135.3	131.2	0.970
2	VH_S031H	356.4	1.37E+05	1.95E-04	1.43E-09	150	144.5	139.8	0.967
2	VH_S031K	380.3	1.30E+05	2.73E-04	2.10E-09	156.7	150.7	144.8	0.961
2	VH_S032A	332.3	1.38E+05	1.36E-04	9.87E-10	140.6	135.6	132.2	0.975
2	VH_S032L	366.7	1.30E+05	1.54E-03	1.19E-08	149.7	139.7	116.8	0.836
2	VH_S032D	364.2	1.07E+05	2.77E-03	2.60E-08	149.3	129.9	95.4	0.734
2	VH_S032Y	313.6	1.39E+05	6.63E-04	4.77E-09	130.1	124.3	114.1	0.918
2	VH_S032Q	545.7	1.32E+05	2.52E-04	1.92E-09	224.6	216.9	208.9	0.963
2	VH_S032W	371.9	1.24E+05	3.25E-04	2.63E-09	144.5	137	130.7	0.954
2	VH_S032H	339.4	1.33E+05	5.65E-04	4.24E-09	141.1	133.6	124.1	0.929
2	VH_S032K	386.6	1.17E+05	8.48E-04	7.24E-09	148.9	138.3	124.8	0.902
2	VH_N033A	355.8	1.21E+05	2.63E-04	2.16E-09	146.2	138.5	133.3	0.962
2	VH_N033K	302.3	1.02E+05	2.65E-04	2.60E-09	116.1	105.8	101.6	0.960
2	VH_N033Q	365.1	1.38E+05	1.65E-04	1.19E-09	156.1	152.2	147.8	0.971

Figure 13

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VH_N033W	381.1	1.31E+05	3.48E-04	2.65E-09	156.5	150.9	143.6	0.952
2	VH_N033S	321.5	1.28E+05	2.41E-04	1.88E-09	134.1	128	123.3	0.963
2	VH_N033L	344	1.29E+05	2.02E-04	1.56E-09	140.6	134.3	129.8	0.966
2	VH_N033D	372.7	1.03E+05	1.25E-03	1.21E-08	148.2	133	115.2	0.866
2	VH_N033Y	377.8	1.38E+05	2.11E-04	1.53E-09	160.5	155.8	150.5	0.966
2	VH_N033H	358.6	1.40E+05	1.41E-04	1.01E-09	153.5	148.6	144.6	0.973
2	VH_N033A	397.2	1.22E+05	2.68E-03	2.20E-08	164.1	148.8	110.1	0.740
2	VH_W034Q	378	1.25E+05	1.90E-03	1.51E-08	153.7	142.4	114.8	0.806
2	Parent clone	361.4	1.41E+05	1.38E-04	9.82E-10	156.5	151.9	147.9	0.974
2	VH_W034S	446	9.21E+04	2.79E-03	3.03E-08	171.1	143.5	105.4	0.734
2	VH_W034L	335.3	1.33E+05	1.17E-03	8.85E-09	140.8	132.4	115.2	0.870
2	VH_W034D	344.6	1.31E+05	3.31E-03	2.53E-08	150	134.3	92.4	0.688
2	VH_W034H	366.3	1.04E+05	2.61E-03	2.51E-08	139.5	121.5	90.7	0.747
2	VH_W035A	23.7	1.04E+05	6.49E-04	6.21E-09	10.6	9.1	8.4	0.923
2	VH_W035K	20.7	9.20E+04	6.04E-04	6.56E-09	12.4	10.5	9.7	0.924
2	VH_W035Q	76.3	9.27E+04	3.20E-04	3.45E-09	31.1	27.7	26.5	0.957
2	VH_W035Y	327.9	1.38E+05	1.77E-04	1.29E-09	140.7	135.8	131.7	0.970

Figure 14

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VH_I029S	334.2	1.39E+05	2.40E-04	2.65E-09	143.3	138.2	133.1	0.963
2	VH_I029D	343.6	1.43E+05	2.52E-04	1.88E-09	152.5	147.5	142.1	0.963
2	VH_I029Y	382.8	1.32E+05	2.09E-04	1.56E-09	159.8	153.7	148.6	0.967
2	VH_W034K	325.8	3.25E+05	4.06E-02	1.21E-08	68.4	48.4	10.8	0.223
2	VL_R091D	1.9	1.05E+05	6.94E-04	1.53E-09	9.3	8.2	7.5	0.915
2	VH_E050S	348.9	1.56E+05	1.86E-03	1.01E-09	155.4	147.7	118.9	0.805
2	VH_E050L	376.3	1.16E+05	7.91E-03	2.20E-08	132.2	105.4	44.2	0.419
2	VH_E050D	367.4	1.35E+05	3.40E-03	1.51E-08	156.5	141.5	96.5	0.682
2	VH_E050Y	379.9	1.07E+05	5.24E-03	9.82E-10	135.7	112.8	63.4	0.562
2	VH_E050H	352.9	1.46E+05	1.02E-03	3.03E-08	152.6	146.2	129	0.882
2	VH_I051A	361.3	1.45E+05	1.84E-04	8.85E-09	158.6	153.9	149.2	0.969
2	VH_I051K	359.9	1.16E+05	3.26E-04	2.53E-08	141.5	132.1	126.2	0.955
2	VH_I051Y	388.4	1.32E+05	1.73E-04	2.51E-08	163.7	156.6	152.1	0.971
2	VL_P055Q	370.6	1.35E+05	1.72E-04	6.21E-09	161.8	155.4	150.9	0.971
2	VL_R054D	377.5	8.42E+04	2.07E-04	6.56E-09	97.6	84.4	81.7	0.968
2	VH_P100Y	350.1	6.91E+04	5.89E-04	3.45E-09	120.7	95.5	89.1	0.933
2	VH_S100aD	393.8	9.83E+04	3.07E-06	3.12E-11	10.1	9.6	9.5	0.990

Figure 15

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
2	VL_S090W	386.1	1.27E+05	4.87E-04	3.84E-09	10.3	10.4	9.9	0.952
2	VL_N089H	400.3	1.40E+05	5.11E-04	3.64E-09	175.2	168.7	157.9	0.936
2	VL_P055H	378.3	1.38E+05	1.44E-04	1.04E-09	164.8	159.7	155.6	0.974
2	VH_Y102A	407.7	1.36E+05	1.20E-04	8.80E-10	173.1	167.7	163.7	0.976
2	VL_N053Y	387.3	1.14E+05	3.56E-04	3.13E-09	157.5	146.8	139.9	0.953
2	VL_S056A	335.5	1.44E+05	1.51E-04	1.05E-09	148.9	144.8	140.8	0.972
2	VL_S056Q	360.8	1.41E+05	1.53E-04	1.09E-09	158.9	153.9	149.8	0.973
3	VH_I097K	479.1	1.38E+05	2.35E-04	1.70E-09	190.3	184.2	173.2	0.940
3	VH_I097S	640.8	1.32E+05	9.43E-04	7.15E-09	259.8	247.3	198.1	0.801
3	VH_I097L	572.5	1.40E+05	3.00E-04	2.15E-09	237.1	229.6	212.9	0.927
3	VH_I097D	585	1.55E+05	4.70E-03	3.04E-08	211.8	192.9	76.3	0.396
3	VH_I097Y	541.7	9.89E+04	2.27E-04	2.29E-09	206.5	186.9	176.6	0.945
3	VH_I097H	559.9	1.22E+05	1.46E-04	1.19E-09	218.6	207.7	199.5	0.961
3	VH_G098K	514	7.22E+04	1.69E-07	2.35E-12	5.7	6.2	7.5	1.210
3	VH_G098W	582.4	1.09E+05	4.29E-07	3.94E-12	4.8	6.5	6.6	1.015
3	VH_G098S	552.6	2.15E+05	3.20E-02	1.48E-07	168.6	111.8	6.6	0.059

Figure 16

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
3	VH_G098D	766.5	1.12E+05	4.84E-02	4.30E-07	153.7	59.5	9.9	0.166
3	VH_G098Y	622.4	7.45E+04	6.00E-09	8.06E-14	5.7	5.9	7	1.186
3	VH_W099A	544.2	9.58E+04	2.74E-07	2.85E-12	5.1	5.9	6.6	1.119
3	VH_W099K	583.7	6.75E+04	9.48E-08	1.40E-12	6	5.4	7	1.296
3	VH_W099Q	564.8	1.65E+05	2.81E-04	1.71E-09	6.4	9.6	8.1	0.844
3	VH_W099Y	610.4	2.12E+05	1.91E-02	9.02E-08	208.5	161.4	13.9	0.086
3	VH_W099S	693.4	1.54E+05	2.69E-07	1.75E-12	5.9	7.4	7.9	1.068
3	VH_W099D	579.5	6.93E+04	3.51E-07	5.08E-12	4.9	5	5.7	1.140
3	VH_W099H	664.4	2.88E+05	3.94E-02	1.37E-07	207.8	139.4	8.4	0.060
3	VH_P100A	600.8	4.80E+05	9.72E-02	2.03E-07	129.4	76.1	7	0.092
3	VH_P100K	532.7	1.00E+05	7.84E-04	7.84E-09	6.1	10.4	7.1	0.683
3	VH_P100Q	638.1	1.47E+05	2.22E-06	1.50E-11	5.5	8.5	7.9	0.929
3	VH_P100W	744.8	9.12E+04	8.95E-07	9.81E-12	6	7.2	8.5	1.181
3	VH_P100S	520.8	7.99E+05	1.93E-01	2.42E-07	109.9	58.3	6.2	0.106
3	VH_P100L	912.7	1.26E+05	2.13E-06	1.69E-11	6.7	10.6	9.9	0.934
3	VH_P100D	679.9	7.17E+04	2.92E-07	4.07E-12	4.8	5.3	6.2	1.170
3	VH_P100H	736.3	1.48E+05	1.32E-04	8.91E-10	15.5	18.5	17.1	0.924

Figure 17

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
3	VH_S100aA	655.9	1.16E+05	2.22E-04	1.92E-09	266.8	250.7	236.9	0.945
3	VH_S100aL	617.3	1.27E+05	7.29E-04	5.75E-09	253.9	240.5	202.3	0.841
3	VH_S100aQ	667.6	1.41E+05	1.77E-04	1.25E-09	282.2	274.5	261.8	0.954
3	VH_S100aW	616.1	1.10E+05	5.59E-04	5.08E-09	243.2	224.7	196.7	0.875
3	VH_S100aH	647.1	1.46E+05	2.06E-04	1.41E-09	281.3	274.2	259.9	0.948
3	VH_S100aK	799.8	3.10E+05	4.10E-02	1.32E-07	234.4	159.1	10.3	0.065
3	VH_F100bA	330.8	8.97E+04	4.80E-04	5.34E-09	123.2	107.5	96.2	0.895
3	VH_F100bK	-2.9	9.43E+04	4.28E-03	4.54E-08	5	5	2.2	0.440
3	VH_F100bQ	283.7	7.88E+04	5.62E-04	7.13E-09	102.3	85	74.7	0.879
3	VH_F100bW	14.1	4.24E+05	6.96E-03	1.64E-08	8.8	7.5	2.7	0.360
3	VH_F100bS	355.8	9.81E+04	3.85E-04	3.92E-09	145.3	129.4	118.4	0.915
3	VH_F100bL	744.1	1.81E+05	3.80E-04	2.10E-09	360.2	355.3	325.5	0.916
3	VH_F100bD	-9.8	8.83E+04	1.34E-02	1.51E-07	6.5	4.6	0	0.000
3	VH_F100bH	-0.8	6.00E+04	1.21E-02	2.02E-07	7.2	4.3	0	0.000
3	VH_D101A	140.8	1.46E+05	4.56E-04	3.13E-09	69.4	68	60.8	0.894
3	VH_D101L	-0.6	7.58E+04	1.47E-02	1.94E-07	6	4	-0.2	-0.050
3	VH_D101Q	735.8	1.83E+05	2.54E-04	1.39E-09	343.1	337.8	319	0.944

Figure 18

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
3	VH_D101S	-2	1.57E+05	5.89E-03	3.76E-08	4.6	5.2	1.8	0.346
3	VH_D101W	245.1	1.51E+05	4.03E-04	2.67E-09	109.9	107.2	97.6	0.910
3	VH_D101H	534.2	2.09E+05	4.27E-04	2.04E-09	259	255.1	232.6	0.912
3	VH_D101K	698.6	2.13E+05	4.12E-04	1.93E-09	321.1	315.4	289.4	0.918
3	VH_Y102K	899.4	2.73E+05	2.21E-04	8.08E-10	450.8	451.8	430.5	0.953
3	VH_Y102Q	763.5	3.30E+05	2.37E-04	7.17E-10	394.6	396.2	376.4	0.950
3	VH_Y102W	660.2	3.26E+05	2.43E-04	7.46E-10	346.9	348.4	330.1	0.947
3	VH_Y102L	778.2	1.33E+05	1.56E-04	1.17E-09	328.1	316.4	303.2	0.958
3	VH_Y102D	339.3	1.51E+05	2.60E-04	1.72E-09	146.5	143.6	134.2	0.935
3	VH_Y102H	720	1.37E+05	1.62E-04	1.19E-09	308.2	298.4	285.7	0.957
3	VH_E095A	819.8	9.76E+04	4.61E-04	4.72E-09	298.7	269.4	241	0.895
3	VH_E095K	621.7	5.79E+10	2.61E-02	4.51E-09	12.5	19.9	11.2	0.563
3	VH_E095Q	0.5	9.82E+04	4.84E-03	4.93E-08	5	4.1	1.1	0.268
3	VH_E095W	735.9	1.09E+05	5.16E-10	4.71E-15	7.6	8.4	10.4	1.238
3	VH_E095S	158	1.13E+05	8.78E-04	7.78E-09	67.4	62.1	50.2	0.808
3	VH_E095L	878.7	9.70E+04	6.37E-04	6.57E-09	314.3	281.6	241.9	0.859
3	VH_E095D	776.9	8.75E+04	9.77E-04	1.12E-08	259.2	224.6	178.5	0.795

Figure 19

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
3	VH_E095Y	23.9	1.10E+05	1.31E-03	1.19E-08	15	14.3	10.6	0.741
3	VH_E095H	694.5	9.06E+04	8.47E-04	9.34E-09	244.1	213.6	175.2	0.820
3	VH_G096A	599	1.06E+05	9.02E-04	8.51E-09	250.1	227.6	184.5	0.811
3	VH_G096K	-1	5.54E+05	8.41E-03	1.52E-08	5	5	2.4	0.480
3	VH_G096Q	609.8	9.98E+04	1.53E-03	1.53E-08	244.5	216.7	152.9	0.706
3	VH_G096W	-2.7	4.37E+05	5.74E-03	1.32E-08	5.4	5.9	3.6	0.610
3	VH_G096S	939.9	1.01E+05	1.07E-03	1.06E-08	382.2	341.9	267.2	0.782
3	VH_G096L	807.4	3.47E+05	4.78E-02	1.38E-07	204.8	140.5	13	0.093

4	VL_S090A	399.4	1.21E+05	2.03E-04	1.68E-09	158.7	149.1	141.2	0.947
4	VL_S090L	382.7	9.53E+04	3.82E-03	4.01E-08	88.6	64.7	34.7	0.536
4	VL_S090D	388.3	9.69E+04	5.99E-03	6.19E-08	126.7	95.9	31.1	0.324
4	VL_S090Y	379.9	7.60E+08	1.15E-02	1.51E-07	37.4	26.4	4.5	0.170
4	VL_S090Q	395.2	1.83E+09	1.40E-02	7.65E-08	20.4	18.3	3.7	0.202
4	VL_S090H	383.2	1.56E+10	2.44E-02	1.56E-08	7.6	9.8	4.3	0.439
4	VL_R091A	421.8	7.20E+04	1.96E-03	2.72E-08	75.7	59.6	37.8	0.634
4	VL_R091K	404.1	1.74E+05	1.59E-02	9.14E-08	142.7	108.8	8.3	0.076

Figure 20

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
4	VL_R091Q	400.5	8.98E+07	2.00E-01	2.23E-07	72.7	38.2	4.4	0.115
4	VL_R091W	397.9	7.93E+04	4.22E-04	5.33E-09	4.4	5.1	4.4	0.863
4	VL_R091L	398.6	8.23E+04	3.12E-04	3.79E-09	4.7	5.2	4.7	0.904
4	VL_R091Y	408.2	1.24E+05	8.09E-04	6.52E-09	4.9	5.1	4.1	0.804
4	VL_R091H	388.3	1.40E+05	5.41E-02	3.87E-07	85	33.2	5.1	0.154
4	VL_D092A	404.3	7.79E+04	3.30E-04	4.24E-09	137.4	114.5	105.6	0.922
4	VL_D092L	393.1	1.85E+05	2.60E-02	1.41E-07	101.3	68.3	5.6	0.082
4	VL_D092Q	382.2	8.07E+04	2.18E-03	2.70E-08	126.2	102.3	62.7	0.613
4	VL_D092Y	380.6	1.15E+05	1.09E-02	9.41E-08	99.1	71.6	14.6	0.204
4	VL_D092S	384.7	1.09E+05	2.35E-04	2.15E-09	148.3	137.9	129.7	0.941
4	VL_D092W	380.4	8.75E+04	2.35E-03	2.68E-08	117.8	95.5	58.7	0.615
4	VL_D092H	380.3	6.82E+04	9.91E-04	1.45E-08	125	98.8	78.6	0.796
4	VL_D092K	396.8	9.43E+04	6.91E-03	7.32E-08	99.2	69.6	22.2	0.319
4	VL_S093A	390.7	1.32E+05	2.29E-04	1.74E-09	162.9	156.4	147.3	0.942
4	VL_S093L	405.5	1.47E+05	1.58E-04	1.08E-09	173.5	169	161.7	0.957
4	VL_S093D	399	1.33E+05	2.62E-04	1.98E-09	167.8	160.9	150.4	0.935
4	VL_S093Y	411.3	1.39E+05	1.72E-04	1.24E-09	171.9	165.9	158.2	0.954

Figure 21

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
4	VL_S093Q	388.9	1.35E+05	2.17E-04	1.61E-09	163.7	158.3	149.5	0.944
4	VL_S093W	413	1.40E+05	1.65E-04	1.18E-09	171.6	166	158.4	0.954
4	VL_S093H	388.9	1.26E+05	2.26E-04	1.79E-09	159.1	152.3	143.6	0.943
4	VL_S093K	396	1.15E+05	2.03E-04	1.77E-09	156.2	146	138.3	0.947
4	VL_S094A	411.6	1.27E+05	2.42E-04	1.91E-09	169	160.4	150.6	0.939
4	VL_S094L	395.2	1.37E+05	2.33E-04	1.70E-09	167.4	162	152.5	0.941
4	VL_S094D	404.5	1.31E+05	2.73E-04	2.08E-09	171	164	153	0.933
4	VL_S094K	409	1.29E+05	2.66E-04	2.07E-09	167.8	160.1	149.6	0.934
4	VL_S094Q	390.5	1.27E+05	2.05E-04	1.62E-09	158.6	150.6	142.7	0.948
4	VL_S094W	418.1	1.35E+05	2.59E-04	1.93E-09	172.5	165.4	154.5	0.934
4	VL_S094H	416.6	1.15E+05	2.50E-04	2.17E-09	164.2	153.2	143.7	0.938
4	VL_S094K	387.2	1.02E+05	2.73E-04	2.68E-09	146.8	134.1	125.1	0.933
4	VL_G095A	396.5	1.17E+05	1.45E-03	1.24E-08	156.5	144.3	103.1	0.714
4	VL_G095K	399.5	1.53E+05	2.34E-03	1.53E-08	8.8	13.8	6.4	0.464
4	VL_G095Q	406.1	1.45E+05	1.18E-02	8.13E-08	25.2	29.7	6.9	0.232
4	VL_G095W	419.5	1.94E+05	5.16E-02	2.66E-07	83.4	39.2	7	0.179
4	VL_G095S	405.3	1.99E+05	1.84E-02	9.23E-08	128.1	95.5	10.3	0.105

Figure 22

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
4	VL_K095aD	408.9	1.68E+05	6.66E-03	3.96E-08	171.9	153.7	39.1	0.254
4	VL_G095L	390.8	1.23E+05	2.37E-02	1.92E-07	113.2	71.1	6.7	0.094
4	VL_G095D	400.3	1.45E+05	3.91E-02	2.70E-07	96.7	49.5	7.1	0.143
4	VL_G095Y	404.5	6.00E+05	9.08E-02	1.51E-07	115.8	71.9	7	0.097
4	VL_G095H	403.3	2.16E+05	2.87E-03	1.33E-08	11.3	18.9	8.6	0.455
4	VL_K095aD	404.9	1.42E+05	4.49E-04	3.17E-09	176.5	171	153.2	0.896
4	VL_K095aL	408.7	1.38E+05	3.36E-04	2.43E-09	177.3	171.4	157.5	0.919
4	VL_K095aQ	406.1	1.49E+05	3.21E-04	2.16E-09	179.2	174.8	161.2	0.922
4	VL_K095aY	438.6	1.35E+05	4.46E-04	3.30E-09	184.6	176.5	158.1	0.896
4	VL_K095aS	410.9	1.41E+05	3.98E-04	2.82E-09	178.2	173	156.7	0.906
4	VL_K095aW	431.4	1.31E+05	1.20E-03	9.11E-09	174.9	164.8	124.1	0.753
4	VL_N095bA	413.5	1.43E+05	2.05E-04	1.43E-09	176.8	172.1	162.8	0.946
4	VL_N095bK	408.6	1.27E+05	1.84E-04	1.45E-09	168.1	160.6	152.7	0.951
4	VL_N095bQ	403	1.36E+05	2.29E-04	1.67E-09	170.1	165	155.3	0.941
4	VL_N095bW	397	1.45E+05	1.91E-04	1.31E-09	170.9	167.3	158.8	0.949
4	VL_N095bS	423.4	1.42E+05	1.92E-04	1.35E-09	181.1	175.7	166.7	0.949
4	VL_N095bL	418.8	1.37E+05	1.97E-04	1.44E-09	177.5	171.6	162.6	0.948

Figure 23

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
4	VL_N095bD	424.5	1.48E+05	2.81E-04	1.90E-09	185.8	180.7	168	0.930
4	VL_N095bY	424.2	1.31E+05	2.87E-04	2.18E-09	170.2	163	151.3	0.928
4	VL_N095bH	395.5	1.40E+05	1.97E-04	1.40E-09	169.2	164.8	156.3	0.948
4	VL_L096A	407.8	1.13E+05	4.70E-04	4.14E-09	161.5	150.8	134.4	0.891
4	VL_L096K	403.1	1.22E+06	1.25E-01	1.02E-07	88.7	67.8	10.2	0.150
4	VL_L096Q	409.3	1.15E+05	2.16E-04	1.88E-09	161.7	152.4	144	0.945
4	VL_L096Y	416.2	1.18E+05	1.32E-03	1.11E-08	171.4	158.9	117	0.736
4	VL_L096S	419.5	1.09E+05	3.64E-04	3.34E-09	163.1	151.1	137.9	0.913
4	VL_L096W	410.5	1.27E+05	2.88E-03	2.27E-08	166.1	152.6	79.5	0.521
4	VL_L096D	-2.8	8.50E+04	1.28E-03	1.51E-08	7.5	6.5	4.6	0.708
4	VL_L096H	410.3	1.26E+05	1.69E-04	1.34E-09	173.8	166.5	159	0.955
4	VL_V097A	408.9	1.36E+05	2.30E-04	1.69E-09	174.3	169.1	159.1	0.941
4	VL_V097K	426.9	1.01E+05	4.58E-04	4.54E-09	163.4	147.6	132	0.894
4	VL_V097Q	427.8	1.24E+05	3.45E-04	2.79E-09	175.9	166.6	152.8	0.917
4	VL_V097W	416.4	1.06E+05	9.69E-04	9.18E-09	163.2	148.6	118.5	0.797
4	VL_V097L	421.7	1.19E+05	4.81E-04	4.03E-09	172.4	162.5	144.5	0.889
4	VL_V097D	440	1.44E+05	2.45E-04	1.71E-09	190.4	185.1	173.5	0.937

Figure 24

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
4	VL_V097Y	427.1	8.66E+04	7.91E-04	9.13E-09	158.5	136	112.9	0.830
4	VL_V097H	440.1	1.07E+05	4.14E-04	3.87E-09	174.5	159.9	144.5	0.904
4	VL_N089A	420	9.54E+04	6.32E-04	6.62E-09	57.7	52.5	44.9	0.855
4	VL_N089K	450.3	8.69E+04	1.09E-03	1.26E-08	154.6	132.1	102.4	0.775
4	VL_N089Q	446.1	1.22E+05	5.22E-04	4.27E-09	184.9	174.1	153.4	0.881
4	VL_N089W	419.9	9.00E+04	6.41E-03	7.12E-08	115.9	82	28.6	0.349
4	VL_N089S	408.9	1.34E+05	2.05E-04	1.53E-09	174.7	169	160	0.947
4	VL_N089L	425.2	1.49E+05	2.02E-04	1.36E-09	186.4	182.5	172.7	0.946
4	VL_N089D	458.8	5.19E+04	5.50E-04	1.06E-08	144.6	101.1	88.7	0.877
4	VL_N089Y	435.4	1.21E+05	8.81E-04	7.28E-09	168.5	157.2	127.4	0.810
4	VL_S090K	411.5	8.16E+04	1.03E-07	1.27E-12	7.7	7.8	8	1.026
4	VL_K095aH	447.6	1.32E+05	4.73E-04	3.59E-09	190.2	181.6	161.8	0.891
4	Parent clone	447	1.42E+05	1.82E-04	1.28E-09	193.4	188	178.9	0.952
4	VL_K051W	489.9	1.28E+05	2.16E-04	1.69E-09	207.5	198.1	187.2	0.945
4	VL_N052Q	434.8	1.26E+05	2.01E-04	1.59E-09	184.6	176.5	167.3	0.948
5	VH_W034Y	477.5	1.55E+05	5.98E-04	3.87E-09	198.1	191.4	165.8	0.866

Figure 25

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
5	VH_G026Q	489.2	1.67E+05	1.77E-04	1.06E-09	213.7	210	200.6	0.955
5	VH_S035aL	504.6	8.75E+04	5.54E-04	6.33E-09	159.3	136.9	120.1	0.877
5	VH_G027A	439.9	1.68E+05	1.63E-04	9.70E-10	192.2	189.3	181.4	0.958
5	VH_S028D	520.7	1.68E+05	1.94E-04	1.15E-09	232.6	227.9	217	0.952
5	VH_S028Q	482.1	1.67E+05	1.82E-04	1.09E-09	212.9	209.5	199.9	0.954
5	VH_I051Q	508.6	1.48E+05	1.91E-04	1.29E-09	205.4	198.8	189.2	0.952
5	VH_I051W	494.9	1.50E+05	2.35E-04	1.57E-09	205.8	199.7	188.3	0.943
5	VH_I051S	477.1	1.63E+05	2.03E-04	1.24E-09	206.2	202.4	192.2	0.950
5	VH_I051L	489.8	1.70E+05	1.70E-04	1.00E-09	211.1	207.8	198.8	0.957
5	VH_I051D	51.2	1.52E+05	5.21E-04	3.43E-09	19.5	17.9	15.8	0.883
5	VH_N060H	497	1.72E+05	1.54E-07	8.94E-10	220	217.1	208.4	0.960
5	VH_I051H	366.2	1.59E+05	2.26E-04	1.42E-09	153.1	149.2	140.9	0.944
5	VH_Y052A	495.6	1.42E+05	8.84E-04	6.22E-09	212.5	202.4	164.5	0.813
5	VH_Y052K	475.6	1.27E+05	1.51E-03	1.19E-08	187.4	174.3	122.9	0.705
5	VH_Y052Q	460.9	1.38E+05	8.48E-04	6.13E-09	196.5	186.9	153.3	0.820
5	VH_Y052W	484.1	1.68E+05	1.36E-04	8.13E-10	210.2	207.1	199.7	0.964
5	VH_Y052S	484.1	1.43E+05	9.42E-04	6.60E-09	209.1	199.5	160	0.802

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Figure 26

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
5	VH_Y052L	512.7	1.54E+05	1.46E-04	9.47E-10	221.9	216.3	208.1	0.962
5	VH_Y052D	526.4	1.47E+05	6.08E-04	4.13E-09	234.6	225.3	195	0.866
5	VH_Y052H	508.9	1.57E+05	2.59E-04	1.64E-09	219.7	214.5	201.1	0.938
5	VH_H053A	528.2	1.52E+05	2.39E-04	1.57E-09	224.6	218.1	205.4	0.942
5	VH_H053L	511.9	1.51E+05	2.80E-04	1.85E-09	217.3	211.1	197	0.933
5	VH_H053Q	507.3	1.61E+05	2.00E-04	1.24E-09	220.6	216.3	205.5	0.950
5	VH_H053Y	518.6	1.60E+05	1.68E-04	1.05E-09	224.4	219.4	210	0.957
5	VH_H053S	519.4	1.56E+05	2.23E-04	1.43E-09	223.8	217.9	205.9	0.945
5	VH_H053W	529.4	1.62E+05	1.68E-04	1.04E-09	230.2	225.6	215.9	0.957
5	VH_H053D	549.6	1.42E+05	3.73E-04	2.63E-09	238.4	228.7	209	0.914
5	VH_H053K	505.8	1.55E+05	1.66E-04	1.07E-09	210.4	205.7	196.8	0.957
5	VH_S054A	539.2	1.68E+05	1.38E-04	8.22E-10	238.3	234.5	226	0.964
5	VH_S054L	515.3	1.68E+05	1.49E-04	8.89E-10	226.1	222.6	214	0.961
5	VH_S054D	489.1	1.43E+05	3.00E-04	2.10E-09	214.6	206.8	192.2	0.929
5	VH_S054Y	540.7	2.24E+05	1.38E-04	6.17E-10	249	248.9	239.7	0.963
5	VH_S054Q	531.1	1.73E+05	1.67E-04	9.70E-10	234.8	231.5	221.5	0.957
5	VH_S054W	532.2	2.69E+05	1.36E-04	5.06E-10	249.8	251	241.7	0.963

Figure 27

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
5	VH_S054H	549.4	1.91E+05	1.45E-04	7.57E-10	248.7	246.5	237.1	0.962
5	VH_S054K	518.7	1.58E+05	3.20E-04	2.03E-09	218.3	213.6	197.2	0.923
5	VH_G055A	548.7	1.66E+05	1.52E-04	9.15E-10	242.6	238.4	228.9	0.960
5	VH_G055K	536.2	1.45E+05	1.65E-04	1.14E-09	222.4	216	206.8	0.957
5	VH_G055Q	544.4	1.64E+05	1.61E-04	9.79E-10	238.8	234.4	224.7	0.959
5	VH_G055W	555.2	1.56E+05	1.81E-04	1.16E-09	234.6	229.1	218.5	0.954
5	VH_G055S	535	1.66E+05	1.58E-04	9.52E-10	235.4	231.3	222	0.960
5	VH_G055L	550	1.62E+05	1.53E-04	9.45E-10	240.3	235.6	226.2	0.960
5	VH_G055D	2.8	1.23E+02	1.74E-03	1.41E-01	0.1	-1	-0.6	0.600
5	VH_G055Y	531	1.60E+05	1.60E-04	1.00E-09	229.1	224.8	215.6	0.959
5	VH_G055H	556.9	1.60E+05	1.53E-04	9.59E-10	242.1	237.3	228	0.961
5	VH_N056A	587.1	1.59E+05	2.04E-04	1.28E-09	255.6	249.9	237.2	0.949
5	VH_N056K	569.3	1.39E+05	5.09E-04	3.67E-09	232.2	222.5	196.9	0.885
5	VH_N056Q	528.2	1.58E+05	1.97E-04	1.25E-09	231.2	226.5	215.3	0.951
5	VH_N056W	551.8	2.16E+05	1.42E-04	6.59E-10	253	253	243.5	0.962
5	VH_N056S	578.6	1.62E+05	2.31E-04	1.42E-09	254.7	249.4	235.4	0.944
5	VH_N056L	562.5	1.80E+05	1.53E-04	8.49E-10	252.4	249.7	239.8	0.960

Figure 28

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
5	VH_N056D	547.5	1.55E+05	1.41E-04	9.11E-10	245.3	239.6	230.9	0.964
5	VH_N056Y	566.6	1.85E+05	1.44E-04	7.78E-10	255.2	253.6	244	0.962
5	VH_N056H	598.7	1.83E+05	1.23E-04	6.74E-10	268	265.5	256.6	0.966
5	VH_N058A	594	1.67E+05	3.39E-04	2.03E-09	262.3	257.1	236.4	0.919
5	VH_N058L	581.7	1.52E+05	1.86E-04	1.23E-09	250.1	243.3	231.8	0.953
5	VH_N058D	528.4	1.49E+05	2.18E-04	1.46E-09	227.5	221.6	209.7	0.946
5	VH_N058Y	568.6	1.48E+05	7.03E-04	4.75E-09	242	233.3	197.5	0.847
5	VH_N058H	569.5	1.31E+05	1.20E-03	9.15E-09	233.9	219.6	166.1	0.756
5	VH_Y059A	192.3	1.88E+05	1.94E-04	1.03E-09	90	89.4	85	0.951
5	VH_Y059K	577.4	1.51E+05	2.14E-04	1.42E-09	247.6	241.2	228.5	0.947
5	VH_Y059Q	604.4	1.67E+05	2.01E-04	1.20E-09	268.4	263.5	250.2	0.950
5	VH_Y059W	587.3	1.61E+05	2.05E-04	1.27E-09	257.8	252.4	239.6	0.949
5	VH_Y059S	596.1	1.72E+05	1.87E-04	1.09E-09	267.1	263.3	250.8	0.953
5	VH_Y059L	598.9	1.67E+05	1.98E-04	1.18E-09	267	262.7	249.7	0.951
5	VH_Y059D	600.1	1.79E+05	1.71E-04	9.57E-10	275.3	272.3	260.5	0.957
5	VH_Y059H	609.9	1.67E+05	1.76E-04	1.05E-09	272	267.3	255.2	0.955
5	VH_N060A	618.5	1.76E+05	1.63E-04	9.24E-10	278.1	274.7	263.1	0.958

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Figure 29

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
5	VH_N060K	613.1	1.67E+05	1.78E-04	1.06E-09	273.2	269	256.9	0.955
5	VH_N060Q	623.1	1.77E+05	1.53E-04	8.66E-10	281.5	278.2	267.1	0.960
5	VH_N060W	605.3	1.77E+05	1.53E-04	8.62E-10	273.6	270.6	259.9	0.960
5	VH_N060L	600.4	1.82E+05	1.38E-04	7.58E-10	272.5	270.1	260.2	0.963
5	VH_N060D	623.6	1.87E+05	1.62E-04	8.66E-10	287.8	285.5	273.5	0.958
5	VH_N060Y	622.3	1.81E+05	1.33E-04	7.33E-10	282.8	280.3	270.2	0.964
5	Parent clone	623.1	1.70E+05	1.66E-04	9.79E-10	278.3	274.1	262.4	0.957

5	VL_S034K	399.8	2.40E+04	3.73E-07	1.56E-11	5	0.9	3.3	3.667
5	VL_G050A	407.9	1.45E+05	1.86E-04	1.28E-09	172.8	167.2	159.4	0.953
5	VL_G050K	392.1	7.58E+04	6.76E-04	8.92E-09	121	99.4	84.9	0.854
5	VL_G050Q	403.2	9.54E+04	2.72E-04	2.85E-09	141.9	126.2	118.1	0.936
5	VL_G050W	393.6	7.54E+04	1.79E-04	2.38E-09	138.1	114.9	110	0.957
5	VL_G050S	401.2	1.35E+05	2.13E-04	1.58E-09	163.5	156.9	148.6	0.947
5	VL_Q024D	419	1.51E+05	1.46E-04	9.66E-10	181.1	176.8	170	0.962
5	VL_Q024S	390.5	1.46E+05	1.39E-04	9.52E-10	166.6	162.3	156.4	0.964
5	VL_Q024H	392.2	1.44E+05	1.44E-04	9.97E-10	166.3	161.5	155.5	0.963

Figure 30

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
6	VL_G025A	383.7	1.17E+05	1.64E-04	1.40E-09	154.6	145.5	139.7	0.960
6	VL_N030A	402.5	1.74E+05	2.95E-04	1.70E-09	177.4	175	162.5	0.929
6	VL_G050H	385.3	9.19E+04	2.67E-04	2.90E-09	141.6	126	118	0.937
6	VL_K051D	400.9	6.14E+04	5.79E-04	9.42E-09	151.1	114.4	100.2	0.876
6	VL_K051H	394.9	1.34E+05	9.78E-05	7.30E-10	171.4	165.4	161.1	0.974
6	VL_N052K	407.2	1.01E+05	1.92E-04	1.90E-09	156.9	142.2	135.7	0.954
6	VL_N052W	403	1.21E+05	2.75E-04	2.27E-09	162.7	153.2	143.2	0.935
6	VL_N052S	382.7	1.42E+05	1.81E-04	1.27E-09	163.3	158.5	151.3	0.955
6	VL_N052L	398	1.06E+05	1.75E-04	1.65E-09	161.9	148.3	142	0.958
6	VL_N052D	398.7	1.50E+05	1.43E-04	9.50E-10	176	172.1	165.7	0.963
6	VL_N052Y	410.3	1.30E+05	2.01E-04	1.55E-09	168.2	160.7	152.7	0.950
6	VL_N052H	413.5	1.27E+05	1.90E-04	1.49E-09	169.3	160.9	153.4	0.953
6	VL_N053A	411.7	1.36E+05	2.23E-04	1.64E-09	172.2	165.6	156.6	0.946
6	VL_N053K	398.1	1.14E+05	2.13E-04	1.88E-09	152.2	142.3	135	0.949
6	VL_N053Q	375.2	1.41E+05	1.93E-04	1.37E-09	159.3	154.6	147.1	0.951
6	VL_N053W	399.4	1.01E+05	3.18E-04	3.14E-09	148.4	134.9	125	0.927
6	VL_N053S	390.8	1.51E+05	1.71E-04	1.14E-09	167.7	164.3	157	0.956

Figure 31

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
6	VL_N053L	411.2	1.32E+05	2.32E-04	1.76E-09	171.9	164.4	155.1	0.943
6	VL_N053D	418.1	1.64E+05	1.59E-04	9.69E-10	188.6	185.6	178.1	0.960
6	VL_N053H	391.1	1.26E+05	2.07E-04	1.65E-09	158.4	151.1	143.5	0.950
6	VL_R054A	401.5	1.45E+05	1.39E-04	9.54E-10	174	169.2	163	0.963
6	VL_R054K	428.1	1.46E+05	1.46E-04	9.99E-10	183.4	178	171.2	0.962
6	VL_R054Q	421.5	1.49E+05	1.33E-04	8.92E-10	182.9	178.2	172	0.965
6	VL_R054W	405.7	1.24E+05	1.18E-04	9.49E-10	165.7	157.6	152.6	0.968
6	VL_R054L	422.4	1.49E+05	1.26E-04	8.45E-10	184.6	179.6	173.6	0.967
6	VL_R054Y	405.2	1.42E+05	1.11E-04	7.84E-10	174.1	169.2	164.2	0.970
6	VL_R054H	413.7	1.45E+05	1.58E-04	1.09E-09	177	171.7	164.7	0.959
6	VL_P055A	395.2	1.37E+05	1.41E-04	1.03E-09	168.6	163.2	157.2	0.963
6	VL_P055K	418.4	1.22E+05	1.55E-04	1.27E-09	169.2	159.8	153.5	0.961
6	VL_P055L	392.7	1.40E+05	1.44E-04	1.03E-09	166.5	161.5	155.5	0.963
6	VL_P055D	412.4	1.41E+05	1.54E-04	1.09E-09	178	172.2	165.5	0.961
6	VL_P055Y	423.8	1.31E+05	1.59E-04	1.22E-09	175.1	167.1	160.3	0.959
6	VL_S056L	395.4	1.48E+05	1.38E-04	9.36E-09	169.6	165.6	159.6	0.964
6	VL_S056D	382.4	1.56E+05	1.40E-04	9.00E-10	168.5	165.5	159.4	0.963

Figure 32

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
6	VL_S056Y	417.4	1.41E+05	1.38E-04	9.79E-10	174.7	169.2	163	0.963
6	VL_S056W	372.2	1.36E+05	1.38E-04	1.02E-09	154.2	149.2	143.8	0.964
6	VL_S056H	428.9	1.45E+05	1.36E-04	9.39E-10	181.9	176.8	170.3	0.963
6	VL_S056K	413.5	1.38E+05	1.40E-04	1.02E-09	171.5	165.9	159.8	0.963
6	VL_Y031L	400.6	1.21E+05	2.56E-02	2.11E-07	106.1	63.5	6.4	0.101
6	VH_W035L	430.2	1.17E+05	1.15E-04	9.82E-10	151.6	142.6	138.1	0.968
6	VH_W035D	84.2	8.74E+04	5.11E-04	5.85E-09	27.7	24.3	21.6	0.889
6	VH_W035H	415.3	1.18E+05	1.93E-04	1.63E-09	162.4	153.1	145.7	0.952
6	VH_S035aA	427.8	1.48E+05	1.26E-04	8.48E-10	180.4	175.8	169.8	0.966
6	VH_S035aD	432.7	1.07E+05	9.84E-04	9.23E-09	167.4	151.1	120.2	0.795
6	VH_S035aY	405.1	4.28E+04	6.71E-07	1.57E-11	5.9	3.7	6.2	1.676
6	VH_S035aQ	393.7	1.58E+05	2.15E-02	1.36E-07	132	90.4	7	0.077
6	VH_S035aW	415.5	5.61E+04	2.71E-06	4.83E-11	4.7	3.5	5.7	1.629
6	VH_S035aH	415.5	9.64E+04	3.19E-02	3.31E-07	86.2	42	6.4	0.152
6	VH_S035aK	419.7	7.61E+04	7.25E-08	9.53E-13	7.3	7.4	7.5	1.014
6	VH_E050A	428.8	1.51E+05	3.53E-03	2.33E-08	177.7	165.1	74.2	0.449
6	VH_E050K	391.5	2.15E+05	2.74E-07	1.27E-12	3.7	3.8	5.8	1.526

Figure 33

Run #	Amino acid Substitution	Capture level	ka (1/Ms)	kd (1/s)	KD (M)	Rmax (RU)	binding early	binding late	binding late/ binding early
6	VH_E050Q	440.4	1.56E+05	5.21E-03	3.33E-08	181.1	163.4	51.7	0.316
6	VH_E050W	434.5	1.59E+05	1.83E-04	1.15E-08	6.1	12.8	5.9	0.461
6	VH_T057A	424.4	1.50E+05	1.94E-04	1.29E-09	181.6	177.1	168.5	0.951
6	VH_T057K	418.5	1.31E+05	1.91E-04	1.46E-09	169.2	161.8	154.1	0.952
6	VH_T057Q	418.3	1.53E+05	1.30E-04	8.52E-10	180.9	177.3	171.1	0.965
6	VH_T057W	406.2	1.52E+05	1.33E-04	8.73E-10	175.6	172.2	166.1	0.965
6	VH_T057S	441.8	1.53E+05	1.55E-04	1.01E-09	190.6	186.3	178.7	0.959
6	VH_T057L	420.7	1.52E+05	1.64E-04	1.08E-09	181.9	177.9	170.2	0.957
6	VH_T057D	433.8	1.65E+05	1.06E-04	6.40E-10	195.2	192.6	187	0.971
6	VH_T057Y	423	1.51E+05	1.50E-04	9.96E-10	182	178.1	171.2	0.961
6	VH_T057H	417.9	1.45E+05	2.02E-04	1.39E-09	177.2	172.5	163.8	0.950
6	VH_N058K	408.4	1.24E+05	7.45E-04	6.01E-09	161.5	151.7	127.3	0.839
6	VH_N058Q	423	1.45E+05	1.11E-04	7.65E-10	180.7	176.1	170.7	0.969
6	VH_N058W	412.4	1.34E+05	4.73E-04	3.52E-09	171.3	164.4	146.8	0.893
6	VH_G098L	408.7	4.32E+04	5.30E-07	1.23E-11	6.1	3.8	6.6	1.737
6	Parent clone	434.6	1.50E+05	1.60E-04	1.07E-09	186.1	181.8	174.3	0.959

Figure 34A

ANTIBODY	Heavy Chain	Light Chain
ANTIBODY 4	Wild type (WT)	Wild type (WT)
ANTIBODY 1	S54F	WT
ANTIBODY 2	S54Y	WT
ANTIBODY 3	S54W	WT
ANTIBODY 6	N56W	WT
ANTIBODY 7	S54F + N56F	WT
ANTIBODY 8	S54Y + N56F	WT
ANTIBODY 9	S54W + N56F	WT
ANTIBODY 10	S54F + N56Y	WT
ANTIBODY 11	S54Y + N56Y	WT
ANTIBODY 12	S54W + N56Y	WT
ANTIBODY 13	S54F + N56W	WT
ANTIBODY 14	S54Y + N56W	WT
ANTIBODY 15	S54W + N56W	WT
ANTIBODY 16	WT	D92S
ANTIBODY 20	S35aA	WT
ANTIBODY 21	W35L	WT
ANTIBODY 22	Y52W	WT
ANTIBODY 23	N56H	WT
ANTIBODY 24	N56L	WT
ANTIBODY 25	T57D	WT
ANTIBODY 26	N58Q	WT
ANTIBODY 27	N60Y	WT
ANTIBODY 29	WT	G50S
ANTIBODY 30	WT	K51A
ANTIBODY 31	WT	K51H

Figure 34B

ANTIBODY	Heavy Chain	Light Chain
ANTIBODY 32	WT	K51L
ANTIBODY 33	WT	R54L
ANTIBODY 34	WT	R54Q
ANTIBODY 35	WT	R54Y
ANTIBODY 36	Y102S	WT
ANTIBODY 37	Y102L	WT
ANTIBODY 38	Y102A	WT
ANTIBODY 39	Y102H	WT
ANTIBODY 40	S54F + N56W	K51H
ANTIBODY 41	S54Y + N56W	K51H
ANTIBODY 42	S54W + N56W	K51H
ANTIBODY 43	S54F + N56W	R54Y
ANTIBODY 44	S54Y + N56W	R54Y
ANTIBODY 45	S54W + N56W	R54Y
ANTIBODY 46	S54W+N60Y	WT
ANTIBODY 47	N56W+N60Y	WT
ANTIBODY 48	S54W+N56W+N60Y	WT
ANTIBODY 49	WT	K51H + R54L
ANTIBODY 50	WT	K51H + R54Y
ANTIBODY 51	WT	N30S
ANTIBODY 52	S54Y + N56W	N30S
ANTIBODY 53	S54Y + N56Y	N30S
ANTIBODY 54	WT	D92E
ANTIBODY 55	S54Y + N56W	D92E
ANTIBODY 56	S54Y + N56Y	D92E
ANTIBODY 57	I82aS	WT
ANTIBODY 58	S54Y + N56W + I82aS	WT
ANTIBODY 59	I82aS	N30S
ANTIBODY 60	S54Y + N56W + I82aS	N30S

Figure 34C

ANTIBODY	Heavy Chain	Light Chain
ANTIBODY 61	I82aS	D92E
ANTIBODY 62	S54Y + N56Y + I82aS	D92E
ANTIBODY 63	S54Y + N56Y + I82aS	WT
ANTIBODY 64	S54Y + N56Y + I82aS	N30S
ANTIBODY 65	S54Y + N56Y + I82aS	D92E
ANTIBODY 66	S54Y + N56Y + I82aS	S93L
ANTIBODY 67	S54Y + N56Y + I82aS	S93E
ANTIBODY 68	S54Y + N56Y + I82aS	S93F
ANTIBODY 69	S54Y + N56Y + I82aS	N30S+92E
ANTIBODY 70	S54Y + N56Y + I82aS	N30S+S93L
ANTIBODY 71	S54Y + N56Y + I82aS	N30S+S93E
ANTIBODY 72	S54Y + N56Y + I82aS	N30S+S93F
ANTIBODY 73	S54Y + N56Y	N30S
ANTIBODY 74	S54Y + N56Y	D92E
ANTIBODY 75	S54Y + N56Y	S93L
ANTIBODY 76	S54Y + N56Y	S93E
ANTIBODY 77	S54Y + N56Y	S93F
ANTIBODY 78	S54Y + N56Y	N30S+D92E
ANTIBODY 79	S54Y + N56Y	N30S+S93L
ANTIBODY 80	S54Y + N56Y	N30S+S93E
ANTIBODY 81	S54Y + N56Y	N30S+S93F

Figure 35

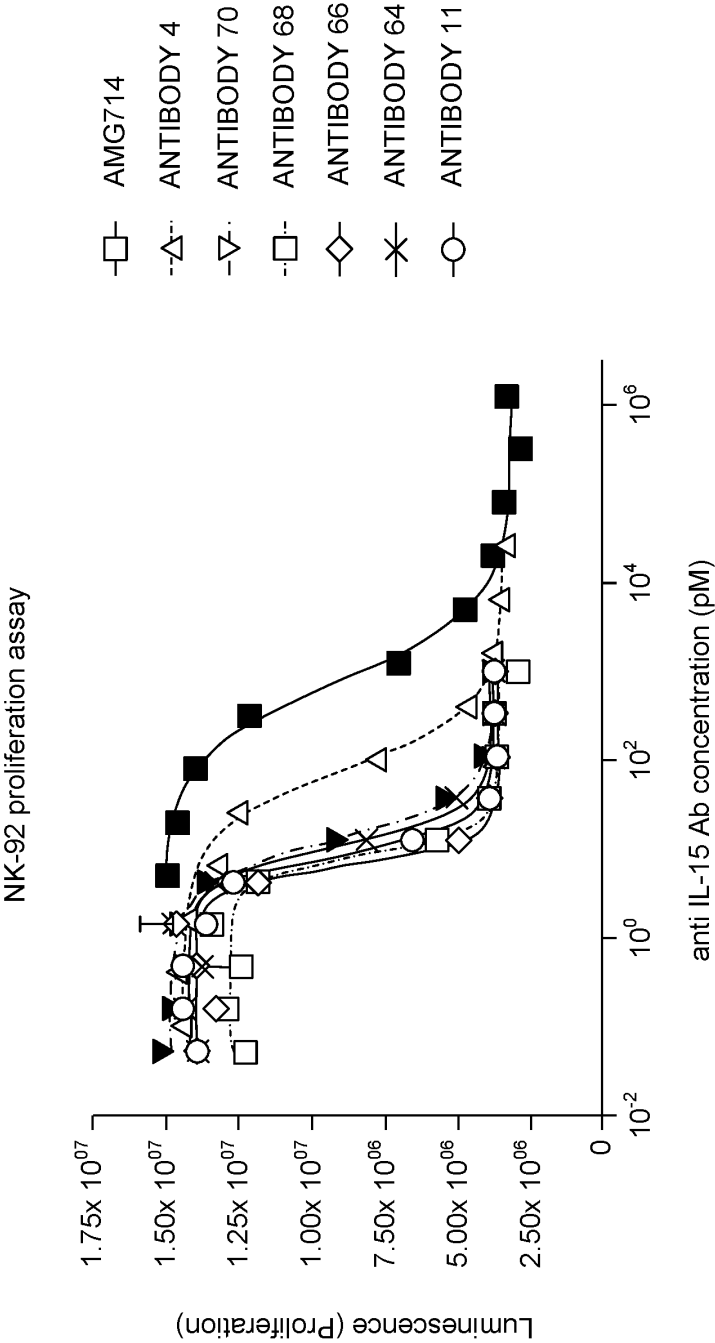


Figure 36

Sample	Ligand	ka (1/Ms)		kd (1/s)		KD (nM)	
Human IL-15 complex	ANTIBODY 70a	2.52e+05	2.61e+05	3.47e-05	3.75e-05	0.133	0.149
	ANTIBODY 70b	2.49e+05	2.54e+05	3.92e-05	3.89e-05	0.154	0.157
	ANTIBODY 70e	2.37e+05	2.47e+05	4.31e-05	4.58e-05	0.174	0.193
	ANTIBODY 70f	2.49e+05	2.60e+05	4.44e-05	4.32e-05	0.171	0.173
	ANTIBODY 4	1.48e+05	1.50e+05	9.43e-05	9.31e-05	0.630	0.628
	AMG714	2.09e+05	2.14e+05	3.98e-04	3.80e-04	1.86	1.82

Figure 37

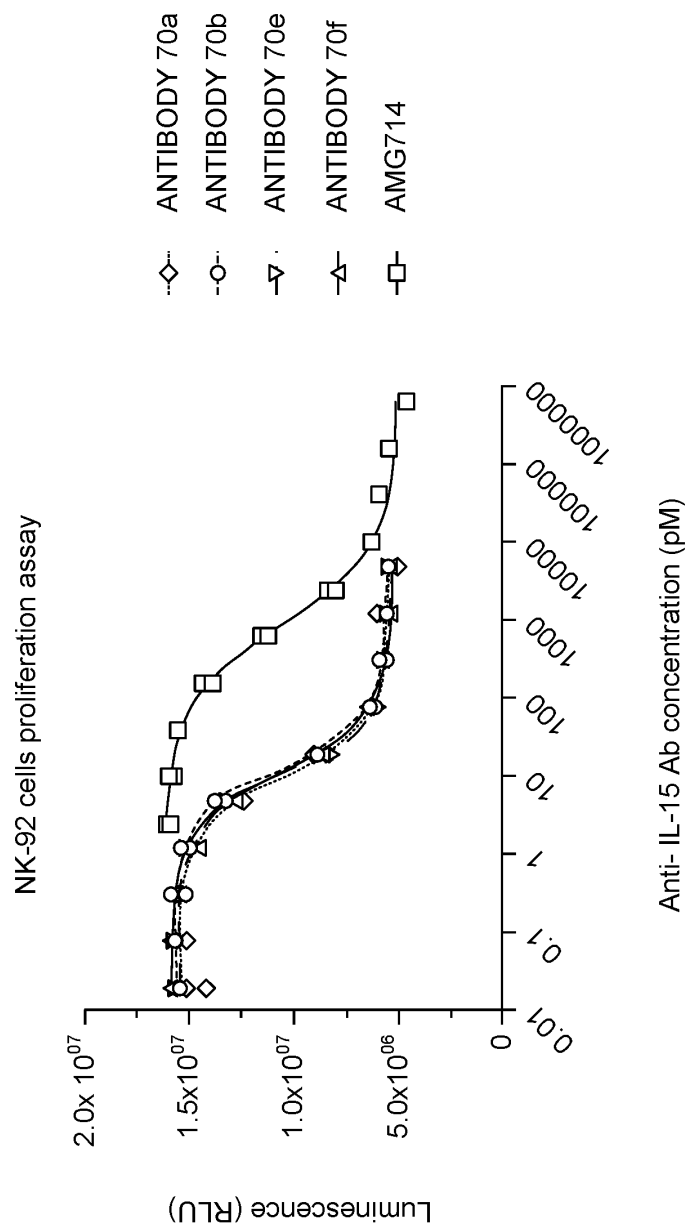


Figure 38

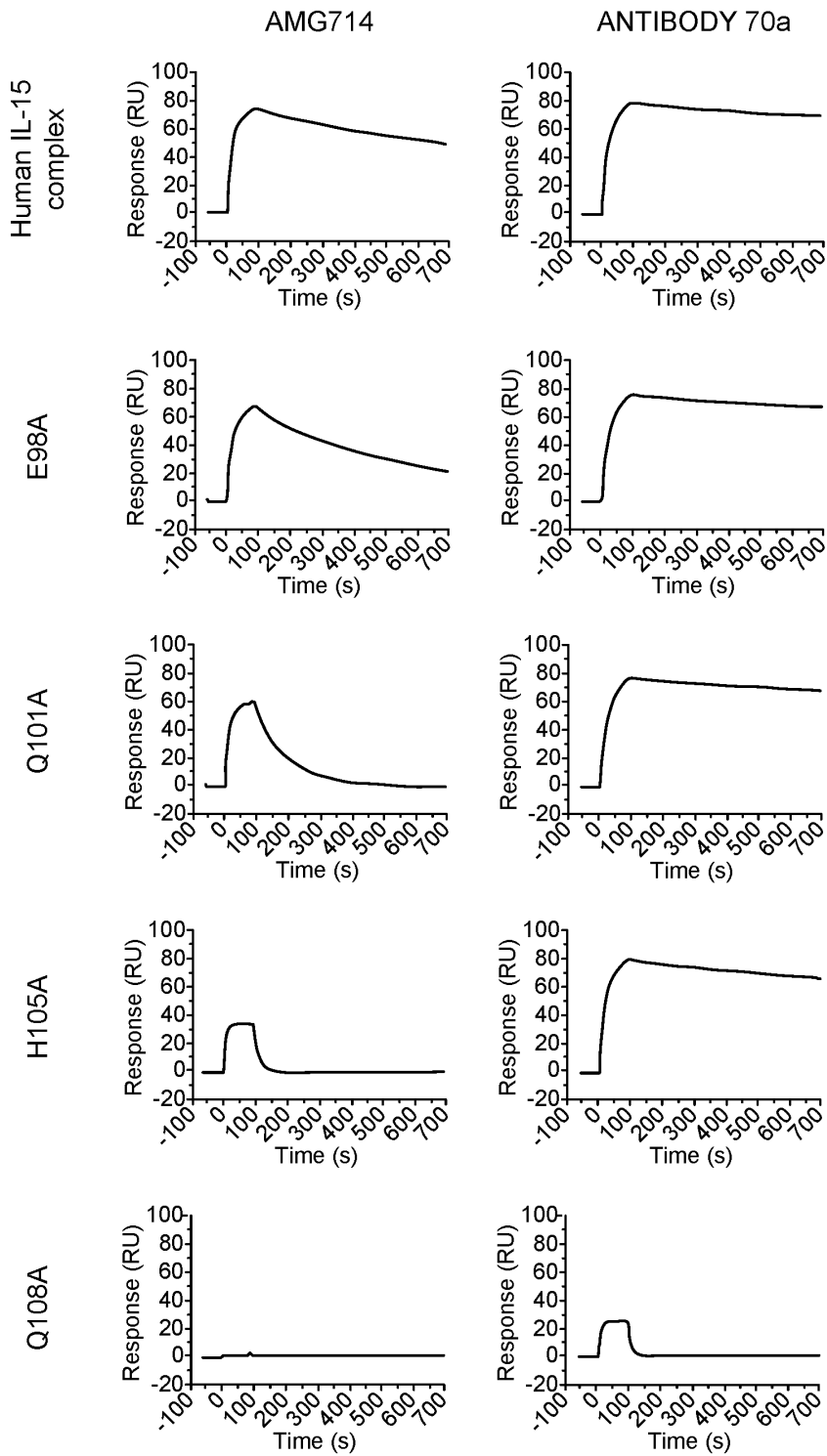


Figure 39B

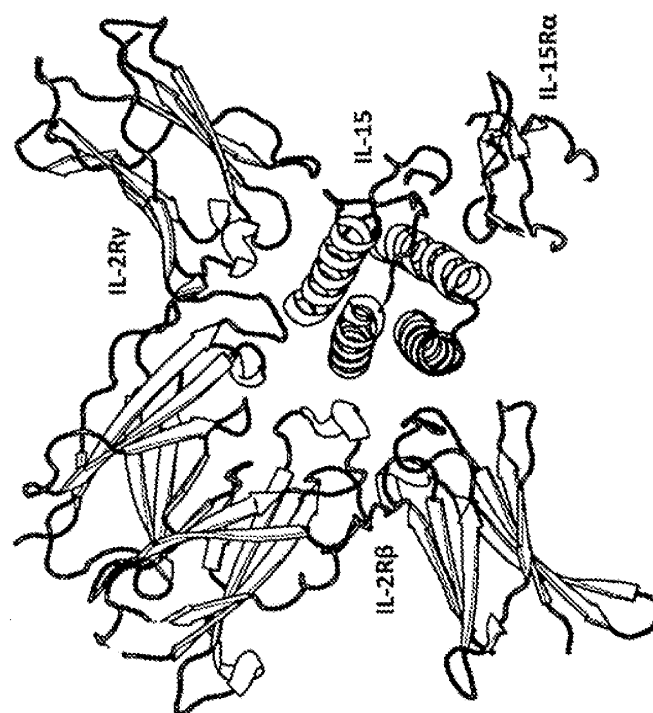


Figure 39A

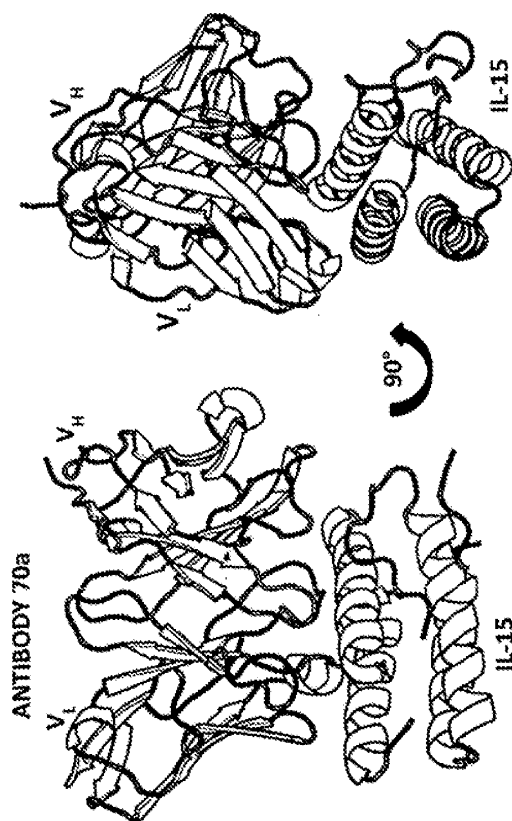


Figure 39E

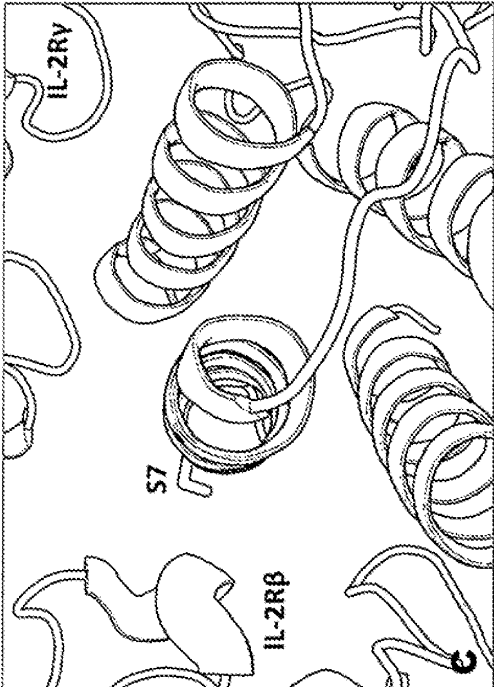


Figure 39C

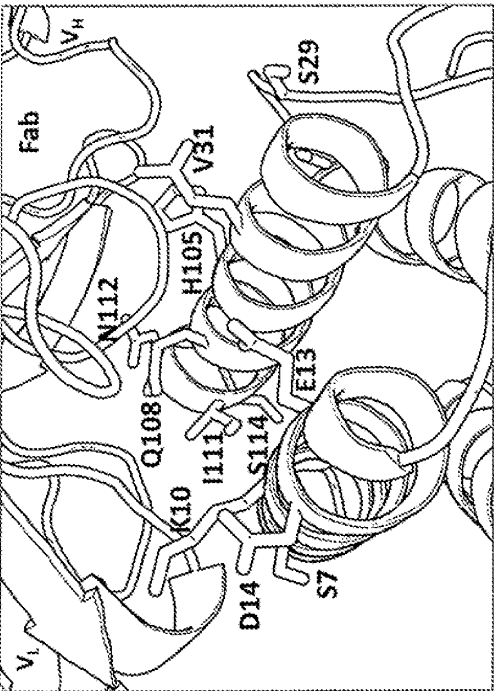


Figure 39D

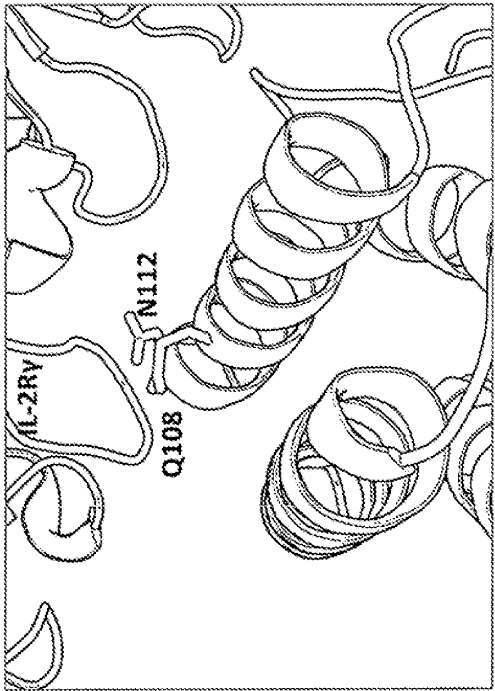


Figure 39H

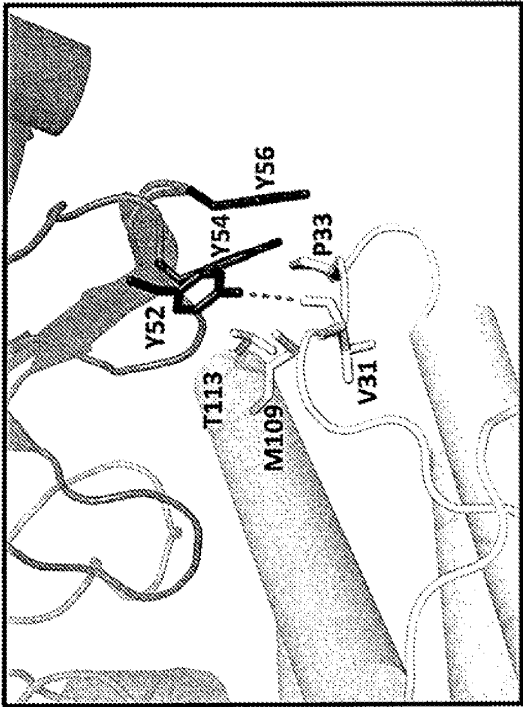


Figure 39G

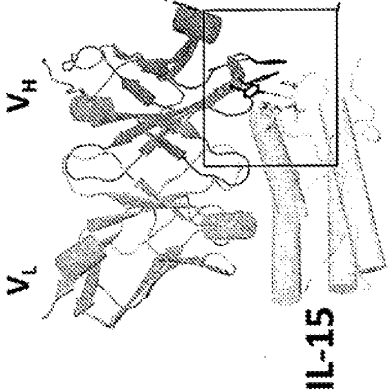


Figure 39F

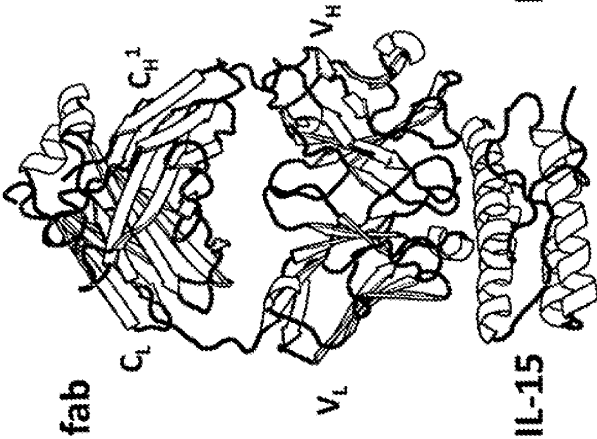


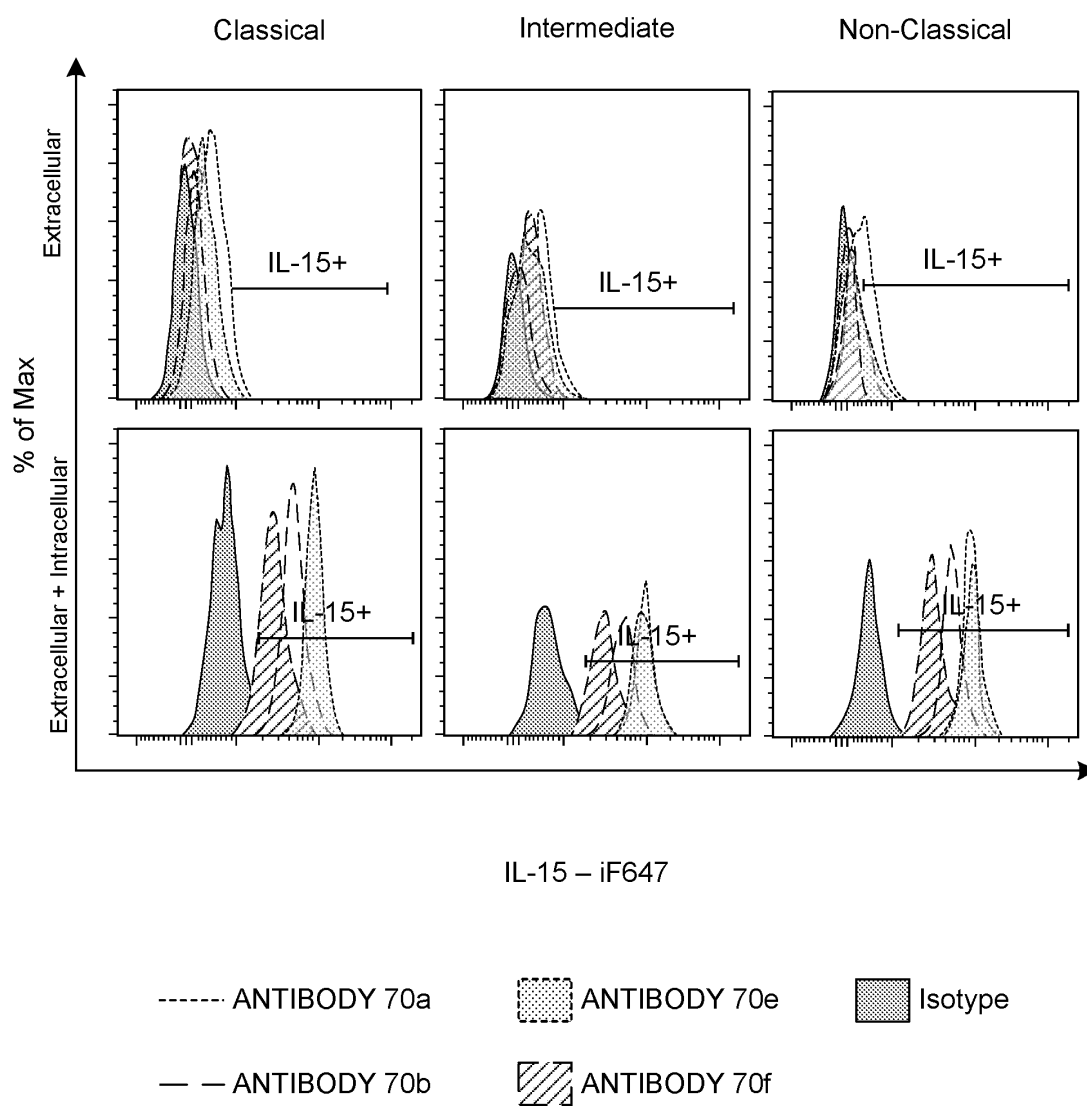
Figure 40

Figure 41

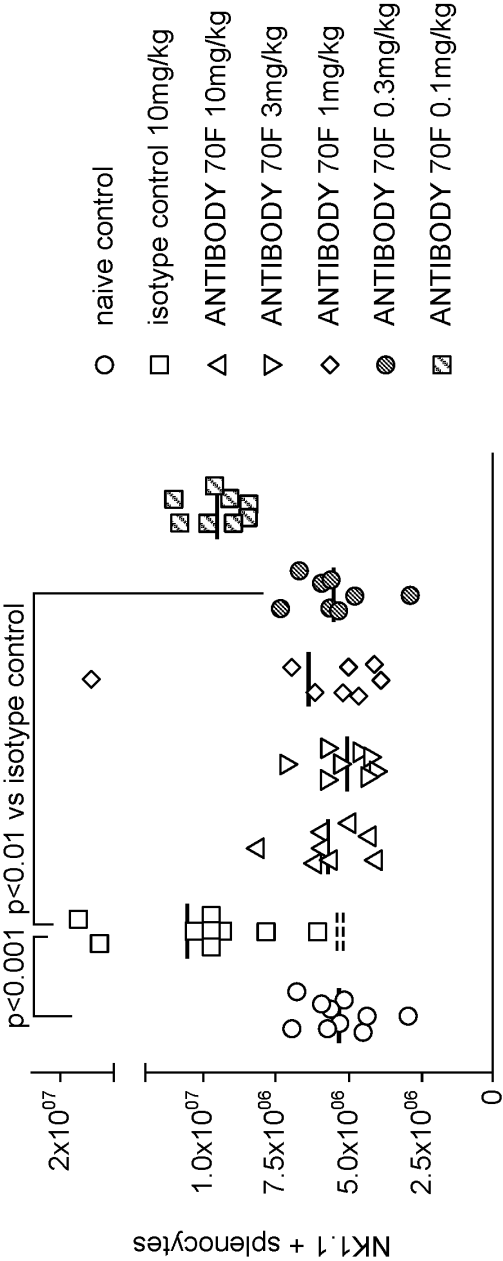


Figure 42

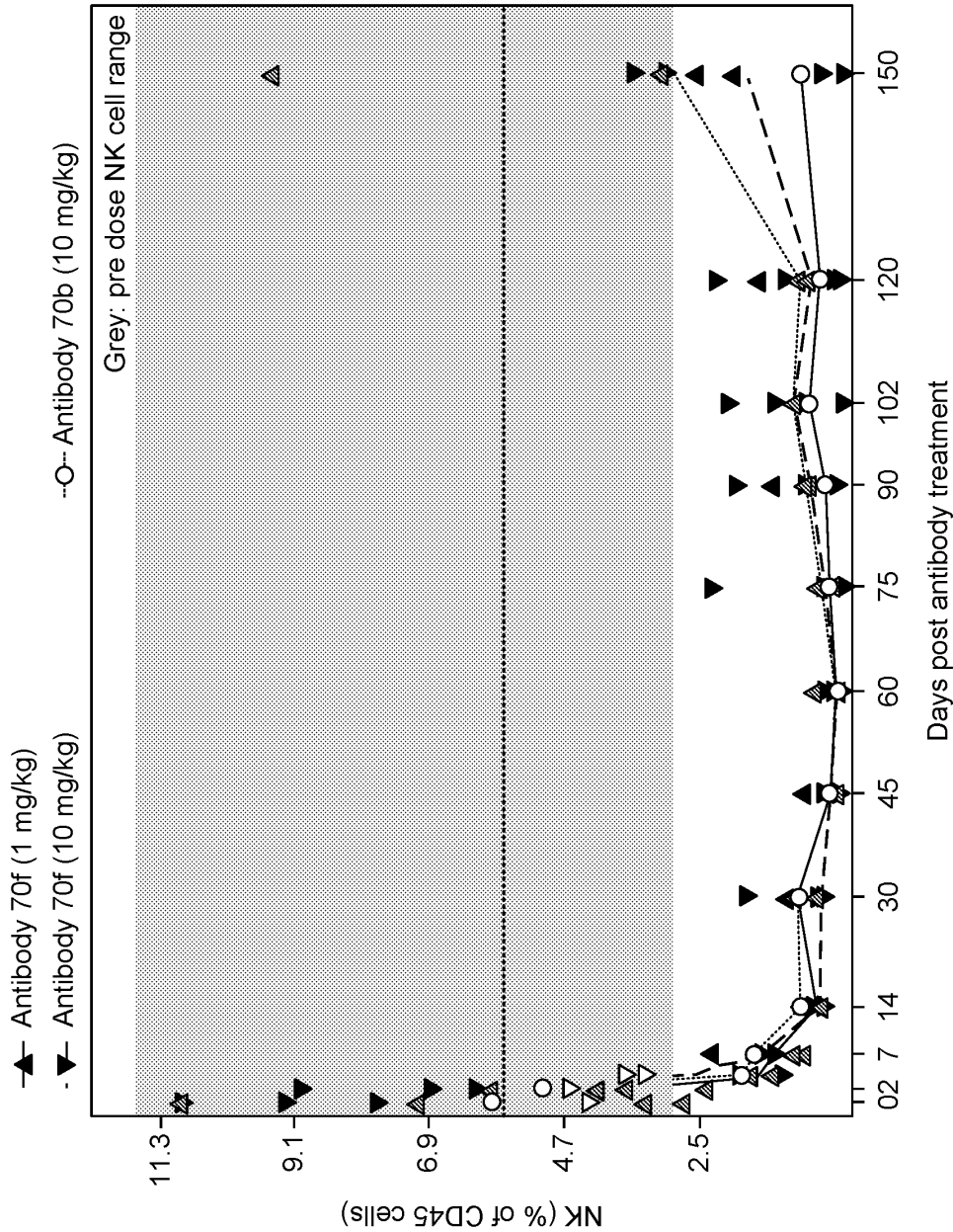


Figure 43A

H1	H2	H3
58	18 or 19	20
59	18 or 19	20
60	18 or 19	20
61	18 or 19	20
62	18 or 19	20
63	18 or 19	20
64	18 or 19	20
65	18 or 19	20
66	18 or 19	20
67	18 or 19	20
68	18 or 19	20
69	18 or 19	20
70	18 or 19	20
71	18 or 19	20
72	18 or 19	20
73	18 or 19	20
74	18 or 19	20
75	18 or 19	20
76	18 or 19	20
77	18 or 19	20
78	18 or 19	20
79	18 or 19	20
80	18 or 19	20
81	18 or 19	20
82	18 or 19	20
83	18 or 19	20
84	18 or 19	20
85	18 or 19	20
86	18 or 19	20
87	18 or 19	20
88	18 or 19	20
89	18 or 19	20
90	18 or 19	20
91	18 or 19	20
92	18 or 19	20
93	18 or 19	20
94	18 or 19	20
95	18 or 19	20
96	18 or 19	20
97	18 or 19	20
98	18 or 19	20

H1	H2	H3
99	18 or 19	20
100	18 or 19	20
101	18 or 19	20
102	18 or 19	20
103	18 or 19	20
104	18 or 19	20
105	18 or 19	20
106	18 or 19	20
107	18 or 19	20
108	18 or 19	20
109	18 or 19	20
110	18 or 19	20
111	18 or 19	20
112	18 or 19	20
113	18 or 19	20
114	18 or 19	20
115	18 or 19	20
116	18 or 19	20
117	18 or 19	20
118	18 or 19	20
119	18 or 19	20
120	18 or 19	20
121	18 or 19	20
122	18 or 19	20
123	18 or 19	20
124	18 or 19	20
125	18 or 19	20
126	18 or 19	20
127	18 or 19	20
128	18 or 19	20
129	18 or 19	20
130	18 or 19	20
131	18 or 19	20
132	18 or 19	20
133	18 or 19	20
134	18 or 19	20
135	18 or 19	20

Figure 43B

H1	H2	H3
453	136	20
453	137	20
453	138	20
453	139	20
453	140	20
453	141	20
453	142	20
453	143	20
453	144	20
453	145	20
453	146	20
453	147	20
453	148	20
453	149	20
453	150	20
453	151	20
453	152	20
453	153	20
453	154	20
453	155	20
453	156	20
453	157	20
453	158	20
453	159	20
453	160	20
453	161	20
453	162	20
453	163	20
453	164	20
453	165	20
453	166	20

H1	H2	H3
453	167	20
453	168	20
453	169	20
453	170	20
453	171	20
453	172	20
453	173	20
453	174	20
453	175	20
453	176	20
453	177	20
453	178	20
453	179	20
453	180	20
453	181	20
453	182	20
453	183	20
453	184	20
453	185	20
453	186	20
453	187	20
453	188	20
453	189	20
453	190	20
453	191	20
453	192	20
453	193	20
453	194	20
453	195	20
453	196	20
453	197	20

H1	H2	H3
453	198	20
453	199	20
453	200	20
453	201	20
453	202	20
453	203	20
453	204	20
453	205	20
453	206	20
453	207	20
453	208	20
453	209	20
453	210	20
453	211	20
453	212	20
453	213	20
453	214	20
453	215	20
453	216	20
453	217	20
453	218	20
453	219	20
453	220	20
453	221	20
453	222	20
453	223	20
453	224	20
453	225	20
453	226	20

Figure 43C

H1	H2	H3
453	18 or 19	227
453	18 or 19	228
453	18 or 19	229
453	18 or 19	230
453	18 or 19	231
453	18 or 19	232
453	18 or 19	233
453	18 or 19	234
453	18 or 19	235
453	18 or 19	236
453	18 or 19	237
453	18 or 19	238
453	18 or 19	239
453	18 or 19	240
453	18 or 19	241
453	18 or 19	242
453	18 or 19	243
453	18 or 19	244
453	18 or 19	245
453	18 or 19	246
453	18 or 19	247
453	18 or 19	248
453	18 or 19	249
453	18 or 19	250
453	18 or 19	251
453	18 or 19	252
453	18 or 19	253
453	18 or 19	254
453	18 or 19	255
453	18 or 19	256
453	18 or 19	257
453	18 or 19	258
453	18 or 19	259
453	18 or 19	260
453	18 or 19	261
453	18 or 19	262
453	18 or 19	263
453	18 or 19	264
453	18 or 19	265
453	18 or 19	266
453	18 or 19	267
453	18 or 19	268

H1	H2	H3
453	18 or 19	269
453	18 or 19	270
453	18 or 19	271
453	18 or 19	272

Figure 44A

L1	L2	L3
273	28	30, 31, or 519
274	28	30, 31, or 519
275	28	30, 31, or 519
276	28	30, 31, or 519
277	28	30, 31, or 519
278	28	30, 31, or 519
279	28	30, 31, or 519
280	28	30, 31, or 519
281	28	30, 31, or 519
282	28	30, 31, or 519
283	28	30, 31, or 519
284	28	30, 31, or 519
285	28	30, 31, or 519
286	28	30, 31, or 519
287	28	30, 31, or 519
288	28	30, 31, or 519
289	28	30, 31, or 519
290	28	30, 31, or 519
291	28	30, 31, or 519
292	28	30, 31, or 519
293	28	30, 31, or 519
294	28	30, 31, or 519
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296	28	30, 31, or 519
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298	28	30, 31, or 519
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308	28	30, 31, or 519
309	28	30, 31, or 519
310	28	30, 31, or 519
311	28	30, 31, or 519
312	28	30, 31, or 519

L1	L2	L3
313	28	30, 31, or 519
314	28	30, 31, or 519
315	28	30, 31, or 519
316	28	30, 31, or 519
317	28	30, 31, or 519
318	28	30, 31, or 519
319	28	30, 31, or 519
320	28	30, 31, or 519
321	28	30, 31, or 519
322	28	30, 31, or 519
323	28	30, 31, or 519
324	28	30, 31, or 519
325	28	30, 31, or 519
326	28	30, 31, or 519
327	28	30, 31, or 519
328	28	30, 31, or 519
329	28	30, 31, or 519

Figure 44B

L1	L2	L3
26 or 27	330	30, 31, or 519
26 or 27	331	30, 31, or 519
26 or 27	332	30, 31, or 519
26 or 27	333	30, 31, or 519
26 or 27	334	30, 31, or 519
26 or 27	335	30, 31, or 519
26 or 27	336	30, 31, or 519
26 or 27	337	30, 31, or 519
26 or 27	338	30, 31, or 519
26 or 27	339	30, 31, or 519
26 or 27	340	30, 31, or 519
26 or 27	341	30, 31, or 519
26 or 27	342	30, 31, or 519
26 or 27	343	30, 31, or 519
26 or 27	344	30, 31, or 519
26 or 27	345	30, 31, or 519
26 or 27	346	30, 31, or 519
26 or 27	347	30, 31, or 519
26 or 27	348	30, 31, or 519
26 or 27	349	30, 31, or 519
26 or 27	350	30, 31, or 519
26 or 27	351	30, 31, or 519
26 or 27	352	30, 31, or 519
26 or 27	353	30, 31, or 519
26 or 27	354	30, 31, or 519
26 or 27	355	30, 31, or 519
26 or 27	356	30, 31, or 519
26 or 27	357	30, 31, or 519
26 or 27	358	30, 31, or 519
26 or 27	359	30, 31, or 519
26 or 27	360	30, 31, or 519
26 or 27	361	30, 31, or 519
26 or 27	362	30, 31, or 519
26 or 27	363	30, 31, or 519
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26 or 27	365	30, 31, or 519
26 or 27	366	30, 31, or 519
26 or 27	367	30, 31, or 519
26 or 27	368	30, 31, or 519
26 or 27	369	30, 31, or 519

L1	L2	L3
26 or 27	370	30, 31, or 519
26 or 27	371	30, 31, or 519
26 or 27	372	30, 31, or 519
26 or 27	373	30, 31, or 519
26 or 27	374	30, 31, or 519
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26 or 27	384	30, 31, or 519
26 or 27	385	30, 31, or 519
26 or 27	386	30, 31, or 519
26 or 27	387	30, 31, or 519
26 or 27	388	30, 31, or 519
26 or 27	389	30, 31, or 519
26 or 27	390	30, 31, or 519

Figure 44C

L1	L2	L3
26 or 27	28	391
26 or 27	28	392
26 or 27	28	393
26 or 27	28	394
26 or 27	28	395
26 or 27	28	396
26 or 27	28	397
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26 or 27	28	424
26 or 27	28	425
26 or 27	28	426
26 or 27	28	427
26 or 27	28	428
26 or 27	28	429
26 or 27	28	430

L1	L2	L3
26 or 27	28	431
26 or 27	28	432
26 or 27	28	433
26 or 27	28	434
26 or 27	28	435
26 or 27	28	436
26 or 27	28	437
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26 or 27	28	464
26 or 27	28	465
26 or 27	28	466
26 or 27	28	467
26 or 27	28	468
26 or 27	28	469
26 or 27	28	470

L1	L2	L3
26 or 27	28	471
26 or 27	28	472
26 or 27	28	473
26 or 27	28	474

Figure 45A

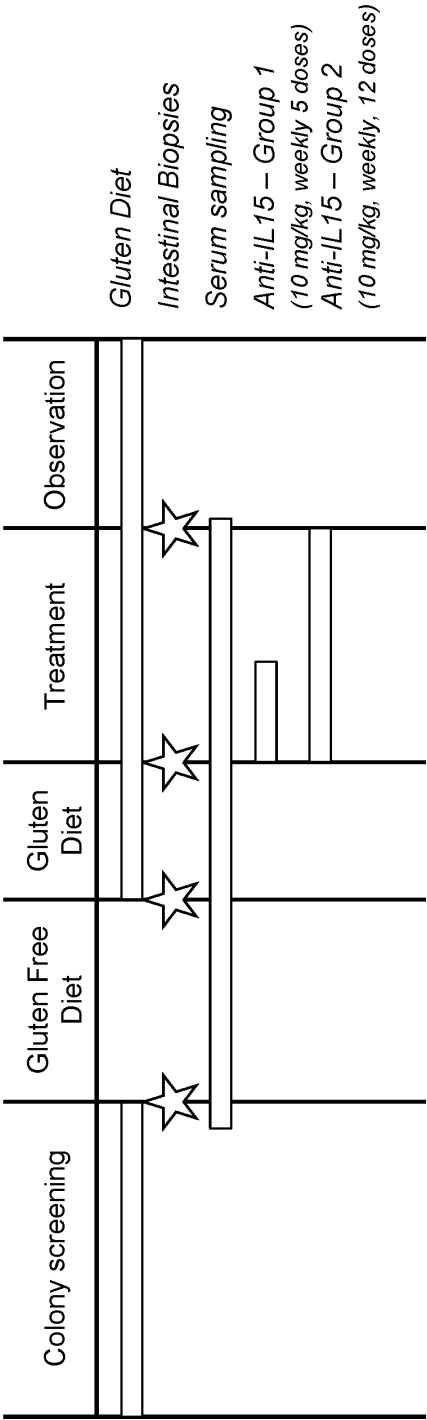


Figure 45B

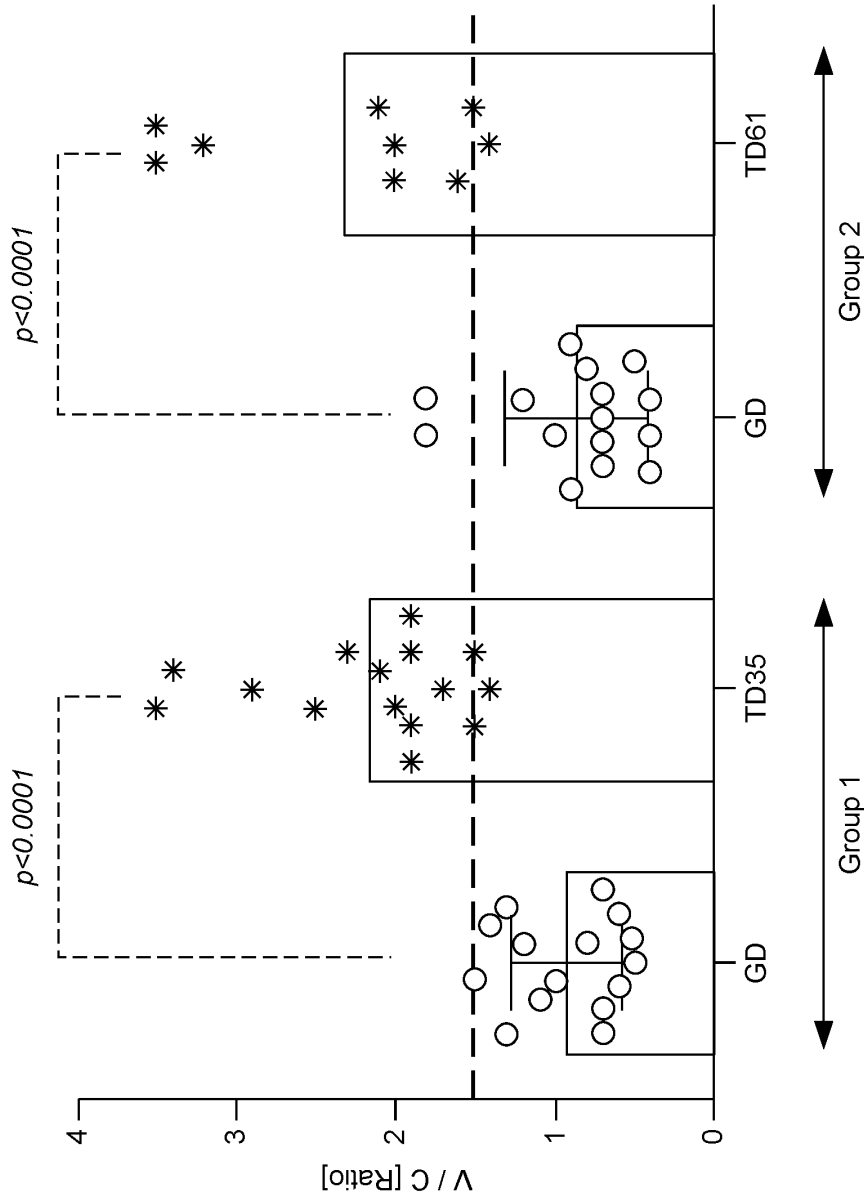


Figure 45C
IEL Counts

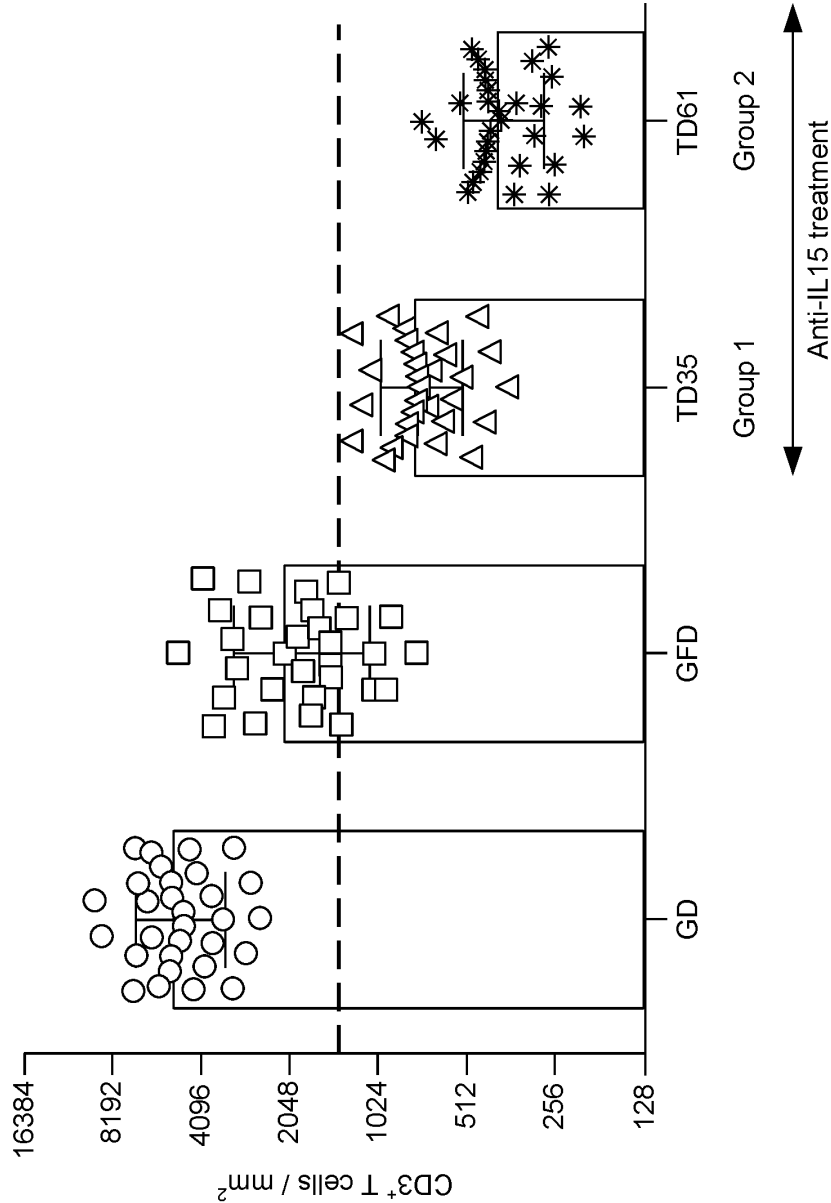


Figure 45D

