

Figure 1

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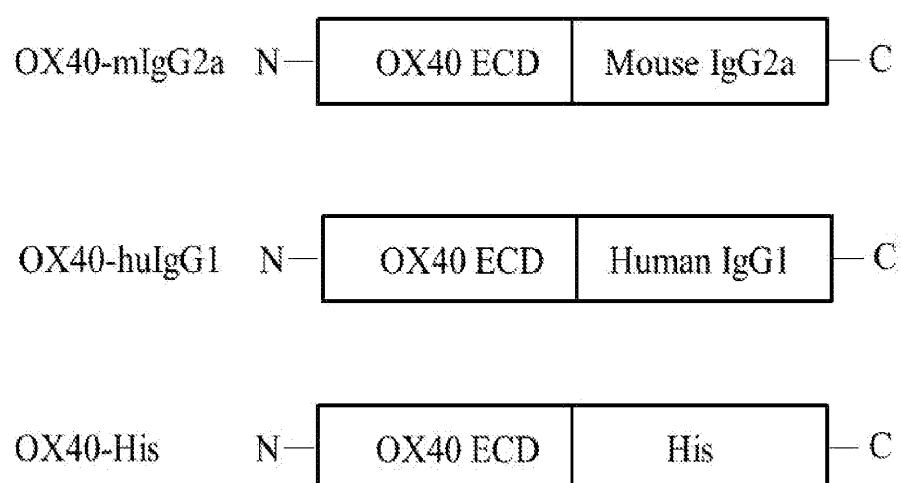


Figure 2
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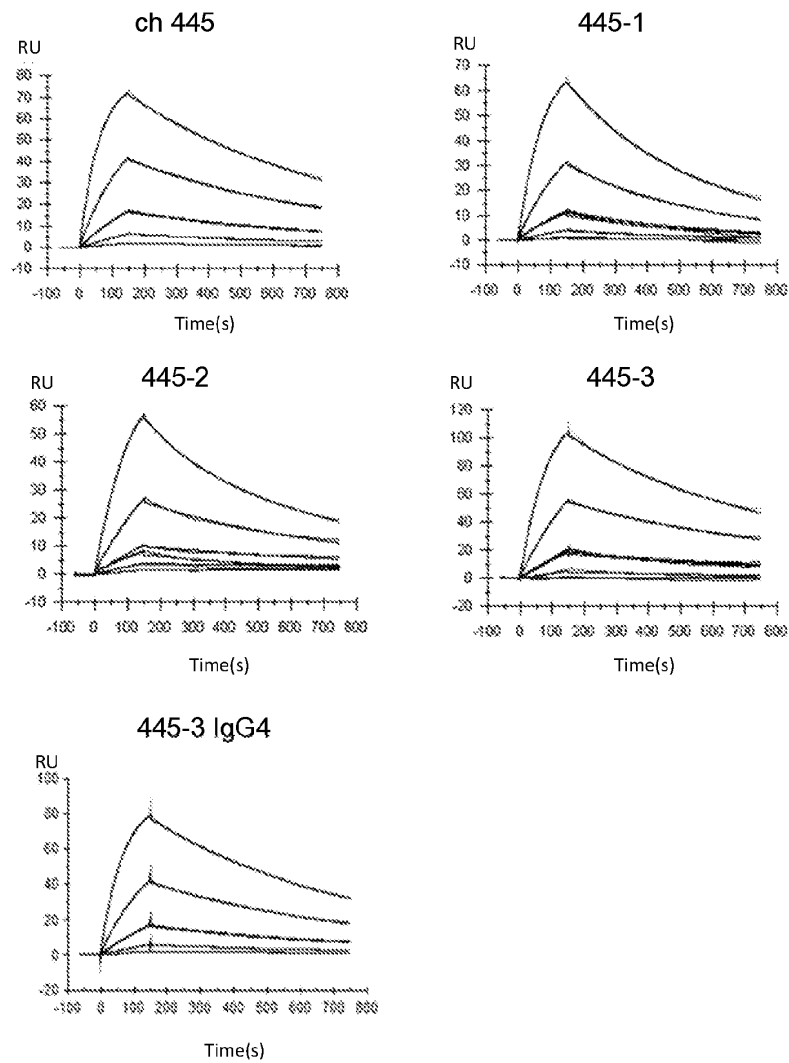


Figure 3
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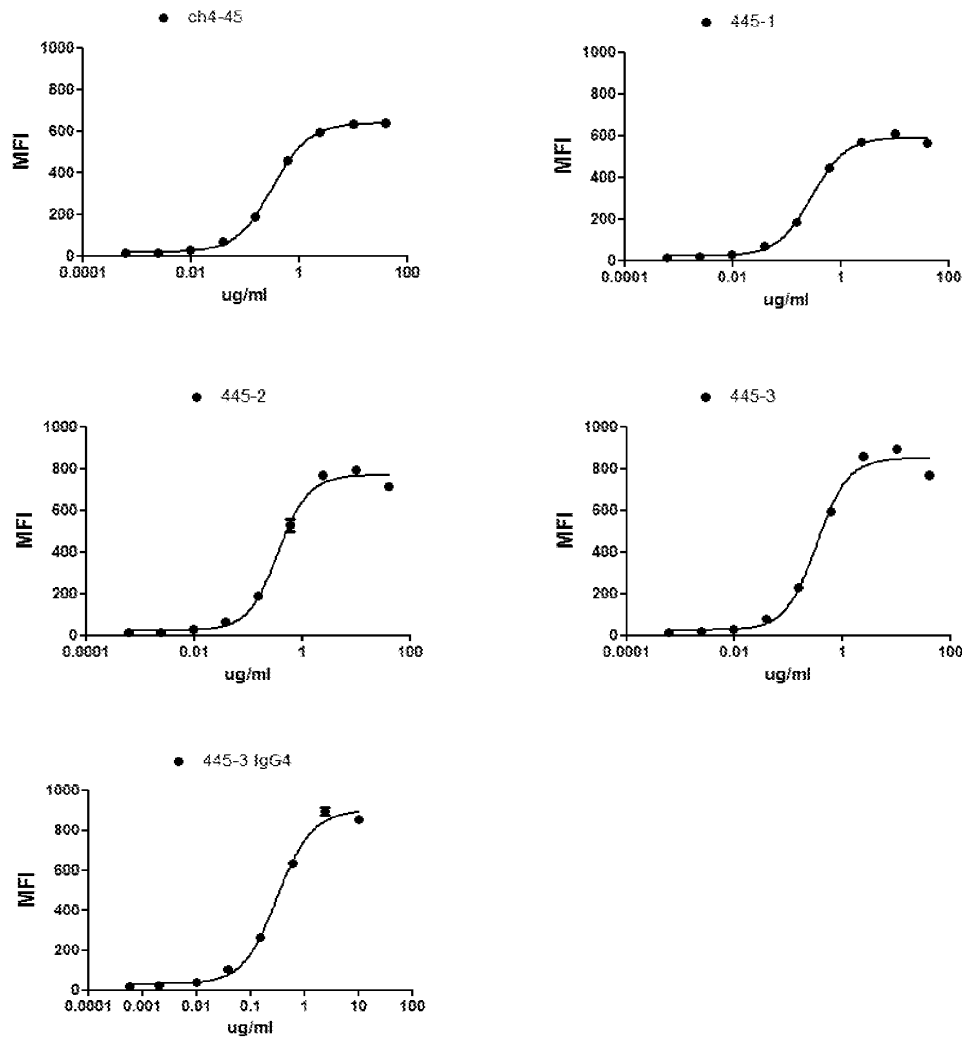


Figure 4
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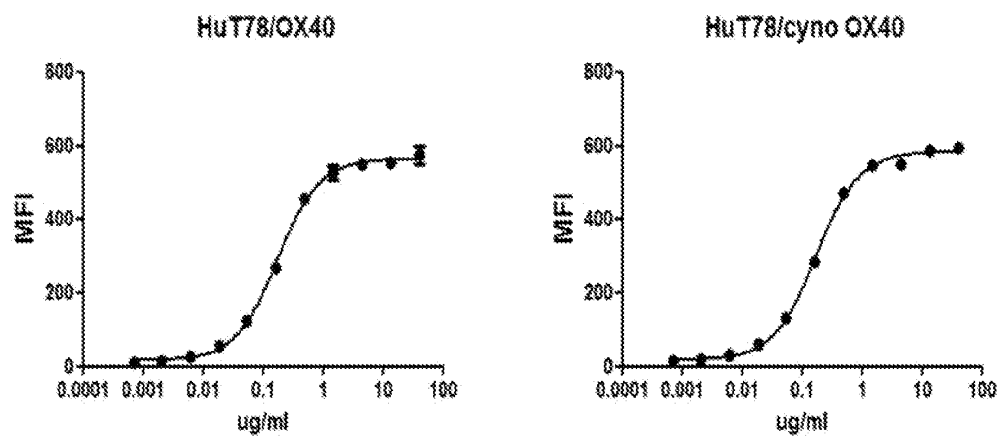


Figure 5
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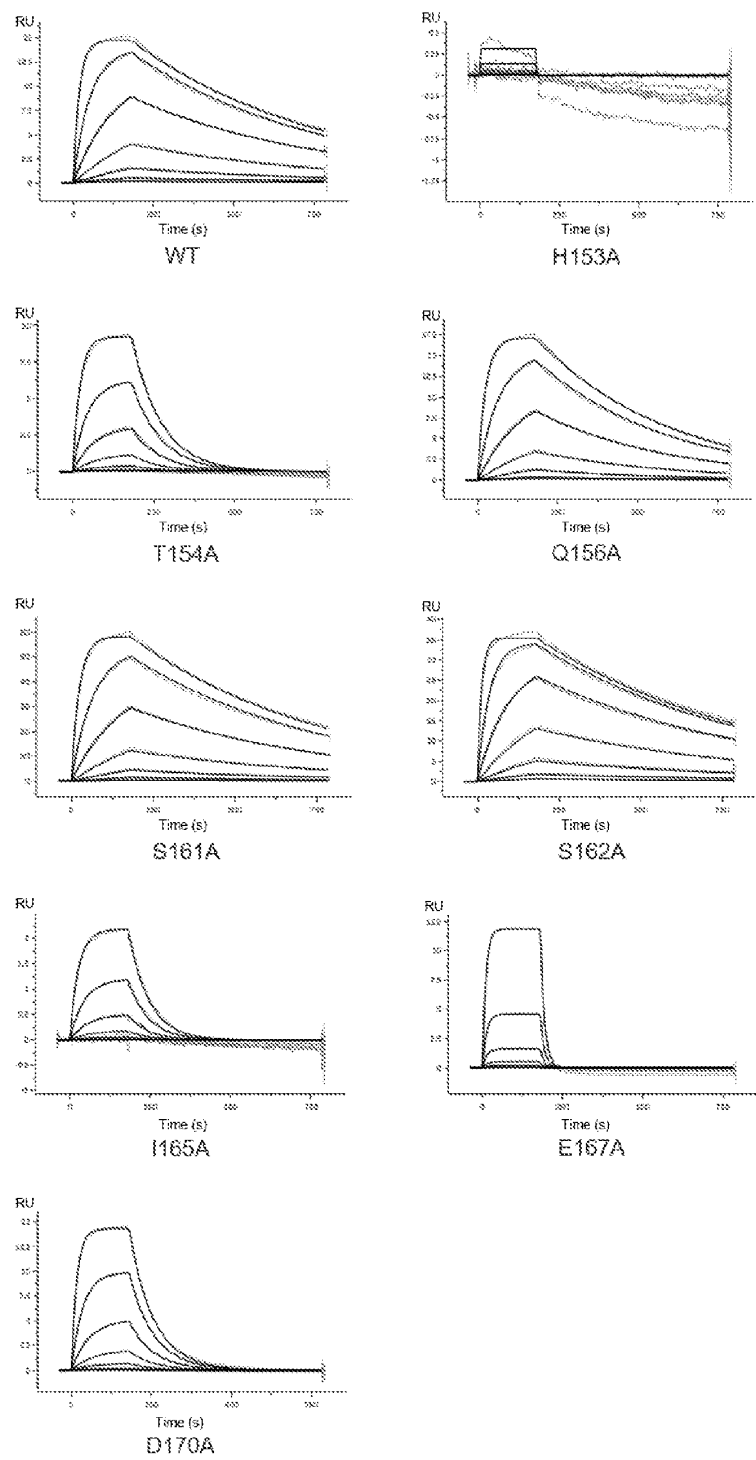


Figure 6
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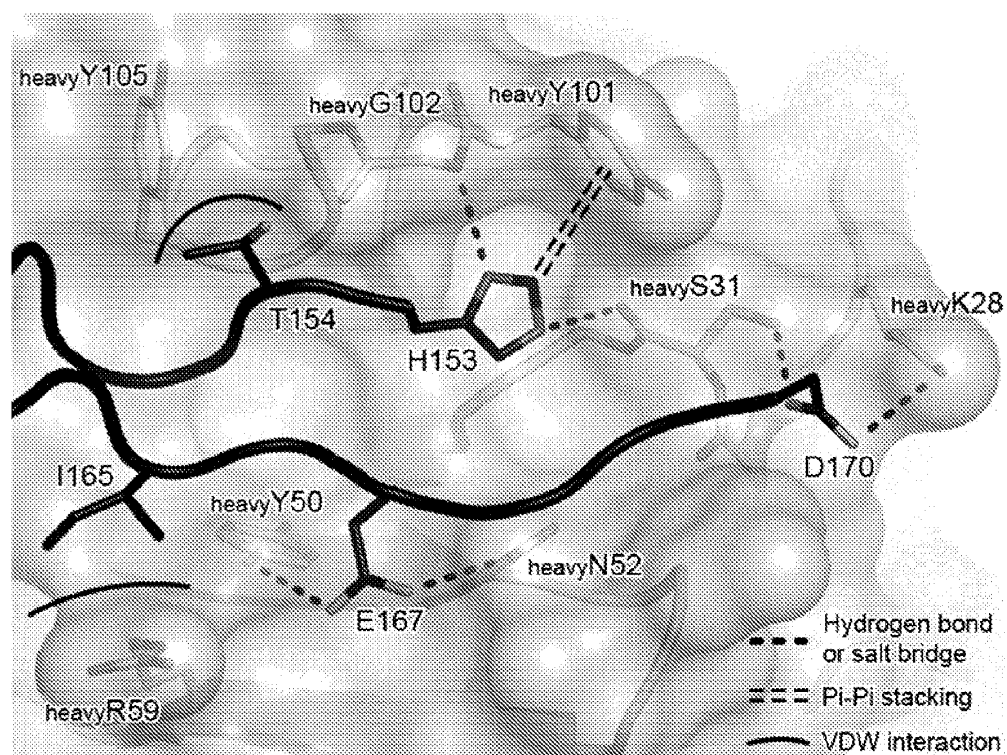


Figure 7
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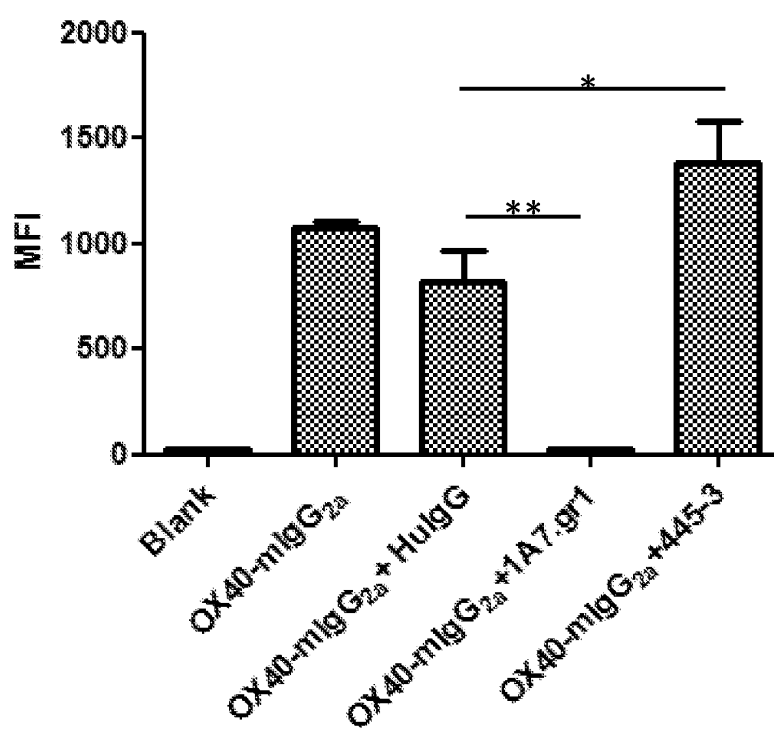


Figure 8
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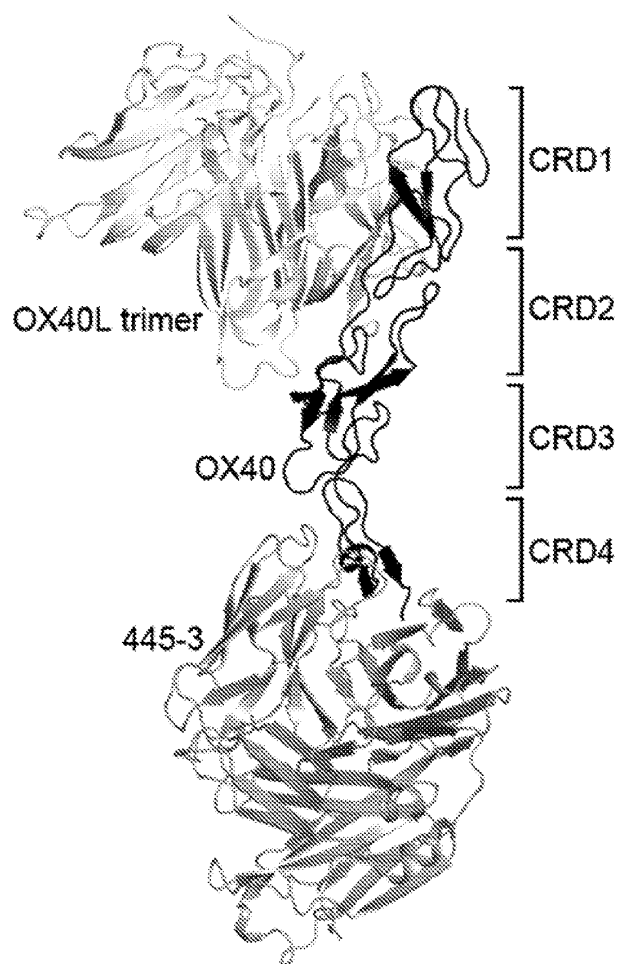


Figure 9A-B
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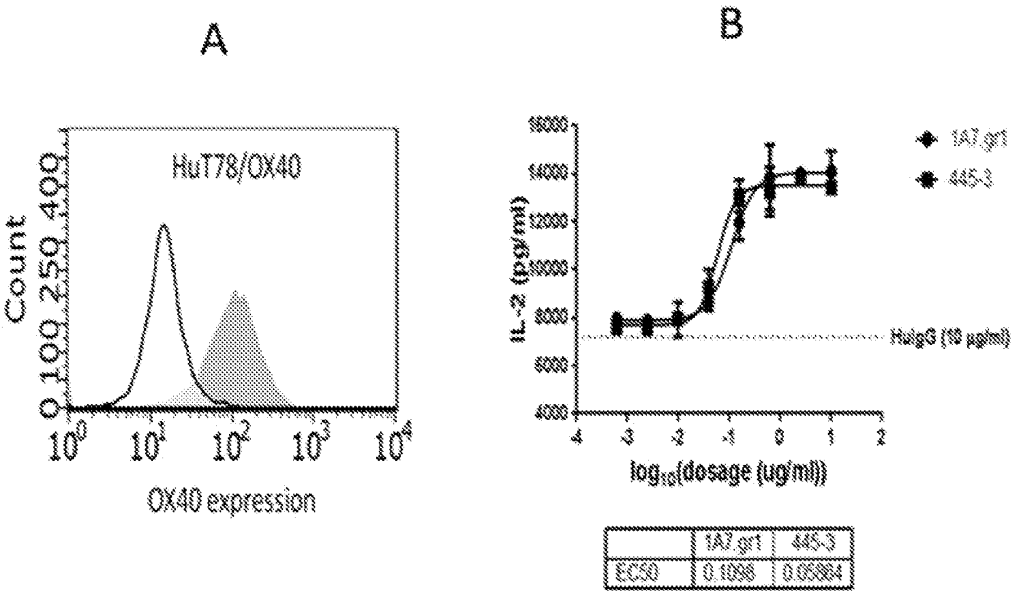


Figure 10
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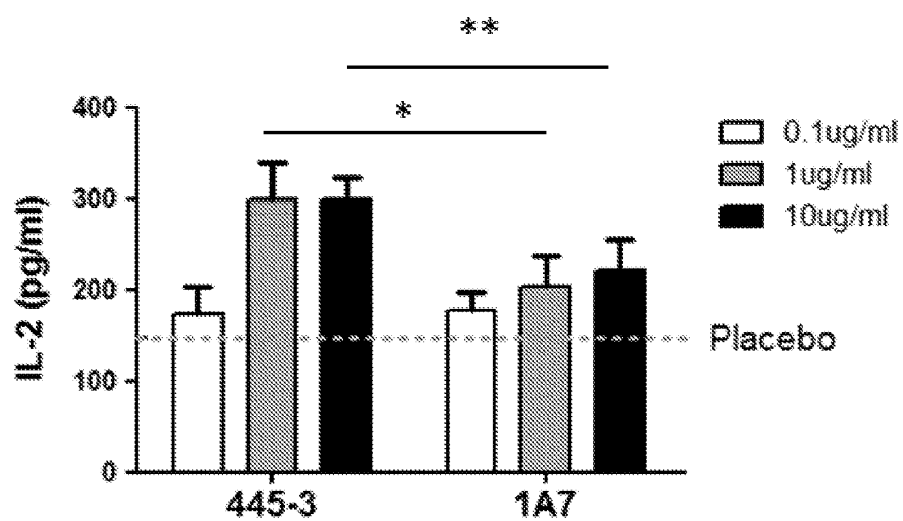


Figure 11
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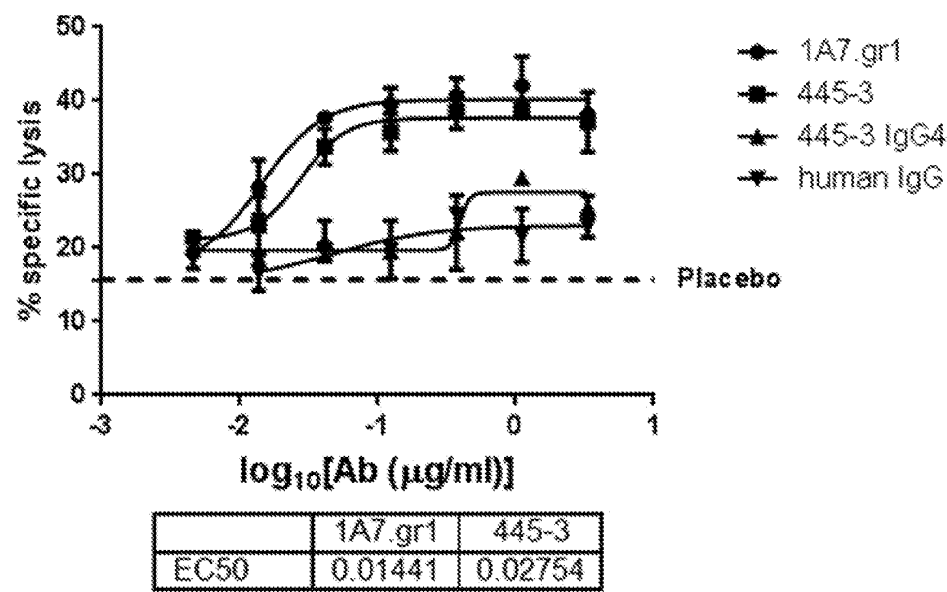


Figure 12A-12C
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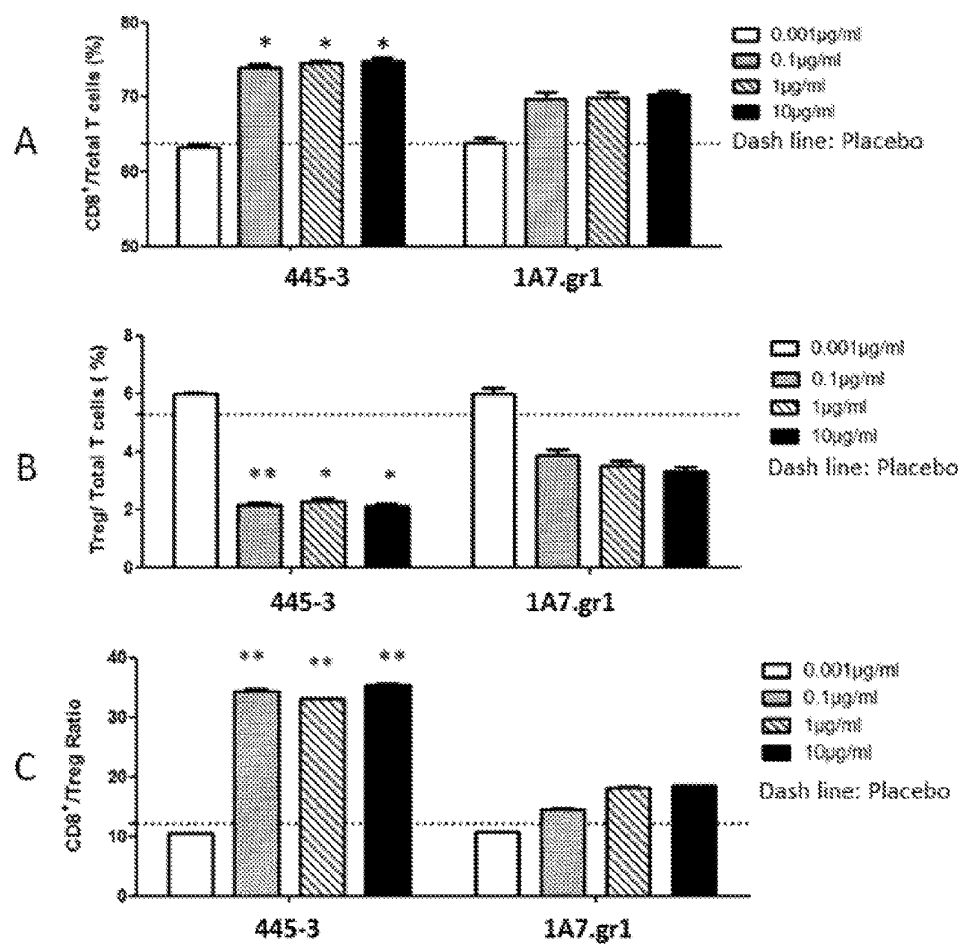


Figure 13A
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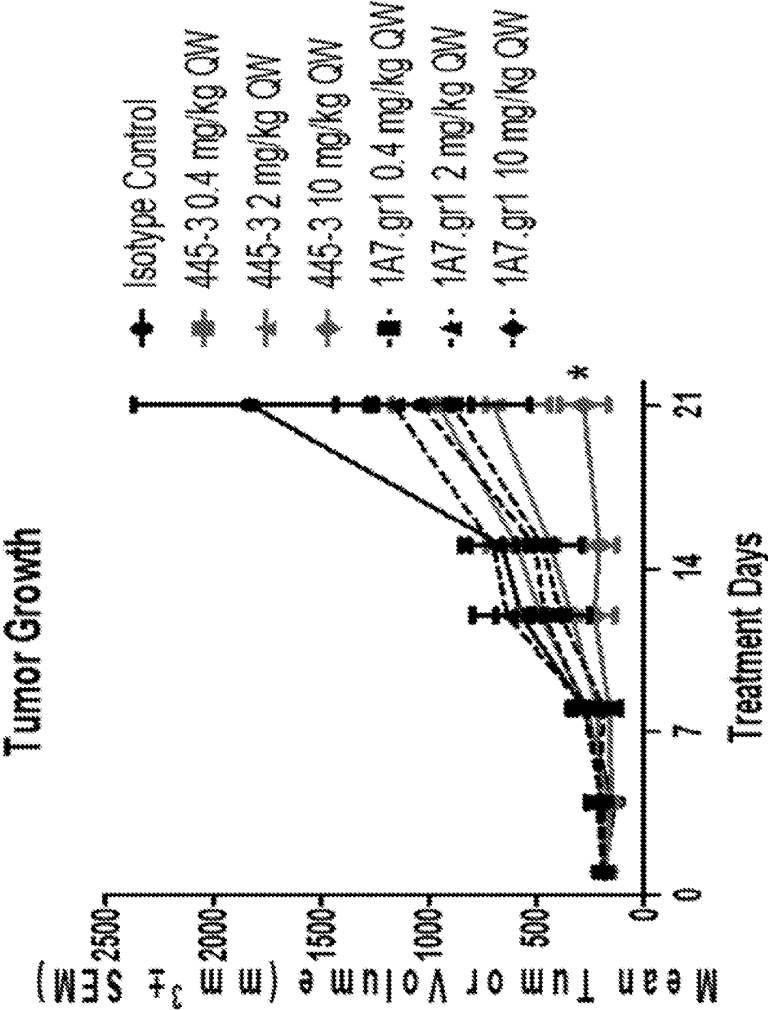


Figure 13B
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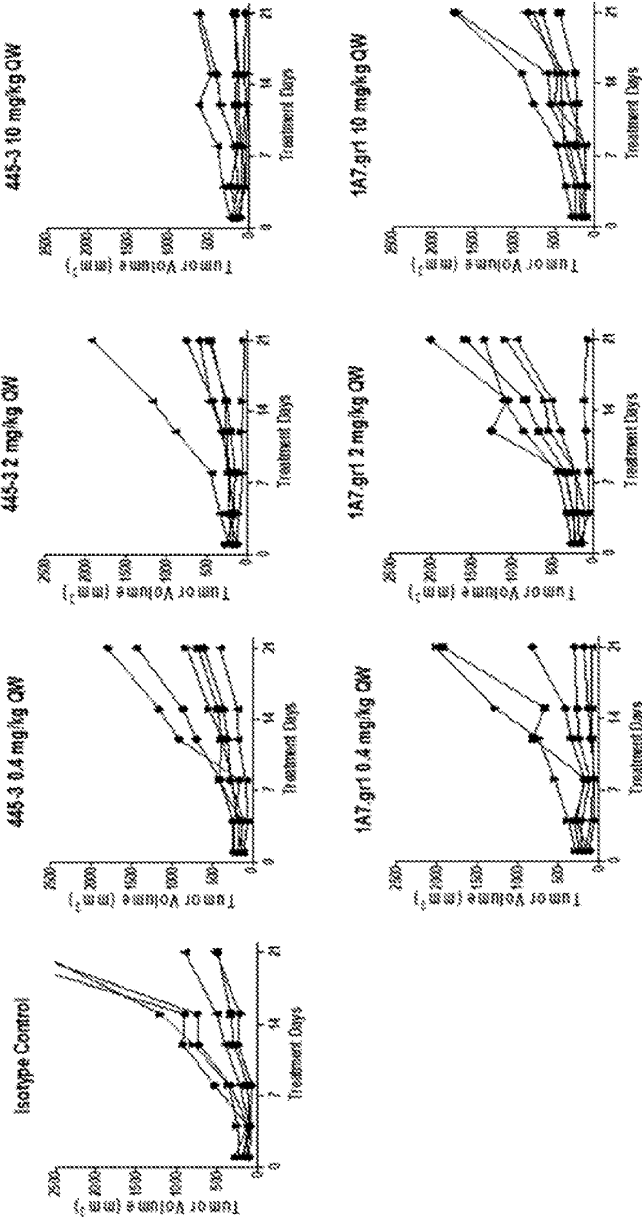


Figure 14A

Heavy chain		Light chain		Co-transfection with heavy chain and light chain	FACS		Biacore		
ID	CDR/FR	ID	CDR/FR		EC ₅₀ (ng/ml)	Top(MFI)	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)	K _D (M)
445-1VH	-	445-1VL	-	445-1	336	500	2.37E+05	3.89E-03	1.64E-08
445-1VH-M48I	FR2	445-1VL	-	445-2(M48I)-1 (445-1 with M48I mutation on VH)	353	480	2.30E+05	3.50E-03	1.55E-08
445-1VH	-	445-1VL-S24G	CDR1	445-1-2(S24G) (445-1 with S24G mutation on VL)	307	470	2.22E+05	3.60E-03	1.62E-08
445-1VH	-	445-1VL-S10T/E8ID/D70E	FR1/FR3	445-1-2(S10T/E8ID/D70E) (445-1 with S10T, E8ID and D70E mutations on VL)	280	510	2.28E+05	3.40E-03	1.49E-08

Figure 14B

Heavy chain		Light chain		Co-transfection with heavy chain and light chain	FACS		Biacore		
ID	CDR/FR	ID	CDR/FR		Ab ID	EC ₅₀ (ng/ml)	Top0(MFI)	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)
445-2VH	-	445-2VL	-	445-2	397	760	2.06E+05	2.64E-03	1.28E-08
445-2VH-Q62E-Q65K	CDR2	445-2VL-S24R	CDR1	445-3(Q62E/Q65K)-3(S24R) (445-2 with Q62E and Q65K mutations on VH and S24R mutation on VL)	318	790	1.87E+05	2.32E-03	1.24E-08
445-2VH-Q62E	CDR2	445-2VL-S24R	CDR1	445-3(Q62E)-3(S24R) (445-2 with Q62E mutation on VH and S24R mutation on VL)	363	760	1.94E+05	2.27E-03	1.17E-08
445-2VH-K28T	FR1	445-2VL-S24R	CDR1	445-3(K28T)-3(S24R) (445-2 with K28T mutation on VH and S24R mutation on VL)	660	750	4.44E+05	5.74E-03	1.29E-08
445-2VH-Y27G	FR1	445-2VL-S24R	CDR1	445-3(Y27G)-3(S24R) (445-2 with Y27G mutation on VH and S24R mutation on VL)	755	630	6.25E+04	1.35E-03	2.15E-08
445-2VH-T30S	FR1	445-2VL-S24R	CDR1	445-3(T30S)-3(S24R) (445-2 with T30S mutation on VH and S24R mutation on VL)	405	800	2.91E+05	3.81E-03	1.31E-08
445-3VH	-	445-3VL	-	445-3	462	990	1.74E+05	1.48E-03	8.51E-09
445-2VH-A61N-K28R	CDR2/FR1	445-3VL	-	445-3(A61N-K28R)-3 (445-2 VH with A61N and K28R mutations and 445-3 VL)	369	1080	1.57E+05	1.15E-03	7.35E-09
445-2VH-A61N-K63R	CDR2	445-3VL	-	445-3(A61N-K63R)-3 (445-2 VH with A61N and K63R mutations and 445-3 VL)	483	1100	1.61E+05	1.55E-03	9.65E-09
445-3VH	-	445-2VL-G41D-K42G-S24R-K93R	FR2/CDR1/CDR3	445-3-3(G41D-K42G-S24R-K93R) (445-3 VH and 445-2 VL with G41D, K42G, S24R and K93R mutations)	337	1050	2.12E+05	1.68E-03	7.90E-09

Figure 15
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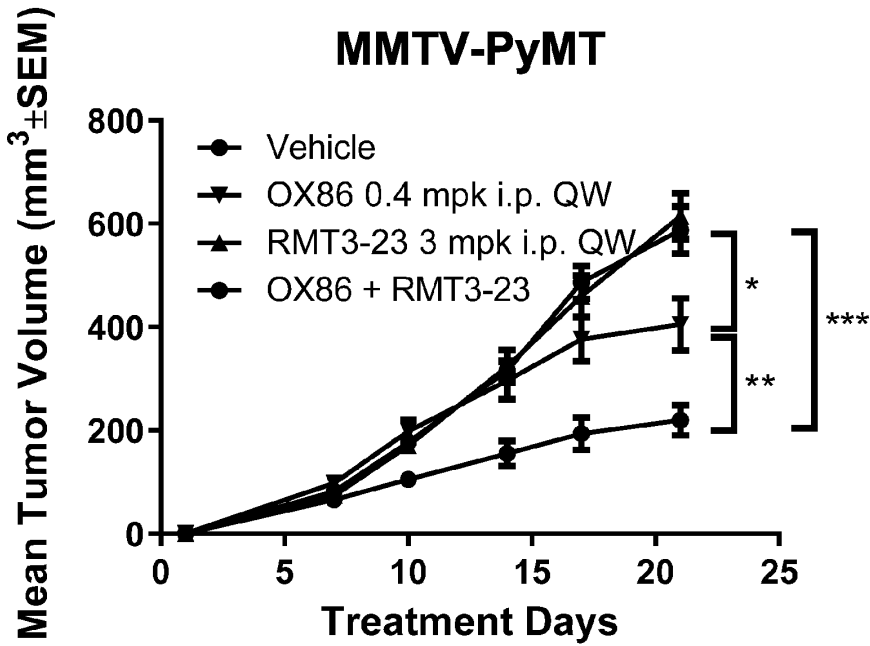


Figure 16
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