FIGURE 1

CDR sequences for anti-CD154 antibody 342

Sequence ID Number	Description	Sequence
SEQ ID NO: 3	CDR-H1	GFSSTNYHVH
SEQ ID NO: 4	CDR-H2	VIWGDGDTSYNSVLKS
SEQ ID NO: 5	CDR-H3	QLTHYYVLAA
SEQ ID NO: 6	CDR-L1	RASEDLYYNLA
SEQ ID NO: 7	CDR-L2	DTYRLAD
SEQ ID NO: 8	CDR-L3	QQYYKFPFT

CDR sequences for anti-CD154 antibody 381

Sequence ID Number	Description	Sequence
SEQ ID NO: 42	CDR-H1	GFTFSDYYMA
SEQ ID NO: 43	CDR-H2	SISYEGSSTYYGDSVKG
SEQ ID NO: 44	CDR-H3	HDDSPGYYFDY
SEQ ID NO: 45	CDR-L1	LAGEDISNVLA
SEQ ID NO: 46	CDR-L2	AANRLQD
SEQ ID NO: 47	CDR-L3	QQTFRYPLT

CDR sequences for anti-CD154 antibody 338

Sequence ID Number	Description	Sequence
SEQ ID NO: 48	CDR-H1	GFSLTSHHIS
SEQ ID NO: 49	CDR-H2	VMWNDGGTLYNSALKS
SEQ ID NO: 50	CDR-H3	GKMHYYVLDA
SEQ ID NO: 51	CDR-L1	RTSEDIYSNLA
SEQ ID NO: 52	CDR-L2	DTNRLAD
SEQ ID NO: 53	CDR-L3	QHYSNFPWT

FIGURE 2

Rat anti-CD154 342 antibody sequences

Sequence ID Number	Description	Sequence
SEQ ID NO: 29 (heavy 342 in Figure 9)	RAT 342 Ab VH region	QVQLKESGPGLVQPSETLSLTCTVSGFSSTNYHVHWVRQPPGKSLEW MGVIWGDGDTSYNSVLKSRLSITRDTSRSQVFLKMSSLQTEDTATYY CARQLTHYYVLAAWGQGASVTVS
SEQ ID NO: 34	RAT 342 Ab VH region with signal sequence	atggctgtcctggtgctgttgctctgcctgatgacatttccaagctg tgtcctgtcccaggtgcagctgaaggagtcaggacctggcctggtgc agccctcagagaccctgtctctcacctgcactgtctctgggttctca tcaaccaattatcatgtgcactgggttcgacagcctccaggaaaaag tcttgagtggatgggagtaatatggggtgatggagacacatcatata attcagttctcaaatcccgactgagcatcaccagggacacctccagg agccaagttttcttaaaaatgagcagtctgcaaacggaggacactgc cacctactattgtgccaggcaattgactcattactatgttctggctg cctggggtcaaggagcttcagtcactgtctcg
SEQ ID NO: 32	RAT 342 Ab VH region without signal sequence	caggtgcagctgaaggagtcaggacctggcctggtgcagccctcaga gaccctgtctctcacctgcactgtctctgggttctcatcaaccaatt atcatgtgcactgggttcgacagcctccaggaaaaagtcttgagtgg atgggagtaatatggggtgatggagacacatcatataattcagttct caaatcccgactgagcatcaccagggacacctccaggagccaagttt tcttaaaaatgagcagtctgcaaacggaggacactgccacctactat tgtgccaggcaattgactcattactatgttctggctgcctggggtca aggagcttcagtcactgtctcg
SEQ ID NO: 30 (light 342 in Figure 9)	RAT 342 Ab VL region	DIQMTQSPASLSASLGETVTVECRASEDLYYNLAWYQRKPGNSPQLL IYDTYRLADGVPSRFSGSGSGTQYSLKINTLPSGDVASYFCQQYYKF PFTFGSGTKLELK
SEQ ID NO: 33	RAT 342 Ab VL region with signal sequence	atgggtgtgcccactcatctcctggggttgttgctactgtggattac agatgccatatgtgacatccagatgacacagtctccagcttccctgt ctgcatctctgggagaaactgtcaccgtcgaatgtcgagcaagtgag gacctttactataatttagcgtggtatcagcggaaaccagggaactc tcctcaactcctgatctatgatacatataggttggcagatggggtcc catcacggttcagtggcagtgggtctggcacacagtattctctaaag ataaacaccctgccatctggagatgtcgcaagttatttctgtcaaca gtattacaaatttccattcacgttcggctcagggaccaagctggaac tgaaa
SEQ ID NO: 31	RAT 342 Ab VL region without signal sequence	gacatccagatgacacagtctccagcttccctgtctgcatctctggg agaaactgtcaccgtcgaatgtcgagcaagtgaggacctttactata atttagcgtggtatcagcggaaaccagggaactctcctcaactcctg atctatgatacatataggttggcagatggggtcccatcacggttcag tggcagtgggtctggcacacagtattctctaaagataaacaccctgc catctggagatgtcgcaagttatttctgtcaacagtattacaaattt ccattcacgttcggctcagggaccaagctggaactgaaa

FIGURE 3

Acceptor Framework Sequences

Sequence ID Number	Description	Sequence
SEQ ID NO: 35 (2 1 1 O12 in Figure 9)	Human VK1 2-1-(1) O12 JK1 acceptor framework	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSL QPEDFATYYCQQSYSTPWTFGQGTKVEIK
SEQ ID NO: 36	Human VK1 2-1-(1) O12 JK1 acceptor framework	gacatccagatgacccagtctccatcctccctgtc tgcatctgtaggagacagagtcaccatcacttgcc gggcaagtcagagcattagcagctatttaaattgg tatcagcagaaaccagggaaagcccctaagctcct gatctatgctgcatccagtttgcaaagtggggtcc catcaaggttcagtggcagtggatctgggacagat ttcactctcaccatcagcagtctgcaacctgaaga ttttgcaacttactactgtcaacagagttacagta ccccttggacgttcggccaagggaccaaggtggaa atcaaa
SEQ ID NO: 37 (1-1 3-66 in Figure 9)	Human VH3 1-1 3-66 JH4 acceptor framework	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQ APGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCARYFDYWGQGTLVTVS
SEQ ID NO: 38	Human VH3 1-1 3-66 JH4 acceptor framework	gaggtgcagctggtggagtctgggggaggcttggt ccagcctgggggtccctgagactctcctgtgcag cctctggattcaccgtcagtagcaactacatgagc tgggtccgccaggctccagggaaggggctggagtg ggtctcagttatttatagcggtggtagcacatact acgcagactccgtgaagggcagattcaccatctcc agagacaattccaagaacacgctgtatcttcaaat gaacagcctgagagccgaggacacggctgtgtatt actgtgcgagatactttgactactggggccaggga accctggtcaccgtctcc
SEQ ID NO: 39 (1-1 4-59 in Figure 9)	Human VH4 1-1 4-59 JH4 acceptor framework	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQ PPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQF SLKLSSVTAADTAVYYCARYFDYWGQGTLVTVS
SEQ ID NO: 40	Human VH4 1-1 4-59 JH4 acceptor framework	caggtgcagctgcaggagtcgggcccaggactggt gaagccttcggagaccctgtccctcacctgcactg tctctggtggctccatcagtagttactactggagc tggatccggcagcccccagggaagggactggagtg gattgggtatatctattacagtgggagcaccaact acaaccctccctcaagagtcgagtcaccatatca gtagacacgtccaagaaccagttctccctgaagct gagctctgtgaccgctgcggacacggccgtgtatt actgtgcgagatactttgactactggggccaggga accctggtcaccgtctcc

FIGURE 4

342 CDR grafts based on acceptor frameworks

Sequence ID Number	Description	Sequence
SEQ ID NO: 10 (VH3 gH7 in Figure 9)	Variable heavy CDR-only graft based on VH3 1-1 3-66 JH4 acceptor framework	EVQLVESGGGLVQPGGSLRLSCAASGFSSTNYHVHWVRQA PGKGLEWVSVIWGDGDTSYNSVLKSRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARQLTHYYVLAAWGQGTLVTVS
SEQ ID NO: 20	Variable heavy CDR-only graft based on VH3 1-1 3-66 JH4 acceptor framework	gaggtgcagctggtcgagtctggaggcgggcttgtccagc ctggtgggagcctgcgtctcttgtgcagcgagcggctt cagctctaccaattaccatgtgcactgggtgcgtcaggca cctgggaagggcctggagtgggtgagtgttatttggggcg acggcgatacatcctacaactccgtcctgaagagccgttt caccatttcccgtgacaactcaaagaatacccttacctc cagatgaactctctccgcgcagaggacacagcagtctatt actgtgcacgtcaactgacccactattacgttttggcagc ctggggtcaagggactctggtcacagtctcg
SEQ ID NO: 9	Variable heavy CDR-only graft based on VH4 1-1 4-59 JH4 acceptor framework	QVQLQESGPGLVKPSETLSLTCTVSGFSSTNYHVHWI RQPPGKGLEWIGVIWGDGDTSYNSVLKSRVTISVDTS KNQFSLKLSSVTAADTAVYYCARQLTHYYVLAAWGQG TLVTVS
SEQ ID NO: 19	Variable heavy CDR-only graft based on VH4 1-1 4-59 JH4 acceptor framework	caggtgcagctgcaggagtctggaccggggcttgtca agcctagtgagaccctgagcctcacttgtaccgtgag cggcttcagctctaccaattaccatgtgcactggatt cgtcagccacctgggaagggcctggagtggattggtg ttatttggggcgacggcgatacatcctacaactccgt cctgaagagccgtgtcaccatttccgttgacacctca aagaatcaattttccctcaagttgagctctgtcaccg cagcggacacagcagtctattactgtgcacgtcaact gacccactattacgttttggcagcctggggtcaaggg actctggtcacagtctcg
SEQ ID NO: 14 (VK1 gL3 in Figure 9)	Variable light CDR-only graft based on VK1 2-1-(1) O12 JK1 acceptor framework	DIQMTQSPSSLSASVGDRVTITCRASEDLYYNLAWYQ QKPGKAPKLLIYDTYRLADGVPSRFSGSGSGTDFTLT ISSLQPEDFATYYCQQYYKFPFTFGQGTKVEIK
SEQ ID NO: 16	Variable light CDR-only graft based on VK1 2-1-(1) O12 JK1 acceptor framework	gatatccagatgacccagagtccaagcagtctctccg ccagcgtaggcgatcgtgtgactattacctgtcgtgc cagtgaggacctctattacaacctggcctggtatcag caaaaaccgggcaaagccccgaagctgctcatctatg atacgtaccgcctggctgacggtgtgccaagccgttt cagtggcagtggcagcggtactgactttaccctcaca atttcgtctctccagccggaagatttcgccacttact attgtcagcaatattacaagttccctttcaccttcgg tcagggcactaaagtagaaatcaaa

FIGURE 5

342 gH1 based on acceptor frameworks

Sequence ID Number	Description	Sequence
SEQ ID NO: 1 (VH3 gH1 in Figure 9)	gH1 based on VH3 1-1 3-66 JH4 acceptor framework	EVQLVESGGGLVQPGGSLRLSCAVSGFSSTNYHV HWVRQAPGKGLEWMGVIWGDGDTSYNSVLKSRFT ISRDTSKNTVYLQMNSLRAEDTAVYYCARQLTHY YVLAAWGQGTLVTVS
SEQ ID NO: 22	gH1 based on VH3 1-1 3-66 JH4 acceptor framework	gaggtgcagctggtcgagtctggaggcgggcttgtcc agcctggtgggagcctgcgtctctcttgtgcagtgag cggcttcagctctaccaattaccatgtgcactgggtg cgtcaggcacctgggaagggcctggagtggatgggtg ttatttggggcgacggcgatacatcctacaactccgt cctgaagagccgtttcaccatttcccgtgacacctca aagaataccgtttacctccagatgaactctctccgcg cagaggacacagcagtctattactgtgcacgtcaact gacccactattacgttttggcagcctggggtcaaggg actctggtcacagtctcg
SEQ ID NO: 11 (VH4 gH1 in Figure 9)	gH1 based on VH4 1-1 4-59 JH4 acceptor framework	QVQLQESGPGLVKPSETLSLTCTVSGFSSTNYHV HWIRQPPGKGLEWMGVIWGDGDTSYNSVLKSRVT ISRDTSKNQVSLKLSSVTAADTAVYYCARQLTHY YVLAAWGQGTLVTVS
SEQ ID NO: 21	gH1 based on VH4 1-1 4-59 JH4 acceptor framework	caggtgcagctgcaggagtctggaccggggcttg tcaagcctagtgagaccctgagcctcacttgtac cgtgagcggcttcagctctaccaattaccatgtg cactggattcgtcagccacctgggaagggcctgg agtggatgggtgttatttggggcgacggcgatac atcctacaactccgtcctgaagagccgtgtcacc atttcccgtgacacctcaaagaatcaagtttccc tcaagttgagctctgtcaccgcagcggacacagc agtctattactgtgcacgtcaactgacccactat tacgttttggcagcctggggtcaagggactctgg tcacagtctcg

FIGURE 6

342 gL4

Sequence ID Number	Description	Sequence
SEQ ID NO: 2 (VK1 gL4 in Figure 9)	gL4 Variable light	DIQMTQSPSSLSASVGDRVTITCRASEDLYYNLA WYQRKPGKAPKLLIYDTYRLADGVPSRFSGSGSG TDYTLTISSLQPEDFASYYCQQYYKFPFTFGQGT KVEIK
SEQ ID NO: 17	gL4 Variable light	gatatccagatgacccagagtccaagcagtctct ccgccagcgtaggcgatcgtgtgactattacctg tcgtgccagtgaggacctctattacaacctggcc tggtatcagcgtaaaccgggcaaagccccgaagc tgctcatctatgatacgtaccgcctggctgacgg tgtgccaagccgtttcagtggcagtggcagcggt actgactataccctcacaatttcgtctctccagc cggaagatttcgcctcttactattgtcagcaata ttacaagttccctttcaccttcggtcagggcact aaagtagaaatcaaa
SEQ ID NO: 25	gL4 Variable Light sequence with sequence encoding signal peptide underlined	atgaaaaagacagctatcgcaattgcagtggcct tggctggtttcgctaccgtagcgcaagctgatat ccagatgacccagagtccaagcagtctctccgcc agcgtaggcgatcgtgtgactattacctgtcgtg ccagtgaggacctctattacaacctggcctggta tcagcgtaaaccgggcaaagccccgaagctgctc atctatgatacgtaccgcctggctgacggtgtgc caagccgtttcagtggcagtggcagcggtactga ctataccctcacaatttcgtctctccagccggaa gatttcgcctcttactattgtcagcaatattaca agttcccttcaccttcggtcagggcactaaagt agaaatcaaa

FIGURE 7: 342 sequences

Sequence ID Number	Description	Sequence
SEQ ID NO: 15	342gL4 light chain (including constant region)	DIQMTQSPSSLSASVGDRVTITCRASEDLYYNLAWYQ RKPGKAPKLLIYDTYRLADGVPSRFSGSGSGTDYTLT ISSLQPEDFASYYCQQYYKFPFTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 18	342gL4 light chain (including constant region)	atgaaaaagacagctatcgcaattgcagtggccttggctg gtttcgctaccgtagcgcaagctgatatccagatgaccca gagtccaagcagtctctccgccagcgtaggcgatcgtgtg actattacctgtcgtgccagtgaggacctctattacaacc tggcctggtatcagcgtaaaccgggcaaagccccgaagct gctcatctatgatacgtaccgcctggctgacggtgtgcca agccgtttcagtggcagtggcagcggtactgactataccc tcacaatttcgtctctccagccggaagatttcgcctctta ctattgtcagcaatattacaagttccctttcaccttcggt cagggcactaaagtagaaatcaaacgtacggtagcggccc catctgtcttcatcttcccgccatctgatgagcagttgaa atctggaactgcctctgttgtgtgcctgctgaataacttc tatcccagagaggccaaagtacagtggaaggtggataacg ccctccaatcgggtaactcccaggagagtgtcacagagca ggacagcaaggacagcacctacagcctcagcagcaccctg acgctgagcaaagcagactacgagaaacacaaagtctacg cctgcgaagtcacccatcagggcctgagctcaccagtaac aaaaagttttaatagaggggagtgt
SEQ ID NO: 12	342gH1 Fab (no hinge) heavy chain (including constant region)	EVQLVESGGGLVQPGGSLRLSCAVSGFSSTNYHVHWV RQAPGKGLEWMGVIWGDGDTSYNSVLKSRFTISRDTS KNTVYLQMNSLRAEDTAVYYCARQLTHYYVLAAWGQG TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

FIGURE 7 continued

Sequence ID Number	Description	Sequence
SEQ ID NO: 26 (SEQ ID NO: 23 without signal sequence)	342gH1 Fab (no hinge) heavy chain (including constant region)	atgaagaagactgctatagcaattgcagtggcgctagctggt ttcgccaccgtggcgcaagctgaggttcagctggtcgagtct ggaggcgggcttgtccagcctggtgggagcctgcgtctctct tgtgcagtgagcggcttcagctctaccaattaccatgtgcac tgggtgcgtcaggcacctgggaagggcctggagtggatgggt gttatttggggcgacggcgatacatcctacaactccgtcctg aagagccgtttcaccatttcccgtgacacctcaaagaatacc gtttacctccagatgaactctctccgcgcagaggacacagca gtctattactgtgcacgtcaactgacccactattacgttttg gcagcctggggtcaagggactctggtcacagtctcgagcgct tctacaaagggcccatcggtcttcccccctggcaccctcctcc aagagcacctctgggggcacagcggccctgggctgcctggtc aaggactacttccccgaaccggtgacggtgtcgtggaactca ggcgccctgaccagcggcgtgcacaccttcccggctgtccta cagtcctcaggactctactccctcagcagcgtggtgaccgtg ccctccagcagcttgggcacccagacctacatctgcaacgtg aatcacaagcccagcaacaccaaggtcgacaagaaagttgag cccaaatcttgt
SEQ ID NO: 13	342gH1 Fab' heavy chain (including constant region)	EVQLVESGGGLVQPGGSLRLSCAVSGFSSTNYHVHWVRQ APGKGLEWMGVIWGDGDTSYNSVLKSRFTISRDTSKNTV YLQMNSLRAEDTAVYYCARQLTHYYVLAAWGQGTLVTVS SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCAA
SEQ ID NO: 27 (SEQ ID NO: 24 without signal sequence)	342gH1 Fab' heavy chain (including constant region)	atgaagaagactgctatagcaattgcagtggcgctagctggt ttcgccaccgtggcgcaagctgaggttcagctggtcgagtct ggaggcgggcttgtccagcctggtgggagcctgcgtctctct tgtgcagtgagcggcttcagctctaccaattaccatgtgcac tgggtgcgtcaggcacctgggaagggcctggagtggatgggt gttatttggggcgacggcgatacatcctacaactccgtcctg aagagccgtttcaccatttcccgtgacacctcaaagaatacc gtttacctccagatgaactctctccgcgcagaggacacagca gtctattactgtgcacgtcaactgacccactattacgttttg gcagcctggggtcaagggactctggtcacagtctcgagcgct tctacaaagggcccatcggtcttcccccctggcaccctcctcc aagagcacctctgggggcacagcggccctgggctgcctggtc aaggactacttccccgaaccggtgacggtgtcgtggaactca ggcgccctgaccagcggcgtgcacaccttcccggctgtccta cagtcctcaggactctactccctcagcagcgtggtgaccgtg ccctccagcagcttgggcacccagacctacatctgcaacgtg aatcacaagcccagcaacaccaaggtcgacaagaaagttgag cccaaatcttgtgacaaaactcacacatgcgccgcg

FIGURE 8

SEQ ID NO: 28: 342gL4gH1 **Fab** (no hinge) vector DNA sequence

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   1  atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac
  51  cgtagcgcaa gctGATATCc agatgaccca gagtccaagc agtctctccg
 101  ccagcgtagg cgatcgtgtg actattacct gtcgtgccag tgaggacctc
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 251  gtggcagtgg cagcggtact gactataccc tcacaatttc gtctctccag
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 351  caccttcggt cagggcacta aagtagaaat caaaCGTACG gtagcggccc
 401  catctgtctt catcttcccg ccatctgatg agcagttgaa atctggaact
 451  gcctctgttg tgtgcctgct gaataacttc tatcccagag aggccaaagt
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 601  acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt
 651  cacccatcag ggcctgagct caccagtaac aaaaagtttt aatagagggg
 701  agtgttaaaa tgaagaagac tgctatagca attgcagtgg cgctagctgg
 751  tttcgccacc gtggcgcaag ctgaggttCA GCTGgtcgag tctggaggcg
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 851  ttcagctcta ccaattacca tgtgcactgg gtgcgtcagg cacctgggaa
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1251  actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag
1301  tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag
1351  cttgggcacc cagacctaca tctgcaacgt gaatcacaag cccagcaaca
1401  ccaaggtcga caagaaagtt gagcccaaat cttgttaa
```

FIGURE 8 continued

SEQ ID NO: 41: 342gL4gH1 **Fab'** vector DNA sequence

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   1  atgaaaaaga cagctatcgc aattgcagtg gccttggctg gtttcgctac
  51  cgtagcgcaa gctGATATCc agatgaccca gagtccaagc agtctctccg
 101  ccagcgtagg cgatcgtgtg actattacct gtcgtgccag tgaggacctc
 151  tattacaacc tggcctggta tcagcgtaaa ccgggcaaag ccccgaagct
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 751  tttcgccacc gtggcgcaag ctgaggttCA GCTGgtcgag tctggaggcg
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1301  tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag
1351  cttgggcacc cagacctaca tctgcaacgt gaatcacaag cccagcaaca
1401  ccaaggtcga caagaaagtt gagcccaaat cttgtgacaa aactcacaca
1451  tgcgccgcg
```

FIGURE 9

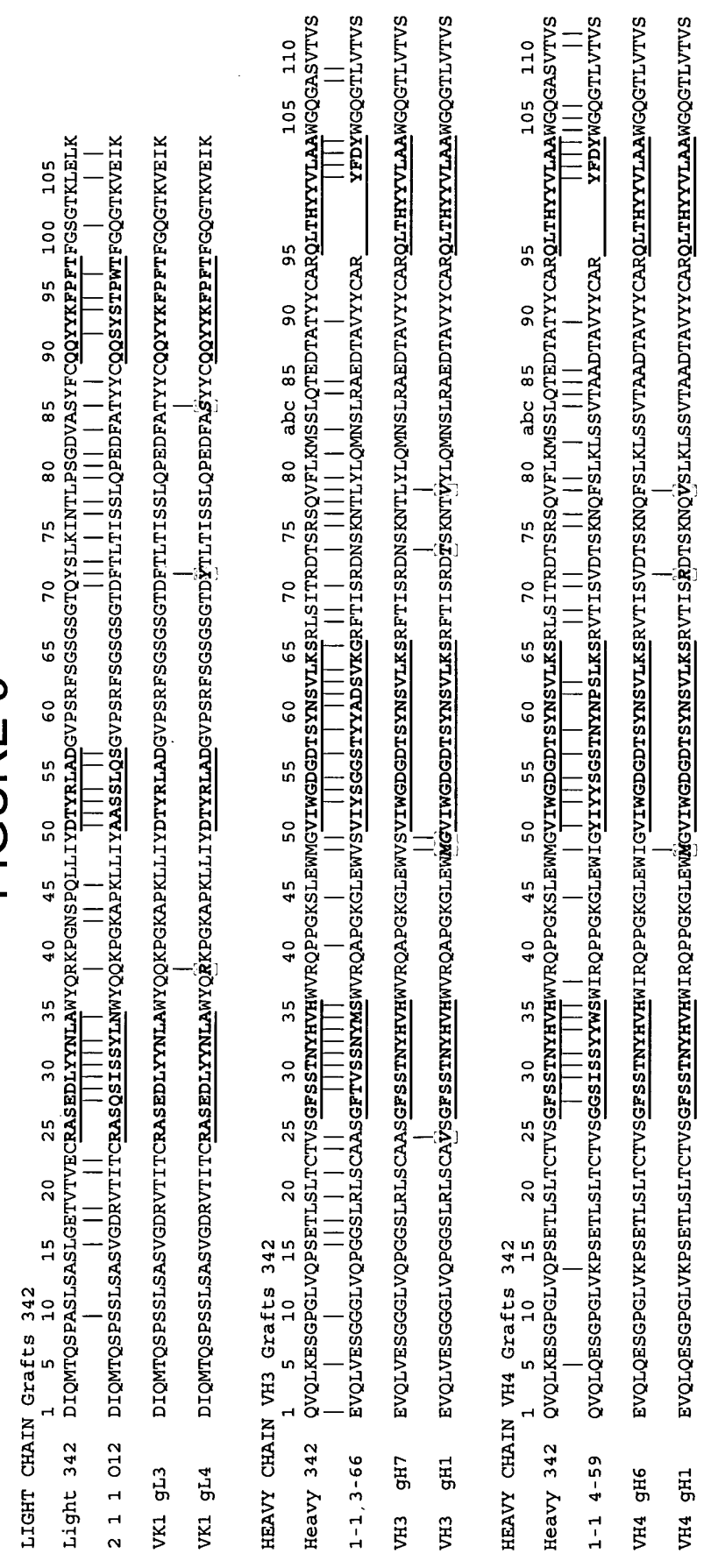

LIGHT CHAIN Grafts 342
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105
Light 342 DIQMTQSPASLSASLGETVTVECRASEDLYYNLAWYQRKPGNSPQLLIYDTYRLADGVPSRFSGSGSGTQYSLKINTLPSGDVASYFCQQYYKFPFTFGSGTKLELK
2 1 1 O12 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKVEIK
VK1 gL3 DIQMTQSPSSLSASVGDRVTITCRASEDLYYNLAWYQQKPGKAPKLLIYDTYRLADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYYKFPFTFGQGTKVEIK
VK1 gL4 DIQMTQSPSSLSASVGDRVTITCRASEDLYYNLAWYQRKPGKAPKLLIYDTYRLADGVPSRFSGSGSGTDYTLTISSLQPEDFASYYCQQYYKFPFTFGQGTKVEIK
HEAVY CHAIN VH3 Grafts 342
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 abc 85 90 95 105 110
Heavy 342 QVQLKESGPGLVQPSETLSLTCTVSGFSSTNYHVHWVRQPPGKSLEWMGVIWGDGDTSYNSVLKSRLSITRDTSRSQVFLKMSSLQTEDTATYYCARQLTHYYVLAAWGQGASVTVS
1-1,3-66 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR YFDYWGQGTLVTVS
VH3 gH7 EVQLVESGGGLVQPGGSLRLSCAASGFSSTNYHVHWVRQAPGKGLEWVSVIWGDGDTSYNSVLKSRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARQLTHYYVLAAWGQGTLVTVS
VH3 gH1 EVQLVESGGGLVQPGGSLRLSCAVSGFSSTNYHVHWVRQAPGKGLEWMGVIWGDGDTSYNSVLKSRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARQLTHYYVLAAWGQGTLVTVS
HEAVY CHAIN VH4 Grafts 342
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 abc 85 90 95 105 110
Heavy 342 QVQLKESGPGLVQPSETLSLTCTVSGFSSTNYHVHWVRQPPGKSLEWMGVIWGDGDTSYNSVLKSRLSITRDTSRSQVFLKMSSLQTEDTATYYCARQLTHYYVLAAWGQGASVTVS
1-1 4-59 QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR YFDYWGQGTLVTVS
VH4 gH6 EVQLQESGPGLVKPSETLSLTCTVSGFSSTNYHVHWIRQPPGKGLEWIGVIWGDGDTSYNSVLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARQLTHYYVLAAWGQGTLVTVS
VH4 gH1 EVQLQESGPGLVKPSETLSLTCTVSGFSSTNYHVHWIRQPPGKGLEWMGVIWGDGDTSYNSVLKSRVTISRDTSKNQVSLKLSSVTAADTAVYYCARQLTHYYVLAAWGQGTLVTVS

FIGURE 10: Anti-CD154 antibody 381

V_L Sequence

SEQ ID NO: 54 (underlined sequence is a CDR sequence)
DIQMTQSPTS LSASLGETVS IECLAGEDIS NVLAWYQQKS GGSPQLLIYA
ANRLQDGVPS RFSGSGSGTR YSLKISGMRP EDEADYFCQQ TFRYPLTFGS
GTKLELK

SEQ ID NO: 55
GACATCCAGA TGACACAGTC TCCAACTTCC CTGTCTGCAT CTCTCGGAGA
AACTGTCTCC ATCGAATGTC TAGCAGGTGA AGACATTTCC AATGTTTTAG
CGTGGTATCA GCAGAAGTCA GGGGGGTCTC CTCAGCTCCT GATCTATGCT
GCAAATAGGT TACAAGACGG GGTCCCCTCA CGGTTCAGTG GCAGTGGATC
TGGCACACGG TATTCTCTCA AGATCAGTGG CATGCGACCT GAAGATGAAG
CAGATTATTT CTGTCAACAG ACTTTCAGGT ATCCGCTCAC GTTCGGTTCT
GGGACCAAGC TGGAATTGAA A

V_H Sequence

SEQ ID NO: 56 (underlined sequence is a CDR sequence)
EVPLVESGGG LVQPGRSMKL SCVASGFTFS DYYMAWVRQA PKKGLEWVAS
ISYEGSSTYY GDSVKGRFTV SRDIAKSTLY LQMHSLKSED TAIYYCARHD
DSPGYYFDYW GQGVMVTVS

SEQ ID NO: 57
GAGGTGCCGC TGGTGGAGTC TGGGGGAGGC TTAGTGCAGC CTGGAAGGTC
CATGAAACTT TCCTGTGTAG CCTCAGGATT CACTTTCAGT GACTATTACA
TGGCCTGGGT CCGCCAGGCT CCAAAGAAGG GTCTGGAGTG GGTCGCATCC
ATTAGTTATG AGGGTAGTAG TACTTACTAT GGAGACTCCG TGAAGGGCCG
ATTCACTGTC TCCAGAGATA TTGCAAAAAG CACCCTATAC CTTCAAATGC
ACAGTCTGAA GTCTGAGGAT ACGGCCATTT ATTATTGTGC ACGACATGAC
GATAGTCCAG GATACTACTT TGATTATTGG GGCCAAGGAG TCATGGTCAC
AGTCTCG

FIGURE 11: Anti-CD154 antibody 338

V_L Sequence

SEQ ID NO: 58 (underlined sequence is a CDR sequence)
DIQMTQSPAS LSASLGETVT IECRTSEDIY SNLAWYRQRP GKSPQLLIYD
TNRLADGVPS RFSGSGSGTQ YSLKINSLQS EDVASYFCQH YSNFPWTFGG
DTKLELK

SEQ ID NO: 59
GACATCCAGA TGACACAGTC TCCGGCTTCC CTGTCTGCAT CTCTGGGAGA
AACTGTCACC ATCGAATGTC GAACAAGTGA GGACATTTAC AGTAATTTAG
CGTGGTATCG GCAGAGACCA GGGAAGTCTC CTCAGCTCCT GATCTATGAT
ACAAATAGAT TGGCTGATGG GGTCCCGTCA CGGTTCAGTG GCAGTGGATC
TGGCACACAA TATTCTCTAA AGATAAACAG CCTGCAATCT GAAGATGTCG
CCAGCTATTT CTGTCAACAC TATAGCAATT TTCCGTGGAC CTTCGGTGGA
GACACCAAGC TGGAATTGAA A

V_H Sequence

SEQ ID NO: 60 (underlined sequence is a CDR sequence)
QVQLTESGPG LVQPSQTLSL TCTVSGFSLT SHHISWVRQP PGKGLEWVGV
MWNDGGTLYN SALKSRPSIS RDTSKSQVFL KMSSLQTEDT ATYYCARGKM
HYYVLDAWGQ GASVTVS

SEQ ID NO: 61
CAGGTGCAGC TGACGGAGTC AGGGCCTGGC CTGGTGCAGC CCTCACAGAC
CCTGTCTCTC ACCTGCACTG TCTCTGGGTT CTCATTAACC AGCCATCATA
TATCCTGGGT TCGACAGCCT CCAGGAAAAG GTCTGGAGTG GGTGGGAGTC
ATGTGGAATG ATGGAGGCAC ATTATATAAT TCAGCTCTCA AGTCTCGACC
GAGCATCAGT AGGGACACCT CCAAGAGTCA GGTCTTCTTA AAAATGAGCA
GTCTGCAAAC TGAAGACACA GCCACTTACT ACTGTGCCAG GGGCAAAATG
CATTACTATG TTCTGGATGC CTGGGGTCAA GGAGCTTCAG TCACTGTCTC
G

FIGURE 12
Anti-Human CD154 (CD40L) Antibodies (Chimaeric Fab')

Antibody	Kd Biacore (pM)	CD40 Binding IC50 (ng/ml)	ICAM-1 Upreg'n IC50 (ng/ml)
Hu5c8 (whole Ig)	23	16 (n=6)	43 (n=10)
CA081-00294 (294)	107	26 (n=2)	364 (n=6)
CA081-00295 (295)	51	15 (n=2)	138 (n=6)
CA081-00300 (300)	43	15 (n=2)	113 (n=7)
CA081-00335 (335)	42	-	279 (n=3)
CA081-00303 (303)	130	51 (n=3)	252 (n=3)
CA081-00338 (338)	15	6 (n=2)	192 (n=6)
CA081-00342 (342)	16	8 (n=5)	53 (n=6)
CA081-00381 (381)	5	22 (n=2)	100 (n=2)
CA081-00402 (402)	48	12 (n=2)	92 (n=2)

FIGURE 13: hu5c8 kappa light chain

SEQ ID NO: 62 (underlined sequence is the signal sequence)

METDTLLLWV LLLWVPGSTG DIVLTQSPAT LSVSPGERAT ISCRASQRVS
SSTYSYMHWY QQKPGQPPKL LIKYASNLES GVPARFSGSG SGTDFTLTIS
SVEPEDFATY YCQHSWEIPP TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK
SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC

SEQ ID NO: 63 (mature protein)

DIVLTQSPAT LSVSPGERAT ISCRASQRVS SSTYSYMHWY QQKPGQPPKL
LIKYASNLES GVPARFSGSG SGTDFTLTIS SVEPEDFATY YCQHSWEIPP
TFGGGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC

SEQ ID NO: 64 (open reading frame)

ATGGAGACAG ACACACTCCT GTTATGGGTG CTGCTGCTCT GGGTTCCAGG
TTCCACTGGT GACATTGTAC TGACACAGTC TCCTGCTACC TTATCTGTAT
CTCCGGGAGA GAGGGCCACC ATCTCATGCA GGGCCAGCCA ACGTGTCAGT
TCATCTACCT ATAGTTATAT GCACTGGTAC CAACAGAAAC CAGGACAGCC
ACCCAAACTC CTCATCAAGT ATGCATCCAA CCTAGAATCT GGGGTCCCTG
CCAGGTTCAG TGGCAGTGGG TCTGGGACTG ACTTCACCCT CACCATCTCT
TCTGTGGAGC CGGAGGATTT TGCAACATAT TACTGTCAGC ACAGTTGGGA
GATTCCTCCG ACGTTCGGTG GAGGGACCAA GCTGGAGATC AAACGAACTG
TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
ACAGGGGAGA GTGTTAG

FIGURE 14: hu5c8 aglyP-huIgG4 heavy chain

SEQ ID NO: 65 (underlined sequence is the signal sequence)

MDWTWRVFCL LAVAPGAHSQ VQLVQSGAEV VKPGASVKLS CKASGYIFTS
YYMYWVKQAP GQGLEWIGEI NPSNGDTNFN EKFKSKATLT VDKSASTAYM
ELSSLRSEDT AVYYCTRSDG RNDMDSWGQG TLVTVSSAST KGPSVFPLAP
CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE
FLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE
VHNAKTKPRE EQFNSAYRVV SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE
KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY PSDIAVEWES
NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF SCSVMHEALH
NHYTQKSLSL SLG

SEQ ID NO: 66 (mature protein: S228P/T299A mutations are underlined and in bold)

QVQLVQSGAE VVKPGASVKL SCKASGYIFT SYYMYWVKQA PGQGLEWIGE
INPSNGDTNF NEKFKSKATL TVDKSASTAY MELSSLRSED TAVYYCTRSD
GRNDMDSWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT
CNVDHKPSNT KVDKRVESKY GPPCP**P**CPAP EFLGGPSVFL FPPKPKDTLM
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNS**A**YRV
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLG

SEQ ID NO: 67

ATGGACTGGA CCTGGAGGGT CTTCTGCTTG CTGGCTGTAG CACCAGGTGC
CCACTCCCAG GTCCAACTGG TGCAGTCAGG GGCTGAAGTG GTGAAGCCTG
GGGCTTCAGT GAAGTTGTCC TGCAAGGCTT CTGGCTACAT CTTCACCAGT
TATTATATGT ACTGGGTGAA GCAGGCGCCC GGACAAGGCC TTGAGTGGAT
TGGAGAGATT AATCCTAGCA ATGGTGATAC TAACTTCAAT GAGAAGTTCA
AGAGTAAGGC CACACTGACT GTAGACAAAT CCGCCAGCAC AGCATACATG
GAGCTCAGCA GCCTGAGGTC TGAGGACACT GCGGTCTATT ACTGTACAAG
ATCGGACGGT AGAAATGATA TGGACTCCTG GGGCCAAGGG ACCCTGGTCA
CCGTCTCCTC AGCTTCCACC AAGGGCCCAT CCGTCTTCCC CCTGGCGCCC
TGCTCCAGAT CTACCTCCGA GAGCACAGCC GCCCTGGGCT GCCTGGTCAA
GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA
CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACGAAGAC
CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA
GAGTTGAGTC CAAATATGGT CCCCCATGCC CACCGTGCCC AGCACCTGAG
TTCCTGGGGG GACCATCAGT CTTCCTGTTC CCCCCAAAAC CCAAGGACAC
TCTCATGATC TCCCGGACCC CTGAGGTCAC GTGCGTGGTG GTGGACGTGA
GCCAGGAAGA CCCCGAGGTC CAGTTCAACT GGTACGTGGA TGGCGTGGAG

FIGURE 14 continued

GTGCATAATG CCAAGACAAA GCCGCGGGAG GAGCAGTTCA ACAGCGCGTA
CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAACGGCA
AGGAGTACAA GTGCAAGGTC TCCAACAAAG GCCTCCCGTC CTCCATCGAG
AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAGCCAC AAGTGTACAC
CCTGCCCCCA TCCCAGGAGG AGATGACCAA GAACCAGGTC AGCCTGACCT
GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA GTGGGAGAGC
AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TCCTCGATTC
CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT
GGCAGGAGGG GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC
AACCACTACA CACAGAAGAG CCTCTCCCTG TCTCTGGGTT GA

FIGURE 15: hu342 kappa light chain

SEQ ID NO: 68 (underlined sequence is the signal sequence)

MDMRVPAQLL GLLLLWLRGA RCDIQMTQSP SSLSASVGDR VTITCRASED
LYYNLAWYQR KPGKAPKLLI YDTYRLADGV PSRFSGSGSG TDYTLTISSL
QPEDFASYYC QQYYKFPFTF GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG
TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

SEQ ID NO: 69 (mature protein)

DIQMTQSPSS LSASVGDRVT ITCRASEDLY YNLAWYQRKP GKAPKLLIYD
TYRLADGVPS RFSGSGSGTD YTLTISSLQP EDFASYYCQQ YYKFPFTFGQ
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG
LSSPVTKSFN RGEC

SEQ ID NO: 70 (open reading frame)

ATGGACATGA GGGTCCCCGC TCAGCTCCTG GGGCTCCTGC TACTCTGGCT
CCGAGGTGCC AGATGTGATA TCCAGATGAC CCAGAGTCCA AGCAGTCTCT
CCGCCAGCGT AGGCGATCGT GTGACTATTA CCTGTCGTGC CAGTGAGGAC
CTCTATTACA ACCTGGCCTG GTATCAGCGT AAACCGGGCA AAGCCCCGAA
GCTGCTCATC TATGATACGT ACCGCCTGGC TGACGGTGTG CCAAGCCGTT
TCAGTGGCAG TGGCAGCGGT ACTGACTATA CCCTCACAAT TTCGTCTCTC
CAGCCGGAAG ATTTCGCCTC TTACTATTGT CAGCAATATT ACAAGTTCCC
TTTCACCTTC GGTCAGGGCA CTAAAGTAGA AATCAAACGT ACGGTGGCTG
CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA
ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA
GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA
AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
GAGAGTGTTA G

FIGURE 16: hu342 aglyP-hulgG4 heavy chain

SEQ ID NO: 71 (underlined sequence is the signal sequence)

MDWTWRVFCL LAVAPGAHSE VQLVESGGGL VQPGGSLRLS CAVSGFSSTN
YHVHWVRQAP GKGLEWMGVI WGDGDTSYNS VLKSRFTISR DTSKNTVYLQ
MNSLRAEDTA VYYCARQLTH YYVLAAWGQG TLVTVSSAST KGPSVFPLAP
CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE
FLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE
VHNAKTKPRE EQFNSAYRVV SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE
KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY PSDIAVEWES
NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF SCSVMHEALH
NHYTQKSLSL SLG

SEQ ID NO: 72 (mature protein: S228P/T299A mutations are underlined and in bold)

EVQLVESGGG LVQPGGSLRL SCAVSGFSST NYHVHWVRQA PGKGLEWMGV
IWGDGDTSYN SVLKSRFTIS RDTSKNTVYL QMNSLRAEDT AVYYCARQLT
HYYVLAAWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT
CNVDHKPSNT KVDKRVESKY GPPCP**P**CPAP EFLGGPSVFL FPPKPKDTLM
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNS**A**YRV
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLG

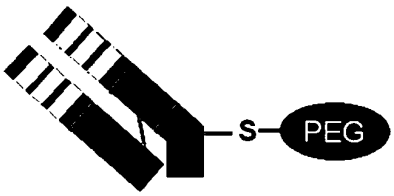
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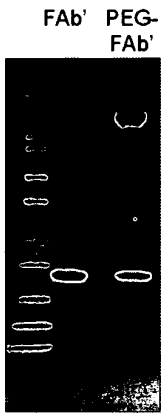
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CCACTCCGAA GTACAATTGG TCGAGTCTGG AGGCGGGCTT GTCCAGCCTG
GTGGGAGCCT GCGTCTCTCT TGTGCAGTGA GCGGCTTCAG CTCTACCAAT
TACCATGTGC ACTGGGTGCG TCAGGCACCT GGGAAGGGCC TGGAGTGGAT
GGGTGTTATT TGGGGCGACG GCGATACATC CTACAACTCC GTCCTGAAGA
GCCGTTTCAC CATTTCCCGT GACACCTCAA AGAATACCGT TTACCTCCAG
ATGAACTCTC TCCGCGCAGA GGACACAGCA GTCTATTACT GTGCACGTCA
ACTGACCCAC TATTACGTTT TGGCAGCCTG GGGTCAAGGG ACTCTGGTCA
CAGTCTCGAG CGCTTCAACC AAGGGCCCAT CCGTCTTCCC CCTGGCGCCC
TGCTCCAGAT CTACCTCCGA GAGCACAGCC GCCCTGGGCT GCCTGGTCAA
GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA
CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACGAAGAC
CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA
GAGTTGAGTC CAAATATGGT CCCCCATGCC CACCGTGCCC AGCACCTGAG
TTCCTGGGGG GACCATCAGT CTTCCTGTTC CCCCCAAAAC CCAAGGACAC
TCTCATGATC TCCCGGACCC CTGAGGTCAC GTGCGTGGTG GTGGACGTGA

FIGURE 16 continued

GCCAGGAAGA CCCCGAGGTC CAGTTCAACT GGTACGTGGA TGGCGTGGAG
GTGCATAATG CCAAGACAAA GCCGCGGGAG GAGCAGTTCA ACAGCGCGTA
CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAACGGCA
AGGAGTACAA GTGCAAGGTC TCCAACAAAG GCCTCCCGTC CTCCATCGAG
AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAGCCAC AAGTGTACAC
CCTGCCCCCA TCCCAGGAGG AGATGACCAA GAACCAGGTC AGCCTGACCT
GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA GTGGGAGAGC
AATGGGCAGC CGGAGAACAA CTACAAGACC ACGCCTCCCG TCCTCGATTC
CGACGGCTCC TTCTTCCTCT ACAGCAGGCT AACCGTGGAC AAGAGCAGGT
GGCAGGAGGG GAATGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC
AACCACTACA CACAGAAGAG CCTCTCCCTG TCTCTGGGTT GA

FIGURE 17





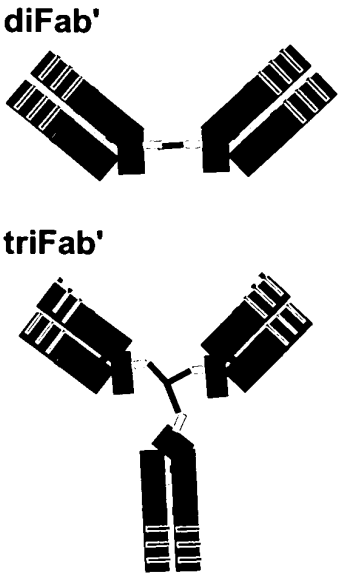


FIGURE 18

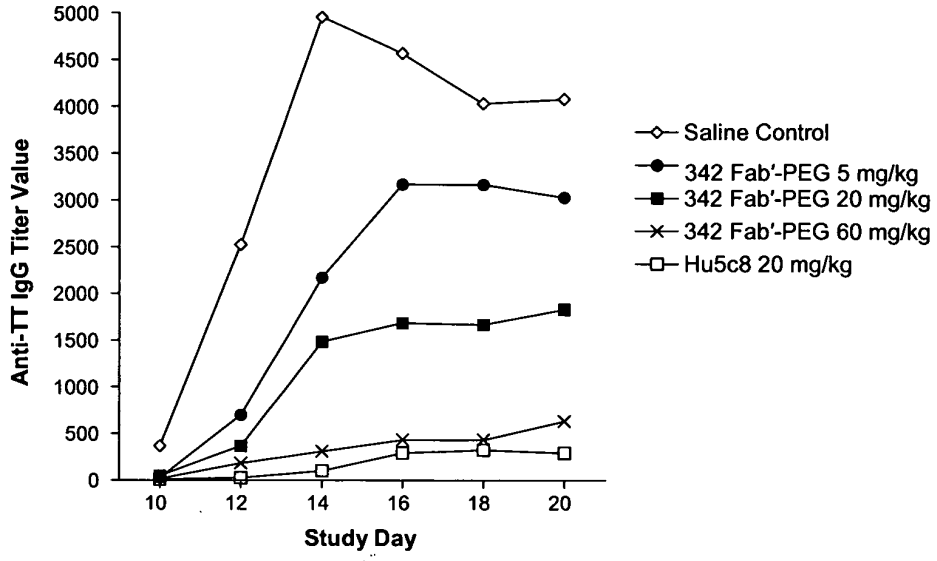
Activity Profile of 342 Fab' & Fab'-PEG Entities

342 = gL4gH1 graft

	Kd Biacore (pM)	CD40 Binding IC50 (ng/ml)	ICAM-1 Upreg'n IC50 (ng/ml)	Competition Binding Assay IC50 (pM)
hu5c8 IgG1	25	31	37	54
342 Fab'	28	12	40	24
342 Fab'-PEG	50	35	127	113
342 Di-Fab'	nd	9	22	nd
342 Di-Fab'-PEG	45	32	58	26
342 Tri-Fab'	nd	9	31	nd
342 Tri-Fab'-PEG	nd	8	36	nd
342 aglycosyl IgG4	nd	25	48	35

FIGURE 19: Inhibition of IgG Immune Response to Tetanus Toxoid in Cynomolgus Monkeys

Primary Immune Response to TT



Immune Response to TT at Days 30-50

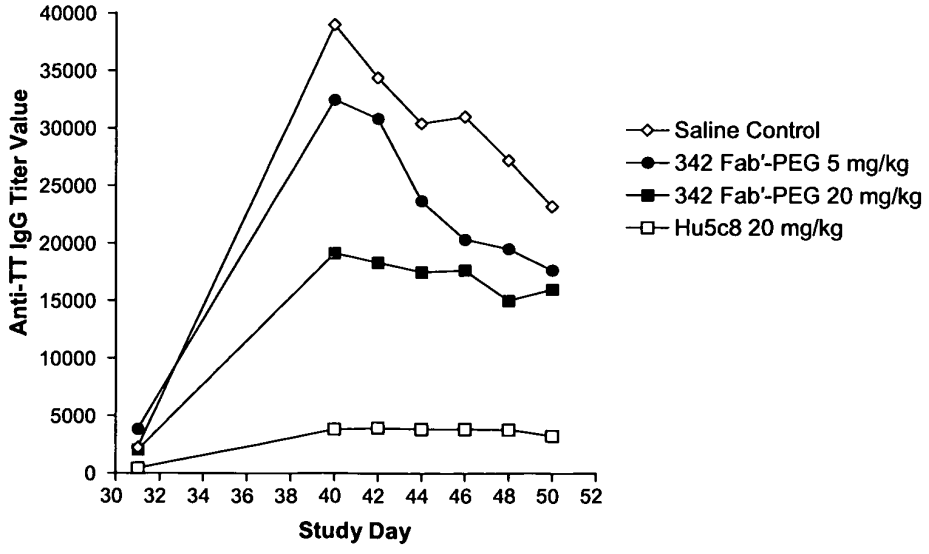


FIGURE 20: Inhibition of IgG Immune Response to Tetanus Toxoid in Cynomolgus Monkeys

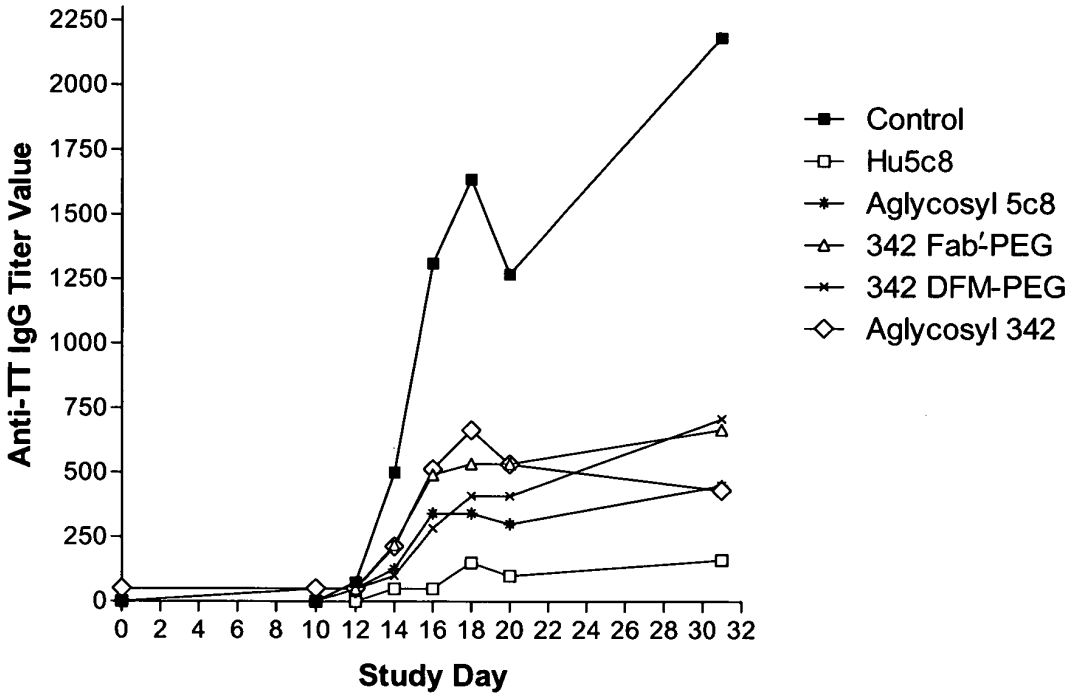


FIGURE 21: Primary IgM Immune Response to Tetanus Toxoid in Cynomolgus Monkeys

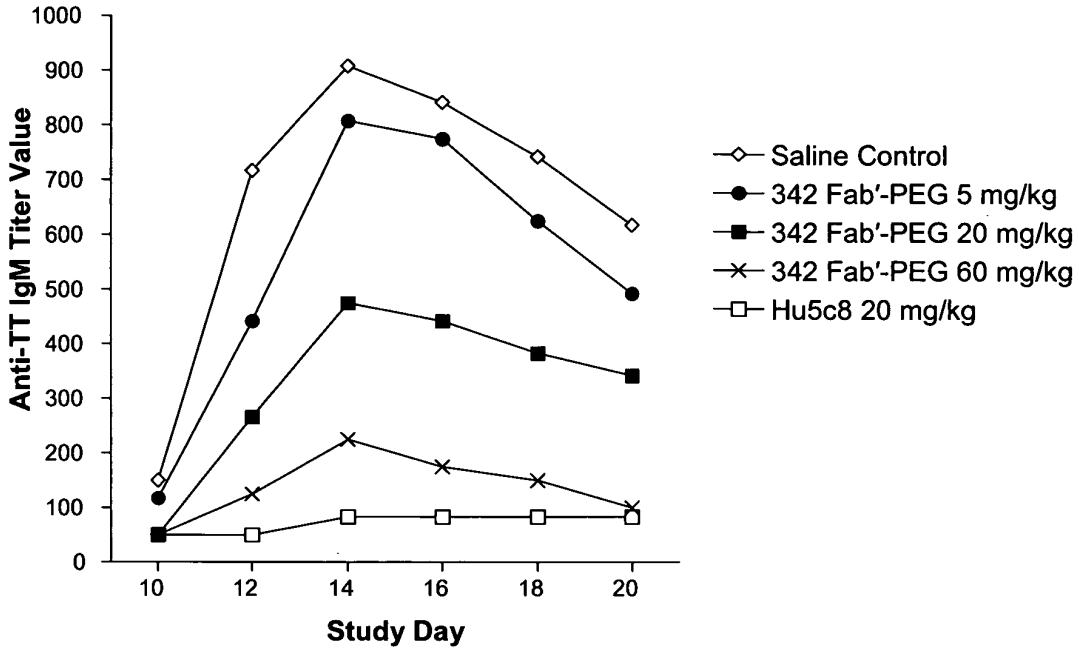


FIGURE 22: Pharmacokinetics of 342 Fab'-PEG in Cynomolgus Monkeys

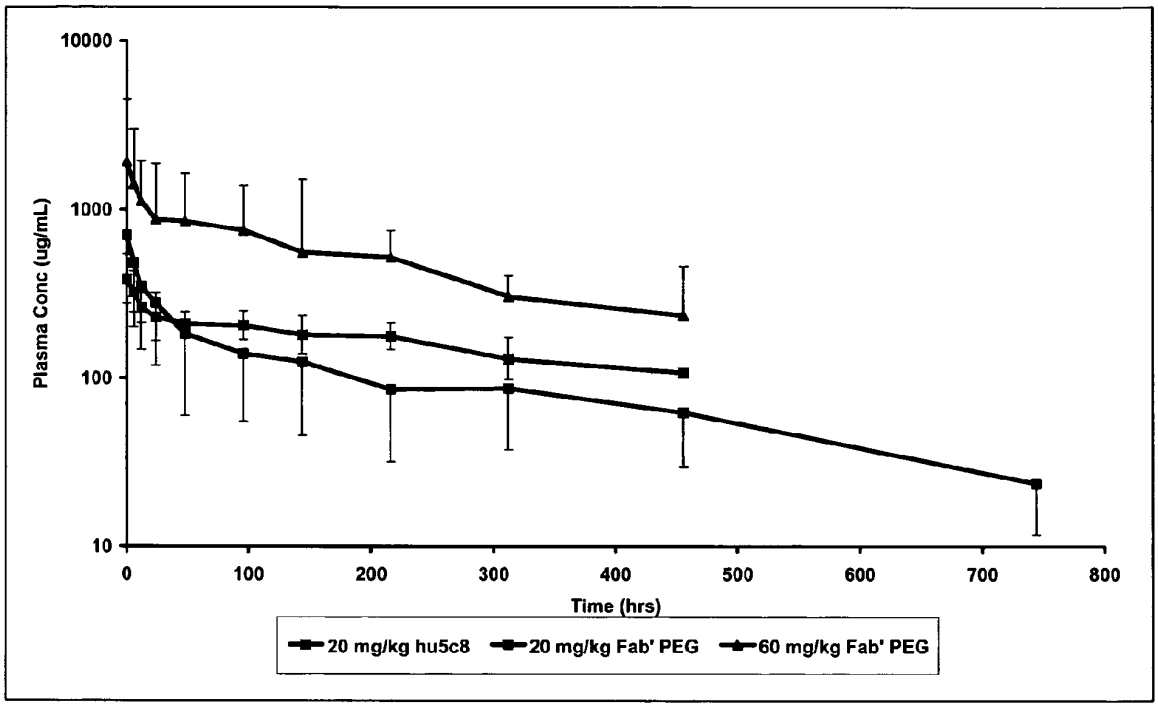


FIGURE 23

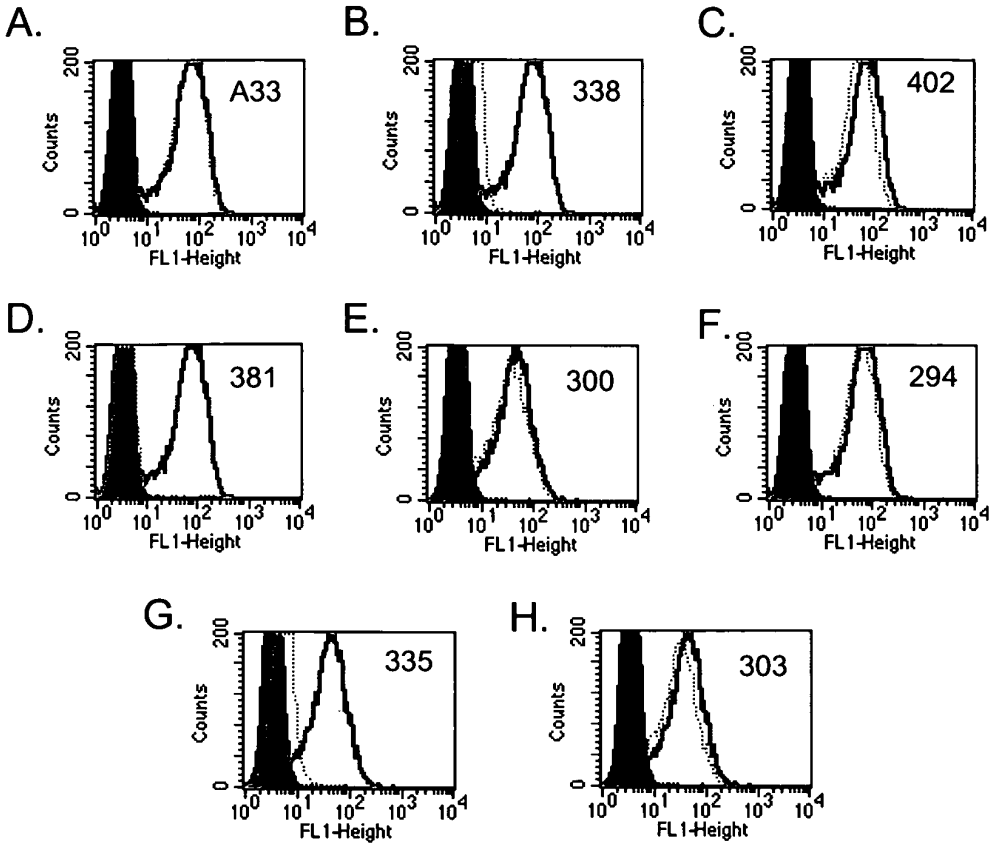


FIGURE 24

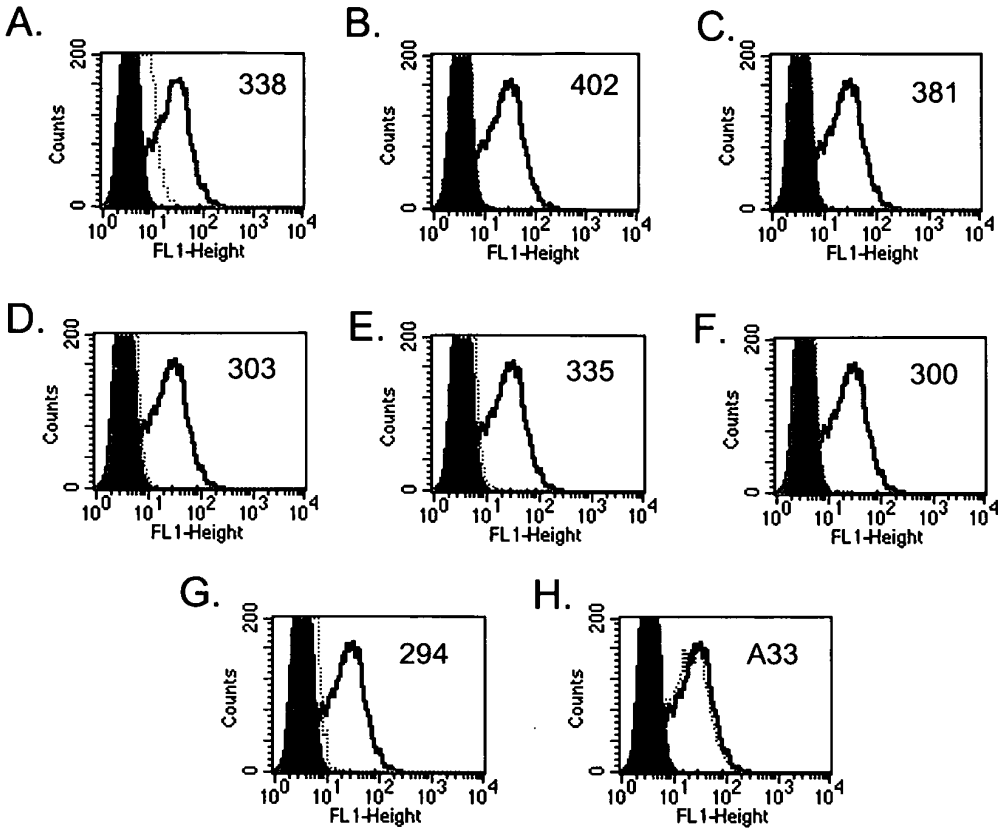
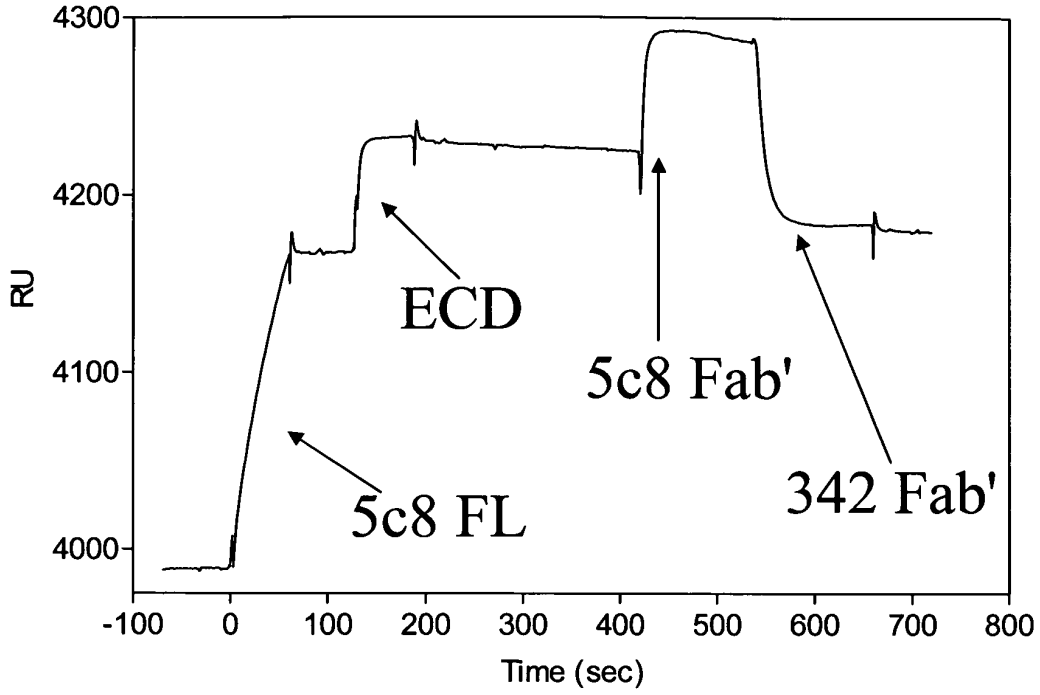


FIGURE 25

A.


4300
4200
4100
4000
RU
ECD
5c8 Fab'
5c8 FL
342 Fab'
-100
0
100
200
300
400
500
600
700
800
Time (sec)

B.

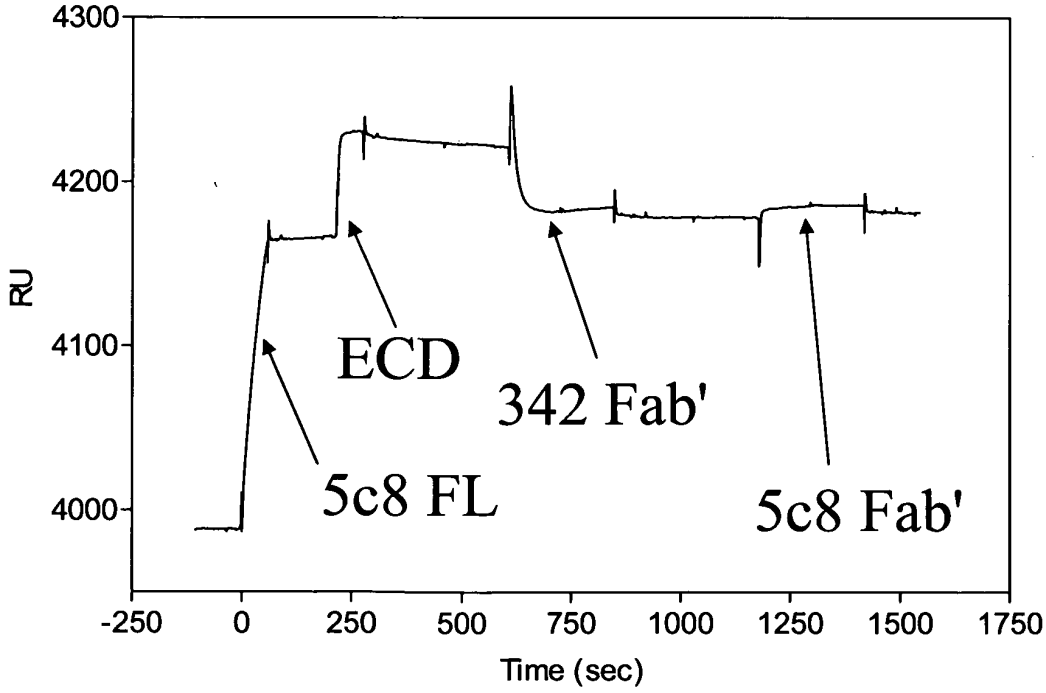

4300
4200
4100
4000
RU
ECD
342 Fab'
5c8 FL
5c8 Fab'
-250
0
250
500
750
1000
1250
1500
1750
Time (sec)

FIGURE 25 continued

C.

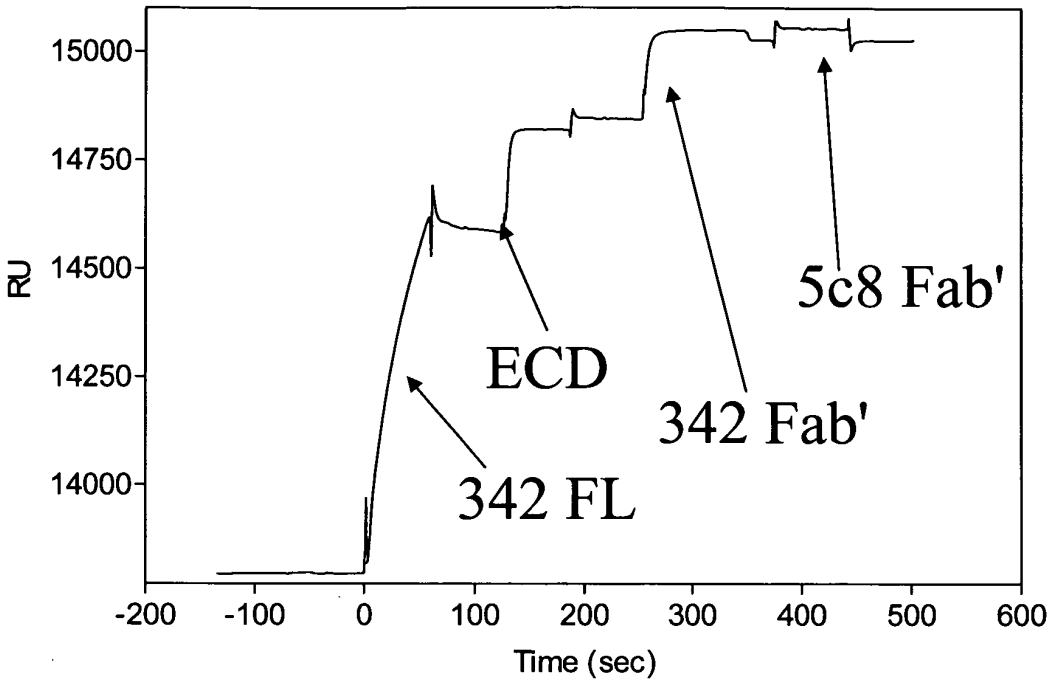
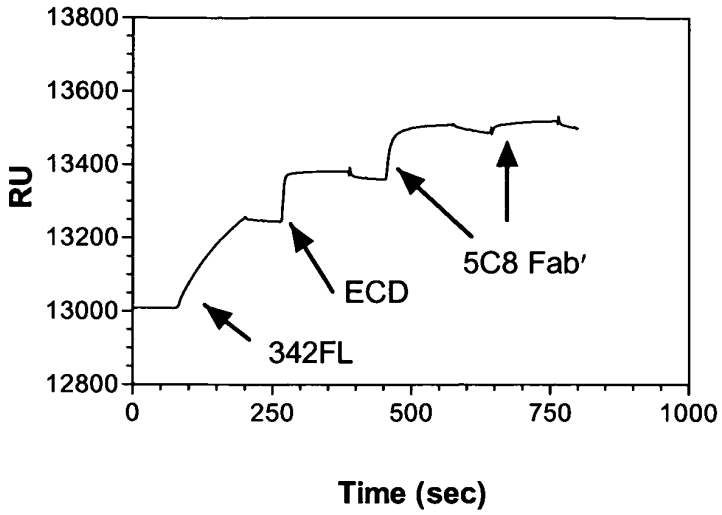
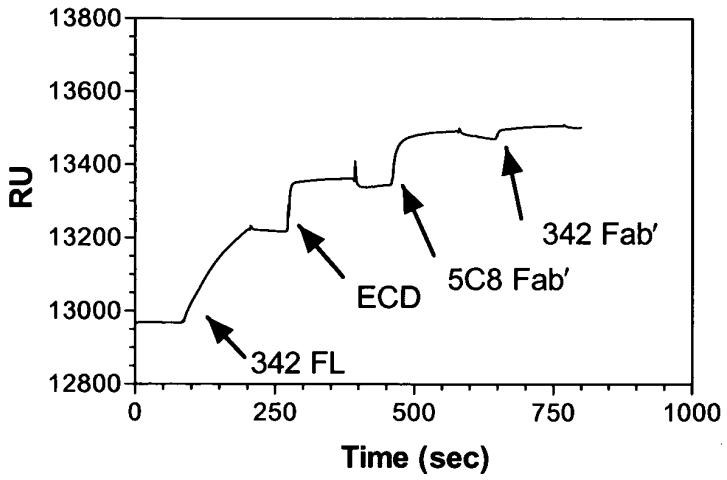


FIGURE 25 continued

D.



E.



F.

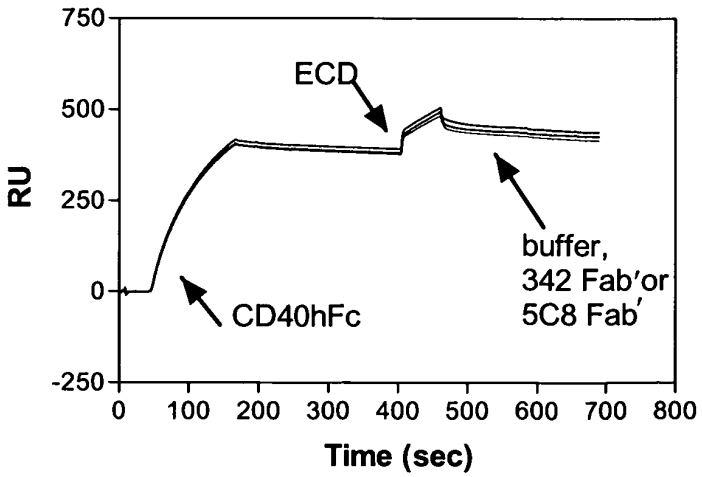
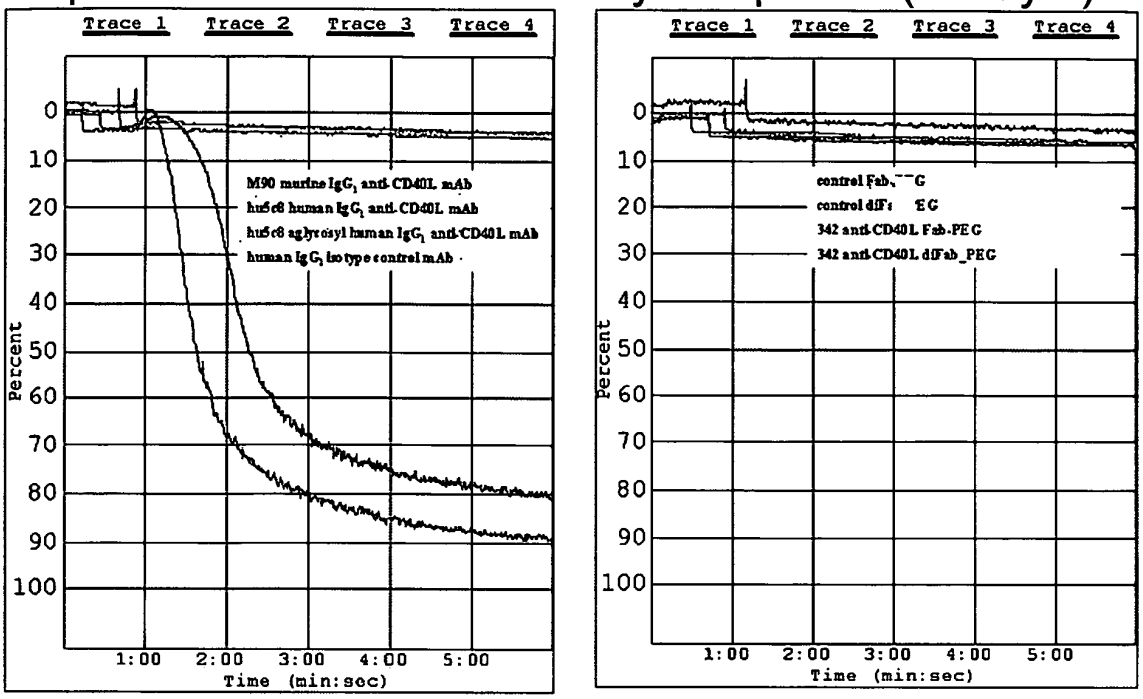


FIGURE 26: Representative platelet aggregation in response to rhsCD40L/antibody complexes (Assay 1)



human IgG_1 isotype control mAb

hu5c8 aglycosyl human IgG_1 anti CD40L mAb

M90 murine IgG_1 anti-CD40L mAb

hu5c8 human IgG_1 anti-CD40L mAb

342 anti CD40L diFab'-PEG

342 anti CD40L Fab'-PEG

control diFab'-PEG

control Fab'-PEG

FIGURE 26 continued

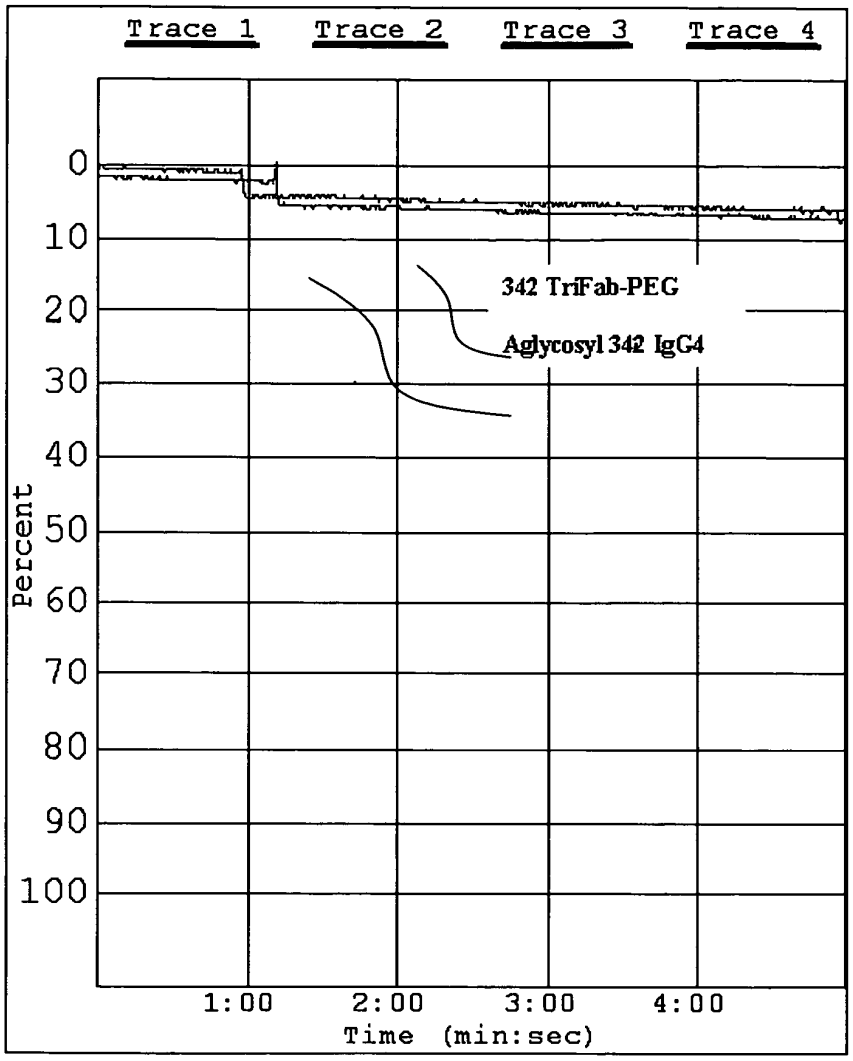


FIGURE 27: Representative platelet aggregation in response to control and anti-CD154 antibodies (Assay 2)

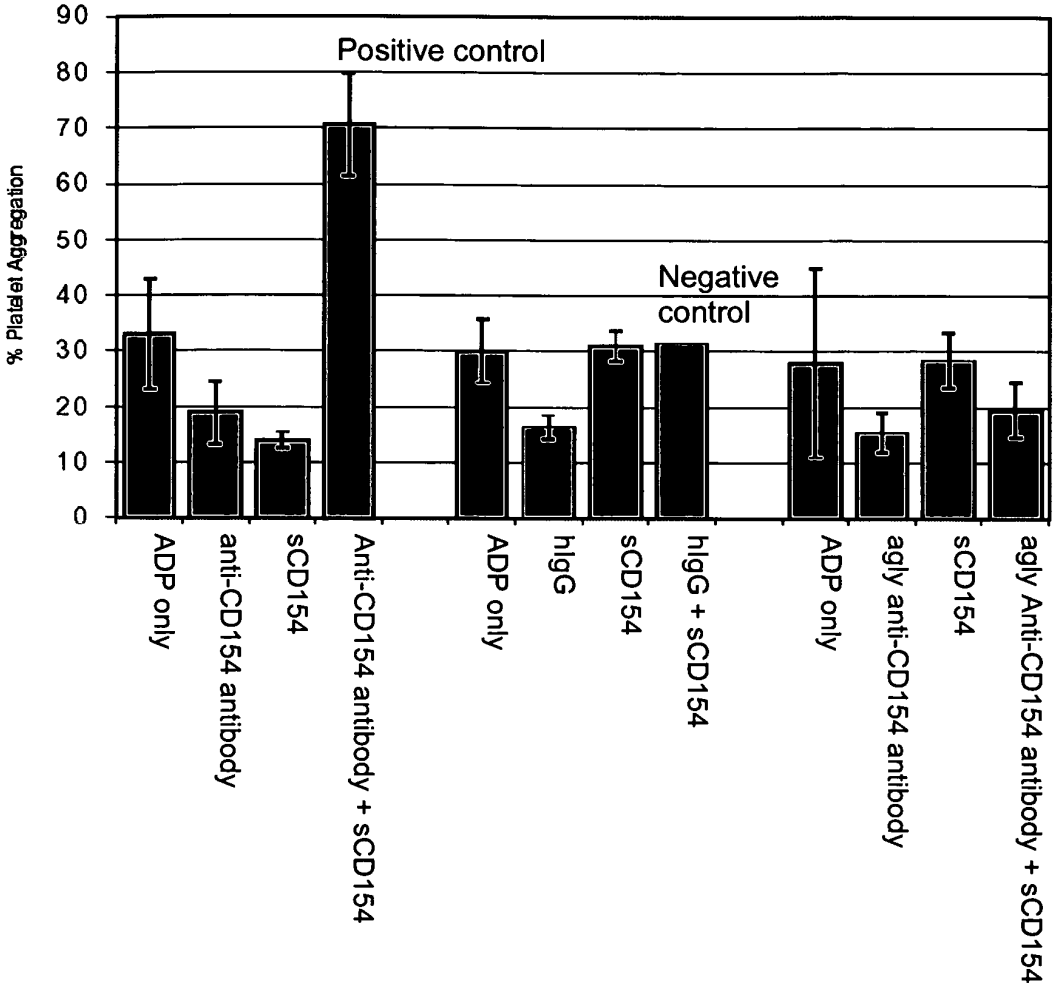


FIGURE 28

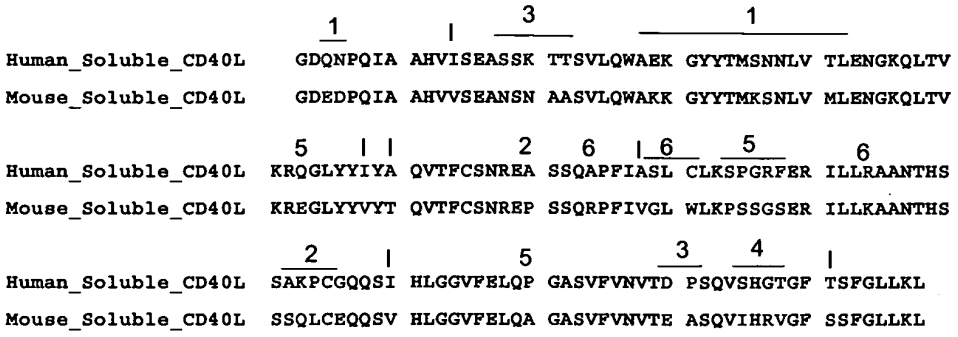
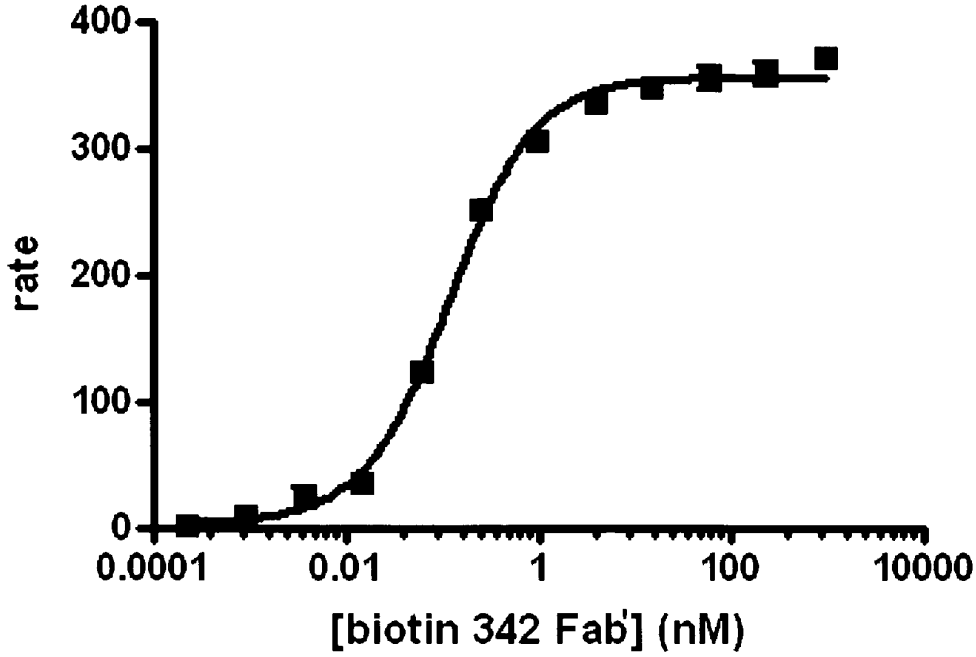

Human_Soluble_CD40L GDQNPQIA AHVISEASSK TTSVLQWAEK GYYTMSNNLV TLENGKQLTV
Mouse_Soluble_CD40L GDEDPQIA AHVVSEANSN AASVLQWAKK GYYTMKSNLV MLENGKQLTV
Human_Soluble_CD40L KRQGLYYIYA QVTFCSNREA SSQAPFIASL CLKSPGRFER ILLRAANTHS
Mouse_Soluble_CD40L KREGLYYVYT QVTFCSNREP SSQRPFIVGL WLKPSSGSER ILLKAANTHS
Human_Soluble_CD40L SAKPCGQQSI HLGGVFELQP GASVFVNVTD PSQVSHGTGF TSFGLLKL
Mouse_Soluble_CD40L SSQLCEQQSV HLGGVFELQA GASVFVNVTE ASQVIHRVGF SSFGLLKL

FIGURE 29

A.


400
300
200
100
0
rate
0.0001
0.01
1
100
10000
[biotin 342 Fab'] (nM)

B.

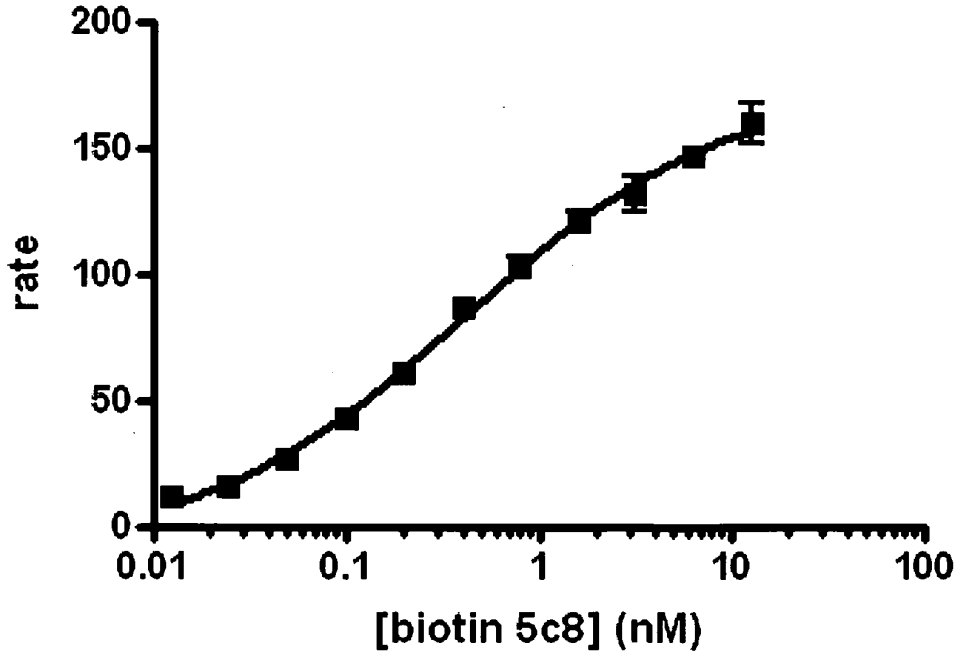
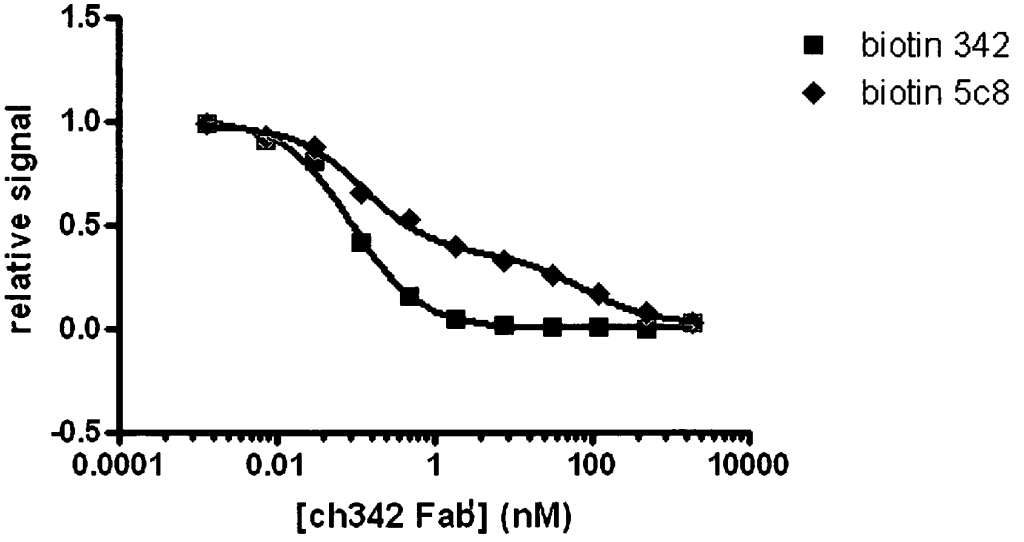

200
150
100
50
0
rate
0.01
0.1
1
10
100
[biotin 5c8] (nM)

FIGURE 29 continued

C.



D.

