Figure 1

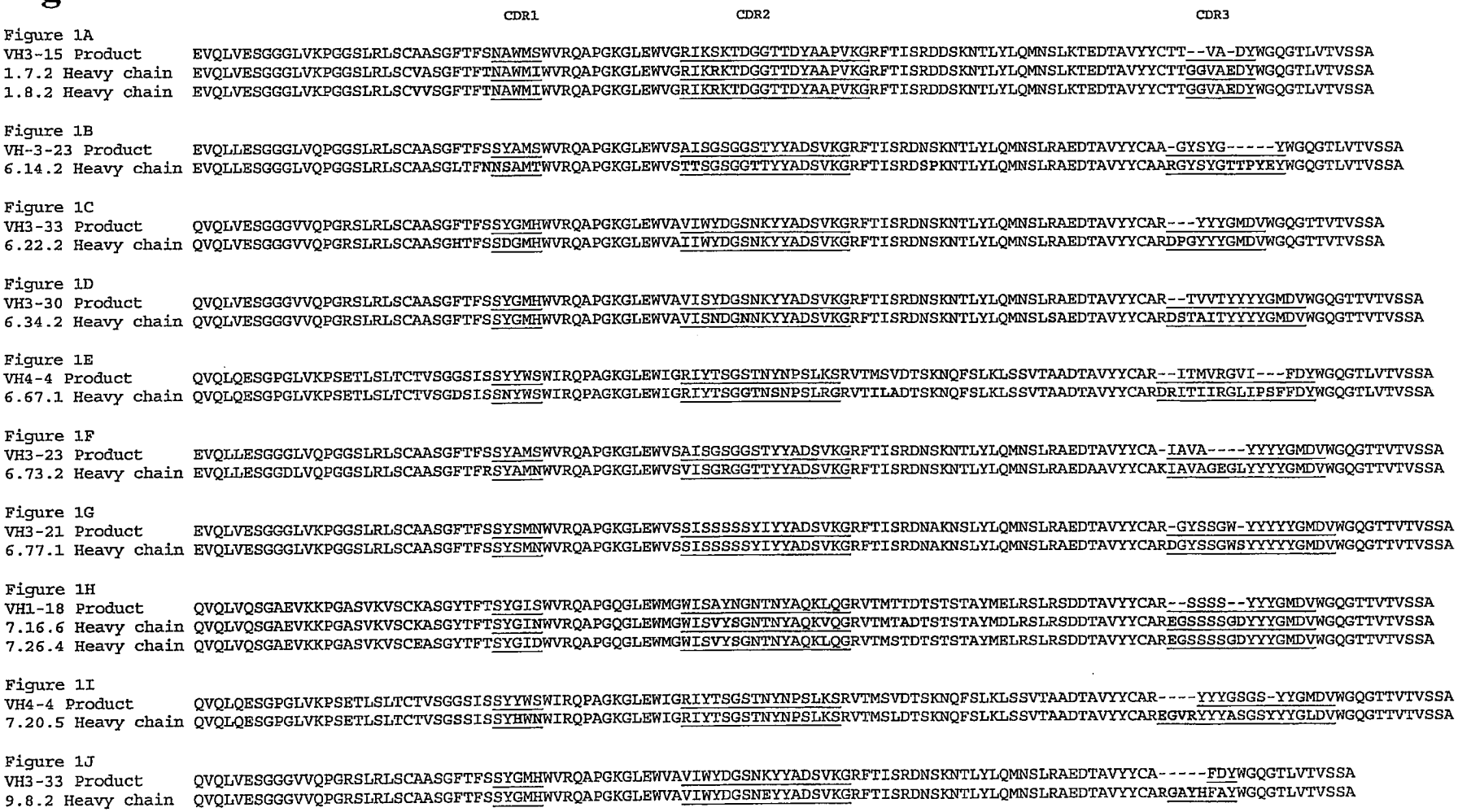

CDR1
CDR2
CDR3
Figure 1A
VH3-15 Product EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT--VA-DYWGQGTLVTVSSA
1.7.2 Heavy chain EVQLVESGGGLVKPGGSLRLSCVASGFTFTNAWMIWVRQAPGKGLEWVGRIKRKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGGVAEDYWGQGTLVTVSSA
1.8.2 Heavy chain EVQLVESGGGLVKPGGSLRLSCVVSGFTFTNAWMIWVRQAPGKGLEWVGRIKRKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGGVAEDYWGQGTLVTVSSA
Figure 1B
VH-3-23 Product EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA-GYSYG-----YWGQGTLVTVSSA
6.14.2 Heavy chain EVQLLESGGGLVQPGGSLRLSCAASGLTFNNSAMTWVRQAPGKGLEWVSTTSGSGGTTYYADSVKGRFTISRDSPKNTLYLQMNSLRAEDTAVYYCAARGYSYGTTPYEYWGQGTLVTVSSA
Figure 1C
VH3-33 Product QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---YYYGMDVWGQGTTVTVSSA
6.22.2 Heavy chain QVQLVESGGGVVQPGRSLRLSCAASGHTFSSDGMHWVRQAPGKGLEWVAIIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDPGYYYGMDVWGQGTTVTVSSA
Figure 1D
VH3-30 Product QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--TVVTYYYYGMDVWGQGTTVTVSSA
6.34.2 Heavy chain QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISNDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLSAEDTAVYYCARDSTAITYYYYGMDVWGQGTTVTVSSA
Figure 1E
VH4-4 Product QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR--ITMVRGVI---FDYWGQGTLVTVSSA
6.67.1 Heavy chain QVQLQESGPGLVKPSETLSLTCTVSGDSISSNYWSWIRQPAGKGLEWIGRIYTSGGTNSNPSLRGRVTILADTSKNQFSLKLSSVTAADTAVYYCARDRITIIRGLIPSFFDYWGQGTLVTVSSA
Figure 1F
VH3-23 Product EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-IAVA----YYYYGMDVWGQGTTVTVSSA
6.73.2 Heavy chain EVQLLESGGDLVQPGGSLRLSCAASGFTFRSYAMNWVRQAPGKGLEWVSVISGRGGTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDAAVYYCAKIAVAGEGLYYYYGMDVWGQGTTVTVSSA
Figure 1G
VH3-21 Product EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR-GYSSGW-YYYYYGMDVWGQGTTVTVSSA
6.77.1 Heavy chain EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGYSSGWSYYYYYGMDVWGQGTTVTVSSA
Figure 1H
VH1-18 Product QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR--SSSS--YYYGMDVWGQGTTVTVSSA
7.16.6 Heavy chain QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGINWVRQAPGQGLEWMGWISVYSGNTNYAQKVQGRVTMTADTSTSTAYMDLRSLRSDDTAVYYCAREGSSSSGDYYYGMDVWGQGTTVTVSSA
7.26.4 Heavy chain QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGIDWVRQAPGQGLEWMGWISVYSGNTNYAQKLQGRVTMSTDTSTSTAYMELRSLRSDDTAVYYCAREGSSSSGDYYYGMDVWGQGTTVTVSSA
Figure 1I
VH4-4 Product QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR----YYYGSGS-YYGMDVWGQGTTVTVSSA
7.20.5 Heavy chain QVQLQESGPGLVKPSETLSLTCTVSGSSISSYHWNWIRQPAGKGLEWIGRIYTSGSTNYNPSLKSRVTMSLDTSKNQFSLKLSSVTAADTAVYYCAREGVRYYYASGSYYYGLDVWGQGTTVTVSSA
Figure 1J
VH3-33 Product QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA-----FDYWGQGTLVTVSSA
9.8.2 Heavy chain QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNEYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGAYHFAYWGQGTLVTVSSA

Figure 1, cont.

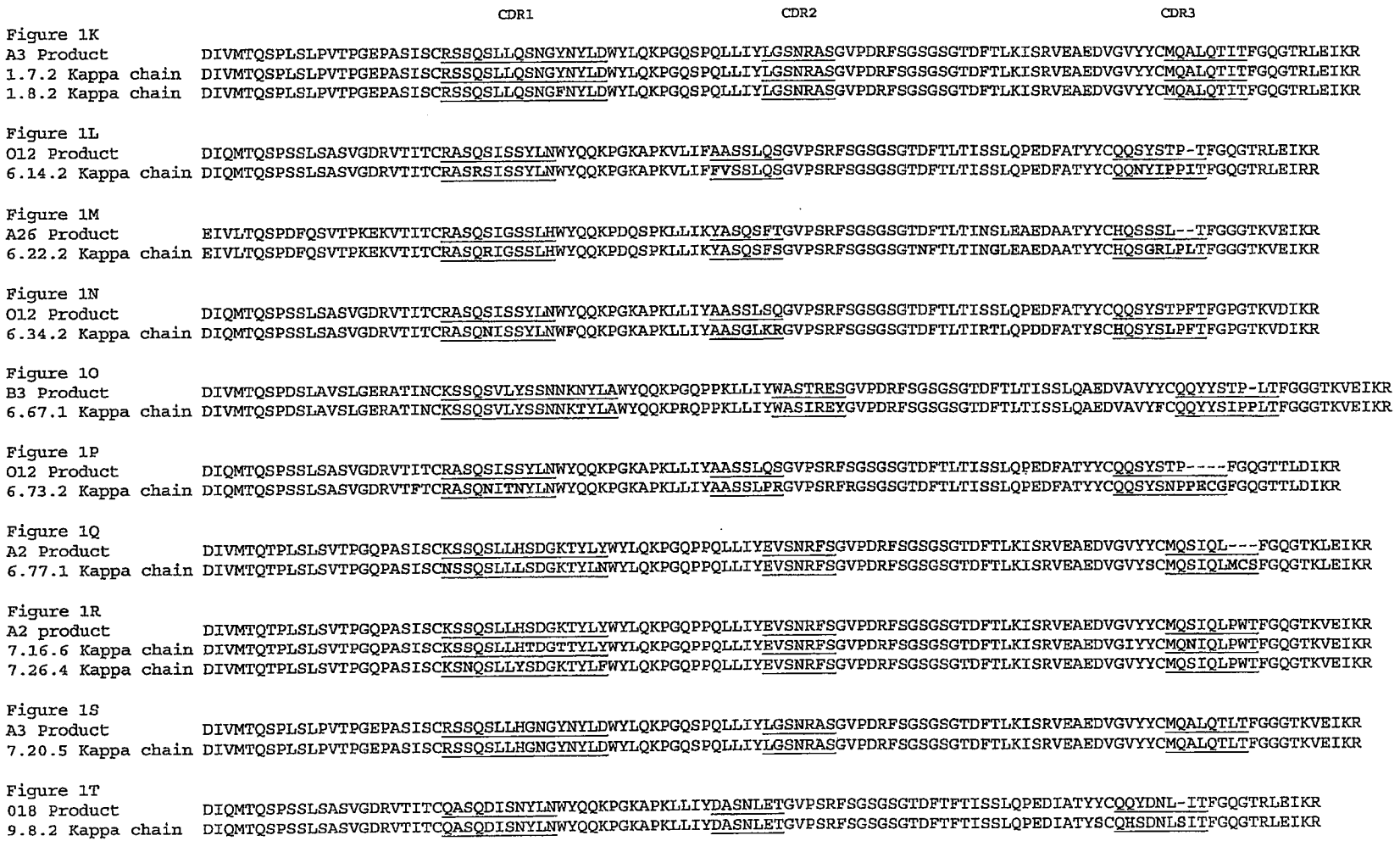


Figure 2

Figure 2A

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1.7.2          --MRLPAQLLGLLMLWVS--GSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLQS-NGY
1.8.2          --MRLPAQLLGLLMLWVS--GSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLQS-NGF
7.20.5         --MRLPAQLLGLLMLWVS--GSSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHG-NGY
7.16.6         --MRLPAQLLGLLMLWIP--GSSADIVMTQTPLSLSVTPGQPASISCKSSQSLLHT-DGT
7.26.4         --MRLPAQLLGLLMLWIP--GSSADIVMTQTPLSLSVTPGQPASISCKSNQSLLYS-DGK
6.77.1         --MRLPAQLLGLLMLWIP--GSSADIVMTQTPLSLSVTPGQPASISCNSSQSLLLS-DGK
6.67.1         --MVLQTQVFISLLLWIS--GAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNK
6.34.2         MDMRVPAQLLGLLLLWLR--GARCDIQMTQSPSSLSASVGDRVTITCRASQNISSY----
6.73.2         MDMRVPAQLLGLLLLWLR--GARCDIQMTQSPSSLSASVGDRVTFTCRASQNITNY----
6.14.2         MDMRVPAQLLGLLLLWLR--GARCDIQMTQSPSSLSASVGDRVTITCRASRSISSY----
9.8.2          MDMRVPAQLLGLLLLWLSVAGARCDIQMTQSPSSLSASVGDRVTITCQASQDISNY----
6.22.2         ---MLPSQLIGFLLLWVP--ASRGEIVLTQSPDFQSVTPKEKVTITCRASQRIGSS----
                   : :*:: *:**:  .:  :* :**:*  ..:  : .::.*.:.: :

1.7.2          NYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
1.8.2          NYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
7.20.5         NYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
7.16.6         TYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQ
7.26.4         TYLFWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
6.77.1         TYLNWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
6.67.1         TYLAWYQQKPRQPPKLLIYWASIREYGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQ
6.34.2         --LNWFQQKPGKAPKLLIYAASGLKRGVPSRFSGSGSGTDFTLTIRTLQPDDFATYSCHQ
6.73.2         --LNWYQQKPGKAPKLLIYAASSLPRGVPSRFRGSGSGTDFTLTISSLQPEDFATYYCQQ
6.14.2         --LNWYQQKPGKAPKVLIFFVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
9.8.2          --LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYSCQH
6.22.2         --LHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTNFTLTINGLEAEDAATYYCHQ
                 * *: *** :.*::**   *    ***.** ******:**:.*  ::.:* . * * :

1.7.2          ALQT---ITFGQGTRLEIKR
1.8.2          ALQT---ITFGQGTRLEIKR
7.20.5         ALQT---LTFGGGTKVEIKR
7.16.6         NIQLP--WTFGQGTKVEIKR
7.26.4         SIQLP--WTFGQGTKVEIKR
6.77.1         SIQLM--CSFGQGTKLEIKR
6.67.1         YYSIPP-LTFGGGTKVEIKR
6.34.2         SYSLP--FTFGPGTKVDIKR
6.73.2         SYSNPPECGFGQGTTLDIKR
6.14.2         NYIPP--ITFGQGTRLEIRR
9.8.2          SDNLS--ITFGQGTRLEIKR
6.22.2         SGRLP--LTFGGGTKVEIKR
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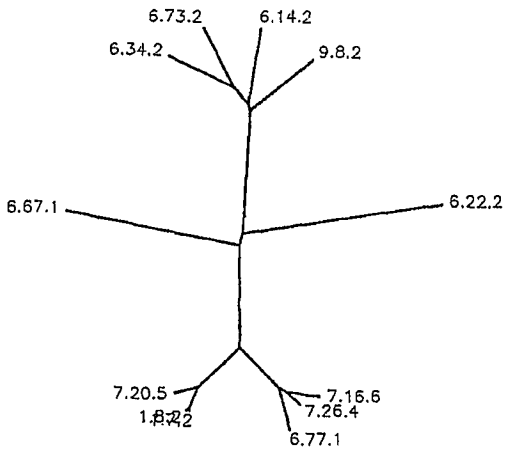


Figure 2B

```
7.16.6      QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGINWVRQAPGQGLEWMGWIS--VYSGNT
7.26.4      QVQLVQSGAEVKKPGASVKVSCEASGYTFTSYGIDWVRQAPGQGLEWMGWIS--VYSGNT
1.7.2       EVQLVESGGGLVKPGGSLRLSCVASGFTFTNAWMIWVRQAPGKGLEWVGRIKRKTDGGTT
1.8.2       EVQLVESGGGLVKPGGSLRLSCVVSGFTFTNAWMIWVRQAPGKGLEWVGRIKRKTDGGTT
6.14.2      EVQLLESGGGLVQPGGSLRLSCAASGLTFNNSAMTWVRQAPGKGLEWVSTTS--GSGGTT
6.73.2      EVQLLESGGDLVQPGGSLRLSCAASGFTFRSYAMNWVRQAPGKGLEWVSVIS--GRGGTT
6.77.1      EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSIS--SSSSYI
6.22.2      QVQLVESGGGVVQPGRSLRLSCAASGHTFSSDGMHWVRQAPGKGLEWVAIIW--YDGSNK
6.34.2      QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIS--NDGNNK
9.8.2       QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW--YDGSNE
7.20.5      QVQLQESGPGLVKPSETLSLTCTVSGSSISSYHWNWIRQPAGKGLEWIGRIY---TSGST
6.67.1      QVQLQESGPGLVKPSETLSLTCTVSGDSISSNYWSWIRQPAGKGLEWIGRIY---TSGGT
            :*** :**  : :*. :: ::* .** :: .    *:**..*:****:.       ..

7.16.6      NYAQKVQGRVTMTADTSTSTAYMDLRSLRSDDTAVYYCAREG-SS--SSGDYYYGMDVWG
7.26.4      NYAQKLQGRVTMSTDTSTSTAFFLLRSLRSDDTAVYYCAREG-SS--SSGDYYYGMDVWG
1.7.2       DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGG------VAEDY-----WG
1.8.2       DYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTGG------VAEDY-----WG
6.14.2      YYADSVKGRFTISRDSPKNTLYLQMNSLRAEDTAVYYCAARG-YSYGTTPYEY-----WG
6.73.2      YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDAAVYYCAKIA-VAGEGLYYYYG-MDVWG
6.77.1      YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDG-YSSGWSYYYYYGMDVWG
6.22.2      YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-------PGYYYG-MDVWG
6.34.2      YYADSVKGRFTISRDNSKNTLYLQMNSLSAEDTAVYYCARDS-TA--ITYYYYG-MDVWG
9.8.2       YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARG----------AYH-FAYWG
7.20.5      NYNPSLKSRVTMSLDTSKNQFSLKLSSVTAADTAVYYCAREGVRYYYASGSYYYGLDVWG
6.67.1      NSNPSLRGRVTILADTSKNQFSLKLSSVTAADTAVYYCARD--RITIIRGLIPSFFDYWG
                 ::.*.*:  * ...   : : *: : *:*****:                    **

7.16.6      QGTTVTVSSA
7.26.4      QGTTVTVSSA
1.7.2       QGTLVTVSSA
1.8.2       QGTLVTVSSA
6.14.2      QGTLVTVSSA
6.73.2      QGTTVTVSSA
6.77.1      QGTTVTVSSA
6.22.2      QGTTVTVSSA
6.34.2      QGTTVTVSSA
9.8.2       QGTLVTVSSA
7.20.5      QGTTVTVSSA
6.67.1      QGTLVTVSSA
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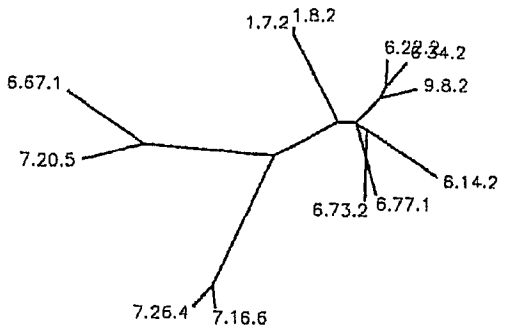


Figure 3

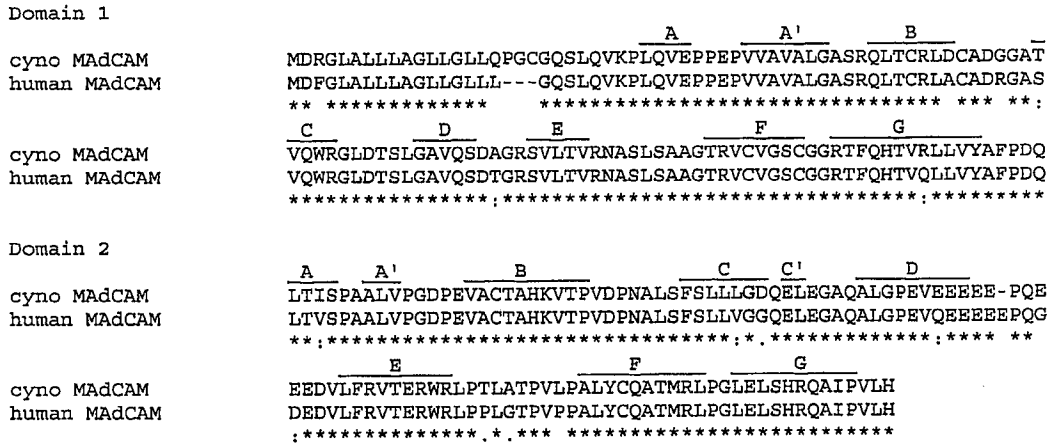

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human MAdCAM MDFGLALLLAGLLGLLL---GQSLQVKPLQVEPPEPVVAVALGASRQLTCRLACADRGAS
C D E F G
cyno MAdCAM VQWRGLDTSLGAVQSDAGRSVLTVRNASLSAAGTRVCVGSCGGRTFQHTVRLLVYAFPDQ
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Domain 2
A A' B C C' D
cyno MAdCAM LTISPAALVPGDPEVACTAHKVTPVDPNALSFSLLLGDQELEGAQALGPEVEEEEE-PQE
human MAdCAM LTVSPAALVPGDPEVACTAHKVTPVDPNALSFSLLVGGQELEGAQALGPEVQEEEEEPQG
E F G
cyno MAdCAM EEDVLFRVTERWRLPTLATPVLPALYCQATMRLPGLELSHRQAIPVLH
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Figure 4

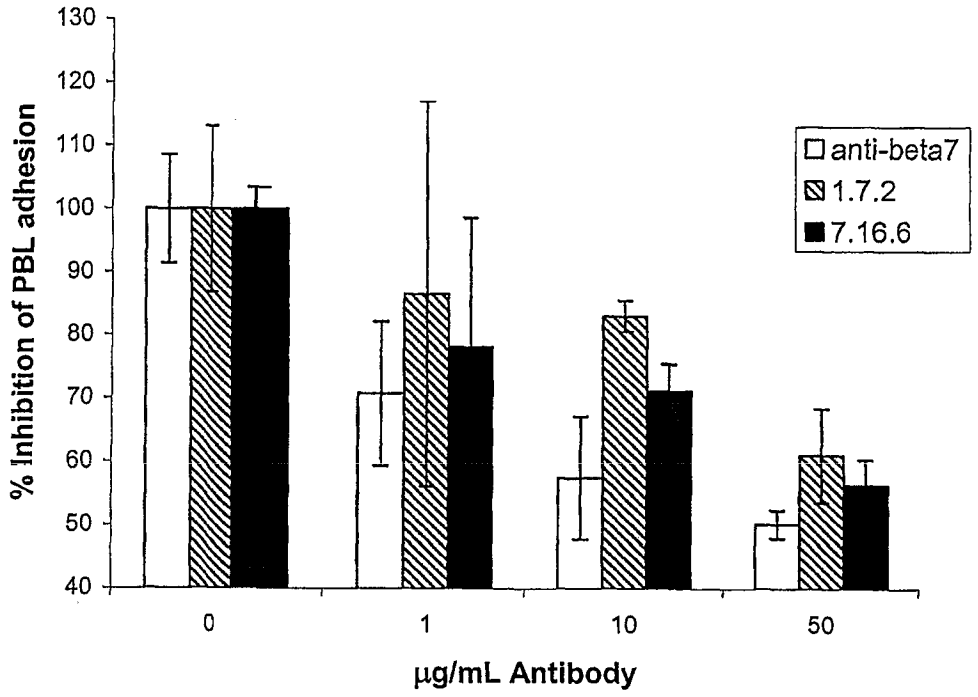

130
120
110
100
90
80
70
60
50
40
% Inhibition of PBL adhesion
0
1
10
50
µg/mL Antibody
anti-beta7
1.7.2
7.16.6

Figure 5

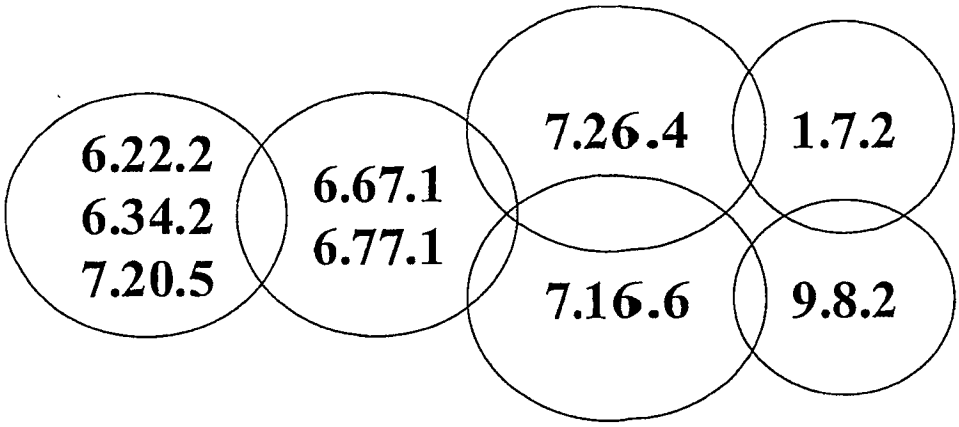


Figure 6

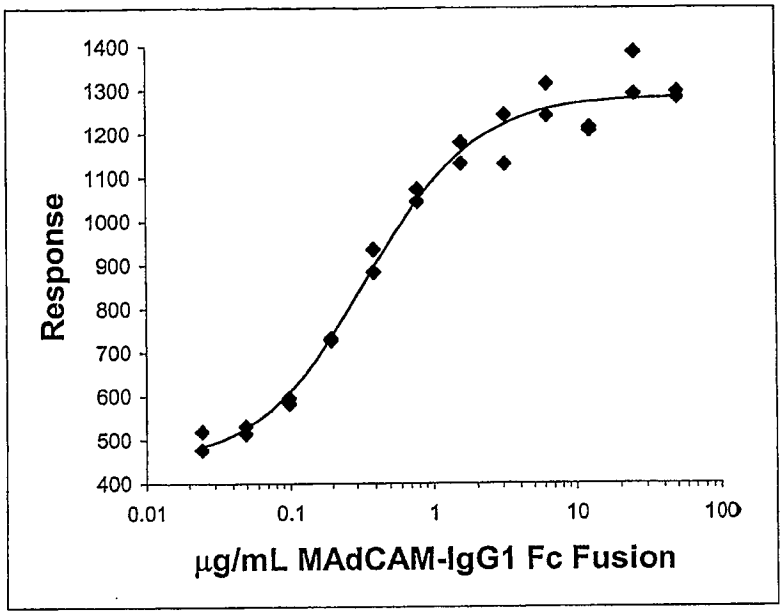
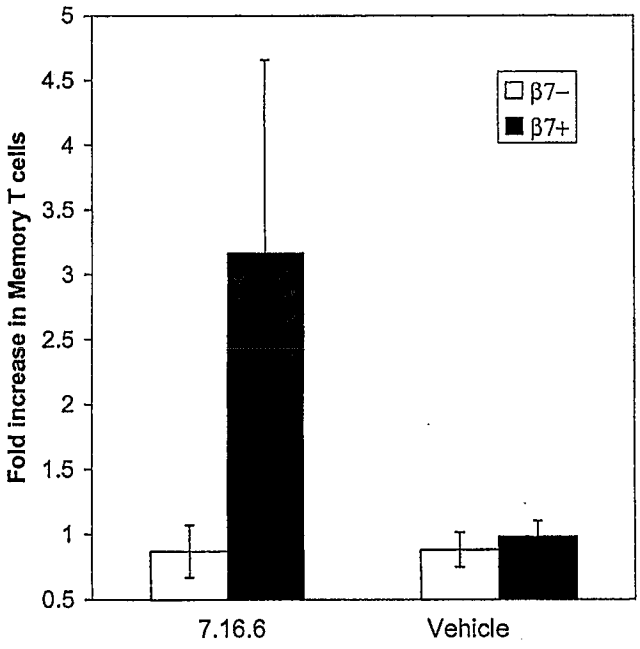

Response
1400
1300
1200
1100
1000
900
800
700
600
500
400
0.01
0.1
1
10
100
µg/mL MAdCAM-IgG1 Fc Fusion

Figure 7


Fold increase in Memory T cells
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
β7−
β7+
7.16.6
Vehicle

Key:
Signal sequence: underlined lower case

Amino acid changes in modified anti-MAdCAM antibodies sequence compared to parent: underlined upper case

SEQ ID NO. 1
1.7.2 Heavy Chain Nucleotide Sequence

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  51  ccagtgtGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCTTG GTGAAGCCTG
 101  GGGGGTCCCT TAGACTCTCC TGTGTAGCCT CTGGATTCAC TTTCACTAAC
 151  GCCTGGATGA TCTGGGTCCG CCAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  TGGCCGTATT AAAAGGAAAA CTGATGGTGG GACAACAGAC TACGCTGCAC
 251  CCGTGAAAGG CAGATTCACC ATCTCAAGAG ATGATTCAAA AAACACGCTG
 301  TATCTGCAAA TGAACAGCCT GAAAACCGAG GACACAGCCG TGTATTACTG
 351  TACCACAGGG GGAGTGGCTG AGGACTACTG GGGCCAGGGA ACCCTGGTCA
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 451  TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA
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 551  CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC
 601  TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC
 651  CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA
 701  CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT
 751  GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT
 801  CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC
 851  ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG
 901  CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG
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1151  TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT
1201  GGGCAGCCGG AGAACAACTA CAAGACCACA CCTCCCATGC TGGACTCCGA
1251  CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC
1301  AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC
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SEQ ID NO. 2
1.7.2 Predicted Heavy Chain Protein Sequence

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 101  YLQMNSLKTE DTAVYYCTTG GVAEDYWGQG TLVTVSSAST KGPSVFPLAP
 151  CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY
 201  SLSSVVTVPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP
 251  VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV
 301  HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK
 351  TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN
 401  GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN
 451  HYTQKSLSLS PGK
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SEQ ID NO. 3
1.7.2 Kappa Light Chain Nucleotide Sequence

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  51  atccagtggg GATATTGTGA TGACTCAGTC TCCACTCTCC CTGCCCGTCA
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 301  AGCAGAGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAGCTCT
 351  ACAAACTATC ACCTTCGGCC AAGGGACACG ACTGGAGATT AAACGAACTG
 401  TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
 451  TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
 501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
 551  AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
 601  AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
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 701  ACAGGGGAGA GTGTTAGTGA
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SEQ ID NO. 4
1.7.2 Predicted Kappa Light Chain Protein Sequence

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 151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
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SEQ ID NO. 5
1.8.2 Heavy Chain Nucleotide Sequence

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   1  atggagtttg ggctgagctg gattttcctt gctgctattt taaaaggtgt
  51  ccagtgtGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCTTG GTGAAGCCTG
 101  GGGGGTCCCT TAGACTCTCC TGTGTAGTCT CTGGATTCAC TTTCACTAAC
 151  GCCTGGATGA TCTGGGTCCG CCAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  TGGCCGTATT AAAAGGAAAA CTGATGGTGG GACAACAGAC TACGCTGCAC
 251  CCGTGAAAGG CAGATTCACC ATCTCAAGAG ATGATTCAAA AAACACGCTG
 301  TATCTGCAAA TGAACAGCCT GAAAACCGAG GACACAGCCG TGTATTACTG
 351  TACCACAGGG GGAGTGGCTG AGGACTACTG GGGCCAGGGA ACCCTGGTCA
 401  CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC
 451  TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA
 501  GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCTCTGA
 551  CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC
 601  TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC
 651  CTACACCTGC AACGTAGATC ACAAGCCCAG CAACACCAAG GTGGACAAGA
 701  CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT
 751  GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT
 801  CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC
 851  ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG
 901  CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG
 951  TGTGGTCAGC GTCCTCACCG TTGTGCACCA GGACTGGCTG AACGGCAAGG
1001  AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA
1051  ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGTACACCCT
1101  GCCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC
1151  TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT
1201  GGGCAGCCGG AGAACAACTA CAAGACCACA CCTCCCATGC TGGACTCCGA
1251  CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC
1301  AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC
1351  CACTACACGC AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GA
```

SEQ ID NO. 6
1.8.2 Predicted Heavy Chain Protein Sequence

```
   1  mefglswifl aailkgvqcE VQLVESGGGL VKPGGSLRLS CVVSGFTFTN
  51  AWMIWVRQAP GKGLEWVGRI KRKTDGGTTD YAAPVKGRFT ISRDDSKNTL
 101  YLQMNSLKTE DTAVYYCTTG GVAEDYWGQG TLVTVSSAST KGPSVFPLAP
 151  CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY
 201  SLSSVVTVPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP
 251  VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV
 301  HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK
 351  TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN
 401  GQPENNYKTT PPMLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN
 451  HYTQKSLSLS PGK
```

SEQ ID NO. 7
1.8.2 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtctctgg
  51  atccagtggg GATATTGTGA TGACTCAGTC TCCACTCTCC CTGCCCGTCA
 101  CCCCTGGAGA GCCGGCCTCC ATCTCCTGCA GGTCTAGTCA GAGCCTCCTG
 151  CAAAGTAATG GATTCAACTA TTTGGATTGG TACCTGCAGA AGCCAGGGCA
 201  GTCTCCACAG CTCCTGATCT ATTTGGGTTC TAATCGGGCC TCCGGGGTCC
 251  CTGACAGGTT CAGTGGCAGT GGGTCAGGCA CAGATTTTAC ACTGAAAATC
 301  AGCAGAGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAGCTCT
 351  ACAAACTATC ACCTTCGGCC AAGGGACACG ACTGGAGATT AAACGAACTG
 401  TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
 451  TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
 501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
 551  AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
 601  AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
 651  CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
 701  ACAGGGGAGA GTGTTAGTGA
```

SEQ ID NO. 8
1.8.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mrlpaqllgl lmlwvsgssg DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL
  51  QSNGFNYLDW YLQKPGQSPQ LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YYCMQALQTI TFGQGTRLEI KRTVAAPSVF IFPPSDEQLK
 151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
 202  STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
```

SEQ ID NO. 9
6.14.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg gcttttttctt gtggctattt taaaaggtgt
  51  ccagtgtGAG GTGCAGCTGT TGGAGTCTGG GGGAGGCTTG GTACAGCCTG
 101  GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGACTCAC CTTTAACAAT
 151  TCTGCCATGA CCTGGGTCCG CCAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  CTCAACTACT AGTGGAAGTG GTGGTACCAC ATACTACGCA GACTCCGTGA
 251  AGGGCCGGTT CACCATCTCC AGAGACTCTC CCAAGAACAC GCTCTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCCGTATATT ACTGTGCGGC
 351  CCGTGGATAC AGCTATGGTA CGACCCCCTA TGAGTACTGG GGCCAGGGAA
 401  CCCTGGTCAC CGTCTCCTCA GCTTCCACCA AGGGCCCATC CGTCTTCCCC
 451  CTGGCGCCCT GTTCCAGGAG CACCTCCGAG AGCACAGCCG CCCTGGGCTG
 501  CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG TGGAACTCAG
 551  GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
 601  GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG
 651  CACGAAGACC TACACCTGCA ACGTAGATCA CAAGCCCAGC AACACCAAGG
 701  TGGACAAGAG AGTTGAGTCC AAATATGGTC CCCCATGCCC ATCATGCCCA
 751  GCACCTGAGT TCCTGGGGGG ACCATCAGTC TTCCTGTTCC CCCCAAAACC
 801  CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TGCGTGGTGG
 851  TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT
 901  GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA
 951  CAGCACGTAC CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC
1001  TGAACGGCAA GGAGTACAAG TGCAAGGTCT CCAACAAAGG CCTCCCGTCC
1051  TCCATCGAGA AAACCATCTC CAAAGCCAAA GGGCAGCCCC GAGAGCCACA
1101  GGTGTACACC CTGCCCCCAT CCCAGGAGGA GATGACCAAG AACCAGGTCA
1151  GCCTGACCTG CCTGGTCAAA GGCTTCTACC CCAGCGACAT CGCCGTGGAG
1201  TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT
1251  GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAGGCTA ACCGTGGACA
1301  AGAGCAGGTG GCAGGAGGGG AATGTCTTCT CATGCTCCGT GATGCATGAG
1351  GCTCTGCACA ACCACTACAC ACAGAAGAGC CTCTCCCTGT CTCTGGGTAA
1401  ATGA
```

SEQ ID NO. 10
6.14.2 Predicted Heavy Chain Protein Sequence

```
   1  mefglswlfl vailkgvqcE VQLLESGGGL VQPGGSLRLS CAASGLTFNN
  51  SAMTWVRQAP GKGLEWVSTT SGSGGTTYYA DSVKGRFTIS RDSPKNTLYL
 101  QMNSLRAEDT AVYYCAARGY SYGTTPYEYW GQGTLVTVSS ASTKGPSVFP
 151  LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS
 201  GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPSCP
 251  APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD
 301  GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS
 351  SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE
 401  WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE
 451  ALHNHYTQKS LSLSLGK
```

SEQ ID NO. 11
6.14.2 Kappa Light Chain Nucleotide Sequence

```
   1  atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct
  51  ccgaggggcc agatgtGACA TCCAGATGAC CCAGTCTCCA TCCTCCCTGT
 101  CTGCATCTGT AGGAGACAGA GTCACCATCA CTTGCCGGGC AAGTCGGAGC
 151  ATTAGCAGCT ATTTAAATTG GTATCAGCAG AAACCAGGGA AAGCCCCTAA
 201  AGTCCTGATC TTTTTTGTGT CCAGTTTGCA AAGTGGGGTC CCATCAAGGT
 251  TCAGTGGCAG TGGCTCTGGG ACAGATTTCA CTCTCACCAT CAGCAGTCTG
 301  CAACCTGAAG ATTTTGCAAC TTACTACTGT CAACAGAATT ACATTCCCCC
 351  TATTACCTTC GGCCAGGGGA CACGACTGGA GATCAGACGA ACTGTGGCTG
 401  CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA
 451  ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
 501  AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA
 551  GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
 601  CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA
 651  AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
 701  GAGAGTGTTA G
```

SEQ ID NO. 12
6.14.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mdmrvpaqll glllwlrga rcDIQMTQSP SSLSASVGDR VTITCRASRS
  51  ISSYLNWYQQ KPGKAPKVLI FFVSSLQSGV PSRFSGSGSG TDFTLTISSL
 101  QPEDFATYYC QQNYIPPITF GQGTRLEIRR TVAAPSVFIF PPSDEQLKSG
 151  TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
 202  LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
```

SEQ ID NO. 13
6.22.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt
  51  ccagtgtCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG
 101  GGAGGTCCCT GAGACTCTCC TGTGCAGCGT CTGGACACAC CTTCAGTAGC
 151  GATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT
 201  GGCAATTATA TGGTATGATG GAAGTAATAA ATATTATGCA GACTCCGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTATATT ACTGTGCGAG
 351  AGATCCCGGC TACTATTACG GTATGGACGT CTGGGGCCAA GGGACCACGG
 401  TCACCGTCTC CTCAGCTTCC ACCAAGGGCC CATCCGTCTT CCCCCTGGCG
 451  CCCTGCTCCA GGAGCACCTC CGAGAGCACA GCCGCCCTGG GCTGCCTGGT
 501  CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCCC
 551  TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC CTCAGGACTC
 601  TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACGAA
 651  GACCTACACC TGCAACGTAG ATCACAAGCC CAGCAACACC AAGGTGGACA
 701  AGAGAGTTGA GTCCAAATAT GGTCCCCCAT GCCCATCATG CCCAGCACCT
 751  GAGTTCCTGG GGGGACCATC AGTCTTCCTG TTCCCCCCAA AACCCAAGGA
 801  CACTCTCATG ATCTCCCGGA CCCCTGAGGT CACGTGCGTG GTGGTGGACG
 851  TGAGCCAGGA AGACCCCGAG GTCCAGTTCA ACTGGTACGT GGATGGCGTG
 901  GAGGTGCATA ATGCCAAGAC AAAGCCGCGG GAGGAGCAGT TCAACAGCAC
 951  GTACCGTGTG GTCAGCGTCC TCACCGTCCT GCACCAGGAC TGGCTGAACG
1001  GCAAGGAGTA CAAGTGCAAG GTCTCCAACA AAGGCCTCCC GTCCTCCATC
1051  GAGAAAACCA TCTCCAAAGC CAAAGGGCAG CCCCGAGAGC CACAGGTGTA
1101  CACCCTGCCC CCATCCCAGG AGGAGATGAC CAAGAACCAG GTCAGCCTGA
1151  CCTGCCTGGT CAAAGGCTTC TACCCCAGCG ACATCGCCGT GGAGTGGGAG
1201  AGCAATGGGC AGCCGGAGAA CAACTACAAG ACCGCGCCTC CCGTGCTGGA
1251  CTCCGACGGC TCCTTCTTCC TCTACAGCAG GCTAACCGTG GACAAGAGCA
1301  GGTGGCAGGA GGGGAATGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG
1351  CACAACCACT ACACACAGAA GAGCCTCTCC CTGTCTCTGG GTAAATGA
```

SEQ ID NO. 14
6.22.2 Predicted Heavy Chain Protein Sequence

```
   1  mefglswvfl vallrgvqcQ VQLVESGGGV VQPGRSLRLS CAASGHTFSS
  51  DGMHWVRQAP GKGLEWVAII WYDGSNKYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLRAEDT AVYYCARDPG YYYGMDVWGQ GTTVTVSSAS TKGPSVFPLA
 151  PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL
 201  YSLSSVVTVP SSSLGTKTYT CNVDHKPSNT KVDKRVESKY GPPCPSCPAP
 251  EFLGGPSVFL FPPKPKDTLM ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV
 301  EVHNAKTKPR EEQFNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI
 351  EKTISKAKGQ PREPQVYTLP PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE
 401  SNGQPENNYK TAPPVLDSDG SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL
 451  HNHYTQKSLS LSLGK
```

SEQ ID NO. 15
6.22.2 Kappa Light Chain Nucleotide Sequence

```
   1  atgttgccat cacaactcat tgggtttctg ctgctctggg ttccagcttc
  51  caggggtGAA ATTGTGCTGA CTCAGTCTCC AGACTTTCAG TCTGTGACTC
 101  CAAAAGAGAA AGTCACCATC ACCTGCCGGG CCAGTCAGAG AATTGGTAGT
 151  AGCTTACACT GGTACCAGCA GAAACCAGAT CAGTCTCCAA AACTCCTCAT
 201  CAAGTATGCT TCCCAGTCCT TCTCAGGGGT CCCCTCGAGG TTCAGTGGCA
 251  GTGGATCTGG GACAAATTTC ACCCTCACCA TCAATGGCCT GGAAGCTGAA
 301  GATGCTGCAA CTTATTACTG TCATCAGAGT GGTCGTTTAC CGCTCACTTT
 351  CGGCGGAGGG ACCAAGGTGG AGATCAAACG AACTGTGGCT GCACCATCTG
 401  TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG AACTGCCTCT
 451  GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG
 501  GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG AGTGTCACAG
 551  AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG
 601  AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA
 651  TCAGGGCCTG AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT
 701  AGTGA
```

SEQ ID NO. 16
6.22.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mlpsqligfl llwvpasrgE IVLTQSPDFQ SVTPKEKVTI TCRASQRIGS
  51  SLHWYQQKPD QSPKLLIKYA SQSFSGVPSR FSGSGSGTNF TLTINGLEAE
 101  DAATYYCHQS GRLPLTFGGG TKVEIKRTVA APSVFIFPPS DEQLKSGTAS
 151  VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL
 201  SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC
```

SEQ ID NO. 17
6.34.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt
  51  ccagtgtCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG
 101  GGAGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC CTTCAGTAGC
 151  TATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT
 201  GGCAGTTATA TCAAATGATG GAAATAATAA ATACTATGCA GACTCCGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAATT CCAAAAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGAGCGC TGAGGACACG GCTGTGTATT ACTGTGCGAG
 351  AGATAGTACG GCGATAACCT ACTACTACTA CGGAATGGAC GTCTGGGGCC
 401  AAGGGACCAC GGTCACCGTC TCCTCAGCTT CCACCAAGGG CCCATCCGTC
 451  TTCCCCCTGG CGCCCTGCTC CAGGAGCACC TCCGAGAGCA CAGCCGCCCT
 501  GGGCTGCCTG GTCAAGGACT ACTTCCCCGA ACCGGTGACG GTGTCGTGGA
 551  ACTCAGGCGC CCTGACCAGC GGCGTGCACA CCTTCCCGGC TGTCCTACAG
 601  TCCTCAGGAC TCTACTCCCT CAGCAGCGTG GTGACCGTGC CCTCCAGCAG
 651  CTTGGGCACG AAGACCTACA CCTGCAACGT AGATCACAAG CCCAGCAACA
 701  CCAAGGTGGA CAAGAGAGTT GAGTCCAAAT ATGGTCCCCC ATGCCCATCA
 751  TGCCCAGCAC CTGAGTTCCT GGGGGGACCA TCAGTCTTCC TGTTCCCCCC
 801  AAAACCCAAG GACACTCTCA TGATCTCCCG GACCCCTGAG GTCACGTGCG
 851  TGGTGGTGGA CGTGAGCCAG GAAGACCCCG AGGTCCAGTT CAACTGGTAC
 901  GTGGATGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA
 951  GTTCAACAGC ACGTACCGTG TGGTCAGCGT CCTCACCGTC CTGCACCAGG
1001  ACTGGCTGAA CGGCAAGGAG TACAAGTGCA AGGTCTCCAA CAAAGGCCTC
1051  CCGTCCTCCA TCGAGAAAAC CATCTCCAAA GCCAAAGGGC AGCCCCGAGA
1101  GCCACAGGTG TACACCCTGC CCCCATCCCA GGAGGAGATG ACCAAGAACC
1151  AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTACCCCAG CGACATCGCC
1201  GTGGAGTGGG AGAGCAATGG ACAGCCGGAG AACAACTACA AGACCACGCC
1251  TCCCGTGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC AGGCTAACCG
1301  TGGACAAGAG CAGGTGGCAG GAGGGGAATG TCTTCTCATG CTCCGTGATG
1351  CATGAGGCTC TGCACAACCA CTACACACAG AAGAGCCTCT CCCTGTCTCT
1401  GGGTAAATGA
```

SEQ ID NO. 18
6.34.2 Predicted Heavy Chain Protein Sequence

```
   1  mefglswvfl vallrgvqcQ VQLVESGGGV VQPGRSLRLS CAASGFTFSS
  51  YGMHWVRQAP GKGLEWVAVI SNDGNNKYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLSAEDT AVYYCARDST AITYYYYGMD VWGQGTTVTV SSASTKGPSV
 151  FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ
 201  SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPS
 251  CPAPEFLGGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY
 301  VDGVEVHNAK TKPREEQFNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL
 351  PSSIEKTISK AKGQPREPQV YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA
 401  VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ EGNVFSCSVM
 451  HEALHNHYTQ KSLSLSLGK
```

SEQ ID NO. 19
6.34.2 Kappa Light Chain Nucleotide Sequence

```
   1  atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct
  51  ccgaggtgcc agatgtGACA TCCAGATGAC CCAGTCTCCA TCCTCCCTGT
 101  CTGCATCTGT CGGAGACAGA GTCACCATCA CTTGCCGGGC AAGTCAGAAT
 151  ATTAGTAGCT ATTTAAATTG GTTTCAGCAG AAACCAGGGA AAGCCCCTAA
 201  GCTCCTGATC TATGCTGCAT CCGGTTTGAA GCGTGGGGTC CCATCACGGT
 251  TCAGTGGTAG TGGATCTGGG ACAGATTTCA CTCTCACCAT CAGGACTCTG
 301  CAACCTGATG ATTTTGCAAC TTACTCCTGT CACCAGAGTT ACAGTCTCCC
 351  ATTCACTTTC GGCCCTGGGA CCAAAGTGGA TATCAAACGA ACTGTGGCTG
 401  CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA
 451  ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
 501  AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA
 551  GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
 601  CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA
 651  AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
 701  GAGAGTGTTA GTGA
```

SEQ ID NO. 20
6.34.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mdmrvpaqll glllwlrga rcDIQMTQSP SSLSASVGDR VTITCRASQN
  51  ISSYLNWFQQ KPGKAPKLLI YAASGLKRGV PSRFSGSGSG TDFTLTIRTL
 101  QPDDFATYSC HQSYSLPFTF GPGTKVDIKR TVAAPSVFIF PPSDEQLKSG
 151  TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
 201  LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
```

SEQ ID NO. 21
6.67.1 Heavy Chain Nucleotide Sequence

```
   1  atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt
  51  cctgtccCAG GTGCAGCTGC AGGAGTCGGG CCCAGGACTG GTGAAGCCTT
 101  CGGAGACCCT GTCCCTCACC TGCACTGTCT CTGGTGACTC CATCAGTAGT
 151  AACTATTGGA GCTGGATCCG GCAGCCCGCC GGGAAGGGAC TGGAGTGGAT
 201  TGGGCGTATC TATACCAGTG GGGGCACCAA CTCCAACCCC TCCCTCAGGG
 251  GTCGAGTCAC CATTTTAGCA GACACGTCCA AGAACCAGTT CTCTCTGAAA
 301  CTGAGTTCTG TGACCGCCGC GGACACGGCC GTGTATTACT GTGCGAGAGA
 351  TCGTATTACT ATAATTCGGG GACTTATTCC ATCCTTCTTT GACTACTGGG
 401  GCCAGGGAAC CCTGGTCACC GTCTCCTCAG CTTCCACCAA GGGCCCATCC
 451  GTCTTCCCCC TGGCGCCCTG CTCCAGGAGC ACCTCCGAGA GCACAGCCGC
 501  CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
 551  GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA
 601  CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG
 651  CAGCTTGGGC ACGAAGACCT ACACCTGCAA CGTAGATCAC AAGCCCAGCA
 701  ACACCAAGGT GGACAAGAGA GTTGAGTCCA AATATGGTCC CCCATGCCCA
 751  TCATGCCCAG CACCTGAGTT CCTGGGGGGA CCATCAGTCT TCCTGTTCCC
 801  CCCAAAACCC AAGGACACTC TCATGATCTC CCGGACCCCT GAGGTCACGT
 851  GCGTGGTGGT GGACGTGAGC CAGGAAGACC CCGAGGTCCA GTTCAACTGG
 901  TACGTGGATG GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA
 951  GCAGTTCAAC AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC
1001  AGGACTGGCT GAACGGCAAG GAGTACAAGT GCAAGGTCTC CAACAAAGGC
1051  CTCCCGTCCT CCATCGAGAA AACCATCTCC AAAGCCAAAG GGCAGCCCCG
1101  AGAGCCACAG GTGTACACCC TGCCCCCATC CCAGGAGGAG ATGACCAAGA
1151  ACCAGGTCAG CCTGACCTGC CTGGTCAAAG GCTTCTACCC CAGCGACATC
1201  GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT ACAAGACCAC
1251  GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAGGCTAA
1301  CCGTGGACAA GAGCAGGTGG CAGGAGGGGA ATGTCTTCTC ATGCTCCGTG
1351  ATGCATGAGG CTCTGCACAA CCACTACACA CAGAAGAGCC TCTCCCTGTC
1401  TCTGGGTAAA TGA
```

SEQ ID NO. 22
6.67.1 Predicted Heavy Chain Protein Sequence

```
   1  mkhlwfflll vaaprwvlsQ VQLQESGPGL VKPSETLSLT CTVSGDSISS
  51  NYWSWIRQPA GKGLEWIGRI YTSGGTNSNP SLRGRVTILA DTSKNQFSLK
 101  LSSVTAADTA VYYCARDRIT IIRGLIPSFF DYWGQGTLVT VSSASTKGPS
 151  VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL
 201  QSSGLYSLSS VVTVPSSSLG TKTYTCNVDH KPSNTKVDKR VESKYGPPCP
 251  SCPAPEFLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS QEDPEVQFNW
 301  YVDGVEVHNA KTKPREEQFN STYRVVSVLT VLHQDWLNGK EYKCKVSNKG
 351  LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI
 401  AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV
 451  MHEALHNHYT QKSLSLSLGK
```

SEQ ID NO. 23
6.67.1 Kappa Light Chain Nucleotide Sequence

```
   1  atggtgttgc agacccaggt cttcatttct ctgttgctct ggatctctgg
  51  tgcctacggg GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT
 101  CTCTGGGCGA GAGGGCCACC ATCAACTGCA AGTCCAGCCA GAGTGTTTTA
 151  TACAGCTCCA ACAATAAGAC CTACTTAGCT TGGTACCAAC AGAAACCAAG
 201  ACAGCCTCCT AAATTGCTCA TTTACTGGGC ATCTATACGG GAATATGGGG
 251  TCCCTGACCG ATTCAGTGGC AGCGGGTCTG GGACAGATTT CACTCTCACC
 301  ATCAGCAGCC TGCAGGCTGA AGATGTGGCA GTTTATTTCT GTCAACAATA
 351  TTATAGTATT CCTCCCCCTCA CTTTCGGCGG AGGGACCAAG GTGGAGATCA
 401  AACGAACTGT GGCTGCACCA TCTGTCTTCA TCTTCCCGCC ATCTGATGAG
 451  CAGTTGAAAT CTGGAACTGC CTCTGTTGTG TGCCTGCTGA ATAACTTCTA
 501  TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC CTCCAATCGG
 551  GTAACTCCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC
 601  AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA
 651  AGTCTACGCC TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA
 701  AGAGCTTCAA CAGGGGAGAG TGTTAGTGA
```

SEQ ID NO. 24
6.67.1 Predicted Kappa Light Chain Protein Sequence

```
   1  mvlqtqvfis lllwisgayg DIVMTQSPDS LAVSLGERAT INCKSSQSVL
  51  YSSNNKTYLA WYQQKPRQPP KLLIYWASIR EYGVPDRFSG SGSGTDFTLT
 101  ISSLQAEDVA VYFCQQYYSI PPLTFGGGTK VEIKRTVAAP SVFIFPPSDE
 151  QLKSGTASVV CLLNNFYPRE AKVQWKVDNA LQSGNSQESV TEQDSKDSTY
 201  SLSSTLTLSK ADYEKHKVYA CEVTHQGLSS PVTKSFNRGE C
```

SEQ ID NO. 25
6.73.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg gctttttctt gtggctattt taaaaggtgt
  51  ccagtgtGAG GTGCAGCTGT TGGAGTCTGG GGGAGACTTG GTCCAGCCTG
 101  GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC CTTTAGAAGT
 151  TATGCCATGA ACTGGGTCCG ACAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  CTCAGTTATT AGTGGTCGTG GTGGTACTAC ATACTACGCA GACTCCGTGA
 251  AGGGCCGGTT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACGCG GCCGTATATT ACTGTGCGAA
 351  GATAGCAGTG GCTGGAGAGG GGCTCTACTA CTACTACGGT ATGGACGTCT
 401  GGGGCCAAGG GACCACGGTC ACCGTCTCCT CAGCTTCCAC CAAGGGCCCA
 451  TCCGTCTTCC CCCTGGCGCC CTGCTCCAGG AGCACCTCCG AGAACACAGC
 501  CGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG GTGACGGTGT
 551  CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT CCCGGCTGTC
 601  CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC
 651  TAGCAGCTTG GGCACGAAGA CCTACACCTG CAACGTAGAT CACAAGCCCA
 701  GCAACACCAA GGTGGACAAG AGAGTTGAGT CCAAATATGG TCCCCCATGC
 751  CCATCATGCC CAGCACCTGA GTTCCTGGGG GGACCATCAG TCTTCCTGTT
 801  CCCCCCAAAA CCCAAGGACA CTCTCATGAT CTCCCGGACC CCTGAGGTCA
 851  CGTGCGTGGT GGTGGACGTG AGCCAGGAAG ACCCCGAGGT CCAGTTCAAC
 901  TGGTACGTGG ATGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA
 951  GGAGCAGTTC AACAGCACGT ACCGTGTGGT CAGCGTCCTC ACCGTCCTGC
1001  ACCAGGACTG GCTGAACGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA
1051  GGCCTCCCGT CCTCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC
1101  CCGAGAGCCA CAGGTGTACA CCCTGCCCCC ATCCCAGGAG GAGATGACCA
1151  AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC
1201  ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC
1251  CACGCCTCCC GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAGGC
1301  TAACCGTGGA CAAGAGCAGG TGGCAGGAGG GGAATGTCTT CTCATGCTCC
1351  GTGATGCATG AGGCTCTGCA CAACCACTAC ACACAGAAGA GCCTCTCCCT
1401  GTCTCTGGGT AAATGATAG
```

SEQ ID NO. 26
6.73.2 Predicted Heavy Chain Protein Sequence

```
   1  mefglswlfl vailkgvqcE VQLLESGGDL VQPGGSLRLS CAASGFTFRS
  51  YAMNWVRQAP GKGLEWVSVI SGRGGTTYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLRAEDA AVYYCAKIAV AGEGLYYYYG MDVWGQGTTV TVSSASTKGP
 151  SVFPLAPCSR STSENTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV
 201  LQSSGLYSLS SVVTVPSSSL GTKTYTCNVD HKPSNTKVDK RVESKYGPPC
 251  PSCPAPEFLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SQEDPEVQFN
 301  WYVDGVEVHN AKTKPREEQF NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK
 351  GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD
 401  IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS
 451  VMHEALHNHY TQKSLSLSLG K
```

SEQ ID NO. 27
6.73.2 Kappa Light Chain Nucleotide Sequence

```
   1  atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct
  51  ccgaggtgcc agatgtGACA TCCAGATGAC CCAGTCTCCA TCCTCCCTGT
 101  CTGCATCTGT AGGTGACAGA GTCACCTTCA CTTGCCGGGC AAGTCAGAAC
 151  ATTACCAACT ATTTAAATTG GTATCAGCAG AAACCAGGGA AGGCCCCTAA
 201  GCTCCTGATC TATGCTGCGT CCAGTTTGCC AAGAGGGGTC CCATCAAGGT
 251  TCCGTGGCAG TGGATCTGGG ACAGATTTCA CTCTCACCAT CAGCAGTCTG
 301  CAACCTGAAG ATTTTGCAAC TTACTACTGT CAACAGAGTT ACAGTAATCC
 351  TCCGGAGTGC GGTTTTGGCC AGGGGACCAC GCTGGATATC AAACGAACTG
 401  TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
 451  TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
 501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
 551  AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
 601  AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
 651  CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
 701  ACAGGGGAGA GTGTTAGTGA
```

SEQ ID NO. 28
6.73.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mdmrvpaqll gllllwlrga rcDIQMTQSP SSLSASVGDR VTFTCRASQN
  51  ITNYLNWYQQ KPGKAPKLLI YAASSLPRGV PSRFRGSGSG TDFTLTISSL
 101  QPEDFATYYC QQSYSNPPEC GFGQGTTLDI KRTVAAPSVF IFPPSDEQLK
 151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
 201  STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
```

SEQ ID NO. 29
6.77.1 Heavy Chain Nucleotide Sequence

```
   1  atggaactgg ggctccgctg ggttttcctt gttgctattt tagaaggtgt
  51  ccagtgtGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCCTG GTCAAGCCTG
 101  GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC CTTCAGTAGC
 151  TATAGCATGA ACTGGGTCCG CCAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  CTCATCCATT AGTAGTAGTA GTAGTTACAT ATACTACGCA GACTCAGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAACG CCAAGAACTC ACTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG
 351  AGATGGGTAT AGCAGTGGCT GGTCCTACTA CTACTACTAC GGTATGGACG
 401  TCTGGGGCCA AGGGACCACG GTCACCGTCT CCTCAGCTTC CACCAAGGGC
 451  CCATCCGTCT TCCCCCTGGC GCCCTGCTCC AGGAGCACCT CCGAGAGCAC
 501  AGCCGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG
 551  TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
 601  GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC
 651  CTCCAGCAGC TTGGGCACGA AGACCTACAC CTGCAACGTA GATCACAAGC
 701  CCAGCAACAC CAAGGTGGAC AAGAGAGTTG AGTCCAAATA TGGTCCCCCA
 751  TGCCCATCAT GCCCAGCACC TGAGTTCCTG GGGGGACCAT CAGTCTTCCT
 801  GTTCCCCCCA AAACCCAAGG ACACTCTCAT GATCTCCCGG ACCCCTGAGG
 851  TCACGTGCGT GGTGGTGGAC GTGAGCCAGG AAGACCCCGA GGTCCAGTTC
 901  AACTGGTACG TGGATGGCGT GGAGGTGCAT AATGCCAAGA CAAAGCCGCG
 951  GGAGGAGCAG TTCAACAGCA CGTACCGTGT GGTCAGCGTC CTCACCGTCC
1001  TGCACCAGGA CTGGCTGAAC GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC
1051  AAAGGCCTCC CGTCCTCCAT CGAGAAAACC ATCTCCAAAG CCAAAGGGCA
1101  GCCCCGAGAG CCACAGGTGT ACACCCTGCC CCCATCCCAG GAGGAGATGA
1151  CCAAGAACCA GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCAGC
1201  GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA
1251  GACCACGCCT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA
1301  GGCTAACCGT GGACAAGAGC AGGTGGCAGG AGGGGAATGT CTTTTCACGC
1351  TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACACAGA AGAGCCTCTC
1401  CCTGTCTCTG GGTAAATGAT AGGAATTCTG ATGA
```

SEQ ID NO. 30
6.77.1 Predicted Heavy Chain Protein Sequence

```
   1  melglrwvfl vailegvqcE VQLVESGGGL VKPGGSLRLS CAASGFTFSS
  51  YSMNWVRQAP GKGLEWVSSI SSSSSYIYYA DSVKGRFTIS RDNAKNSLYL
 101  QMNSLRAEDT AVYYCARDGY SSGWSYYYYY GMDVWGQGTT VTVSSASTKG
 151  PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA
 201  VLQSSGLYSL SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP
 251  CPSCPAPEFL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSQEDPEVQF
 301  NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV LTVLHQDWLN GKEYKCKVSN
 351  KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL TCLVKGFYPS
 401  DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSR
 451  SVMHEALHNH YTQKSLSLSL GK
```

SEQ ID NO. 31
6.77.1 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct ggatacctgg
  51  atccagtgca GATATTGTGA TGACCCAGAC TCCACTCTCT CTGTCCGTCA
 101  CTCCTGGACA GCCGGCCTCC ATCTCCTGCA ACTCTAGTCA GAGCCTCCTG
 151  CTTAGTGATG GAAAGACCTA TTTGAATTGG TACCTGCAGA AGCCCGGCCA
 201  GCCTCCACAG CTCCTGATCT ATGAAGTTTC CAACCGGTTC TCTGGAGTGC
 251  CAGACAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTCAC ACTGAAAATC
 301  AGCCGGGTGG AGGCTGAGGA TGTTGGGGTT TATTCCTGCA TGCAAAGTAT
 351  ACAGCTTATG TGCAGTTTTG GCCAGGGGAC CAAGCTGGAG ATCAAACGAA
 401  CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG
 451  AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT TCTATCCCAG
 501  AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT
 551  CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
 601  AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA
 651  CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT
 701  TCAACAGGGG AGAGTGTTAG TGA
```

SEQ ID NO. 32
6.77.1 Predicted Kappa Light Chain Protein Sequence

```
   1  mrlpaqllgl lmlwipgssa DIVMTQTPLS LSVTPGQPAS ISCNSSQSLL
  51  LSDGKTYLNW YLQKPGQPPQ LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YSCMQSIQLM CSFGQGTKLE IKRTVAAPSV FIFPPSDEQL
 151  KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL
 201  SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNRGEC
```

SEQ ID NO. 33
7.16.6 Heavy Chain Nucleotide Sequence

```
   1  atggactgga cctggagcat ccttttcttg gtggcagcag caacaggtgc
  51  ccactccCAG GTTCAGCTGG TGCAGTCTGG AGCTGAGGTG AAGAAGCCTG
 101  GGGCCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGTTACAC CTTTACCAGC
 151  TATGGTATCA ACTGGGTGCG ACAGGCCCCT GGACAAGGGC TTGAGTGGAT
 201  GGGATGGATC AGCGTTTACA GTGGTAACAC AAACTATGCA CAGAAGGTCC
 251  AGGGCAGAGT CACCATGACC GCAGACACAT CCACGAGCAC AGCCTACATG
 301  GACCTGAGGA GCCTGAGATC TGACGACACG GCCGTGTATT ACTGTGCGAG
 351  AGAGGGTAGC AGCTCGTCCG GAGACTACTA TTACGGTATG GACGTCTGGG
 401  GCCAAGGGAC CACGGTCACC GTCTCCTCAG CCTCCACCAA GGGCCCATCG
 451  GTCTTCCCCC TGGCGCCCTG CTCCAGGAGC ACCTCCGAGA GCACAGCGGC
 501  CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
 551  GGAACTCAGG CGCTCTGACC AGCGGCGTGC ACACCTTCCC AGCTGTCCTA
 601  CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG
 651  CAACTTCGGC ACCCAGACCT ACACCTGCAA CGTAGATCAC AAGCCCAGCA
 701  ACACCAAGGT GGACAAGACA GTTGAGCGCA AATGTTGTGT CGAGTGCCCA
 751  CCGTGCCCAG CACCACCTGT GGCAGGACCG TCAGTCTTCC TCTTCCCCCC
 801  AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACGTGCG
 851  TGGTGGTGGA CGTGAGCCAC GAAGACCCCG AGGTCCAGTT CAACTGGTAC
 901  GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCAC GGGAGGAGCA
 951  GTTCAACAGC ACGTTCCGTG TGGTCAGCGT CCTCACCGTT GTGCACCAGG
1001  ACTGGCTGAA CGGCAAGGAG TACAAGTGCA AGGTCTCCAA CAAAGGCCTC
1051  CCAGCCCCCA TCGAGAAAAC CATCTCCAAA ACCAAAGGGC AGCCCCGAGA
1101  ACCACAGGTG TACACCCTGC CCCCATCCCG GGAGGAGATG ACCAAGAACC
1151  AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTACCCCAG CGACATCGCC
1201  GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACACC
1251  TCCCATGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC AAGCTCACCG
1301  TGGACAAGAG CAGGTGGCAG CAGGGGAACG TCTTCTCATG CTCCGTGATG
1351  CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT CCCTGTCTCC
1401  GGGTAAATGA
```

SEQ ID NO. 34
7.16.6 Predicted Heavy Chain Protein Sequence

```
   1  mdwtwsilfl vaaatgahsQ VQLVQSGAEV KKPGASVKVS CKASGYTFTS
  51  YGINWVRQAP GQGLEWMGWI SVYSGNTNYA QKVQGRVTMT ADTSTSTAYM
 101  DLRSLRSDDT AVYYCAREGS SSSGDYYYGM DVWGQGTTVT VSSASTKGPS
 151  VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL
 201  QSSGLYSLSS VVTVPSSNFG TQTYTCNVDH KPSNTKVDKT VERKCCVECP
 251  PCPAPPVAGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVQFNWY
 301  VDGVEVHNAK TKPREEQFNS TFRVVSVLTV VHQDWLNGKE YKCKVSNKGL
 351  PAPIEKTISK TKGQPREPQV YTLPPSREEM TKNQVSLTCL VKGFYPSDIA
 401  VEWESNGQPE NNYKTTPPML DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
 451  HEALHNHYTQ KSLSLSPGK
```

SEQ ID NO. 35
7.16.6 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct ggatacctgg
  51  atccagtgca GATATTGTGA TGACCCAGAC TCCACTCTCT CTGTCCGTCA
 101  CCCCTGGACA GCCGGCCTCC ATCTCCTGCA AGTCTAGTCA GAGCCTCCTG
 151  CATACTGATG GAACGACCTA TTTGTATTGG TACCTGCAGA AGCCAGGCCA
 201  GCCTCCACAG CTCCTGATCT ATGAAGTTTC CAACCGGTTC TCTGGAGTGC
 251  CAGATAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTCAC ACTGAAAATC
 301  AGCCGGGTGG AGGCTGAGGA TGTTGGGATT TATTACTGCA TGCAAAATAT
 351  ACAGCTTCCG TGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA
 401  CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG
 451  AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT TCTATCCCAG
 501  AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT
 551  CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
 601  AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA
 651  CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT
 701  TCAACAGGGG AGAGTGTTAG TGA
```

SEQ ID NO. 36
7.16.6 Kappa Light Chain Protein Sequence

```
   1  mrlpaqllgl lmlwipgssa DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL
  51  HTDGTTYLYW YLQKPGQPPQ LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGI YYCMQNIQLP WTFGQGTKVE IKRTVAAPSV FIFPPSDEQL
 151  KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL
 201  SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNRGEC
```

SEQ ID NO. 37
7.20.5 Heavy Chain Nucleotide Sequence

```
   1  atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt
  51  cctgtccCAG GTGCAGCTGC AGGAGTCGGG CCCAGGACTG GTGAAGCCTT
 101  CGGAGACCCT GTCCCTCACC TGCACTGTCT CTGGTAGCTC CATCAGTAGT
 151  TACCACTGGA ACTGGATCCG GCAGCCCGCC GGGAAGGGAC TGGAGTGGAT
 201  TGGGCGTATC TATACCAGTG GGAGCACCAA CTACAACCCC TCCCTCAAGA
 251  GTCGAGTCAC CATGTCACTA GACACGTCCA AGAACCAGTT CTCCCTGAAG
 301  CTGAGCTCTG TGACCGCCGC GGACACGGCC GTGTATTACT GTGCGAGAGA
 351  GGGGGTCAGG TATTACTATG CTTCGGGGAG TTATTACTAC GGTCTGGACG
 401  TCTGGGGCCA AGGGACCACG GTCACCGTCT CCTCAGCCTC CACCAAGGGC
 451  CCATCGGTCT TCCCCCTGGC GCCCTGCTCC AGGAGCACCT CCGAGAGCAC
 501  AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG
 551  TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGCACAC CTTCCCAGCT
 601  GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC
 651  CTCCAGCAAC TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC
 701  CCAGCAACAC CAAGGTGGAC AAGACAGTTG AGCGCAAATG TTGTGTCGAG
 751  TGCCCACCGT GCCCAGCACC ACCTGTGGCA GGACCGTCAG TCTTCCTCTT
 801  CCCCCCAAAA CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA
 851  CGTGCGTGGT GGTGGACGTG AGCCACGAAG ACCCCGAGGT CCAGTTCAAC
 901  TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCACGGGA
 951  GGAGCAGTTC AACAGCACGT TCCGTGTGGT CAGCGTCCTC ACCGTTGTGC
1001  ACCAGGACTG GCTGAACGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA
1051  GGCCTCCCAG CCCCCATCGA GAAAACCATC TCCAAAACCA AAGGGCAGCC
1101  CCGAGAACCA CAGGTGTACA CCCTGCCCCC ATCCCGGGAG GAGATGACCA
1151  AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC
1201  ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC
1251  CACACCTCCC ATGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC
1301  TCACCGTGGA CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC
1351  GTGATGCATG AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT
1401  GTCTCCGGGT AAATGA
```

SEQ ID NO. 38
7.20.5 Predicted Heavy Chain Protein Sequence

```
   1  mkhlwfflll vaaprwvlsQ VQLQESGPGL VKPSETLSLT CTVSGSSISS
  51  YHWNWIRQPA GKGLEWIGRI YTSGSTNYNP SLKSRVTMSL DTSKNQFSLK
 101  LSSVTAADTA VYYCAREGVR YYYASGSYYY GLDVWGQGTT VTVSSASTKG
 151  PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA
 201  VLQSSGLYSL SSVVTVPSSN FGTQTYTCNV DHKPSNTKVD KTVERKCCVE
 251  CPPCPAPPVA GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVQFN
 301  WYVDGVEVHN AKTKPREEQF NSTFRVVSVL TVVHQDWLNG KEYKCKVSNK
 351  GLPAPIEKTI SKTKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD
 401  IAVEWESNGQ PENNYKTTPP MLDSDGSFFL YSKLTVDKSR WQQGNVFSCS
 451  VMHEALHNHY TQKSLSLSPG K
```

SEQ ID NO. 39
7.20.5 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtctctgg
  51  atccagtggg GATATTGTGA TGACTCAGTC TCCACTCTCC CTGCCCGTCA
 101  CCCCTGGAGA GCCGGCCTCC ATCTCCTGCA GGTCTAGTCA GAGCCTCCTG
 151  CATGGTAATG GATACAACTA TTTGGATTGG TACCTGCAGA AGCCAGGGCA
 201  GTCTCCACAG CTCCTGATCT ATTTGGGTTC TAATCGGGCC TCCGGGGTCC
 251  CTGACAGGTT CAGTGGCAGT GGATCAGGCA CAGATTTTAC ACTGAAAATC
 301  AGCAGAGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAGCTCT
 351  ACAAACTCTC ACTTTCGGCG GAGGGACCAA GGTGGAGATC AAACGAACTG
 401  TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
 451  TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA
 501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
 551  AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
 601  AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
 651  CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
 701  ACAGGGGAGA GTGTTAGTGA
```

SEQ ID NO. 40
7.20.5 Predicted Kappa Light Chain Protein Sequence

```
   1  mrlpaqllgl lmlwvsgssg DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL
  51  HGNGYNYLDW YLQKPGQSPQ LLIYLGSNRA SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YYCMQALQTL TFGGGTKVEI KRTVAAPSVF IFPPSDEQLK
 151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
 201  STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
```

SEQ ID NO. 41
7.26.4 Heavy Chain Nucleotide Sequence

```
   1  atggactgga cctggagcat ccttttcttg gtggcagcag caacaggtgc
  51  ccactccCAG GTTCAGCTGG TGCAGTCTGG AGCTGAGGTG AAGAAGCCTG
 101  GGGCCTCAGT GAAGGTCTCC TGCGAGGCTT CTGGTTACAC CTTTACCAGC
 151  TATGGTATCG ACTGGGTGCG ACAGGCCCCT GGACAAGGGC TTGAGTGGAT
 201  GGGATGGATC AGCGTTTACA GTGGTAACAC AAACTATGCA CAGAAGCTCC
 251  AGGGCAGAGT CACCATGTCC ACAGACACAT CCACGAGCAC AGCCTACATG
 301  GAGCTGAGGA GCCTGAGATC TGACGACACG GCCGTGTATT ACTGTGCGAG
 351  AGAGGGTAGC AGCTCGTCCG GAGACTACTA CTACGGTATG GACGTCTGGG
 401  GCCAAGGGAC CACGGTCACC GTCTCCTCAG CCTCCACCAA GGGCCCATCG
 451  GTCTTCCCCC TGGCGCCCTG CTCCAGGAGC ACCTCCGAGA GCACAGCGGC
 501  CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
 551  GGAACTCAGG CGCTCTGACC AGCGGCGTGC ACACCTTCCC AGCTGTCCTA
 601  CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG
 651  CAACTTCGGC ACCCAGACCT ACACCTGCAA CGTAGATCAC AAGCCCAGCA
 701  ACACCAAGGT GGACAAGACA GTTGAGCGCA AATGTTGTGT CGAGTGCCCA
 751  CCGTGCCCAG CACCACCTGT GGCAGGACCG TCAGTCTTCC TCTTCCCCCC
 801  AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACGTGCG
 851  TGGTGGTGGA CGTGAGCCAC GAAGACCCCG AGGTCCAGTT CAACTGGTAC
 901  GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCAC GGGAGGAGCA
 951  GTTCAACAGC ACGTTCCGTG TGGTCAGCGT CCTCACCGTT GTGCACCAGG
1001  ACTGGCTGAA CGGCAAGGAG TACAAGTGCA AGGTCTCCAA CAAAGGCCTC
1051  CCAGCCCCCA TTGAGAAAAC CATCTCCAAA ACCAAAGGGC AGCCCCGAGA
1101  ACCACAGGTG TACACCCTGC CCCCATCCCG GGAGGAGATG ACCAAGAACC
1151  AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTACCCCAG CGACATCGCC
1201  GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACACC
1251  TCCCATGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC AAGCTCACCG
1301  TGGACAAGAG CAGGTGGCAG CAGGGGAACG TCTTCTCATG CTCCGTGATG
1351  CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT CCCTGTCTCC
1402  GGGTAAATGA
```

SEQ ID NO. 42
7.26.4 Predicted Heavy Chain Protein Sequence

```
   1  mdwtwsilfl vaaatgahsQ VQLVQSGAEV KKPGASVKVS CEASGYTFTS
  51  YGIDWVRQAP GQGLEWMGWI SVYSGNTNYA QKLQGRVTMS TDTSTSTAYM
 101  ELRSLRSDDT AVYYCAREGS SSSGDYYYGM DVWGQGTTVT VSSASTKGPS
 151  VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL
 201  QSSGLYSLSS VVTVPSSNFG TQTYTCNVDH KPSNTKVDKT VERKCCVECP
 251  PCPAPPVAGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVQFNWY
 301  VDGVEVHNAK TKPREEQFNS TFRVVSVLTV VHQDWLNGKE YKCKVSNKGL
 351  PAPIEKTISK TKGQPREPQV YTLPPSREEM TKNQVSLTCL VKGFYPSDIA
 401  VEWESNGQPE NNYKTTPPML DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
 451  HEALHNHYTQ KSLSLSPGK
```

SEQ ID NO. 43
7.26.4 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct ggatacctgg
  51  atccagtgcg GATATTGTGA TGACCCAGAC TCCACTCTCT CTGTCCGTCA
 101  CCCCTGGACA GCCGGCCTCC ATCTCCTGCA AGTCTAATCA GAGCCTCCTG
 151  TATAGTGATG GAAAGACCTA TTTGTTTTGG TACCTGCAGA AGCCAGGCCA
 201  GCCTCCACAG CTCCTGATCT ATGAAGTTTC CAACCGATTC TCTGGAGTGC
 251  CAGATAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTCAC ACTGAAAATC
 301  AGCCGGGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAAGTAT
 351  ACAGCTTCCG TGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA
 401  CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG
 451  AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT TCTATCCCAG
 501  AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT
 551  CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
 601  AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA
 651  CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT
 701  TCAACAGGGG AGAGTGTTAG TGA
```

SEQ ID NO. 44
7.26.4 Predicted Kappa Light Chain Protein Sequence

```
   1  mrlpaqllgl lmlwipgssa DIVMTQTPLS LSVTPGQPAS ISCKSNQSLL
  51  YSDGKTYLFW YLQKPGQPPQ LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YYCMQSIQLP WTFGQGTKVE IKRTVAAPSV FIFPPSDEQL
 151  KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL
 201  SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNRGEC
```

SEQ ID NO. 45
9.8.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt
  51  ccagtgtCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG
 101  GGAGGTCCCT GAGACTCTCC TGTGCAGCGT CTGGATTCAC CTTCAGTAGC
 151  TATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT
 201  GGCAGTTATA TGGTATGATG GAAGTAATGA ATACTATGCA GACTCCGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG
 351  GGGGGCGTAC CACTTTGCCT ACTGGGGCCA GGGAACCCTG GTCACCGTCT
 401  CCTCAGCTTC CACCAAGGGC CCATCCGTCT TCCCCCTGGC GCCCTGCTCC
 451  AGGAGCACCT CCGAGAGCAC AGCCGCCCTG GGCTGCCTGG TCAAGGACTA
 501  CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG
 551  GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
 601  AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACGA AGACCTACAC
 651  CTGCAACGTA GATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAGAGTTG
 701  AGTCCAAATA TGGTCCCCCA TGCCCATCAT GCCCAGCACC TGAGTTCCTG
 751  GGGGGACCAT CAGTCTTCCT GTTCCCCCCA AAACCCAAGG ACACTCTCAT
 801  GATCTCCCGG ACCCCTGAGG TCACGTGCGT GGTGGTGGAC GTGAGCCAGG
 851  AAGACCCCGA GGTCCAGTTC AACTGGTACG TGGATGGCGT GGAGGTGCAT
 901  AATGCCAAGA CAAAGCCGCG GGAGGAGCAG TTCAACAGCA CGTACCGTGT
 951  GGTCAGCGTC CTCACCGTCC TGCACCAGGA CTGGCTGAAC GGCAAGGAGT
1001  ACAAGTGCAA GGTCTCCAAC AAAGGCCTCC CGTCCTCCAT CGAGAAAACC
1051  ATCTCCAAAG CCAAAGGGCA GCCCCGAGAG CCACAGGTGT ACACCCTGCC
1101  CCCATCCCAG GAGGAGATGA CCAAGAACCA GGTCAGCCTG ACCTGCCTGG
1151  TCAAAGGCTT CTACCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG
1201  CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG
1251  CTCCTTCTTC CTCTACAGCA GGCTAACCGT GGACAAGAGC AGGTGGCAGG
1301  AGGGGAATGT CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC
1351  TACACACAGA AGAGCCTCTC CCTGTCTCTG GGTAAATGA
```

SEQ ID NO. 46
9.8.2 Predicted Heavy Chain Chain Protein Sequence

```
   1  mefglswvfl vallrgvqcQ VQLVESGGGV VQPGRSLRLS CAASGFTFSS
  51  YGMHWVRQAP GKGLEWVAVI WYDGSNEYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLRAEDT AVYYCARGAY HFAYWGQGTL VTVSSASTKG PSVFPLAPCS
 151  RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL
 201  SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPSCPAPEFL
 251  GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH
 301  NAKTKPREEQ FNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT
 351  ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL TCLVKGFYPS DIAVEWESNG
 401  QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC SVMHEALHNH
 451  YTQKSLSLSL GK
```

SEQ ID NO. 47
9.8.2 Kappa Light Chain Nucleotide Sequence

```
   1  atggacatga gggtccctgc tcagctcctg gggctcctgc tgctctggct
  51  ctcagtcgca ggtgccagat gtGACATCCA GATGACCCAG TCTCCATCCT
 101  CCCTGTCTGC ATCTGTAGGA GACAGAGTCA CCATCACTTG CCAGGCGAGT
 151  CAGGACATTA GCAACTATTT AAATTGGTAT CAGCAGAAAC CAGGGAAAGC
 201  CCCTAAGCTC CTGATCTACG ATGCATCCAA TTTGGAAACA GGGGTCCCAT
 251  CAAGGTTCAG TGGAAGTGGA TCTGGGACAG ATTTTACTTT CACCATCAGC
 301  AGCCTGCAGC CTGAAGATAT TGCAACATAT TCCTGTCAAC ACTCTGATAA
 351  TCTCTCGATC ACCTTCGGCC AGGGGACACG ACTGGAGATT AAACGAACTG
 401  TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA
 451  TCTGGAACTG CCTCTGTTGT GTGCCTGCTG AATAACTTCT ACCCCAGAGA
 501  GGCCAAAGTA CAGTGGAAGG TGGATAACGC CCTCCAATCG GGTAACTCCC
 551  AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
 601  AGCACCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC
 651  CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
 701  ACAGGGGAGA GTGTTAGTGA
```

SEQ ID NO. 48
9.8.2 Predicted Kappa Light Chain Protein Sequence

```
   1  mdmrvpaqll gllllwlsva garcDIQMTQ SPSSLSASVG DRVTITCQAS
  51  QDISNYLNWY QQKPGKAPKL LIYDASNLET GVPSRFSGSG SGTDFTFTIS
 101  SLQPEDIATY SCQHSDNLSI TFGQGTRLEI KRTVAAPSVF IFPPSDEQLK
 151  SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS
 201  STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC
```

SEQ ID NO. 49
Nucleotide Sequence of cynomolgus MAdCAM $\alpha_4\beta_7$ binding domain

```
   1  ATGGATCGGG GCCTGGCCCT CCTGCTGGCG GGGCTTCTGG GGCTCCTCCA
  51  GCCGGGCTGC GGCCAGTCCC TCCAGGTGAA GCCCCTGCAG GTGGAGCCCC
 101  CGGAGCCGGT GGTGGCCGTG GCCCTGGGCG CCTCTCGCCA GCTCACCTGC
 151  CGCCTGGACT GCGCGGACGG CGGGGCCACG GTGCAGTGGC GGGGCCTGGA
 201  CACCAGCCTG GGCGCGGTGC AGTCGGACGC GGGCCGCAGC GTCCTCACCG
 251  TGCGCAACGC CTCGCTGTCG GCGGCCGGGA CCCGTGTGTG CGTGGGCTCC
 301  TGCGGGGGCC GCACCTTCCA GCACACCGTG CGGCTCCTTG TGTACGCCTT
 351  CCCGGACCAG CTGACCATCT CCCCGGCAGC CCTGGTGCCT GGTGACCCGG
 401  AGGTGGCCTG TACGGCTCAC AAAGTCACGC CTGTGGACCC CAATGCGCTC
 451  TCCTTCTCCC TGCTCCTGGG GGACCAGGAA CTGGAGGGGG CCCAGGCTCT
 501  GGGCCCGGAG GTGGAGGAGG AGGAGGAGCC CCAGGAGGAG GAGGACGTGC
 551  TGTTCAGGGT GACAGAGCGC TGGCGGCTGC CGACCCTGGC AACCCCTGTC
 601  CTGCCCGCGC TCTACTGCCA GGCCACGATG AGGCTGCCTG GCTTGGAGCT
 651  CAGCCACCGC CAGGCCATCC CGGTCCTGCA C
```

SEQ ID NO. 50
Amino acid sequence of cynomolgus MAdCAM $\alpha_4\beta_7$ binding domain

```
   1  MDRGLALLLA GLLGLLQPGC GQSLQVKPLQ VEPPEPVVAV ALGASRQLTC
  51  RLDCADGGAT VQWRGLDTSL GAVQSDAGRS VLTVRNASLS AAGTRVCVGS
 101  CGGRTFQHTV RLLVYAFPDQ LTISPAALVP GDPEVACTAH KVTPVDPNAL
 151  SFSLLLGDQE LEGAQALGPE VEEEEEPQEE EDVLFRVTER WRLPTLATPV
 201  LPALYCQATM RLPGLELSHR QAIPVLH
```

SEQ ID NO. 51
Modified 6.22.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt
  51  ccagtgtCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG
 101  GGAGGTCCCT GAGACTCTCC TGTGCAGCGT CTGGATTCAC CTTCAGTAGC
 151  GATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT
 201  GGCAATTATA TGGTATGATG GAAGTAATAA ATATTATGCA GACTCCGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTATATT ACTGTGCGAG
 351  AGATCCCGGC TACTATTACG GTATGGACGT CTGGGGCCAA GGGACCACGG
 401  TCACCGTCTC CTCAGCTTCC ACCAAGGGCC CATCCGTCTT CCCCCTGGCG
 451  CCCTGCTCTA GAAGCACCTC CGAGAGCACA GCGGCCCTGG GCTGCCTGGT
 501  CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TCAGGCGCTC
 551  TGACCAGCGG CGTGCACACC TTCCCAGCTG TCCTACAGTC CTCAGGACTC
 601  TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAACT TCGGCACCCA
 651  GACCTACACC TGCAACGTAG ATCACAAGCC CAGCAACACC AAGGTGGACA
 701  AGACAGTTGA GCGCAAATGT TGTGTCGAGT GCCCACCGTG CCCAGCACCA
 751  CCTGTGGCAG GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC
 801  CCTCATGATC TCCCGGACCC CTGAGGTCAC GTGCGTGGTG GTGGACGTGA
 851  GCCACGAAGA CCCCGAGGTC CAGTTCAACT GGTACGTGGA CGGCGTGGAG
 901  GTGCATAATG CCAAGACAAA GCCACGGGAG GAGCAGTTCA ACAGCACGTT
 951  CCGTGTGGTC AGCGTCCTCA CCGTTGTGCA CCAGGACTGG CTGAACGGCA
1001  AGGAGTACAA GTGCAAGGTC TCCAACAAAG GCCTCCCAGC CCCCATCGAG
1051  AAAACCATCT CCAAAACCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC
1101  CCTGCCCCCA TCCCGGGAGG AGATGACCAA GAACCAGGTC AGCCTGACCT
1151  GCCTGGTCAA AGGCTTCTAC CCCAGCGACA TCGCCGTGGA GTGGGAGAGC
1201  AATGGGCAGC CGGAGAACAA CTACAAGACC ACACCTCCCA TGCTGGACTC
1251  CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT
1301  GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC
1351  AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGATAG
```

SEQ ID NO. 52
Modified 6.22.2 Heavy Chain Amino Acid Sequence

```
   1  mefglswvfl vallrgvqcQ VQLVESGGGV VQPGRSLRLS CAASGFTFSS
  51  DGMHWVRQAP GKGLEWVAII WYDGSNKYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLRAEDT AVYYCARDPG YYYGMDVWGQ GTTVTVSSAS TKGPSVFPLA
 151  PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL
 201  YSLSSVVTVP SSNFGTQTYT CNVDHKPSNT KVDKTVERKC CVECPPCPAP
 251  PVAGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV QFNWYVDGVE
 301  VHNAKTKPRE EQFNSTFRVV SVLTVVHQDW LNGKEYKCKV SNKGLPAPIE
 351  KTISKTKGQP REPQVYTLPP SREEMTKNQV SLTCLVKGFY PSDIAVEWES
 401  NGQPENNYKT TPPMLDSDGS FFLYSKLTVD KSRWQQGNVF SCSVMHEALH
 451  NHYTQKSLSL SPGK
```

SEQ ID NO. 53
Modified 6.22.2 Kappa Light Chain Nucleotide Sequence

```
   1  atgttgccat cacaactcat tgggtttctg ctgctctggg ttccagcttc
  51  caggggtGAA ATTGTGCTGA CTCAGTCTCC AGACTTTCAG TCTGTGACTC
 101  CAAAAGAGAA AGTCACCATC ACCTGCCGGG CCAGTCAGAG AATTGGTAGT
 151  AGCTTACACT GGTACCAGCA GAAACCAGAT CAGTCTCCAA AACTCCTCAT
 201  CAAGTATGCT TCCCAGTCCT TCTCAGGGGT CCCCTCGAGG TTCAGTGGCA
 251  GTGGATCTGG GACAGATTTC ACCCTCACCA TCAATAGCCT GGAAGCTGAA
 301  GATGCTGCAA CTTATTACTG TCATCAGAGT GGTCGTTTAC CGCTCACTTT
 351  CGGCGGAGGG ACCAAGGTGG AGATCAAACG AACTGTGGCT GCACCATCTG
 401  TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG AACTGCCTCT
 451  GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG
 501  GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG AGTGTCACAG
 551  AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG
 601  AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA
 651  TCAGGGCCTG AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT
 701  AGTGA
```

SEQ ID NO. 54
Modified 6.22.2 Kappa Light Chain Amino Acid Sequence

```
   1  mlpsqligfl llwvpasrgE IVLTQSPDFQ SVTPKEKVTI TCRASQRIGS
  51  SLHWYQQKPD QSPKLLIKYA SQSFSGVPSR FSGSGSGTDF TLTINSLEAE
 101  DAATYYCHQS GRLPLTFGGG TKVEIKRTVA APSVFIFPPS DEQLKSGTAS
 151  VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL
 201  SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC
```

SEQ ID NO. 55
Modified 6.34.2 Heavy Chain Nucleotide Sequence

```
   1  atggagtttg ggctgagctg ggttttcctc gttgctcttt taagaggtgt
  51  ccagtgtCAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG
 101  GGAGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC CTTCAGTAGC
 151  TATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT
 201  GGCAGTTATA TCAAATGATG GAAATAATAA ATACTATGCA GACTCCGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAATT CCAAAAACAC GCTGTATCTG
 301  CAAATGAACA GCCTGCGCGC TGAGGACACG GCTGTGTATT ACTGTGCGAG
 351  AGATAGTACG GCGATAACCT ACTACTACTA CGGAATGGAC GTCTGGGGCC
 401  AAGGGACCAC GGTCACCGTC TCCTCAGCTT CCACCAAGGG CCCATCCGTC
 451  TTCCCCCTGG CGCCCTGCTC TAGAAGCACC TCCGAGAGCA CAGCGGCCCT
 501  GGGCTGCCTG GTCAAGGACT ACTTCCCCGA ACCGGTGACG GTGTCGTGGA
 551  ACTCAGGCGC TCTGACCAGC GGCGTGCACA CCTTCCCAGC TGTCCTACAG
 601  TCCTCAGGAC TCTACTCCCT CAGCAGCGTG GTGACCGTGC CCTCCAGCAA
 651  CTTCGGCACC CAGACCTACA CCTGCAACGT AGATCACAAG CCCAGCAACA
 701  CCAAGGTGGA CAAGACAGTT GAGCGCAAAT GTTGTGTCGA GTGCCCACCG
 751  TGCCCAGCAC CACCTGTGGC AGGACCGTCA GTCTTCCTCT TCCCCCCAAA
 801  ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACGTGCGTGG
 851  TGGTGGACGT GAGCCACGAA GACCCCGAGG TCCAGTTCAA CTGGTACGTG
 901  GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCACGGG AGGAGCAGTT
 951  CAACAGCACG TTCCGTGTGG TCAGCGTCCT CACCGTTGTG CACCAGGACT
1001  GGCTGAACGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGGCCTCCCA
1051  GCCCCCATCG AGAAAACCAT CTCCAAAACC AAAGGGCAGC CCCGAGAACC
1101  ACAGGTGTAC ACCCTGCCCC CATCCCGGGA GGAGATGACC AAGAACCAGG
1151  TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT ACCCCAGCGA CATCGCCGTG
1201  GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA CCACACCTCC
1251  CATGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG
1301  ACAAGAGCAG GTGGCAGCAG GGGAACGTCT TCTCATGCTC CGTGATGCAT
1351  GAGGCTCTGC ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG
1401  TAAATGATAG
```

SEQ ID NO. 56
Modified 6.34.2 Heavy Chain Amino Acid Sequence

```
   1  mefglswvfl vallrgvqcQ VQLVESGGGV VQPGRSLRLS CAASGFTFSS
  51  YGMHWVRQAP GKGLEWVAVI SNDGNNKYYA DSVKGRFTIS RDNSKNTLYL
 101  QMNSLRAEDT AVYYCARDST AITYYYYGMD VWGQGTTVTV SSASTKGPSV
 151  FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ
 201  SSGLYSLSSV VTVPSSNFGT QTYTCNVDHK PSNTKVDKTV ERKCCVECPP
 251  CPAPPVAGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVQFNWYV
 301  DGVEVHNAKT KPREEQFNST FRVVSVLTVV HQDWLNGKEY KCKVSNKGLP
 351  APIEKTISKT KGQPREPQVY TLPPSREEMT KNQVSLTCLV KGFYPSDIAV
 401  EWESNGQPEN NYKTTPPMLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH
 451  EALHNHYTQK SLSLSPGK
```

SEQ ID NO. 57
Modified 6.34.2 Kappa Light Chain Nucleotide Sequence

```
   1  atggacatga gggtccccgc tcagctcctg gggctcctgc tactctggct
  51  ccgaggtgcc agatgtGACA TCCAGATGAC CCAGTCTCCA TCCTCCCTGT
 101  CTGCATCTGT CGGAGACAGA GTCACCATCA CTTGCCGGGC AAGTCAGAGT
 151  ATTAGTAGCT ATTTAAATTG GTATCAGCAG AAACCAGGGA AAGCCCCTAA
 201  GCTCCTGATC TATGCTGCAT CCGGTTTGAA GCGTGGGGTC CCATCACGGT
 251  TCAGTGGTAG TGGATCTGGG ACAGATTTCA CTCTCACCAT CAGTTCTCTG
 301  CAACCTGAGG ATTTTGCAAC TTACTACTGT CACCAGAGTT ACAGTCTCCC
 351  ATTCACTTTC GGCCCTGGGA CCAAAGTGGA TATCAAACGA ACTGTGGCTG
 401  CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA
 451  ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA
 501  AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA
 551  GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC
 601  CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA
 651  AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG
 701  GAGAGTGTTA GTGA
```

SEQ ID NO. 58
Modified 6.34.2 Kappa Light Chain Amino Acid Sequence

```
   1  mdmrvpaqll gllllwlrga rcDIQMTQSP SSLSASVGDR VTITCRASQS
  51  ISSYLNWYQQ KPGKAPKLLI YAASGLKRGV PSRFSGSGSG TDFTLTISSL
 101  QPEDFATYYC HQSYSLPFTF GPGTKVDIKR TVAAPSVFIF PPSDEQLKSG
 151  TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST
 201  LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
```

SEQ ID NO. 59
Modified 6.67.1 Heavy Chain Nucleotide Sequence

```
   1  atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt
  51  cctgtccCAG GTGCAGCTGC AGGAGTCGGG CCCAGGACTG GTGAAGCCTT
 101  CGGAGACCCT GTCCCTCACC TGCACTGTCT CTGGTGACTC CATCAGTAGT
 151  AACTATTGGA GCTGGATCCG GCAGCCCGCC GGGAAGGGAC TGGAGTGGAT
 201  TGGGCGTATC TATACCAGTG GGGGCACCAA CTCCAACCCC TCCCTCAGGG
 251  GTCGAGTCAC CATGTCAGTA GACACGTCCA AGAACCAGTT CTCTCTGAAA
 301  CTGAGTTCTG TGACCGCCGC GGACACGGCC GTGTATTACT GTGCGAGAGA
 351  TCGTATTACT ATAATTCGGG GACTTATTCC ATCCTTCTTT GACTACTGGG
 401  GCCAGGGAAC CCTGGTCACC GTCTCCTCAG CTTCCACCAA GGGCCCATCC
 451  GTCTTCCCCC TGGCGCCCTG CTCTAGAAGC ACCTCCGAGA GCACAGCGGC
 501  CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG ACGGTGTCGT
 551  GGAACTCAGG CGCTCTGACC AGCGGCGTGC ACACCTTCCC AGCTGTCCTA
 601  CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG
 651  CAACTTCGGC ACCCAGACCT ACACCTGCAA CGTAGATCAC AAGCCCAGCA
 701  ACACCAAGGT GGACAAGACA GTTGAGCGCA AATGTTGTGT CGAGTGCCCA
 751  CCGTGCCCAG CACCACCTGT GGCAGGACCG TCAGTCTTCC TCTTCCCCCC
 801  AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACGTGCG
 851  TGGTGGTGGA CGTGAGCCAC GAAGACCCCG AGGTCCAGTT CAACTGGTAC
 901  GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCAC GGGAGGAGCA
 951  GTTCAACAGC ACGTTCCGTG TGGTCAGCGT CCTCACCGTT GTGCACCAGG
1001  ACTGGCTGAA CGGCAAGGAG TACAAGTGCA AGGTCTCCAA CAAAGGCCTC
1051  CCAGCCCCCA TCGAGAAAAC CATCTCCAAA ACCAAAGGGC AGCCCCGAGA
1101  ACCACAGGTG TACACCCTGC CCCCATCCCG GGAGGAGATG ACCAAGAACC
1151  AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTACCCCAG CGACATCGCC
1201  GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACACC
1251  TCCCATGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC AAGCTCACCG
1301  TGGACAAGAG CAGGTGGCAG CAGGGGAACG TCTTCTCATG CTCCGTGATG
1351  CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT CCCTGTCTCC
1401  GGGTAAATGA TAG
```

SEQ ID NO. 60
Modified 6.67.1 Heavy Chain Amino Acid Sequence

```
   1  mkhlwfflll vaaprwvlsQ VQLQESGPGL VKPSETLSLT CTVSGDSISS
  51  NYWSWIRQPA GKGLEWIGRI YTSGGTNSNP SLRGRVTMSV DTSKNQFSLK
 101  LSSVTAADTA VYYCARDRIT IIRGLIPSFF DYWGQGTLVT VSSASTKGPS
 151  VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL
 201  QSSGLYSLSS VVTVPSSNFG TQTYTCNVDH KPSNTKVDKT VERKCCVECP
 251  PCPAPPVAGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVQFNWY
 301  VDGVEVHNAK TKPREEQFNS TFRVVSVLTV VHQDWLNGKE YKCKVSNKGL
 351  PAPIEKTISK TKGQPREPQV YTLPPSREEM TKNQVSLTCL VKGFYPSDIA
 401  VEWESNGQPE NNYKTTPPML DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM
 451  HEALHNHYTQ KSLSLSPGK
```

SEQ ID NO. 61
Modified 6.67.1 Kappa Light Chain Nucleotide Sequence

```
   1  atggtgttgc agacccaggt cttcatttct ctgttgctct ggatctctgg
  51  tgcctacggg GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT
 101  CTCTGGGCGA GAGGGCCACC ATCAACTGCA AGTCCAGCCA GAGTGTTTTA
 151  TACAGCTCCA ACAATAAGAA CTACTTAGCT TGGTACCAAC AGAAACCAGG
 201  ACAGCCTCCT AAATTGCTCA TTTACTGGGC ATCTATACGG GAATATGGGG
 251  TCCCTGACCG ATTCAGTGGC AGCGGGTCTG GGACAGATTT CACTCTCACC
 301  ATCAGCAGCC TGCAGGCTGA AGATGTGGCA GTTTATTTCT GTCAACAATA
 351  TTATAGTATT CCTCCCCCTCA CTTTCGGCGG AGGGACCAAG GTGGAGATCA
 401  AACGAACTGT GGCTGCACCA TCTGTCTTCA TCTTCCCGCC ATCTGATGAG
 451  CAGTTGAAAT CTGGAACTGC CTCTGTTGTG TGCCTGCTGA ATAACTTCTA
 501  TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC CTCCAATCGG
 551  GTAACTCCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC
 601  AGCCTCAGCA GCACCCTGAC GCTGAGCAAA GCAGACTACG AGAAACACAA
 651  AGTCTACGCC TGCGAAGTCA CCCATCAGGG CCTGAGCTCG CCCGTCACAA
 701  AGAGCTTCAA CAGGGGAGAG TGTTAGTGA
```

SEQ ID NO. 62
Modified 6.67.1 Kappa Light Chain Amino Acid Sequence

```
   1  mvlqtqvfis lllwisgayg DIVMTQSPDS LAVSLGERAT INCKSSQSVL
  51  YSSNNKNYLA WYQQKPGQPP KLLIYWASIR EYGVPDRFSG SGSGTDFTLT
 101  ISSLQAEDVA VYFCQQYYSI PPLTFGGGTK VEIKRTVAAP SVFIFPPSDE
 151  QLKSGTASVV CLLNNFYPRE AKVQWKVDNA LQSGNSQESV TEQDSKDSTY
 201  SLSSTLTLSK ADYEKHKVYA CEVTHQGLSS PVTKSFNRGE C
```

SEQ ID NO. 63
Modified 6.77.1 Heavy Chain Nucleotide Sequence

```
   1  atggaactgg ggctccgctg ggttttcctt gttgctattt tagaaggtgt
  51  ccagtgtGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCCTG GTCAAGCCTG
 101  GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC CTTCAGTAGC
 151  TATAGCATGA ACTGGGTCCG CCAGGCTCCA GGGAAGGGGC TGGAGTGGGT
 201  CTCATCCATT AGTAGTAGTA GTAGTTACAT ATACTACGCA GACTCAGTGA
 251  AGGGCCGATT CACCATCTCC AGAGACAACG CCAAGAACTC ACTGTATCTG
 301  CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG
 351  AGATGGGTAT AGCAGTGGCT GGTCCTACTA CTACTACTAC GGTATGGACG
 401  TCTGGGGCCA AGGGACCACG GTCACCGTCT CCTCAGCTTC CACCAAGGGC
 451  CCATCCGTCT TCCCCCTGGC GCCCTGCTCT AGAAGCACCT CCGAGAGCAC
 501  AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG
 551  TGTCGTGGAA CTCAGGCGCT CTGACCAGCG GCGTGCACAC CTTCCCAGCT
 601  GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC
 651  CTCCAGCAAC TTCGGCACCC AGACCTACAC CTGCAACGTA GATCACAAGC
 701  CCAGCAACAC CAAGGTGGAC AAGACAGTTG AGCGCAAATG TTGTGTCGAG
 751  TGCCCACCGT GCCCAGCACC ACCTGTGGCA GGACCGTCAG TCTTCCTCTT
 801  CCCCCCAAAA CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA
 851  CGTGCGTGGT GGTGGACGTG AGCCACGAAG ACCCCGAGGT CCAGTTCAAC
 901  TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCACGGGA
 951  GGAGCAGTTC AACAGCACGT TCCGTGTGGT CAGCGTCCTC ACCGTTGTGC
1001  ACCAGGACTG GCTGAACGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA
1051  GGCCTCCCAG CCCCCATCGA GAAAACCATC TCCAAAACCA AAGGGCAGCC
1101  CCGAGAACCA CAGGTGTACA CCCTGCCCCC ATCCCGGGAG GAGATGACCA
1151  AGAACCAGGT CAGCCTGACC TGCCTGGTCA AAGGCTTCTA CCCCAGCGAC
1201  ATCGCCGTGG AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC
1251  CACACCTCCC ATGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC
1301  TCACCGTGGA CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC
1351  GTGATGCATG AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT
1401  GTCTCCGGGT AAATGATAG
```

SEQ ID NO. 64
Modified 6.77.1 Heavy Chain Protein Sequence

```
   1  melglrwvfl vailegvqcE VQLVESGGGL VKPGGSLRLS CAASGFTFSS
  51  YSMNWVRQAP GKGLEWVSSI SSSSSYIYYA DSVKGRFTIS RDNAKNSLYL
 101  QMNSLRAEDT AVYYCARDGY SSGWSYYYYY GMDVWGQGTT VTVSSASTKG
 151  PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA
 201  VLQSSGLYSL SSVVTVPSSN FGTQTYTCNV DHKPSNTKVD KTVERKCCVE
 251  CPPCPAPPVA GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVQFN
 301  WYVDGVEVHN AKTKPREEQF NSTFRVVSVL TVVHQDWLNG KEYKCKVSNK
 351  GLPAPIEKTI SKTKGQPREP QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD
 401  IAVEWESNGQ PENNYKTTPP MLDSDGSFFL YSKLTVDKSR WQQGNVFSCS
 451  VMHEALHNHY TQKSLSLSPG K
```

SEQ ID NO. 65
Modified 6.77.1 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct ggatacctgg
  51  atccagtgca GATATTGTGA TGACCCAGAC TCCACTCTCT CTGTCCGTCA
 101  CTCCTGGACA GCCGGCCTCC ATCTCCTGCA AGTCTAGTCA GAGCCTCCTG
 151  CTTAGTGATG GAAAGACCTA TTTGAATTGG TACCTGCAGA AGCCCGGCCA
 201  GCCTCCACAG CTCCTGATCT ATGAAGTTTC CAACCGGTTC TCTGGAGTGC
 251  CAGACAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTCAC ACTGAAAATC
 301  AGCCGGGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAAGTAT
 351  ACAGCTTATG TGCAGTTTTG GCCAGGGGAC CAAGCTGGAG ATCAAACGAA
 401  CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG
 451  AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT TCTATCCCAG
 501  AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT
 551  CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
 601  AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA
 651  CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT
 701  TCAACAGGGG AGAGTGTTAG TGA
```

SEQ ID NO. 66
Modified 6.77.1 Kappa Light Chain Amino Acid Sequence

```
   1  mrlpaqllgl lmlwipgssa DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL
  51  LSDGKTYLNW YLQKPGQPPQ LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YSCMQSIQLM SSFGQGTKLE IKRTVAAPSV FIFPPSDEQL
 151  KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL
 201  SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNRGEC
```

SEQ ID NO. 67
Modified 7.26.4 Kappa Light Chain Nucleotide Sequence

```
   1  atgaggctcc ctgctcagct cctggggctg ctaatgctct ggatacctgg
  51  atccagtgcg GATATTGTGA TGACCCAGAC TCCACTCTCT CTGTCCGTCA
 101  CCCCTGGACA GCCGGCCTCC ATCTCCTGCA AGTCTAGTCA GAGCCTCCTG
 151  TATAGTGATG GAAAGACCTA TTTGTTTTGG TACCTGCAGA AGCCAGGCCA
 201  GCCTCCACAG CTCCTGATCT ATGAAGTTTC CAACCGATTC TCTGGAGTGC
 251  CAGATAGGTT CAGTGGCAGC GGGTCAGGGA CAGATTTCAC ACTGAAAATC
 301  AGCCGGGTGG AGGCTGAGGA TGTTGGGGTT TATTACTGCA TGCAAAGTAT
 351  ACAGCTTCCG TGGACGTTCG GCCAAGGGAC CAAGGTGGAA ATCAAACGAA
 401  CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA TGAGCAGTTG
 451  AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT TCTATCCCAG
 501  AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA TCGGGTAACT
 551  CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC
 601  AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAAGTCTA
 651  CGCCTGCGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT
 701  TCAACAGGGG AGAGTGTTAG TGA
```

SEQ ID NO. 68
Modified 7.26.4 Kappa Light Chain Amino Acid Sequence

```
   1  mrlpaqllgl lmlwipgssa DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL
  51  YSDGKTYLFW YLQKPGQPPQ LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI
 101  SRVEAEDVGV YYCMQSIQLP WTFGQGTKVE IKRTVAAPSV FIFPPSDEQL
 151  KSGTASVVCL LNNFYPREAK VQWKVDNALQ SGNSQESVTE QDSKDSTYSL
 201  SSTLTLSKAD YEKHKVYACE VTHQGLSSPV TKSFNRGEC
```

IN THE UNITED STATES RECEIVING OFFICE
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Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

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INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 1.7.2 in the description on page 81, line 2.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090901.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

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IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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P.O. Box 1450
Alexandria, Virginia 22313-1450

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INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 1.8.2 in the description on page 81, line 3.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090902.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

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Applicants : PFIZER INC. et al.

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Alexandria, Virginia 22313-1450

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INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.14.2 in the description on page 81, line 4.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090903.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104 (4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation :

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

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Applicants : PFIZER INC. et al.

Filed : Herewith

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INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.22.2 in the description on page 81, line 5.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090904.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

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INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.34.2 in the description on page 81, line 6.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090905.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

VIA EXPRESS MAIL

HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.67.1 in the description on page 81, line 7.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090906.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.73.2 in the description on page 81, line 8.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090907.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 6.77.1 in the description on page 81, line 9.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090908.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 7.16.6 in the description on page 81, line 10.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090909.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

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HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 7.20.5 in the description on page 81, line 11.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090910.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

VIA EXPRESS MAIL

HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 7.26.4 in the description on page 81, line 12.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090911.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.

ABX-PF/6 PCT

IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

Applicants : PFIZER INC. et al.

Filed : Herewith

For : ANTIBODIES TO MAdCAM

VIA EXPRESS MAIL

HON. COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450

MAIL STOP PCT - RO/US

INDICATIONS RELATING TO THE
EXPERT SOLUTION IN RESPECT OF DEPOSITED
BIOLOGICAL MATERIAL REFERRED TO IN THE DESCRIPTION

Sir:

The indications relating to deposited biological material are all contained in the description. The following additional indications are not required to be part of the description and should be treated as "separate indications." They relate only to the expert solution.

The additional indications made below relate to the deposited biological material referred to as Hybridoma 9.8.2 in the description on page 81, line 13.

The deposit was made in:

European Collection of Cell Cultures (ECACC)
Health Protection Agency
Porton Down
Salisbury, Wiltshire SP4 0JG
UNITED KINGDOM

on 09 September 2003 (09.09.2003), under Deposit Number 03090912.

The additional indications are:

For CA (Canada) designation:

In respect of the designation of Canada, samples of the deposited biological material will be made available until the grant of the Canadian patent, or until the date on which the application is refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, as provided in Rules 107 and 108 of the Patent Rules under the Canadian Patent Act, only by the issue of a sample to an independent expert nominated by the Commissioner (Rule 104(4)).

For EP (European Patent) designation:

In respect of the designation of the EPO, samples of the deposited biological material will be made available until the publication of the mention of the grant of the European patent, or until 20 years from the date of filing if the application is refused or withdrawn or is deemed to be withdrawn, as provided in Rule 28(3) of the Implementing Regulations under the EPC, only by the issue of a sample to an expert nominated by requester (Rule 28(4) EPC).

For FI (Finland) designation:

In respect of the designation of Finland, until the publication of the mention of grant by the National Board of Patents and Registration, or for 20 years from the date of filing if the application has been finally decided upon without resulting in the grant of a patent by the National Board of Patents and Registration, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For GB (United Kingdom) designation:

In respect of the designation of the United Kingdom, the applicant(s) hereby give(s) notice of my/our intention that the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For IS (Iceland) designation:

In respect of the designation of Iceland, until a patent has been granted by the Icelandic Patent Office, or a final decision taken by the Icelandic Patent Office if the application has been finally decided upon without resulting in the grant of a patent, the furnishing of samples of the deposited biological material will only be effected to an expert in the art.

For SE (Sweden) designation:

In respect of the designation of Sweden, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of samples of the deposited biological material will be made available only to an expert in the art.

For SG (Singapore) designation:

Applicant(s) hereby give notice of my/our intention that samples of the above-identified culture shall be available only to experts in accordance with paragraph 3 of the Fourth Schedule to the Patents Rules 1995.