Figure 1a

Variable Heavy Chain DNA

3076_VH1A (SEQ ID NO: 1):
CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAGCTGC
AAAGCCTCCGGAGGCACTTTTTCTTCTAATGCTATTTCTTGGGTGCGCCAAGCCCCTGGGCAGGGTC
TCGAGTGGATGGGCAATATCTGGCCGATTTTTGGCACTGCGAATTACGCGCAGAAGTTTCAGGGCC
GGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGCG
AAGATACGGCCGTGTATTATTGCGCGCGTAATGGTTATCTTGATACTAATACTTATATTGATTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

3078_VH3 (SEQ ID NO: 2):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTGATTATGCTATGTCTTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCGCTATCCGTTATGATGGTAGCAATACCTATTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTTATTATTCTGGTATTTATCAGCATATTGATTATTGGGGC
CAAGGCACCCTGGTGACGGTTAGCTCA

3081_ VH3 (SEQ ID NO: 3):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTCTTCATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTCTATCTCTGGTCTTGGTAGCACTACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTTATCATTATGAGTATCATTATTTTTCTTCTGGTTTTGATAA
TTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3085_ VH1A (SEQ ID NO: 4):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGCTG
CAAAGCCTCCGGATATACCTTTACTGGTTATTATATTAATTGGGTCCGCCAAGCCCCTGGGCAGGGT
CTCGAGTGGATGGGCTGGATCTTTCCGAATGGTGGCTCTACGGGTTACGCGCAGAAGTTTCAGGGC
CGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGC
GAAGATACGGCCGTGTATTATTGCGCGCGTGGTAATATTTTTATTTTTGATTATTGGGGCCAAGGCAC
CCTGGTGACGGTTAGCTCA

3086_VH3 (SEQ ID NO: 5):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTACTTCTTATTATATGCATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATCGATTCTTCTGGTAGCTCTACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTCAGCTTATGCCTTTTGGTGGTTATTTTGATGTTTGGGGC
CAAGGCACCCTGGTGACGGTTAGCTCA

3087_ VH3 (SEQ ID NO: 6):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG

TCTCGAGTGGGTGAGCGGTATCTCTGGTGATCCTAGCAATACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

3088_ VH3 (SEQ ID NO: 7):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCGGTATCTCTTCTTGGGGTAGCTCTACCTATTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

3089_ VH2 (SEQ ID NO: 8):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTTCTGATGGTATGGGTGTGGGTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCTTATCGATTGGGATGATGATAAGCGTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTTTTAATTGGTTTTATCGTCTTGCTTTTGTTAATCCTGAT
GTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3101_ VH2 (SEQ ID NO: 9):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTACTTCTCGTGTTGGTGTGTCTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCATATCGATTGGAATGATGATAAGTATTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTGAGGATCGTCTTCTTGGTGGTTATGGTTATGATGTTT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3102_ VH4 (SEQ ID NO: 10):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACCTG
CACCGTTTCCGGAGGCAGCATTTCTGGTAATTATTGGTCTTGGATTCGCCAGGCCCCTGGGAAGGG
TCTCGAGTGGATTGGCGATTATCATGGCTCTACCTATTATAATCCGAGCCTGAAAGGCCGGGTGACC
ATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCGGAAGATACGG
CCGTGTATTATTGCGCGCGTGAGCAGTATCATTGGGGTCTTGCTTGGACTGGTTTTGATAATTGGGG
CCAAGGCACCCTGGTGACGGTTAGCTCA

3127_ VH5 (SEQ ID NO: 11):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAGCTGC
AAAGGTTCCGGATATTCCTTTTCTACTTCTTGGGTTGGTTGGGTGCGCCAGATGCCTGGGAAGGGTC
TCGAGTGGATGGGCATTATCGATCCGGATATTAGCTATACCTCTTATTCTCCGAGCTTTCAGGGCCA
GGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTATCTTCAATGGAGCAGCCTGAAAGCGAG
CGATACGGCCATGTATTATTGCGCGCGTTATCTTATGGGTCTTGGTTATGATGTTTGGGGCCAAGGC
ACCCTGGTGACGGTTAGCTCA

3128_ VH2 (SEQ ID NO: 12):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTTCTTCTGGTATGTCTGTGTCTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTCGTATCTATTCTGATGATTCTAAGTCTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTGCTGCTCATTGGAATGGTCCTCTTTTTGATGTTTGGG
GCCAAGGCACCCTGGTGACGGTTAGCTCA

3129_ VH3 (SEQ ID NO: 13):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTAATTATTCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATCTATGGTGGTGGTAGCTATACCTATTATGCGGATAGCGTGAAAGGC
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTCAGGCTGGTATGTATTTTGATGTTTGGGGCCAAGGCACC
CTGGTGACGGTTAGCTCA

3130_ VH4 (SEQ ID NO: 14):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACCTG
CACCGTTTCCGGAGGCAGCATTGGTTATTATTGGAATTGGATTCGCCAGGCCCCTGGGAAGGGTCT
CGAGTGGATTGGCCATATCTCTCGTTTTGGCTCTACCAATTATAATCCGAGCCTGAAAGGCCGGGTG
ACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCGGAAGATA
CGGCCGTGTATTATTGCGCGCGGGAGTATACTGGTAATGATTGGTATCGTCAGCAGGGTCAGCATG
CTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3131_ VH2 (SEQ ID NO: 15):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACCTGT
ACCTTTTCCGGATTTAGCCTGTCTAATTCTGGTGTTGGTGTGGGTTGGATTCGCCAGCCGCCTGGGA
AAGCCCTCGAGTGGCTGGCTGATATCTATTCTGATACTACTAAGCGTTATAGCACCAGCCTGAAAAC
GCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACATGGACCCG
GTGGATACGGCCACCTATTATTGCGCGCGTTATGGTGAGGCTTATTTTGATTATTGGGGCCAAGGCA
CCCTGGTGACGGTTAGCTCA

6183_VH3 (SEQ ID NO: 77)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGGTATTAATATGGAGTCTACTCGTATTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6184_VH3 (SEQ ID NO: 78)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTCATGATGGTAATGTTAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6185_VH3 (SEQ ID NO: 79)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGAATGGTGATTATATTTCTTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6186_VH3 (SEQ ID NO: 80)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTAATCTTTCTGGTTCTGCTAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6187_VH3 (SEQ ID NO: 81)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTTCTAATGGTGATATTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6188_VH3 (SEQ ID NO: 82)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTACTAATGGTTGGCAGACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6189_VH3 (SEQ ID NO: 83)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTAATATGATTGGTAATGTTACTAATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6190_VH3 (SEQ ID NO: 84)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCTATATTAATCCTAATGGTATGATGACTAATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6192_VH3 (SEQ ID NO: 85)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGTTATTTCTCCTGGTGGTGAGGCTAAGTCTTATGCTGATTCTGTTAAGGGT
CGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGA
AGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

6195_VH3 (SEQ ID NO: 86)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTGGTAATGGTGGTCATACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6197_VH3 (SEQ ID NO: 87)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGGATGGTGTTTATAAGTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6200_VH3 (SEQ ID NO: 88)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTAATAATGGTAATGTTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6201_VH3 (SEQ ID NO: 89)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGAAGGG
TCTCGAGTGGGTGAGCGCTATTTCTATGCATGGTGATACTACTTATTATGCTGATTCTGTTAAGGGTC
GTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAA
GATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGCTTATTGGGGCCA
AGGCACCCTGGTGACGGTTAGCTCA

6204_VH3 (SEQ ID NO: 90)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCCATATTCGTAAGAAGAATACTTCTTATACTACTGAGTATGCTGCTTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCG

TGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTT
ATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6214_VH3 (SEQ ID NO: 91)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATTCAGCGTGTTGGTTCTACTTATTATGCTGATTCTGTTAAGGGTCGT
TTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGGAAGA
TACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTTGCTTATTGGGGCC
AAGGCACCCTGGTGACGGTTAGCTCA

3077_VH1B (SEQ ID NO: 111)
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGCTG
CAAAGCCTCCGGATATACCTTTACTTCTTATTCTATTAATTGGGTCCGCCAAGCCCCTGGGCAGGGT
CTCGAGTGGATGGGCTATATCGATCCGAATCGTGGCAATACGAATTACGCGCAGAAGTTTCAGGGC
CGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGCCTGCGTAGC
GAAGATACGGCCGTGTATTATTGCGCGCGTGAGTATATTTATTTTATTCATGGTATGCTTGATTTTTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3079_VH3 (SEQ ID NO: 112)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTAATTATGGTATGCATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATCCGTTCTGATGGTAGCTGGACCTATTATGCGGATAGCGTGAAAG
GCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCG
GAAGATACGGCCGTGTATTATTGCGCGCGTCGTTATTGGTCTAAGTCTCATGCTTCTGTTACTGATTA
TTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3080_ VH3 (SEQ ID NO: 113)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAGCT
GCGCGGCCTCCGGATTTACCTTTTCTTCTTATGGTATGCATTGGGTGCGCCAAGCCCCTGGGAAGG
GTCTCGAGTGGGTGAGCAATATCTATTCTGATGGTAGCAATACCTTTTATGCGGATAGCGTGAAAGG
CCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGCGTGCGG
AAGATACGGCCGTGTATTATTGCGCGCGTAATATGTATCGTTGGCCTTTTCATTATTTTTTTGATTATT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

~~Figure 1b~~

Variable Heavy Chain Peptide

(CDR Regions in **Bold** or <u>underlined</u>)

3076_VH1A (SEQ ID NO: 16):
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSNAIS**WVRQAPGQGLEWMG**NIWPIFGTANYAQKFQGR**
VTITADESTSTAYMELSSLRSEDTAVYYCAR**NGYLDTNTYIDY**WGQGTLVTVSS

3078_VH3 (SEQ ID NO: 17):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSDYAMSWVRQAPGKGLEWV**SAIRYDGSNTYYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YYSGIYQHIDY**WGQGTLVTVSS

3081_ VH3 (SEQ ID NO: 18):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYALHWVRQAPGKGLEWV**SSISGLGSTTYYADSVKGRF**
TISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YHYEYHYFSSGFDN**WGQGTLVTVSS

3085_ VH1A (SEQ ID NO: 19):
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTGYYIN**WVRQAPGQGLEWMG**WIFPNGGSTGYAQKFQGR**
VTMTRDTSISTAYMELSSLRSEDTAVYYCAR**GNIFIFDY**WGQGTLVTVSS

3086_VH3 (SEQ ID NO: 20):
QVQLVESGGGLVQPGGSLRLSCAASGFTFTSYYMHWVRQAPGKGLEWV**SYIDSSGSSTYYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QLMPFGGYFDV**WGQGTLVTVSS

3087_ VH3 (SEQ ID NO: 21):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWV**SGISGDPSNTYYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**DLPLVYTGFAY**WGQGTLVTVSS

3088_ VH3 (SEQ ID NO: 22):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWV**SGISSWGSSTYYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**EDGSYMTDYFAY**WGQGTLVTVSS

3089_ VH2 (SEQ ID NO: 23):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSDGMGVG**WIRQPPGKALEWLA**LIDWDDDKRYSTSLKTRL**
TISKDTSKNQVVLTMTNMDPVDTATYYCAR**FNWFYRLAFVNPDV**WGQGTLVTVSS

3101_ VH2 (SEQ ID NO: 24):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSRVGVS**WIRQPPGKALEWLA**HIDWNDDKYYSTSLKTRLT**
ISKDTSKNQVVLTMTNMDPVDTATYYCAR**EDRLLGGYGYDV**WGQGTLVTVSS

3102_VH4 (SEQ ID NO: 25):
QVQLQESGPGLVKPGETLSLTCTVSGGSISGNYWSWIRQAPGKGLEWIGDYHGSTYYNPSLKGRVTISV
DTSKNQFSLKLSSVTAEDTAVYYCAREQYHWGLAWTGFDNWGQGTLVTVSS

3127_VH5 (SEQ ID NO: 26):
QVQLVQSGAEVKKPGESLKISCKGSGYSFSTSWVGWVRQMPGKGLEWMGIIDPDISYTSYSPSFQGQV
TISADKSISTAYLQWSSLKASDTAMYYCARYLMGLGYDVWGQGTLVTVSS

3128_VH2 (SEQ ID NO: 27):
QVQLKESGPALVKPTQTLTLTCTFSGFSLSSSGMSVSWIRQPPGKALEWLARIYSDDSKSYSTSLKTRLTI
SKDTSKNQVVLTMTNMDPVDTATYYCARAAHWNGPLFDVWGQGTLVTVSS

3129_VH3 (SEQ ID NO: 28):
QVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMNWVRQAPGKGLEWVSYIYGGGSYTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARQAGMYFDVWGQGTLVTVSS

3130_VH4 (SEQ ID NO: 29):
QVQLQESGPGLVKPGETLSLTCTVSGGSIGYYWNWIRQAPGKGLEWIGHISRFGSTNYNPSLKGRVTISV
DTSKNQFSLKLSSVTAEDTAVYYCAREYTGNDWYRQQGQHADYWGQGTLVTVSS

3131_VH2 (SEQ ID NO: 30):
QVQLKESGPALVKPTQTLTLTCTFSGFSLSNSGVGVGWIRQPPGKALEWLADIYSDTTKRYSTSLKTRLTI
SKDTSKNQVVLTMTNMDPVDTATYYCARYGEAYFDYWGQGTLVTVSS

6183_VH3 (SEQ ID NO: 92)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSGINMESTRIYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6184_VH3 (SEQ ID NO: 93)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISHDGNVKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6185_VH3 (SEQ ID NO: 94)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMNGDYISYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6186_VH3 (SEQ ID NO: 95)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINLSGSAKYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6187_VH3 (SEQ ID NO: 96)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISSNGDITYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6188_VH3 (SEQ ID NO: 97)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISTNGWQTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6189_VH3 (SEQ ID NO: 98)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINMIGNVTNYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6190_VH3 (SEQ ID NO: 99)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSYINPNGMMTNYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6192_VH3 (SEQ ID NO: 100)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSVISPGGEAKSYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6195_VH3 (SEQ ID NO: 101)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISGNGGHTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6197_VH3 (SEQ ID NO: 102)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMDGVYKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6200_VH3 (SEQ ID NO: 103)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISNNGNVTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6201_VH3 (SEQ ID NO: 104)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMHGDTTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6204_VH3 (SEQ ID NO: 105)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSHIRKKNTSYTTEYAASVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

6214_VH3 (SEQ ID NO: 106)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSNIQRVGSTYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

3077_VH1B (SEQ ID NO: 114)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYSINWVRQAPGQGLEWMGYIDPNRGNTNYAQKFQGR
VTMTRDTSISTAYMELSSLRSEDTAVYYCAREYIYFIHGMLDFWGQGTLVTVSS

3079_VH3 (SEQ ID NO: 115)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVSNIRSDGSWTYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRYWSKSHASVTDYWGQGTLVTVSS

3080_VH3 (SEQ ID NO: 116)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSNIYSDGSNTFYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCARNMYRWPFHYFFDYWGQGTLVTVSS

Figure 2a

Variable Light Chain DNA

3076_Vl lambda 2 (SEQ ID NO: 31):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGTGT
ACGGGTACTAGCAGCGATATTGGTGCTTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGGCGCCG
AAACTTATGATTTATGAGGTTTCTTCTCGTCCCTCAGGCGTGAGCAACCGTTTTAGCGGATCCAAAAG
CGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATTATTATTGCTC
TTCTTATGATCTTACTCCTCCTGGTAAGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3078_Vl lambda 3 (SEQ ID NO: 32):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGCTTC
TGATGTTGGTTCTCTTGATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3081_ Vk kappa 3 (SEQ ID NO: 33):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTGAG
CTGCAGAGCGAGCCAGACTGGTTCTACTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCAAGCA
CCGCGTCTATTAATTTATGATGCTTCTAAGCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGCTCTG
GATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGACTTATTATTG
CCATCAGTATTATAACGTTCCTCATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

3085_ Vl lambda 1 (SEQ ID NO: 34):
GATATCGTGCTGACCCAGCCGCCTTCAGTGAGTGGCGCACCAGGTCAGCGTGTGACCATCTCGTGT
AGCGGCAGCAGCAGCAACATTGGTAATAATTATGTGTCTTGGTACCAGCAGTTGCCCGGGACGGCG
CCGAAACTTCTGATTTATGGTGATGATCAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGCGGATCCA
AAAGCGGCACCAGCGCGAGCCTTGCGATTACGGGCCTGCAAAGCGAAGACGAAGCGGATTATTATT
GCCAGTCTTATGGTACTTTTTCTTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3086_Vk kappa 1 (SEQ ID NO: 35):
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTACC
TGCAGAGCGAGCCAGAATATTTCTCAGTGGCTGAATTGGTACCAGCAGAAACCAGGTAAAGCACCG
AAACTATTAATTTATGGTGCTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTCTGGATC
CGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATTATTGCCAG
CAGTATTATGATCTTCCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

3087_ Vl lambda 3 (SEQ ID NO: 36):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTCGTCATTATTATGTTTATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGGTGATTCTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGAC
TTATAGTGGTGGTGCTTCTCTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3088_ Vl lambda 3 (SEQ ID NO: 37):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TTATAATGGTACTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3089_ Vk kappa 3 (SEQ ID NO: 38):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTGAG
CTGCAGAGCGAGCCAGTCTGTTTCTTCTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCAAGCA
CCGCGTCTATTAATTTATGGTGCTTCTTCTCGTGCAACTGGGGTCCCGGCGCGTTTTAGCGGCTCTG
GATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGTTTATTATTG
CCAGCAGGGTTATAATTCTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

3101_ Vl lambda 3 (SEQ ID NO: 39):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATTCTCTTGGTTCTTATTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTGGTGATGATACTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCG
GCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGGTT
CTCGTACTGGTTATAATAATTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3102_ V'l lambda 3 (SEQ ID NO: 40):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGATGATTCTGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCGGTGC
TTATGCTATGCATATGACTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3127_ Vl lambda 2 (SEQ ID NO: 41):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGTGT
ACGGGTACTAGCAGCGATGTTGGTGCTATTAATTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGG
CGCCGAAACTTATGATTTATGATGTTAATAAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGCGGATC
CAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATTATTA
TTGCGGTTCTTATACTATGCAGGTTGGTTCTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTG
GCCAG

3128_ Vl lambda 3 (SEQ ID NO: 42):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGCTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTG
TTGTGATTTATGATGATAATGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGGC
TTATACTGGTGATGGTGGTCGTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3129_ Vl lambda 3 (SEQ ID NO: 43):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATGTTGGTTCTAAGGTTGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTT

CTTGTGATTTATTATGATAATAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCG
GCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGT
CTTATACTTTTGAGTCTGGTTCTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3130_ Vl lambda 3 (SEQ ID NO: 44):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTCATTATTATGTTGATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGCTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TATTCTCAGCAGTCTATGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3131_ Vl lambda 3 (SEQ ID NO: 45):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATCTTGGTAATTTTTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATGAGGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TGGGATATGTATCGTACTATTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

6278_Vl lambda 3 (SEQ ID NO: 107)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TGCTGATAATTTTCCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGTCAG

6279_ Vl lambda 3 (SEQ ID NO: 108)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTC
TTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCCAGTC
TTATACTATGTCTGATGTTCTTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGTCAG

3077_Vk kappa 2 (SEQ ID NO: 117)
GATATCGTGATGACCCAGAGCCCACTGAGCCTGCCAGTGACTCCGGGCGAGCCTGCGAGCATTAGC
TGCAGAAGCAGCCAAAGCCTGCTTTTTATTGATGGCAATAATTATCTGAATTGGTACCTTCAAAAACC
AGGTCAAAGCCCGCAGCTATTAATTTATCTTGGTTCTAATCGTGCCAGTGGGGTCCCGGATCGTTT
TAGCGGCTCTGGATCCGGCACCGATTTTACCCTGAAAATTAGCCGTGTGGAAGCTGAAGACGTGGG
CGTGTATTATTGCCAGCAGTATTCTTCTAAGTCTGCTACCTTTGGCCAGGGTACGAAAGTTGAAATTA
AACGTACG

3079_Vk kappa 1 (SEQ ID NO: 118)
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTACC
TGCAGAGCGAGCCAGGATATTTCTGCTTTTCTGAATTGGTACCAGCAGAAACCAGGTAAAGCACCGA
AACTATTAATTTATAAGGTTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTCTGGATCC
GGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATTATTGCCAGCA
GGCTTATTCTGGTTCTATTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGTACG

3080_Vl lambda 3 (SEQ ID NO: 119)

GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGTGT
AGCGGCGATAATATTGGTAATAAGTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCCAGTTG
TTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAACAGCGG
CAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTATTGCTCTTCT
TATGATTCTTCTTATTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

Figure 2b

Variable Light Chain Peptide

(CDR Regions in **Bold** or <u>underlined</u>)

3076_Vl lambda 2 (SEQ ID NO: 46):
DIALTQPASVSGSPGQSITISCTGTSSDIGAYVSWYQQHPGKAPKLMIYEVSSRPSGVSNRFSGSKSGNT
ASLTISGLQAEDEADYYCSSYDLTPPGKVFGGGTKLTVLGQ

3078_Vl lambda 3 (SEQ ID NO: 47):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYGDNNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCASDVGSLDVFGGGTKLTVLGQ

3081_ Vk kappa 3 (SEQ ID NO: 48):
DIVLTQSPATLSLSPGERATLSCRASQTGSTSYLAWYQQKPGQAPRLLIYDASKRATGVPARFSGSGSGT
DFTLTISSLEPEDFATYYCHQYYNVPHTFGQGTKVEIKRT

3085_ Vl lambda 1 (SEQ ID NO: 49):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGNNYVS**WYQQLPGTAPKLLIY**GDDQRPS**GVPDRFSGSKSG
TSASLAITGLQSEDEADYYC**QSYGTFSSF**VFGGGTKLTVLGQ

3086_Vk kappa 1 (SEQ ID NO: 50):
DIQMTQSPSSLSASVGDRVTITCRASQNISQWLNWYQQKPGKAPKLLIYGASNLQSGVPSRFSGSGSGT
DFTLTISSLQPEDFATYYCQQYYDLPNTFGQGTKVEIKRT

3087_ Vl lambda 3 (SEQ ID NO: 51):
DIELTQPPSVSVAPGQTARISCSGDNLRHYYVYWYQQKPGQAPVLVIYGDSKRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCQTYTGGASLVFGGGTKLTVLGQ

3088_ Vl lambda 3 (SEQ ID NO: 52):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYNGTYVFGGGTKLTVLGQ

3089_ Vk kappa 3 (SEQ ID NO: 53):
DIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGVPARFSGSGSGT
DFTLTISSLEPEDFAVYYCQQGYNSPFTFGQGTKVEIKRT

3101_ Vl lambda 3 (SEQ ID NO: 54):
DIELTQPPSVSVAPGQTARISCSGDSLGSYYVHWYQQKPGQAPVLVIGDDTKRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCGSRTGYNNSFVFGGGTKLTVLGQ

3102_ Vl lambda 3 (SEQ ID NO: 55):
DIELTQPPSVSVAPGQTARISCSGDNLGHYYVSWYQQKPGQAPVLVIYDDSDRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCGAYAMHMTVFGGGTKLTVLGQ

3127_ Vl lambda 2 (SEQ ID NO: 56):
DIALTQPASVSGSPGQSITISCTGTSSDVGAINYVSWYQQHPGKAPKLMIYDVNKRPSGVPDRFSGSKSG
NTASLTISGLQAEDEADYYCGSYTMQVGSYVFGGGTKLTVLGQ

3128_ Vl lambda 3 (SEQ ID NO: 57):
DIELTQPPSVSVAPGQTARISCSGDNIGHYYAHWYQQKPGQAPVVVIYDDNDRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCQAYTGDGGRVFGGGTKLTVLGQ

3129_ Vl lambda 3 (SEQ ID NO: 58):
DIELTQPPSVSVAPGQTARISCSGDNLGSKVVSWYQQKPGQAPVLVIYYDNKRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYTFESGSVVFGGGTKLTVLGQ

3130_ Vl lambda 3 (SEQ ID NO: 59):
DIELTQPPSVSVAPGQTARISCSGDNLGHYYVDWYQQKPGQAPVLVIYADNNRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCSSYSQQSMVFGGGTKLTVLGQ

3131_ Vl lambda 3 (SEQ ID NO: 60):
DIELTQPPSVSVAPGQTARISCSGDNLGNFYVHWYQQKPGQAPVLVIYEDSNRPSGIPERFSGSNSGNT
ATLTISGTQAEDEADYYCSSWDMYRTIFVFGGGTKLTVLGQ

6278_ Vl lambda 3 (SEQ ID NO: 109)
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSADNFPFVFGGGTKLTVLGQ

6279_ Vl lambda 3 (SEQ ID NO: 110)
DIELTQPPSVSVAPGQTARISCSGDNIGHYYVSWYQQKPGQAPVLVIYSDSNRPSGIPERFSGSNSGNTA
TLTISGTQAEDEADYYCQSYTMSDVLVVFGGGTKLTVLGQ

3077_Vk kappa 2 (SEQ ID NO: 120)
DIVMTQSPLSLPVTPGEPASISCRSSQSLLFIDGNNYLNWYLQKPGQSPQLLIYLGSNRASGVPDRFSGS
GSGTDFTLKISRVEAEDVGVYYCQQYSSKSATFGQGTKVEIKRT

3079_Vk kappa 1 (SEQ ID NO: 121)
DIQMTQSPSSLSASVGDRVTITC**RASQDISAFLN**WYQQKPGKAPKLLI**YKVSNLQS**GVPSRFSGSGSGT
DFTLTISSLQPEDFATYYC**QQAYSGSI**TFGQGTKVEIKRT

3080_Vl lambda3 (SEQ ID NO: 122)
DIELTQPPSVSVAPGQTARISC**SGDNIGNKYVS**WYQQKPGQAPVVVIY**GDNNRPS**GIPERFSGSNSGNT
ATLTISGTQAEDEADYYC**SSYDSSYFVF**GGGTKLTVLGQ

Figure 3

Variable Heavy Chain Consensus Sequences

(CDR Regions in **Bold**)

VH1A Consensus (SEQ ID NO: 61):

QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYAIS**WVRQAPGQGLEWMG**GIIPIFGTANYAQKFQG**RVTI
TADESTSTAYMELSSLRSEDTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS.

VH2 Consensus (SEQ ID NO: 62)

QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPPGKALEWLA**LIDWDDDKYYSTSLKT**RLT
ISKDTSKNQVVLTMTNMDPVDTATYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

VH3 Consensus (SEQ ID NO: 63):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS SYAMS**WVRQA PGKGLEWVS**A**
(51) **ISGSGGSTYY ADSVKG**RFTI SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**
(101) **GDGFYAMDYW** GQGTLVTVS S

VH4 Consensus (SEQ ID NO: 64):

QVQLQESGPGLVKPSETLSLTCTVS**GGSISSYYWS**WIRQPPGKGLEWIG**YIYYSGSTNYNPSLKS**RVTIS
VDTSKNQFSLKLSSVTAADTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

VH5 Consensus (SEQ ID NO: 65):

QVQLVQSGAEVKKPGESLKISCKGS**GYSFTSYWIG**WVRQMPGKGLEWMG**IIYPGDSDTRYSPSFQG**QVTI
SADKSISTAYLQWSSLKASDTAMYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

Figure 4

Variable Light Chain Consensus Sequences

(CDR Regions in Bold)

Vl_λ1 Consensus (SEQ ID NO: 66):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGSNYVS**WYQQLPGTAPKLLIY**DNNQRPS**GVPDRFSGSKSGT
SASLAITGLQSEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

Vl_λ2 Consensus (SEQ ID NO: 67):
DIALTQPASVSGSPGQSITISC**TGTSSDVGGYNYVS**WYQQHPGKAPKLMIY**DVSNRPS**GVSNRFSGSKSG
NTASLTISGLQAEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

Vl_λ3 Consensus (SEQ ID NO: 68):

(1) DIELTQPPSV SVAPGQTARI SC**SGDALGDK YAS**WYQQKPG QAPVLVIY**DD**
(51) **SDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTTPP**VFGGG
(101) TKLTVLG

Vl_k1 Consensus (SEQ ID NO: 69):

(1) DIQMTQSPSS LSASVGDRVT ITC**RASQGIS SYLA**WYQQKP GKAPKLLIY**A**
(51) **ASSLQS**GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC**QQ HYTTPP**TFGQ
(101) GTKVEIKR

Vl_k3 Consensus (SEQ ID NO: 70):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSGSGT
DFTLTISSLEPEDFAVYYC**QQHYTTPP**TFGQGTKVEIKRT

Figure 5

Peptide Sequence of CD38

(SEQ ID NO: 71):

```
1     mancefspvs gdkpccrlsr raqlclgvsi lvlilvvvla vvvprwrqqw sgpgttkrfp
61    etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn
121   killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181   snnpvsvfwk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea
241   wvihggreds rdleqdptik elesiiskrn iqfsekniyr pdkflqcvkn pedssctsei
```

Figure 6

Nucleotide Sequence of Chimeric OKT10

Heavy Chain (SEQ ID NO: 72):

caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc gattttagta
gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg attggagaaa ttaatccaga
tagcagtacg ataaactata cgacatctct aaaggataaa ttcatcatct ccagagacaa cgccaaaaat
acgctgtacc tgcaaatgac caaagtgaga tctgaggaca cagcccttta ttactgtgca agatatggta
actggtttcc ttattggggc caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggt
cttccccctg gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac accttcccgg
ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac
ccagacctac atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagaaagt tgagcccaaa
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg tcagtcttcc
tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga
cgtgagccac gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag
acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg
actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac
catctccaaa gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc gtggagtggg
agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt
cctctacagc aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Light Chain (SEQ ID NO: 73):

gatatcctga tgacccagtc tcaaaaaatc atgcccacat cagtgggaga cagggtcagc gtcacctgca
aggccagtca aaatgtggat actaatgtag cctggtatca acagaaacca ggacagtctc ctaaagcact
gatttactcg gcatcctacc gatacagtgg agtccctgat cgcttcacag gcagtggatc tgggacagat

ttcactctca ccatcaccaa tgtgcagtct gaggacttgg cagagtattt ctgtcagcaa tatgacagct

atcctctcac gttcggtgct gggaccaagc tggacctgaa acgtacggtg gctgcaccat ctgtcttcat

cttcccgcca tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat

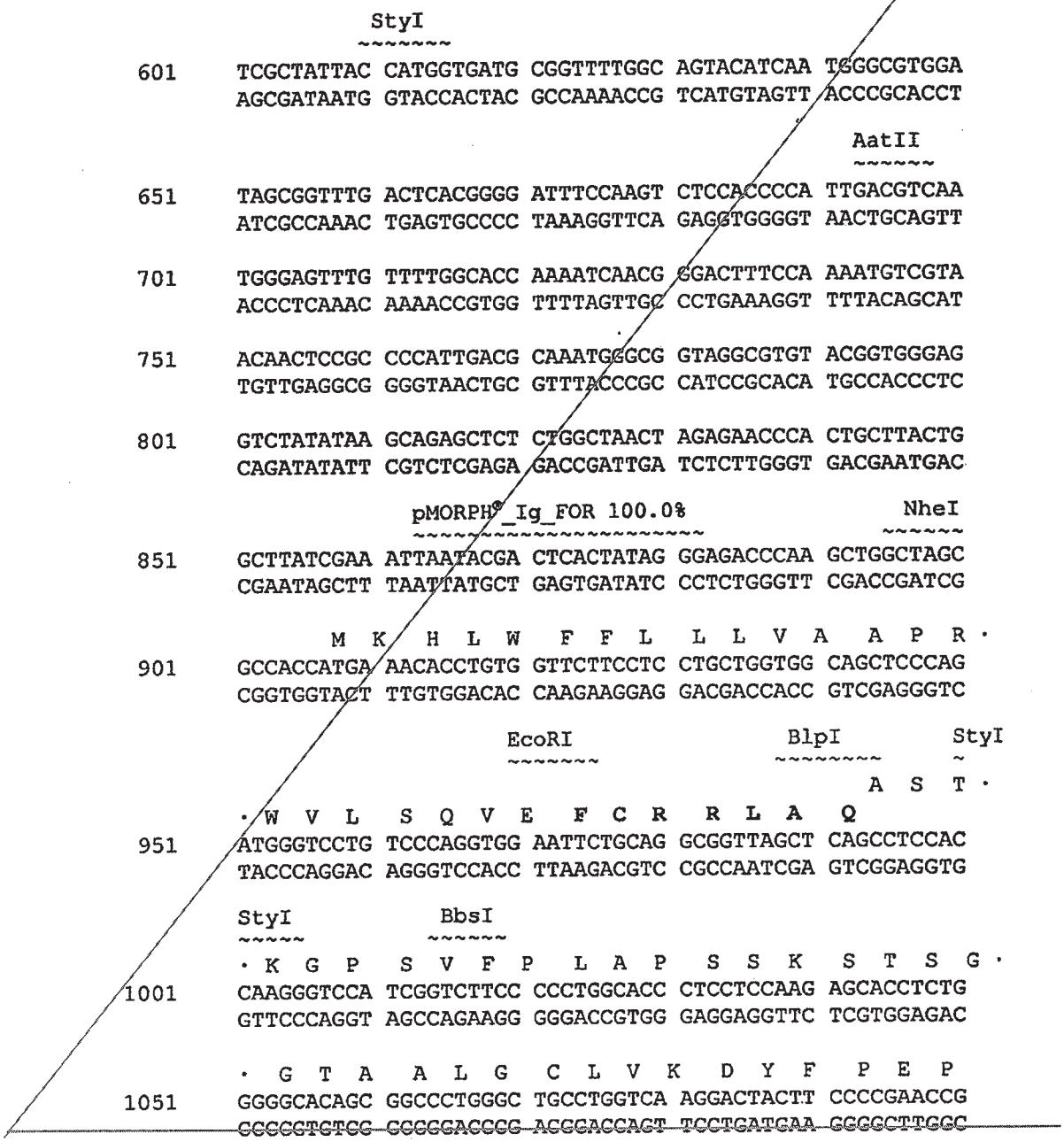
cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag gagagtgtca

cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg ctgagcaaag cagactacga

gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc ctgagctcgc ccgtcacaaa gagcttcaac

aggggagagt gt

Figure 7: DNA sequence of pMOPRH®_h_IgG1_1



```
          V  T  V  S   W  N  S   G  A  L   T  S  G  V   H  T  F  ·
1101      GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
          CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA

          ·  P  A  V   L  Q  S  S   G  L  Y   S  L  S   S  V  V  T  ·
1151      CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
          GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACT

          ·  V  P  S   S  S  L   G  T  Q  T   Y  I  C   N  V  N
1201      CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT
          GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA

                              StyI
                            ~~~~~~~
          H  K  P  S   N  T  K   V  D  K   K  V  E  P   K  S  C  ·
1251      CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
          GTGTTCGGGT CGTTGTGGTT CCACCTGTTC TTTCAACTCG GGTTTAGAAC

          ·  D  K  T   H  T  C  P   P  C  P   A  P  E   L  L  G  G  ·
1301      TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG
          ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

                    BbsI                        StyI
                  ~~~~~~~                     ~~~~~~
          ·  P  S  V   F  L  F   P  P  K  P   K  D  T   L  M  I
1351      GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
          CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG

                                                          BbsI
                                                         ~~~~~
          S  R  T  P   E  V  T   C  V  V   V  D  V  S   H  E  D  ·
1401      TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
          AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT

          BbsI
          ~
          ·  P  E  V   K  F  N  W   Y  V  D   G  V  E   V  H  N  A  ·
1451      CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
          GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

          ·  K  T  K   P  R  E   E  Q  Y   N  S  T  Y   R  V  V
1501      CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
          GGTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCGTGCAT GGCCCACCAG

          S  V  L  T   V  L  H   Q  D  W   L  N  G  K   E  Y  K  ·
1551      AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
          TCGCAGGAGT GGCAGGACGT GGTCCTGACC GACTTACCGT TCCTCATGTT

          ·  C  K  V   S  N  K  A   L  P  A   P  I  E   K  T  I  S  ·
1601      GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
          CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

                                                    BsrGI
                                                   ~~~~~~
          ·  K  A  K   G  Q  P   R  E  P   Q  V  Y   T  L  P  P
1651      CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA
```

```
          GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT
           S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  V  K  ·
1701      TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
          AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT

          ·  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  ·
1751      AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
          TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG

          ·  E  N  N  Y  K  T  T  P  P  V  L  D  S  D  G  S
1801      CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC
          GCCTCTTGTT GATGTTCTGG TGCGGAGGGC ACGACCTGAG GCTGCCGAGG

           F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q  G  ·
1851      TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
          AAGAAGGAGA TGTCGTTCGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

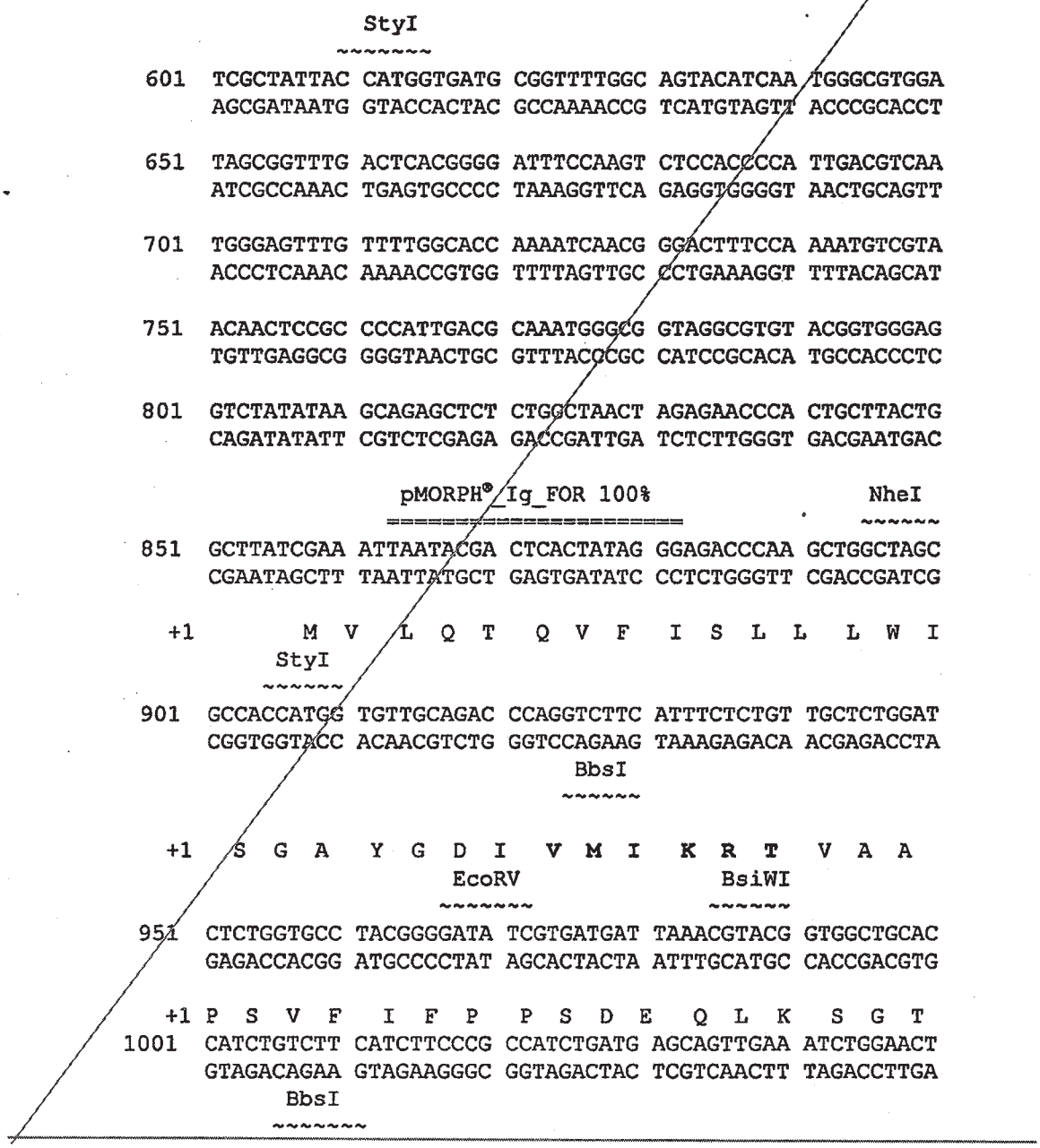
                BbsI                    NsiI
              ~~~~~~~~                ~~~~~~
          ·  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  ·
1901      GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
          CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

                SapI                                        PmeI
              ~~~~~~~~                                   ~~~~~~~~
          ·  Q  K  S  L  S  L  S  P  G  K  *
1951      CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGGGCC CGTTTAAACC
          GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTACTCCCGG GCAAATTTGG

2001      CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
          GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

                    ~~~~~~~~~~~~~~~~~~~
                    pMORPH® Ig_REV 100.0%
2051      CCCCTCCCCC GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC
          GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG
```

Figure 8: DNA Sequence of Ig kappa light chain expression vector pMORPH®_h_Igκ_1



```
   +1  A  S  V  V   C  L  L   N  N  F   Y  P  R  E   A  K  V
1051  GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
      CGGAGACAAC ACACGGACGA CTTATTGAAG ATAGGGTCTC TCCGGTTTCA

   +1   Q  W  K   V  D  N  A   L  Q  S   G  N  S   Q  E  S
1101  ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
      TGTCACCTTC CACCTATTGC GGGAGGTTAG CCCATTGAGG GTCCTCTCAC

   +1 V  T  E  Q   D  S  K   D  S  T  Y   S  L  S   S  T  L
1151  TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG
      AGTGTCTCGT CCTGTCGTTC CTGTCGTGGA TGTCGGAGTC GTCGTGGGAC

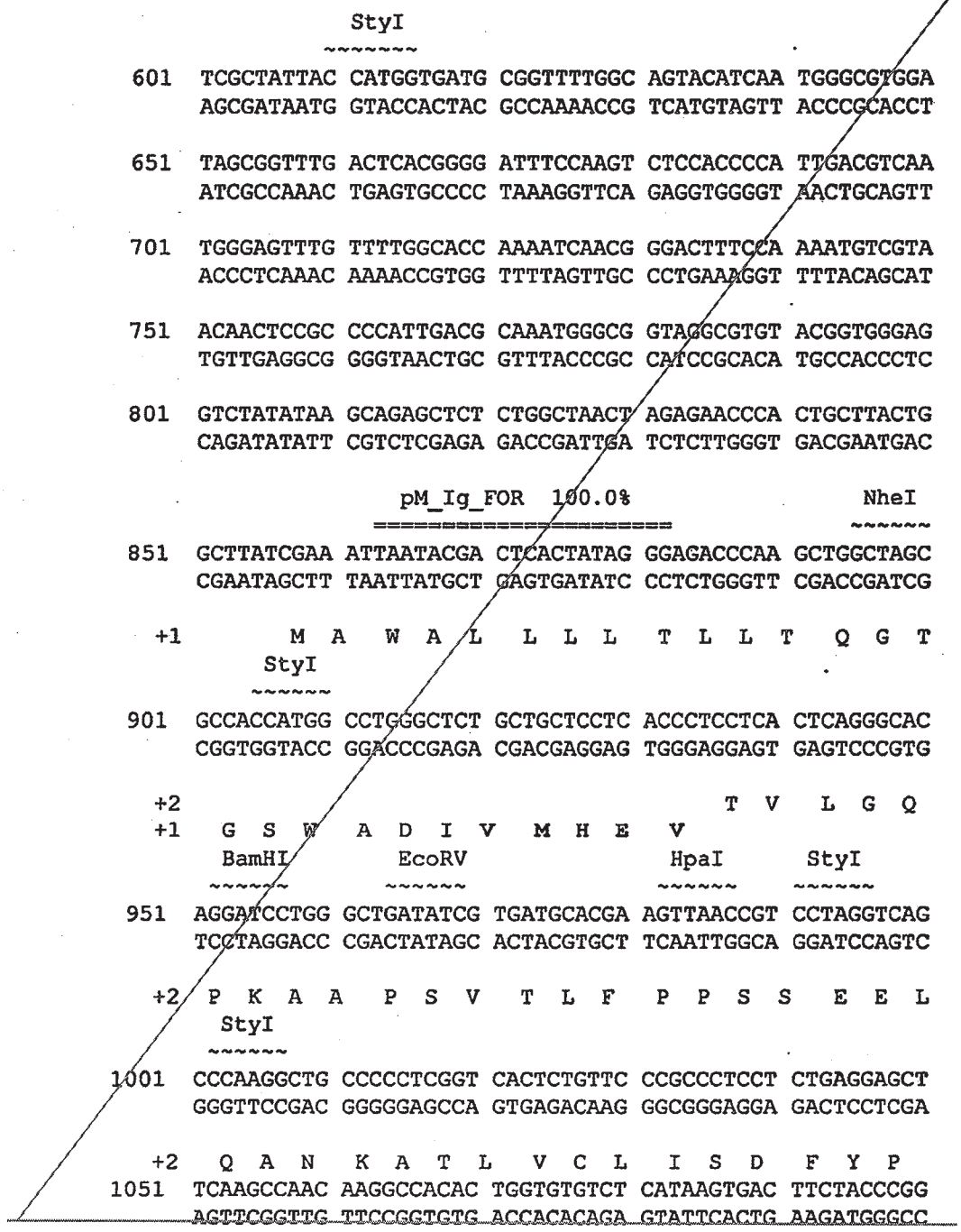
   +1  T  L  S  K   A  D  Y   E  K  H   K  V  Y  A   C  E  V
         BlpI
       ~~~~~~~
1201  ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
      TGCGACTCGT TTCGTCTGAT GCTCTTTGTG TTTCAGATGC GGACGCTTCA

   +1   T  H  Q   G  L  S  S   P  V  T   K  S  F   N  R  G
1251  CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
      GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC

   +1 E  C  *
                          PmeI                  pMORPH®_Ig_REV 100%
                        ~~~~~~~~~               ==========
1301  AGTGTTAGGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
      TCACAATCCC CGGGCAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA

      =
1351  AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT CCTTGACCCT
      TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAACTGGGA
```

Figure 9: DNA Sequence of HuCAL® Ig lambda light chain vector pMORPH®_h_Igλ_1



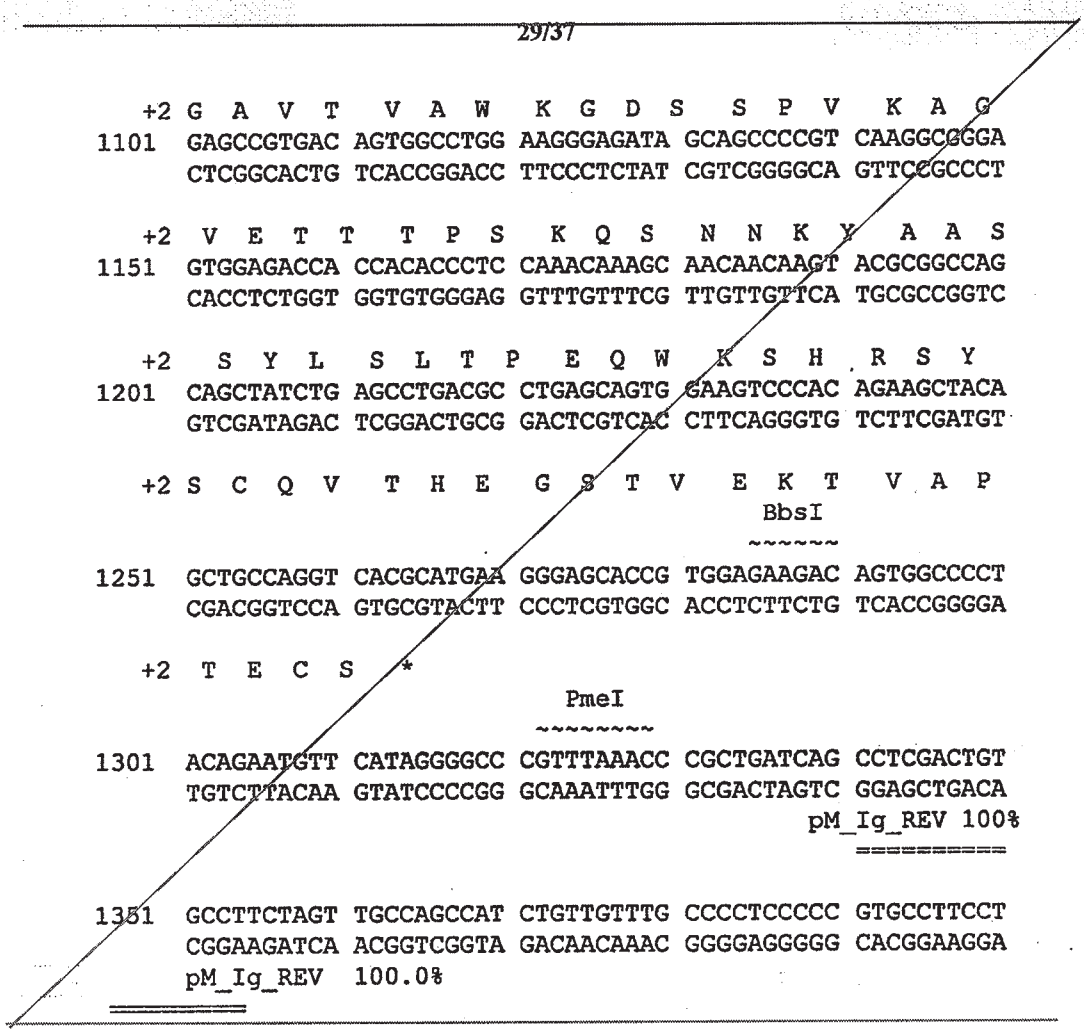

+2 G A V T V A W K G D S S P V K A G
1101 GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT
+2 V E T T T P S K Q S N N K Y A A S
1151 GTGGAGACCA CCACACCCTC CAAACAAAGC AACAACAAGT ACGCGGCCAG
CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC
+2 S Y L S L T P E Q W K S H R S Y
1201 CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA
GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT
+2 S C Q V T H E G S T V E K T V A P
BbsI
1251 GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCT
CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA
+2 T E C S *
PmeI
1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
pM_Ig_REV 100%
1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
pM_Ig_REV 100.0%

Figure 10

Designation:	Format	Affinity Maturation	Heavy chain from:	Light chain from:
MOR06183	Fab/IgG1	new H-CDR2	MOR06183	MOR03087 (parental)
MOR06184	Fab/IgG1	new H-CDR2	MOR06184	MOR03087 (parental)
MOR06185	Fab/IgG1	new H-CDR2	MOR06185	MOR03087 (parental)
MOR06186	Fab/IgG1	new H-CDR2	MOR06186	MOR03087 (parental)
MOR06187	Fab/IgG1	new H-CDR2	MOR06187	MOR03087 (parental)
MOR06188	Fab/IgG1	new H-CDR2	MOR06188	MOR03087 (parental)
MOR06189	Fab/IgG1	new H-CDR2	MOR06189	MOR03087 (parental)
MOR06190	Fab/IgG1	new H-CDR2	MOR06190	MOR03087 (parental)
MOR06192	Fab/IgG1	new H-CDR2	MOR06192	MOR03087 (parental)
MOR06195	Fab/IgG1	new H-CDR2	MOR06195	MOR03087 (parental)
MOR06197	Fab/IgG1	new H-CDR2	MOR06197	MOR03087 (parental)
MOR06200	Fab/IgG1	new H-CDR2	MOR06200	MOR03087 (parental)
MOR06201	Fab/IgG1	new H-CDR2	MOR06201	MOR03087 (parental)
MOR06204	Fab/IgG1	new H-CDR2	MOR06204	MOR03088 (parental)
MOR06214	Fab/IgG1	new H-CDR2	MOR06214	MOR03088 (parental)
MOR06278	Fab	new L-CDR3	MOR03088 (parental)	MOR06278
MOR06279	Fab	new L-CDR3	MOR03088 (parental)	MOR06279
MOR06347	IgG1	new L-CDR3	MOR03088 (parental)	MOR06278
MOR06348	IgG1	new L-CDR3 & H-CDR2	MOR06214	MOR06278

FIGURE 11: CD38-expression analysis of Lymphocytes and Erythrocytes

A: MOR 3087

B: MOR 3088

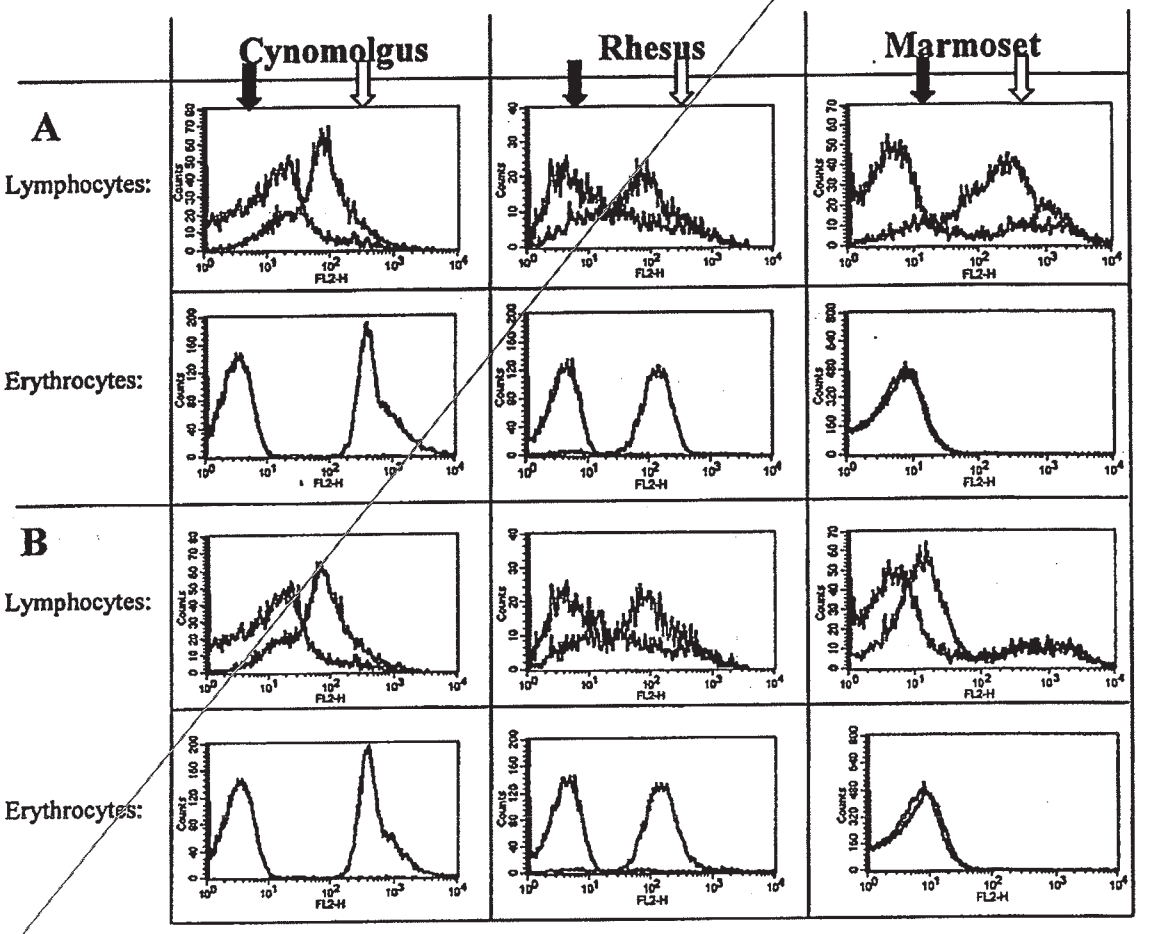


Figure 12: CD38 expression analysis of Lymphocytes and Erythrocytes

MOR 03087:

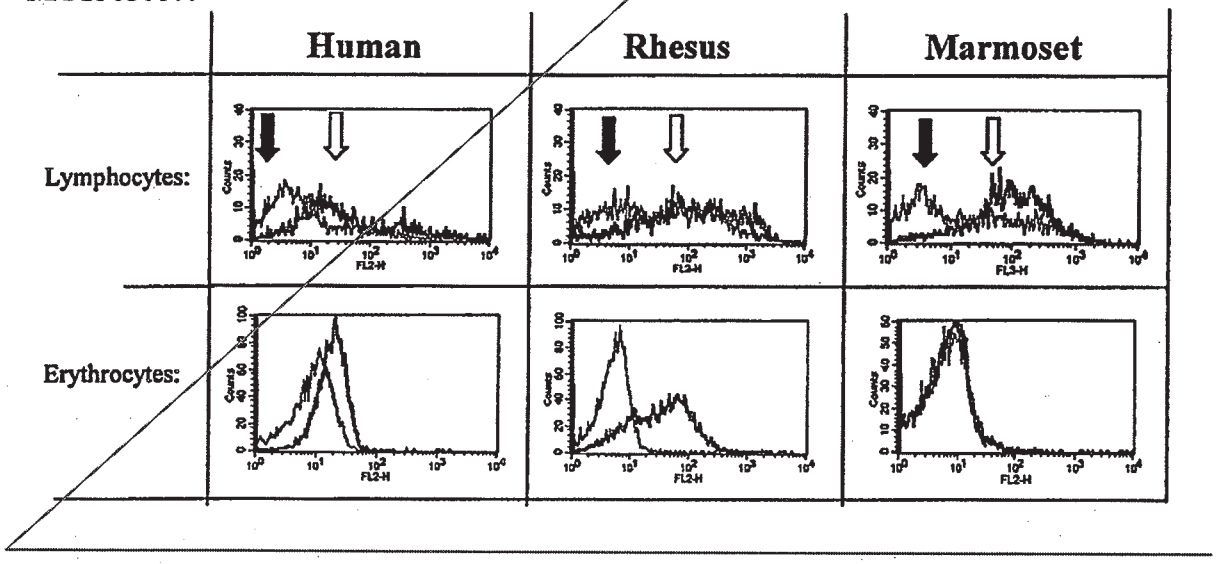


Figure 13: Overview Cross-Reactivity Anti-CD38 Antibodies

	Human		Rhesus		Cynomolgus		Marmoset	
Species/Tissue: / Anti-CD38 MAbs:	PBMCs	Erythr.	PBMCs	Erythr.	PBMCs	Erythr.	PBMCs	Erythr.
3076	+	n.d.	-	-	-	-	-	-
3077	+	-	-	-	-	-	-	-
3078	+	n.d.	-	-	-	-	-	-
3079	+	+	-	-	-	-	-	-
3080	+	+/-	+	-	+	-	-	-
3081	+	n.d.	-	-	-	-	-	-
3085	+	n.d.	-	-	-	-	-	-
3086	+	n.d.	-	-	-	-	-	-
3087	+	+/-	+	+	+	+	+	-
3088	+	-	+	+	+	+	+	-
3089	+	n.d.	-	-	-	-	-	-
3101	+	n.d.	-	-	-	-	-	-
3102	+	n.d.	-	-	-	-	-	-
3127	+	n.d.	-	-	-	-	-	-
3128	+	n.d.	-	-	-	-	-	-
3129	+	n.d.	-	-	-	-	-	-
3130	+	n.d.	-	-	-	-	-	-
3131	+	n.d.	-	-	-	-	-	-

+ : positive staining
+/- : weak positive staining
- : negative staining
n.d.: not determined

Figure 14a:

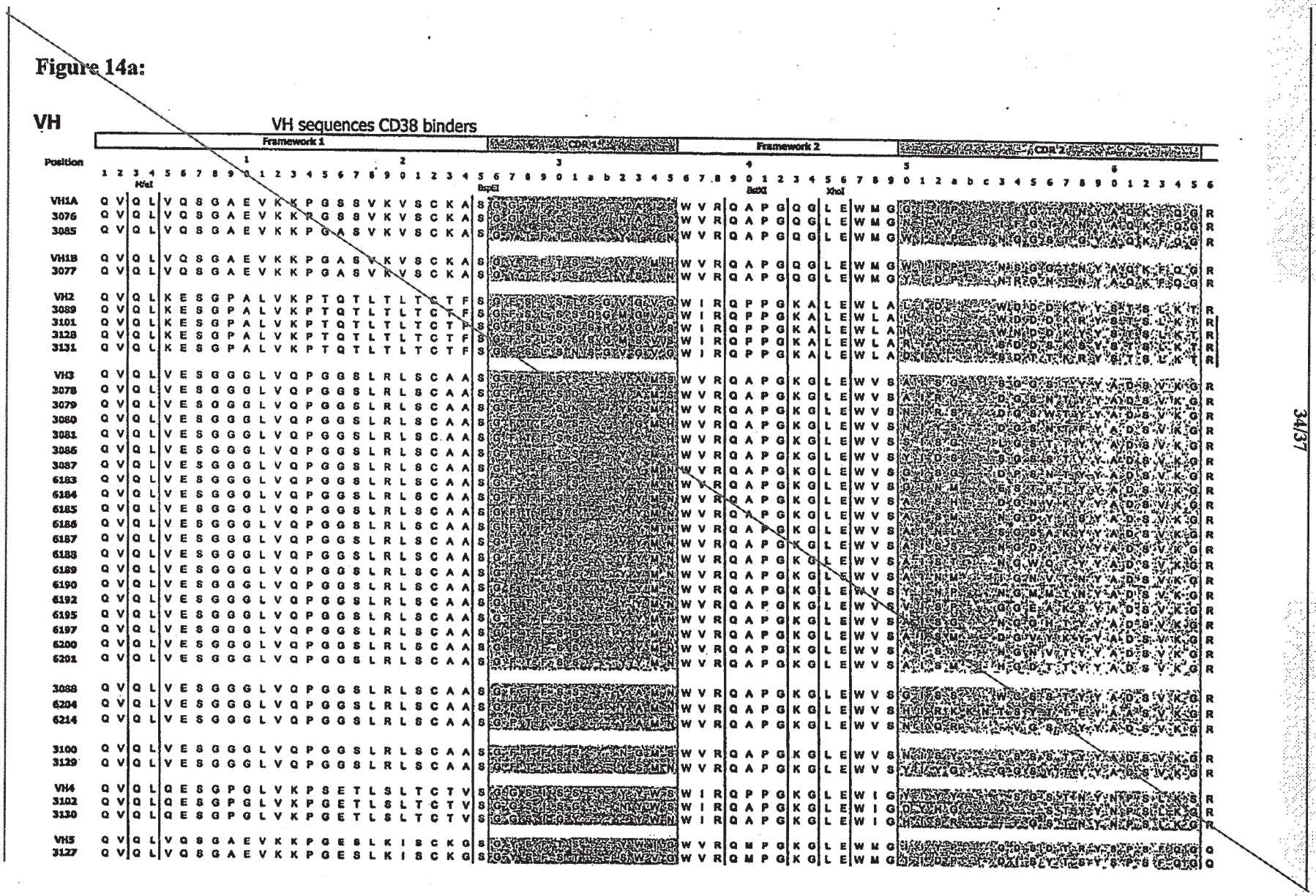

VH
VH sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
MfeI
BspEI
BstXI
XhoI
VH1A
3076
3085
VH1B
3077
VH2
3089
3101
3128
3131
VH3
3078
3079
3080
3081
3086
3087
6183
6184
6185
6186
6187
6188
6189
6190
6192
6195
6197
6200
6201
3088
6204
6214
3100
3129
VH4
3102
3130
VH5
3127

Figure 14a to be continued :

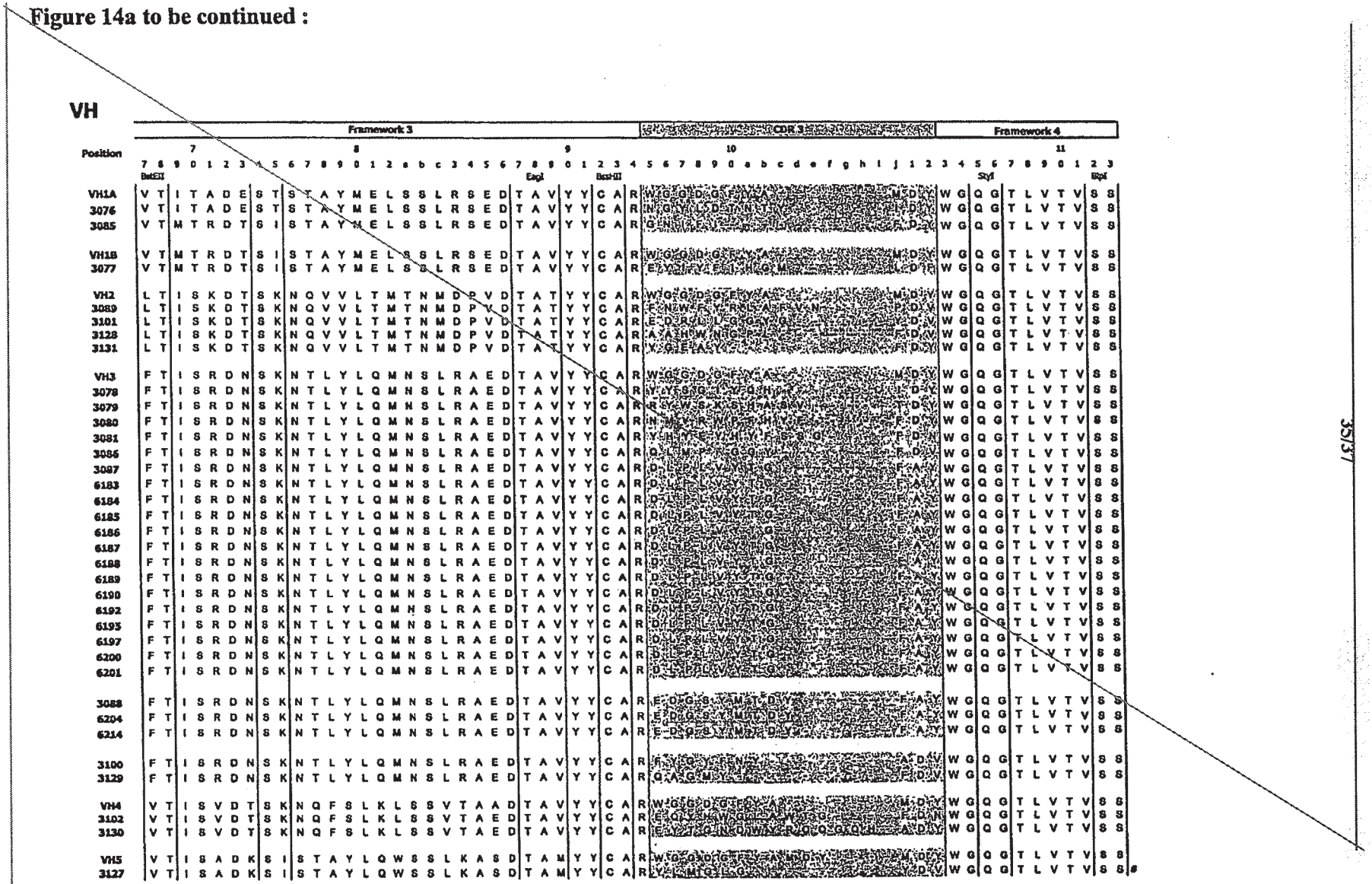


Figure 14b:

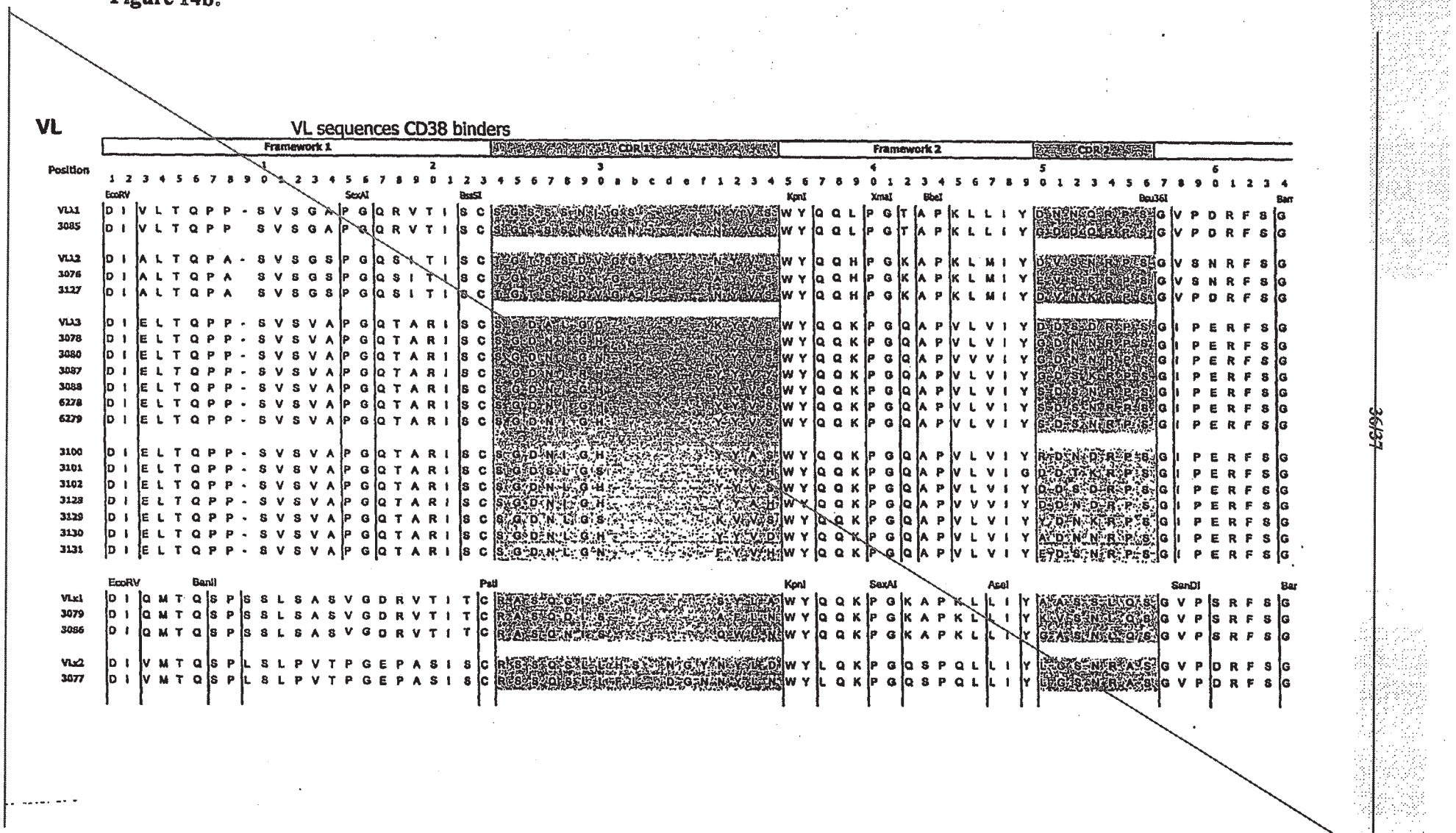

VL
VL sequences CD38 binders
Framework 1
CDR1
Framework 2
CDR2
Position
EcoRV
SexAI
BssSI
KpnI
XmaI
BbeI
Bsu36I
BarI
VLk1
3085
VLk2
3076
3127
VLk3
3078
3080
3087
3088
6278
6279
3100
3101
3102
3128
3129
3130
3131
EcoRV
BanII
PstI
KpnI
SexAI
AseI
SanDI
BarI
VLx1
3079
3086
VLx2
3077

Figure 14b to be continued:

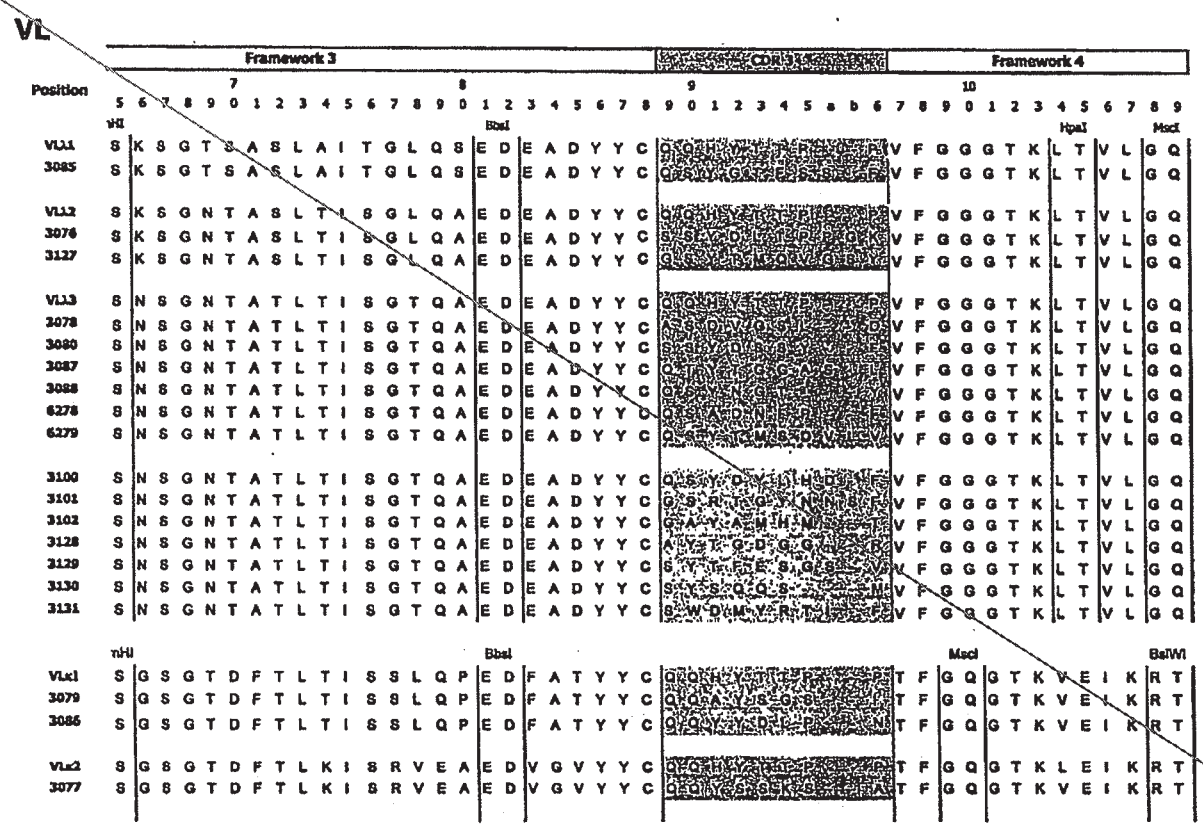


Figure 1a

Variable Heavy Chain DNA

3076_VH1A (SEQ ID NO: 1):
CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGAGGCACTTTTTCTTCTAATGCTATTTCTTGGGTGCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCAATATCTGGCCGATTTTTGGCACTGCGAATTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATGGTTATCTTGATACTAATACTTA
TATTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3078_VH3 (SEQ ID NO: 2):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTGATTATGCTATGTCTTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCGCTATCCGTTATGATGGTAGCAATACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTTATTATTCTGGTATTTATCAGCATAT
TGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3081_ VH3 (SEQ ID NO: 3):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTCTTCATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTCTATCTCTGGTCTTGGTAGCACTACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTTATCATTATGAGTATCATTATTTTTCTT
CTGGTTTTGATAATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3085_ VH1A (SEQ ID NO: 4):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGATATACCTTTACTGGTTATTATATTAATTGGGTCCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCTGGATCTTTCCGAATGGTGGCTCTACGGGTTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTAATATTTTTATTTTTGATTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

3086_VH3 (SEQ ID NO: 5):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTACTTCTTATTATATGCATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATCGATTCTTCTGGTAGCTCTACCTATTATGCGGATAGCGTG
AAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCAGCTTATGCCTTTTGGTGGTTATTTTG
ATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3087_ VH3 (SEQ ID NO: 6):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGGTATCTCTGGTGATCCTAGCAATACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTT
GCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1a (Continued)

3088_ VH3 (SEQ ID NO: 7):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCGGTATCTCTTCTTGGGGTAGCTCTACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATT
ATTTTGCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3089_ VH2 (SEQ ID NO: 8):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTTCTGATGGTATGGGTGTGGGTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCTTATCGATTGGGATGATGATAAGCGTTATAGCACCAGC
CTGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAA
CATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTTTTAATTGGTTTTATCGTCTTGCTT
TTGTTAATCCTGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3101_ VH2 (SEQ ID NO: 9):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTACTTCTCGTGTTGGTGTGTCTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCATATCGATTGGAATGATGATAAGTATTATAGCACCAGC
CTGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAA
CATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTGAGGATCGTCTTCTTGGTGGTTAT
GGTTATGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3102_ VH4 (SEQ ID NO: 10):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACC
TGCACCGTTTCCGGAGGCAGCATTTCTGGTAATTATTGGTCTTGGATTCGCCAGGCCCCTGGGA
AGGGTCTCGAGTGGATTGGCGATTATCATGGCTCTACCTATTATAATCCGAGCCTGAAAGGCCG
GGTGACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCG
GAAGATACGGCCGTGTATTATTGCGCGCGTGAGCAGTATCATTGGGGTCTTGCTTGGACTGGTT
TTGATAATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3127_ VH5 (SEQ ID NO: 11):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAGCT
GCAAAGGTTCCGGATATTCCTTTTCTACTTCTTGGGTTGGTTGGGTGCGCCAGATGCCTGGGAA
GGGTCTCGAGTGGATGGGCATTATCGATCCGGATATTAGCTATACCTCTTATTCTCCGAGCTTTC
AGGGCCAGGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTATCTTCAATGGAGCAGCCT
GAAAGCGAGCGATACGGCCATGTATTATTGCGCGCGTTATCTTATGGGTCTTGGTTATGATGTTT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3128_ VH2 (SEQ ID NO: 12):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTTCTTCTGGTATGTCTGTGTCTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCGTATCTATTCTGATGATTCTAAGTCTTATAGCACCAGCC
TGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAAC
ATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTGCTGCTCATTGGAATGGTCCTCTTT
TTGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1a (Continued)

3129_ VH3 (SEQ ID NO: 13):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTAATTATTCTATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATCTATGGTGGTGGTAGCTATACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCAGGCTGGTATGTATTTTGATGTTTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3130_ VH4 (SEQ ID NO: 14):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACC
TGCACCGTTTCCGGAGGCAGCATTGGTTATTATTGGAATTGGATTCGCCAGGCCCCTGGGAAGG
GTCTCGAGTGGATTGGCCATATCTCTCGTTTTGGCTCTACCAATTATAATCCGAGCCTGAAAGGC
CGGGTGACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGG
CGGAAGATACGGCCGTGTATTATTGCGCGCGGGAGTATACTGGTAATGATTGGTATCGTCAGCA
GGGTCAGCATGCTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3131_ VH2 (SEQ ID NO: 15):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTAATTCTGGTGTTGGTGTGGGTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTGATATCTATTCTGATACTACTAAGCGTTATAGCACCAGCC
TGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAAC
ATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTTATGGTGAGGCTTATTTTGATTATTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6183_VH3 (SEQ ID NO: 77)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGGTATTAATATGGAGTCTACTCGTATTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6184_VH3 (SEQ ID NO: 78)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTCATGATGGTAATGTTAAGTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6185_VH3 (SEQ ID NO: 79)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGAATGGTGATTATATTTCTTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1a (Continued)

6186_VH3 (SEQ ID NO: 80)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTAATCTTTCTGGTTCTGCTAAGTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6187_VH3 (SEQ ID NO: 81)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTTCTAATGGTGATATTACTTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6188_VH3 (SEQ ID NO: 82)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTACTAATGGTTGGCAGACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6189_VH3 (SEQ ID NO: 83)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTAATATGATTGGTAATGTTACTAATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6190_VH3 (SEQ ID NO: 84)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATTAATCCTAATGGTATGATGACTAATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6192_VH3 (SEQ ID NO: 85)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGTTATTTCTCCTGGTGGTGAGGCTAAGTCTTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1a (Continued)

6195_VH3 (SEQ ID NO: 86)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTGGTAATGGTGGTCATACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6197_VH3 (SEQ ID NO: 87)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGGATGGTGTTTATAAGTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6200_VH3 (SEQ ID NO: 88)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTAATAATGGTAATGTTACTTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6201_VH3 (SEQ ID NO: 89)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGCATGGTGATACTACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6204_VH3 (SEQ ID NO: 90)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCCATATTCGTAAGAAGAATACTTCTTATACTACTGAGTATGCTGC
TTCTGTTAAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAA
CAGCCTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACT
GATTATTTTGCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

6214_VH3 (SEQ ID NO: 91)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATTCAGCGTGTTGGTTCTACTTATTATGCTGATTCTGTTAA
GGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGC
GTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTT
GCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1a (Continued)

3077_VH1B (SEQ ID NO: 111)
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGATATACCTTTACTTCTTATTCTATTAATTGGGTCCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCTATATCGATCCGAATCGTGGCAATACGAATTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGAGTATATTTATTTTATTCATGGTAT
GCTTGATTTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3079_VH3 (SEQ ID NO: 112)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTAATTATGGTATGCATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATCCGTTCTGATGGTAGCTGGACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCGTTATTGGTCTAAGTCTCATGCTTC
TGTTACTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

3080_ VH3 (SEQ ID NO: 113)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGGTATGCATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATCTATTCTGATGGTAGCAATACCTTTTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTAATATGTATCGTTGGCCTTTTCATTAT
TTTTTTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

Figure 1b

Variable Heavy Chain Peptide

(CDR Regions in **Bold** or underlined)

3076_VH1A (SEQ ID NO: 16):
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSNAIS**WVRQAPGQGLEWMG**NIWPIFGTANYAQKFQ**
GRVTITADESTSTAYMELSSLRSEDTAVYYCAR**NGYLDTNTYIDY**WGQGTLVTVSS

3078_VH3 (SEQ ID NO: 17):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSDYAMS**WVRQAPGKGLEWVS**AIRYDGSNTYYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YYSGIYQHIDY**WGQGTLVTVSS

3081_ VH3 (SEQ ID NO: 18):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYALH**WVRQAPGKGLEWVS**SISGLGSTTYYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YHYEYHYFSSGFDN**WGQGTLVTVSS

3085_ VH1A (SEQ ID NO: 19):
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTGYYIN**WVRQAPGQGLEWMG**WIFPNGGSTGYAQKF**
QGRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR**GNIFIFDY**WGQGTLVTVSS

3086_VH3 (SEQ ID NO: 20):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFTSYYMH**WVRQAPGKGLEWVS**YIDSSGSSTYYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QLMPFGGYFDV**WGQGTLVTVSS

3087_ VH3 (SEQ ID NO: 21):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYYMN**WVRQAPGKGLEWVS**GISGDPSNTYYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**DLPLVYTGFAY**WGQGTLVTVSS

3088_ VH3 (SEQ ID NO: 22):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYAMN**WVRQAPGKGLEWVS**GISSWGSSTYYADSV**
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**EDGSYMTDYFAY**WGQGTLVTVSS

3089_ VH2 (SEQ ID NO: 23):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSDGMGVG**WIRQPPGKALEWLA**LIDWDDDKRYSTSLK**
TRLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**FNWFYRLAFVNPDV**WGQGTLVTVSS

3101_ VH2 (SEQ ID NO: 24):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSRVGVS**WIRQPPGKALEWLA**HIDWNDDKYYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**EDRLLGGYGYDV**WGQGTLVTVSS

Figure 1b (Continued)

3102_ VH4 (SEQ ID NO: 25):
QVQLQESGPGLVKPGETLSLTCTVS**GGSISGNYWS**WIRQAPGKGLEWIG**DYHGSTYYNPSLKG**RVT
ISVDTSKNQFSLKLSSVTAEDTAVYYCAR**EQYHWGLAWTGFDN**WGQGTLVTVSS

3127_ VH5 (SEQ ID NO: 26):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFSTSWVG**WVRQMPGKGLEWMGI**IDPDISYTSYSPSFQG**
QVTISADKSISTAYLQWSSLKASDTAMYYCAR**YLMGLGYDV**WGQGTLVTVSS

3128_ VH2 (SEQ ID NO: 27):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSSGMSVS**WIRQPPGKALEWLA**RIYSDDSKSYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**AAHWNGPLFDV**WGQGTLVTVSS

3129_ VH3 (SEQ ID NO: 28):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYSMN**WVRQAPGKGLEWVS**YIYGGGSYTYYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QAGMYFDV**WGQGTLVTVSS

3130_ VH4 (SEQ ID NO: 29):
QVQLQESGPGLVKPGETLSLTCTVS**GGSIGYYWN**WIRQAPGKGLEWIG**HISRFGSTNYNPSLKG**RV
TISVDTSKNQFSLKLSSVTAEDTAVYYCAR**EYTGNDWYRQQGQHADY**WGQGTLVTVSS

3131_ VH2 (SEQ ID NO: 30):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSNSGVGVG**WIRQPPGKALEWLA**DIYSDTTKRYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**YGEAYFDY**WGQGTLVTVSS

6183_VH3 (SEQ ID NO: 92)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSGINMESTRIYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6184_VH3 (SEQ ID NO: 93)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISHDGNVKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6185_VH3 (SEQ ID NO: 94)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMNGDYISYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6186_VH3 (SEQ ID NO: 95)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINLSGSAKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

Figure 1b (Continued)

6187_VH3 (SEQ ID NO: 96)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISSNGDITYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6188_VH3 (SEQ ID NO: 97)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISTNGWQTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6189_VH3 (SEQ ID NO: 98)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINMIGNVTNYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6190_VH3 (SEQ ID NO: 99)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSYINPNGMMTNYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6192_VH3 (SEQ ID NO: 100)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSVISPGGEAKSYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6195_VH3 (SEQ ID NO: 101)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISGNGGHTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6197_VH3 (SEQ ID NO: 102)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMDGVYKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6200_VH3 (SEQ ID NO: 103)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISNNGNVTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6201_VH3 (SEQ ID NO: 104)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMHGDTTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

6204_VH3 (SEQ ID NO: 105)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSHIRKKNTSYTTEYAAS
VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

Figure 1b (Continued)

6214_VH3 (SEQ ID NO: 106)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSNIQRVGSTYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

3077_VH1B (SEQ ID NO: 114)
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTSYSIN**WVRQAPGQGLEWMGY**IDPNRGNTNYAQKFQ**
GRVTMTRDTSISTAYMELSSLRSEDTAVYYCAR**EYIYFIHGMLDF**WGQGTLVTVSS

3079_VH3 (SEQ ID NO: 115)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYGMH**WVRQAPGKGLEWVS**NIRSDGSWTYYADSV**
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**RYWSKSHASVTDY**WGQGTLVTVSS

3080_ VH3 (SEQ ID NO: 116)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYGMH**WVRQAPGKGLEWVS**NIYSDGSNTFYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**NMYRWPFHYFFDY**WGQGTLVTVSS

Figure 2a

Variable Light Chain DNA

3076_Vl lambda 2 (SEQ ID NO: 31):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGT
GTACGGGTACTAGCAGCGATATTGGTGCTTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGGC
GCCGAAACTTATGATTTATGAGGTTTCTTCTCGTCCCTCAGGCGTGAGCAACCGTTTTAGCGGAT
CCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATT
ATTATTGCTCTTCTTATGATCTTACTCCTCCTGGTAAGGTGTTTGGCGGCGGCACGAAGTTAACC
GTTCTTGGCCAG

3078_Vl lambda 3 (SEQ ID NO: 32):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGCTTCTGATGTTGGTTCTCTTGATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

3081_ Vk kappa 3 (SEQ ID NO: 33):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG
AGCTGCAGAGCGAGCCAGACTGGTTCTACTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTC
AAGCACCGCGTCTATTAATTTATGATGCTTCTAAGCGTGCAACTGGGGTCCCGGCGCGTTTTAGC
GGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGA
CTTATTATTGCCATCAGTATTATAACGTTCCTCATACCTTTGGCCAGGGTACGAAAGTTGAAATTA
AACGTACG

3085_ Vl lambda 1 (SEQ ID NO: 34):
GATATCGTGCTGACCCAGCCGCCTTCAGTGAGTGGCGCACCAGGTCAGCGTGTGACCATCTCGT
GTAGCGGCAGCAGCAGCAACATTGGTAATAATTATGTGTCTTGGTACCAGCAGTTGCCCGGGAC
GGCGCCGAAACTTCTGATTTATGGTGATGATCAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGC
GGATCCAAAAGCGGCACCAGCGCGAGCCTTGCGATTACGGGCCTGCAAAGCGAAGACGAAGCG
GATTATTATTGCCAGTCTTATGGTACTTTTTCTTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACC
GTTCTTGGCCAG

3086_Vk kappa 1 (SEQ ID NO: 35):
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTA
CCTGCAGAGCGAGCCAGAATATTTCTCAGTGGCTGAATTGGTACCAGCAGAAACCAGGTAAAGC
ACCGAAACTATTAATTTATGGTGCTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCT
CTGGATCCGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTAT
TATTGCCAGCAGTATTATGATCTTCCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGT
ACG

3087_ Vl lambda 3 (SEQ ID NO: 36):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTCGTCATTATTATGTTTATTGGTACCAGCAGAAACCCGGGCAGGCGCCA
GTTCTTGTGATTTATGGTGATTCTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAA
CAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTA
TTGCCAGACTTATACTGGTGGTGCTTCTCTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTG
GCCAG

Figure 2a (Continued)

3088_ Vl lambda 3 (SEQ ID NO: 37):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATAATGGTACTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

3089_ Vk kappa 3 (SEQ ID NO: 38):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG
AGCTGCAGAGCGAGCCAGTCTGTTTCTTCTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCA
AGCACCGCGTCTATTAATTTATGGTGCTTCTTCTCGTGCAACTGGGGTCCCGGCGCGTTTTAGCG
GCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGT
TTATTATTGCCAGCAGGGTTATAATTCTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA
ACGTACG

3101_ Vl lambda 3 (SEQ ID NO: 39):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATTCTCTTGGTTCTTATTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTGGTGATGATACTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGGTTCTCGTACTGGTTATAATAATTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTT
CTTGGCCAG

3102_ V'l lambda 3 (SEQ ID NO: 40):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGATGATTCTGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGGTGCTTATGCTATGCATATGACTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

3127_ Vl lambda 2 (SEQ ID NO: 41):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGT
GTACGGGTACTAGCAGCGATGTTGGTGCTATTAATTATGTGTCTTGGTACCAGCAGCATCCCGG
GAAGGCGCCGAAACTTATGATTTATGATGTTAATAAGCGTCCCTCAGGCGTGCCGGATCGTTTTA
GCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAG
CGGATTATTATTGCGGTTCTTATACTATGCAGGTTGGTTCTTATGTGTTTGGCGGCGGCACGAAG
TTAACCGTTCTTGGCCAG

3128_ Vl lambda 3 (SEQ ID NO: 42):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGCTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTGTTGTGATTTATGATGATAATGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGGCTTATACTGGTGATGGTGGTCGTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCT
TGGCCAG

Figure 2a (Continued)

3129_ Vl lambda 3 (SEQ ID NO: 43):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTTCTAAGGTTGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTATGATAATAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATACTTTTGAGTCTGGTTCTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTT
CTTGGCCAG

3130_ Vl lambda 3 (SEQ ID NO: 44):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTCATTATTATGTTGATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGCTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTATTCTCAGCAGTCTATGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

3131_ Vl lambda 3 (SEQ ID NO: 45):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTAATTTTTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGAGGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTGGGATATGTATCGTACTATTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTC
TTGGCCAG

6278_Vl lambda 3 (SEQ ID NO: 107)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTGCTGATAATTTTCCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGT
CAG

6279_ Vl lambda 3 (SEQ ID NO: 108)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATACTATGTCTGATGTTCTTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTC
CTAGGTCAG

3077_Vk kappa 2 (SEQ ID NO: 117)
GATATCGTGATGACCCAGAGCCCACTGAGCCTGCCAGTGACTCCGGGCGAGCCTGCGAGCATT
AGCTGCAGAAGCAGCCAAAGCCTGCTTTTTATTGATGGCAATAATTATCTGAATTGGTACCTTCAA
AAACCAGGTCAAAGCCCGCAGCTATTAATTTATCTTGGTTCTAATCGTGCCAGTGGGGTCCCGGA
TCGTTTTAGCGGCTCTGGATCCGGCACCGATTTTACCCTGAAAATTAGCCGTGTGGAAGCTGAA
GACGTGGGCGTGTATTATTGCCAGCAGTATTCTTCTAAGTCTGCTACCTTTGGCCAGGGTACGAA
AGTTGAAATTAAACGTACG

Figure 2a (Continued)

3079_Vk kappa 1 (SEQ ID NO: 118)
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTA
CCTGCAGAGCGAGCCAGGATATTTCTGCTTTTCTGAATTGGTACCAGCAGAAACCAGGTAAAGCA
CCGAAACTATTAATTTATAAGGTTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTC
TGGATCCGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATT
ATTGCCAGCAGGCTTATTCTGGTTCTATTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGT
ACG

3080_Vl lambda 3 (SEQ ID NO: 119)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTAATAAGTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTGTTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTATGATTCTTCTTATTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCC
AG

Figure 2b

Variable Light Chain Peptide

(CDR Regions in **Bold** or underlined)

3076_Vl lambda 2 (SEQ ID NO: 46):
DIALTQPASVSGSPGQSITISC**TGTSSDIGAYVS**WYQQHPGKAPKLMIY**EVSSRPS**GVSNRFSGSKSG
NTASLTISGLQAEDEADYYC**SSYDLTPPGK**VFGGGTKLTVLGQ

3078_Vl lambda 3 (SEQ ID NO: 47):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**GDNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**ASDVGSLD**VFGGGTKLTVLGQ

3081_ Vk kappa 3 (SEQ ID NO: 48):
DIVLTQSPATLSLSPGERATLSC**RASQTGSTSYLA**WYQQKPGQAPRLLIY**DASKRAT**GVPARFSGSG
SGTDFTLTISSLEPEDFATYYC**HQYYNVPH**TFGQGTKVEIKRT

3085_ Vl lambda 1 (SEQ ID NO: 49):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGNNYVS**WYQQLPGTAPKLLIY**GDDQRPS**GVPDRFSGSK
SGTSASLAITGLQSEDEADYYC**QSYGTFSSF**VFGGGTKLTVLGQ

3086_Vk kappa 1 (SEQ ID NO: 50):
DIQMTQSPSSLSASVGDRVTITC**RASQNISQWLN**WYQQKPGKAPKLLIY**GASNLQS**GVPSRFSGSG
SGTDFTLTISSLQPEDFATYYC**QQYYDLPN**TFGQGTKVEIKRT

3087_ Vl lambda 3 (SEQ ID NO: 51):
DIELTQPPSVSVAPGQTARISC**SGDNLRHYYVY**WYQQKPGQAPVLVIY**GDSKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QTYTGGASL**VFGGGTKLTVLGQ

3088_ Vl lambda 3 (SEQ ID NO: 52):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSYNGTY**VFGGGTKLTVLGQ

3089_ Vk kappa 3 (SEQ ID NO: 53):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSG
SGTDFTLTISSLEPEDFAVYYC**QQGYNSPF**TFGQGTKVEIKRT

3101_ Vl lambda 3 (SEQ ID NO: 54):
DIELTQPPSVSVAPGQTARISC**SGDSLGSYYVH**WYQQKPGQAPVLVIG**DDTKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**GSRTGYNNSF**VFGGGTKLTVLGQ

3102_ Vl lambda 3 (SEQ ID NO: 55):
DIELTQPPSVSVAPGQTARISC**SGDNLGHYYVS**WYQQKPGQAPVLVIY**DDSDRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**GAYAMHMT**VFGGGTKLTVLGQ

3127_ Vl lambda 2 (SEQ ID NO: 56):
DIALTQPASVSGSPGQSITISC**TGTSSDVGAINYVS**WYQQHPGKAPKLMIY**DVNKRPS**GVPDRFSGS
KSGNTASLTISGLQAEDEADYYC**GSYTMQVGSY**VFGGGTKLTVLGQ

Figure 2b (Continued)

3128_ Vl lambda 3 (SEQ ID NO: 57):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYAH**WYQQKPGQAPVVVIY**DDNDRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCQ**AYTGDGGR**VFGGGTKLTVLGQ

3129_ Vl lambda 3 (SEQ ID NO: 58):
DIELTQPPSVSVAPGQTARISC**SGDNLGSKVVS**WYQQKPGQAPVLVIY**YDNKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCQ**SYTFESGSV**VFGGGTKLTVLGQ

3130_ Vl lambda 3 (SEQ ID NO: 59):
DIELTQPPSVSVAPGQTARISC**SGDNLGHYYVD**WYQQKPGQAPVLVIY**ADNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCS**SYSQQSM**VFGGGTKLTVLGQ

3131_ Vl lambda 3 (SEQ ID NO: 60):
DIELTQPPSVSVAPGQTARISC**SGDNLGNFYVH**WYQQKPGQAPVLVIY**EDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCS**SWDMYRTIF**VFGGGTKLTVLGQ

6278_ Vl lambda 3 (SEQ ID NO: 109)
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSADNFPF**VFGGGTKLTVLGQ

6279_ Vl lambda 3 (SEQ ID NO: 110)
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSYTMSDVLV**VFGGGTKLTVLGQ

3077_Vk kappa 2 (SEQ ID NO: 120)
DIVMTQSPLSLPVTPGEPASISC**RSSQSLLFIDGNNYLN**WYLQKPGQSPQLLIY**LGSNRAS**GVPDRFS
GSGSGTDFTLKISRVEAEDVGVYYC**QQYSSKSA**TFGQGTKVEIKRT

3079_Vk kappa 1 (SEQ ID NO: 121)
DIQMTQSPSSLSASVGDRVTITC**RASQDISAFLN**WYQQKPGKAPKLLIY**KVSNLQS**GVPSRFSGSGS
GTDFTLTISSLQPEDFATYYC**QQAYSGSI**TFGQGTKVEIKRT

3080_Vl lambda3 (SEQ ID NO: 122)
DIELTQPPSVSVAPGQTARISC**SGDNIGNKYVS**WYQQKPGQAPVVVIY**GDNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**SSYDSSYF**VFGGGTKLTVLGQ

Figure 3

Variable Heavy Chain Consensus Sequences

(CDR Regions in **Bold**)

VH1A Consensus (SEQ ID NO: 61):
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYAIS**WVRQAPGQGLEWMG**GIIPIFGTANYAQKFQG**RV
TITADESTSTAYMELSSLRSEDTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

VH2 Consensus (SEQ ID NO: 62)
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPPGKALEWLA**LIDWDDDKYYSTSLKT**R
LTISKDTSKNQVVLTMTNMDPVDTATYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

VH3 Consensus (SEQ ID NO: 63):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS SYAMS**WVRQA PGKGLEWVS**A**
(51) **ISGSGGSTYY ADSVKG**RFTI SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**
(101) **GDGFYAMDY**W GQGTLVTVS S

VH4 Consensus (SEQ ID NO: 64):
QVQLQESGPGLVKPSETLSLTCTVS**GGSISSYYWS**WIRQPPGKGLEWIG**YIYYSGSTNYNPSLKS**RVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

VH5 Consensus (SEQ ID NO: 65):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFTSYWIG**WVRQMPGKGLEWMG**IIYPGDSDTRYSPSFQGQ**V
TISADKSISTAYLQWSSLKASDTAMYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

Figure 4

Variable Light Chain Consensus Sequences

(CDR Regions in **Bold**)

Vl_λ1 Consensus (SEQ ID NO: 66):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGSNYVS**WYQQLPGTAPKLLIY**DNNQRPS**GVPDRFSGSKS
GTSASLAITGLQSEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

Vl_λ2 Consensus (SEQ ID NO: 67):
DIALTQPASVSGSPGQSITISC**TGTSSDVGGYNYVS**WYQQHPGKAPKLMIY**DVSNRPS**GVSNRFSGSK
SGNTASLTISGLQAEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

Vl_λ3 Consensus (SEQ ID NO: 68):

(1) DIELTQPPSV SVAPGQTARI SC**SGDALGDK YAS**WYQQKPG QAPVLVIY**DD**
(51) **SDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTTPP**VFGGG
(101) TKLTVLG

Vl_k1 Consensus (SEQ ID NO: 69):

(1) DIQMTQSPSS LSASVGDRVT ITC**RASQGIS SYLA**WYQQKP GKAPKLLIY**A**
(51) **ASSLQS**GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC**QQ HYTTP**PTFGQ
(101) GTKVEIKR

Vl_k3 Consensus (SEQ ID NO: 70):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSGS
GTDFTLTISSLEPEDFAVYYC**QQHYTTPP**TFGQGTKVEIKRT

Figure 5

Peptide Sequence of CD38

(SEQ ID NO: 71):

```
1     mancefspvs gdkpccrlsr raqlclgvsi lvlilvvvla vvvprwrqqw sgpgttkrfp

61    etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn

121   killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc

181   snnpvsvfwk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea

241   wvihggreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei
```

Figure 6

Nucleotide Sequence of Chimeric OKT10

Heavy Chain (SEQ ID NO: 72):

caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc

gattttagta gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg

attggagaaa ttaatccaga tagcagtacg ataaactata cgacatctct aaaggataaa

ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaatgac caaagtgaga

tctgaggaca cagcccttta ttactgtgca agatatggta actggtttcc ttattggggc

caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggt cttccccctg

gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac

tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac

accttcccgg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg

ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacaa gcccagcaac

accaaggtgg acaagaaagt tgagcccaaa tcttgtgaca aaactcacac atgcccaccg

tgcccagcac ctgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag

gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag

acaaagccgc gcgaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc

ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg

tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg

gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag

aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Figure 6 (Continued)

Light Chain (SEQ ID NO: 73):

gatatcctga tgacccagtc tcaaaaaatc atgcccacat cagtgggaga cagggtcagc

gtcacctgca aggccagtca aaatgtggat actaatgtag cctggtatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcatcctacc gatacagtgg agtccctgat

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct

gaggacttgg cagagtattt ctgtcagcaa tatgacagct atcctctcac gttcggtgct

gggaccaagc tggacctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

Figure 7: DNA sequence of pMOPRH®_h_IgG1_1

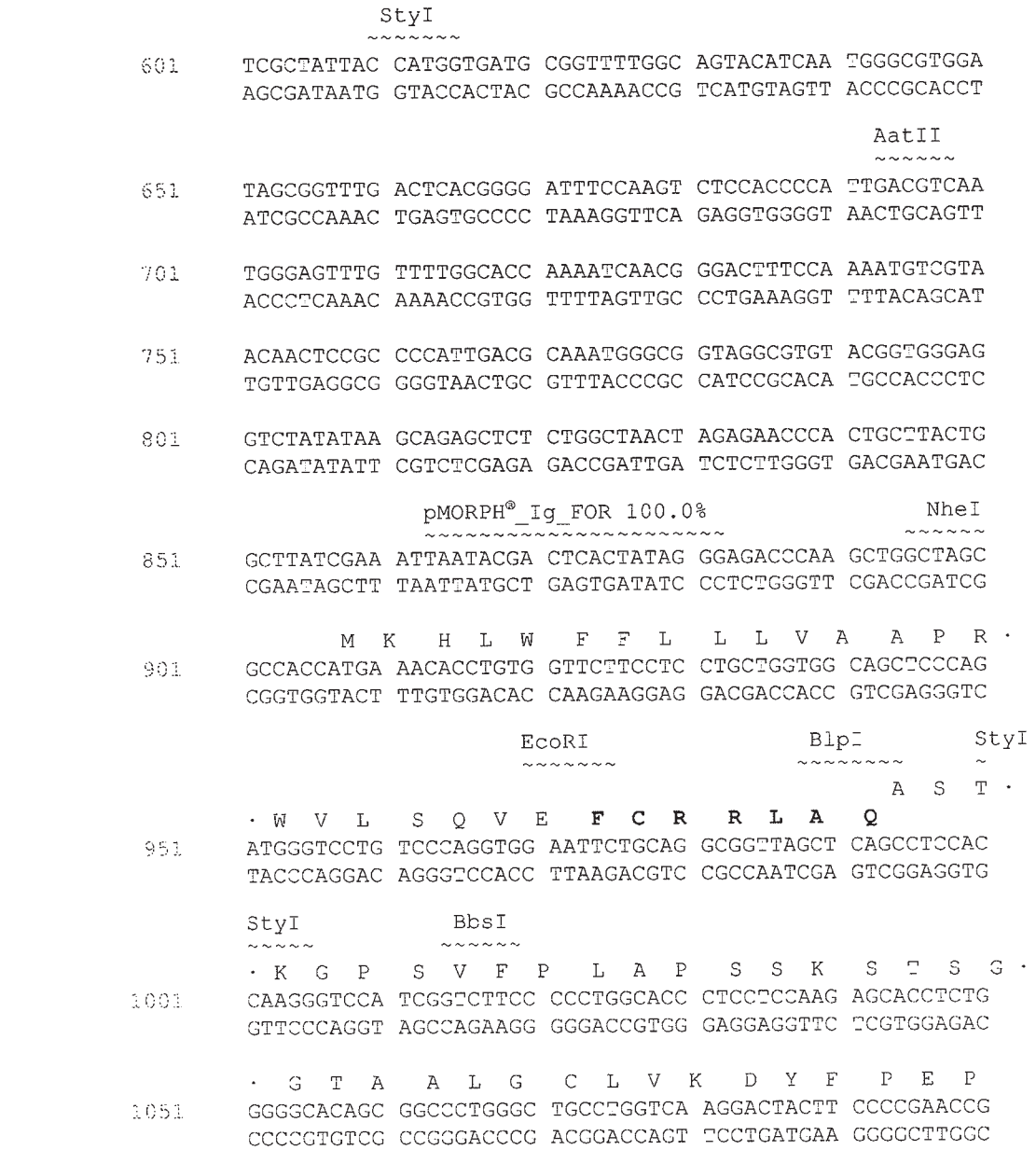


Figure 7 (Continued)

```
          V  T  V  S   W  N  S   G  A  L   T  S  G  V   H  T  F ·
1101      GTGACGGTGT CGTGGAACTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
          CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA

          · P  A  V   L  Q  S  S   G  L  Y   S  L  S   S  V  V  T ·
1151      CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
          GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCACT

          · V  P  S   S  S  L   G  T  Q  T   Y  I  C   N  V  N
1201      CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT
          GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACTTA

                              StyI
                              ~~~~~~~
          H  K  P  S   N  T  K   V  D  K   K  V  E  P   K  S  C ·
1251      CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG
          GTGTTCGGGT CGTTGTGGTT CCACCTGTTC TTTCAACTCG GGTTTAGAAC

          · D  K  T   H  T  C  P   P  C  P   A  P  E   L  L  G  G ·
1301      TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG
          ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC

                    BbsI                        StyI
                    ~~~~~~~                     ~~~~~~
          · P  S  V   F  L  F   P  P  K  P   K  D  T   L  M  I
1351      GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
          CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG

                                                          BbsI
                                                          ~~~~~
          S  R  T  P   E  V  T   C  V  V   V  D  V  S   H  E  D ·
1401      TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA
          AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT

          BbsI
          ~
          · P  E  V   K  F  N  W   Y  V  D   G  V  E   V  H  N  A ·
1451      CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
          GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC

          · K  T  K   P  R  E   E  Q  Y  N   S  T  Y   R  V  V
1501      CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
          GGTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCGTGCAT GGCCCACCAG

          S  V  L  T   V  L  H   Q  D  W   L  N  G  K   E  Y  K ·
1551      AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
          TCGCAGGAGT GGCAGGACGT GGTCCTGACC GACTTACCGT TCCTCATGTT

          · C  K  V   S  N  K  A   L  P  A   P  I  E   K  T  I  S ·
1601      GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
          CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

                                                  BsrGI
                                                  ~~~~~~
```

Figure 7 (Continued)

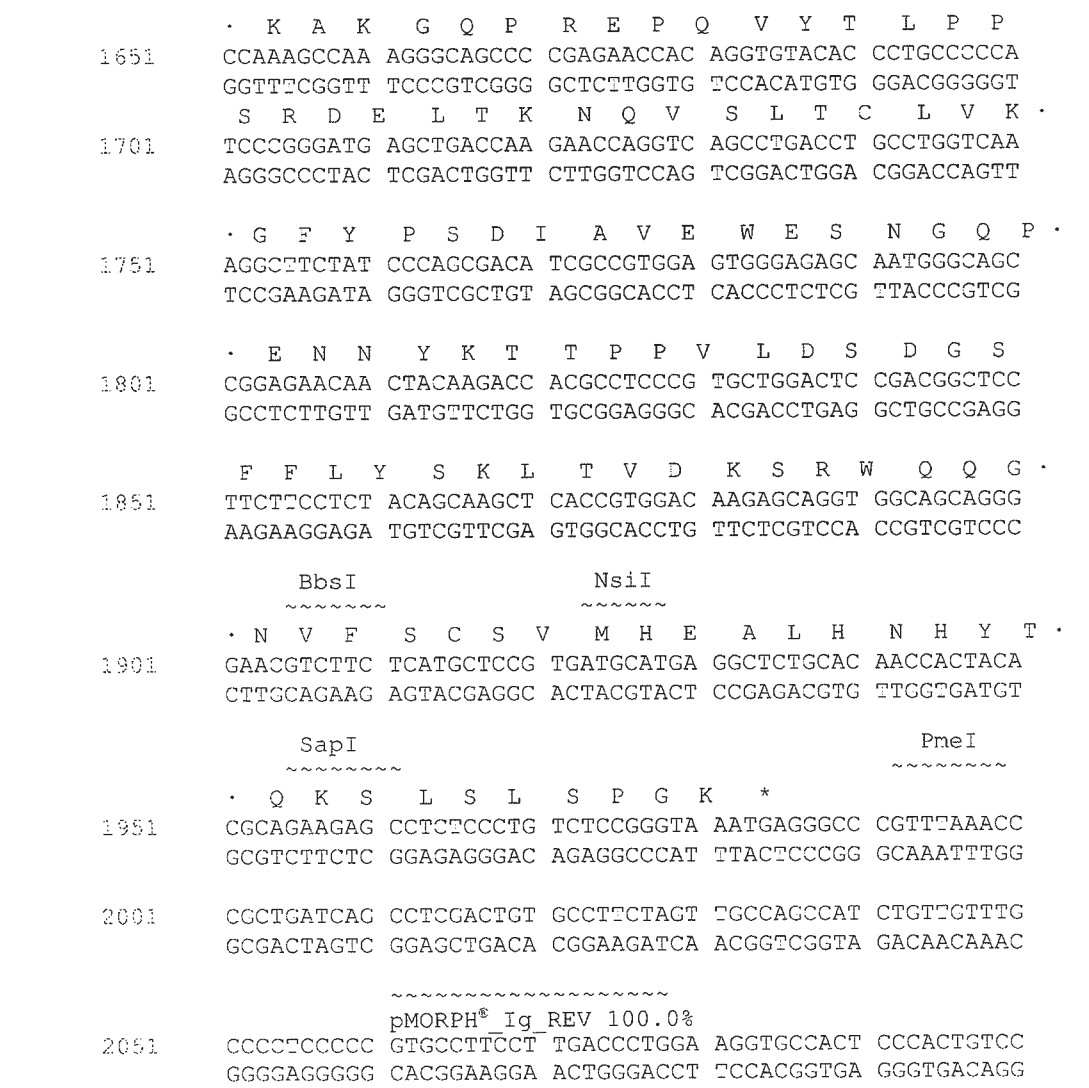


Figure 8: DNA Sequence of Ig kappa light chain expression vector pMORPH®_h_Igκ_1

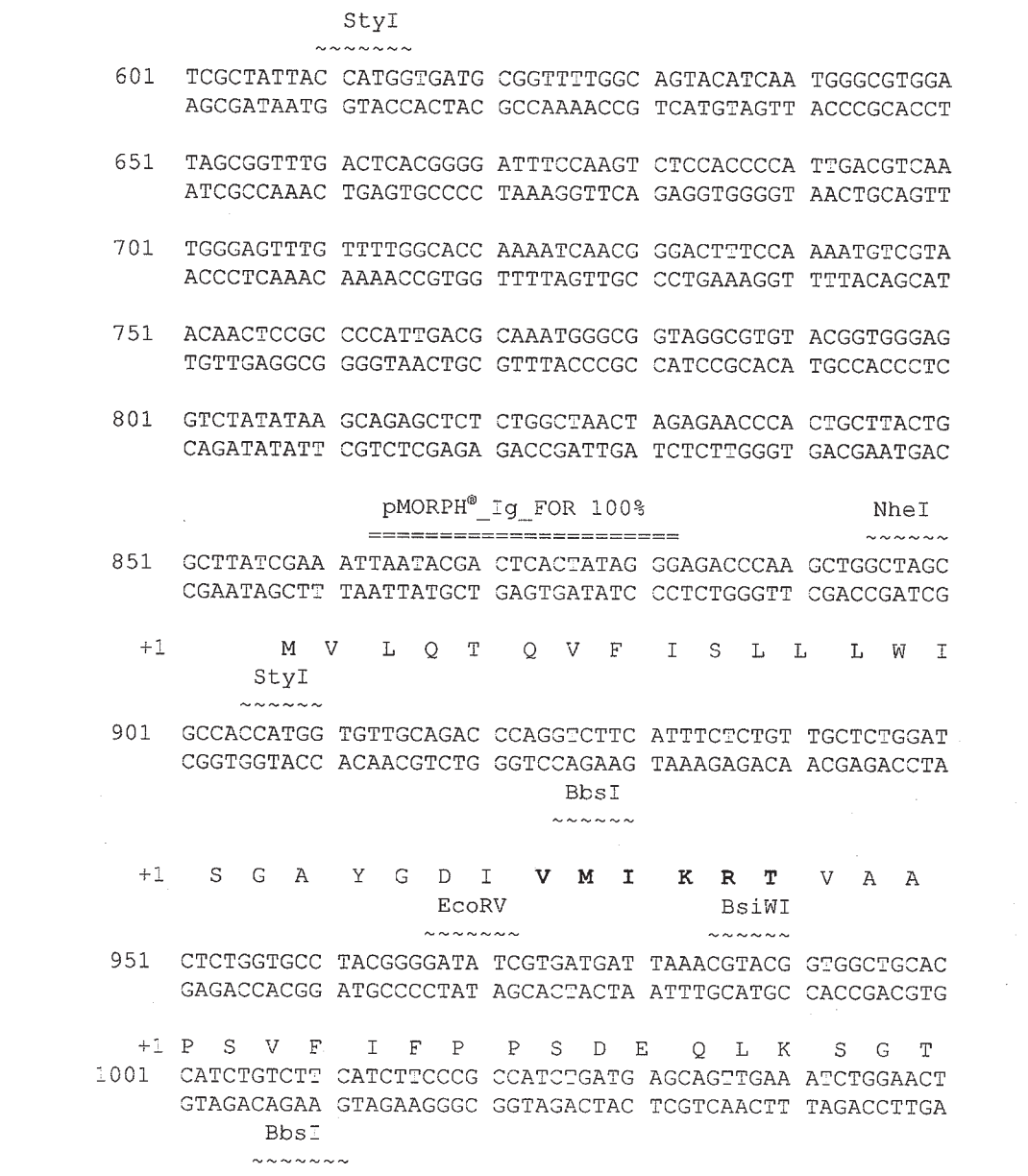


Figure 8 (Continued)

```
   +1  A  S  V  V   C  L  L   N  N  F   Y  P  R  E   A  K  V
1051  GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
      CGGAGACAAC ACACGGACGA CTTATTGAAG ATAGGGTCTC TCCGGTTTCA

   +1   Q  W  K   V  D  N  A   L  Q  S   G  N  S   Q  E  S
1101  ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
      TGTCACCTTC CACCTATTGC GGGAGGTTAG CCCATTGAGG GTCCTCTCAC

   +1 V  T  E  Q   D  S  K   D  S  T  Y   S  L  S   S  T  L
1151  TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCTG
      AGTGTCTCGT CCTGTCGTTC CTGTCGTGGA TGTCGGAGTC GTCGTGGGAC

   +1  T  L  S  K   A  D  Y   E  K  H   K  V  Y  A   C  E  V
         BlpI
       ~~~~~~~
1201  ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
      TGCGACTCGT TTCGTCTGAT GCTCTTTGTG TTTCAGATGC GGACGCTTCA

   +1   T  H  Q   G  L  S  S   P  V  T   K  S  F   N  R  G
1251  CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
      GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC

   +1 E  C  *
                        PmeI                    pMORPH®_Ig_REV 100%
                     ~~~~~~~~~                  ==================
1301  AGTGTTAGGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
      TCACAATCCC CGGGCAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA


      =
1351  AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT CCTTGACCCT
      TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAACTGGGA
```

Figure 9: DNA Sequence of HuCAL® Ig lambda light chain vector pMORPH®_h_Igλ_1

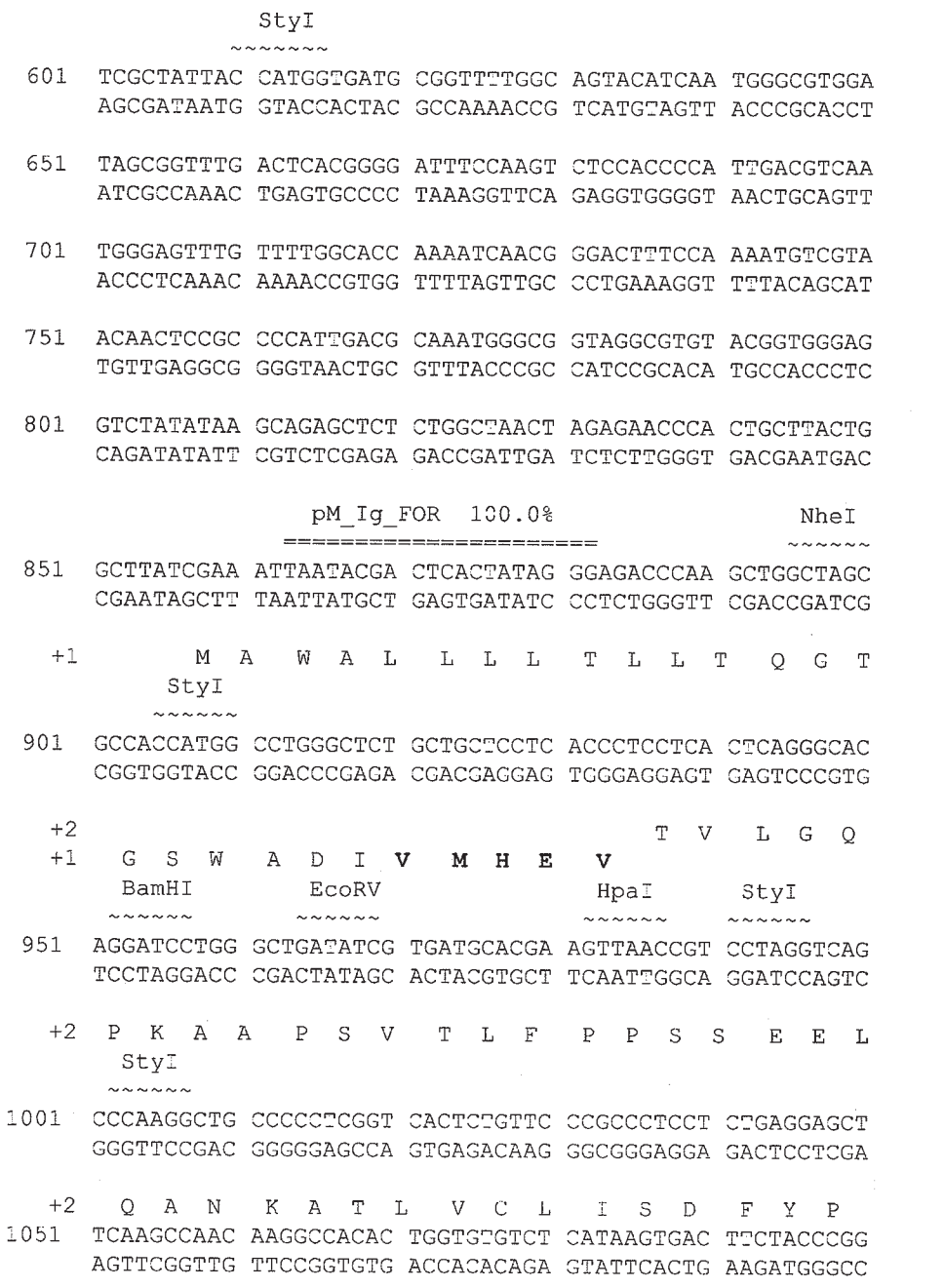


Figure 9 (Continued)

```
   +2 G  A  V  T   V  A  W   K  G  D  S   S  P  V   K  A  G
1101  GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
      CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

   +2  V  E  T  T   T  P  S   K  Q  S   N  N  K  Y   A  A  S
1151  GTGGAGACCA CCACACCCTC CAAACAAAGC AACAACAAGT ACGCGGCCAG
      CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

   +2   S  Y  L   S  L  T  P   E  Q  W   K  S  H   R  S  Y
1201  CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA
      GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT

   +2 S  C  Q  V   T  H  E   G  S  T  V   E  K  T   V  A  P
                                            BbsI
                                           ~~~~~~
1251  GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCT
      CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

   +2  T  E  C  S   *
                          PmeI
                         ~~~~~~~~
1301  ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
      TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
                                              pM_Ig_REV 100%
                                                 ==========

1351  GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
      CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
      pM_Ig_REV  100.0%
 ========
```

Figure 10

Designation:	Format	Affinity Maturation	Heavy chain from:	Light chain from:
MOR06183	Fab/IgG1	new H-CDR2	MOR06183	MOR03087 (parental)
MOR06184	Fab/IgG1	new H-CDR2	MOR06184	MOR03087 (parental)
MOR06185	Fab/IgG1	new H-CDR2	MOR06185	MOR03087 (parental)
MOR06186	Fab/IgG1	new H-CDR2	MOR06186	MOR03087 (parental)
MOR06187	Fab/IgG1	new H-CDR2	MOR06187	MOR03087 (parental)
MOR06188	Fab/IgG1	new H-CDR2	MOR06188	MOR03087 (parental)
MOR06189	Fab/IgG1	new H-CDR2	MOR06189	MOR03087 (parental)
MOR06190	Fab/IgG1	new H-CDR2	MOR06190	MOR03087 (parental)
MOR06192	Fab/IgG1	new H-CDR2	MOR06192	MOR03087 (parental)
MOR06195	Fab/IgG1	new H-CDR2	MOR06195	MOR03087 (parental)
MOR06197	Fab/IgG1	new H-CDR2	MOR06197	MOR03087 (parental)
MOR06200	Fab/IgG1	new H-CDR2	MOR06200	MOR03087 (parental)
MOR06201	Fab/IgG1	new H-CDR2	MOR06201	MOR03087 (parental)
MOR06204	Fab/IgG1	new H-CDR2	MOR06204	MOR03088 (parental)
MOR06214	Fab/IgG1	new H-CDR2	MOR06214	MOR03088 (parental)
MOR06278	Fab	new L-CDR3	MOR03088 (parental)	MOR06278
MOR06279	Fab	new L-CDR3	MOR03088 (parental)	MOR06279
MOR06347	IgG1	new L-CDR3	MOR03088 (parental)	MOR06278
MOR06348	IgG1	new L-CDR3 & H-CDR2	MOR06214	MOR06278

FIGURE 11: CD38-expression analysis of Lymphocytes and Erythrocytes

A: MOR 3087

B: MOR 3088

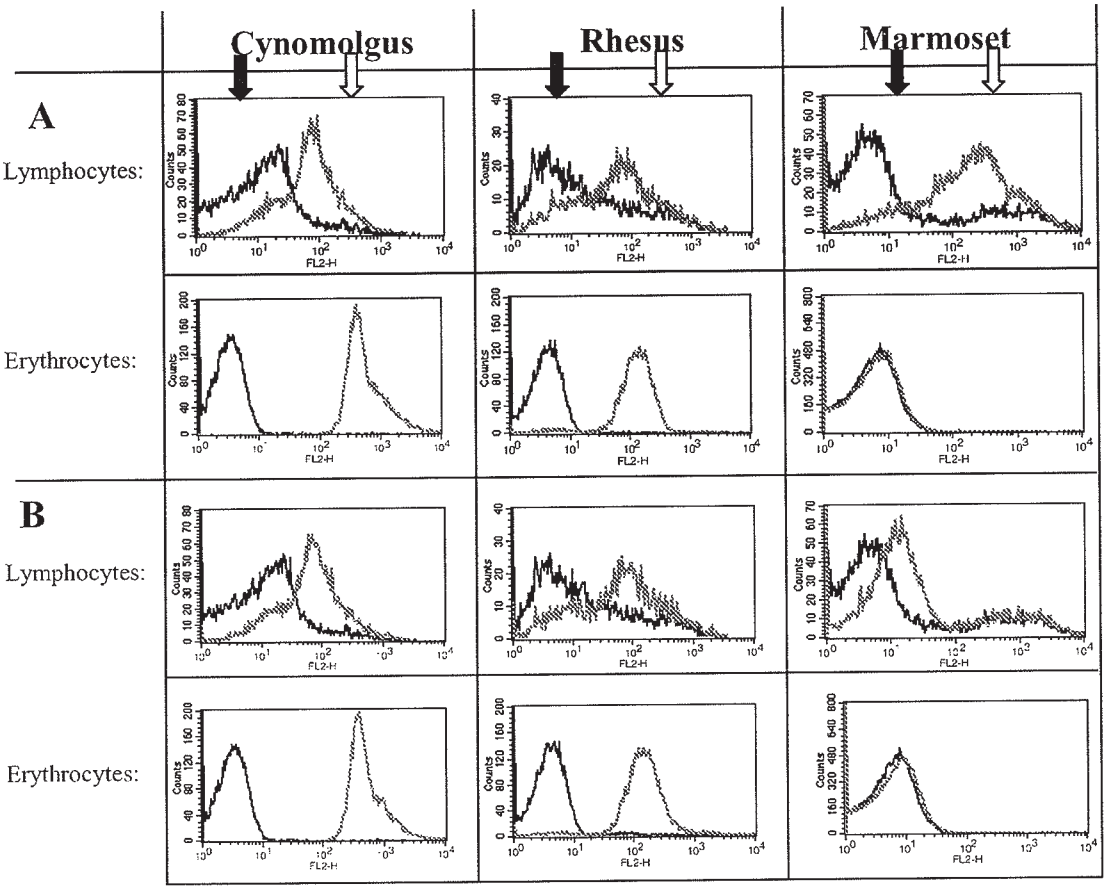


Figure 12: CD38 expression analysis of Lymphocytes and Erythrocytes

MOR 03087:

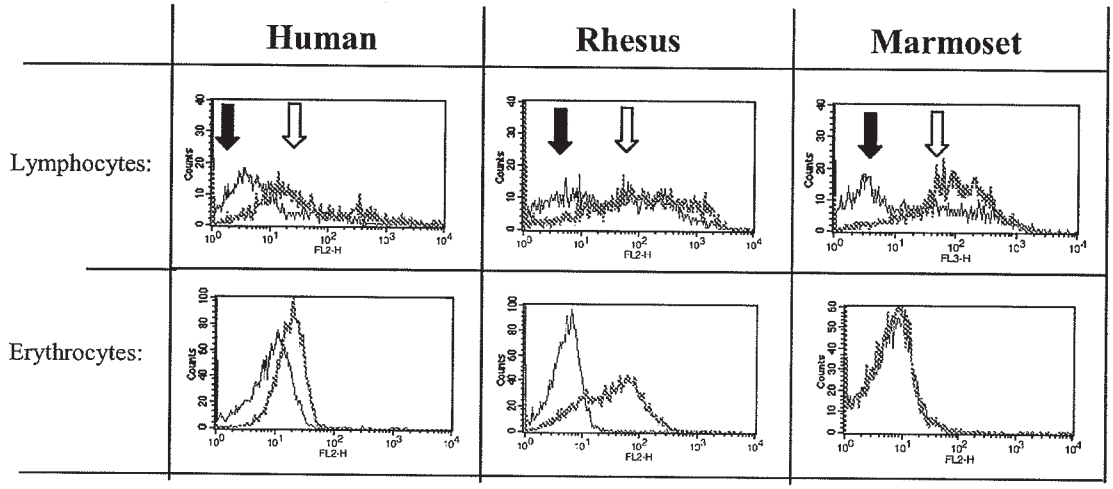


Figure 13: Overview Cross-Reactivity Anti-CD38 Antibodies

	Human		Rhesus		Cynomolgus		Marmoset	
Species/Tissue: / Anti-CD38 MAbs:	PBMCs	Erythr.	PBMCs	Erythr.	PBMCs	Erythr.	PBMCs	Erythr.
3076	+	n.d.	-	-	-	-	-	-
3077	+	-	-	-	-	-	-	-
3078	+	n.d.	-	-	-	-	-	-
3079	+	+	-	-	-	-	-	-
3080	+	+/-	+	-	+	-	-	-
3081	+	n.d.	-	-	-	-	-	-
3085	+	n.d.	-	-	-	-	-	-
3086	+	n.d.	-	-	-	-	-	-
3087	+	+/-	+	+	+	+	+	-
3088	+	-	+	+	+	+	+	-
3089	+	n.d.	-	-	-	-	-	-
3101	+	n.d.	-	-	-	-	-	-
3102	+	n.d.	-	-	-	-	-	-
3127	+	n.d.	-	-	-	-	-	-
3128	+	n.d.	-	-	-	-	-	-
3129	+	n.d.	-	-	-	-	-	-
3130	+	n.d.	-	-	-	-	-	-
3131	+	n.d.	-	-	-	-	-	-

+ : positive staining
+/-: weak positive staining
- : negative staining
n.d.: not determined

Figure 14a

VH

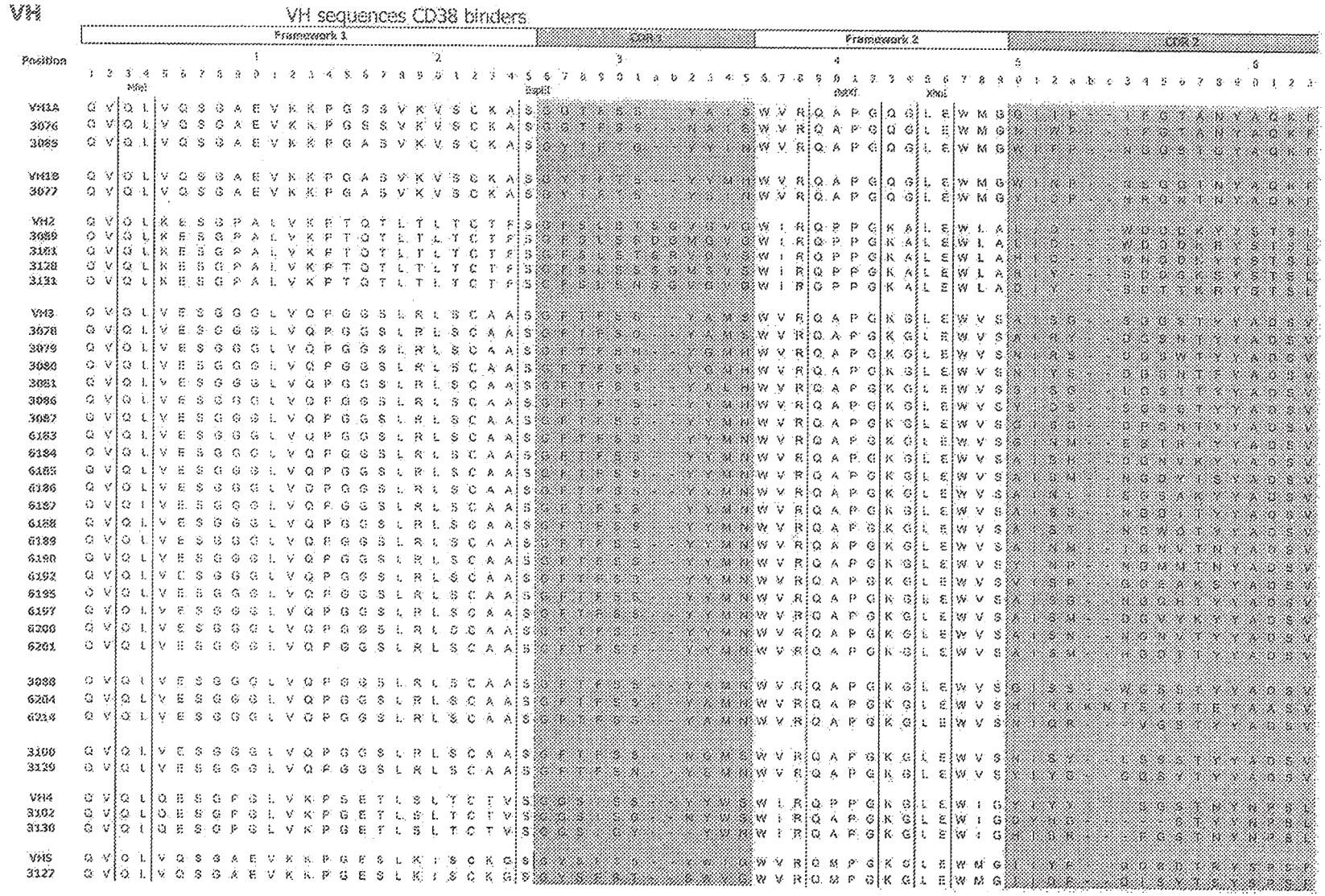


Figure 14a (Continued)

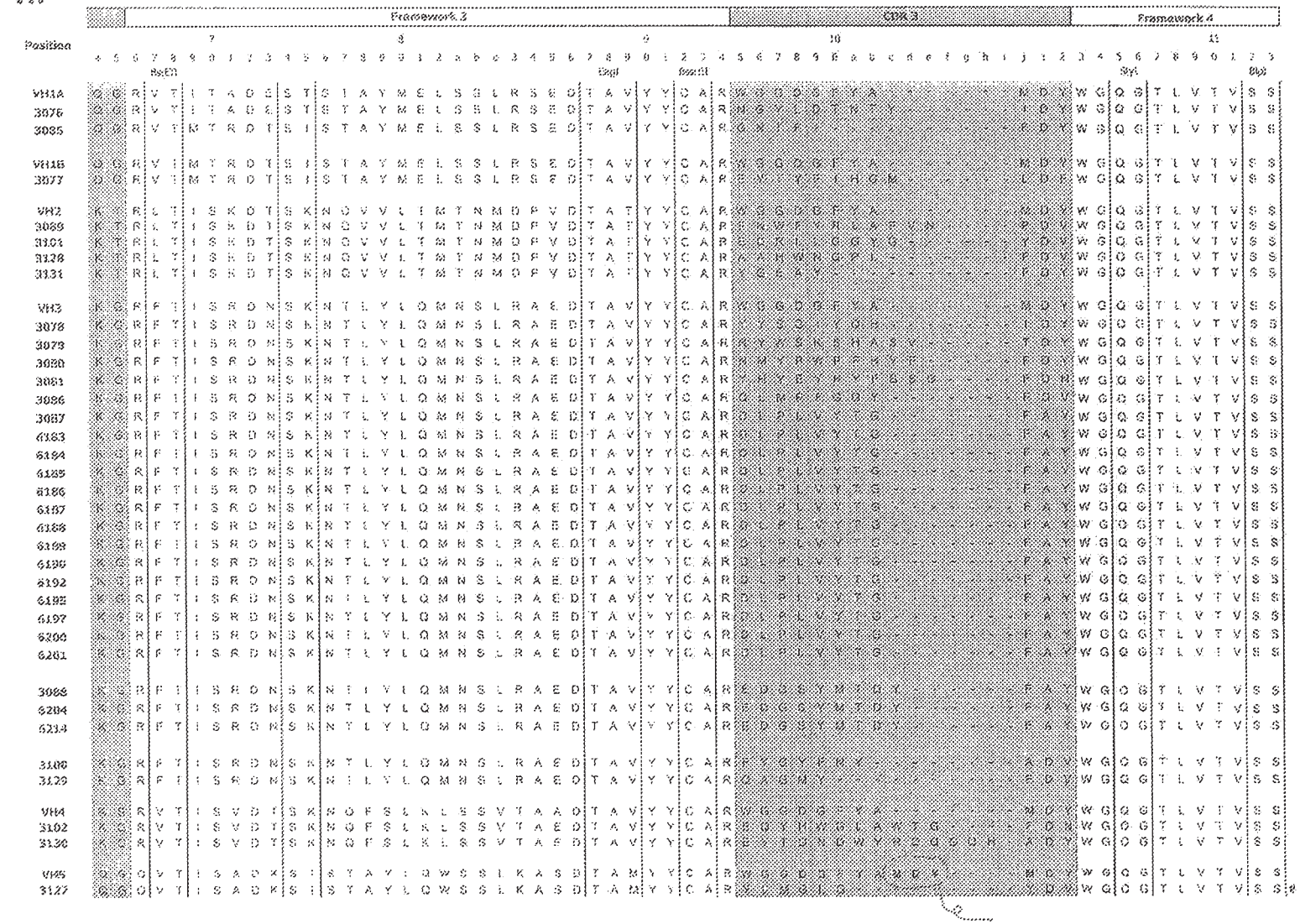


Figure 14b

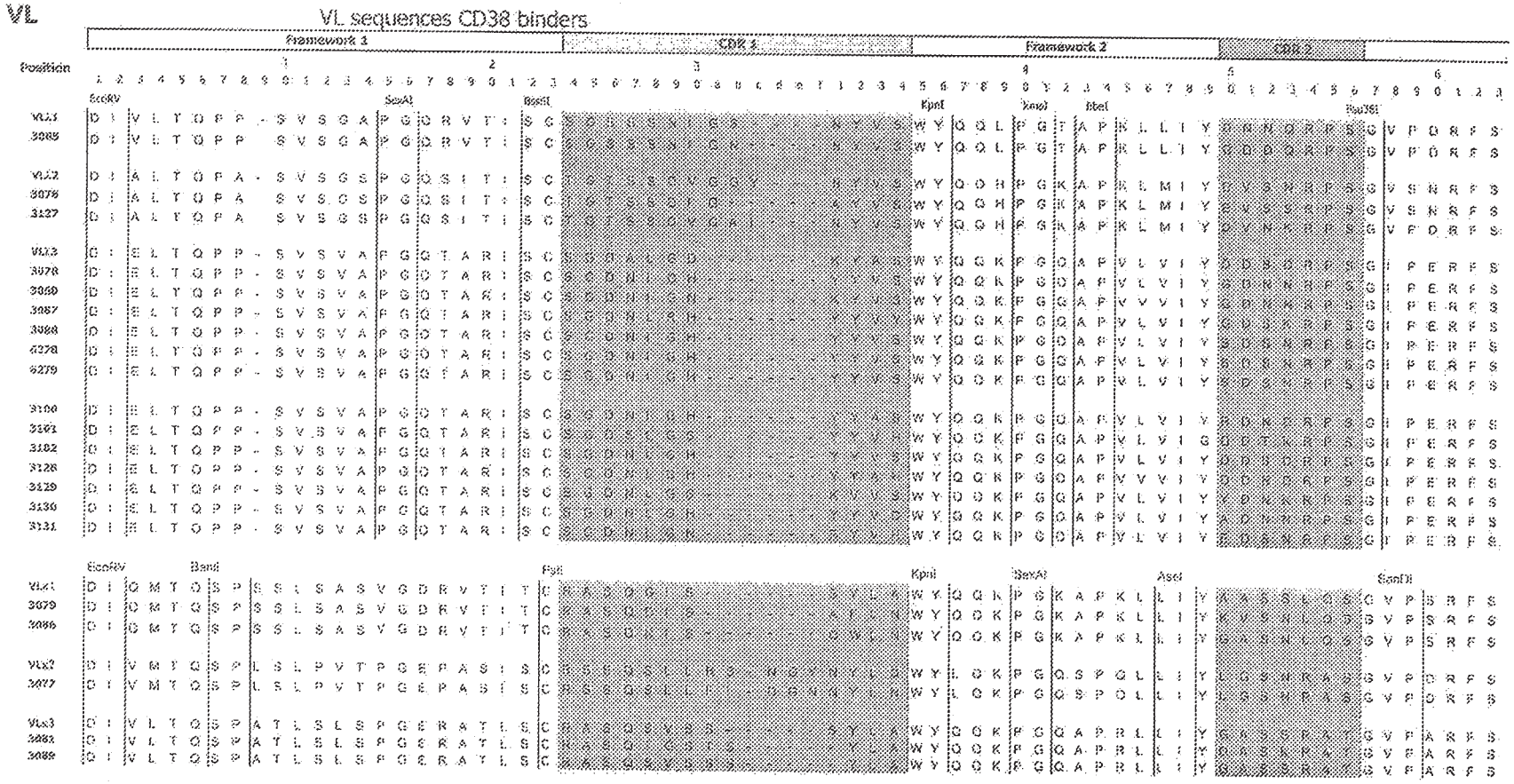

VL
VL sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
EcoRV
SexAI
BssHI
KpnI
XmaI
BbeI
SpeI/BlpI
EcoRV
BamHI
PstI
KpnI
SexAI
AscI
SanDI

Figure 14b (Continued)

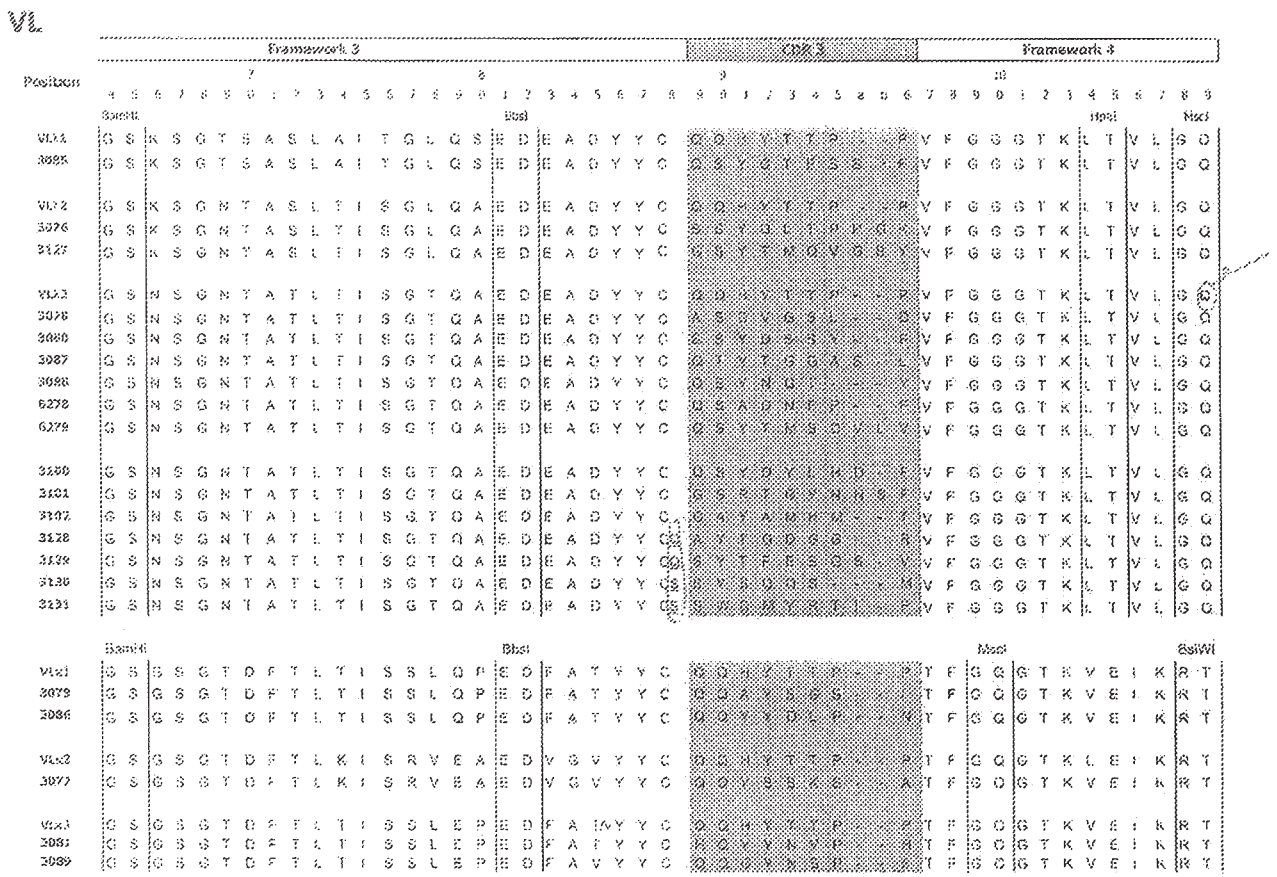


Figure 14a

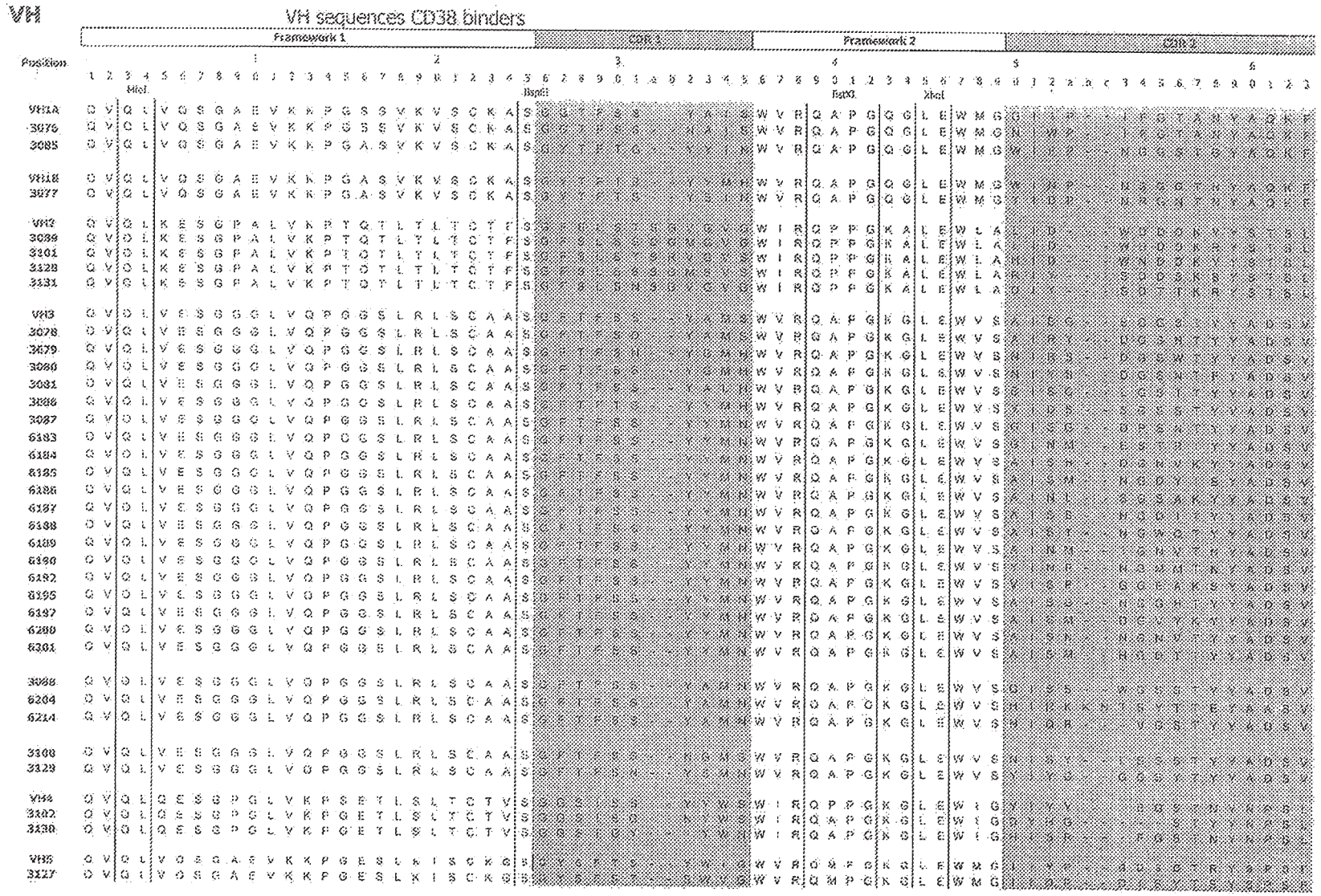

VH
VH sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
MfeI
BspEI
BstXI
XbaI
VH1A
3076
3085
VH18
3077
VH2
3089
3101
3128
3131
VH3
3078
3079
3080
3081
3086
3087
6183
6184
6185
6186
6187
6188
6189
6190
6192
6195
6197
6200
6201
3088
6204
6214
3108
3129
VH4
3102
3130
VH5
3127

Figure 14a (Continued)

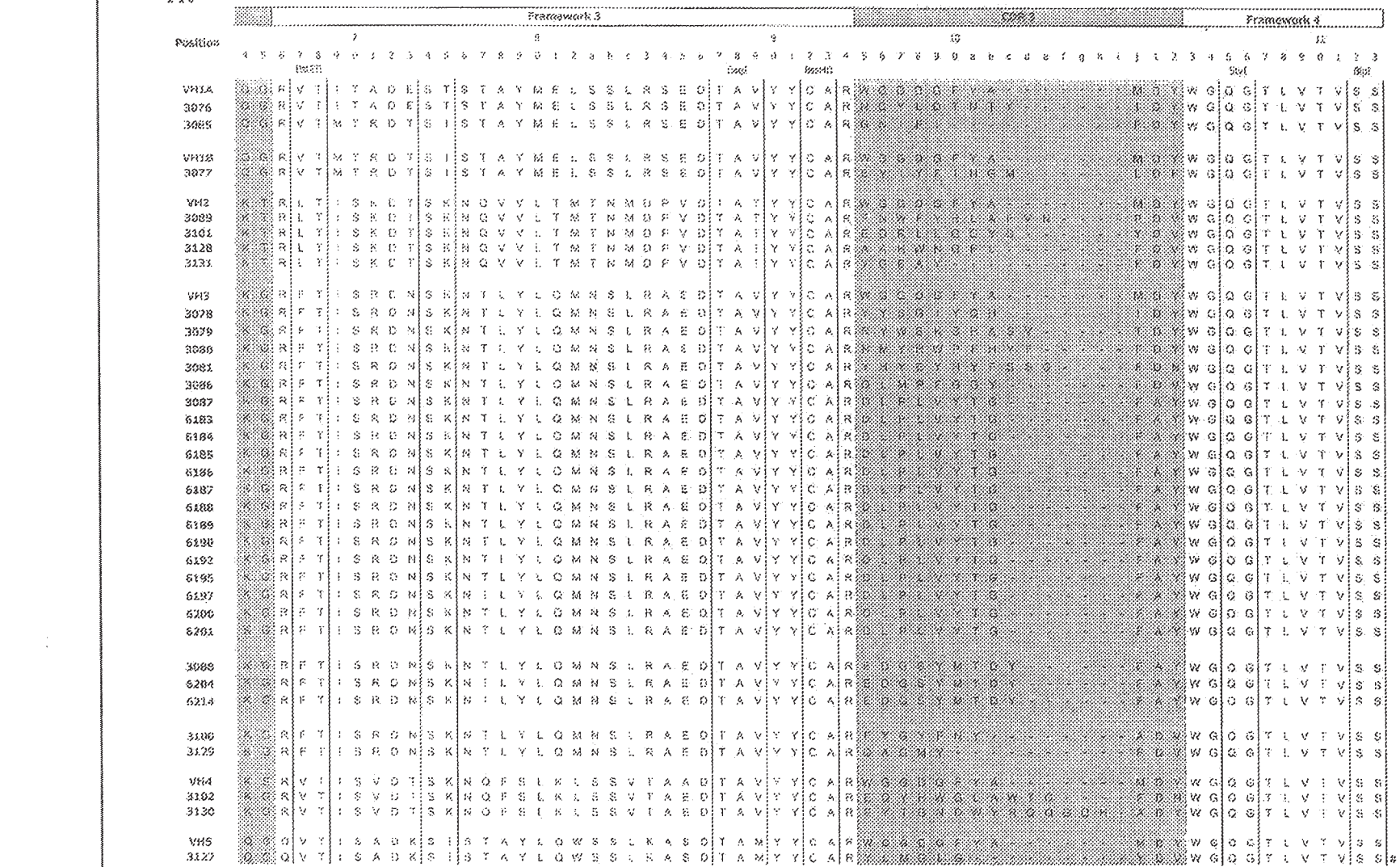


Figure 14b

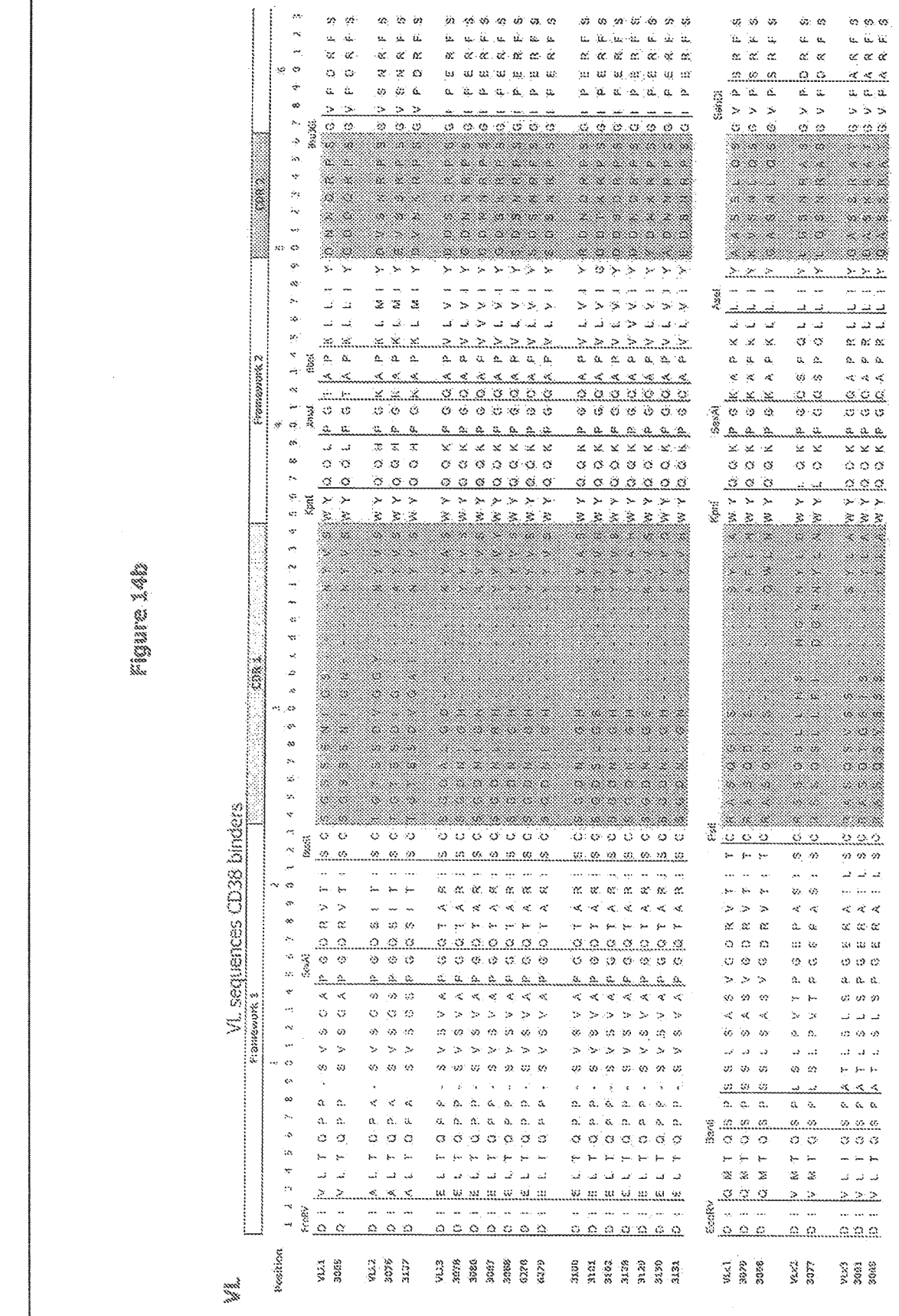

VL
VL sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Framework 3
Position
EcoRV
BsiWI
AscI
NheI
KpnI
BamHI
VLk1
3035
VLk2
3076
3077
VLk3
3078
3086
3087
3088
3228
3229
3100
3101
3102
3126
3129
3130
3131
VLk1
3079
3036
VLk2
3077
VLk3
3081
3049

Figure 14b (Continued)

