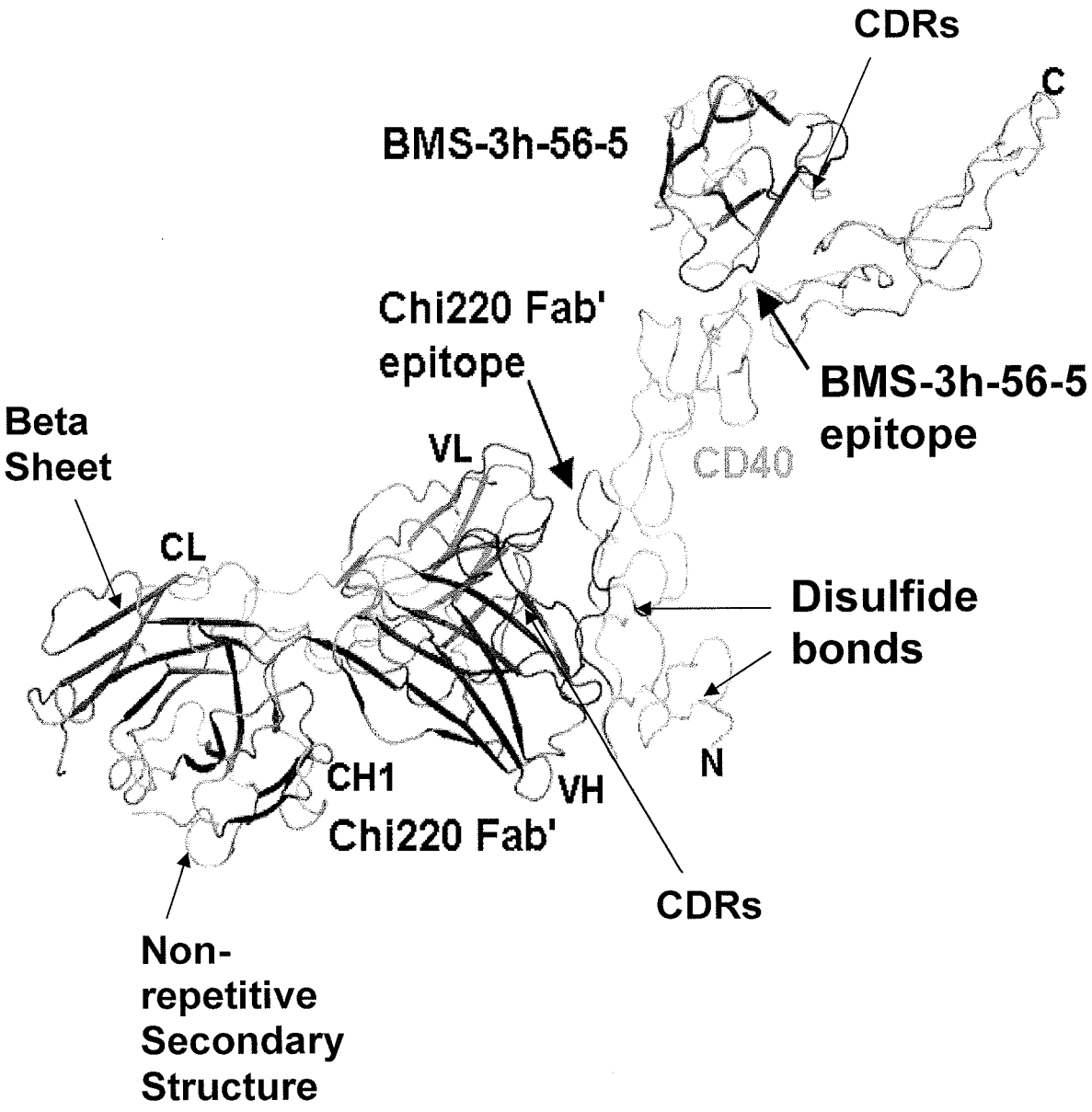
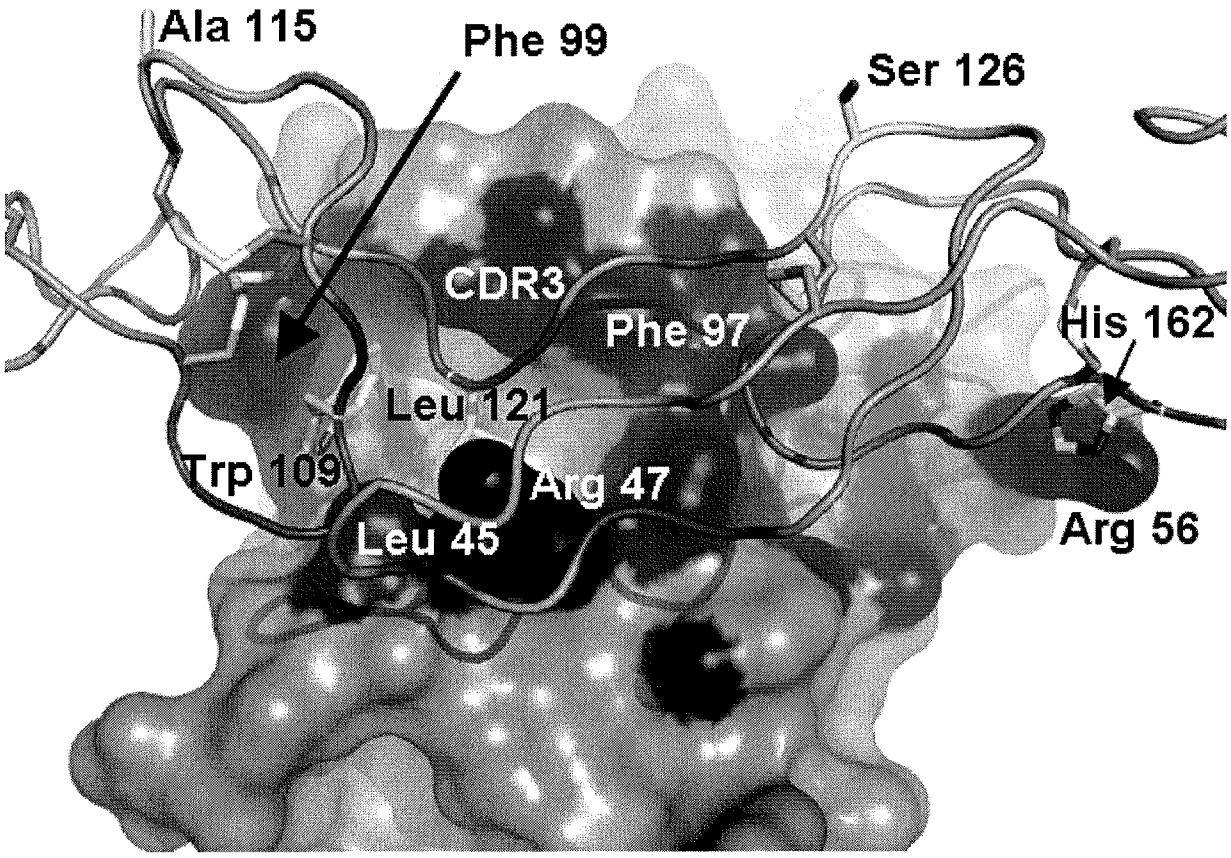
# FIG. 1


CDRs
C
BMS-3h-56-5
Chi220 Fab'
epitope
BMS-3h-56-5
epitope
Beta
Sheet
VL
CD40
CL
Disulfide
bonds
N
CH1
VH
Chi220 Fab'
CDRs
Non-
repetitive
Secondary
Structure

# FIG. 2


Ala 115
Phe 99
Ser 126
CDR3
Phe 97
His 162
Leu 121
Trp 109
Arg 47
Leu 45
Arg 56

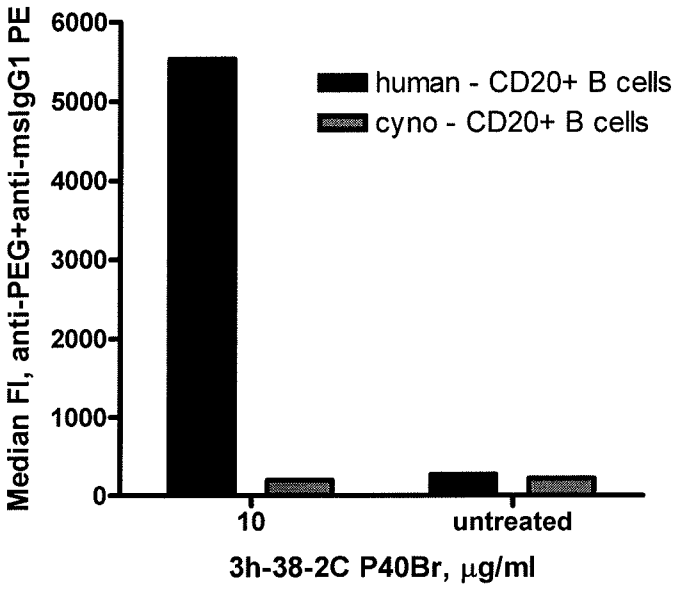

Median FI, anti-PEG+anti-mslgG1 PE
6000
5000
4000
3000
2000
1000
0
human - CD20+ B cells
cyno - CD20+ B cells
10
untreated
3h-38-2C P40Br, μg/ml

FIG. 3A

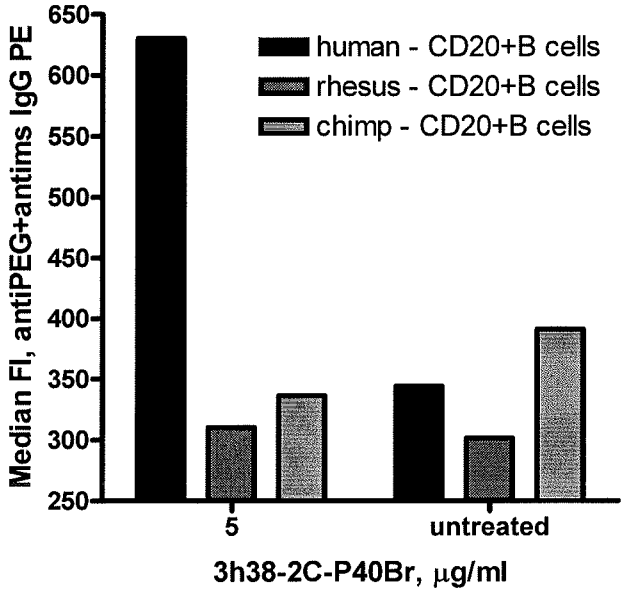
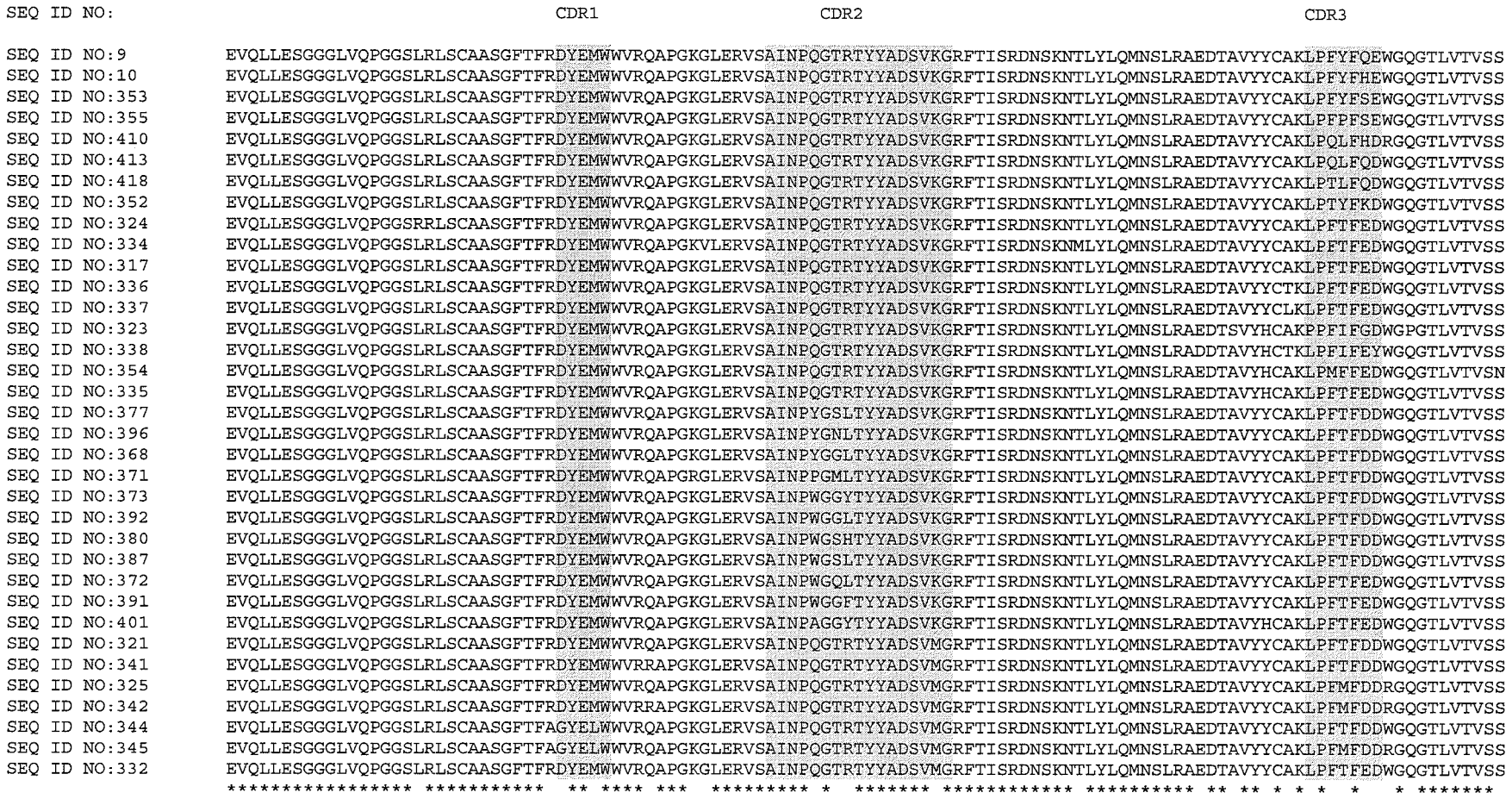
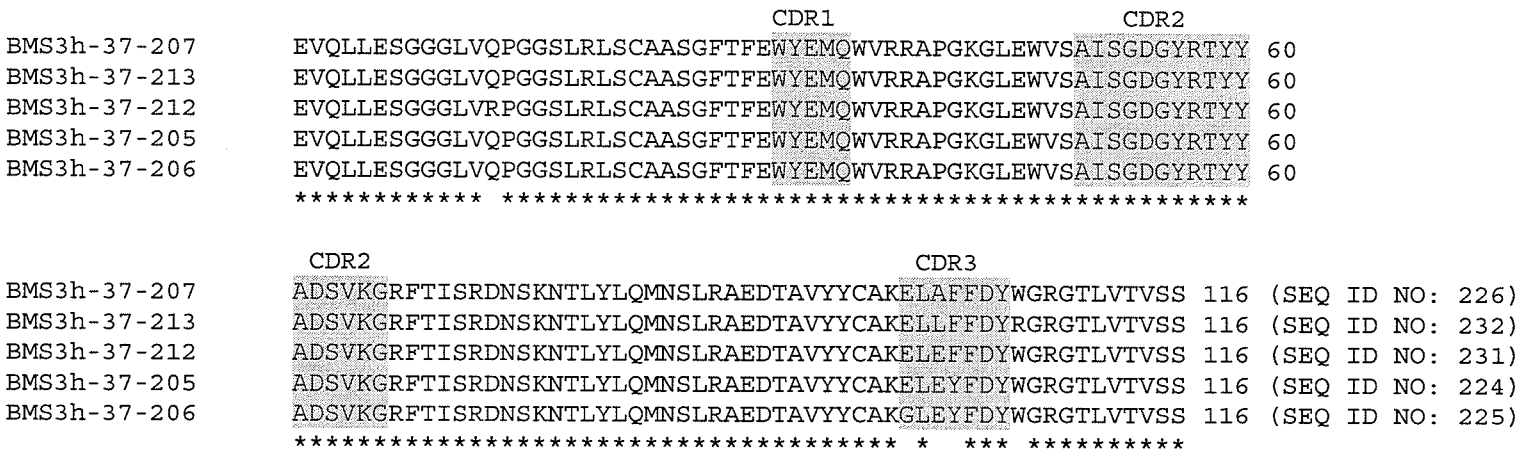

Median FI, antiPEG+antims IgG PE
650
600
550
500
450
400
350
300
250
human - CD20+B cells
rhesus - CD20+B cells
chimp - CD20+B cells
5
untreated
3h38-2C-P40Br, μg/ml

FIG. 3B

# FIG. 4


SEQ ID NO:
CDR1
CDR2
CDR3
SEQ ID NO:9 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLVTVSS
SEQ ID NO:10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLVTVSS
SEQ ID NO:353 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFSEWGQGTLVTVSS
SEQ ID NO:355 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFPFSEWGQGTLVTVSS
SEQ ID NO:410 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPQLFHDRGQGTLVTVSS
SEQ ID NO:413 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPQLFQDWGQGTLVTVSS
SEQ ID NO:418 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPTLFQDWGQGTLVTVSS
SEQ ID NO:352 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPTYFKDWGQGTLVTVSS
SEQ ID NO:324 EVQLLESGGGLVQPGGSRRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:334 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKVLERVSAINPQGTRTYYADSVKGRFTISRDNSKNMLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:317 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:336 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTKLPFTFEDWGQGTLVTVSS
SEQ ID NO:337 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCLKLPFTFEDWGQGTLVTVSS
SEQ ID NO:323 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTSVYHCAKPPFIFGDWGPGTLVTVSS
SEQ ID NO:338 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRADDTAVYHCTKLPFIFEYWGQGTLVTVSS
SEQ ID NO:354 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYHCAKLPMFFEDWGQGTLVTVSN
SEQ ID NO:335 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYHCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:377 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGSLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:396 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:368 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:371 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGRGLERVSAINPPGMLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:373 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:392 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:380 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:387 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:372 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGQLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:391 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:401 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGGYTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYHCAKLPFTFEDWGQGTLVTVSS
SEQ ID NO:321 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:341 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRRAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:325 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFMFDDRGQGTLVTVSS
SEQ ID NO:342 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRRAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFMFDDRGQGTLVTVSS
SEQ ID NO:344 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS
SEQ ID NO:345 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFMFDDRGQGTLVTVSS
SEQ ID NO:332 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS

# FIG. 5

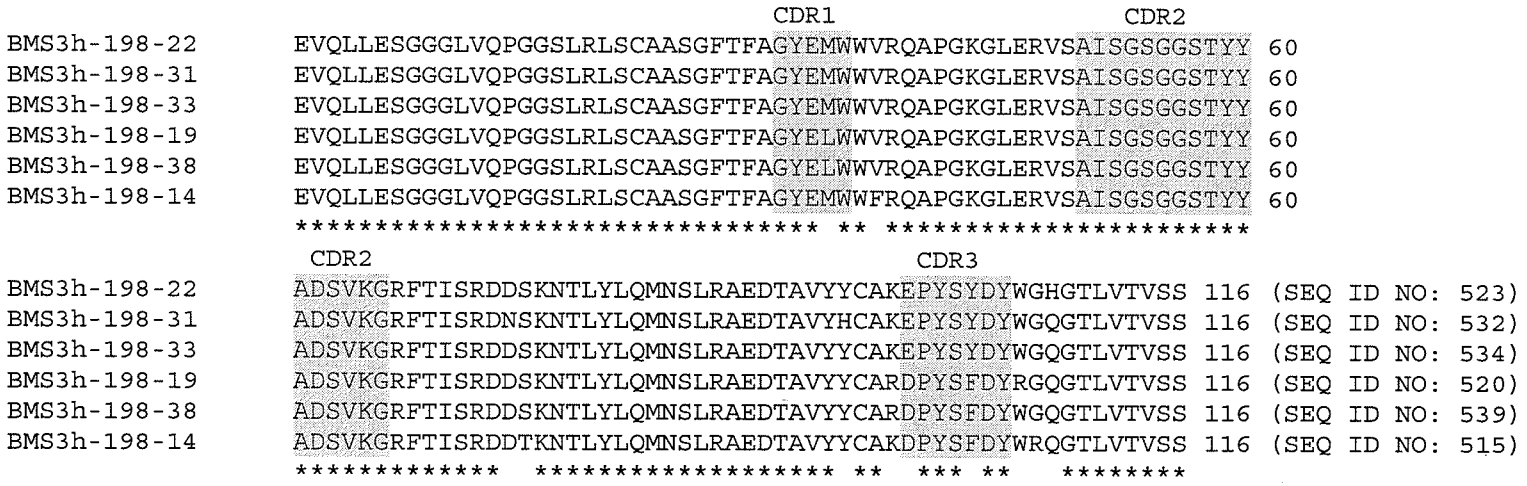

CDR1
CDR2
BMS3h-37-207 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY 60
BMS3h-37-213 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY 60
BMS3h-37-212 EVQLLESGGGLVRPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY 60
BMS3h-37-205 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY 60
BMS3h-37-206 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY 60
CDR2
CDR3
BMS3h-37-207 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKELAFFDYWGRGTLVTVSS 116 (SEQ ID NO: 226)
BMS3h-37-213 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKELLFFDYRGRGTLVTVSS 116 (SEQ ID NO: 232)
BMS3h-37-212 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTVSS 116 (SEQ ID NO: 231)
BMS3h-37-205 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKELEYFDYWGRGTLVTVSS 116 (SEQ ID NO: 224)
BMS3h-37-206 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGLEYFDYWGRGTLVTVSS 116 (SEQ ID NO: 225)

# FIG. 6

```
                                        CDR1                    CDR2
BMS3h-38-217    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRRGYSTYY 60
BMS3h-38-238    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRSGYSTYY 60
BMS3h-38-228    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGFSTYY 60
BMS3h-38-235    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGYSTYY 60
BMS3h-38-231    EVQLLASGGGLVQPGGSLRLSCAASGFPFEEEEMIWVRQAPGKGLEWVSAISRQGWSTYY 60
BMS3h-38-237    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRGGWSTYY 60
BMS3h-38-218    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRHGWSTYY 60
BMS3h-38-215    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGLGWSTYY 60
BMS3h-38-223    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYY 60
BMS3h-38-224    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYY 60
BMS3h-38-225    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGGTYY 60
BMS3h-38-219    EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSSISRSGGSTYY 60
                ************************** ********************  **  *  ***

                 CDR2                                   CDR3
BMS3h-38-217    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 264)
BMS3h-38-238    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 285)
BMS3h-38-228    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 275)
BMS3h-38-235    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 282)
BMS3h-38-231    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 278)
BMS3h-38-237    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 284)
BMS3h-38-218    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 265)
BMS3h-38-215    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 262)
BMS3h-38-223    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFMYDYWGQGTLVTVSS 116 (SEQ ID NO: 270)
BMS3h-38-224    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFPYDYWGQGTLVTVSS 116 (SEQ ID NO: 271)
BMS3h-38-225    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 272)
BMS3h-38-219    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS 116 (SEQ ID NO: 266)
                ************************************** **************
```

# FIG. 7


CDR1
CDR2
BMS3h-198-22 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY 60
BMS3h-198-31 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY 60
BMS3h-198-33 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY 60
BMS3h-198-19 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAISGSGGSTYY 60
BMS3h-198-38 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAISGSGGSTYY 60
BMS3h-198-14 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYY 60
CDR2
CDR3
BMS3h-198-22 ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGHGTLVTVSS 116 (SEQ ID NO: 523)
BMS3h-198-31 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGTLVTVSS 116 (SEQ ID NO: 532)
BMS3h-198-33 ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGQGTLVTVSS 116 (SEQ ID NO: 534)
BMS3h-198-19 ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYRGQGTLVTVSS 116 (SEQ ID NO: 520)
BMS3h-198-38 ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLVTVSS 116 (SEQ ID NO: 539)
BMS3h-198-14 ADSVKGRFTISRDDTKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWRQGTLVTVSS 116 (SEQ ID NO: 515)