

Figure 1

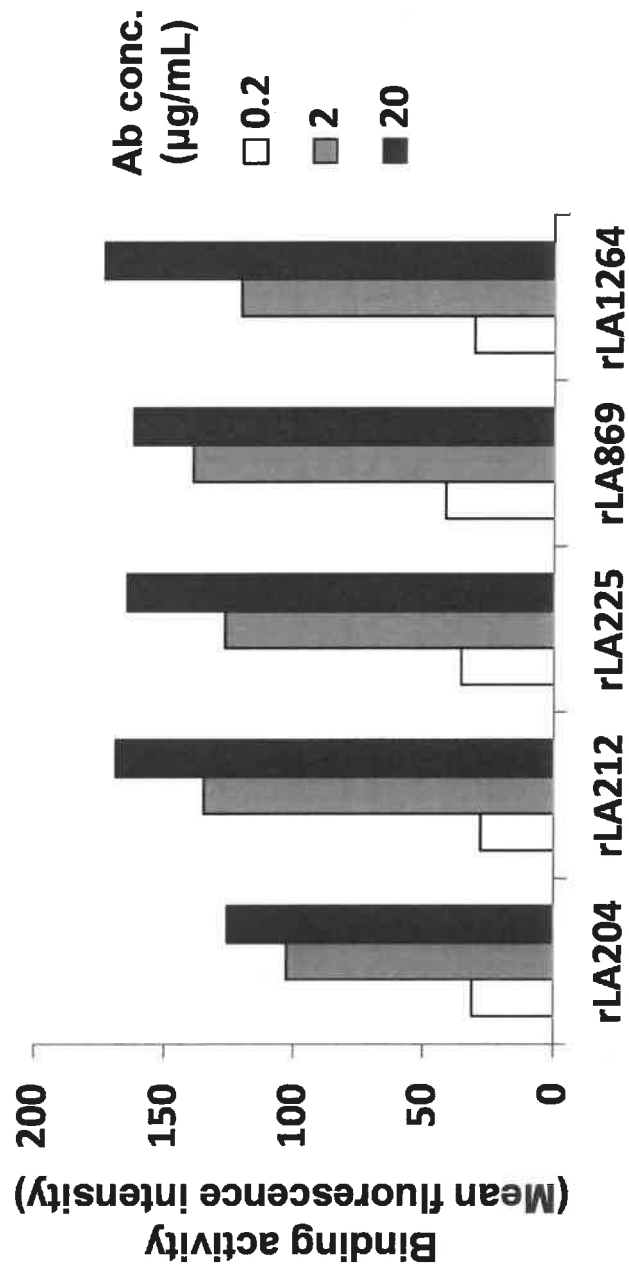


Figure 2

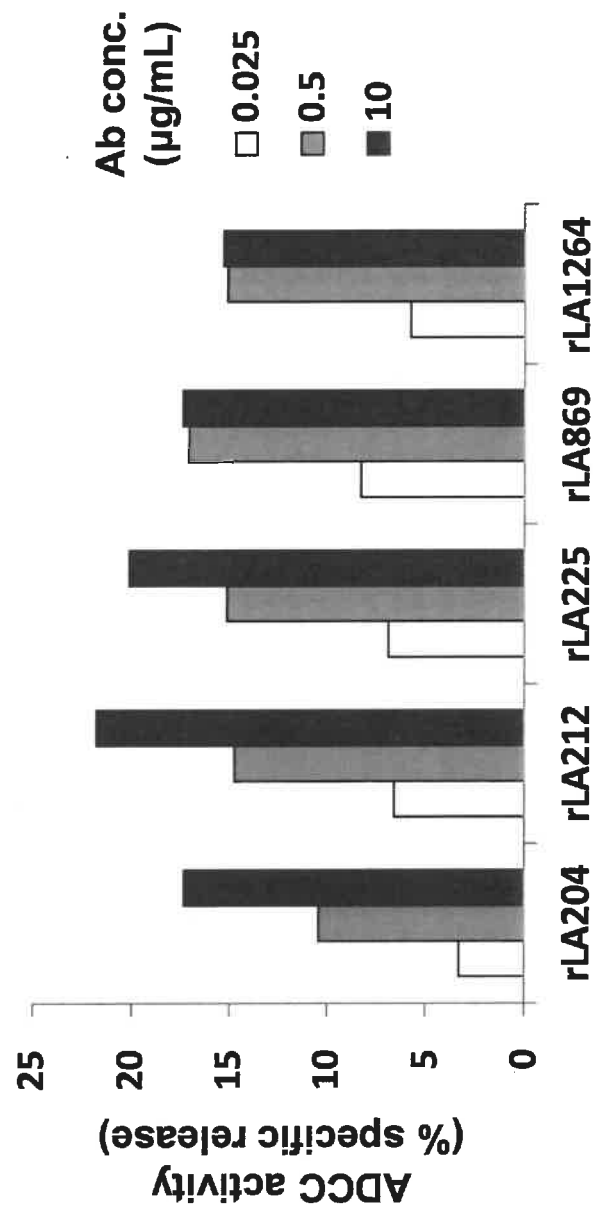


Figure 3

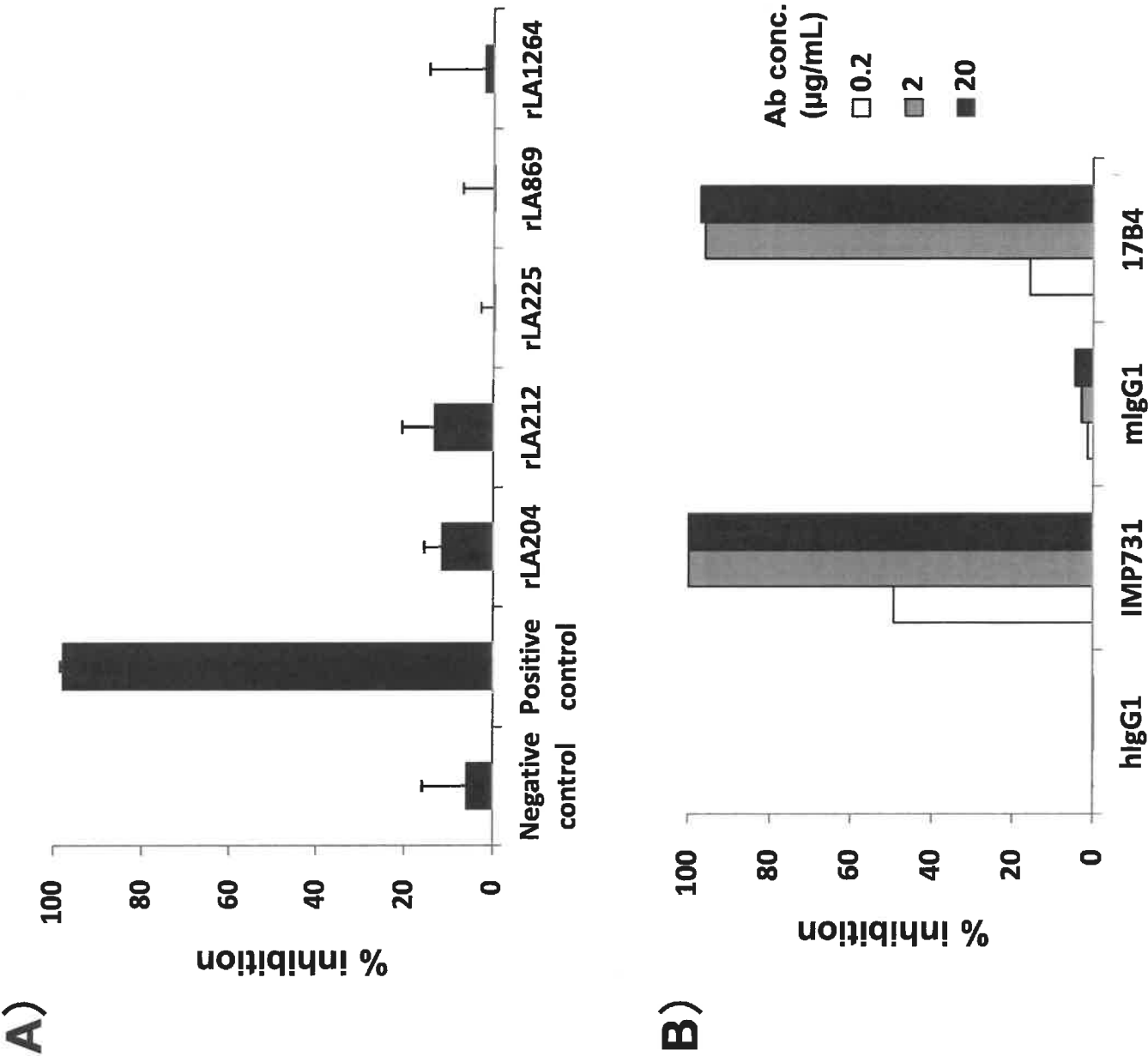


Figure 4

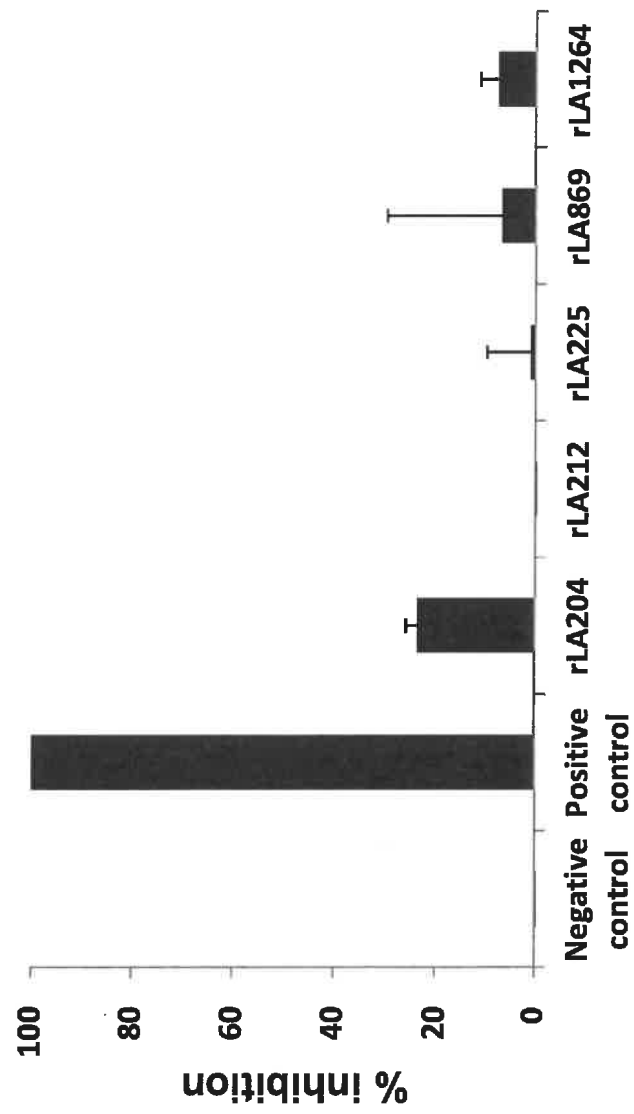
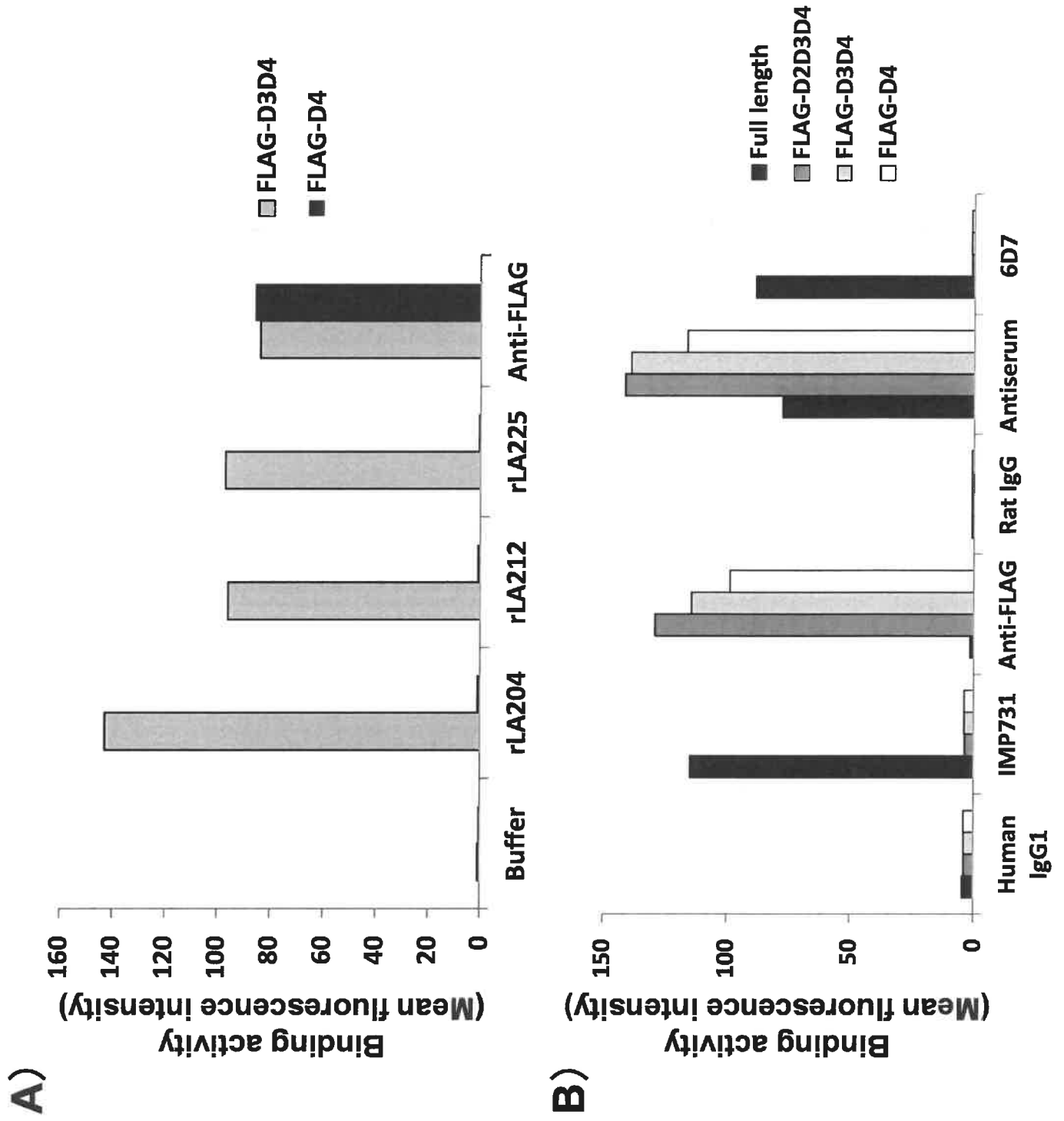


Figure 5



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Figure 6

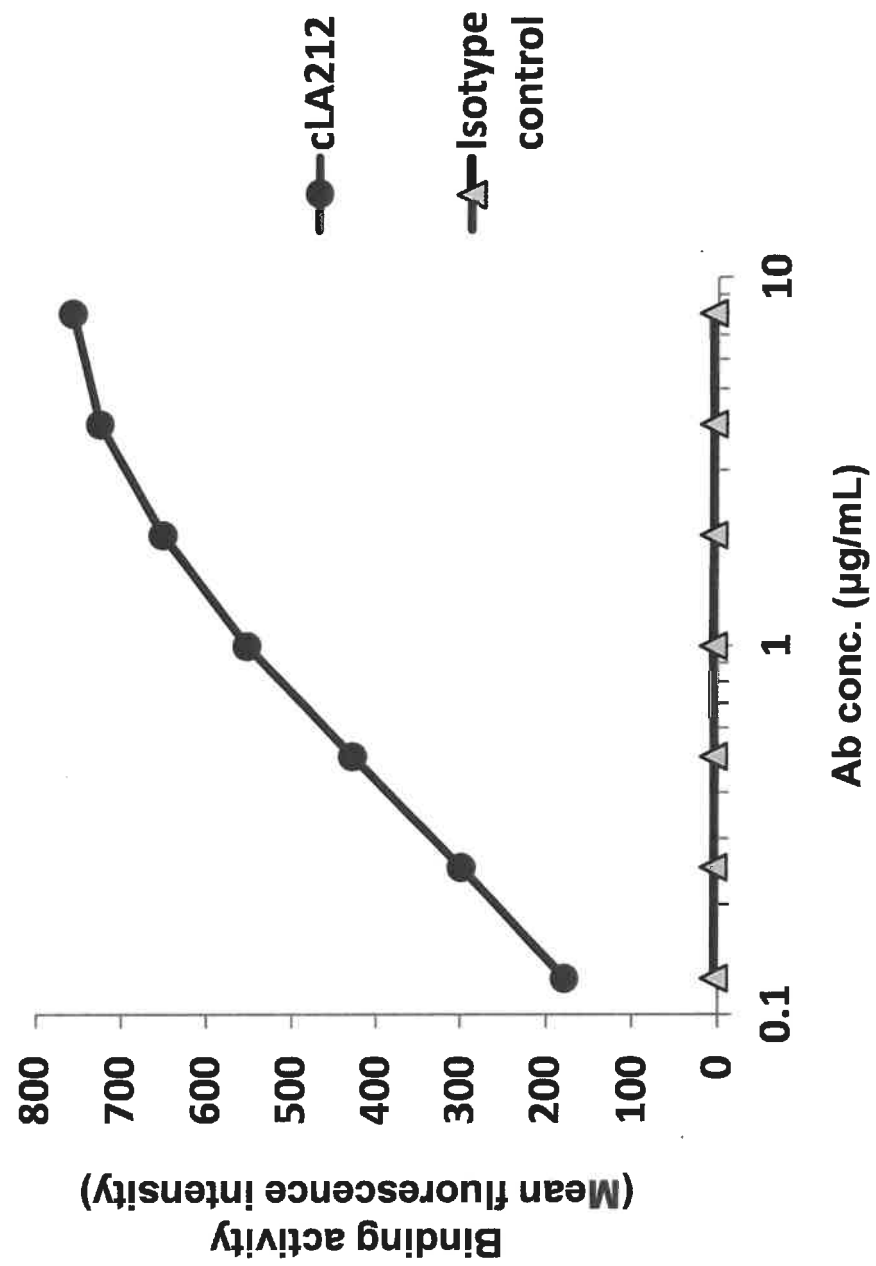


Figure 7

|    | Antibodies   | KD<br>(nM) |
|----|--------------|------------|
| 1  | hLA212_H2/L1 | 0.11       |
| 2  | hLA212_H2/L2 | 0.12       |
| 3  | hLA212_H2/L3 | 0.15       |
| 4  | hLA212_H2/L4 | 0.096      |
| 5  | hLA212_H2/L5 | 0.12       |
| 6  | hLA212_H3/L1 | 0.092      |
| 7  | hLA212_H3/L2 | 0.062      |
| 8  | hLA212_H3/L3 | 0.10       |
| 9  | hLA212_H3/L4 | 0.076      |
| 10 | hLA212_H3/L5 | 0.10       |

Figure 8

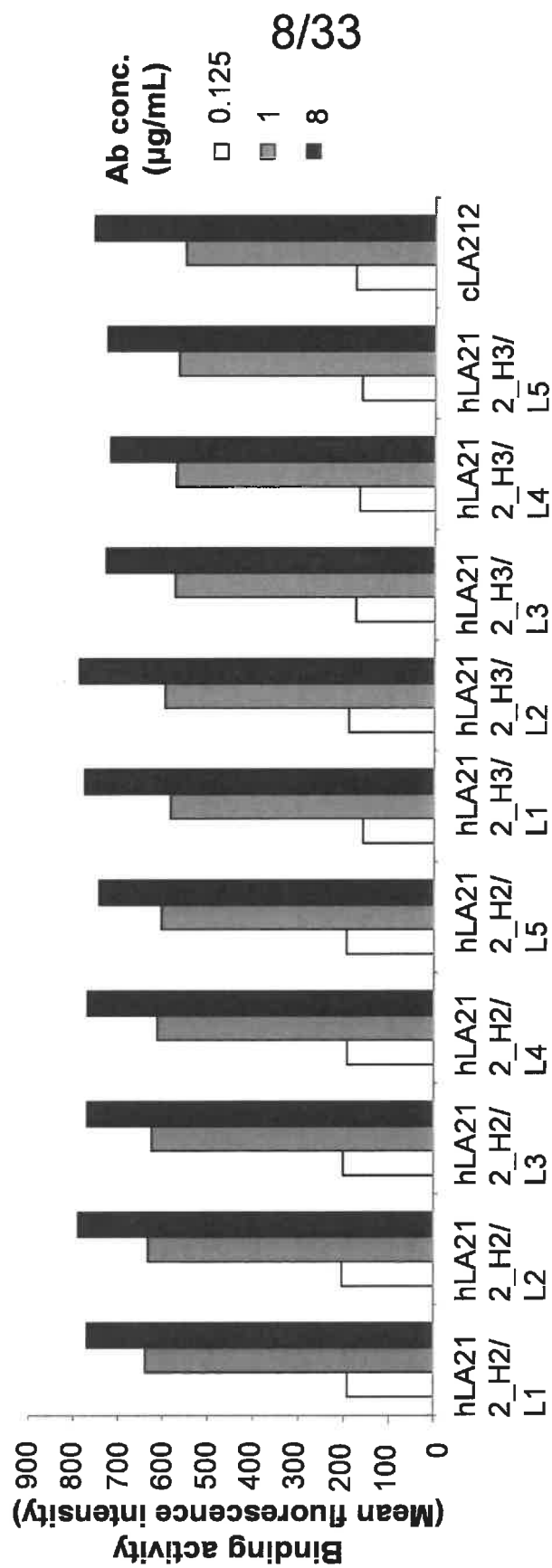


Figure 9

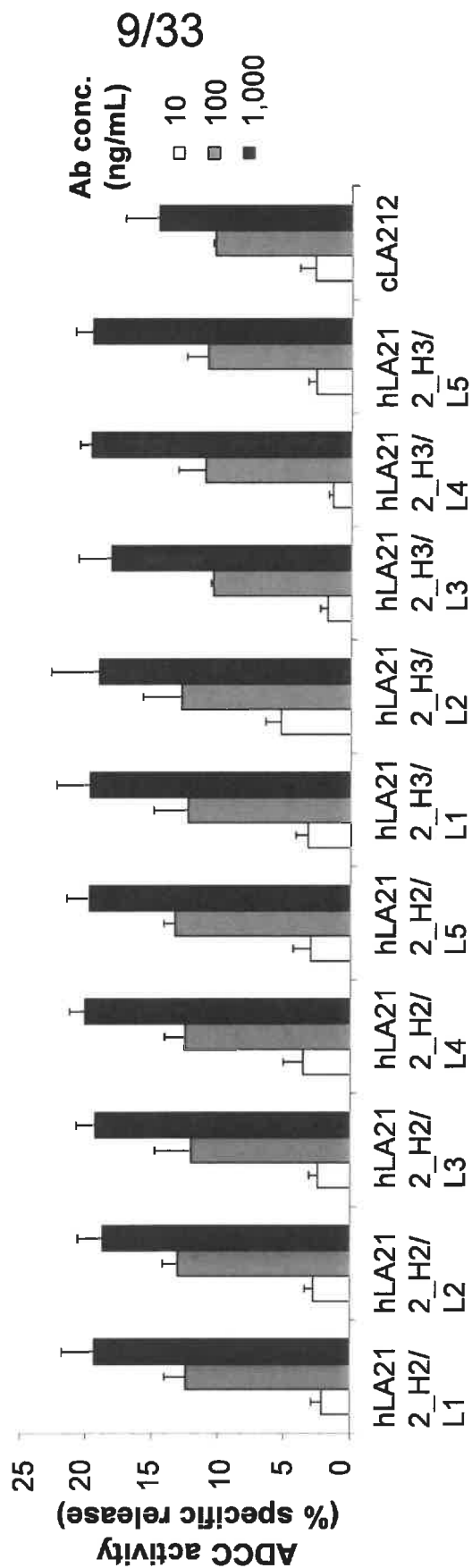


Figure 10

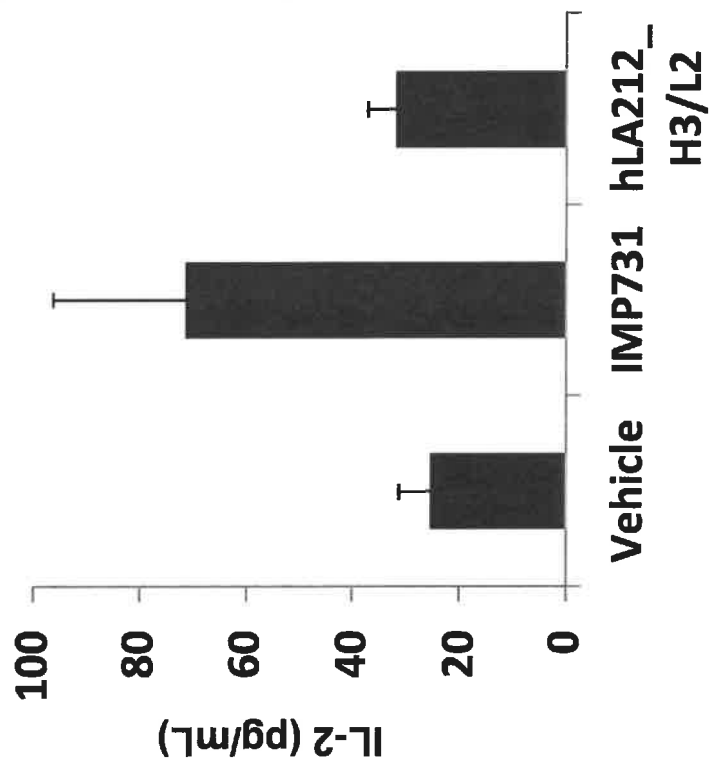


Figure 11

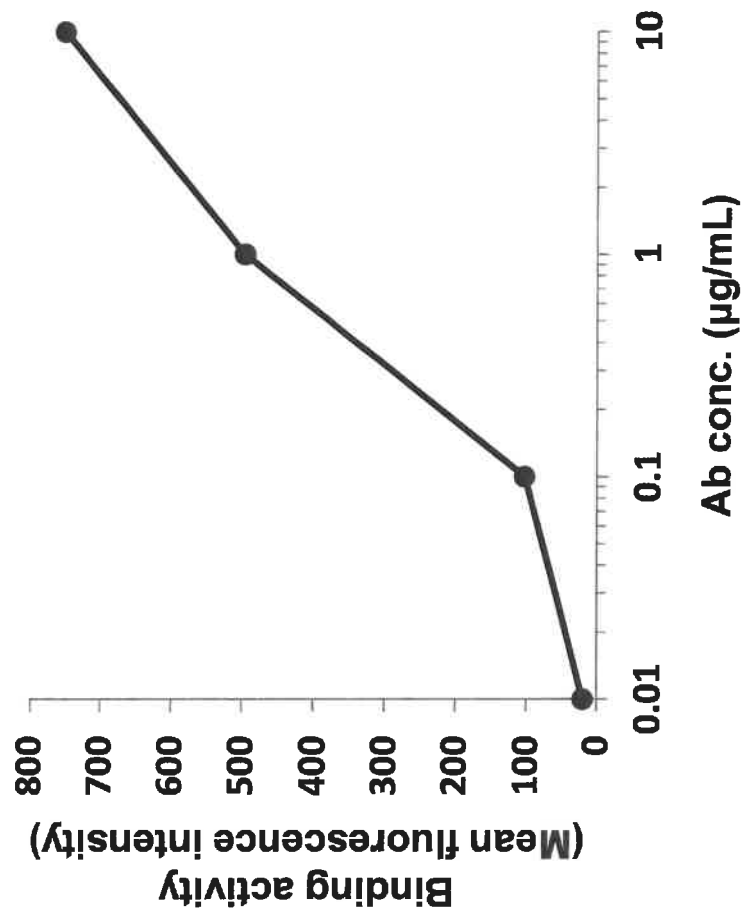


Figure 12

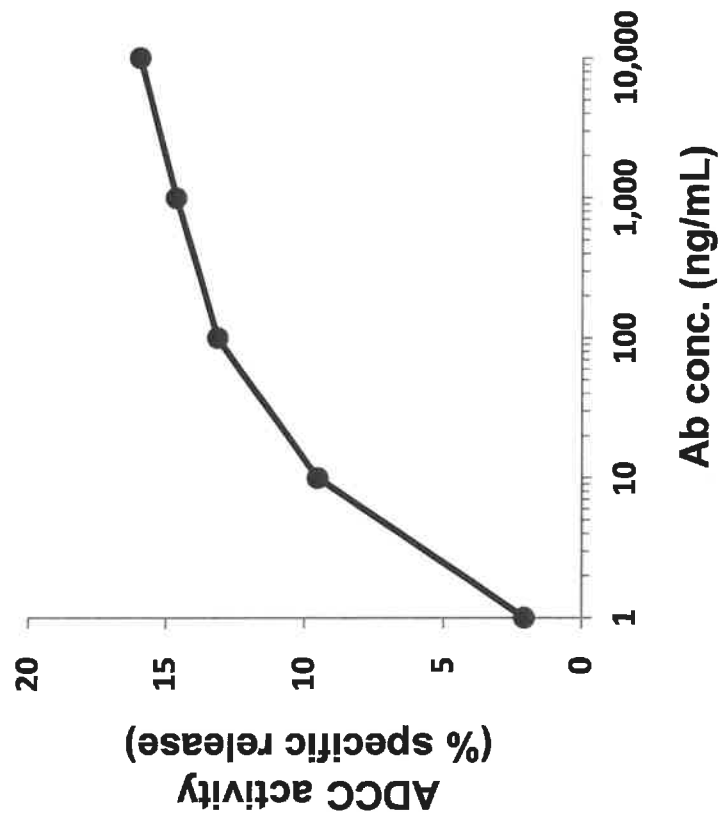


Figure 13

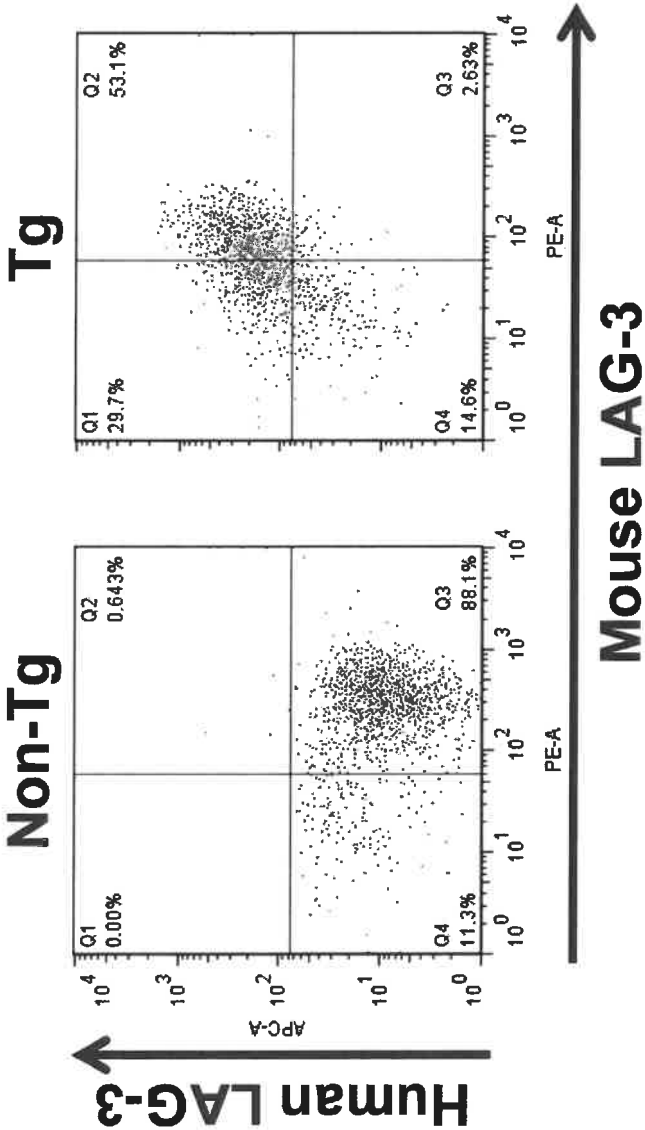


Figure 14

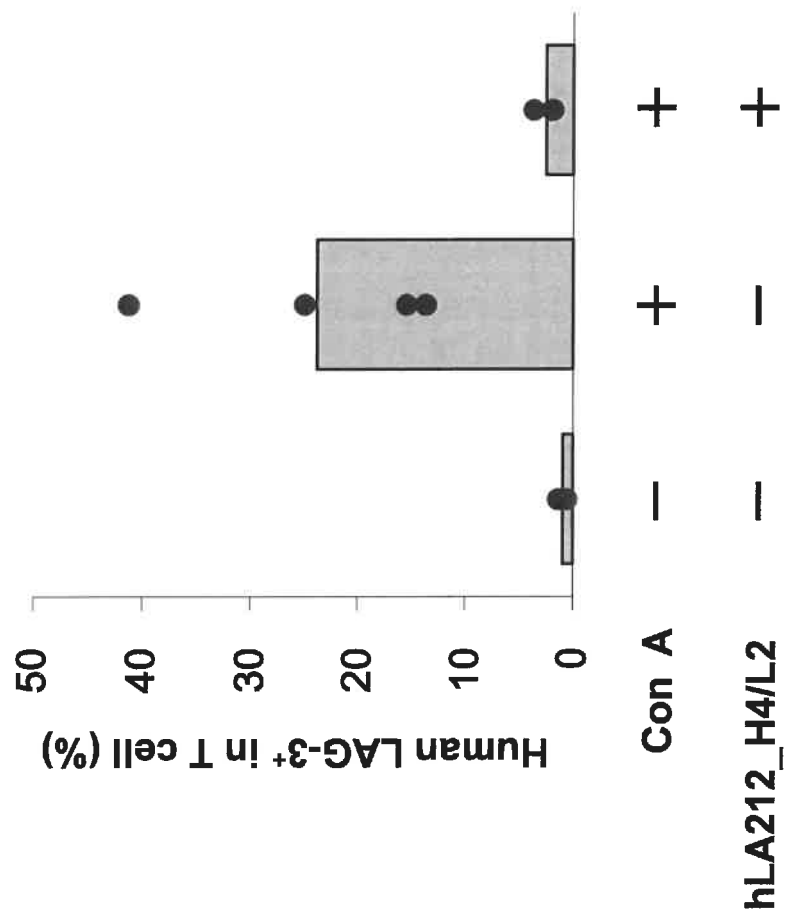


Figure 15

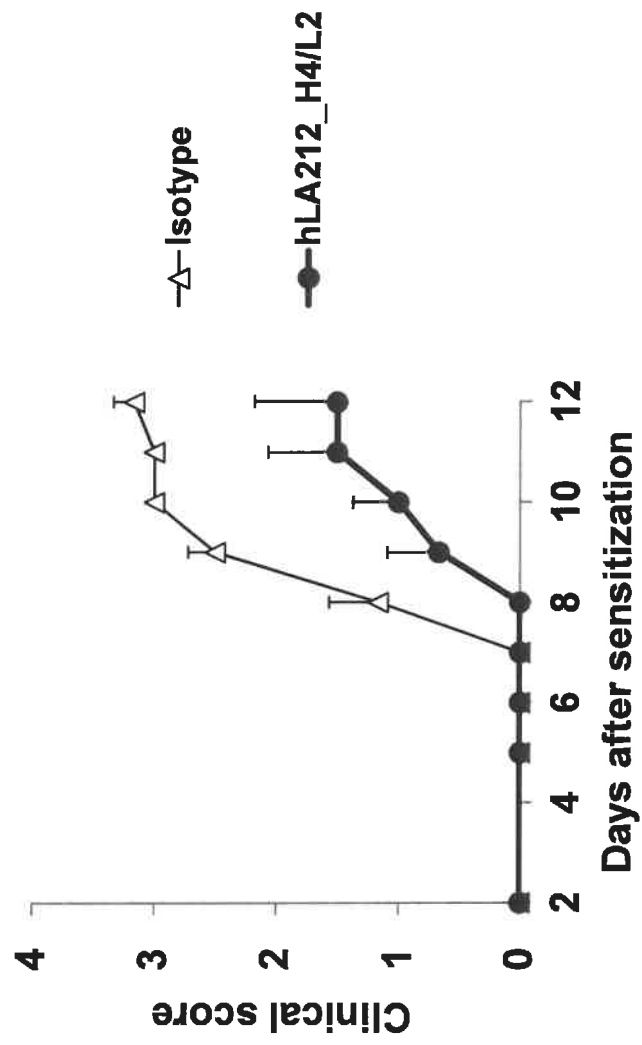


Figure 16

GAGGTAGAGCTGGTGGAGTCTGGGGGCGGCTTAGTGCAGCCTGGAAGGTCCATGAAACTCTCCT  
GTGCAGCCTCAGGATTCACTTTCAGAACCTATGGCATGGCCTGGGTCCGCCAGGCTCCAACGAAG  
GGTCTGGAGTGGGTCGCATCCATTAGTACTGGTGGTGGTAGCACTTACTATCGCGACTCCGTGAA  
GGGCCGATTCACTATCTCCAGAGATAATGCAAAAAGCACCCCTATACCTGCAAATGGACAGTCTGA  
GGTCTGAGGACACGGCCACTTATTACTGTACAACAGATCTAATTAACACCCGGGTATAGGGGGG  
TTTGCTTCTGGGGCCAAGGCACTCTGGTCACTGTCTCTTCA

variable region(1-366)

(SEQ ID No:1)

Figure 17

EVELVESGGGLVQPGRSMKLSCAASGFTFRITYGMAWVRQAPTKGLEWVASISTGGGSTYYRDSVKG  
RFTISRDNASTLYLQMDSLRSEDATYYCTTDLINYPGIGGFAFWGQGTLTVSS

variable region(1-122)

(SEQ ID No:2)

Figure 18

AACATTGTGATGACCCAGTCTCCCAAATCCATGTCCATATCAGTAGGAGACAGGGTCACCATGAAC  
TGCAAGGCCAGTCAGAATGTGTATAATAATATAGCCTGGTATCAACAGAAGCCAGGGAAATCTCC  
TAAACTGTTGATCTACTATGCATCTAACCGGTACACTGGGGTCCCTGATCGCTTACAGGCAGTGG  
CTCTGGGACAGATTTCACTCTCACCATCCATAGTGTGCAAGCTGAAGATGCAGCCTTTTATTACTGT  
CAGCGTCTTTACAATTCTCCTCCGACGTTCCGGTGGAGGCACCAAGCTGGAATTGAAACGGGCT

variable region(1-327)

(SEQ ID No:3)

Figure 19

NIVMTQSPKSMISVGDRTVMNCKASQNVYNNIAWYQQKPGKSPKLLIYYASNRYTGVPDRFTGSGS  
GDTFTLIHSVQAEDAAFYYCQRLYNPPTFGGGTKLELKRA

variable region(1-109)

(SEQ ID No:4)

Figure 20

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTCTCCT  
GTGCAGCCTCAGGATTCACTTACCGTAGCTATGTCATGGCCTGGGTCCGCCAGGCTCCAACGAGG  
GGTCTGGAGTGGGTCGCATCCATTAGTACTGGTGGTGGTAACACTTACTATCGAGACTCCGTGAA  
GGGCCGATTCACTATCTCCAGAGATAATGCAAAGAACACCCTATACCTACAAATGGACAGTCTGA  
GGTCTGAGGACACGGCCACTTATTACTGTGCAGAAGACATGAGTAATTCGGGATACGGGCTCTTT  
GATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCA

variable region(1-363)

(SEQ ID No:5)

Figure 21

EVQLVESGGGLVQPGRSLKLSCAASGFTYRSYVMAWVRQAPTRGLEWVASISTGGGNTYYRDSVKGR  
FTISRDNAKNTLYLQMDSLRS EDTATYYCAEDMSNSGYGLFDYWGQGVMVTVSS

variable region(1-121)

(SEQ ID No:6)

Figure 22

AACATTGTGATGACCCAGTCTCCCAAATCCATGTCCATATCAGTAGGAGACAGGGTCACCATGAAC  
TGCAAGGCCGGTCAGAATGTGGATAATAATATAGCCTGGTATCAAAGAAACCAGGGCAGTCTCC  
TAAACTGTTGATCTACTATGCATCTAACCAGGAACACTGGGGTCCCTGATCGCTTCACAGGCGGTGG  
ATATGGGACAGATTTCACTCTCACCATCAATAGTGTGCAAGCTGAAGATGCAGCCTTTTATTACTG  
TCAGCGTATTTCCAATTCTCCGTACACGTTTGGCGCTGGGACCGAGCTGGAAGTAAAACGGGCT

variable region(1-327)

(SEQ ID No:7)

Figure 23

NIVMTQSPKSMISVGDRTVMNCKAGQNVNNAWYQKKPGQSPKLLIYYASNRNTGVPDRFTGGG  
YGTDFLTINSVQAEDAAFYQCQRISNSPYTFGAGTELELKRA

variable region(1-109)

(SEQ ID No:8)

Figure 24

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCATGAACTCTCCT  
GTGTAGCCTCAGGATTCACCTTCAGTAACTATTACATGGCCTGGGTCCGCCAGGCTCCAACGAAGG  
GTCTGGAGTGGGTGCGATCCATTAGTACTGGTGGTGGTAACACTTACTATCGAGACTCCGTGAAG  
GGCCGATTCATCTCCAGAGATAATGCAAAAAGCACCTATACCTGCAAATGGACAGTCTGAG  
GTCTGAGGACACGGCCACTTATTACTGTGCAAGACCCCATATGGCTATAACTACGGTTGGTTTAC  
TTACTGGGGCCAAGGCACTCTGGTCACTGTCTCTTCA

variable region(1-363)

(SEQ ID No:9)

Figure 25

EVQLVESGGGLVQPGRSMKLSCVASGFTFSNYVMAWVRQAPTKGLEWVASISTGGGNTYYRDSVKG  
RFTISRDNASTLYLQMDSLRS EDTATYYCARPPYGYNYGWFTYWGQGLTVTVSS

variable region(1-121)

(SEQ ID No:10)

Figure 26

GACATCCAGATGACACAGTCTCCAGCTTCCCTGTCTGCATCTCTGGGAGAACTGTCACCATCGAA  
TGTCGAGCAAGTGAGGACATTCACAATGGTTTAGTATGGTATCAGCAGAAGCCAGGGAAATCTCC  
TCAGCTCCTGATCTATAATGCAAATAGTATGCATACTGGGGTCCCATCACGGTTCAGTGGCAGTGG  
ATCTGGTACACAGTATTCTCTCAAGATAAACAGCCTGCAGTCTGAAGATGTCGCAAGTTATTTCTG  
TCAACAGTATTACAATTATCCTCGGACGTTGGTGGAGGCACCAAGCTGGAATTGAAACGGGCT  
variable region(1-327)  
(SEQ ID No:11)

Figure 27

DIQMTQSPASLSASLGETVTIECRASEDIHNGLVWYQQKPGKSPQLLIYNANSMHTGVPSRFSGSGSG  
TQYSLKINSLQSEDVASYFCQQYYNYPRTFGGGTKLELKRA  
variable region(1-109)  
(SEQ ID No:12)

Figure 28

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTCTCCT  
GTGCAGCCTCAGGATTCATTATCGTACCTATGTCATGGCCTGGGTCCGCCAGGGTCCAACGCAG  
GGTCTGGAGTGGGTGCGATCCATTAGTACTGGTGGTGTTAGCACTTATTATCGAGACTCCGTGAA  
GGGCCGATTCACTATCTCCAGAGATAATGCAAAAAACACCCTATACTTGCAATGGACAGTCTGA  
GGTCTGAGGACACGGCCACTTATTACTGTGCAAAAGACATGTTGAATGGTTATAACTCTCAGGGG  
CTTTTTGATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCA  
variable region(1-369)  
(SEQ ID No:13)

Figure 29

EVQLVESGGGLVQPGRSLKLSAASGFTYRITYVMAWVRQGPTQGLEWVASISTGGVSTYYRDSVKGR  
FTISRDNAKNTLYLQMDSLRSEDATYYCAKDMLNGYNSQGLFDYWQGVMVTVSS  
variable region(1-123)  
(SEQ ID No:14)

Figure 30

AACATTGTGATGACCCAGTCTCCCAAATCCATGTCCATATCAGTGGGAGACAGGGTCACCATGAAC  
TGCAGGGCCAGTCAGAATGTGGATAATACTATAGCCTGGTATCAACAGAAACCAGGGCAGTCTCC  
TAAACTGTTGATCTACTTTGCATCTGACCGGTACACTGGGGTCCCTGATCGCTTCACAGGCGGTGG  
ATATGGGACAGATTTCACTCTCACCATCAATAGTGTGCAAGCTGAAGATGCAGCCTTTTATTACTG  
TCAGCGTATTTACAATTCTCCACTCACGTTTCGGTTCTGGGACCAAGCTGGAGATCAGACGGGCT  
variable region(1-327)  
(SEQ ID No:15)

Figure 31

NIVMTQSPKMSISVGDRVMTMNCRASQNVDNTIAWYQQKPGQSPKLLIYFASDRYTGVPDRFTGGG  
YGTDFTLTINSVQAEDAAFYYCQRIYNSPLTFGSGTKLEIRRA  
variable region(1-109)  
(SEQ ID No:16)

Figure 32

GAGGTGCAGCTGGTGAATCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTCTCCT  
GTGCAGCCTCAGGATTCACCTTCAGTTCCTATTACATGGCCTGGGTCCGCCAGGCTCCAACGAAGG  
GTCTGGAGTGGGTGCGATACATCAGTAATGGTGGTTATAGCACTTACTATCGAGACTCCGTGAAG  
GGCCGATTCATATCTCCAGAGAAAATGCAAAAAGCACCCCTTACCTGCAAATGGACAGTCTGAG  
GTCTGAGGACACGGCCACTTATTACTGTACAATCACAGATCATTCGGGGTACAGGTTTACTTACTG  
GGGCCAAGGCACTCTGGTCACTGTCTCTTCA  
variable region (1-357)  
(SEQ ID No:17)

Figure 33

EVQLVESGGGLVQPGRSLKLSAASGFTFSSYYMAWVRQAPTKGLEWVAYISNGGYSTYYRDSVKGR  
FTISRENAKSTLYLQMDSLRS EDTATYYCTITDHS GYRFTYWGQGTLVTVSS  
variable region (1-119)  
(SEQ ID No:18)

Figure 34

GACATCCAGATGACCCAGTCTCCTTCACTCCTGTCAGCATCTGTGGGAGACAGAGTCACTCTCAGC  
TGCAAAGCAAGTCAGAGTATTTACAACAGCTTAGCCTGGTATCAGCAAAAACCTGGAGAAGCTCC  
CAAACCTCATATATGATGCAAACAGTTTGCAAACGGGCATCCCATCAAGGTTCAAGTGGCAGTG  
GATCTGGTACAGATTTCACTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACATATTTCT  
GCCAGAAGTATTATAGCGGGAACACGTTTGGAGCTGGGACCAAGCTGGAAGTAAACGGGCT  
variable region (1-324)  
(SEQ ID No:19)

Figure 35

DIQMTQSPSLLSASVGDRVTLSCASQSIYNSLAWYQQKLGEAPKLLIYDANSLQTGIPSRFSGSGSGTD  
FTLTISLQPEDVATYFCQKYSGNTFGAGTKLELKRA  
variable region (1-108)  
(SEQ ID No:20)

Figure 36

gcctccggactctagagccaccATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCG  
GCGCGTACGGCGATATCGTGATGATTAAACGTACGGTGGCCGCCCCCTCCGTGTTTCATCTTCCCCC  
CCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTGTGCCTGCTGAATAACTTCTACCCCA  
GAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGTCCGGGAACTCCCAGGAGAGCG  
TGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGCAGCACCTGACCCTGAGCAAAGC  
CGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCCACCAGGGCCTGAGCTCCCCCGTC  
ACCAAGAGCTTCAACAGGGGGGAGTGTtaggggcccgtttaacgggggaggcta  
(SEQ ID No:21)

Figure 37

gcctccggactctagagccaccATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGG  
TGCTGAGCCAGGTGCAATTGTGCAGGCGGTTAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCC  
CCCTGGCACCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGAC  
TACTTCCCCGAACCCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTT  
CCCCGCTGTCTGCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAG  
CTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGA  
GAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAACTCCTGG  
GGGACCCCTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTG  
AGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT  
GGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTA  
CCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC  
AAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCAAAGCCAAAGGCCAGCC  
CCGGGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGC  
CTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCA  
GCCCCGAGAACAACCTACAAGACCACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAG  
CAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATG  
AGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAAtgagatatcgggcccgt  
ttaacgggggaggcta  
(SEQ ID No:22)

Figure 38

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCGAGGTGCA  
 GCTGGTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAAGGTCCCTGAAACTCTCCTGTGCAGCCT  
 CAGGATTCACCTACCGTAGCTATGTCATGGCCTGGGTCCGCCAGGCTCCAACGAGGGGTCTGGAG  
 TGGGTGCGATCCATTAGTACTGGTGGTGGTAACACTTACTATCGAGACTCCGTGAAGGGCCGATT  
 CACTATCTCCAGAGATAATGCAAAGAACACCCTATACCTACAAATGGACAGTCTGAGGTCTGAGG  
 ACACGGCCACTTATTACTGTGCAGAAGACATGAGTAATTCGGGATACGGGCTCTTTGATTACTGG  
 GGCCAAGGAGTCATGGTCACAGTCAGCTCAGCCTCCACCAAGGGGCCAAGCGTCTTCCCCCTGGC  
 ACCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC  
 CGAACCCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCCGCTG  
 TCCTGCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA  
 CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAG  
 CCCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAACTCCTGGGGGGACCC  
 TCAGTCTTCTCTTCCCCC AAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAT  
 GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT  
 GGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTC  
 AGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA  
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAACCAC  
 AGGTGTACACCCTGCCCCCATCCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTG  
 GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCGAGAACAA  
 ACTACAAGACCACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGT  
 GGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  
 AACCCTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAA

signal sequence(1-57), heavy chain variable region(58-420), heavy chain  
 constant region(421-1410)

(SEQ ID No:23)

Figure 39

MKHLWFFLLLVAAAPRWVLSEVQLVESGGGLVQPGRSLKLSCAASGFTYRSYVMAWVRQAPTRGLEW  
 VASISTGGGNTYYRDSVKGRFTISRDNKNTLYLQMDSLRSEDATYYCAEDMSNSGYGLFDYWQQG  
 VMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL  
 YSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD  
 TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN  
 GQPENNYKTTTPVLDSGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

signal sequence(1-19), heavy chain variable region(20-140), heavy chain  
 constant region(141-470)

(SEQ ID No:24)

Figure 40

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCAACATT  
 GTGATGACCCAGTCTCCCAAATCCATGTCCATATCAGTAGGAGACAGGGTCACCATGAACTGCAA  
 GGCCGGTCAGAATGTGGATAATAATATAGCCTGGTATCAAAAGAAACCAGGGCAGTCTCCTAAAC  
 TGTTGATCTACTATGCATCTAACCGGAACACTGGGGTCCCTGATCGCTTCACAGGCGGTGGATATG  
 GGACAGATTTCACTCTCACCATCAATAGTGTGCAAGCTGAAGATGCAGCCTTTTATTACTGTCAGC  
 GTATTTCCAATTCTCCGTACACGTTTGGCGCTGGGACCGAGCTGGAAGTGAAACGGGCTGTGGCC  
 GCCCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTG  
 TGCCTGCTGAATAACTTCTACCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCA  
 GTCCGGGAACTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTGAGC  
 AGCACCTGACCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGACCC  
 ACCAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:25)

Figure 41

MVLQTQVFISLLLWISGAYGNIVMTQSPKSMISVGDRTVMNCKAGQNVDNNIWYQKKPGQSPKL  
 LIYYASNRNTGVPDRFTGGGYGTDFTLTINSVQAEDAAFYQCQRISNSPYTFGAGTELELKRAVAAPSVF  
 IFPPSDEQLKSGTASVVCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKAD  
 YEKHKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence(1-20), light chain variable region(21-129), light chain  
 constant region(130-234)

(SEQ ID No:26)

Figure 42

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCGAAGTGCA  
 GCTGGTGGAATCTGGCGGCGGACTGGTGCAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCC  
 AGCGGCTTCACCTACCGGTCTTACGTGATGGCCTGGGTGCGCCAGGCCCCTGGAAAAGGACTGGA  
 ATGGGTGGGATCCATCAGCACCGGCGGAGGCAACACCTACTACCGGGATAGCGTGAAGGGCCGG  
 TTCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGA  
 GGACACCGCCGTGTACTATTGCGCCGAGGATATGAGCAACAGCGGCTACGGCCTGTTCGACTACT  
 GGGGCCAGGGAACCCCTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCAAGCGTCTTCCCCCTG  
 GCACCCTCCTCCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTT  
 CCCCAGAACCCGTGACCGTGAGCTGGAAGTCAAGCGCCCTGACCAGCGGCGTGACACCTTCCCCG  
 CTGTCCTGCAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG  
 GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT  
 GAGCCCCAAATCTTGTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGAACTCCTGGGGGG  
 ACCCTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC  
 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG  
 GCGTGGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGGGT  
 GGTGAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT  
 CCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGGGAA  
 CCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTG  
 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCCGAG  
 AACAACCTACAAGACCACCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC  
 ACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT  
 GCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAA

signal sequence(1-57), heavy chain variable region(58-420), heavy chain  
 constant region(421-1410)

(SEQ ID No:27)

Figure 43

MKHLWFFLLVAAAPRWVLSEVQLVESGGGLVQPGGSLRLSCAASGFTYRSYVMAWVRQAPGKGL  
 WVGSISSGGNTYYRDSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAEDMSNSGYGLFDYW  
 QGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS  
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKCDKHTCPPCPAPELLGGPSVFLFPPKP  
 KDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL  
 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES  
 NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

signal sequence(1-19), heavy chain variable region(20-140), heavy chain  
 constant region(141-470)

(SEQ ID No:28)

Figure 44

ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTGCTGAGCGAAGTGCA  
 GCTGGTGGGAATCTGGCGGCGGACTGGTGCAGCCTGGCGGATCTCTGAGACTGAGCTGTGCCGCC  
 AGCGGCTTCACCTACCGGTCTTACGTGATGGCCTGGGTGCGCCAGGCCCCCTGGAAAAGGACTGGA  
 ATGGGTGGCCAGCATCAGCACCGGCGGAGGCAACACCTACTACCGGGATAGCGTGAAGGGCCG  
 GTTCACCATCAGCCGGGACAACGCCAAGAACACCCTGTACCTGCAGATGGACAGCCTGCGGGCCG  
 AGGATACCGCCGTGTACTACTGTGCCGAGGACATGAGCAACAGCGGCTACGGCCTGTTCTGACTAC  
 TGGGGCCAGGGAACCCCTCGTGACCGTCAGCTCAGCCTCCACCAAGGGCCCCAAGCGTCTTCCCCCT  
 GGCACCCCTCTCAAGAGCACCTCTGGCGGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACT  
 TCCCCGAACCCGTGACCGTGAGCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCC  
 GCTGTCTGCACTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG  
 GGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAG  
 TTGAGCCCCAAATCTTGACAAAACTCACACATGCCCCACCCTGCCCAGCACCTGAACTCCTGGGGG  
 GACCCTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT  
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC  
 GCGTGAGGTGCATAATGCCAAGACAAAGCCCCGGGAGGAGCAGTACAACAGCACGTACCGG  
 GTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG  
 TCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCCAGCCCCGG  
 GAACCACAGGTGTACACCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAGGTGAGCCTGAC  
 CTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCCAGCCCG  
 AGAACAATAACAAGACCACCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGC  
 TCACCGTGGACAAGAGCAGGTGGCAGCAGGGCAACGTCTTCTCATGCTCCGTGATGCATGAGGCT  
 CTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCCGGCAAA

signal sequence(1-57), heavy chain variable region(58-420), heavy chain  
 constant region(421-1410)

(SEQ ID No:29)

Figure 45

MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGGSLRLSCAASGFTYRSYVMAWVRQAPGKGLE  
 WVASISTGGGNTYYRDSVKGRFTISRDNAKNTLYLQMDSLRAEDTAVYYCAEDMSNSGYGLFDYWG  
 QGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSS  
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVKPKCDKHTHTCPPCPAPPELLGGPSVFLFPPKP  
 KDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL  
 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES  
 NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

signal sequence(1-19), heavy chain variable region(20-140), heavy chain  
 constant region(141-470)

(SEQ ID No:30)

Figure 46

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGACATC  
 CAGATGACCCAGAGCCCTAGCAGCCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACCTGTA  
 AAGCCGGCCAGAACGTGGACAACAATATCGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCCTAA  
 GCTGCTGATCTACTACGCCAGCAACCGGAACACCGGCGTGCCAGCAGATTTTCTGGCAGCGGCT  
 CCGGCACCGACTTCACCCTGACAATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCC  
 AGAGAATCAGCAACAGCCCCCTACACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGCGTACGGT  
 GGCCGCCCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGT  
 GGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCC  
 CTGCAGTCCGGGAACTCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCC  
 TGAGCAGCACCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGT  
 GACCCACCAAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:31)

Figure 47

MVLQTQVFISLLLWISGAYGDIQMTQSPSSLSASVGDRTITCKAGQNVNINIAWYQQKPGQAPKLLI  
 YYASNRNTGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQRISNSPYTFGQGTKVEIKRTVAAPSVFIFP  
 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence(1-20), light chain variable region(21-129), light chain  
 constant region(130-234)

(SEQ ID No:32)

Figure 48

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGACATC  
 CAGATGACCCAGAGCCCTAGCAGCCTGAGCGCCAGCGTGGGCGACAGAGTGACCATCACCTGTA  
 AAGCCGGCCAGAACGTGGACAACAATATCGCCTGGTATCAGCAGAAGCCCGGCCAGAGCCCCAA  
 GCTGCTGATCTACTACGCCAGCAACCGGAACACCGGCGTGCCAGCAGATTTTCCGGCAGCGGCT  
 ACGGCACCGACTTCACCCTGACAATCAGCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCC  
 AGAGAATCAGCAACAGCCCCCTACACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGCGTACGGT  
 GGCCGCCCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGT  
 GGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCC  
 CTGCAGTCCGGGAACTCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCC  
 TGAGCAGCACCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGT  
 GACCCACCAAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:33)

Figure 49

MVLQTQVFISLLLWISGAYGDIQMTQSPSSLSASVGDRVITITCKAGQNVDNNIWYQQKPGQSPKLLI  
 YYASNRNTGVPSRFSGSGYGTDFLTISLQPEDFATYYCQRISNSPYTFGQGTKVEIKRTVAAPSVFIFP  
 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence(1-20), light chain variable region(21-129), light chain  
 constant region(130-234)

(SEQ ID No:34)

Figure 50

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCAACATC  
 CAGATGACCCAGAGCCCCAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACATGCAA  
 GGCCGGCCAGAACGTGGACAACAATATCGCCTGGTATCAGAAGAAGCCCGGCCAGTCCCCCAAG  
 CTGCTGATCTACTACGCCAGCAACCGGAACACCGGCGTGCCCGACAGATTTTCCGGCGGAGGCTA  
 CGGCACCGACTTCACCCTGACCATCAGCTCCCTGCAGCCCGAGGACTTCGCCTTCTACTACTGTCA  
 GCGGATCAGCAACAGCCCCTACACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGCGTACGGTG  
 GCCGCCCCCTCCGTGTTTCATCTTCCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTG  
 GTGTGCCTGCTGAATAACTTCTACCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCT  
 GCAGTCCGGGAATCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCCTG  
 AGCAGCACCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTGA  
 CCCACCAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:35)

Figure 51

MVLQTQVFISLLLWISGAYGNIQMTQSPSSLSASVGDRVITITCKAGQNVDNNIWYQKKPGQSPKLLI  
 YYASNRNTGVPPDRFSGGGYGTDFLTISLQPEDFAFYCQRISNSPYTFGQGTKVEIKRTVAAPSVFIFP  
 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence(1-20), light chain variable region(21-129), light chain  
 constant region(130-234)

(SEQ ID No:36)

Figure 52

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCGACATC  
 CAGATGACCCAGAGCCCCAGCAGCATGAGCATCAGCGTGGGCGACAGAGTGACCATGACCTGCA  
 AGGCCGGCCAGAACGTGGACAACAATATCGCCTGGTATCAGAAGAAGCCCCGGCCAGTCCCCAA  
 GCTGCTGATCTACTACGCCAGCAACCGGAACACCGGCGTGCCCGAGCAGATTTTCTGGCAGCGGCT  
 CCGGCACCGACTTCACCCTGACAATCAGCAGCGTGACGCCCAGGACTTCGCCACCTACTACTGCC  
 AGAGAATCAGCAACAGCCCCTACACCTTCGGCCAGGGCACCAAGCTGGAAGTGAAGCGTACGGT  
 GGCCGCCCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGT  
 GGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCC  
 CTGCAGTCCGGGAAGTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCC  
 TGAGCAGCACCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGT  
 GACCCACCAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:37)

Figure 53

MVLQTQVFISLLLWISGAYGDIQMTQSPSSMSISVGDRVMTCKAGQNVDNNAWYQKKPGQSPKL  
 LIYYASNRNTGVPSRFSGSGSGTDFTLTISVVQPEDFATYYCQRISNSPYTFGQGTKLELKRTVAAPSVFIF  
 PPSDEQLKSGTASVVCLLNFPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYE  
 KHKVYACEVTHQGLSSPVTKSFNREGC

signal sequence(1-20), light chain variable region(21-129), light chain  
 constant region(130-234)

(SEQ ID No:38)

Figure 54

ATGGTGCTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGCGTACGGCAACATC  
 CAGATGACCCAGAGCCCCAGCAGCATGAGCATCAGCGTGGGCGACAGAGTGACCATGACCTGCA  
 AGGCCGGCCAGAACGTGGACAACAATATCGCCTGGTATCAGAAGAAGCCCCGGCCAGTCCCCAA  
 GCTGCTGATCTACTACGCCAGCAACCGGAACACCGGCGTGCCCGACAGATTTTCCGGCGGAGGCT  
 ACGGCACCGACTTCACCCTGACAATCAGCAGCGTGACGCCCAGGACGCCGCCTTCTACTACTGTC  
 AGCGGATCAGCAACAGCCCCTACACCTTCGGCCAGGGCACCAAGCTGGAAGTGAAGCGTACGGT  
 GGCCGCCCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGT  
 GGTGTGCCTGCTGAATAACTTCTACCCCAGAGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCC  
 CTGCAGTCCGGGAAGTCCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGACAGCACCTACAGCC  
 TGAGCAGCACCTGACCCTGAGCAAAGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGT  
 GACCCACCAGGGCCTGAGCTCCCCCGTCACCAAGAGCTTCAACAGGGGGGAGTGT

signal sequence(1-60), light chain variable region(61-387), light chain  
 constant region(388-702)

(SEQ ID No:39)

Figure 55

MVLQTQVFISLLWISGAYGNIQMTQSPSSMSISVGDRVTMTCKAGQNVDNNAWYQKKPGQSPKL  
LIYYASNRNTGVPDRFSGGGYGTDFTLTISSVQPEDAAFYYCQRISNSPYTFGQGTKLELKRTVAAPSVFI  
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADY  
EKHKVYACEVTHQGLSSPVTKSFNRGEC

signal sequence(1-20), light chain variable region(21-129), light chain  
constant region(130-234)

(SEQ ID No:40)

Figure 56

**GFTFRTYGMA**

(SEQ ID No:41)

Figure 57

**SISTGGGSTYYRDSVKG**

(SEQ ID No:42)

Figure 58

**DLINYPGIGGFAF**

(SEQ ID No:43)

Figure 59

**KASQNVYNNIA**

(SEQ ID No:44)

Figure 60

**YASNRYT**

(SEQ ID No:45)

Figure 61

**QRLYNPPT**

(SEQ ID No:46)

Figure 62

**GFTYRSYVMA**

(SEQ ID No:47)

Figure 63  
**SISTGGGNTYYRDSVKG**  
(SEQ ID No:48)

Figure 64  
**DMSNSGYGLFDY**  
(SEQ ID No:49)

Figure 65  
**KAGQNVDDNIA**  
(SEQ ID No:50)

Figure 66  
**YASNRNT**  
(SEQ ID No:51)

Figure 67  
**QRISNSPYT**  
(SEQ ID No:52)

Figure 68  
**GFTFSNYMA**  
(SEQ ID No:53)

Figure 69  
**SISTGGGNTYYRDSVKG**  
(SEQ ID No:54)

Figure 70  
**PPYGYNYGWFTY**  
(SEQ ID No:55)

Figure 71  
**RASEDIHNGLV**  
(SEQ ID No:56)

Figure 72  
**NANSMHT**  
(SEQ ID No:57)

Figure 73  
**QQYYNYPRT**  
(SEQ ID No:58)

Figure 74  
**GFTYRTYVMA**  
(SEQ ID No:59)

Figure 75  
**SISTGGVSTYYRDSVKG**  
(SEQ ID No:60)

Figure 76  
**DMLNGYNSQGLFDY**  
(SEQ ID No:61)

Figure 77  
**RASQNV DNTIA**  
(SEQ ID No:62)

Figure 78  
**FASDRYT**  
(SEQ ID No:63)

Figure 79  
**QRIYNSPLT**  
(SEQ ID No:64)

Figure 80  
**GFTFSSYYMA**  
(SEQ ID No:65)

Figure 81  
**YISNGGYSTYYRDSVKG**  
(SEQ ID No:66)

Figure 82  
TDHSGYRFTY  
(SEQ ID No:67)

Figure 83  
KASQSIYNLSA  
(SEQ ID No:68)

Figure 84  
DANSLQT  
(SEQ ID No:69)

Figure 85  
QKYSGNT  
(SEQ ID No:70)

Figure 86  
CTCCAGAGTTCCAGGTCACGGTGACTGGC  
(SEQ ID No:71)

Figure 87  
TCAGTAACACTGTCCAGGACACCATCTC  
(SEQ ID No:72)

Figure 88  
TATACCGTCGACCTCTAGCTAGAGCTTGGC  
(SEQ ID No:73)

Figure 89  
GCTATGGCAGGGCCTGCCGCCCCGACGTTG  
(SEQ ID No:74)

Figure 90  
CCAGATGGGTGCTGAGCGAGGTGCAGCTGGTGGAGTCTGGGGGAGG  
(SEQ ID No:75)

Figure 91  
CTTGGTGGAGGCTGAGCTGACTGTGACCATGACTCCTTGGCCCCAG  
(SEQ ID No:76)

Figure 92

ATCTCCGGCGCGTACGGCAACATTGTGATGACCCAGTCTCCCAAATCC  
(SEQ ID No:77)

Figure 93

GGAGGGGGCGGCCACAGCCCGTTTCAGTTCCAGCTCGGTCCCAGC  
(SEQ ID No:78)

Figure 94

ATGTGGGAGGCTCAGTTCCTGGGCTTGCTGTTTC  
(SEQ ID No:79)

Figure 95

GCCCGAGCCCGAGCCCGAGCCGGAGCAGCTCTGA  
(SEQ ID No:80)

Figure 96

GAGTATGTGTTGACTGGTTGATAACTATCG  
(SEQ ID No:81)

Figure 97

GCCATGACAGATTAGCCATGTCTGCAGCAC  
(SEQ ID No:82)

Figure 98

CAGGACCTTTTCTAACCTCCCTTGGAGGGCTGGGGAGGCCCGGGCCATAGAGGAG  
(SEQ ID No:83)

Figure 99

CCTGGAGCCGAGGCAGCCAGCAGGTCTCAGCAGCTCCGCCCCGCCGCCGCCGCC  
(SEQ ID No:84)

Figure 100

ATGTGGGAGGCTCAGTTCCTGGGCTTGCTGTTTCTGCAGCCGCTTTGGGTGGCTCCAGTGAAGCC  
 TCTCCAGCCAGGGGCTGAGGTCCCGGTGGTGTGGGCCAGGAGGGGGCTCCTGCCAGCTCCCC  
 TGCAGCCCCACAATCCCCCTCCAGGATCTCAGCCTTCTGCGAAGAGCAGGGGTCACTTGGCAGCA  
 TCAGCCAGACAGTGGCCCCCGCTGCCGCCCCGGCCATCCCCTGGCCCCGGCCCTCACCCGG  
 CGGCGCCCTCCTCCTGGGGGCCAGGCCCCGCGCTACACGGTGTGAGCGTGGGTCCCGGAGG  
 CCTGCGCAGCGGGAGGCTGCCCTGCAGCCCCGCGTCCAGCTGGATGAGCGCGGCCGGCAGCGC  
 GGGGACTTCTCGCTATGGCTGCGCCCAGCCCCGGCGCGCGGACGCCGGCGAGTACCGCGCCGCGG  
 TGCACCTCAGGGACCGCGCCCTCTCCTGCCGCTCCGTCTGCGCCTGGGCCAGGCCTCGATGACTG  
 CCAGCCCCCAGGATCTCTCAGAGCCTCCGACTGGGTCAATTTGAACTGCTCCTTCAGCCGCCCTG  
 ACCGCCCAGCCTCTGTGCATTGGTTCCGGAACCGGGGCCAGGGCCGAGTCCCTGTCCGGGAGTCC  
 CCCCATCACCCTTAGCGGAAAGCTTCTCTTCTGCCCAAGTCAGCCCCATGGACTCTGGGCCCT  
 GGGGCTGCATCCTCACCTACAGAGATGGCTTCAACGTCTCCATCATGTATAACCTCACTGTTCTGG  
 GTCTGGAGCCCCCAACTCCCTTGACAGTGTACGCTGGAGCAGGTTCCAGGGTGGGGCTGCCCTGC  
 CGCCTGCCTGCTGGTGTGGGGACCCGGTCTTTCCTCACTGCCAAGTGGACTCCTCCTGGGGGAGG  
 CCCTGACCTCCTGGTGAAGTGGAGACAATGGCGACTTTACCCTTCGACTAGAGGATGTGAGCCAGG  
 CCCAGGCTGGGACCTACACCTGCCATATCCATCTGCAGGAACAGCAGCTCAATGCCACTGTCACAT  
 TGGCAATCATCAGTGACTCCCAAATCCTTGGGTCACTGGATCCCTGGGGAAGCTGCTTTGTG  
 AGGTGACTCCAGTATCTGGACAAGAACGCTTGTGTGGAGCTCTCTGGACACCCATCCCAGAGG  
 AGTTTCTCAGGACCTTGGCTGGAGGCACAGGAGGCCAGCTCCTTCCCAGCCTTGGCAATGCCA  
 GCTGTACCAGGGGGAGAGGCTTCTTGGAGCAGCAGTGTACTTCACAGAGCTGTCTAGCCAGGT  
 GCCCAACGCTCTGGGAGAGCCCCAGGTGCCCTCCCAGCAGGCCACCTCCTGCTGTTTCTATCCTT  
 GGTGTCCTTTCTCTGCTCCTTTTGGTGAAGTGGAGCCTTTGGCTTTACCTTTGGAGAAGACAGTGG  
 CGACCAAGACGATTTTCTGCCTTAGAGCAAGGGATTACCCTCCGCAGGCTCAGAGCAAGATAGA  
 GGAGCTGGAGCAAGAACCGGAGCCGGAGCCGGAGCCGGAACCGGAGCCCGAGCCCGAGCCCGA  
 GCCGGAGCAGCTC

(SEQ ID No:85)

Figure 101

MWEAQFLGLLFLQPLWVAPVKPLQPGAEPVWVAQEGAPAQLPCSPTIPLQDLSLLRRAGVTWQH  
 QPDSGPPAAAPGHPLAPGPHPAAPSSWGPRPRRYTVLSVGPGLRSGRLPLQPRVQLDERGRQRGD  
 FSLWLRPARRADAGEYRAAVHLRDRALSCRLRLRLGQASMTASPPGSLRASDWVILNCSFSRPRPAS  
 VHWFRNRGQGRVPVRESPPHHLAESFLFPQVSPMDSGPWGCILTYRDGFNVSIMYNLTVLGLPPT  
 PLTVYAGAGSRVGLPCRLPAGVGTRSFLLAKWTPPGGGPDLLVTGDNGDFTLRLEDVSSQAQAGTYTC  
 HIHLQEQQLNATVTLAIITVTPKSFSGPSGLKLLCEVTPVSGQERFVWSSLDTPSQRFSFSGPWLEAQE  
 AQLLSQPWQCQLYQGERLLGAAYFTLSSPGAQRSGRAPGALPAGHLLLFLILGVLSLLLLVTGAFGF  
 HLWRRQWRPRRFSALEQGIHPPQAQSKIEELEQEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEQL

(SEQ ID No:86)