FIG. 1

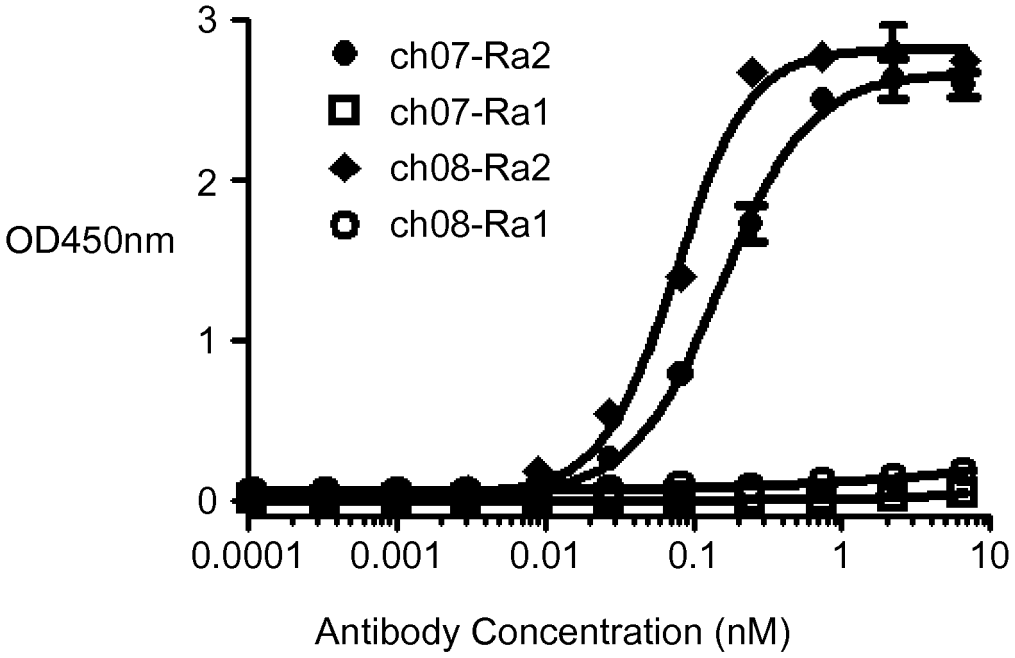

3
2
1
0
OD450nm
ch07-Ra2
ch07-Ra1
ch08-Ra2
ch08-Ra1
0.0001
0.001
0.01
0.1
1
10
Antibody Concentration (nM)

FIG. 2A

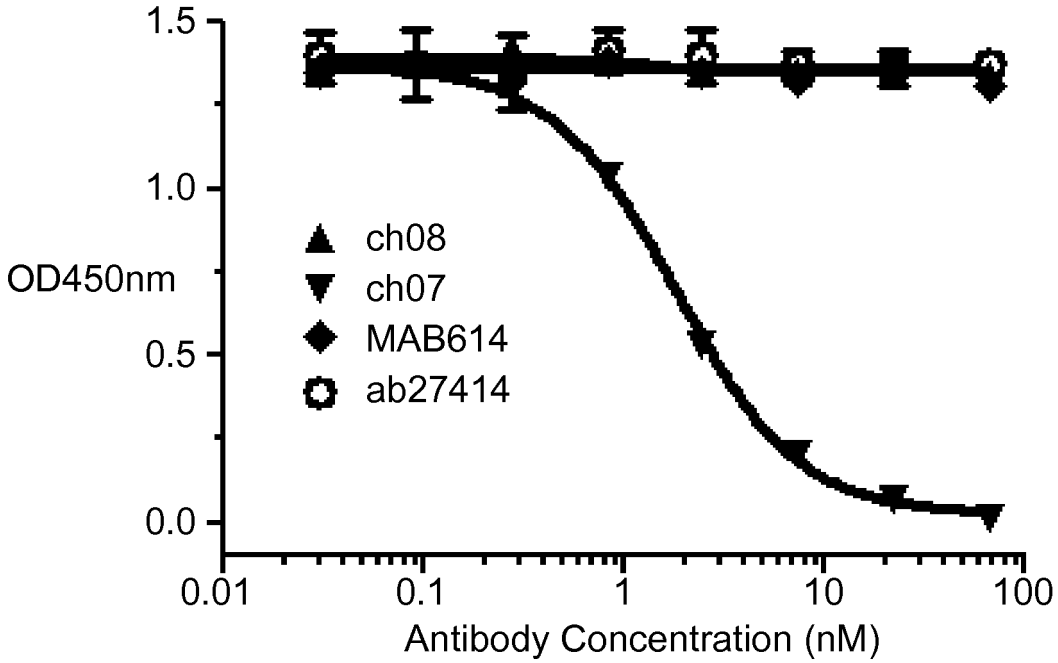

1.5
1.0
0.5
0.0
OD450nm
ch08
ch07
MAB614
ab27414
0.01
0.1
1
10
100
Antibody Concentration (nM)

FIG. 2B

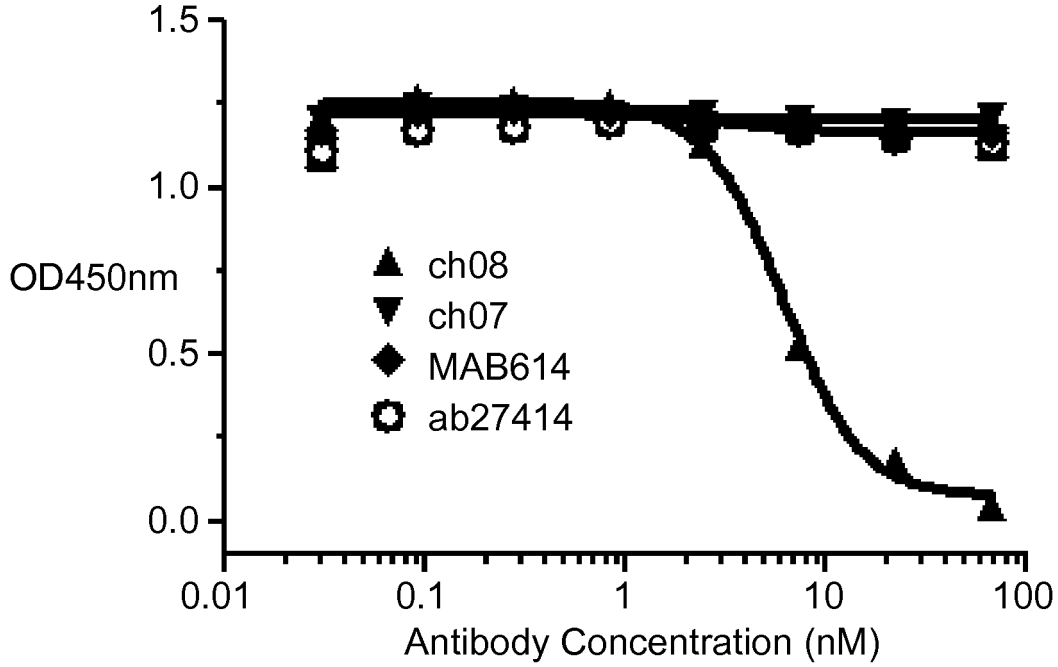

1.5
1.0
0.5
0.0
OD450nm
ch08
ch07
MAB614
ab27414
0.01
0.1
1
10
100
Antibody Concentration (nM)

FIG. 2C

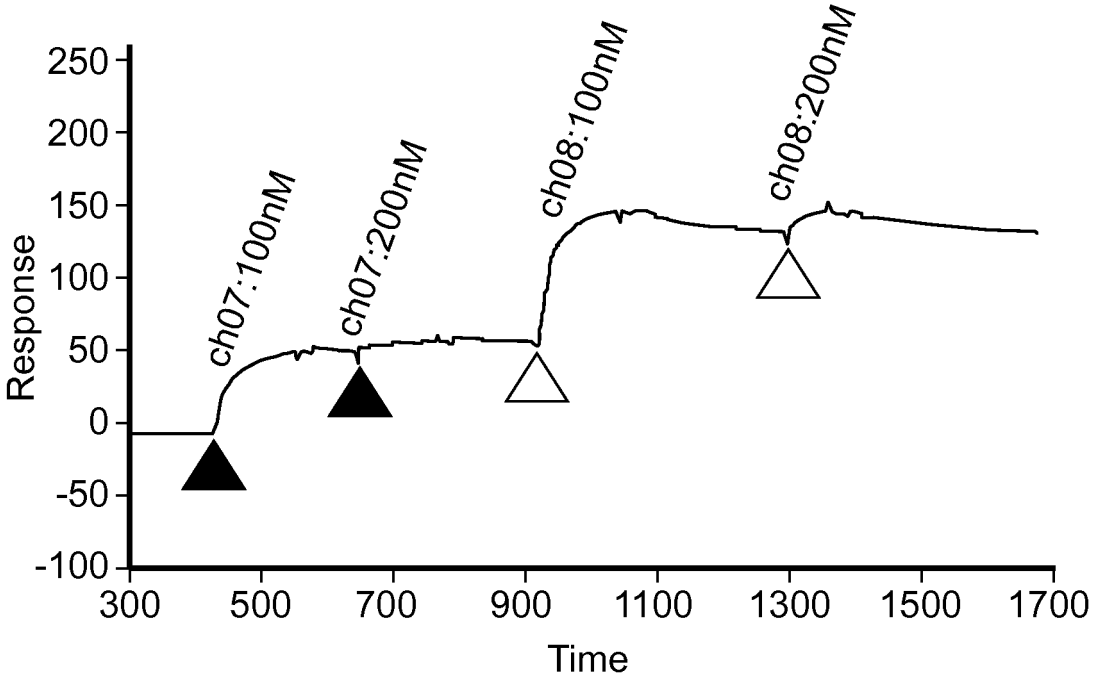

250
200
150
100
50
0
-50
-100
Response
ch07:100nM
ch07:200nM
ch08:100nM
ch08:200nM
300
500
700
900
1100
1300
1500
1700
Time

FIG. 3

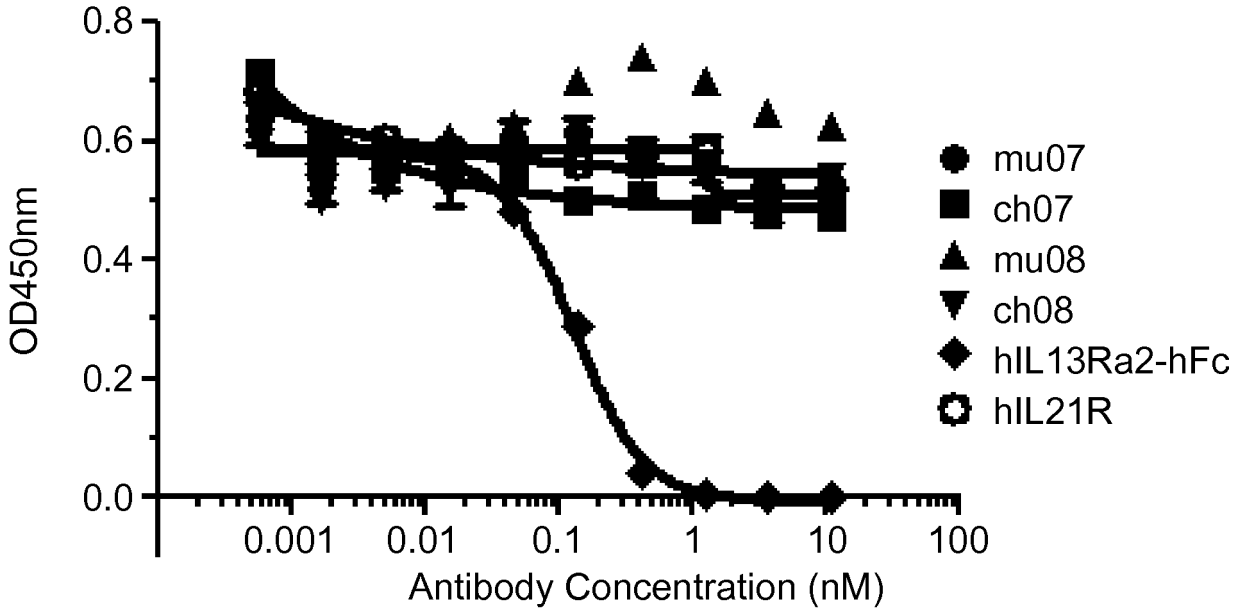

0.8
0.6
0.4
0.2
0.0
OD450nm
0.001
0.01
0.1
1
10
100
Antibody Concentration (nM)
mu07
ch07
mu08
ch08
hIL13Ra2-hFc
hIL21R

FIG. 4A

SEQ ID NO: 1 hu08-VH v1.0

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSS

SEQ ID NO: 2 hu08 HCDR1

SRNGMS

SEQ ID NO: 3 hu08 HCDR2

TVSSGGSYIYYADSVKG

SEQ ID NO: 4 hu08 HCDR3

QGTTALATRFFDV

SEQ ID NO: 5 hu08-VL v1.0

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYSASYRSTGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCQHHYSAPWTFGGGTKVEIK

SEQ ID NO: 6 hu08 LCDR1

KASQDVGTAVA

SEQ ID NO: 7 hu08 LCDR2

SASYRST

SEQ ID NO: 8 hu08 LCDR3

QHHYSAPWT

SEQ ID NO: 9 hu07-VH v1.0

EVQLVESGGGLVQPGGSLRLSCAASGFTFTKYGVHWVRQAPGKGLEWVAVKWAGGSTDYNSALMSRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

SEQ ID NO: 10 hu07 HCDR1

TKYGVH

SEQ ID NO: 11 hu07 HCDR2

VKWAGGSTDYNSALMS

SEQ ID NO: 12 hu07 HCDR3

DHRDAMDY

SEQ ID NO: 13 hu07-VL v1.0

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPGKAPKLLIYSTSNLASGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 14 hu07 LCDR1

TASLSVSSTYLH

SEQ ID NO: 15 hu07 LCDR2

STSNLAS

SEQ ID NO: 16 hu07 LCDR3

HQYHRSPLT

FIG. 4B

SEQ ID NO: 17 hu08-VH v1.0

GAGGTGCAGCTGGTGGAGTCTGGCGGCGGACTGGTGCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCC
TCCGGCTTCACCTTCAGTAGGAATGGCATGTCTTGGGTGAGGCAGGCCCCTGGCAAGGGCCTGGAGTGGGTGG
CCACCGTTAGTAGTGGTGGTAGTTACATCTACTATGCAGACAGTGTGAAGGGGCGGTTCACCATCTCCAGGGAC
AACGCCAAGAACTCCCTGTACCTCCAGATGAACTCCCTGAGGGCCGAGGATACCGCCGTGTACTACTGTGCCA
GACAAGGGACTACGGCACTAGCTACGAGGTTCTTCGATGTCTGGGGCCAGGGCACCCTGGTGACCGTGTCCTC
T

SEQ ID NO: 18 hu08-VL v1.0

GACATCCAGATGACCCAGTCCCCCTCTTCTCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACCTGTAAGGC
CAGTCAGGATGTAGGTACTGCTGTAGCCTGGTATCAGCAGAAGCCTGGCAAGGCTCCCAAGCTGCTGATCTACT
CGGCATCCTACCGGTCCACTGGCGTGCCTTCCAGATTCTCCGGCTCTGGCTCTGGCACCGATTTCACCCTGACC
ATCTCCTCCCTCCAGCCTGAGGATTTCGCCACCTACTACTGCCAGCACCATTATAGTGCTCCGTGGACGTTTGG
CGGCGGAACAAAGGTGGAGATCAAG

SEQ ID NO: 19 hu08-VH v1.1

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQ**T**P**D**K**R**LEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQM**S**SLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSS

SEQ ID NO: 20 hu08-VH v1.1

GAGGTGCAGCTGGTGGAGTCTGGCGGCGGACTGGTGCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCC
TCCGGCTTCACCTTCAGTAGGAATGGCATGTCTTGGGTGAGGCAGACCCCTGACAAGCGCCTGGAGTGGGTGG
CCACCGTTAGTAGTGGTGGTAGTTACATCTACTATGCAGACAGTGTGAAGGGGCGGTTCACCATCTCCAGGGAC
AACGCCAAGAACTCCCTGTACCTCCAGATGAGCTCCCTGAGGGCCGAGGATACCGCCGTGTACTACTGTGCCA
GACAAGGGACTACGGCACTAGCTACGAGGTTCTTCGATGTCTGGGGCCAGGGCACCCTGGTGACCGTGTCCTC
T

SEQ ID NO: 21 hu08-VL v1.1

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQ**I**PGKAPKLLIYSASYRSTGVP**D**RFSGSGSGTDF**S**FIISSLQ
PEDFATYYCQHHYSAPWTFGGGTKVEIK

SEQ ID NO: 22 hu08-VL v1.1

GACATCCAGATGACCCAGTCCCCCTCTTCTCTGTCTGCCTCTGTGGGCGACAGAGTGACCATCACCTGTAAGGC
CAGTCAGGATGTAGGTACTGCTGTAGCCTGGTATCAGCAGATCCCTGGCAAGGCTCCCAAGCTGCTGATCTACT
CGGCATCCTACCGGTCCACTGGCGTGCCTGACAGATTCTCCGGCTCTGGCTCTGGCACCGATTTCTCCTTTATC
ATCTCCTCCCTCCAGCCTGAGGATTTCGCCACCTACTACTGCCAGCACCATTATAGTGCTCCGTGGACGTTTGG
CGGCGGAACAAAGGTGGAGATCAAG

FIG. 4C

SEQ ID NO: 23 mu08 VH

EVQLVESGGDLVRPGGSLQLSCAASGFTFSRNGMSWVRQTPDRRLEWVATVSSGGSYIYYADSVKGRFTISRDNAR
NTLYLQMSSLKSEDTAMYYCARQGTTALATRFFDVWGAGTTVTVSS

SEQ ID NO: 24 mu08 VL

DIVMTQSHKFISTSVGDRVSITCKASQDVGTAVAWYQQIPGQSPKLLIYSASYRST
GIPDRFTGSGSGTDFSFIISSVQAEDLALYYCQHHYSAPWTFGGGTTLDIK

SEQ ID NO: 25 mu07 VH

QVQLKESGPGLVAPSQSLSINCTVSGFSLTKYGVHWIRQSPGKGLEWLGVKWAGGSTDYNSALMSRLTISKDNNKS
QVFLKMNSLQSDDSAMYYCARDHRDAMDYWGQGTSVTVSS

SEQ ID NO: 26 mu07 VL

QVVLTQSPAIMSASPGERVTMTCTASLSVSSTYLHWYHQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISS
MEAEDAATYYCHQYHRSPLTFGSGTKLELK

SEQ ID NO: 27 cyno IL-13Ra2

DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDNFKECTVEYELKYRNIGSETWTTIITKNLHYKDGFDLNKGIEAKIH
TLLPWQCTNGSEVQSSWAEATYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDRAL
QCVDYIKVDGQNIGCRFPYLESSDYKDFYICVNGSSETKPIRSSYFTFQLQNIVKPLPPVCLTCTQESLYEIKLKWSIPL
GPIPARCFVYEIEIREDDTTLVTTTVENETYTLKITNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEVEELLKKTLL
LFLLPFGFILILVIFVTGLLL

SEQ ID NO: 28 hu08 HC 1.0 L443C

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNY**K**TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS**C**SPGK

FIG. 4D

SEQ ID NO: 29 hu08 HC 1.0 Q347C

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP**C**VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS**L**SPGK

SEQ ID NO: 30 hu08 KC 1.0 kA111C

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYSASYRSTGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCQHHYSAPWTFGGGTKVEIKRTVA**C**PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 31 hu08 KC 1.0 kK183C

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYSASYRSTGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCQHHYSAPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLS**C**ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 32 hu08 KC 1.0 kK188C

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYSASYRSTGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCQHHYSAPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYE**C**HKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 33 hu08 HC 1.0 L443C/K392C

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNY**C**TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS**C**SPGK

SEQ ID NO: 34 hu08 HC 1.0 L443C/V422C

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNY**K**TTPPVLDSDGSFFLYSKLTVDKSRWQQGN**C**FSCSVMHEALHNHYTQKSLS**C**SPGK

FIG. 4E

SEQ ID NO: 35 hu07-HC-v1.5

EVQLVESGGGLVQPGGSLRLSCAASGF**SL**TKYGVHWVRQAPGKGLEWV**G**VKWAGGSTDYNSALMSRFTIS**K**DNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 36 hu07-LC-v1.7

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPG**SS**PKL**W**IYSTSNLASGVPSRFSGSGSGT**SY**TLTISS
LQPEDFATYYCHQYHRSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKAAYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 37 hu07 VH 1.1

EVQLVESGGGLVQPGGSLRLSCAASGF**SL**TKYGVHWVRQAPGKGLEWV**G**VKWAGGSTDYNSALMSR**L**TISRDNAK
SSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

SEQ ID NO: 38 hu07 VH 1.2

EVQLVESGGGLVQPGGSLRLSCAASGFTFTKYGVHWVRQAPGKGLEWVAVKWAGGSTDYNSALMSRFTIS**K**DNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

SEQ ID NO: 39 hu07 VH 1.3

EVQLVESGGGLVQPGGSLRLSCAASGF**SL**TKYGVHWVRQAPGKGLEWVAVKWAGGSTDYNSALMSRFTIS**K**DNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

SEQ ID NO: 40 hu07 VH 1.4

EVQLVESGGGLVQPGGSLRLSCAASGF**SL**TKYGVHWVRQAPGKGLEWVAVKWAGGSTDYNSALMSRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

SEQ ID NO: 41 hu07 VH 1.5

EVQLVESGGGLVQPGGSLRLSCAASGF**SL**TKYGVHWVRQAPGKGLEWV**G**VKWAGGSTDYNSALMSRFTIS**K**DNAK
NSLYLQMNSLRAEDTAVYYCARDHRDAMDYWGQGTLVTVSS

FIG. 4F

SEQ ID NO: 42 hu07 VL 1.1

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPG**SS**PKLLIYSTSNLASGVPSRFSGSGSGT**S**FTLTISSL
QPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 43 hu07 VL 1.2

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPGKAPKL**W**IYSTSNLASGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 44 hu07 VL 1.3

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPGKAPKLLIYSTSNLASGVPSRFSGSGSGTD**Y**TLTISSL
QPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 45 hu07 VL 1.4

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPGKAPKL**W**IYSTSNLASGVPSRFSGSGSGTD**Y**TLTISS
LQPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 46 hu07 VL 1.5

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPG**SS**PKL**W**IYSTSNLASGVPSRFSGSGSGT**S**FTLTISSL
QPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 47 hu07 VL 1.6

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPG**SS**PKLLIYSTSNLASGVPSRFSGSGSGT**SY**TLTISSL
QPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO: 48 hu07 VL 1.7

DIQMTQSPSSLSASVGDRVTITCTASLSVSSTYLHWYQQKPG**SS**PKL**W**IYSTSNLASGVPSRFSGSGSGT**SY**TLTISS
LQPEDFATYYCHQYHRSPLTFGGGTKVEIK

SEQ ID NO:49 hu08 heavy chain constant region

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

FIG. 4G

SEQ ID NO: 50 hu08-HC v1.0

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRNGMSWVRQAPGKGLEWVATVSSGGSYIYYADSVKGRFTISRDNAK
NSLYLQMNSLRAEDTAVYYCARQGTTALATRFFDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 51 hu08 LC v1.0

DIQMTQSPSSLSASVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYSASYRSTGVPSRFSGSGSGTDFTLTISSL
QPEDFATYYCQHHYSAPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKAAYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 52 hu08 LC constant region Km(3) D77A mutant

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAAY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 53 hu08 LC constant region 45, 77, 83 genus

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN**x**LQSGNSQESVTEQDSKDSTYSLSSTLTLSKA**x**Y
EKHK**x**YACEVTHQGLSSPVTKSFNRGEC

Wherein x at position 45 is A or V, x at position 77 is selected from the group consisting of A, G, I, V, L, R, S, T, Q, P, N, M, H and W, and x at position 83 is L or V.

SEQ ID NO: 54 hu08 LC constant region Km(3) D77 genus mutation

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA**x**Y
EKHKVYACEVTHQGLSSPVTKSFNRGEC

Wherein x at position 77 is selected from the group consisting of A, G, I, V, L, R, S, T, Q, P, N, M, H and W.

SEQ ID NO: 55 hu08 LC constant region Km(3) Wild Type

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKAD
YEKHKVYACEVTHQGLSSPVTKSFNRGEC