

FIG. 1**Minibodies****IAB57M1-1: SEQ ID No. 1**METDTLLLVLLLLVWPGSTG

1 EIVMTQSPAT LSVSPGERAT LSCKASQSVS NDVVWYQQKP GQAPRLLIYY ASNRYTGIPA 60
61 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ DYTSPTWFGQ GTKLEIKGST SGGSGGGSG 120
121 GGGSSQVQLV QSGAEVKKPG ASVKVSKAS GYTFTNYGMN WVRQAPGQGL EWMGWINTYT 180
181 GEPTYADDFK GRVTMTDTS TSTAYMELRS LRSDDTAVYY CARIGDSSPS DYWGQGLVT 240
241 VSSEPKSSDK THTCPPCPPC GGGSSGGSG GQPREPQVYT LPPSREEMTK NQVSLTCLVK 300
301 GFYPSDIAVE WESNGQPENN YKTPPVLD S DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE 360
361 ALHNHYTQKS LSLSPG 376

IAB57M2-2: SEQ ID No. 2METDTLLLVLLLLVWPGSTG

QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTS
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGLVTVSSGSTSGGSGGGSGGGSSSEIVMTQSPATLSVSPGER
ATLSCKASQSVSNDVVWYQQKPGQAPRLLIYYASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSP
WTFGQGTKLEIKEPKSSDKTHTCPPCPPCGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M1-3 SEQ ID No. 3METDTLLLVLLLLVWPGSTG

EIVMTQSPATLSVSPGERATLSCKASQSVSNDVVWYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPTWFGQGTKLEIKGSTSGGSGGGSGGGSSQVQLVQSGAEVKKPGASVKVSKASGYTF
TNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTSSTAYMELRSLRSDDTAVYYCARIGDSSPSD
YWGQGLVTVVSSEPKSSDKTHTCPPCPPCGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M2-4 SEQ ID No. 4METDTLLLVLLLLVWPGSTG

QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTS
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGLVTVSSGSTSGGSGGGSGGGSSSEIVMTQSPATLSVSPGER
ATLSCKASQSVSNDVVWYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSP
WTFGQGTKLEIKEPKSSDKTHTCPPCPPCGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M1-5 SEQ ID No. 5METDTLLLVLLLLVWPGSTG

EIVMTQSPATLSVSPGERATLSCKASQSVSNDVVWYQQKPGQAPRLLIYYASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPTWFGQGTKLEIKGSTSGGSGGGSGGGSSQVQLVQSGAEVKKPGASVKVSKASGYTF
TNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTSSTAYMELRSLRSDDTAVYYCARIGDSSPSD
YWGQGLVTVVSSEPKSSDKTHTCPPCPPCGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M2-6 SEQ ID No. 6METDTLLLVLLLLVWPGSTG

QVQLVQSGAEVKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTS
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGLVTVSSGSTSGGSGGGSGGGSSSEIVMTQSPATLSVSPGER
ATLSCKASQSVSNDVVWYQQKPGQAPRLLIYYASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSP
WTFGQGTKLEIKEPKSSDKTHTCPPCPPCGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M1-7 SEQ ID No. 7METDTLLLVLLLLVWPGSTG

EIVMTQSPATLSVSPGERATLSCKASQSVSNDVVWYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPTWFGQGTKLEIKGSTSGGSGGGSGGGSSQVQLVQSGAEVKKPGASVKVSKASGYTF
TNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTDTSSTAYMELRSLRSDDTAVYYCARIGDSSPSD

FIG. 1 Continued

YWGQGTTLVTVSSEPKSSDKHTHTCPPPCPGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
IAB57M2-8 SEQ ID No. 8
METDTLLLVVLLLWVPGSTG
QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTST
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGTTLVTVSSGSTSGGGSGGGSGGGSSSEIVMTQSPATLSVSPGER
ATLSCASQSVSNVWVYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSP
WTFGQGTKLEIKKPKSSDKHTHTCPPPCPGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M1-13 SEQ ID No. 9

METDTLLLVVLLLWVPGSTG
EIVMTQSPATLSVSPGERATLSCASQSVSNVWVYQQKPGQAPQLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPWTFGQGTKLEIKGSTSGGGSGGGSGGGSSQVQLVQSGAEVKKPGASVKVSCKASGYTF
ITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARIGDSSPSD
YWGQGTTLVTVSSEPKSSDKHTHTCPPPCPGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

IAB57M1-14 SEQ ID No. 10

METDTLLLVVLLLWVPGSTG
EIVMTQSPATLSVSPGERATLSCASQSVSNVWVYQQKPGQSPQLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPWTFGQGTKLEIKGSTSGGGSGGGSGGGSSQVQLVQSGAEVKKPGASVKVSCKASGYTF
ITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARIGDSSPSD
YWGQGTTLVTVSSEPKSSDKHTHTCPPPCPGGGSSGGSGGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

FIG. 2

Cys-diabodies**IAB57C1-9 SEQ ID No. 11**

METDTLLLVVLLLWVPGSTG
EIVMTQSPATLSVSPGERATLSCASQSVSNVWVYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPWTFGQGTKLEIKSGGGGQVQLVQSGAEVKKPGASVKVSCKASGYTFITNYGMNWVRQAPG
QGLEWMGWINTYTGEPTYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGTTLTVSSG
GCPPCPPC

IAB57C2-10 SEQ ID No. 12

METDTLLLVVLLLWVPGSTG
QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTST
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGTTLTVSSSGGGGEIVMTQSPATLSVSPGERATLSCASQSVSN
DVWVYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSPWTFGQGTKLEIKG
GCPPCPPC

IAB57C3-11 SEQ ID No. 13

METDTLLLVVLLLWVPGSTG
EIVMTQSPATLSVSPGERATLSCASQSVSNVWVYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTIS
LQSEDFAVYYCQQDYTSPWTFGQGTKLEIKGGSGGGGQVQLVQSGAEVKKPGASVKVSCKASGYTFITNYGMNWVRQ
APGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGTTLTV
SSGGCPPCPPC

IAB57C4-12 SEQ ID No. 14

METDTLLLVVLLLWVPGSTG
QVQLVQSGAEVKKPGASVKVSCKASGYTFITNYGMNWVRQAPGQGLEWMGWINTYTGEPTYADDFKGRVTMTTDTST
TAYMELRSLRSDDTAVYYCARIGDSSPSDYWGQGTTLTVSSGGGGGEIVMTQSPATLSVSPGERATLSCASQSV
SNVWVYQQKPGQAPRLLIYDASNRYTGIPARFSGSGSGTEFTLTISLQSEDFAVYYCQQDYTSPWTFGQGTKLE
IKGGCPPCPPC

FIG. 3 - Component sequences**LCDRs****SEQ ID No. 15 - LCDR1**

KASQSVSNDVVW

SEQ ID No. 16 - LCDR1

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Val Trp

SEQ ID No. 17 - LCDR2

YASNRYTG

SEQ ID No. 18 - LCDR2

Tyr Ala Ser Asn Arg Tyr Thr Gly

SEQ ID No. 19 - LCDR2

DASNRYTG

SEQ ID No. 20 - LCDR2

Asp Ala Ser Asn Arg Tyr Thr Gly

SEQ ID No. 21 - LCDR2

YASNRNTG

SEQ ID No. 22 - LCDR2

Tyr Ala Ser Asn Arg Asn Thr Gly

SEQ ID No. 23 - LCDR2

DASNRNTG

SEQ ID No. 24 - LCDR2

Asp Ala Ser Asn Arg Asn Thr Gly

SEQ ID No. 25 - LCDR3

QQDYTSPWT

SEQ ID No. 26 - LCDR3

Gln Gln Asp Tyr Thr Ser Pro Trp Thr

HCDRs**SEQ ID No. 27 - HCDR1**

KASGYTFTNYGMN

SEQ ID No. 28 - HCDR1

Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn

SEQ ID No. 29 - HCDR2

WINTYTGEPT

SEQ ID No. 30 - HCDR2

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr

SEQ ID No. 31 - HCDR3

ARIGDSSPSDY

FIG. 3 Continued

SEQ ID No. 32 - HCDR3

Ala Arg Ile Gly Asp Ser Ser Pro Ser Asp Tyr Asp Ala Ser Asn Arg Asn
Thr Gly

FRs**SEQ ID No. 33 - LFR2**

YQQKPGQAPRLLIY

SEQ ID No. 34 - LFR2

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr

SEQ ID No. 35 - LFR2

YQQKPGQAPQLLIY

SEQ ID No. 36 - LFR2

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gln Leu Leu Ile Tyr

SEQ ID No. 37 - LFR2

YQQKPGQSPQLLIY

SEQ ID No. 38 - LFR2

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr

Linkers**SEQ ID No. 39 - Linker**

SGGGG

SEQ ID No. 40 - Linker

Ser Gly Gly Gly Gly

SEQ ID No. 41 - Linker

GGSGGGG

SEQ ID No. 42 - Linker

Gly Gly Gly Ser Gly Gly Gly Gly

SEQ ID No. 43 - Linker

GSTSGGGSGGGSGGGSS

SEQ ID No. 44 - Linker

Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
Ser

SEQ ID No. 45 - Signal Peptide

1 METDTLLLWV LLLWVPGSTG 20

SEQ ID No. 46 - Signal Peptide

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly
Ser Thr Gly

FIG. 3 Continued

VH/VL

SEQ ID NO: 47 - Parental VH

QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWRQAPGGLEWMGWINTYTGEPYADDFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARI GDSSPSDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPEC

APELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO: 48 - Parental LC

EIVMTQSPATLSVSPGERATLSCASQSVSNDVVWYQQKPGQAPRLLIYYASNRYTGIPARFSGSGSGTEFTLTIS LQSEDFAVYYCQQDYTSPWTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 49 - Parental VL

EIVMTQSPATLSVSPGERATLSCASQSVSNDVVWYQQKPGQAPRLLIYYASNRYTGIPARFSGSGSGTEFTLTIS LQSEDFAVYYCQQDYTSPWTFGQGTKLEIK

FIG. 4

IAB57M1-7 annotated sequence with CDRs:

CDR definitions: North, IMGT, Kabat, CHOTIA

EIVMTQSPATLSVSPGERATLSC KASQSVSNDVVWYQQKPGQAPRLLIY DASNRNT GIPARFSGSGSGT
EFTLTISLQSEDFAVYYC QQDYTSPWT FGQGTKLEIKGSTSGGSGGGSGGGSSQVQLVQSGAEVKKPGA
SVKVSCKAS GYTFTNY GMNWRQAPGGLEWMGW INTYTGEP TYADDFKGRVTMTTDTSTSTAYMELRSLR
SDDTAVYYC ARIGDSSPSDY WGQGT LVTVSSSEPKSSDKTHTCPPCPGCGGSSGGSGGQPREPQVYTLPPS
REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPG (SEQ ID NO:142)

FIG. 5

IAB57M1-3, IAB57M2-6, Rovalpituzumab: variable regions alignment

Rovalpituzumab-HC	QVQLVQSGAEVKKFGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT
IAB57M1-3-HC	QVQLVQSGAEVKKFGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT
IAB57M2-6-HC	QVQLVQSGAEVKKFGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT

Rovalpituzumab-HC	YTGEPTYADDFKGRVTMTTDTSTSTAYMELASLRSDDTAVYYCARIGDSSPSDY
IAB57M1-3-HC	YTGEPTYADDFKGRVTMTTDTSTSTAYMELASLRSDDTAVYYCARIGDSSPSDY
IAB57M2-6-HC	YTGEPTYADDFKGRVTMTTDTSTSTAYMELASLRSDDTAVYYCARIGDSSPSDY

SEQ ID NO:

Rovalpituzumab-HC	WGQGTLLVTVSS	86
IAB57M1-3-HC	WGQGTLLVTVSS	87
IAB57M2-6-HC	WGQGTLLVTVSS	88

	1		53
Rovalpituzumab-LC	EIVMTQSPATLSVSPGERATLSCRASQSVSNQVWYQQKPKAPRLLIYYASN		
IAB57M1-3-LC	EIVMTQSPATLSVSPGERATLSCRASQSVSNQVWYQQKPKAPRLLIYYASN		
IAB57M2-6-LC	EIVMTQSPATLSVSPGERATLSCRASQSVSNQVWYQQKPKAPRLLIYYASN		
		SEQ ID NO:	
Rovalpituzumab-LC	RYTGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQDYTSFWTFGQGTLEIK		89
IAB57M1-3-LC	RYTGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQDYTSFWTFGQGTLEIK		90
IAB57M2-6-LC	RNTGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQDYTSFWTFGQGTLEIK		91

54

FIG. 6

SEQ ID NO. 50

Human-DLL3

MVSPRM3GLLSQTVILALIFLPQTRPAGVFELQIHSFGPGPGPGAPRSPCSARLPCLRFVCLKPGLSSEAAESPC
ALGAALSARGPVYTEQPGAPADLPLPDGLLQVFFRDANPGTFSPFIETWREELGDQIGGPAWSLLARVAGRRRLAA
GGPWARDIQRAGAWELRFSYRACEFFAVGTACTRLCKRPSAPSRCGPGRLRCPABLEDECEAPLVCRAGCSPENGF
EQPGECRCLLEGWTGPLCTVPVSTSSCLSPRGPSAATGCLVPGGPGCDGNPCANGSSCSETPRSFECTCPRGFVGLR
CEVSGVTCADGPCFNGGLCVGGADPDSAYICHCPFGFGQ3NCEKRVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAG
PRCEHDLDDCAGRACANGGTCVEGGGAHRCSALGFGGRDCRERADPCAARPCAANGGRCYAHF3GLVCACAPGYMGA
RCEFPVHPDGASALPAAPFGLRFGDFQRYLLPPALGLLVAAGVAGAALLLVHVRRRGH3QDAGSRLLAGTPEPSVHA
LPDALNNLRTQEGSGDGPSSSVDNRPEDVDPQGIYVISAPSIYAREVATPLFPPLHTGRAGQRQHLLFPYPSSILS
VK

FIG. 7

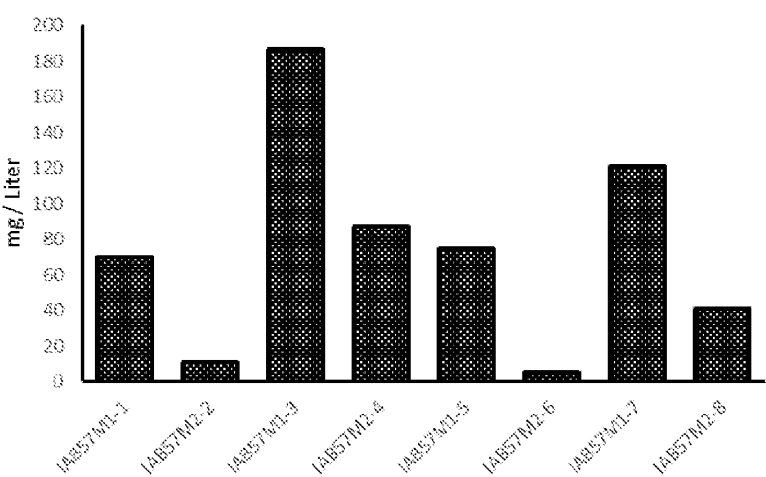


FIG. 8

Binding to recombinant antigen (ELISA):

DLL3 ELISA

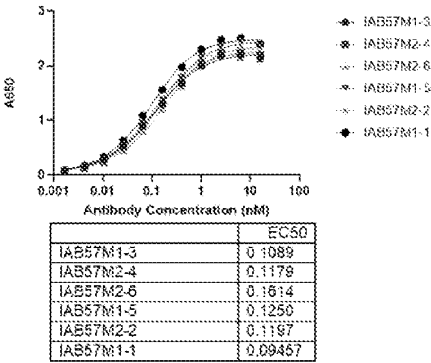
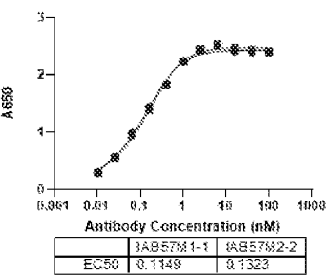


FIG. 8 Continued

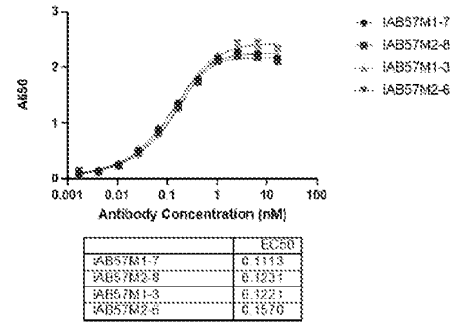


FIG. 9

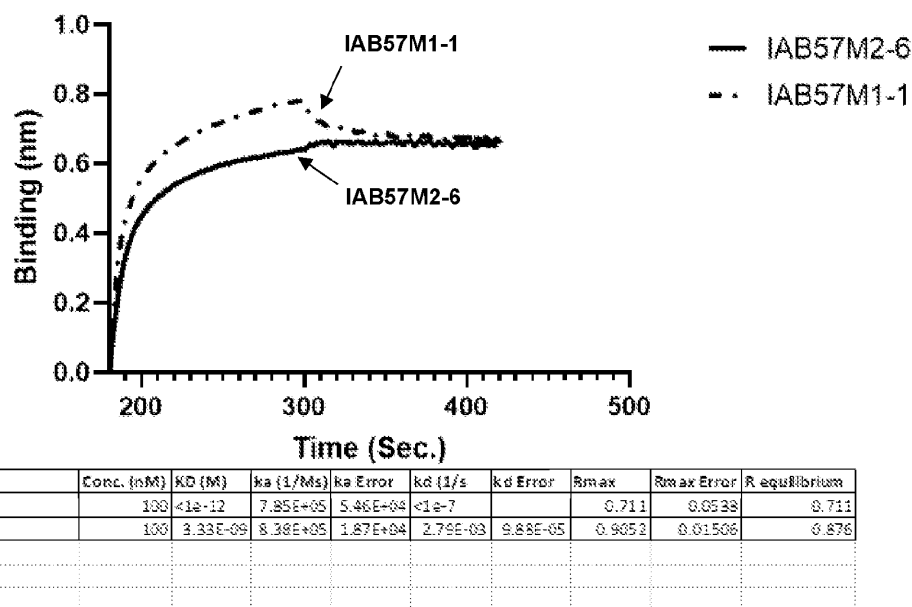
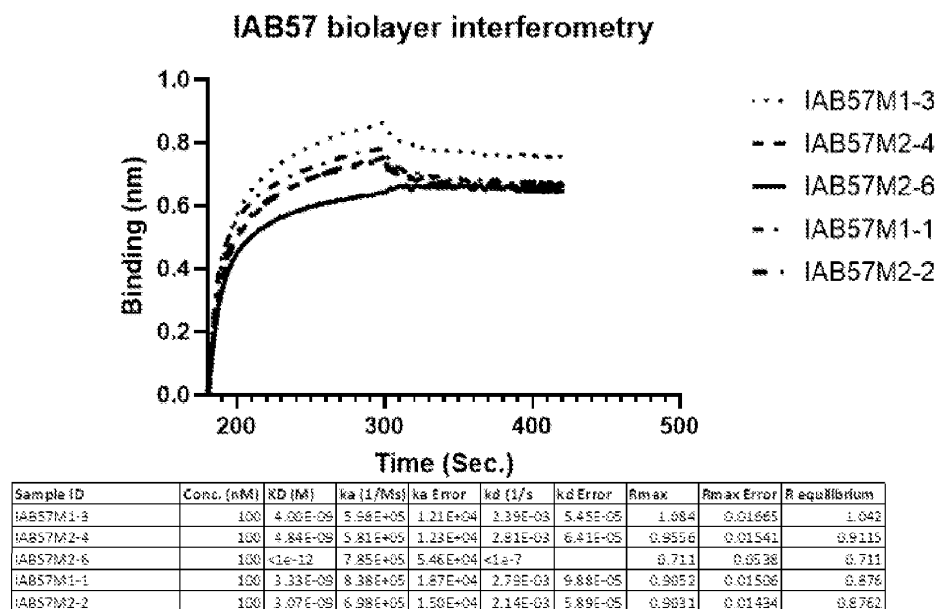
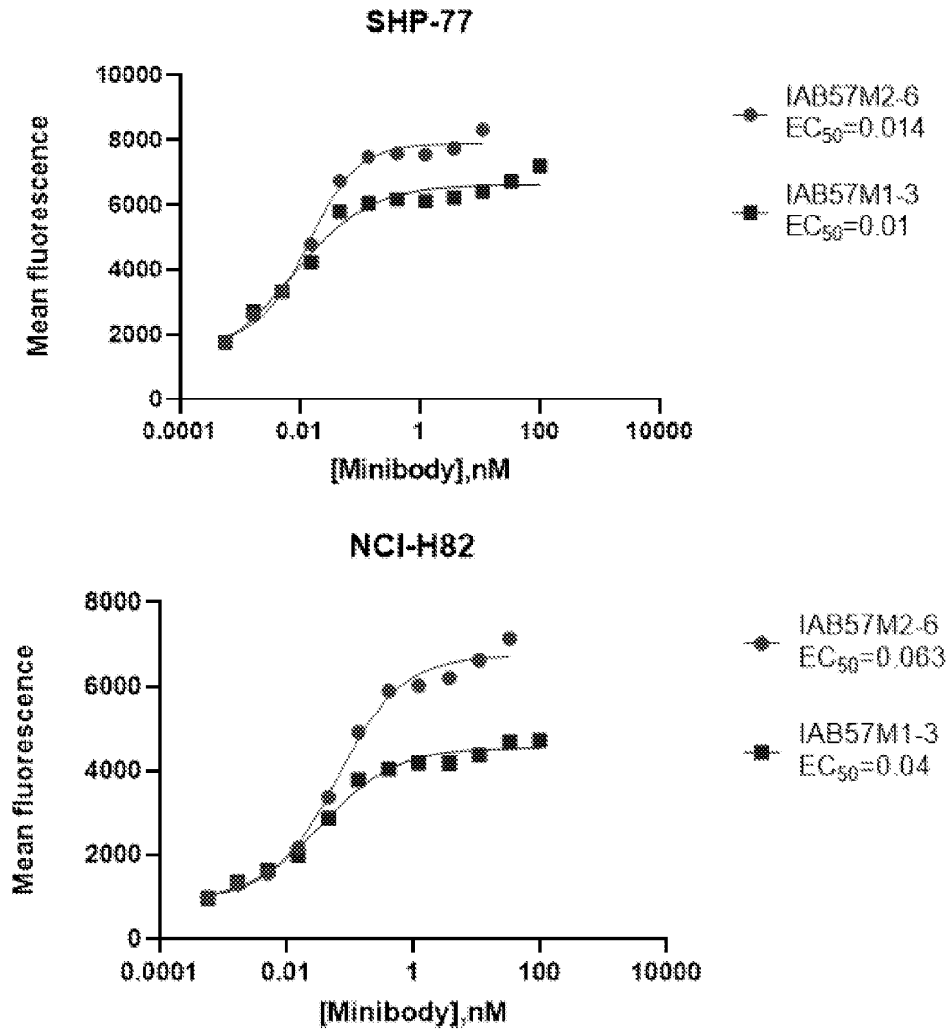


FIG. 10

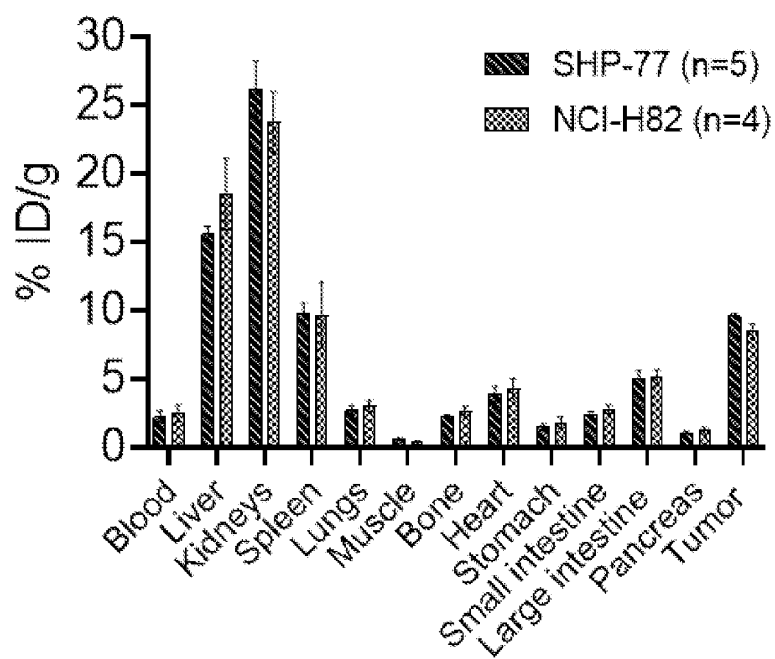
Binding to tumor cells (Flow Cytometry):



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FIG. 11

In-vivo biodistribution:

Biodistribution of ^{89}Zr -desferoxamine-IAB57M1-3 in NCr nude mice bearing SHP77 and NCI-H82 tumors

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FIG. 12

In-vivo biodistribution of ^{89}Zr -desferoxamine-IAB57M1-3, ^{89}Zr -desferoxamine-IAB57M1-13, and ^{89}Zr -desferoxamine-IAB57M1-14 in NCr nude mice bearing SHP77 and NCI-H82 tumors

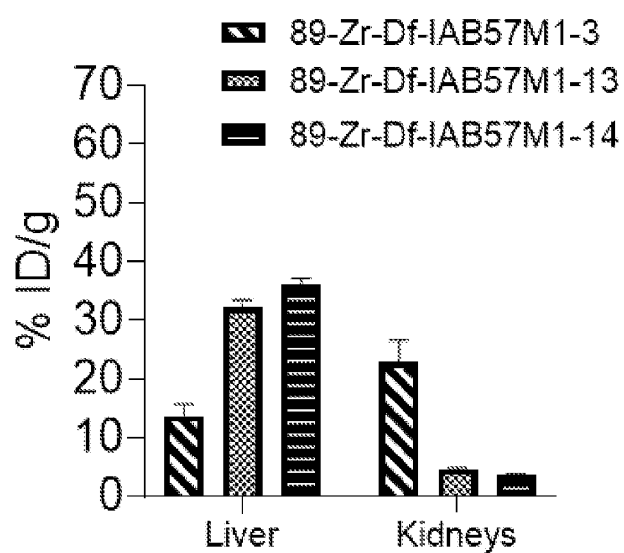


FIG. 13 Nucleic acids:

IAB57M1-1

SEQ ID No.: 51

ATGGAGACCGACACCCCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGGCAGCACCGGCGAGATCGTGA
TGACACAGAGCCCCGGCAGACTCAGCGTGAGTCCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGCCAAGCCCCCTAGACTGCTGATCTACTAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTACGCGGCAGCGGCAGCGGCACCGAGTTACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAAATTAAGGGCAGCACCTCTGGAGGCGGGTCGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGCAGCTGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGGTATACCTTCACCAACTACGGCATGAAGTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCG
ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCAACCCCAAGAGCTCCGACAAGACCCACACgTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M2-2

SEQ ID No.: 52

ATGGAGACCGATACCCCTGCTACTGTGGGTCTCCTACTGTGGGTGCCCCGGCAGCACCGGGCAAGTGCAGC
TGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCCGGCGCTAGCGTGAAGGTGAGCTGCAAGGCAAGCGGTGA
CACCTTCACCAACTACGGCATGAAGTGGGTGAGACAAGCCCCCGCCAAGGCCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGGCGAGCCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTTTACTACTGTGC
GAGAATCGGCGACAGCAGCCCTAGCGACTATTGGGGTCAAGGCACCTTGGTACTGTGTCAAGCGGCTCC
ACCTCCGGCGGCGGATCGGGCGGAGGAAGCGGTGGCGGCGGCAGCAGCGAGATCGTGATGACACAGAGCC
CCGCCACCTTAAGCGTTAGCCCCGGCGAGAGAGCAACCTTTCTTGCAAAGCTAGCCAAAGTGTGAGCAA
CGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCTAGACTGCTGATCTACTACGCTAGCAACAGA
TACACCGGCATCCCCGCTAGATTACGCGGCAGCGGCAGCGGCACCGAGTTCACCCTGACCATCAGCAGCC
TGCAGAGCGAGGACTTCGCTGTGTATTATTGCCAACAAGACTACACAAGCCCCCTGGACCTTCGGTCAAGG
GACCAAGCTGGAGATCAAGGAACCCCAAGAGCTCCGACAAGACCCACACgTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M1-3

SEQ ID No.: 53

ATGGAGACCGACACCCCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGGCAGCACCGGCGAGATCGTGA
TGACACAGAGCCCCGGCAGACTCAGCGTGAGTCCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGCCAAGCCCCCTAGACTGCTGATCTACGAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTACGCGGCAGCGGCAGCGGCACCGAGTTACCCCTGA

FIG. 13 Continued.

CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAAATTAAGGGCAGCACCTCTGGAGGCGGGTCGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGCAGCTGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGTATACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACC GCCTACATGGAGCTGAGAAGCCTGAGAAGCG
ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCGAACCCAAGAGCTCCGACAAGACCCACACgTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M2-4

SEQ ID No.: 54

ATGGAGACCGATACCCCTGCTACTGTGGGTCTCCTACTGTGGGTGCCCCGGCAGCACCGGGCAAGTGCAGC
TGGTGCAGAGCGGCGCGGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGGTGAGCTGCAAGGCAAGCGGTTA
CACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGGCAAGGCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGCGAGCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACC GCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTTTACTACTGTGC
GAGAATCGGCGACAGCAGCCCTAGCGACTATTGGGGTCAAGGCACCTTGGTTACTGTGTCAAGCGGCTCC
ACCTCCGGCGGCGGATCGGGCGGAGGAAGCGGTGGCGGCGCAGCAGCGAGATCGTGATGACACAGAGCC
CCGCCACCTTAAGCGTTAGCCCCGGCGAGAGAGCAACCCTTTCTTGCAAAGCTAGCCAAAGTGTGAGCAA
CGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCTAGACTGCTGATCTACGACGCTAGCAACAGA
TACACCGGCATCCCCGTAGATTAGCGGCGAGCGGCAGCGGCACCGAGTTACCCCTGACCATCAGCAGCC
TGCAGAGCGAGGACTTCGCTGTGTATTATTGCCAACAGACTACACAAGCCCCCTGGACCTTCGGTCAAGG
GACCAAGCTGGAGATCAAGGAACCCAAGAGCTCCGACAAGACCCACACgTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M1-5

SEQ ID No.: 55

ATGGAGACCGACACCCCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGGCAGCACCGGCGAGATCGTGA
TGACACAGAGCCCCGCGCACTCAGCGTGAGTCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCCCTAGACTGCTGATCTACTAC
GCTAGCAACAGAAACACCGGCATCCCCGTAGATTAGCGGCGAGCGGCAGCGGCACCGAGTTACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAAATTAAGGGCAGCACCTCTGGAGGCGGGTCGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGCAGCTGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGTATACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACC GCCTACATGGAGCTGAGAAGCCTGAGAAGCG

FIG. 13 Continued.

ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCGAACCCAAGAGCTCCGACAAGACCCACACGTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M2-6

SEQ ID No.: 56

ATGGAGACCGATACCTGCTACTGTGGGTCTCCTACTGTGGGTGCCCCGGCAGCACCCGGGCAAGTGCAGC
TGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGGTGAGCTGCAAGGCAAGCGGTTA
CACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCGGCCAAGGCCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGCGAGCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTTTACTACTGTGC
GAGAATCGGCGACAGCAGCCCTAGCGACTATTGGGGTCAAGGCACCTTGGTTACTGTGTCAAGCGGCTCC
ACCTCCGGCGGCGGATCGGGCGGAGGAAGCGGTGGCGGCGGCAGCAGCGAGATCGTGATGACACAGAGCC
CCGCCACCTTAAGCGTTAGCCCCGGCGAGAGAGCAACCTTTCTTGCAAAGCTAGCCAAAGTGTGAGCAA
CGAGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCTAGACTGCTGATCTACTACGCTAGCAACAGA
AACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGCGGCACCGAGTTCACCCTGACCATCAGCAGCC
TGCAGAGCGAGGACTTCGCTGTGTATTATTGCCAACAAAGACTACACAAGCCCCTGACCTTCGGTCAAGG
GACCAAGCTGGAGATCAAGGAACCCAAGAGCTCCGACAAGACCCACACgTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M1-7

SEQ ID No.: 57

ATGGAGACCGACACCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGGCAGCACCCGGCGAGATCGTGA
TGACACAGAGCCCCGCGACACTCAGCGTGAGTCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCCCTAGACTGCTGATCTACGAC
GCTAGCAACAGAAACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGCGGCACCGAGTTACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAAATTAAGGGCAGCACCTCTGGAGGCGGGTGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGCAGCTGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGGTATACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCG
ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCGAACCCAAGAGCTCCGACAAGACCCACACGTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

FIG. 13 Continued

IAB57M2-8

SEQ ID No.: 58

ATGGAGACCGATACCCTGCTACTGTGGGTCTCCTACTGTGGGTGCCCCGGCAGCACCGGGCAAGTGCAGC
TGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGGTGAGCTGCAAGGCAAGCGGTTA
CACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCGGCCAAGGCCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGCGAGCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTTTACTACTGTGC
GAGAATCGGCGACAGCAGCCCTAGCGACTATTGGGGTCAAGGCACCTTGGTTACTGTGTCAAGCGGCTCC
ACCTCCGGCGGGGATCGGGCGGAGGAAGCGGTGGCGGCGGCAGCAGCGAGATCGTGATGACACAGAGCC
CCGCCACCTTAAGCGTTAGCCCCGGCGAGAGAGCAACCCTTTCTTGCAAAGCTAGCCAAAGTGTGAGCAA
CGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCTAGACTGCTGATCTACGACGCTAGCAACAGA
AACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGCGGCACCGAGTTCACCCTGACCATCAGCAGCC
TGCAGAGCGGAGGACTTCGCTGTGTATTATTGCCAACAAAGACTACACAAGCCCCCTGGACCTTCGGTCAAGG
GACCAAGCTGGAGATCAAGGAACCCAAGAGCTCCGACAAAGACCCACACGTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCCCTCCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57C1-9

SEQ ID No.: 59

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTCCTGTGGGTGCCCCGGTAGCACCGGCGAGATCGTGA
TGACACAGAGCCCCGCGACCCTCAGCGTCAGTCCCGGCGAGAGAGCCACGCTGAGCTGCAAGGCATCTCA
GAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCTAGACTGCTGATCTACGAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGCGGCACCGAGTTCACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCTGTGTACTACTGCCAACAAAGACTACACAAGCCCCCTGGAC
CTTCGGGCAAGGCACCAAACTGGAATTAAGAGCGGAGGTGGTGGGCAAGTGCAGCTGGTGCAGAGCGGC
GCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAAGTGAGCTGCAAGGCCTCCGGATACACCTTCACCAACT
ACGGCATGAACTGGGTGAGACAAGCCCCCGGCCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACAC
CGGCGAGCCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACACAAGCACAAGCACC
GCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTGTACTATTGCGCGCGGATCGGCGACA
GCAGCCCTAGCGACTACTGGGGCCAAGGCACCCTGGTTACCGTGAGCAGCGGCGGCTGCCCCCCTGCCC
ACCCTGCTGA

IAB57C2-10

SEQ ID No.: 60

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTCCTGCTGTGGGTTCGGGATCCACCGGCCAAGTGCAGC
TGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGGTAAGCTGCAAGGCTAGCGGGTA
CACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGGCCAAGGCCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCTGTGTACTACTGCGC
TCGCATCGGCGACAGCAGCCCTAGCGACTACTGGGGGCAAGGCACCCTTGTACCCGTGAGCTCGAGCGGT
GGCGGCGGTGAGATCGTGATGACACAGAGCCCCGCTACACTGAGCGTGAGCCCCGGCGAGAGGCCACGC
TGAGCTGCAAAGCCTCTCAGAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCC
TAGACTGCTGATCTACGACGCTAGCAACAGATACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGC

FIG. 13 Continued

GGCACCAGATTACCCCTGACCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTGTACTATTGCCAACAAG
ACTACACAAGCCCCCTGGACCTTCGGCCAAGGAACCAAGCTGGAGATCAAGGGCGGCTGCCCCCCTGCCC
ACCCGTGCTGA

IAB57C3-11**SEQ ID No.: 61**

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTGCTCCTGTGGGTGCCCCGTAGCACC GGCGAGATCGTGA
TGACACAGAGCCCCGCGACCCTCAGCGTCAGTCCCGGCGAGAGAGCCACGCTGAGCTGCAAGGCATCTCA
GAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCCCTAGACTGCTGATCTACGAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTACGCGGCAGCGGCAGCGGCACCGAGTTACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCTGTGTACTACTGCCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGGCAAGGCACCAAAGCTGGAATTAAGGGCGGAGGTAGCGGAGGTGGTGGGCAAGTGCAGCTGGTG
CAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGTGAGCTGCAAGGCCTCCGGATACACCT
TCACCAACTACGGCATGAAGTGGGTGAGACAAGCCCCCGGCCAAGGCCTGGAGTGGATGGGCTGGATCAA
CACCTACACCGGCGAGCCACCTACGCCGACGACTTCAGGGCAGAGTGACCATGACCACCGACACAAGC
ACAAGCACC GCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCCGTGTACTATTGCGCGCGGA
TCGGCGACAGCAGCCCTAGCGACTACTGGGGCCAAGGCACCCTGGTTACCGTGAGCAGCGGCGGCTGCCC
CCCTGCCCACCTGCTGA

IAB57C4-12**SEQ ID No.: 62**

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTCCTGCTGTGGGTTCGGGATCCACCGGCCAAGTGCAGC
TGGTGCAAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGAAGGTAAGCTGCAAGGCTAGCGGGTA
CACCTTCACCAACTACGGCATGAAGTGGGTGAGACAAGCCCCCGGCCAAGGCCTGGAGTGGATGGGCTGG
ATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAGGGCAGAGTGACCATGACCACCGACA
CAAGCACAAGCACC GCCTACATGGAGCTGAGAAGCCTGAGAAGCGACGACACCGCTGTGTACTACTGCGC
TCGCATCGGCGACAGCAGCCCTAGCGACTACTGGGGGCAAGGCACCCTTGTCACCGTGAGCTCGGGGGGC
GGAAGCGGTGGCGGCGGTGAGATCGTGATGACACAGAGCCCCGCTACACTGAGCGTGAGCCCCGGCGAGA
GAGCCACGCTGAGCTGCAAAGCCTCTCAGAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGG
CCAAGCCCCCTAGACTGCTGATCTACGACGCTAGCAACAGATACACCGGCATCCCCGCTAGATTACGCGGC
AGCGGCAGCGGCACCGAGTTCACCCCTGACCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTGTACTATT
GCCAACAAGACTACACAAGCCCCCTGGACCTTCGGCCAAGGAACCAAGCTGGAGATCAAGGGCGGCTGCCC
CCCTGCCCACCTGCTGA

IAB57M1-13**SEQ ID No.: 63**

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGCGAGCACC GGCGAGATCGTGA
TGACACAGAGCCCCGCGACACTCAGCGTGAGTCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAGCCCCCTCAACTGCTGATCTACGAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTACGCGGCAGCGGCAGCGGCACCGAGTTACCCCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAATTAAGGGCAGCACCTCTGGAGGCGGTCGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGCAGCTGGTGCAGAGCGGCGCCGAGGTGAAGAAGCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGGTATACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCG
ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCGAACCCAAGAGCTCCGACAAGACCCACACGTGTCCCCCTTGCCCTCCTTGT

FIG. 13 Continued

GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

IAB57M1-14

SEQ ID No.: 64

ATGGAGACCGACACCCTGCTGCTGTGGGTGCTCCTACTGTGGGTGCCCCGGCAGCACCGGCGAGATCGTGA
TGACACAGAGCCCCGCGACACTCAGCGTGAGTCCCGGCGAGAGAGCGACGCTCAGCTGCAAGGCAAGCCA
AAGCGTGAGCAACGACGTGGTGTGGTATCAGCAGAAGCCCGGCCAAAGCCCTCAACTGCTGATCTACGAC
GCTAGCAACAGATACACCGGCATCCCCGCTAGATTGAGCGGCAGCGGCAGCGGCACCGAGTTCACCTGA
CCATCAGCAGCCTGCAGAGCGAGGACTTCGCCGTTTACTACTGTCAACAAGACTACACAAGCCCCCTGGAC
CTTCGGCCAAGGCACCAAGCTGGAAATTAAGGGCAGCACCTCTGGAGGCGGGTCGGGCGGAGGATCGGGA
GGCGGCGGAAGCAGCCAAGTGAGCTGGTGCAGAGCGGCGCGGAGGTGAAGAAGCCCGGCGCTAGCGTGA
AGGTATCTTGCAAGGCTAGCGGGTATACCTTCACCAACTACGGCATGAACTGGGTGAGACAAGCCCCCGG
CCAAGGCCTGGAGTGGATGGGCTGGATCAACACCTACACCGGCGAGCCACCTACGCCGACGACTTCAAG
GGCAGAGTGACCATGACCACCGACACAAGCACAAGCACCGCCTACATGGAGCTGAGAAGCCTGAGAAGCG
ACGACACCGCTGTGTATTATTGCGCGCGGATCGGCGACAGCAGCCCTAGCGACTACTGGGGACAAGGCAC
CCTGGTTACCGTGAGCAGCGAACCCAAGAGCTCCGACAAGACCCACACGTGTCCCCCTTGCCCTCCTTGT
GGCGGAGGAAGCTCCGGAGGCGGAAGCGGAGGACAGCCTAGGGAGCCCCAGGTGTATACCTCCCCCT
CCAGGGAAGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTCGTGAAGGGCTTTTATCCCTCCGATAT
CGCCGTGGAGTGGGAGAGCAACGGCCAGCCTGAGAACAATTACAAGACCACCCCCCTGTGCTGGACTCC
GATGGCAGCTTCTTCTGTATTCCAAGCTGACCGTCGACAAGTCCAGGTGGCAACAGGGCAACGTCTTCA
GCTGCAGCGTGATGCACGAGGCCCTGCACAATCACTACACCAGAAGTCCCTCTCCCTGAGCCCCGGCTG
A

FIG. 14

Unique IgG sequences (with allotypes and isoallotypes):

IgG1:

SEQ ID No.: 65

IGHG1*01

GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 66

IGHG1*03

GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 67

IGHG1*04

GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

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FIG. 14 Continued

SEQ ID No.: 68

IGHG1*07

GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEGLHNHYTQKSLSLSPGK

IgG2:

SEQ ID No.: 69

IGHG2*01

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 70

IGHG2*06

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDISVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 71

IGHG2*15

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

IgG3:

SEQ ID No.: 72

IGHG3*01

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNRTQKSLSLSPGK

SEQ ID No.: 73

IGHG3*03

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFCSS
VMHEALHNRTQKSLSLSPGK

SEQ ID No.: 74

IGHG3*06

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNRTQKSLSLSPGK

SEQ ID No.: 75

IGHG3*08

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNRTQKSLSLSPGK

SEQ ID No.: 76

IGHG3*13

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQEGNIFSCS
VMHEALHNRTQKSLSLSPGK

SEQ ID No.: 77

IGHG3*14

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNRYTQKSLSLSPGK

SEQ ID No.: 78

IGHG3*15

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNRYTQKSLSLSPGK

FIG. 14 Continued.

SEQ ID No.: 79
IGHG3*17
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAMEWESSGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 80
IGHG3*20
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQRENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 81
IGHG3*22
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNHYTQKSLSLSPGK

SEQ ID No.: 82
IGHG3*23
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNIFSCS
VMHEALHNHYTQKSLSLSPGK

IgG4:
SEQ ID No.: 83
IGHG4*01
GQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS
VMHEALHNHYTQKSLSLSLGK

SEQ ID No.: 84
IGHG4*03
GQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCS
VMHEALHNHYTQKSLSLSLGK

SEQ ID No.: 85
IGHG4*05
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCS
VMHEALHNHYTQKSLSLSLGK