

## Figure 1

## SEQUENCE ID NO: 1

|                                                                         |    |     |     |
|-------------------------------------------------------------------------|----|-----|-----|
|                                                                         | 40 | 50  | 60  |
| MDTSR LGVLL SLPVL LQLAT GGSSP RSGVL LRGCP THCHC EPDGR MLLRV DCSDL GLSEL |    |     |     |
|                                                                         | 90 | 100 | 110 |
| PSNLS VFTSY LDLSM NNISQ LLPNP LPSLR FLEEL RLAGN ALTYI PKGAF TGLYS LKVLM |    |     |     |
|                                                                         |    |     | 180 |
| LQNNQ LRHVP TEALQ NLRSL QSLRL DANHI SYVPP SCFSG LHSLR HLWLD DNALT EIPVQ |    |     |     |
|                                                                         |    |     | 240 |
| AFRSL SALQA MTLAL NKIHH IPDYA FGNLS SLVVL HLHNN RIHSL GKKCF DGLHS LETLD |    |     |     |
|                                                                         |    |     | 300 |
| LNYYN LDEFP TAIRT LSNLK ELGFH SNNIR SIPEK AFVGN PSLIT IHFYD NPIQF VGRSA |    |     |     |
|                                                                         |    |     | 360 |
| FQHLP ELRTL TLNGA SQITE FPDLT GTANL ESLTL TGAQI SSLPQ TVCNQ LPNLQ VLDLS |    |     |     |
|                                                                         |    |     | 420 |
| YNLLE DLPSF SVCQK LQKID LRHNE IYEIK VDTFQ QLLSL RSLNL AWNKI AIIHP NAFST |    |     |     |
|                                                                         |    |     | 480 |
| LPSLI KDLDS SNLLS SFPIT GLHGL THLKL TGNHA LQSLI SSENF PELKV IEMPY AYQCC |    |     |     |
|                                                                         |    |     | 540 |
| AFGVC ENAYK ISNQW NKGDN SSMDL LHKKD AGMFQ AQDER DLEDF LLDPE EDLKA LHSVQ |    |     |     |
|                                                                         |    |     | 600 |
| CSPSP GPFPK CEHLL DGWLI RIGVW TIAVL ALTCN ALVTS TVFRS PLYIS PIKLL IGZIA |    |     |     |
|                                                                         |    |     | 660 |
| AVNML TGVSS AVLAG VDAFT FGSFA RHGAW WENGW GCHVI GFLSI FASES SVFLL TLAAL |    |     |     |
|                                                                         |    |     | 720 |
| ERGFV VKYSA KFETK APFSS LKVII LLCAL LALTM AAVPL LGGSK YGASP LCLPL PFGEF |    |     |     |
|                                                                         |    |     | 780 |
| STMGY MVALI LLNSL CFLMM TIAYT KLYCN LDKGD LENIW DCSMV KHIAL LLFTN CILNC |    |     |     |
|                                                                         |    |     | 840 |
| PVAFV SFSSL INLTF ISPEV IKFIL LVVVP LPACL NPLLY ILFNP HFKEF LVSLR KQTYV |    |     |     |
|                                                                         |    |     | 900 |
| WTRSK HPSLM SINSF DVEKQ SCDST QALVT FTSSS ITYDL PPSSV PSPAY PVTES CHLSS |    |     |     |
| VAFVP CL                                                                |    |     |     |

**Figure 2****Sequence ID NO: 2**

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                                30          40          50
MRPSG TAGAA LLALL AALCP ASRAL EEKKV CQGTS NKLTQ LGTFE DHFLS
                                100
LQRMF NNCEV VLGNL EITYV QRNYD LSFLK TIQEV AGYVL IALNT VERIP
LENLQ IIRGN MYZEN SYALA VLSNY DANKT GLKEL PMRNL QEILH GAVRF
                                200
SNNPA LCNVE SIQWR DIVSS DFLSN MSMDF QNHLG SCQKC DPSCP NGSCW
GAGEE NCQKL TKIIC AQQCS GRCRG KSPSD CCHNQ CAAGC TGPPE SDCLV
                                300
CRKFR DEATC KDTCP PLMLY NPTTY QMDVN PEGKY SFGAT CVKKC PRNYV
VTDHG SCVRA CGADS YEMEE DGVKR CKKCE GPCRK VCNGI GIGEF KDSLS
                                400
INATN IKHFK NCTSI SGDLH ILPVA FRGDS FTHTP PLDPQ ELDIL KTVKE
ITGFL LIQAW PENRT DLHAF ENLEI IRGRT KQHGO FSLAV VSLNI TSLGL
                                500
RSLKE ISDGD VIISG NKNLC YANTI NWKKL FGTSG QKTKI ISNRG ENSCK
ATGQV CHALC SPEGC WGPEP RDCVS CRNVS RGREC VDKCN LLEGE PREFV
                                600
ENSEC IQCHP ECLPQ AMNIT CTGRG PDNCI QCAHY IDGPH CVKTC PAGVM
GENNT LVWKY ADAGH VCHLC HPNCT YGCTG PGLEG CPTNG PKIPS IATGM
                                700
VGALL LLLVV ALGIG LFMRR RHIVR KRTLK RLLQE RELVE PLTPS GEAPN
QALLR ILKET EFKKI KVLGS GAFGT VYKGL WIPEG EKVKI PVAIK ELREA
                                800
TSPKA NKEIL DEAYV MASVD NPHVC RLLGI CLTST VQLIT QLMPF GCLLD
YVREH KDNIG SQYLL NWCYQ IAKGM NYLED RRLVH RDLAA RNVLV KTPQH
                                900
VKITD FGLAK LLGAE EKEYH AEGGK VPIKW MALES ILHRI YTHQS DVWSY
GVTWV ELMTF GSKPY DGIPA SEISS ILEKG ERLPQ PPICT IDVYM IMVKC
                                1000
WMIDA DSRPK FRELI IEFSE MARDP QRYLV IQGDE RMHLP SPTDS NFYRA
LMDEE DMDDV VDADE YLIPQ QGFFS SPSTS RTPLL SLSA TSNNS TVACI
                                1100
DRNGL QSCPI KEDSF LQRYE SDPTG ALTED SIDDT FLPVP EYINQ SVPKR
PAGSV QNPVY HNQPL NPAPS RDPHY QDPHS TAVGN PEYLN TVQPT CVNST
                                1200
FDSPA HWAQK GSHQI SLDNP DYQQD FFPKE AKPNG IFKGS TAENA EYLRV
APQSS EFIGA

```

Figure 3 a)

| SEQ ID NO: | MF   | Target | VH                                                                                                                                 |
|------------|------|--------|------------------------------------------------------------------------------------------------------------------------------------|
| 3          | 3370 | EGFR   | QVQLVQSGAEVKKPGASVKVCKASGYTFTSYGISWVRQAPGGLEWMGWISAYNGNTNYAQKLQ<br>GRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRHWHHWLDAFDYWGQGTLVTVSS       |
| 4          | 3755 | EGFR   | QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWNVRQAPGHGLEWMGWINANTGDPPTYAQGF<br>TGRFVFSLDTSVSTAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGQGTLVTVSS     |
| 5          | 4280 | EGFR   | QVQLVQSGAEVKKPGASVKVCKVSGYITLTLSMHWVRQAPGKGLEWMGGFDPEYGGKTFFAQNF<br>QGRVTMTEDTSADTAYMELSSLRSEDTAVYYCATEGYYETTTTYYYNLFDSWGQGTLVTVSS |
| 6          | 4289 | EGFR   | QVQLVQSGSELKKPGASVKVCKTSGYITFTDYAMTWVRQAPGGLEWMGWITNTGDPPTYAPGFT<br>GRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARVYHWIRGFEFWGQGTLVTVSS         |
| 7          | 5790 | LGR5   | QVQLQESGPGGLVKPSETLSLTCTVSGGSFSSSSSYWGWRQPPGKGLEWIGSFYSGNTYYNPSLKS<br>RVTISEDTSKNQFSLKLSVTAADTAVYYCARQTYSSSWDGVLYYFDYWGQGTLVTVSS   |
| 8          | 5803 | LGR5   | QVQLQESGPGGLVKPSETLSLTCTVSNNGSISTYYWSWRQPPGKGLEWIGYVYYTGRTKYNPSLKS RV<br>TISVDTSKNQFSLNLSVTAADTAVYYCARGGIVVPAARDYYYMDVWVGKGTIVTVSS |
| 9          | 5805 | LGR5   | EVQLVQSGAEVKKPGESLKIACKGSGFSFTSHWIGWVRQKPRGRGLEWMGVYTPGDS DTRYSPSFQG<br>QVTVSADKSI NTAYLQWNLSKASDTAIYYCARPN SGSPRYFEFFWGRGTLVTVSS  |

Figure 3 a) cont.

|    |      |      |                                                                                                                                      |
|----|------|------|--------------------------------------------------------------------------------------------------------------------------------------|
| 10 | 5808 | LGR5 | QVQLQESGPGLVKPSETLSLTCTVSGGSSSSSYWGWIRQPPCKGLEWIGSFYSGNTYYNP SLKS<br>RVTISVDTSKNQFSLKLSSVTAADTAVYYCARQEYYYGSGSPSYFDYWGGGTLVTVSS      |
| 11 | 5809 | LGR5 | EVQLVQSGAEVKKPGESLKISCKSGDSFISHWIAWVRQMPPCKGLEWMGIVYPGDS DTRYSPSFQG<br>QVTISADKSIITAYLQWSSLKASDTAMYYCARHEWELLGPFDYWGGGTLVTVSS        |
| 12 | 5814 | LGR5 | EVQLVQSGAEVKKPGSSVKVSKKASGGTSTND AISWVRQTPGQGLEWMGSIPIILDTTDHAQKFQG<br>RVTITADKSTNTAYMELNSLRSDDTAVYYCAREHIAARQDYFDYWGGGTLVTVSS       |
| 13 | 5816 | LGR5 | EVQLVQSGSKLKKPGASVKVSKKASGYTFTSYTMN WVRQAPGQGLEWMGWINTDGTGPTYAQQFT<br>GRFVFSLDTSVSTAFLQINSLKAEDTAVYYCARGDCDSTSCYRYSYGYEDYWGGGTLVTVSS |
| 14 | 5817 | LGR5 | QVQLVQSGAEVKKPGSSVKVSKKSGGTFRSYAISWVRQAPGQGLEWMGGIPIFDTRNYAQILQGR<br>VTITADLSTSTAYMELNSLRSEDTAIYYCARGSDGDFDWPWGQGTLLVTVSS            |
| 15 | 5818 | LGR5 | EVQLVQSGTEVRKPGSSVKVSKKASGGTFSN YAISWVRQAPGQGLEWMGSIPIILGTTDHAQKFQD<br>RVTITADKSSNTTYMELSSLRSDDTAVYYCAREYIAARLDYFDSWGQGTLLVTVSS      |

Figure 3 b)

| MF   | Target: | SEQ ID Nos | FW1                                | CDR1   | FW2                | CDR2                  | FW3                                       | CDR3                 | FW4              |
|------|---------|------------|------------------------------------|--------|--------------------|-----------------------|-------------------------------------------|----------------------|------------------|
| 3370 | EGFR    | 16-22      | QVQLVQSGAEVKKPG<br>ASVKVSCKASGYTFT | SYGIS  | WVRQAPGQGLEW<br>MG | WISAYNGNTNIA<br>QKLGQ | RVVTMTDTSSTAYMEIR<br>SLRSDDTAVYYCAK       | DRHHHWLDAF<br>DY     | WGQGTLLV<br>VSS  |
| 3755 | EGFR    | 23-29      | QVQLVQSGSELKKPG<br>ASVKISCKASGYDFT | NYAMN  | WVRQAPGHG<br>LEWMG | WINANTGDP<br>YAQGTG   | RFVFSLDTSVSTAYLQ<br>ISSLKAEDSAVYYCTR      | ERFLEWLHF<br>DY      | WGQGTLL<br>VTVSS |
| 4280 | EGFR    | 30-36      | QVQLVQSGAEVKKPG<br>ASVKVSCKVSQYTLT | ELSMH  | WVRQAPGKG<br>LEWMG | GFDPEYGKTF<br>FAQNFQG | RVVTMTEDTSADTAYM<br>ELSSLRSEDTAVYYCA<br>T | EGYYETTTY<br>YNLFDS  | WGQGTLL<br>VTVSS |
| 4289 | EGFR    | 37-43      | QVQLVQSGSELKKPG<br>ASVKVSCKTSGYTFT | DYAMT  | WVRQAPGQG<br>LEWMG | WITNTGDP<br>YAPGTG    | RFVFSLDTSVSTAYLQ<br>ISSLKAEDTAVYYCAR      | VYHWIRGFE<br>F       | WGQGTLL<br>VTVSS |
| 5790 | LGR5    | 44-50      | QVQLQESGPGLVKPS<br>ETLSLTCTVSGGSFS | SSSYWG | WIRQPPGKGL<br>EWIG | SFYYSNGNTYY<br>NPSLKS | RVTISEDTSKNQFSLK<br>LSSVTAADTAVYYCAR      | QTYSSWDG<br>VLYYFDY  | WGQGTLL<br>VTVSS |
| 5803 | LGR5    | 51-57      | QVQLQESGPGLVKPS<br>ETLSLTCTVSNGLS  | TTYWS  | WIRQPPGKGL<br>EWIG | YVYTGRTKY<br>NPSLKS   | RVTISVDTSKNQFSLN<br>LSSVTAADTAVYYCAR      | GGIVVPAAR<br>DYVYMDV | WGKGT<br>VTVSS   |
| 5805 | LGR5    | 58-64      | EVQLVQSGAEVKKPG<br>ESLKIACKGSGFSFT | SHWIG  | WVRQKPGRG<br>LEWMG | VIYPGDSDR<br>YSPSFQG  | QVTVSADKSINTAYLQ<br>WNSLKASDTAIIYYCAR     | PNSGSPRYFE<br>F      | WGRGTLL<br>VTVSS |
| 5808 | LGR5    | 65-71      | QVQLQESGPGLVKPS<br>ETLSLTCTVSGGSIS | SSSYWG | WIRQPPGKGL<br>EWIG | SFYYSNGNTYY<br>NPSLKS | RVTISVDTSKNQFSLK<br>LSSVTAADTAVYYCAR      | QEYYGSGS<br>PSYFDY   | WGQGTLL<br>VTVSS |

Figure 3 b) cont.

|      |      |             |                                    |       |                    |                       |                                          |                        |                    |
|------|------|-------------|------------------------------------|-------|--------------------|-----------------------|------------------------------------------|------------------------|--------------------|
| 5809 | LGR5 | 72-78       | EVQLVQSGAEVKKPG<br>ESLKISCKGSGDSFI | SHWIA | WVRQMPGKG<br>LEWMG | IVYPGSDPTR<br>YSPSFQG | QVTISADKSIITAYLQ<br>WSSLKASDTAMYYCA<br>R | HEWELLGPF<br>DY        | WGQGT<br>L<br>VTSS |
| 5814 | LGR5 | 79-85       | EVQLVQSGAEVKKPG<br>SSVKVCKASGGTST  | NDAIS | WVRQTPGQG<br>LEWMG | SIIPILDTTDH<br>AQKFQG | RVTITADKSTNTAYME<br>LNSLRSDDTAVYYCAR     | EHIAARQDY<br>FDY       | WGQGT<br>L<br>VTSS |
| 5816 | LGR5 | 86-92       | EVQLVQSGSKLKKPG<br>ASVKVCKASGYTFT  | SYTMN | WVRQAPGQG<br>LEWMG | WINTDTGDP<br>YAQFTG   | RFVFLDTSVSTAFLQ<br>INSLKAEDTAVYYCAR      | GDCDSTSCY<br>RYSYGYEDY | WGQGT<br>L<br>VTSS |
| 5817 | LGR5 | 93-99       | QVQLVQSGAEVKKPG<br>SSVKVCKVSGGTFR  | SYAIS | WVRQAPGQG<br>LEWMG | GIPIFDTRNY<br>AQILQG  | RVTITADLSTSTAYME<br>LNSLRSEDTAIYYCAR     | GSDEGDWFD<br>P         | WGQGT<br>L<br>VTSS |
| 5818 | LGR5 | 100-<br>106 | EVQLVQSGTEVRKPG<br>SSVKVCKASGGTFS  | NYAIS | WVRQAPGQG<br>LEWMG | SIIPILGTTDH<br>AQKFQD | RVTITADKSSNTTYME<br>LSSLRSDDTAVYYCAR     | EYIAARLDYF<br>DS       | WGQGT<br>L<br>VTSS |

Figure 3

c)

MF1337: Sequence ID NO: 107

gaggtgcagctggtggagactggggtgaggtgaagaagccggggcctcagtgaaggtctcctgcaagg  
cttctgactacatcttcacaaatatgacatcaactgggtgcgccaggccccctggacaagggttgaatg  
gatgggatggatgagcgtaacactggaaacacgggctatgcacagaagtccagggcagagtcaccatg  
accaggggacacgtccataaacacagcctacatggagctgagcagcctgacatctggtgacacggccgtt  
atttctgtgcgaggagtagtctttcaagacagagacggcgccctactatcacttcgctctggacgtctg  
gggccaagggaaccaggtcaccgtctccagt

MF3370: Sequence ID NO: 108

caggttcagctggtgcagctctggagctgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg  
cttctggttacacctttaccagctatggtatcagctgggtgcgacaggccccctggacaagggttgaatg  
gatgggatggatcagcgcttacaatggtaacacaaactatgcacagaagctccagggcagagtcaccatg  
accacagacacatccacgagcacagcctacatggagctgaggagcctgagatctgacgacacggctgtg  
attactgtgcaaaagatcgctcattggcattgggtggctggacgcctttgattattggggccaaggtaccct  
ggtcaccgtctccagt

MF3755: Sequence ID NO: 109

caggtgcagctggtgcagctctgggtctgagttgaagaagcctggggcctcagtgaagatttcctgcaagg  
cttctggatacgaacttcaactatgctatgaattgggtgcgacaggccccctggacacgggttgaatg  
gatgggatggatcaacccaacactggggaccaacgtatgccagggttcacaggacggtttgtcttc  
tccttggacacctctgtcagcacggcatactgcagatcagcagtttaaggtgaggactctgccgtgt  
attactgtacgagagagcgattttggagtggttacactttgactactggggccagggaaccctggtcac  
cgctctccagt

MF4280: Sequence ID NO: 110

caggtgcagctggtgcagctctggggtgaggtgaagaagcctggggcctcagtgaaggtctcctgcaagg  
ttccggatacacctcactgaattatccatgcactgggtgcgacaggctcctggttaagggttgaatg  
gatgggaggtcttgcctgagtatggtaaaacattcttcgacagaactccagggcagagtcaccatg  
accgaggacacatctgcagacacagcctacatggagctaagcagcctgagatctgaggacacggccgtgt  
attactgtgcaacagaggggtattatgagactactacttattactacaaccttttgactcctggggcca  
gggaaccctggtcaccgtctccagt

MF4289: Sequence ID NO: 111

caggtgcagctggtgcaatctgggtctgaattgaagaagcctggggcctcagtgaaggttctcctgcaaga  
cttctggatacaccttcaactgactatgctatgacttgggtgcgacaggccccctggacaagggttgaatg  
gatgggatggatcaccaccaacactggggaccaacgtatgccccgggttcacaggacggtttgtcttc  
tccttggacacctctgtcagcacggcatactgcagatcagcagcctaaaggccgaggacactgccgtat  
attactgtgcgagagtgatcattggatacgggatttgagtttggggccagggaaccctggtcaccgt  
ctccagt

MF5790: Sequence ID NO: 112

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg

Figure 3c) cont.

tctctggtggctccttcagcagtagtagttcctactggggctggatccgccagccccaggggaaggggct  
ggagtggtggattgggagtttctattatagtggaacacctactacaacccgtccctcaagagtcgagtcacc  
atatccgaagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgagacacggctg  
tgtattactgtgcgagacagacgtatagcagcagctgggacggggctcgtactactttgactactgggg  
ccagggaaacctggtcaccgtctccagt

MF5803: Sequence ID NO: 113

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg  
tctctaattggctccatcagtagtactactggagctggatccggcagccccaggggaaggggctggagtg  
gattggatatgtctattacactgggcgcaccaagtacaacccctccctcaagagtcgagtcaccatatca  
gtagacacgtccaagaaccagttctccctgaacctgagttctgtgaccgtgcggacacggccgtgtatt  
actgtgcgagagggggtatttagtagtccagctgcgcgggactattactactacatggacgtctgggg  
caaagggaccacggtcaccgtctccagt

MF5805: Sequence ID NO: 114

gaggtgcaactggtgcagctcggagcagaggtgaaaaagcccgaggagttctgaagatcgcctgtaagg  
gttctggattcagttttaccagccactggatcggtgggtgcgcagaaagcccgaggagggcctggagtg  
gatgggggtcatctatcctggtgactctgataccagatacagccgtccttccaaggccaggtcaccgtc  
tcagccgacaagtccatcaataaccgcctacctgcagtggaaacagcctgaaggcctcggacaccgccat  
attactgtgcgagaccgaacagtgggagtcgccgtacttcgagttctggggccgtggcacctggtcac  
cgtctccagt

MF5808: Sequence ID NO: 115

caggtgcagctgcaggagtcggggccaggactggtgaagccttcggagaccctgtccctcacctgcactg  
tctctggtggctccatcagcagtagtagttactactggggctggatccgccagccccaggggaaggggct  
ggagtggtggattgggagtttctattatagtggaacacctactacaacccgtccctcaagagtcgagtcacc  
atatccgtagacacgtccaagaaccagttctccctgaagctgagctctgtgaccgccgagacacggctg  
tgtattactgtgcgagacaggagtattactatggttcggggagtccttcgtactactttgactactgggg  
ccagggaaacctggtcaccgtctccagt

MF5809: Sequence ID NO: 116

gaggtgcagctggtgcagctcggagcagaggtgaaaaagcccgaggagttctgaagatcctcgtgaagg  
gttctggagacagttttatcagccactggatcgctgggtgcgcagatgccgggaaaggcctggagtg  
gatggggatcgtctatcctggtgactctgataccagatacagccgtccttccaaggccaggtcaccatc  
tcagccgacaagtccatcaccaccgcctacttgagtgagcagcctgaaggcctcggacaccgccatgt  
attactgtgcgagacacagtgggaaactacttgcccccttgactactggggccagggaaacctggtcac  
cgtctccagt

MF5814: Sequence ID NO: 117

gaggtgcagctggtgcagctcggggctgaggtgaagaagcctgggtcctcgggtgaaggtctcctgcaagg  
cttctggaggcacctccactaacgatgctatcagttgggtgcgacagaccctggacaagggttgagtg  
gatgggaagtatcatcctatccttgataacaacagaccacgcacagaagtccagggcagagtcacgatt  
accgcggacaaatccacgaacacagcctacatggagctgaacagcctgagatctgatgacacggccgtgt  
attactgtgcgagagagcatatagcagctcgtcaggactactttgactattggggccagggaaacctggt

Figure 3c) cont.

caccgtctccagt

MF5816: Sequence ID NO: 118

gaggtgcagctggtgcagctctgggtctaaattgaagaagcctggggcctcagtgaaggtttcctgcaagg  
cttctggatacaccttcactagctatactatgaattgggtgcgacaggcccctggacaagggttgagt  
gatgggatggatcaacaccgacactggggaccaacgtatgccagggttcacaggacggtttgtcttc  
tccttggacacctctgtcagcacggcatttctacagatcaacagcctaaaggctgaggacactgccgtat  
attactgtgcgagaggagattgtgatagtagtaccagctgctatagatacagttatggttacaggactactg  
gggccagggaaccctggtcaccgtctccagt

MF5817: Sequence ID NO: 119

caggtgcagctggtgcagctctggggctgaggtgaagaagcctgggtcctcggtgaaggtctcctgcaagg  
tttctggaggcaccttcaggagctatgctatcagctgggtgcgacaggcccctggacaagggttgagt  
gatgggagggatcatccctatctttgatacaagaaactacgcacagattcttcagggcagagtcacgatt  
accgcggacttatccacgagcacagcctacatggagctgaacagtctgagatctgaggacacggccattt  
attactgtgcgagaggagcgcagagggggactggttcgaccctggggccaagggaaccctggtcaccgt  
ctccagt

MF5818: Sequence ID NO: 120

gaggtgcagctggtgcagctctgggactgaggtgaggaagcctgggtcctcggtgaaggtctcctgcaagg  
cttctggaggcaccttcagcaactatgctatcagctgggtgcgacaggcccctggacaggggttgagt  
gatgggaagtatcatccctatccttgaacaacagaccacgcacagaagttccaggacagagtcacgatt  
accgcggacaaatcctcgaacacaacctacatggagctgagcagcctgagatctgatgacacggccgtat  
attactgtgcgagagagtatatagcagctcgtctggactactttgactcttggggccagggaaccctggt  
caccgtctccagt

Figure 4

a) Sequence ID NO: 121

DIQMTQSPSSLSASVGDRVTTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP  
SRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPTFGQGTKVEIK  
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT  
EQDSKDYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

b)

Sequence ID NO: 122

DIQMTQSPSSLSASVGDRVTTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVP  
SRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPPTFGQGTKVEIK

Sequence ID NO: 123

gacatccagatgaccagtcctccatcctccctgtctgcatctgtaggagacagagtcaccatcacttgccgggcaagtcagagca  
ttagcagctacttaaattggtatcagcagaaaccagggaaagccctaagctcctgatctatgctgcatccagtttcaaagtgg  
ggtcccatcaaggttcagtggcagtgatctgggacagatttcactctcaccatcagcagctctgcaacctgaagattttgcaactt  
actactgtcaacagagttacagtacccctccaacgttcggccaagggaccaaggtggagatcaaa

c)

Sequence ID NO: 124

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT  
EQDSKDYSLSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Sequence ID NO: 125

gaactgtggtgcaccatctgtcttcatcttcccgcctctgatgagcagttgaaatctggaactgcctctgttgtgcctgctga  
ataacttctatcccagagaggccaaagtacagtggaaggtggataacgccctccaatcgggtaactcccaggagagtgctcaca  
gagcaggacagcaaggacagcacctacagcctcagcagaccctgacgctgagcaaagcagactacgagaaacacaaagtc  
tacgctgcgaagtcacccatcagggcctgagctcgccgctcacaagagcttcaacaggggagagtg

d)

Sequence ID NO: 126

DIQMTQSPSSLSASVGDRVTTITCRASQSISSYLNWYQQKPGKAPKLLIYAA  
SSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTP

e)

CDR1 - QSISSY, Sequence ID NO: 127

CDR2 – AAS Sequence ID NO: 128

CDR3 – QQSYSTPPT Sequence ID NO: 129

## Figure 5

a)

CH1:

Sequence ID NO: 130

gctagcaccaagggcccatcggtcttccccctggcaccctctccaagagcacctctgggggcacagcggccctgggctgcctggt  
caaggactacttccccgaaccggtgacggtgtcgtggaactcaggcgcctgaccagcggcgtgcacaccttcccggtgtccta  
cagtcctcaggactctactccctcagcagcgtcgtgaccgtgcctccagcagcttgggcacccagacctacatctgcaacgtgaa  
tcacaagcccagcaacaccaaggtggacaagagagtt

Sequence ID NO: 131

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ  
SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRV

b)

Hinge:

Sequence ID NO: 132

gagccaaatcttgtgacaaaactcacacatgccaccgtgccca

Sequence ID NO: 133

EPKSCDKTHTCPPCP

c)

CH2:

Sequence ID NO: 134

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

Sequence ID NO: 135

gcacctgaactctggggggaccgtcagttctcttccccccaaaacccaaggacacctcatgatctccggaccctgaggt  
cacatgcgtggtggtggacgtgagccacgaagacctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatg  
ccaagacaaagccgaggagcagtagacaacagcacgtaccgtgtggtcagcgtcctcaccgtctgcaccaggactggctg  
aatggcaaggagtacaagtgaaggtctccaacaaagccctccagccccatcgagaaaaccatctccaaagccaaa

Figure 5 d)

CH3: L351K and T366K

Sequence ID NO: 136

GQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTPPV  
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG-

Sequence ID NO: 137

gggcagccccgagaaccacaggtgtacaccaagcccccatcccgggaggagatgaccaagaaccaggtcagcctgaagtgcct  
ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctc  
ccgtgctggactccgacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctc  
atgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagccttccctgtctccgggttga

e)

CH3: L351D and L368E

Sequence ID NO: 138

GQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPENNYKTTPPV  
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG-

Sequence ID NO: 139

gggcagccccgagaaccacaggtgtacaccgaccccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcga  
ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctc  
ccgtgctggactccgacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctc  
atgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagccttccctgtctccgggttga

Figure 6 a)



