

Sequence Listing

SEQ ID NO:1 HCDR1-F018/F063/J004/J042/N049
GGSI

SEQ ID NO:2 HCDR2-F018/F063/J004/J042/N049
IYSSGST

SEQ ID NO:3 HCDR3-F018
VAWFGDLLSLKGVEL

SEQ ID NO:4 HCDR3-F063/J004/J042/N049
VWVFGDLLSLKGVEL

SEQ ID NO:5 LCDR1-F018/J042
SSNIGSNY

SEQ ID NO:6 LCDR1-F063/N049
SSNIGSKN

SEQ ID NO:7 LCDR1-J004
SSNIGSSY

SEQ ID NO:8 LCDR2-F018/F063/J004/J042/N049
RNN

SEQ ID NO:9 LCDR3-F018
AAWDDSLSAWV

SEQ ID NO:10 LCDR3-F063/J004/J042/N049
AAWDDSLSGWV

SEQ ID NO:11 HCDR1-I022
GGSISSTSY

SEQ ID NO:12 HCDR2-I022
ISYSGST

SEQ ID NO:13 HCDR3-I022
ARILWFGEYLGDY

SEQ ID NO:14 LCDR1-I022
QSVSNY

SEQ ID NO:15 LCDR2-I022
GAS

SEQ ID NO:16 LCDR3-I022
QQYYSTPWT

SEQ ID NO:17 HCDR1-N038

GYSISSGY

SEQ ID NO:18 HCDR2-N038
SNHSGST

SEQ ID NO:19 HCDR3-N038
AREAGYSSSWYFDY

SEQ ID NO:20 LCDR1-N038
SSNIGNNY

SEQ ID NO:21 LCDR2-N038
DNN

SEQ ID NO:22 LCDR3-N038
GTWDSSLSAWV

SEQ ID NO:23 VH-F018 (aa7-117 of 117, NA)
TCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGG
CTCCATCTGGGGCTGGATCCGCCAGCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCT
ATTCTAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCACATCCGTAGAC
ACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTA
TTACTGTGTGGCGTGGTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGG
GAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:24 VH-F018 (aa7-117 of 117, AA)
SGPGLVKPSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNP SLKSRVTTSVD
TSKNQFSLRLSSVTAADTAVYYCVAWFGDLLSLKGVELWGQGLVTVSS

SEQ ID NO:25 VL-F018 (aa5-107 of 110, NA)
ACTCAGCCACCTTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAG
CAGCTCCAACATCGGAAGTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA
AACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTA
TTACTGTGCAGCATGGGATGACAGCCTGAGTGCTTGGGTGTTCTGGCGGAGGCACCCAGCTG

SEQ ID NO:26 VL-F018 (aa5-107 of 110, AA)
TQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVPDRFSGS
KSGTSASLAISGLRSEDEADYYCAAWDDSLSAWVFGGGTQL

SEQ ID NO:27 VH-F063 (aa7-117 of 117, NA)
TCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGG
CTCCATCTGGGGCTGGATCCGCCAGCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCT
ATTCTAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGAC
ACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTA
TTACTGTGTGGTGTGGTTCGGGGACTTATTATCGTTGAAGGGGGTCAATTGTGGGGCCAGG
GAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:28 VH-F063-J042 (aa7-117 of 117, AA)
SGPGLVKPSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNP SLKSRVTISVD
TSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLVTVSS

SEQ ID NO:29 VH-J042 (aa7-117 of 117, NA)

TCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGG
CTCCATCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCT
ATTCTAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGAC
ACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTA
TTACTGTGTGGTGTGGTTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGG
GAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:30 VL-F063 (aa5-107 of 110, NA)

ACTCAGCCACCCCTCAGTGTCTGGGACCCCCGGGCAGAGGGTCACCGTCTCTTGTCTGGAAG
CAGCTCTAACATCGGAAGTAAAAATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA
AACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTA
TTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTGTTTCAGCGGAGGCACCAAGGTG

SEQ ID NO:31 VL-F063 (aa5-107 of 110, AA)

TQPPSVSGTPGQRVTVSCSGSSSNIGSKNVYWYQQLPGTAPKLLIYRNNQRPSPGVDPDRFSGS
KSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFSGGTKV

SEQ ID NO:32 VH-J004 (aa7-117 of 117, NA)

TCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCACACCTGCACTGTCTCTGGTGG
CTCCATCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCT
ATTCTAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGAC
ACGTCCAAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTA
TTACTGTGTGGTGTGGTTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGG
GAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:33 VH-J004 (aa7-117 of 117, AA)

SGPGLVKPSETLSHTCTVSGGSIWGWIQPPGKGLEWIGSIYSSGSTYYNPSLKSRTISVD
TSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLVTVSS

SEQ ID NO:34 VL-J004 (aa5-107 of 110, NA)

ACGCAGCCGCCCTCAGTGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAG
CAGCTCCAACATCGGAAGTAGTTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA
AACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTA
TTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTGTTTCGGCGGAGGCACCGAGCTG

SEQ ID NO:35 VL-J004 (aa5-107 of 110, AA)

TQPPSVSGTPGQRVTVISCSGSSSNIGSSYVYWYQQLPGTAPKLLIYRNNQRPSPGVDPDRFSGS
KSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTEL

SEQ ID NO:36 VL-J042 (aa5-107 of 110, NA)

ACCCAGGAGCCCTCAGTGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAG
CAGCTCCAACATCGGAAGTAATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA
AACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTA
TTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTGTTTCGGCGGAGGGACCAAGCTG

SEQ ID NO:37 VL-J042 (aa5-107 of 110, AA)

TQEPSVSGTPGQRVTIISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSPGAPDRFSGS
KSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKL

SEQ ID NO:38 VH-N049 (aa7-117 of 117, NA)

TCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGG
TTCCATCTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCT
ATTCTAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGAC
ACGTCCGAGAACCAGTTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTA
TTACTGTGTGGTGTGGTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGG
GAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:39 VH-N049 (aa7-117 of 117, AA)

SGPGLVKPSETLSLTCTVSGGSIWGWIQPPGKGLEWIGSIYSSGSTYYNPSLKSRVTISVD
TSENQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLVTVSS

SEQ ID NO:40 VL-N049 (aa5-107 of 110, NA)

ACTCAGCCACCCACAGTGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAG
CAGCTCCAACATCGGAAGTAAAAATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCA
AACTCCTCATCTATAGGAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTA
TTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTGGGTGTTGGCGGAGGCACCAAGGTG

SEQ ID NO:41 VL-N049 (aa5-107 of 110, AA)

TQPPTVSGTPGQRVTIISCSGSSSNIGSKNVYWYQQLPGTAPKLLIYRNNQRPSPGVPDRFSGS
KSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKV

SEQ ID NO:42 VH-I022 (aa7-121 of 121, NA)

TCGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGG
CTCCATCAGCAGTACTAGTTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGG
AGTGGATTGGGAGTATCTCTTATAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTCGA
GTCACCATATCCGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGACCTCTGTGACCGC
CGCAGACACGGCTGTGTATTACTGTGCGAGGATACTATGGTTCGGAGAGTACCTAGGGGACT
ACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

SEQ ID NO:43 VH-I022 (aa7-121 of 121, AA)

SGPGLVKPSETLSLTCTVSGGSISSTSYWGWIRQPPGKGLEWIGSISYSGSTYYNPSLKSR
VTISVDTSKNQFSLKLTSVTAADTAVYYCARILWFGEYLGDYWGQGLVTVSS

SEQ ID NO:44 VL-I022 (aa5-104 of 107, NA)

ACCCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGC
CAGTCAGAGTGTTAGCAACTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGC
TCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGTTTCAGTGGCAGTGGG
TCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATCA
CTGTCAGCAATATTATAGTACTCCGTGGACGTTTCGGCCAAGGGACCAAAGTG

SEQ ID NO:45 VL-I022 (aa5-104 of 107, AA)

TQSPGTLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSG
SGTDFTLTISRLEPEDFAVYHCQQYYSTPWTFGQGTKV

SEQ ID NO:46 VH-N038 (aa7-121 of 121, NA)

TCTGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTTA
CTCCATCAGCAGTGGTTACTACTGGGGCTGGATCCGGCAGCCCCCAGGGAAGGGGCTGGAGT
GGATTGGGAGTAGCAATCATAGTGGGAGCACCTACTACAACCCGTCCCTCAGGAGTCGAGTC
ACCATATCAGTAGACACGTCCAAGAACCAATTCTCCCTGAAGGTGAACTCTGTGACCGCCGC
AGACACGGCCGTTTATTACTGTGCGAGAGAGGCGGGGTATAGCAGCAGCTGGTACTTTGACT
ACTGGGGTCAGGGAACCCTGGTCACCGTCTCTCTCA

SEQ ID NO:47 VH-N038 (aa7-121 of 121, AA)
SGPGLVKPSETLSLTCAVSGYSISSGYWGWIRQPPGKLEWIGSSNHSGSTYYNPSLRSRV
TISVDTSKNQFSLKVNSVTAADTAVYYCAREAGYSSSWYFDYWGQGLVTVSS

SEQ ID NO:48 VL-N038 (aa5-107 of 110, NA)
ACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAGGTCACCATCTCCTGCTCTGGAAG
CAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCA
AACTCCTCATTTATGACAATAATAAGCGACCCCTCAGGGATTCTGACCGATTCTCTGGCTCC
AAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGACTGGGGACGAGGCCGATTA
TTACTGCGGAACATGGGATAGCAGCCTGAGTGCTTGGGTGTTTCGGCGGAGGGACCCAGCTG

SEQ ID NO:49 VL-N038 (aa5-107 of 110, AA)
TQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGS
KSGTSATLGITGLQTGDEADYYCGTWDSSLSAWVFEGGTQL

SEQ ID NO:50 VH (aa1-6, preferred sequence for all, AA)
QX₁QLQX₂, wherein X₁ is selected from V and L, and wherein X₂ is
selected from E and Q

SEQ ID NO:51 VL (aa1-4, preferred sequence for F018, F063,
J004, J042, N049, N038, AA)
QSVL

SEQ ID NO:52 VL (aa1-4, preferred sequence for I022, AA)
EIVX₁, wherein X₁ is selected from L and M

SEQ ID NO:53 VL (aa108-110, preferred sequence for F018, F063,
J004, J042, N049, N038, AA)
TVL

SEQ ID NO:54 VL (aa105-107, preferred sequence for I022, AA)
X₁IK, wherein A₁ is selected from D and E

SEQ ID NO:55 F018 gamma 2 heavy chain (with flanking sequence
and signal peptide)
MDWTWRILFLVAAATGAHSQMQLLES GPGLVKPSETLSLTCTVSGGSIWGWIRQPPGKLEW
IGSIYSSGSTYYNPSLKS RVTTSDTSKNQFSLRLSSVTAADTAVYYCVAWFGDLLSLKGVE
LWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:56 F018 lambda light chain (with flanking sequences and signal peptide)

MAWALLLLTLLTQGTGSWAQSELTQPPSASGTPGQRTVISCSSSSNIGSNYVYWYQQLPGT
APKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAWVFGGGT
QLDILGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT
PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:57 fully human F018 gamma 2 heavy chain (with flanking sequence and signal peptide)

MKHLWFFLLLVAAAPRWVLSQLQLQESGPGLVKPSSETLSLTCTVSGGSIWGWIRQPPGKGLEW
IGSIYSSGSTYYNPSLKSRTTSVDTSKNQFSLRLSSVTAADTAVYYCVAWFGDLLSLKGV
LWGQGTLLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTFRVVSFLTIVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:58 fully human F018 lambda light chain (with flanking sequences and signal peptide)

MAGFPLLLTLLTHCAGSWAQSVLTQPPSASGTPGQRTVISCSSSSNIGSNYVYWYQQLPGT
APKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAWVFGGGT
QLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT
PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:59 scFv-F018 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCTCGTGCTGACTCAGCCACCTTCAGCGTCTGGGACCCCCGGGCAG
AGGGTCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTA
CCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCAG
GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGCTTG
GGTGTTTCGGCGGAGGCACCCAGCTGACCGTCTCGGTGGTGGTTCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGGGAGGTGCAGCTGGTGCAGTCTGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCTGGGGCTG
GATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTCTAGTGGGAGCA
CCTACTACAACCGTCCCTCAAGAGTCGAGTCACCACATCCGTAGACACGTCCAAGAACCAG
TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGTGGCGTG
GTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCTTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:60 scFv-F018 Sfil-fragment (AA)

XAELVLTQPPSASGTPGQRTVISCSSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAWVFGGGTQLTVLGGGSSRSSSSGG
GGSGGGGEVQLVQSGPGLVKPSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYY
NPSLKSRTTSVDTSKNQFSLRLSSVTAADTAVYYCVAWFGDLLSLKGVLELWGQGTLLTVSS
ASTKGPSVTSQA

SEQ ID NO:61 scFv-F063 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCTCGTGCTGACTCAGCCACCTCAGTGTCTGGGACCCCCGGGCAG
AGGGTCACCGTCTCTTGTCTGGAAGCAGCTCTAACATCGGAAGTAAAAATGTATACTGGTA
CCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCAG

GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTG
GGTGTTTCAGCGGAGGCACCAAGGTGACCGTCCTAGGTGGTGGTTCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGGGAGGTGCAGCTGGTGGAGTCTGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCTGGGGCTG
GATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTCTAGTGGGAGCA
CCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAGAACCAG
TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGTGGTGTG
GTTTCGGGGACTTATTATCGTTGAAGGGGGTCAATTGTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCTTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:62 scFv-F063 Sfil-fragment (AA)

XAELVLTQPPSVSGTPGQRTVSCSGSSSNIGSKNVYWYQQLPGTAPKLLIYRNNQRPSGVP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFSGGTKVTVLGGGSSRSSSSSG
GGSGGGGEVQLVESGPGLVKPSETLSLTCTVSGSISGWIRQPPGKLEWIGSIYSSGSTYY
NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLTVTVSS
ASTKGPSVTSGQA

SEQ ID NO:63 scFv-J004 Sfil-fragment (NA)

NGGCCCAGGCGGCCGGGCTCGTGGTGACGCAGCCGCCCTCAGTGTCTGGGACCCCCGGGCAG
AGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAGTTATGTATACTGGTA
CCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCAG
GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTG
GGTGTTTCGGCGGAGGCACCGAGCTGACCGTCCCTCGGTGGTGGTTCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGGGAGGTGCAGCTGGTGGAGTCTGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCACACCTGCACTGTCTCTGGTGGCTCCATCTGGGGCTG
GATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTCTAGTGGGAGCA
CCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAGAACCAG
TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGTGGTGTG
GTTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCTTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:64 scFv-J004 Sfil-fragment (AA)

XAGLVVTQPPSVSGTPGQRTVISCSGSSSNIGSSYVYWYQQLPGTAPKLLIYRNNQRPSGVP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTELTVLGGGSSRSSSSSG
GGSGGGGEVQLVESGPGLVKPSETLSHTCTVSGSISGWIRQPPGKLEWIGSIYSSGSTYY
NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLTVTVSS
ASTKGPSVTSGQA

SEQ ID NO:65 scFv-J042 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCACGTGGTGACCCAGGAGCCCTCAGTGTCTGGGACCCCCGGGCAG
AGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTA
CCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCAG
GGGCCCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTG
GGTGTTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGCGGTGGTTCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGGCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCTGGGGCTG
GATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTCTAGTGGGAGCA
CCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAGAACCAG

TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGTGGTGTG
GTTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCTTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:66 scFv-J042 Sfil-fragment (AA)

XAEHVVTQEPSVSGTPGQRTVISCSSSSNIGSNYVYQQLPGTAPKLLIYRNNQRPSGAP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLGGGSSRSSSSSG
GGSGGGGGQVQLQESGPGLVKPSSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYY
NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLTVTVSS
ASTKGPSVTSGQA

SEQ ID NO:67 scFv-N049 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCTCGTGCTGACTCAGCCACCCACAGTGTCTGGGACCCCCGGGCAG
AGGGTCACCATCTCTTGTCTGGAAGCAGCTCCAACATCGGAAGTAAAAATGTATACTGGTA
CCAGCAGCTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGGAATAATCAGCGGCCCTCAG
GGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAGTGGTTG
GGTGTTTCGGCGGAGGCACCAAGGTGACCGTCTAGGTGGTGGTTCCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGGCAGATCACCTTGAAGGAGTCTGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGTTCCATCTGGGGCTG
GATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTATTCTAGTGGGAGCA
CCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCGAGAACCAG
TTCTCCCTGAGGCTGAGCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGTGGTGTG
GTTTCGGGGACTTATTATCGTTGAAGGGGGTTGAATTGTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCTTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:68 scFv-N049 Sfil-fragment (AA)

XAELVLTQPPTVSGTPGQRTVISCSSSSNIGSKNVYQQLPGTAPKLLIYRNNQRPSGVP
DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKVTVLGGGSSRSSSSSG
GGSGGGGGQITLKESGPGLVKPSSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYY
NPSLKSRTVISVDTSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVELWGQGLTVTVSS
ASTKGPSVTSGQA

SEQ ID NO:69 scFv-I022 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCTCCACATGACCCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGG
GAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAACTACTTAGCCTGGTACCA
GCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCA
TCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTG
GAGCCTGAAGATTTTGCAGTGTATCACTGTGAGCAATATTATAGTACTCCGTGGACGTTTCGG
CCAAGGGACCAAAGTGGATATCAAAGGTGGTTCCTCTAGATCTTCCTCCTCTGGTGGCGGTG
GCTCGGGCGGTGGTGGGCAGGTGCAGCTGCAGGAGTCGGGCCAGGACTGGTGAAGCCTTCG
GAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTACTAGTTACTACTG
GGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTATCTCTTATAGTG
GGAGCACCTACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAG
AACCAGTTCTCCCTGAAGCTGACCTCTGTGACCGCCGCAGACACGGCTGTGTATTACTGTGC
GAGGATACTATGGTTCGGAGAGTACCTAGGGGACTACTGGGGCCAGGGAACCCTGGTCACCG
TCTCCTCAGCCTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGCCN

SEQ ID NO:70 scFv-I022 Sfil-fragment (AA)

XAELHMTQSPGTLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLLIYGASSRATGIPD
RFSGSGSGTDFTLTISRLEPEDFAVYHCQQYYSTPWTFGQGTKVDIKGGSSRSSSSSGGGGSG

GGGQVQLQESGPGLVKPSSETLSLTCTVSGGSISSTSYWGWIRQPPGKGLEWIGSISYSGST
YYNPSLKSRTISVDTSKNQFSLKLTSVTAADTAVYYCARILWFGEYLG DYWGQGT LVT VSS
ASTKGPSVTSGQA

SEQ ID NO:71 scFv-N038 Sfil-fragment (NA)

NGGCCCAGGCGGCCGAGCTCCTGGTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAG
AAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTA
CCAGCAGCTCCCAGGAACAGCCCCCAAACCTCCTCATTTATGACAATAATAAGCGACCCTCAG
GGATTCTGACCGATTCTCTGGCTCCAAGTCTGGCAGCTCAGCCACCCTGGGCATCACCAGGA
CTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTTG
GGTGTTTCGGCGGAGGGACCCAGCTGACCGTCTCTCGGCGGTGGTTTCCTCTAGATCTTCCTCCT
CTGGTGGCGGTGGCTCGGGCGGTGGTGGAGAGGTGCAGCTGGTGCAGTCTGGCCCAGGACTG
GTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCTGTCTCTGGTTACTCCATCAGCAGTGG
TTACTACTGGGGCTGGATCCGGCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGAGTAGCA
ATCATAGTGGGAGCACCTACTACAACCCGTCCCTCAGGAGTCGAGTCACCATATCAGTAGAC
ACGTCCAAGAACCAATTCTCCCTGAAGGTGAACTCTGTGACCGCCGCAGACACGGCCGTTTA
TTACTGTGCGAGAGAGGCGGGGTATAGCAGCAGCTGGTACTTTGACTACTGGGGTCAGGGAA
CCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCACTAGTGGCCAGGCCGGC
CN

SEQ ID NO:72 scFv-N038 Sfil-fragment (AA)

XAELLVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP
DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAWVFGGGTQLTVLGGGSSRSSSSGG
GGSGGGGEVQLVQSGPGLVKPSETLSLTCAVSGYSISSGYWGWIRQPPGKGLEWIGSSNHS
GSTYYNPSLRSRTISVDTSKNQFSLKVN SVTAADTAVYYCAREAGYSSSWYFDYWGQGT LVT
VSSASTKGPSVTSGQA

SEQ ID NO:73 fully human F018 gamma 2 heavy chain

QLQLQESGPGLVKPSSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNPSLKS
VTTSVDTSKNQFSLRLSSVTAADTAVYYCVAWFGLDLSLKGVELWGQGT LVT VSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
TVPSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM
ISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLT TVVH QDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPMLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQ
KSLSLSPGK

SEQ ID NO:74 fully human F018 lambda light chain

QSVLTQPPSASGTPGQRTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVPDR
FSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSAWVFGGGTQLTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:75 fully human F063 and J042 gamma 2 heavy chain

QLQLQESGPGLVKPSSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNPSLKS
VTISVDTSKNQFSLRLSSVTAADTAVYYCVWFGLDLSLKGVELWGQGT LVT VSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
TVPSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM
ISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLT TVVH QDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD

I AVEWESNGQPENNYKTTPMLSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPGK

SEQ ID NO:76 fully human F063 lambda light chain
QSVLTQPPSVSGTPGQRVTVSCSGSSSNIGSKNVYWYQQLPGTAPKLLIYRNNQRPSGVPDR
FSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGTKVTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:77: fully human J004 gamma 2 heavy chain
QLQLQESGPGLVKPSETLSHTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNPSLKSR
VTISVDTSKNQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVLELWGQGTLLTVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM
ISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
I AVEWESNGQPENNYKTTPMLSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPGK

SEQ ID NO:78 fully human J004 lambda light chain
QSVLTQPPSVSGTPGQRVTISCSGSSSNIGSSYVYWYQQLPGTAPKLLIYRNNQRPSGVPDR
FSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTELTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:79 fully human J042 lambda light chain
QSVLTQEPSVSGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGAPDR
FSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:80 fully human N049 gamma 2 heavy chain
QLQLQESGPGLVKPSETLSLTCTVSGGSIWGWIRQPPGKGLEWIGSIYSSGSTYYNPSLKSR
VTISVDTSSENQFSLRLSSVTAADTAVYYCVVWFGDLLSLKGVLELWGQGTLLTVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLM
ISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD
I AVEWESNGQPENNYKTTPMLSDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPGK

SEQ ID NO:81 fully human N049 lambda light chain
QSVLTQPPTVSGTPGQRVTISCSGSSSNIGSKNVYWYQQLPGTAPKLLIYRNNQRPSGVPDR
FSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGWVFGGGTKVTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:82 fully human I022 gamma 2 heavy chain
QLQLQESGPGLVKPSETLSLTCTVSGGISSTSYWGWIRQPPGKGLEWIGSISYSGSTYYN
PSLKSRVTISVDTSKNQFSLKLTSVTAADTAVYYCARILWFGEYLGDIWGQGTLLTVTVSSAST
KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL

SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVH
QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN
HYTQKSLSLSPGK

SEQ ID NO:83 fully human I022 kappa light chain

EIVMTQSPGTLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLLIYGASSRATGIPDRF
SGSGSGTDFTLTISRLEPEDFAVYHCQQYYSTPWTFGQGTKLEIKRTVAAPS VFIFPPSDEQ
LKSGTASVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:84 fully human N038 gamma 2 heavy chain

QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWI RQPPGKGLEWIGSSNHS GSTYYNP
SLRSRVTISVDTSKNQFSLKVN SVTAADTAVYYCAREAGYSSSWYFDYWGQGT LVTVSSAST
KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVH
QDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN
HYTQKSLSLSPGK

SEQ ID NO:85 fully human N038 lambda light chain

QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDR
FSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAWVFGGGTQLTVLGQPKAAPSVTLFPP
SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLT
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

SEQ ID NO:86 HSC-F018-B

CCTGGCCGCGCCTGGCCACTAGTGACCGATGGGCCCTTGGTGGAAGC