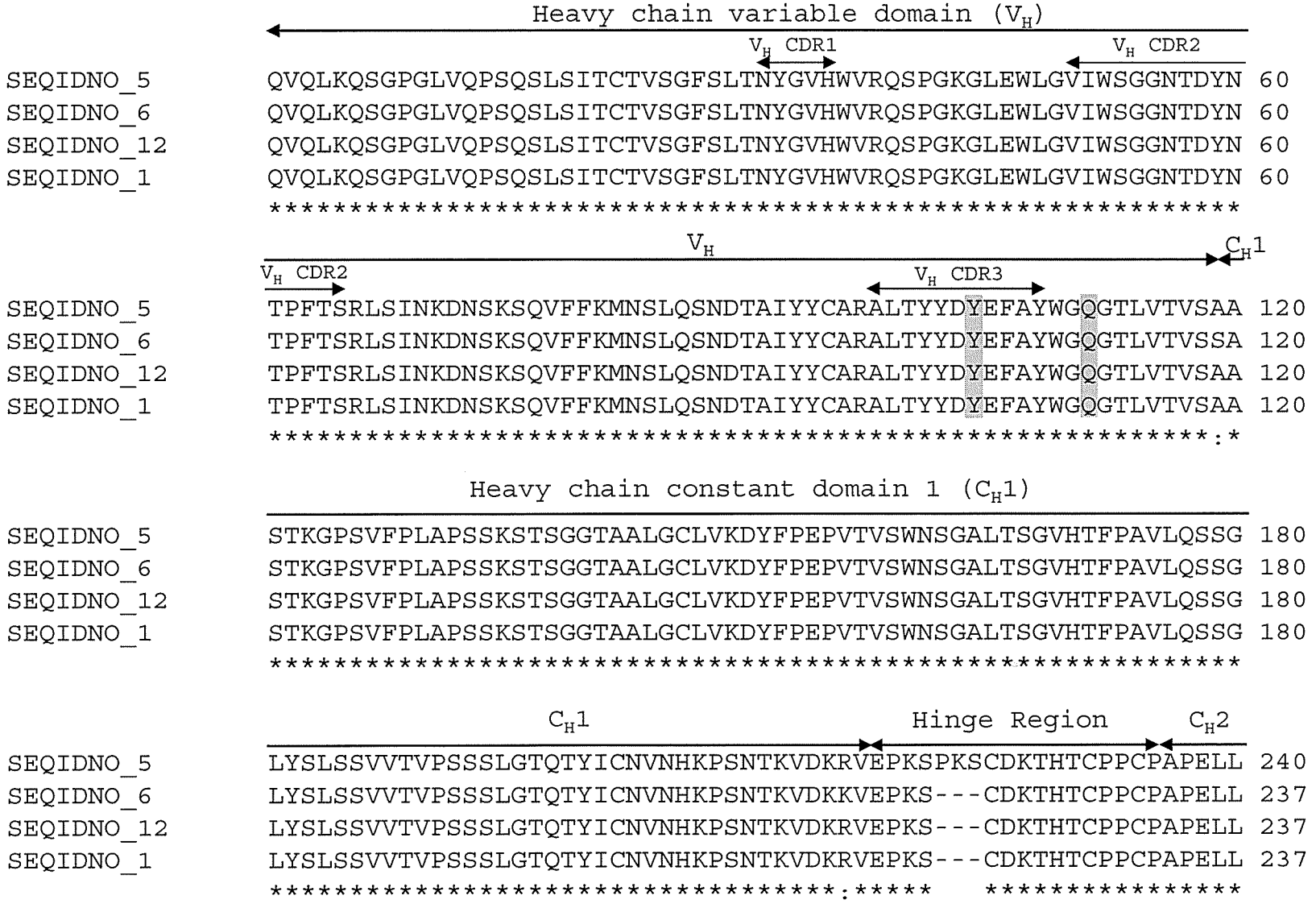

Heavy chain variable domain (V_H)
V_H CDR1
V_H CDR2
SEQIDNO_5 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
SEQIDNO_6 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
SEQIDNO_12 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
SEQIDNO_1 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
V_H
C_H1
V_H CDR2
V_H CDR3
SEQIDNO_5 TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSAA 120
SEQIDNO_6 TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSSA 120
SEQIDNO_12 TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSAA 120
SEQIDNO_1 TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSAA 120
Heavy chain constant domain 1 (C_H1)
SEQIDNO_5 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
SEQIDNO_6 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
SEQIDNO_12 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
SEQIDNO_1 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
C_H1
Hinge Region
C_H2
SEQIDNO_5 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSPKSCDKTHTCPPCPAPELL 240
SEQIDNO_6 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS---CDKTHTCPPCPAPELL 237
SEQIDNO_12 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS---CDKTHTCPPCPAPELL 237
SEQIDNO_1 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS---CDKTHTCPPCPAPELL 237

FIG. 1A

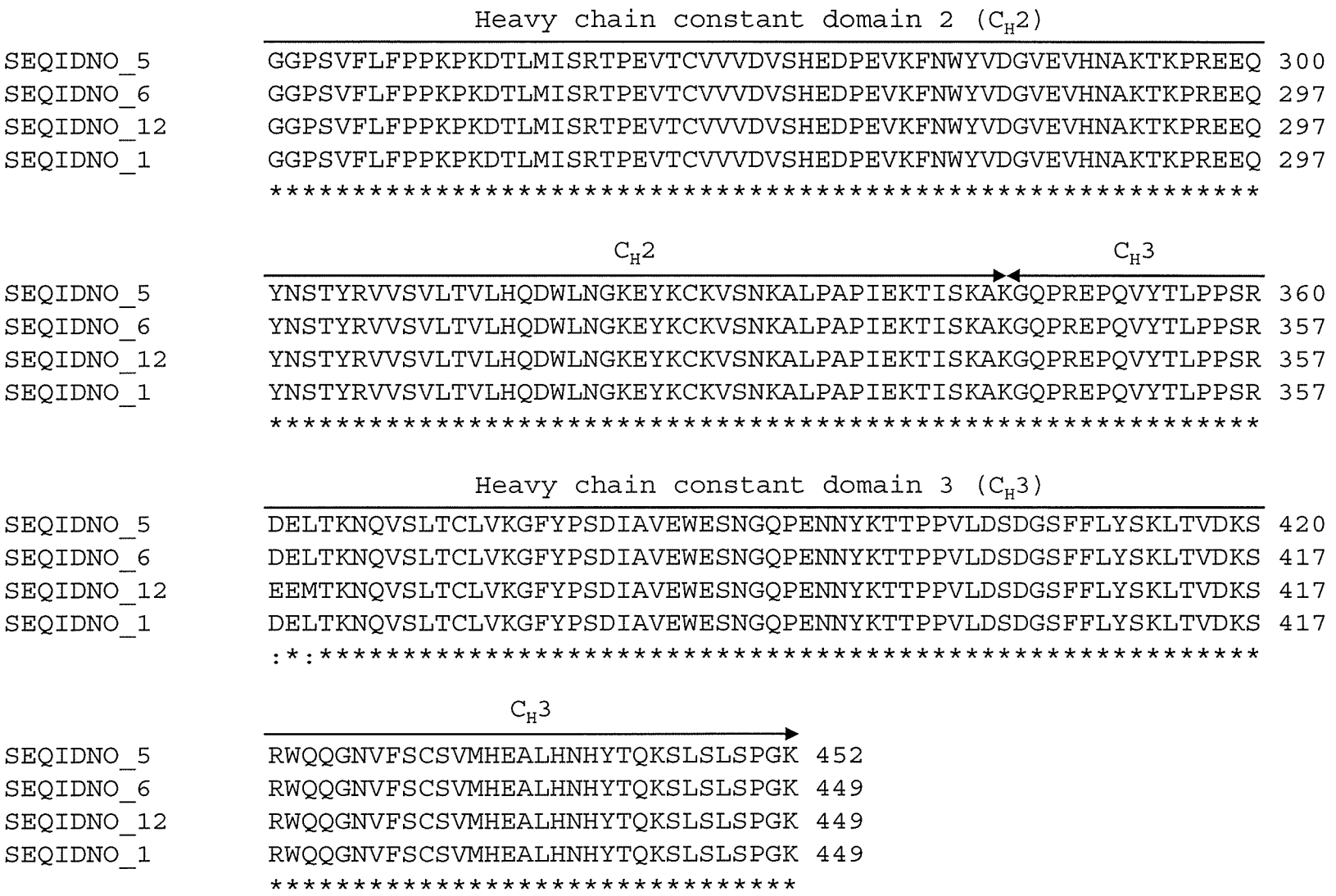

Heavy chain constant domain 2 (C_H2)
SEQIDNO_5 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
SEQIDNO_6 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
SEQIDNO_12 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
SEQIDNO_1 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
C_H2
C_H3
SEQIDNO_5 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
SEQIDNO_6 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
SEQIDNO_12 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
SEQIDNO_1 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
Heavy chain constant domain 3 (C_H3)
SEQIDNO_5 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420
SEQIDNO_6 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
SEQIDNO_12 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
SEQIDNO_1 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
C_H3
SEQIDNO_5 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
SEQIDNO_6 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
SEQIDNO_12 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
SEQIDNO_1 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

FIG. 1A


Light chain variable domain (V_L)
V_L CDR1
V_L CDR2
SEQIDNO_3 DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_10 DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_13 DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_8 DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
V_L
C_L
V_L CDR3
SEQIDNO_3 RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPP 120
SEQIDNO_10 RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKLELKRTVAAPSVFIFPP 120
SEQIDNO_13 RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELKRTVAAPSVFIFPP 120
SEQIDNO_8 RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKVEIKRTVAAPSVFIFPP 120
Light chain constant domain (C_L)
SEQIDNO_3 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
SEQIDNO_10 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
SEQIDNO_13 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
SEQIDNO_8 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
C_L
SEQIDNO_3 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGA- 213
SEQIDNO_10 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGA- 213
SEQIDNO_13 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
SEQIDNO_8 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

FIG. 1B

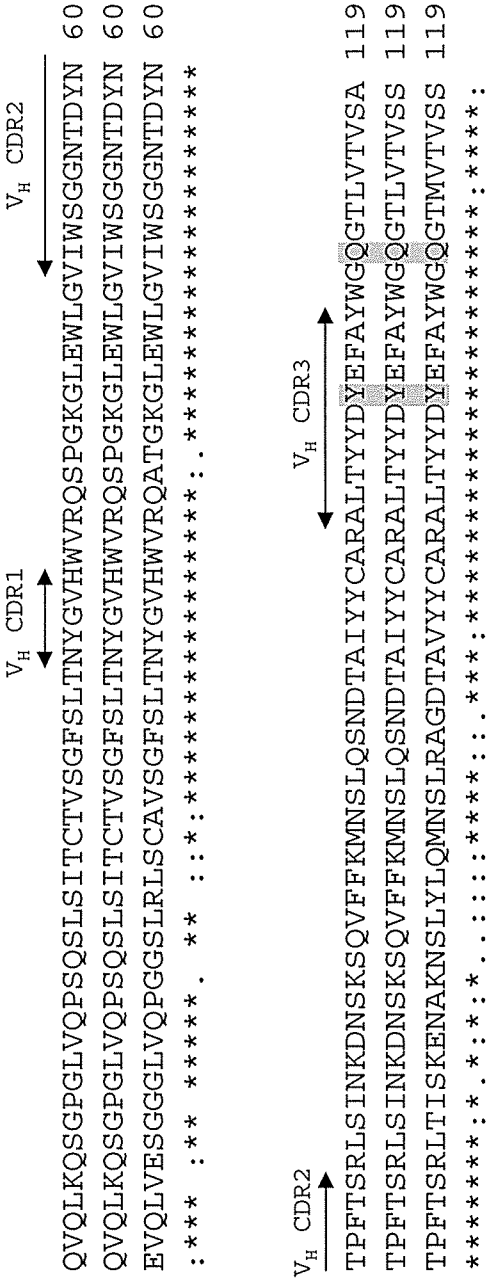

V_H CDR1
V_H CDR2
V_H CDR3
V_H CDR2
SEQIDNO_2
SEQIDNO_7
SEQIDNO_14
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
EVQLVESGGGLVQPGGSLRLSCAVSGFSLTNYGVHWVRQATGKGLEWLGVIWSGGNTDYN 60
TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSA 119
TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSS 119
TPFTSRLTISKENAKNSLYLQMNSLRAGDTAVYYCARALTYYDYEFAYWGQGTMVTVSS 119

FIG. 2A

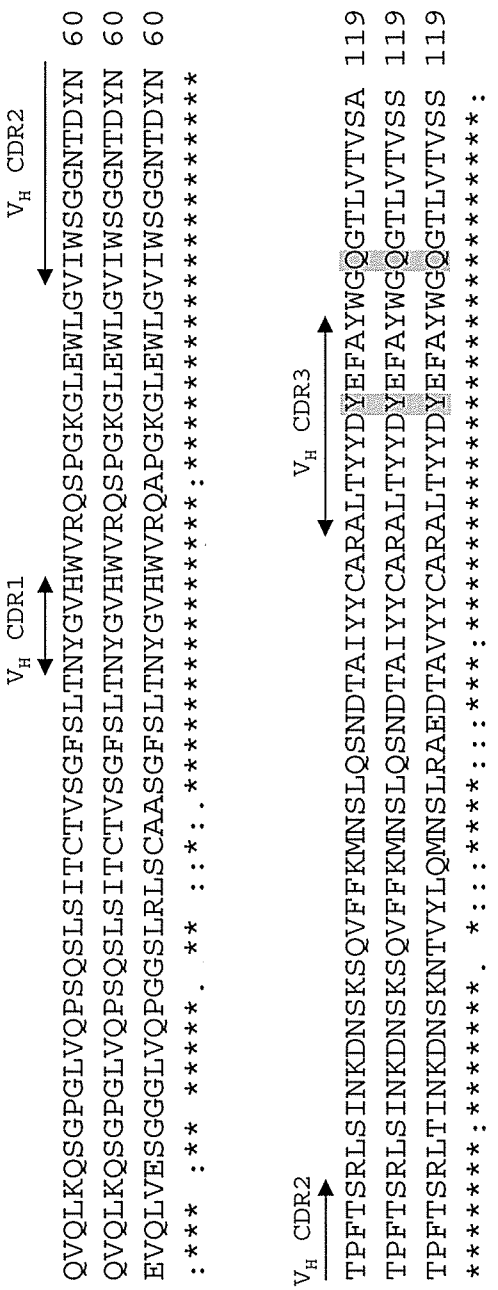

V_H CDR1
V_H CDR2
V_H CDR3
V_H CDR2
SEQIDNO_2
SEQIDNO_7
SEQIDNO_16
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLGVIWSGGNTDYN 60
EVQLVESGGGLVQPGGSLRLSCAASGFSLTNYGVHWVRQAPGKGLEWLGVIWSGGNTDYN 60
TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSA 119
TPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARALTYYDYEFAYWGQGTLVTVSS 119
TPFTSRLTINKDNSKNTVYLQMNSLRAEDTAVYYCARALTYYDYEFAYWGQGTLVTVSS 119

FIG. 2B

```
                                         VL CDR1                    VL CDR2
                                    <---------->               <------>
SEQIDNO_4     DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_11    DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_9     DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_15    EIVLTQSPATLSLSPGERATLSCRASQSIGTNIHWYQQRPGQAPRLLIKYASESISGIPA 60
              :*:*****. **:*****.::*****************.. :***************:

                                             VL CDR3
                                        <--------->
SEQIDNO_4     RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELK 107
SEQIDNO_11    RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKLELK 107
SEQIDNO_9     RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKVEIK 107
SEQIDNO_15    RFSGSGSGTDFTLTISSLEPEDFAVYYCQQNNNWPTTFGGGTKVEIK 107
              ************:*.*:*.**:* ************* ***:*:*
```

FIG. 2C

```
                                          VL CDR1                 VL CDR2
                                       <----------->             <------>
SEQIDNO_4     DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_11    DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_9     DILLTQSPVILSVSPGERVSFSCRASQSIGTNIHWYQQRTNGSPRLLIKYASESISGIPS 60
SEQIDNO_17    DILLTQSPGTLSLSPGERATLSCRASQSIGTNIHWYQQKPGQAPRLLIKYASESISGIPD 60
              ********  **:*****.::****************:..  :***************.

                                             VL CDR3
                                          <---------->
SEQIDNO_4     RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGAGTKLELK 107
SEQIDNO_11    RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKLELK 107
SEQIDNO_9     RFSGSGSGTDFTLSINSVESEDIADYYCQQNNNWPTTFGQGTKVEIK 107
SEQIDNO_17    RFSGSGSGTDFTLTISRLEPEDFAVYYCQQNNNWPTTFGQGTKLEIK 107
              *************:*. :*.**:* ************* ***:*:*
```

FIG. 2D