```
Kabat    1         10          22          31---35     40          50--abc------60---65
AbM      1         10          22    26--------35     40          50--abc-----58      65
Chothia  1         10          22    26------32       40             abc-55           65
Contact  1         10          22        30----35     40      47------abc----58       65
IMGT     1                     23    27------38  41                56-------65       74
AHon     1                     23    27          42                57                76
5H23     QVQLQQSGPELVKPGALVKISCKAS GYTFTS-YDIN WVKQRPGQGLEWIG WIYP--GDGSTKYNEKFKG
1C17     QVQLQESGPGLVKPSQSLSLTCSVT GYSITSGYYWN WIRQFPGNKLEWMG YIN---YDGNSNYTPSLKN
1D19     QVQPQESGPELVKPGALVKISCKAS GYTFTR-YDIN WMKQRPGQGLEWIG WIYP--GDSSTKFNENFKD
2L12     QVQLQQSGPELVKPGALVKISCKAS GYTFTR-YDIN WVKKRPGQGLEWIG WIYP--GDDSTKYNEKFKG
3L3      QVQPQESGPELVKPGTLVKISCKAS GYTFTS-YDIN WVKQRPGQGLEWIG WIYP--GDGSPKYDEKFKG
3N20     QVQLQESGAELARPGASVKLSCKVS GYIFTN-YGIS WVKQRTGQGLEWIG EIYP--RSGNTYYNEKFKG
4P5      QVQLQQSGPELVKPGALVKISCKAS GYTFTR-YDIN WVKKRPGQGLEWIG WIYP--GDDSTKYNEKFKG
5C23     QVQPQESGPELVKPGALVKISCKAS GYTFTR-YDIN WVKKRPGQGLEWIG WIYP--GDGSTKYNEKFEG
5F7      QVQPQESGPELVKPGALVKISCKAS GYTFTR-YDIN WVKQRPGQGLEWIG WIYP--GDISTKYNEKFKG
1G19     QVQLQESGPGLVKPSQSLSLTCSVT GYSITSGYYWN WIRQFPGNKLEWMG YIN---YGGSNNYNPSLKN

Kabat       70         80  abc       90     95--100----102       110
AbM         70         80  abc       90     95--100----102       110
Chothia     70         80  abc       90      96-100---101        110
Contact     70         80  abc       90  93-----100---101        110
IMGT    75              89             105-----------117
AHon                                106 109          138
5H23     KATLTADKSSRTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--AY WGQGTLVTVSA (SEQ ID NO:25)
1C17     RISITRDTSKNQFFLKLNSVTPEDTATYYCAR KGAYYSNYDSFDV WGTGTTVTVSS (SEQ ID NO:51)
1D19     KATLTADKSSSTAYMQLSSLTSENSTVYFCAR SDYYGSRSF--TY WGQGTLVTVSA (SEQ ID NO:77)
2L12     KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:103)
3L3      KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:129)
3N20     KATLTADMSSSTAYMDLRSLTSEDSAVYFCAR HWDGVLDYF--DY WGQGTSLTVSS (SEQ ID NO:155)
4P5      KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:181)
5C23     KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:207)
5F7      KATLTADKSSSTAYMQLNSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:233)
1G19     RISITRDTSKNQFFLKLTSVTTEDTATYYCAR RGAYYSNYDSFDV WGTGTTVTVSS (SEQ ID NO:259)
```

FIGURE 1A

```
Kabat    1         10         20    24-27abcd-------34      40          50-----56
AbM      1         10         20    24-----30abcd----34      40          50-----56
Chothia  1         10         20      26--30abcd--32         40          50--
Contact  1         10         20           30abcd-------36   40     46---------55
IMGT     1                       23    27----------38  41                56-65 69
                                                                        | |
AHon     1                       23                    42                58    72
5H23     DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYVYMH WNQQKPGQPPKLLIY LASYLES
1C17     DIKMTQSPSSMYASLGERVTITC KASQDINS------YLS WVQQKPGKSPKTLIY RANRLVD
1D19     DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
2L12     DIVLTQSPASLPVSLGQRATISC RASKSVST--SGYSYLH WYQQKPGQPPKLLIY LASNLES
3L3      DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYVH WYQQKPGQPPKLLIY LASNLES
3N20     DIVMTQSPSSLSVSAGEKVTMSC KSSQSLLNSGNQKNYLA WYQQKPGQPPKLLIY GASTRES
4P5      DILLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
5C23     DIVLTQSPDSLTVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
5F7      DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
1G19     DIKMTQSPSSMYASLGERVTITC KASQDINS------YLS WFQQKPGKSPKTLIY RANRLVD
```

```
Kabat       60         70         80         89------97
AbM         60         70         80         89------97
Chothia     60         70         80           91---96
Contact     60         70         80         89-----96
IMGT    70                89                105-----117
AHon    73                91                107     138
5H23     GVPARFSGSGSGTDFTLNIHPVEEEDAAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:26)
1C17     GVPSRFSGSGSGQDYSLTISSLEYEDMGIYYC LQYDEFPFT FGSGTKLEIK (SEQ ID NO:52)
1D19     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKLEIK (SEQ ID NO:78)
2L12     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSGELPYT FGGGTKLEIK (SEQ ID NO:104)
3L3      GVPARFSGRGSGTDFTLNIHPVEEEDAATYYC QHSGELPYT FGGGTKLEIK (SEQ ID NO:130)
3N20     GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC LNDHSYPFT FGAGTKLELK (SEQ ID NO:156)
4P5      GVPARFSGRGSGTDFTLNIHPVEEEDAATYYC HHSGELPYT FGGGTKLEIK (SEQ ID NO:182)
5C23     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKLEIK (SEQ ID NO:208)
5F7      GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKVEIK (SEQ ID NO:234)
1G19     GVPSRFSGSGSGQDYSLTISSLEYEEMGIYYC LQYDEFPYT FGGGTKLEIK (SEQ ID NO:260)
```

FIGURE 1B

VH Domain

Kabat	1 10 22	**31---35**	40	**50--abc------60---65**
AbM	1 10 22	**26---------35**	40	**50--abc----58** 65
Chothia	1 10 22	**26-----32**	40	**abc-55** 65
Contact	1 10 22	**30----35**	40	**47------abc----58** 65
IMGT	1 23	**27------38**	41	**56--------65** 74
AHon	1 23	27 42		57 76
5H23	QVQLQQSGPELVKPGALVKISCKAS	GYTFTS-YDIN	WVKQRPGQGLEWIG	WIYP--GDGSTKYNEKFKG
1D19	QVQPQESGPELVKPGALVKISCKAS	GYTFTR-YDIN	WMKQRPGQGLEWIG	WIYP--GDSSTKFNENFKD
2L12	QVQLQQSGPELVKPGALVKISCKAS	GYTFTR-YDIN	WVKKRPGQGLEWIG	WIYP--GDDSTKYNEKFKG
3L3	QVQPQESGPELVKPGTLVKISCKAS	GYTFTS-YDIN	WVKQRPGQGLEWIG	WIYP--GDGSPKYDEKFKG
4P5	QVQLQQSGPELVKPGALVKISCKAS	GYTFTR-YDIN	WVKKRPGQGLEWIG	WIYP--GDDSTKYNEKFKG
5C23	QVQPQESGPELVKPGALVKISCKAS	GYTFTR-YDIN	WVKKRPGQGLEWIG	WIYP--GDGSTKYNEKFEG
5F7	QVQPQESGPELVKPGALVKISCKAS	GYTFTR-YDIN	WVKQRPGQGLEWIG	WIYP--GDISTKYNEKFKG
consensus		**GYTFTR-YDIN** (SEQ ID NO:1)		**WIYP--GDX$_1$STKYNEKFKG** where X_1 = G,D,S,I (SEQ ID NO:262)
or				
consensus		**GYTFT X$_1$-YDIN** where X_1 = R,S (SEQ ID NO:261)		**WIYP--GDX$_1$STKYNEKFKG** where X_1 = G,D,S,I (SEQ ID NO:262)
1C17	QVQLQESGPGLVKPSQSLSLTCSVT	GYSITSGYYWN	WIRQFPGNKLEWMG	YIN---YDGNSNYTPSLKN
1G19	QVQLQESGPGLVKPSQSLSLTCSVT	GYSITSGYYWN	WIRQFPGNKLEWMG	YIN---YGGSNNYNPSLKN
consensus		**GYSITSGYYWN** (SEQ ID NO:27)		**YIN---YX$_1$GX$_2$X$_3$NYX$_4$PSLKN** where X_1 = D,G; where X_2 = N,S; where X_3 = S,N; where X_4 = T,N (SEQ ID NO:264)
3N20	QVQLQESGAELARPGASVKLSCKVS	GYIFTN-YGIS	WVKQRTGQGLEWIG	EIYP--RSGNTYYNEKFKG

FIGURE 2A-1

VH Domain (continued)

```
Kabat       70         80  abc       90     95--100-----102       110
AbM         70         80  abc       90     95--100-----102       110
Chothia     70         80  abc       90      96-100---101         110
Contact     70         80  abc       90  93------100---101        110
IMGT   75                89            105-------------117
AHon                                 106 109          138
5H23     KATLTADKSSRTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--AY WGQGTLVTVSA (SEQ ID NO:25)
1D19     KATLTADKSSSTAYMQLSSLTSENSTVYFCAR SDYYGSRSF--TY WGQGTLVTVSA (SEQ ID NO:77)
2L12     KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:103)
3L3      KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:129)
4P5      KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:181)
5C23     KATLTADKSSSTAYMQLSSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:207)
5F7      KATLTADKSSSTAYMQLNSLTSENSAVYFCAR SDYYGSRSF--VY WGQGTLVTVSA (SEQ ID NO:233)
consensus                                 SDYYGSRSF--VY
or                                        (SEQ ID NO:81)

consensus                                 SDYYGSRSF--X1Y  where X1 = V,T,A
                                          (SEQ ID NO:263)
1C17     RISITRDTSKNQFFLKLNSVTPEDTATYYCAR KGAYYSNYDSFDV WGTGTTVTVSS (SEQ ID NO:51)
1G19     RISITRDTSKNQFFLKLTSVTTEDTATYYCAR RGAYYSNYDSFDV WGTGTTVTVSS (SEQ ID NO:259)
consensus                                 X1GAYYSNYDSFDV  where X1 = K,R
                                          (SEQ ID NO:265)
3N20     KATLTADMSSSTAYMDLRSLTSEDSAVYFCAR HWDGVLDYF--DY WGQGTSLTVSS (SEQ ID NO:155)
```

FIGURE 2A-2

VL Domain

```
Kabat    1         10         20    24-27abcd-------34      40          50-----56
AbM      1         10         20    24-----30abcd----34      40          50-----56
Chothia  1         10         20      26--30abcd--32         40          50--
Contact  1         10         20           30abcd-------36   40     46---------55
IMGT     1                      23    27----------38  41                56-65 69
                                                                        | |
AHon     1                      23                  42                 58    72
5H23     DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYVYMH WNQQKPGQPPKLLIY LASYLES
1D19     DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
2L12     DIVLTQSPASLPVSLGQRATISC RASKSVST--SGYSYLH WYQQKPGQPPKLLIY LASNLES
3L3      DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYVH WYQQKPGQPPKLLIY LASNLES
4P5      DILLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
5C23     DIVLTQSPDSLTVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
5F7      DIVLTQSPASLAVSLGQRATISC RASKSVST--SGYSYMH WYQQKPGQPPKLLIY LASNLES
consensus                        RASKSVST--SGYSYMH                  LASNLES
or                                (SEQ ID NO:56)                (SEQ ID NO: 57)

consensus                        RASKSVST--SGYSYX1H                  LASNLES
                                           where X1 = M,L,V
                                  (SEQ ID NO:266)                (SEQ ID NO: 57)

1C17     DIKMTQSPSSMYASLGERVTITC KASQDINS------YLS WVQQKPGKSPKTLIY RANRLVD
1G19     DIKMTQSPSSMYASLGERVTITC KASQDINS------YLS WFQQKPGKSPKTLIY RANRLVD
consensus                        KASQDINS------YLS                  RANRLVD
or                                (SEQ ID NO:30)                (SEQ ID NO: 31)
3N20     DIVMTQSPSSLSVSAGEKVTMSC KSSQSLLNSGNQKNYLA WYQQKPGQPPKLLIY GASTRES
```

FIGURE 2B-1

VL Domain (continued)

```
Kabat      60         70         80         89-------97
AbM        60         70         80         89-------97
Chothia    60         70         80           91---96
Contact    60         70         80         89------96
IMGT   70                89                105------117
AHon   73                91                107     138
5H23     GVPARFSGSGSGTDFTLNIHPVEEEDAAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:26)
1D19     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKLEIK (SEQ ID NO:78)
2L12     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSGELPYT FGGGTKLEIK (SEQ ID NO:104)
3L3      GVPARFSGRGSGTDFTLNIHPVEEEDAATYYC QHSGELPYT FGGGTKLEIK (SEQ ID NO:130)
4P5      GVPARFSGRGSGTDFTLNIHPVEEEDAATYYC HHSGELPYT FGGGTKLEIK (SEQ ID NO:182)
5C23     GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKLEIK (SEQ ID NO:208)
5F7      GVPARFSGSGSGTDFTLNIHPVEEEDAATYYC QHSRELPYT FGGGTKVEIK (SEQ ID NO:234)
consensus                                  X1HSX2ELPYT where X1 = Q,H; where X2 = R,G
                                         (SEQ ID NO:267)

1C17     GVPSRFSGSGSGQDYSLTISSLEYEDMGIYYC LQYDEFPFT FGSGTKLEIK (SEQ ID NO:52)
1G19     GVPSRFSGSGSGQDYSLTISSLEYEEMGIYYC LQYDEFPYT FGGGTKLEIK (SEQ ID NO:260)
consensus                                  LQYDEFPX1T where X1 = F,Y
                                         (SEQ ID NO:268)
3N20     GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC LNDHSYPFT FGAGTKLELK (SEQ ID NO:156)
```

FIGURE 2B-2

VH Domain

```
Kabat      1         10          22      31--35    40        50--a------60---65
AbM        1         10          22  26-------35   40        50--a----58      65
Chothia    1         10          22  26----32      40            a-55         65
Contact    1         10          22      30---35   40     47------a----58     65
IMGT       1                     23  27-----38  41            56-----65       74
AHon       1                     23  27       42              57              76
5H23       QVQLQQSGPELVKPGALVKISCKAS GYTFTSYDIN WVKQRPGQGLEWIG WIYPGDGSTKYNEKFKG
5H23v1-3   QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYDIN WVRQAPGQRLEWMG WIYPGDGSTKYNEKFKG
vH1        QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWMG WIYPGDGSTKYNEKFKG
vH2        QVQLVQSGPEVKKPGASVKVSCKAS GYTFTSYDIN WVRQRPGQGLEWMG WIYPGDGSTKYNEKFKG
vH3        QVQLQQSGAEVKKPGASVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWIG WIYPGDGSTKYNEKFKG
vH4        QVQLVQSGPEVKKPGASVKVSCKAS GYTFTSYDIN WVRQRPGQGLEWIG WIYPGDGSTKYNEKFKG
vH5        QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWIG WIYPGDGSTKYNEKFKG
vH6        QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYDIN WVKQAPGQGLEWIG WIYPGDGSTKYNEKFKG

5H23v1-69  QVQLVQSGAEVKKPGSSVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWMG WIYPGDGSTKYNEKFKG
vH7        QVQLVQSGAEVKKPGSSVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWIG WIYPGDGSTKYNEKFKG
vH8        QVQLVQSGAEVKKPGSSVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWIG WIYPGDGSTKYNEKFKG
vH9        QVQLVQSGAEVKKPGSSVKVSCKAS GYTFTSYDIN WVRQAPGQGLEWIG WIYPGDGSTKYNEKFKG
```

FIGURE 3A-1

VH Domain (continued)

```
Kabat          70         80  abc       90     95--100--102       110
AbM            70         80  abc       90     95--100--102       110
Chothia        70         80  abc       90      96-100-101        110
Contact        70         80  abc       90  93------100-101       110
IMGT      75                 89            105-----------117
AHon                                   106 109       138
5H23       KATLTADKSSRTAYMQLSSLTSENSAVYFCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:25)
5H23v1-3   RVTITRDTSASTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:323)
vH1        RVTITRDTSASTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:269)
vH2        RVTITADKSARTAYMELSSLTSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:270)
vH3        KATITRDTSASTAYMELSSLRSEDTAVYFCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:271)
vH4        RVTITADKSARTAYMELSSLTSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:272)
vH5        KATLTADTSASTAYMELSSLRSENTAVYFCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:273)
vH6        KATLTADKSARTAYMELSSLRSENTAVYFCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:274)

5H23v1-69  RVTITADESTSTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:414)
vH7        RATLTADKSTSTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:320)
vH8        RATLTADKSTRTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:321)
vH9        RATITADKSTSTAYMELSSLRSEDTAVYYCAR SDYYGSRSFAY WGQGTLVTVSS (SEQ ID NO:322)
```

FIGURE 3A-2

VL Domain

```
Kabat       1         10         20    24-27abcd-----34      40          50-----56
AbM         1         10         20    24-----30ab-----34    40          50-----56
Chothia     1         10         20      26--30ab--32        40          50--
Contact     1         10         20           30ab--------36 40     46---------55
IMGT        1                       23   27--------38  41                56-65 69
                                                                          | |
AHon        1                        23                42                58    72
5H23      DIVLTQSPASLAVSLGQRATISC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
5H23v4-1  DIVMTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WYQQKPGQPPKLLIY LASYLES
vL1       DIVLTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
vL2       DIVMTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WYQQKPGQPPKLLIY LASYLES
vL3       DIVMTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
vL4       DIVLTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
vL5       DIVMTQSPDSLAVSLGERATINC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES


Kabat       60         70         80         89-------97
AbM         60         70         80         89-------97
Chothia     60         70         80           91---96
Contact     60         70         80         89------96
IMGT    70                 89               105------117
AHon    73                 91               107      138
5H23      GVPARFSGSGSGTDFTLNIHPVEEEDAAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:26)
5H23v4-1  GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:355)
vL1       GVPDRFSGSGSGTDFTLTISSVQAEDAAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:275)
vL2       GVPDRFSGSGSGTDFTLTISSVQAEDVAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:276)
vL3       GVPDRFSGSGSGTDFTLTISSVQAEDVAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:277)
vL4       GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QHSRDLTFP FGGGTKVEIK (SEQ ID NO:325)
vL5       GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QHSRDLTFP FGGGTKVEIK (SEQ ID NO:326)
```

FIGURE 3B

VL Domain

```
Kabat      1         10         20    24-27abcd-----34      40          50----56
AbM        1         10         20    24-----30ab----34     40          50-----56
Chothia    1         10         20      26--30ab--32        40          50--
Contact    1         10         20          30ab--------36  40     46---------55
IMGT       1                       23   27--------38  41                56-65 69
                                                                        | |
AHon       1                        23               42                58    72
5H23       DIVLTQSPASLAVSLGQRATISC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
5H23v1-39  DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39a     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39b     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39c     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WNQQKPGKAPKLLIY LASYLES
v1-39d     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39e     DIQLTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39f     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39g     DIQLTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39h     DIQLTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WNQQKPGKPPKLLIY LASYLES
v1-39i     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39j     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKAPKLLIY LASYLES
v1-39k     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WNQQKPGKPPKLLIY LASYLES
v1-39l     DIQLTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WNQQKPGKPPKLLIY LASYLES
v1-39m     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39n     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39o     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
v1-39p     DIQMTQSPSSLSASVGDRVTITC RASKSVSTSGYVYMH WYQQKPGKPPKLLIY LASYLES
```

FIGURE 3C-1

VL Domain (continued)

Kabat		60	70	80	**89------97**		
AbM		60	70	80	**89------97**		
Chothia		60	70	80	**91---96**		
Contact		60	70	80	**89------96**		
IMGT	70		89		**105------117**		
AHon	73		91		107	138	
5H23	GVPARFSGSGSGTDFTLNIHPVEEEDAAIYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:26)
5H23v1-39	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:353)
v1-39a	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				QHSRDLTFP	FG**Q**GTKLEIK	(SEQ ID NO:327)
v1-39b	GVPSRFSGSGSGTDFTLTISS**V**QPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:328)
v1-39c	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:329)
v1-39d	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:330)
v1-39e	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:331)
v1-39f	GVPSRFSGSGSGTDFTLTISS**V**QPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:332)
v1-39g	GVPSRFSGSGSGTDFTLTISS**V**QPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:333)
v1-39h	GVPSRFSGSGSGTDFTLTISS**V**QPEDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:334)
v1-39i	GVPSRFSGSGSGTDFTLTISSLQ**E**EDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:335)
v1-39j	GVPSRFSGSGSGTDFTLTISS**V**Q**E**EDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:336)
v1-39k	GVPSRFSGSGSGTDFTLTISS**V**Q**E**EDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:337)
v1-39l	GVPSRFSGSGSGTDFTLTISS**V**Q**E**ED**A**ATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:338)
v1-39m	GVPSRFSGSGSGTDFTLTISS**V**Q**E**EDFATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:339)
v1-39m	GVPSRFSGSGSGTDFTLTISS**V**Q**E**ED**A**ATYYC				QHSRDLTFP	FGGGTKLEIK	(SEQ ID NO:340)
v1-39o	GVPSRFSGSGSGTDFTLTISS**V**QPEDFATYYC				QHSRDLTFP	FG**Q**GTKLEIK	(SEQ ID NO:341)
v1-39p	GVPSRFSGSGSGTDFTLTISS**V**Q**E**EDFATYYC				QHSRDLTFP	FG**Q**GTKLEIK	(SEQ ID NO:342)

FIGURE 3C-2

VL Domain

```
Kabat      1         10         20    24-27abcd-----34      40          50----56
AbM        1         10         20    24-----30ab----34     40          50----56
Chothia    1         10         20      26--30ab--32        40          50--
Contact    1         10         20          30ab-------36   40     46---------55
IMGT       1                       23   27-------38  41                56-65 69
                                                                        | |
AHon       1                       23              42                  58    72
5H23       DIVLTQSPASLAVSLGQRATISC RASKSVSTSGYVYMH WNQQKPGQPPKLLIY LASYLES
5H23v3-20  EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQAPRLLIY LASYLES
v3-20a     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQAPRLLIY LASYLES
v3-20b     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQAPRLLIY LASYLES
v3-20c     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WNQQKPGQAPRLLIY LASYLES
v3-20d     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQPPRLLIY LASYLES
v3-20e     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQAPRLLIY LASYLES
v3-20f     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WNQQKPGQAPRLLIY LASYLES
v3-20g     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQPPRLLIY LASYLES
v3-20h     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WYQQKPGQAPRLLIY LASYLES
v3-20i     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WNQQKPGQAPRLLIY LASYLES
v3-20j     EIVLTQSPATLSLSPGERATLSC RASKSVSTSGYVYMH WNQQKPGQPPRLLIY LASYLES
```

FIGURE 3D-1

VL Domain (continued)

```
Kabat          60         70         80         89------97
AbM            60         70         80         89------97
Chothia        60         70         80           91---96
Contact        60         70         80         89------96
IMGT       70                 89                105-----117
AHon       73                 91                107     138
5H23        GVPARFSGSGSGTDFTLNIHPVEEEDAAIYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:26)
5H23v3-20   GIPARFSGSGSGTDFTLTISRLEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:354)
v3-20a      GIPARFSGSGSGTDFTLTISRLEPEDFAVYYC QHSRDLTFP FGQGTKLEIK (SEQ ID NO:343)
v3-20b      GIPARFSGSGSGTDFTLTISRVEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:344)
v3-20c      GIPARFSGSGSGTDFTLTISRLEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:345)
v3-20d      GIPARFSGSGSGTDFTLTISRLEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:346)
v3-20e      GIPARFSGSGSGTDFTLTISRLEPEDAAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:347)
v3-20f      GIPARFSGSGSGTDFTLTISRVEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:348)
v3-20g      GIPARFSGSGSGTDFTLTISRVEPEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:349)
v3-20h      GIPARFSGSGSGTDFTLTISRLEEEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:350)
v3-20i      GIPARFSGSGSGTDFTLTISRVEEEDFAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:351)
v3-20j      GIPARFSGSGSGTDFTLTISRVEEEDAAVYYC QHSRDLTFP FGGGTKLEIK (SEQ ID NO:352)
```

FIGURE 3D-2

FIGURE 4A


40
80
human MKPGCAAGSPGNEWIFFSTDEITTRYRNTMSNGGLQRSVILSALILLRAVTGFSGDGRAIWSKNPNFTPVNESQLFLYDT
chMoHu MKTGCAAGSPGNEWIFFSSDERNTRSRKTMSNRALQRSAVLSAFVLLRAVTGFSGDGKAIWDKKQYVSPVNPSQLFLYDT
chHuMo MKPGCAAGSPGNEWIFFSTDEITTRYRNTMSNGGLQRSVILSALILLRAVTGFSGDGRAIWSKNPNFTPVNESQLFLYDT
mouse MKTGCAAGSPGNEWIFFSSDERNTRSRKTMSNRALQRSAVLSAFVLLRAVTGFSGDGKAIWDKKQYVSPVNPSQLFLYDT
120
160
human FPKNFFWGIGTGALQVEGSWKKDGKGPSIWDHFIHTHLKNVSSTNGSSDSYIFLEKDLSALDFIGVSFYQFSISWPRLFP
chMoHu FPKNFSWGVGTGAFQVEGSWKTDGRGPSIWDRYVYSHLRGVNGTDRSTDSYIFLEKDLLALDFLGVSFYQFSISWPRLFP
chHuMo FPKNFFWGIGTGALQVEGSWKKDGKGPSIWDHFIHTHLKNVSSTNGSSDSYIFLEKDLSALDFIGVSFYQFSISWPRLFP
mouse FPKNFSWGVGTGAFQVEGSWKTDGRGPSIWDRYVYSHLRGVNGTDRSTDSYIFLEKDLLALDFLGVSFYQFSISWPRLFP
200
240
human DGIVTVANAKGLQYYSTLLDALVLRNIEPIVTLYHWDLPLALQEKYGGWKNDTIIDIFNDYATYCFQMFGDRVKYWITIH
chMoHu NGTVAAVNAQGLRYYRALLDSLVLRNIEPIVTLYHWDLPLTLQEEYGGWKNATMIDLFNDYATYCFQTFGDRVKYWITIH
chHuMo DGIVTVANAKGLQYYSTLLDALVLRNIEPIVTLYHWDLPLALQEKYGGWKNDTIIDIFNDYATYCFQMFGDRVKYWITIH
mouse NGTVAAVNAQGLRYYRALLDSLVLRNIEPIVTLYHWDLPLTLQEEYGGWKNATMIDLFNDYATYCFQTFGDRVKYWITIH
280
320
human NPYLVAWHGYGTGMHAPGEKGNLAAVYTVGHNLIKAHSKVWHNYNTHFRPHQKGWLSITLGSHWIEPNRSENTMDIFKCQ
chMoHu NPYLVAWHGFGTGMHAPGEKGNLTAVYTVGHNLIKAHSKVWHNYDKNFRPHQKGWLSITLGSHWIEPNRTDNMEDVINCQ
chHuMo NPYLVAWHGYGTGMHAPGEKGNLAAVYTVGHNLIKAHSKVWHNYNTHFRPHQKGWLSITLGSHWIEPNRSENTMDIFKCQ
mouse NPYLVAWHGFGTGMHAPGEKGNLTAVYTVGHNLIKAHSKVWHNYDKNFRPHQKGWLSITLGSHWIEPNRTDNMEDVINCQ
360
400
human QSMVSVLGWFANPIHGDGDYPEGMRKKLFSVLPIFSEAEKHEMRGTADFFAFSFGPNNFKPLNTMAKMGQNVSLNLREAL
chMoHu HSMSSVLGWFANPIHGDGDYPEFMKTG--AMIPEFSEAEKEEVRGTADFFAFSFGPNNFRPSNTVVKMGQNVSLNLRQVL
chHuMo QSMVSVLGWFANPIHGDGDYPEGMRKKLFSVLPIFSEAEKHEMRGTADFFAFSFGPNNFKPLNTMAKMGQNVSLNLREAL
mouse HSMSSVLGWFANPIHGDGDYPEFMKTG--AMIPEFSEAEKEEVRGTADFFAFSFGPNNFRPSNTVVKMGQNVSLNLRQVL
440
480
human NWIKLEYNNPRILIAENGWFTDSRVKTEDTTAIYMMKNFLSQVLQAIRLDEIRVFGYTAWSLLDGFEWQDAYTIRRGLFY
chMoHu NWIKLEYDDPQILISENGWFTDSYIKTEDTTAIYMMKNFLNQVLQAIKFDEIRVFGYTAWTLLDGFEWQDAYTTRRGLFY
chHuMo NWIKLEYNNPRILIAENGWFTDSRVKTEDTTAIYMMKNFLSQVLQAIRLDEIRVFGYTAWSLLDGFEWQDAYTIRRGLFY
mouse NWIKLEYDDPQILISENGWFTDSYIKTEDTTAIYMMKNFLNQVLQAIKFDEIRVFGYTAWTLLDGFEWQDAYTTRRGLFY

FIGURE 4B

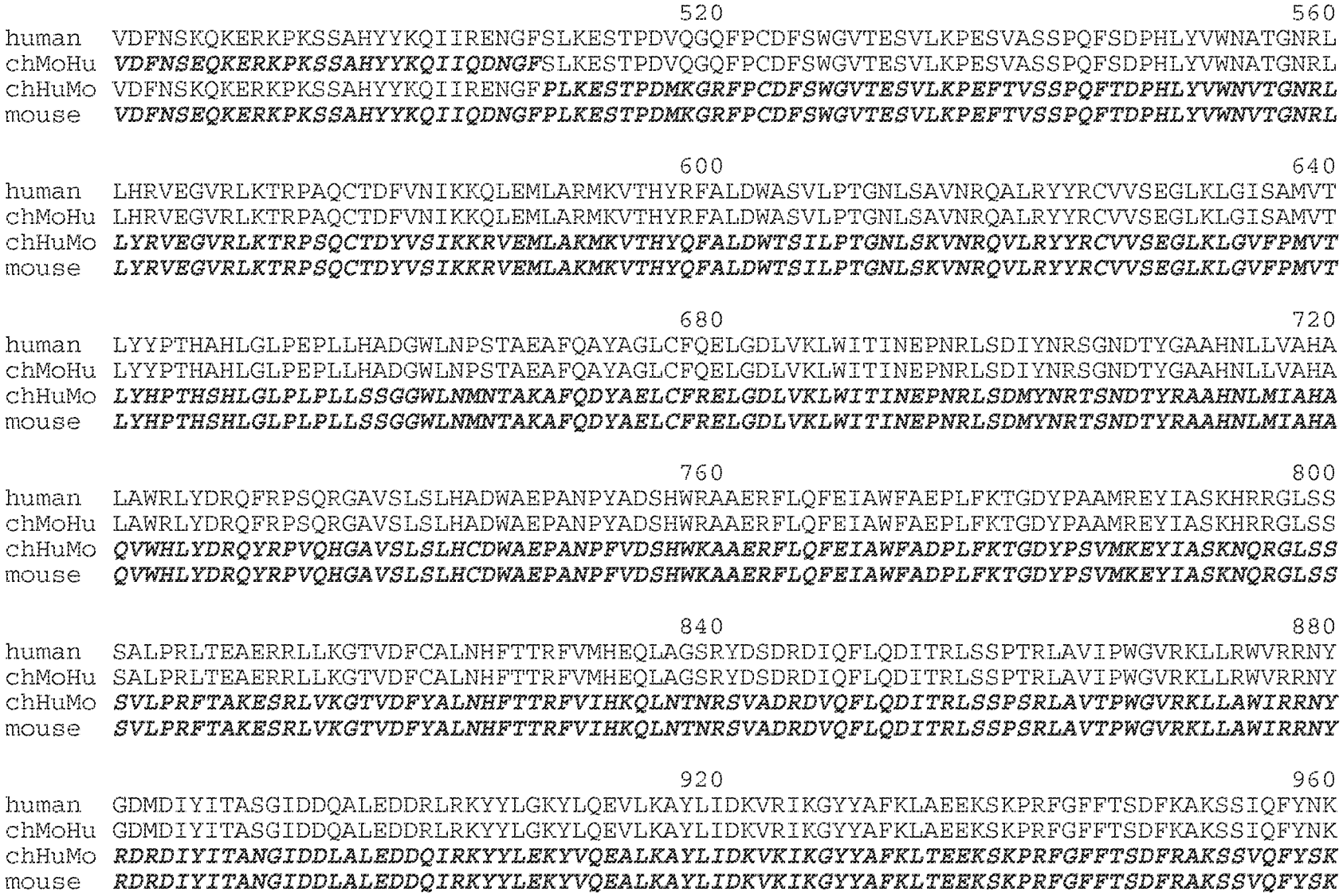

520
560
human VDFNSKQKERKPKSSAHYYKQIIRENGFSLKESTPDVQGQFPCDFSWGVTESVLKPESVASSPQFSDPHLYVWNATGNRL
chMoHu VDFNSEQKERKPKSSAHYYKQIIQDNGFSLKESTPDVQGQFPCDFSWGVTESVLKPESVASSPQFSDPHLYVWNATGNRL
chHuMo VDFNSKQKERKPKSSAHYYKQIIRENGFPLKESTPDMKGRFPCDFSWGVTESVLKPEFTVSSPQFTDPHLYVWNVTGNRL
mouse VDFNSEQKERKPKSSAHYYKQIIQDNGFPLKESTPDMKGRFPCDFSWGVTESVLKPEFTVSSPQFTDPHLYVWNVTGNRL
600
640
human LHRVEGVRLKTRPAQCTDFVNIKKQLEMLARMKVTHYRFALDWASVLPTGNLSAVNRQALRYYRCVVSEGLKLGISAMVT
chMoHu LHRVEGVRLKTRPAQCTDFVNIKKQLEMLARMKVTHYRFALDWASVLPTGNLSAVNRQALRYYRCVVSEGLKLGISAMVT
chHuMo LYRVEGVRLKTRPSQCTDYVSIKKRVEMLAKMKVTHYQFALDWTSILPTGNLSKVNRQVLRYYRCVVSEGLKLGVFPMVT
mouse LYRVEGVRLKTRPSQCTDYVSIKKRVEMLAKMKVTHYQFALDWTSILPTGNLSKVNRQVLRYYRCVVSEGLKLGVFPMVT
680
720
human LYYPTHAHLGLPEPLLHADGWLNPSTAEAFQAYAGLCFQELGDLVKLWITINEPNRLSDIYNRSGNDTYGAAHNLLVAHA
chMoHu LYYPTHAHLGLPEPLLHADGWLNPSTAEAFQAYAGLCFQELGDLVKLWITINEPNRLSDIYNRSGNDTYGAAHNLLVAHA
chHuMo LYHPTHSHLGLPLPLLSSGGWLNMNTAKAFQDYAELCFRELGDLVKLWITINEPNRLSDMYNRTSNDTYRAAHNLMIAHA
mouse LYHPTHSHLGLPLPLLSSGGWLNMNTAKAFQDYAELCFRELGDLVKLWITINEPNRLSDMYNRTSNDTYRAAHNLMIAHA
760
800
human LAWRLYDRQFRPSQRGAVSLSLHADWAEPANPYADSHWRAAERFLQFEIAWFAEPLFKTGDYPAAMREYIASKHRRGLSS
chMoHu LAWRLYDRQFRPSQRGAVSLSLHADWAEPANPYADSHWRAAERFLQFEIAWFAEPLFKTGDYPAAMREYIASKHRRGLSS
chHuMo QVWHLYDRQYRPVQHGAVSLSLHCDWAEPANPFVDSHWKAAERFLQFEIAWFADPLFKTGDYPSVMKEYIASKNQRGLSS
mouse QVWHLYDRQYRPVQHGAVSLSLHCDWAEPANPFVDSHWKAAERFLQFEIAWFADPLFKTGDYPSVMKEYIASKNQRGLSS
840
880
human SALPRLTEAERRLLKGTVDFCALNHFTTRFVMHEQLAGSRYDSDRDIQFLQDITRLSSPTRLAVIPWGVRKLLRWVRRNY
chMoHu SALPRLTEAERRLLKGTVDFCALNHFTTRFVMHEQLAGSRYDSDRDIQFLQDITRLSSPTRLAVIPWGVRKLLRWVRRNY
chHuMo SVLPRFTAKESRLVKGTVDFYALNHFTTRFVIHKQLNTNRSVADRDVQFLQDITRLSSPSRLAVTPWGVRKLLAWIRRNY
mouse SVLPRFTAKESRLVKGTVDFYALNHFTTRFVIHKQLNTNRSVADRDVQFLQDITRLSSPSRLAVTPWGVRKLLAWIRRNY
920
960
human GDMDIYITASGIDDQALEDDRLRKYYLGKYLQEVLKAYLIDKVRIKGYYAFKLAEEKSKPRFGFFTSDFKAKSSIQFYNK
chMoHu GDMDIYITASGIDDQALEDDRLRKYYLGKYLQEVLKAYLIDKVRIKGYYAFKLAEEKSKPRFGFFTSDFKAKSSIQFYNK
chHuMo RDRDIYITANGIDDLALEDDQIRKYYLEKYVQEALKAYLIDKVKIKGYYAFKLTEEKSKPRFGFFTSDFRAKSSVQFYSK
mouse RDRDIYITANGIDDLALEDDQIRKYYLEKYVQEALKAYLIDKVKIKGYYAFKLTEEKSKPRFGFFTSDFRAKSSVQFYSK

FIGURE 4C

```
                                                1000                                                1040
human   VISSRGFPFENSSSRCSQTQENTECTVCLFLVQKKPLIFLGCCFFSTLVLLLSIAIFQRQKRRKFWKAKNLQHIPLKKGK
chMoHu  VISSRGFPFENSSSRCSQTQENTECTVCLFLVQKKPLIFLGCCFFSTLVLLLSIAIFQRQKRRKFWKAKNLQHIPLKKGK
chHuMo  LISSSGLPAENRSPACGQPAEDTDCTICSFLVEKKPLIFFGCCFISTLAVLLSITVFHHQKRRKFQKARNLQNIPLKKGH
mouse   LISSSGLPAENRSPACGQPAEDTDCTICSFLVEKKPLIFFGCCFISTLAVLLSITVFHHQKRRKFQKARNLQNIPLKKGH

human   -RVVS (SEQUENCE ID 297)
chMoHu  -RVVS (SEQUENCE ID 376)
chHuMo  SRVFS (SEQUENCE ID 374)
mouse   SRVFS (SEQUENCE ID 301)
```

FIGURE 5A

```
                                      30                                  60
human    MKPGCAAGSPGNEWIFFSTDEITTRYRNTMSNGGLQRSVILSALILLRAVTGFSGDGRAI
cyno     MKPGCAAGSPGNEWIFFSTDEITIRYRNTMSNGGLQRSVILSALTLLRAVTGFSGDGRAV
mouse    MKTGCAAGSPGNEWIFFSSDERNTRSRKTMSNRALQRSAVLSAFVLLRAVTGFSGDGKAI
rabbit   MKPGCAAGSPGNEWVSFCTDERNRRCRETMSSGRLRRSVMLSAFILLRAVTGFPGDGRAV
hamster  MKAGCAAGSPGNEWIFLSSYERNTRSKKTMSNRALQRSVVLSAFVLLRAVTGLSGDGKAI
rat      MKTGCAAGSPGNEWVFFSSDERSTRSRKTMSNGALQRSAVLSALVLLRAVTGFSGDGKAI
dog      MKPGCAAGSPGNEWIFLSTDESNTHYRKTMCNHGLQRSVILSAFILLGAVPGFSGDGRAI
         ** ***********       *        **    * **  ***  ** ** *  *** *

                                      90                                 120
human    WSKNPNFTPVNESQLFLYDTFPKNFFWGIGTGALQVEGSWKKDGKGPSIWDHFIHTHLKN
cyno     WSKNPNFTPVNESQLFLYDTFPKNFFWGVGTGALQVEGSWKKDGKGPSIWDHFVHTHLKN
mouse    WDKKQYVSPVNPSQLFLYDTFPKNFSWGVGTGAFQVEGSWKTDGRGPSIWDRYVYSHLRG
rabbit   WSQNPNLSPVNESQLFLYDTFPKNFFWGVGTGAFQVEGSWKKDGKGLSVWDHFIATHLN-
hamster  WDKKQYVSPVNASQLFLYDTFPKNFFWGVGTGAFQVEGNWQADGRGPSIWDRFIYTHLRD
rat      WDKKQYVSPVNPGQLFLYDTFPKNFSWGVGTGAFQVEGSWKADGRGPSIWDRYVDSHLRG
dog      WSKNPHFSPVNESQLFLYDTFPKNFFWGVGTGAFQVEGNWKTDGKGPSIWDHFIHTHLKN
         *       ***  ************ ** **** **** *  ** * * **     **

                                     150                                 180
human    VSSTNGSSDSYIFLEKDLSALDFIGVSFYQFSISWPRLFPDGIVTVANAKGLQYYSTLLD
cyno     VSSTNGSSDSYIFLEKDLSALDFIGVSFYQFSISWPRLFPDGIVTVANAKGLQYYNTLLD
mouse    VNGTDRSTDSYIFLEKDLLALDFLGVSFYQFSISWPRLFPNGTVAAVNAQGLRYYRALLD
rabbit   VSSRDGSSDSYIFLEKDLSALDFLGVSFYQFSISWPRLFPDGTVAVANAKGLQYYNRLLD
hamster  VSITEKSADSYIFLEKDLLALDFLGVSFYQFSISWPRLFPNGTVASVNAKGLQYYNKLLD
rat      VNSTDRSTDSYVFLEKDLLALDFLGVSFYQFSISWPRLFPNGTVAAVNAKGLQYYRALLD
dog      VNSMNSSSDSYIFLEKDLSALDFIGVSFYQFSISWPRLFPDGIAAVANAKGLQYYNSLLD
         *     * *** ****** **** **************** *     ** ** **  ***
```

FIGURE 5B

```
                                    210                                 240
human    ALVLRNIEPIVTLYHWDLPLALQEKYGGWKNDTIIDIFNDYATYCFQMFGDRVKYWITIH
cyno     SLVLRNIEPIVTLYHWDLPLALQEKYGGWKNDTIIDIFNDYATYCFQTFGDRVKYWITIH
mouse    SLVLRNIEPIVTLYHWDLPLTLQEEYGGWKNATMIDLFNDYATYCFQTFGDRVKYWITIH
rabbit   SLLLRNIEPVVTLYHWDLPWALQEKYGGWKNETLIDLFNDYATYCFQTFGDRVKYWITIH
hamster  SLILRNIEPVVTLYHWDLPLALQEDYGGWKNATMIDLFNDYATYCFQTFGDRVKYWITIH
rat      SLVLRNIEPIVTLYHWDLPLTLQEEYGGWKNATMIDLFNDYATYCFQTFGDRVKYWITIH
dog      ALVLRNIEPIVTLYHWDLPLALQEKYGGWKNETITDIFNDYATYCFQTFGDRVKYWITIH
          * ****** *********  *** ****** *  * ********** ************

                                    270                                 300
human    NPYLVAWHGYGTGMHAPGEKGNLAAVYTVGHNLIKAHSKVWHNYNTHFRPHQKGWLSITL
cyno     NPYLVAWHGYGTGMHAPGEKGNLAAVYTVGHNLIKAHSKVWHNYNTHFRPHQKGWLSITL
mouse    NPYLVAWHGFGTGMHAPGEKGNLTAVYTVGHNLIKAHSKVWHNYDKNFRPHQKGWLSITL
rabbit   NPYLVAWHGYGTGLHAPGEKGNVAAVYTVGHNLLKAHSKVWHNYNRNFRPHQKGWLSITL
hamster  NPYLVAWHGFATGMHAPGETGNLTAVYIVGHNLIKAHSKVWHNYDKNFRPHQKGLLSITL
rat      NPYLVAWHGFGTGMHAPGEKGNLTAVYTVGHNLIKAHSKVWHNYDKNFRPHQKGWLSITL
dog      NPYLVAWHGYGTGMHAPGEKGNLAAVYTVGHNLIKAHSKVWHNYNTNFRPYQKGLLSITL
         *********  ** ***** **  *** ***** **********   *** *** *****

                                    330                                 360
human    GSHWIEPNRSENTMDIFKCQQSMVSVLGWFANPIHGDGDYPEGMRKKLFSVLPIFSEAEK
cyno     GSHWIEPNRSENTMDILKCQQSMVSVLGWFANPIHGDGDYPEGMKKKLLSILPLFSEAEK
mouse    GSHWIEPNRTDNMEDVINCQHSMSSVLGWFANPIHGDGDYPEFMKT--GAMIPEFSEAEK
rabbit   GSHWIEPNRAESIVDILKCQQSMVSVLGWFANPIHGDGDYPEVMTKKLLSVLPAFSEAEK
hamster  GSHWIEPNKTENMADTISCQHSMAFVLGWFANPIHADGDYPEFMKT--LSTMPVFSEAEK
rat      GSHWIEPNRTENMEDVINCQHSMSSVLGWFANPIHGDGDYPEFMKT--SSVIPEFSEAEK
dog      GSHWIEPNRSENMMDILKCQQSMVSVLGWFANPIHGNGDYPEVMKKKLLSTLPLFSEAEK
         ********       *   ** **  **********  ***** *         * ******
```

FIGURE 5C

```
                                    390                                 420
human    HEMRGTADFFAFSFGPNNFKPLNTMAKMGQNVSLNLREALNWIKLEYNNPRILIAENGWF
cyno     NEVRGTADFFAFSFGPNNFKPLNTMAKMGQNVSLNLREALNWIKLEYNNPRILIAENGWF
mouse    EEVRGTADFFAFSFGPNNFRPSNTVVKMGQNVSLNLRQVLNWIKLEYDDPQILISENGWF
rabbit   NEVRGTADFFAFSFGPNNFKPLNTMAKMGQNVSLNLRQVLNWIKLEYGNPRILIAENGWF
hamster  EEVRGTADFFAFSFGPNNFRPSNTVVKMGQNVSLNLRQVLNWIKLEYDNPRILISENGWF
rat      EEVRGTADFFAFSFGPNNFRPSNTVVKMGQNVSLNLRQVLNWIKLEYDNPRILISENGWF
dog      NEVRGTADFFAFSFGPNNFKPQNTMAKMGQNVSLNLREVLNWIKLEYGNPRILIAENGWF
          * ***************** * **  ***********  ********  * *** *****

                                    450                                 480
human    TDSRVKTEDTTAIYMMKNFLSQVLQAIRLDEIRVFGYTAWSLLDGFEWQDAYTIRRGLFY
cyno     TDSHVKTEDTTAIYMMKNFLSQVLQAIRLDEIRVFGYTAWSLLDGFEWQDAYTIRRGLFY
mouse    TDSYIKTEDTTAIYMMKNFLNQVLQAIKFDEIRVFGYTAWTLLDGFEWQDAYTTRRGLFY
rabbit   TDSYVQTEDTTAIYMMKNFLNQVLQAIRLDGVRVFGYTAWSLLDGFEWQDAYNTRRGLFY
hamster  TDSDIKTEDTTAIYMMKHFLNQVLQAIQFDEIRVFGYTAWSLLDGFEWQYAYTSRRGLFY
rat      TDSYIKTEDTTAIYMMKNFLNQVLQAIKFDEIQVFGYTAWTLLDGFEWQDAYTTRRGLFY
dog      TDSHVKTEDTTAIYMMKNFLNQVLQAIRFDEIQVFGYTAWSLLDGFEWQDAYSTRRGLFY
         ***   *********** ** ******  *   ******* ******** **  ******

                                    510                                 540
human    VDFNSKQKERKPKSSAHYYKQIIRENGFSLKESTPDVQGQFPCDFSWGVTESVLKPESVA
cyno     VDFNSKQKERKPKSSAHYYKQIIRENGFSLKEATPDVQGQFPCDFSWGVTESVLKPESVA
mouse    VDFNSEQKERKPKSSAHYYKQIIQDNGFPLKESTPDMKGRFPCDFSWGVTESVLKPEFTV
rabbit   VDFNSEQRERRPKSSAHYYKQVIGENGFTLREATPDLQGQFPCDFSWGVTESVLKPESVA
hamster  VDFNSEQKERKPKTSAHYYKQIIQENGFPLKESTPDMQGQFPCDFSWGVTESVLKPEFMV
rat      VDFNSEQKERKPKSSAHYYKQIIQDNGFPLQESTPDMKGQFPCDFSWGVTESVLKPEFTV
dog      VDFNSKQKERKPKSSAYYYKQIIQENGFTFKESTPDVQGQFPCDFSWGVTESVLKPKVVA
         ***** * ** ** ** **** *  ***   * ***  * ****************
```

FIGURE 5D

```
                                        570                                 600
human      SSPQFSDPHLYVWNATGNRLLHRVEGVRLKTRPAQCTDFVNIKKQLEMLARMKVTHYRFA
cyno       SSPQFSDPYLYVWNATGNRLLHRVEGVRLKTRPAQCTDFVNIKKQLEMLARMKVTHYRFA
mouse      SSPQFTDPHLYVWNVTGNRLLYRVEGVRLKTRPSQCTDYVSIKKRVEMLAKMKVTHYQFA
rabbit     SSPQFSDPHLYVWNATGNRMLHRVEGVRLKTRPAQCTDFITIKKQLEMLARMKVTHFRFA
hamster    SSPQFTDPHLYVWNATGNRLLQRVEGVRLKTKPSHCTDYVSIKKRVEMLAKMKVTHYQFA
rat        SSPQFTDPHLYVWNVTGNRLLYRVEGVRLKTRPSQCTDYVSIKKRVEMLAKMKVTHYQFA
dog        SSPQFSDPHLYVWNVTGNRLLHRVEGVRLKTRPAQCTDFVSIKRQLEMLARMNVTHYRFA
           ***** ** ***** **** * ********* *  ***   **   **** * ***  **

                                        630                                 660
human      LDWASVLPTGNLSAVNRQALRYYRCVVSEGLKLGISAMVTLYYPTHAHLGLPEPLLHADG
cyno       LDWASVLPTGNLSAVNRQALRYYRCVVSEGLKLGISAMVTLYYPTHAHLGLPEPLLHAGG
mouse      LDWTSILPTGNLSKVNRQVLRYYRCVVSEGLKLGVFPMVTLYHPTHSHLGLPLPLLSSGG
rabbit     LDWASVLPTGNLSEVNRQALRYYRCVVTEGLKLNISPMVTLYYPTHAHLGLPAPLLHSGG
hamster    LDWATILPTGNLSEVNRQVLRYYRCVVSEGLKLGVSPMVTLYHPTHSHLGLPEPLLNSGG
rat        LDWTSILPTGNLSKINRQVLRYYRCVVSEGLKLGISPMVTLYHPTHSHLGLPMPLLSSGG
dog        LDWPSILPTGNLSTVNRQALRYYRCVVSESLKLSISPMVTLYYPTHAHLGLPSPLLHSGG
           ***   *******  *** ******** * ***    ***** *** ***** ***   *

                                        690                                 720
human      WLNPSTAEAFQAYAGLCFQELGDLVKLWITINEPNRLSDIYNRSGNDTYGAAHNLLVAHA
cyno       WLNPSTVEAFQAYAGLCFQELGDLVKLWITINEPNRLSDIYNRSGNDTYGAAHNLLVAHA
mouse      WLNMNTAKAFQDYAELCFRELGDLVKLWITINEPNRLSDMYNRTSNDTYRAAHNLMIAHA
rabbit     WLDPSTAKAFRDYAGLCFRELGDLVKLWITINEPNRLSDVYNRTSNDTYQAAHNLLIAHA
hamster    WLNTYTAKAFQDYAGLCFQELGDLVKLWITINEPNRLSDMYNRTSNDTYRAAHNLMIAHA
rat        WLNTNTAKAFQDYAGLCFKELGDLVKLWITINEPNRLSDMYNRTSNDTYRAAHNLMIAHA
dog        WLNASTARAFQDYAGLCFQELGDLVKLWITINEPNRLSDVYSHTSSDTYRAAHNLLIAHA
           **   *  **  ** *** ********************* *     *** *****  ***
```

FIGURE 5E

```
                                    750                                 780
human    LAWRLYDRQFRPSQRGAVSLSLHADWAEPANPYADSHWRAAERFLQFEIAWFAEPLFKTG
cyno     LAWRLYDRQFRPSQRGAVSLSLHADWAEPANPYADSHWRAAERFLQFEIAWFAEPLFKTG
mouse    QVWHLYDRQYRPVQHGAVSLSLHCDWAEPANPFVDSHWKAAERFLQFEIAWFADPLFKTG
rabbit   LVWHLYDRQYRPSQRGALSLSLHSDWAEPANPYVASHWQAAERFLQFEIAWFAEPLFKTG
hamster  QVWRLYDRQYRPVQHGAVSLSLHSDWVEPANPYVDSHWKAAERFLLFEIAWFADPLFKTG
rat      QVWHLYDRQYRPVQHGAVSLSLHSDWAEPANPYVESHWKAAERFLQFEIAWFADPLFKTG
dog      LVWHLYDRRYRPAQRGAVSLSLHSDWAEPANPYADSHWKAAERFLQFEIAWFAEPLFKTG
           * ****  ** * ** ***** ** *****   *** ****** ******* ******

                                    810                                 840
human    DYPAAMREYIASKHRRGLSSSALPRLTEAERRLLKGTVDFCALNHFTTRFVMHEQLAGSR
cyno     DYPAAMREYIASKHRRGLSSSALPRLTEAERRLLKGTVDFCALNHFTTRFVMHEQLAGSR
mouse    DYPSVMKEYIASKNQRGLSSSVLPRFTAKESRLVKGTVDFYALNHFTTRFVIHKQLNTNR
rabbit   DYPVAMREYIASKTRRGLSSSVLPRFSDAERRLVKGAADFYALNHFTTRFVMHEQQNGSR
hamster  DYPLAMKEYIASKNQQGLSRSVLPRFTPEESRLVKGTIDFYALNHFTTRFVIHKQLNSSR
rat      DYPLAMKEYIASKKQRGLSSSVLPRFTLKESRLVKGTIDFYALNHFTTRFVIHKQLNTNC
dog      DYPPAMREYIASKNRQGLSRSTLPRFTDEERRLVKGAADFYALNHFTTRFVMHARQNGSR
         ***  * ******   *** * ***    * ** **  ** ********** *

                                    870                                 900
human    YDSDRDIQFLQDITRLSSPTRLAVIPWGVRKLLRWVRRNYGDMDIYITASGIDDQALEDD
cyno     YDSDRDIQFLQDITRLSSPTRLAVIPWGVRKLLRWVRRNYGDMDIYITASGIDDQALEDD
mouse    SVADRDVQFLQDITRLSSPSRLAVTPWGVRKLLAWIRRNYRDRDIYITANGIDDLALEDD
rabbit   YDSDRDVQFLQDITRLASPSRLAVMPWGEGKLLRWMRNNYGDLDVYITANGIDDQALQND
hamster  SMADRDVQFLQDITRLSSPSRLAVMPWGARKLLGWIQRNYGDMDIYITANGIDDLALEND
rat      SVADRDVQFLQDITRLSSPSRLAVTPWGMRKLLGWIRRNYRDMDIYVTANGIDDLALEDD
dog      YDADRDVQFLQDITCLSSPSRLAVLPWGERKVLRWIQKNYGDVDVYITASGIDDQSLEND
           *** ******* * ** **** ***  * * *   ** * * * ** ****  *  *
```

FIGURE 5F

```
                                      930                                 960
human    RLRKYYLGKYLQEVLKAYLIDKVRIKGYYAFKLAEEKSKPRFGFFTSDFKAKSSIQFYNK
cyno     RLRKYYLEKYLQEVLKAYLIDKVRIKGYYAFKLAEEKSKPRFGFFTSDFKAKSSIQFYNK
mouse    QIRKYYLEKYVQEALKAYLIDKVKIKGYYAFKLTEEKSKPRFGFFTSDFRAKSSVQFYSK
rabbit   QLRQYYLEKYVQEALKAYLIDKIKIKGYYAFKLTEEKSKPRFGFFTSDFKAKSSIQFYNK
hamster  GIRKYYLEKYIQEALKAYLIDKVKIKGYYAFKLTEEKSKPRFGFFTSDFKAKSSVEFYSK
rat      QIRKYYLEKYVQEALKAYLIDKVKIKGYYAFKLTEEKSKPRFGFFTSDFKAKSSVQFYSK
dog      ELRKYYLEKYIQEALKAHLIDKVKVKGYYAFKLTEEKSKPRFGFFTSEFKAKSSVQLYNK
           * *** ** ** *** ****   ******** ************ * ****   * *

                                      990                                1020
human    VISSRGFPFENSSSRCSQTQENTECTVCLFLVQKKPLIFLGCCFFSTLVLLLSIAIFQRQ
cyno     MISSSGFPSENSSSRCSQTQKNTECTVCLFLVQKKPLIFLGCCFFSTLVLLLSITIFHRQ
mouse    LISSSGLPAENRSPACGQPAEDTDCTICSFLVEKKPLIFFGCCFISTLAVLLSITVFHHQ
rabbit   LITSNGFPSENGGPRCNQTQGNPECTVCLLLLQKKPLIFFSCCFFCTLVLLSSITIFHRR
hamster  LISRSGFPSETSNPACGQPPEDTDCTICSFFTQKKSLIFFGCCFISTLAVLLSITIFHHR
rat      LISSSGFSSENRSPACGQPPEDTECAICSFLTQKKPLIFFGCCFISTLAALLSITIFHHR
dog      LISNSGFPSENRSPRCSETQRNTECMVCLFLVQKKPLIFFSCCFFSTLVLLSSITILHKR
          *   *   *     *        * *     ** ***  ***  **  * **

                                   1045
human    KRRKFWKAKNLQHIPLKKGKRVVS-  (SEQ ID NO:297)
cyno     KRRKFWKAKNLQHIPLKKGKRVLS-  (SEQ ID NO:299)
mouse    KRRKFQKARNLQNIPLKKGHSRVFS  (SEQ ID NO:301)
rabbit   KRRKFWKAKDLQHIPLKKGHKRVLS  (SEQ ID NO:410)
hamster  KRR-FHKSKNLENIPLKEGHSRVLS  (SEQ ID NO:408)
rat      KRRKFQKARNLQNIPLKKGHSRVFS  (SEQ ID NO:356)
dog      KRRKIWKAKNLQHIPLKKSKNSLQS  (SEQ ID NO:412)
         ***   *   *  ****
```

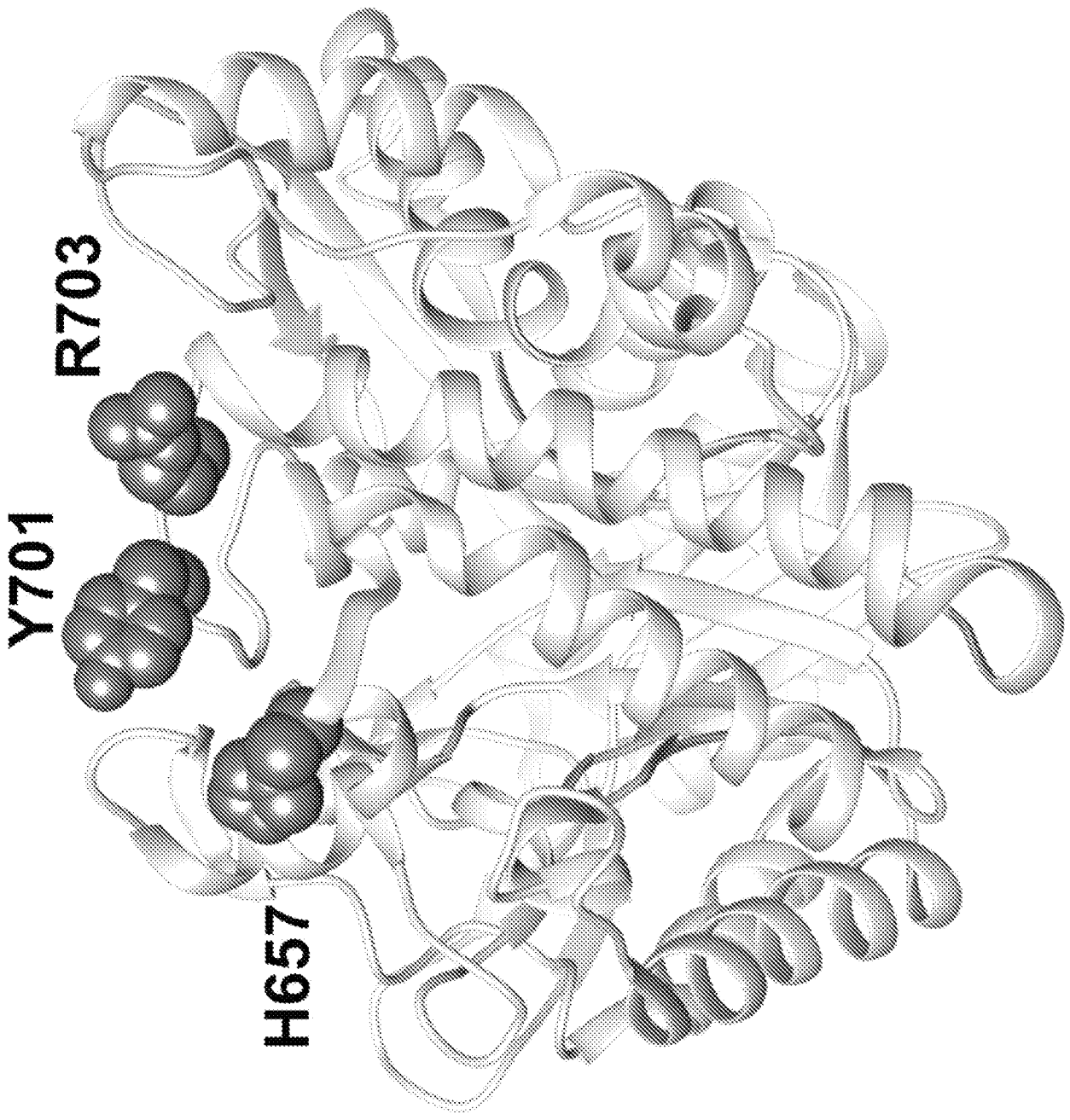


FIGURE 6