FIG. 1A

9B3 VH1 QVQLVESGGGVVQPGRSLRLSCAAS***GFTFSNYALH***WVRQAPGKGLE
WVALISYDGSDKYYADSVKGRFAISRDNSKNTLYLQMNSLRAEDTAVY
YCARDREYCTYSSCSYDAFDIWGQGTMVTVSS

9B3 VH2 QVQLVESGGGVVQPGRSLRLSCAAS***GFTFSSFAMH***WVRQAPGKGLE
WVALIPFDGSSNYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY
YCARDRNYYGSGSFSFDAFDIWGQGTLVTVSS

9B3 VL DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLI
YAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDYATYYCQQYNSYPY
TFGQGTKLEIK

15A9 VH QVQLVQSGAEVKKPGASLKVSCKAS***GYPFTNYGIS***WVRQAPGQGLE
WMGWISTYNGNTHYAQKLQGRVTMTTDTSTTTAYMDLRSLRSDDTA
VYYCARENYYGSGSYRGGMDVWGQGTTVTVSS

15A9 VL EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLI
YDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP
WTFGQGTKVEIK

15C11 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTTYGIS***WVRQAPGQGLE
WMGWISTYNGNTHYAQKLQGRVTMTTDTSTRTAYMELRSLRSDDTA
VYYCARENYYGSGSYRGGMDVWGQGTTVTVSS

15C11 VL EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLI
YDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP
WT

22F9 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYTFTSYAMH***WVRQAPGQRLE
WMGWINAGNGNTKYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAV
YYCARGYSSAWFDAFDIWGQGTMVTVSS

22F9 VL AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIY
DASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPLT
FGGGTKVEIK

FIG. 1B

26B11 VH1 QVQLVESGGGVVQPGRSLRLSCAAS***GFTFSNYALH***WVRQAPGKGLEW
VALISYDGSDKYYADSVKGRFAISRDNSKNTLYLQMNSLRAEDTAVYYC
ARDREYCTYSSCSYDAFDIWGQGTMVTVSS

26B11 VH2 QVQLVESGGGVVQPGRSLRLSCAAS***GFTFSSFAMH***WVRQAPGKGLE
WVALIPFDGSSNYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY
CARDRNYYGSGSFSFDAFDIWGQGTLVTVSS

26B11 VH MDX QVQLVESGGGVVQPGRSLRLSCEAS***GFTFSNYAIH***WVRQAPGKGLEW
VALIPYDGSNNYYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
ARDRNYYGSGSFSFDAFDIWGQGTMVTVSS

26B11 VL DIQMTQSPSSLSASVGDRVTITCRASQGISNWLAWYQQKPEKAPKSLIY
AASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPYTF
GQGTKLEIK

7D4 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYTFTSYGIN***WVRQAPGQGLEW
MGWISTYNGNTNSAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYY
CARAHSSSWFDAFDIWGQGTMVTVSS

7D4 VL AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYD
ASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYPLTFG
GGTKVEIK

1D1 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVYY
CARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 VL EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIY
DASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPWTF
GQGTKVEIK

FIG. 1C

1D1 D5 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGNTNYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGAFRGGMDG</u>WGQGTTVTVSS

1D1 D18 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D21 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGKTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D24 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISPYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D25 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGATHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D28 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGKTHYARMHQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D29 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISSYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D31 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGL
EWMG<u>WISTYNGNKHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDD
TAVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D37 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGGTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDT
AVYYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

FIG. 1D

1D1 D38 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISTYNGVTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 D39 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISTYNGNTNYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGAYRGGMDA</u>WGQGTTVTVSS

1D1 DH3 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISTYNGNTHYAQMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 DH8 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISAYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 DH9 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISPYNGKTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 DH10 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MG<u>WISTYNGNTNYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAVY
YCAR<u>ENYYGSGAYRGGMDV</u>WGQGTTVTVSS

FIG. 1E

1D1 1.1 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.2 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYNFTYYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.3 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYQFTYYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.4 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTHYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.5 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYNFRYYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.6 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYNFTHYGIS***WVRQAPGQGLE
WMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.7 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGKTNYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.8 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFRYYGIS***WVRQAPGQGLE
WMGWISTYNGNTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGSYRGGMDVWGQGTTVTVSS

1D1 1.9 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGNTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDVWGQGTTVTVSS

FIG. 1F

1D1 1.10 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGKTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDVWGQGTTVTVSS

1D1 1.11 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFRYYGIS***WVRQAPGQGLE
WMGWISTYNGNTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGAYRGGMDVWGQGTTVTVSS

1D1 1.12 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYNFTYYGIS***WVRQAPGQGLE
WMGWISPYNGKTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGAYRGGMDVWGQGTTVTVSS

1D1 1.13 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTHYGIS***WVRQAPGQGLE
WMGWISPYNGKTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGAYRGGMDVWGQGTTVTVSS

1D1 1.14 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYNFTHYGIS***WVRQAPGQGLE
WMGWISPYNGKTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAV
YYCARENYYGSGAYRGGMDVWGQGTTVTVSS

1D1 1.15 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGGTHYAQMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.16 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGVTHYAQMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.17 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGATHYAQMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.18 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGNKHYAQMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

FIG. 1G

1D1 1.19 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGGTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.20 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISPYNGNTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.21 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGNTHYAQMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.22 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGVTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.23 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGATHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.24 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGNKHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.25 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGKTHYARMHQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

1D1 1.26 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYSFTYYGIS***WVRQAPGQGLEW
MGWISTYNGNTHYARMLQGRVTMTTDTSTRTAYMELRSLRSDDTAVY
YCARENYYGSGAYRGGMDAWGQGTTVTVSS

FIG. 1H

1D1 1.27 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 1.28 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGNKHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 1.29 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGGTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 1.30 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGVTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGSYRGGMDV</u>WGQGTTVTVSS

1D1 1.31 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGNTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGAYRGGMDV</u>WGQGTTVTVSS

1D1 1.32 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGGTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGAYRGGMDA</u>WGQGTTVTVSS

1D1 1.33 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGVTHYARMLQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGAYRGGMDA</u>WGQGTTVTVSS

1D1 1.34 VH QVQLVQSGAEVKKPGASVKVSCKAS***GYDFTYYGIS***WVRQAPGQGLE
WMG<u>WISTYNGKTHYARMHQG</u>RVTMTTDTSTRTAYMELRSLRSDDTAV
YYCAR<u>ENYYGSGAYRGGMDA</u>WGQGTTVTVSS

FIG. 1I

Alignment of Light Chain Variable Domains:

```
26B11    1 DIQMTQSPSSLSASVGDRVTITCRASQGISNWLAWYQQKPEKAP 44
7D4      1 AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAP 44
1D1      1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAP 44

26B11   45 KSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPE 81
7D4     45 KLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPE 81
1D1     45 RLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPE 81

26B11   82 DFATYYCQQYNSYPYTFGQGTKLEIK 107
7D4     82 DFATYYCQQFNSYPLTFGGGTKVEIK 107
1D1     82 DFAVYYCQQRSNWPWTFGQGTKVEIK 107
```

Alignment of Heavy Chain Variable Domains:

```
1D1      1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTYYGISWVRQAPGQGL 45
7D4      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGINWVRQAPGQGL 45
26B11    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFAMHWVRQAPGKGL 45

1D1     46 EWMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYM 80
7D4     46 EWMGWISTYNGNTNSAQKLQGRVTMTTDTSTSTAYM 80
26B11   46 EWVALIPFDGSSNYYADSVKGRFTISRDNSKNTLYL 80

1D1     81 ELRSLRSDDTAVYYCARENYYGSG..SYRGGMDVWGQGTTVTVSS 113
7D4     81 ELRSLRSDDTAVYYCARAHSS.....SWFDAFDIWGQGTMVTVSS 113
26B11   81 QMNSLRAEDTAVYYCARDRNYYGSGSFSFDAFDIWGQGTLVTVSS 113
```

FIG. 1J

Alignment of Light Chain Variable Domains:

```
22F9 VL   1 AIQLTQSPSSLSASVGDRVTITCRASQGISSALA 34
7D4  VL   1 AIQLTQSPSSLSASVGDRVTITCRASQGISSALA 34

22F9 VL  35 WYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPE 81
7D4  VL  35 WYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPE 81

22F9 VL  82 DFATYYCQQFNSYPLTFGGGTKVEIK 107
7D4  VL  82 DFATYYCQQFNSYPLTFGGGTKVEIK 107
```

Alignment of Heavy Chain Variable Domains:

```
                                                  ***
7D4  VH   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGINWVR 38
22F9 VH   1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVR 38

                          ***     ***   *
7D4  VH  39 QAPGQGLEWMGWISTYNGNTNSAQKLQGRVTMTTDTSTSTAYM 80
22F9 VH  39 QAPGQRLEWMGWINAGNGNTKYSQKFQGRVTITRDTSASTAYM 80

                   *          **   *
7D4  VH  81 ELRSLRSDDTAVYYCARAHSSSWFDAFDIWGQGTMVTVSS 113
22F9 VH  81 ELSSLRSEDTAVYYCARGYSSAWFDAFDIWGQGTMVTVSS 113
                   |
                   85
```

FIG. 1K

Alignment of Light Chain Variable Domains:

```
                                                *
26B11 VL   1 DIQMTQSPSSLSASVGDRVTITCRASQGISNWLA 34
9B3   VL   1 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLA 34


26B11 VL 35 WYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPE 81
9B3   VL 35 WYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPE 81

              *
26B11 VL 82 DFATYYCQQYNSYPYTFGQGTKLEIK 107
9B3   VL 82 DYATYYCQQYNSYPYTFGQGTKLEIK 107
              |
              83
```

Alignment of Heavy Chain Variable Domains VH1 and VH2 of antibodies 9B3 and 26B11, and MDX-VH of 26B11(9B3 and 26B11 produce multiple functional heavy chains which have the same sequences)

```
                                                  ** *
9B3/26B11 VH1   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYALHWVR 38
9B3/26B11 VH2   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFAMHWVR 38
26B11     MDX   1 QVQLVESGGGVVQPGRSLRLSCEASGFTFSNYAIHWVR 38


                                  **   **          *
9B3/26B11 VH1 39 QAPGKGLEWVALISYDGSDKYYADSVKGRFAISRDNSKNTLYL 80
9B3/26B11 VH2 39 QAPGKGLEWVALIPFDGSSNYYADSVKGRFTISRDNSKNTLYL 80
26B11     MDX 39 QAPGKGLEWVALIPYDGSNNYYAASVKGRFTISRDNSKNTLYL 80
                                              |
                                              68

                                        * **** * *          *
9B3/26B11 VH1 81 QMNSLRAEDTAVYYCARDREYCTYSSCSYDAFDIWGQGTMVTVSS 113
9B3/26B11 VH2 81 QMNSLRAEDTAVYYCARDRNYYGSGSFSFDAFDIWGQGTLVTVSS 113
26B11     MDX 81 QMNSLRAEDTAVYYCARDRNYYGSGSFSFDAFDIWGQGTMVTVSS 113
                                                       |
                                                       108
```

FIG. 1L

Alignment of Light Chain Variable Domains:

```
15C11    1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLA 34
1D1      1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLA 34
15A9     1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLA 34

15C11   35 WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSL 78
1D1     35 WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSL 78
15A9    35 WYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSL 78

15C11   79 EPEDFAVYYCQQRSNWPWTFGQGTKVEIK 107
1D1     79 EPEDFAVYYCQQRSNWPWTFGQGTKVEIK 107
15A9    79 EPEDFAVYYCQQRSNWPWTFGQGTKVEIK 107
```

Alignment of Heavy Chain Variable Domains:

```
                                        *  *
15A9     1 QVQLVQSGAEVKKPGASLKVSCKASGYPFTNYGIS 35
15C11    1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTTYGIS 35
1D1      1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTYYGIS 35

                                       **              *
15A9    36 WVRQAPGQGLEWMGWISTYNGNTHYAQKLQGRVTMTTDTSTTTAYM 80
15C11   36 WVRQAPGQGLEWMGWISTYNGNTHYAQKLQGRVTMTTDTSTRTAYM 80
1D1     36 WVRQAPGQGLEWMGWISTYNGNTNYARMLQGRVTMTTDTSTRTAYM 80
                                                    |
                                                    76
           *
15A9    81 DLRSLRSDDTAVYYCARENYYGSGSYRGGMDVWGQGTTVTVSS 113
15C11   81 ELRSLRSDDTAVYYCARENYYGSGSYRGGMDVWGQGTTVTVSS 113
1D1     81 ELRSLRSDDTAVYYCARENYYGSGSYRGGMDVWGQGTTVTVSS 113
           |
           81
```

FIG. 1M

Percentage identity of variable heavy domains for 1D1 and variants (1D1 variants share the same light chain as parent antibody 1D1)

	1D1	1.27	1.28	1.29	1.30	1.31	1.32	1.33	1.34
1D1	100	98.4	97.6	97.6	97.6	97.6	96.0	96.0	95.2
1.27	98.4	100	99.2	99.2	99.2	99.2	97.6	97.6	96.8
1.28	97.6	99.2	100	98.4	98.4	98.4	96.8	96.8	96.0
1.29	97.6	99.2	98.4	100	99.2	98.4	98.4	97.6	96.8
1.30	97.6	99.2	98.4	99.2	100	98.4	97.6	98.4	96.8
1.31	97.6	99.2	98.4	98.4	98.4	100	98.4	98.4	97.6
1.32	96.0	97.6	96.8	98.4	97.6	98.4	100	99.2	98.4
1.33	96.0	97.6	96.8	97.6	98.4	98.4	99.2	100	98.4
1.34	95.2	96.8	96.0	96.8	96.8	97.6	98.4	98.4	100

Variable Light Chain % identity of TL1A antibodies

	1D1	15A9	15C11	9B3	26B11	7D4	22F9
1D1	100	100	100	68.2	68.2	72.9	72.9
15A9	100	100	100	68.2	68.2	72.9	72.9
15C11	100	100	100	68.2	68.2	72.9	72.9
9B3	68.2	68.2	68.2	100	98.1	88.8	88.8
26B11	68.2	68.2	68.2	98.1	100	88.8	88.8
7D4	72.9	72.9	72.9	88.8	88.8	100	100
22F9	72.9	72.9	72.9	88.8	88.8	100	100

Variable heavy chain % identity of TL1A antibodies

	1D1	15A9	15C11	9B3/ 26B11 VH1	9B3/ 26B11 VH2	26B11 MDX	7D4	22F9
1D1	100	93.5	96.8	56.6	57.0	59.4	86.0	75.2
15A9	93.5	100	96.0	56.1	55.6	58.9	85.1	75.2
15C11	96.8	96.0	100	54.5	54.8	57.3	86.8	76.9
9B3/26B11 VH1	56.6	56.1	54.5	100	87.3	88.9	59.2	60.3
9B3/26B11 VH2	57.0	55.6	54.8	87.3	100	93.7	59.2	61.2
26B11 MDX	59.4	58.9	57.3	88.9	93.7	100	61.7	62.0
7D4	86.0	85.1	86.8	59.2	59.2	61.7	100	84.3
22F9	75.2	75.2	76.9	60.3	61.2	62.0	84.3	100

FIG. 2

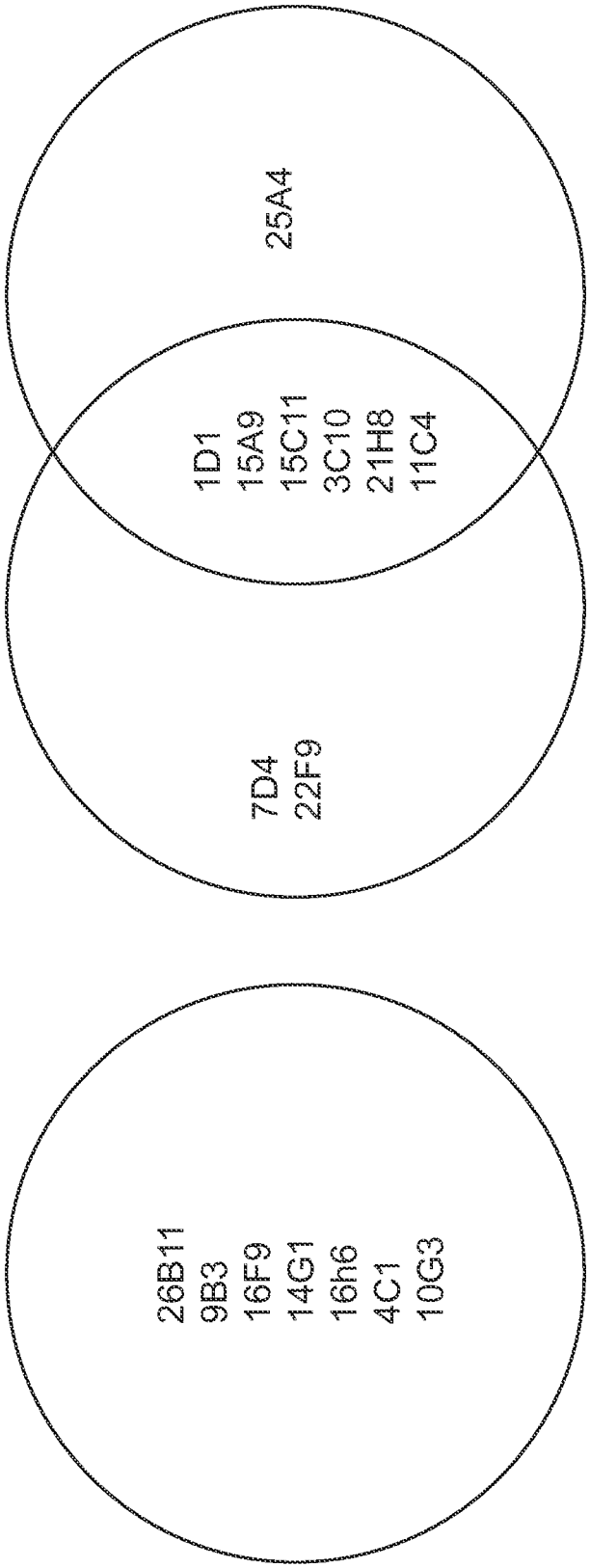

25A4
1D1
15A9
15C11
3C10
21H8
11C4
7D4
22F9
26B11
9B3
16F9
14G1
16h6
4C1
10G3

FIG. 3

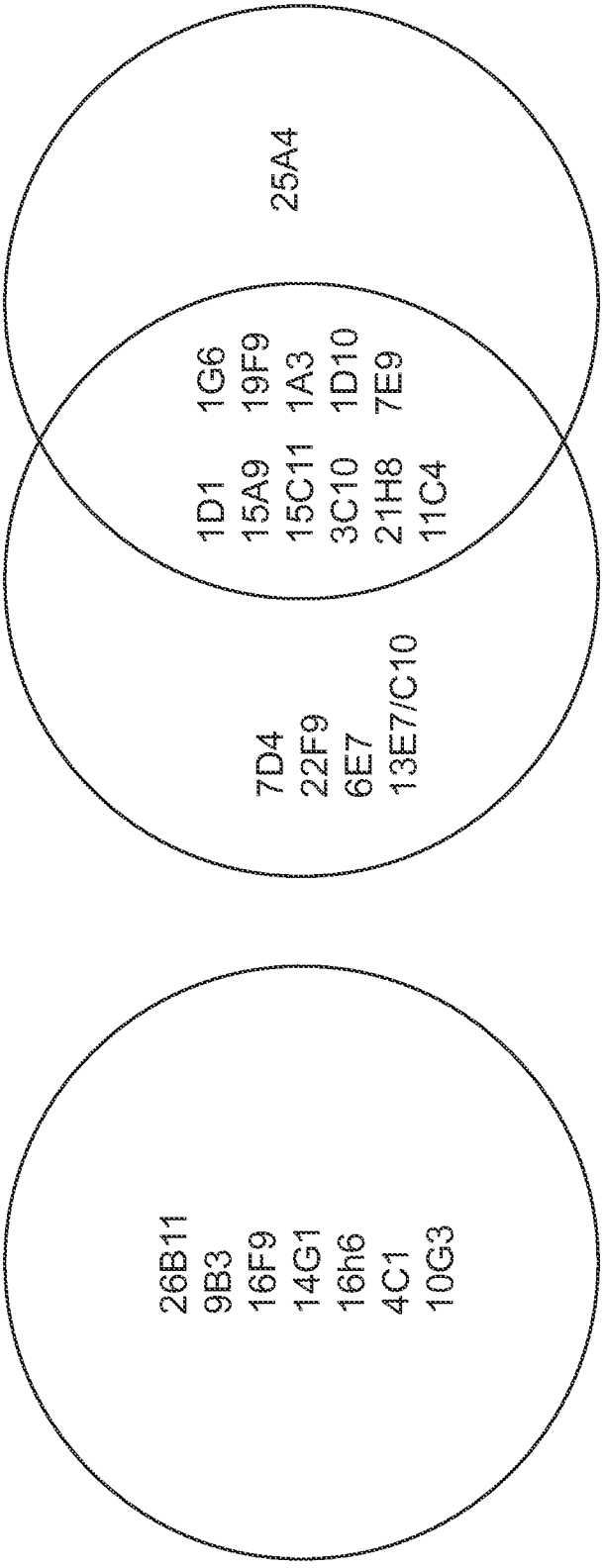

26B11
9B3
16F9
14G1
16h6
4C1
10G3
7D4
22F9
6E7
13E7/C10
1D1
15A9
15C11
3C10
21H8
11C4
1G6
19F9
1A3
1D10
7E9
25A4

FIG. 4

Epitope Binning with Murine TL1A

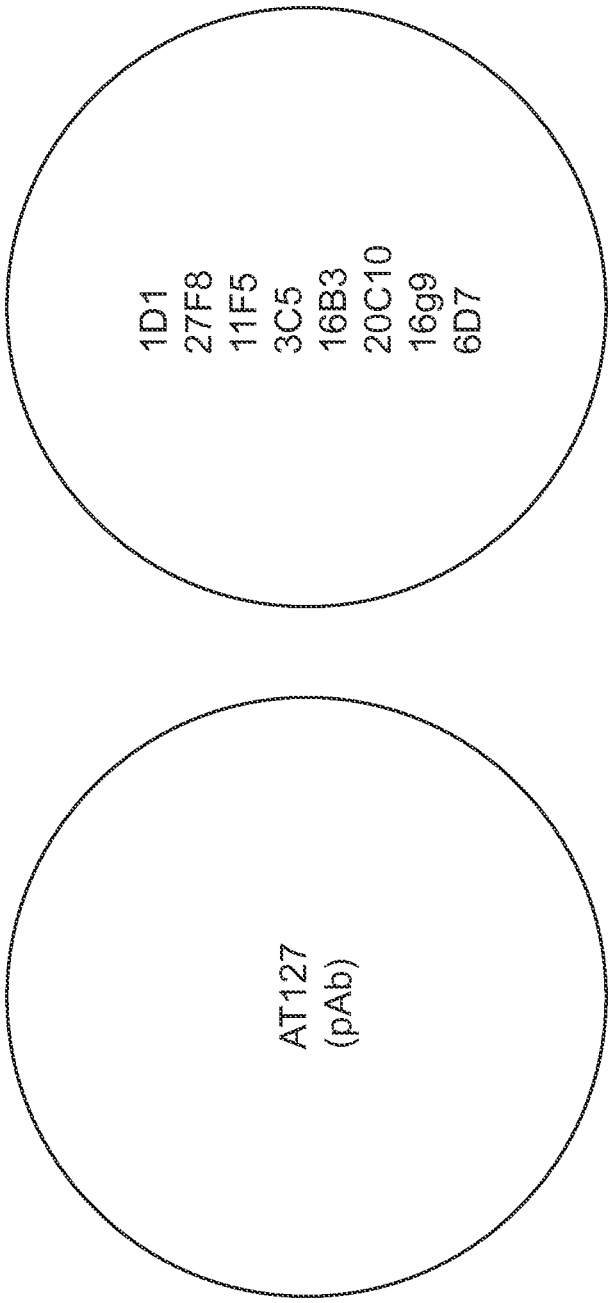


FIG. 5

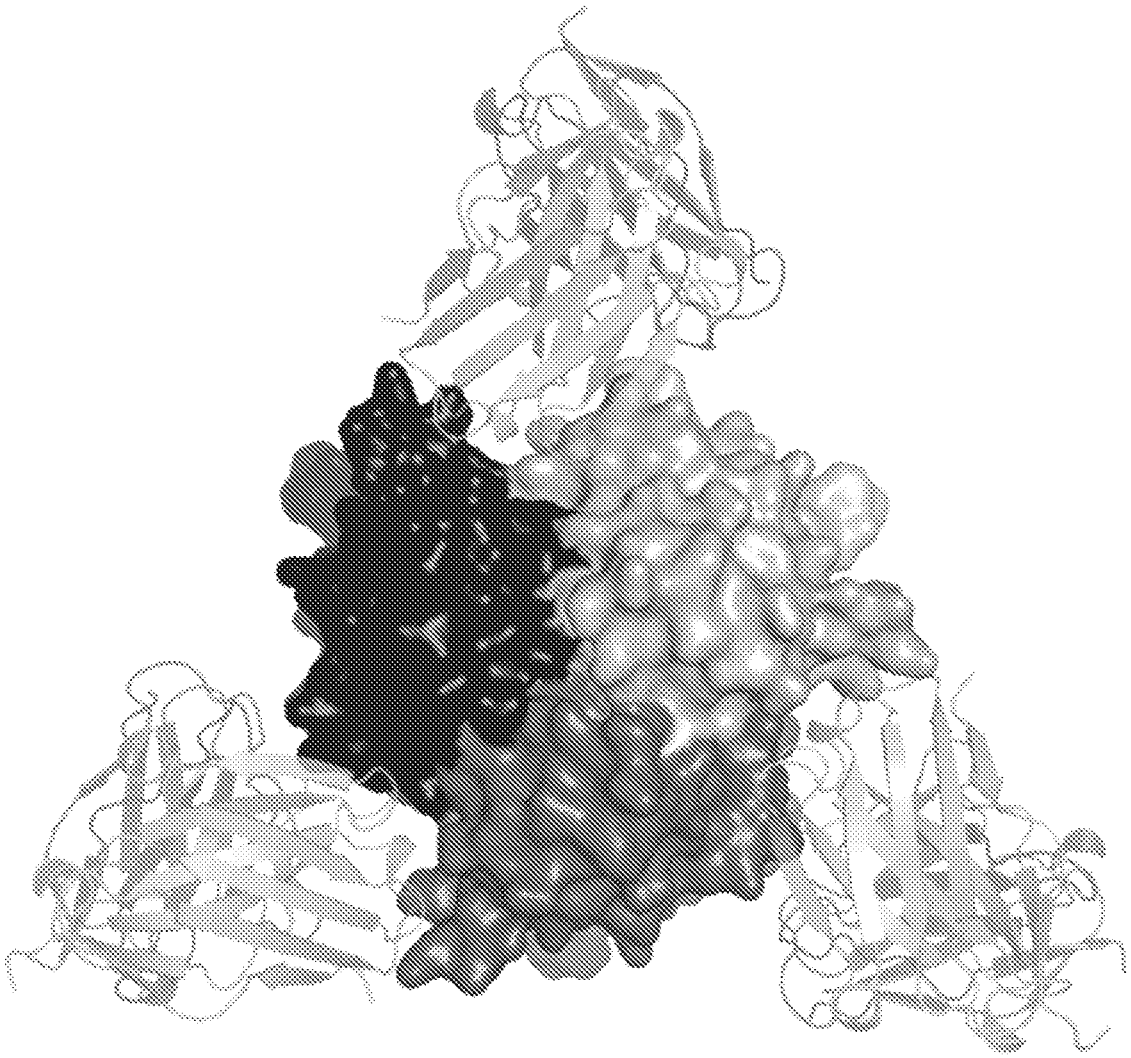


FIG. 6

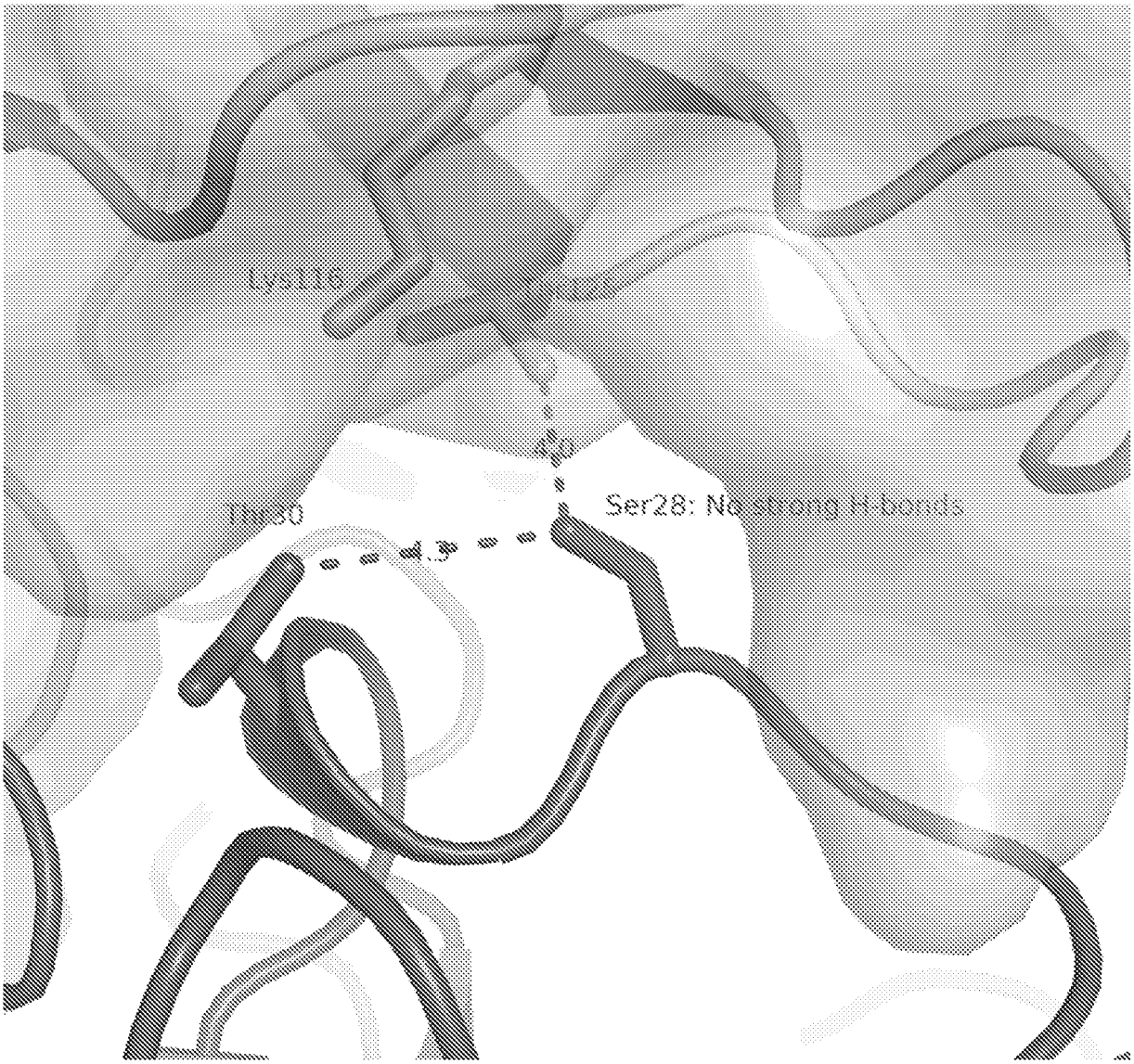


FIG. 7

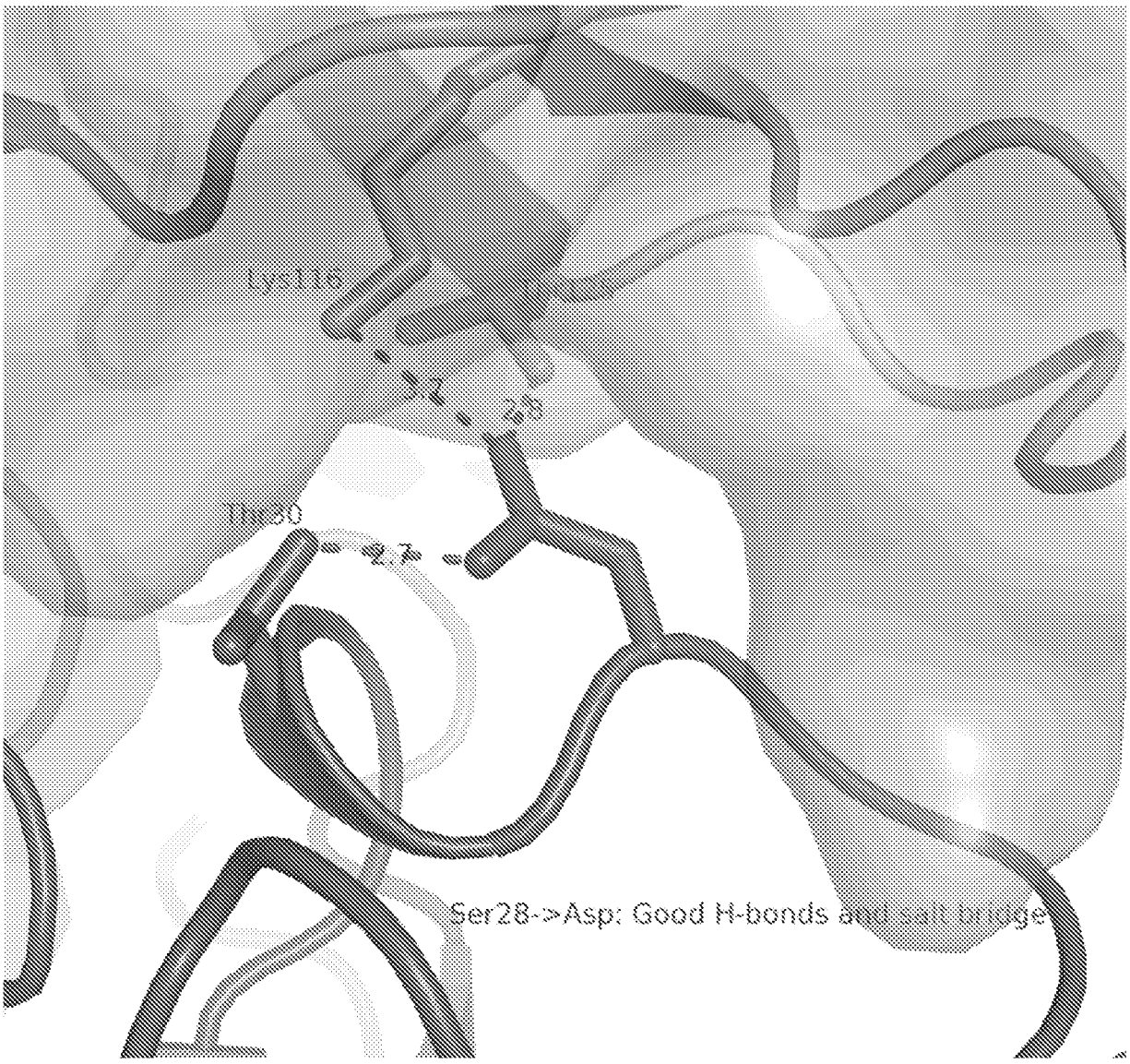


FIG. 8

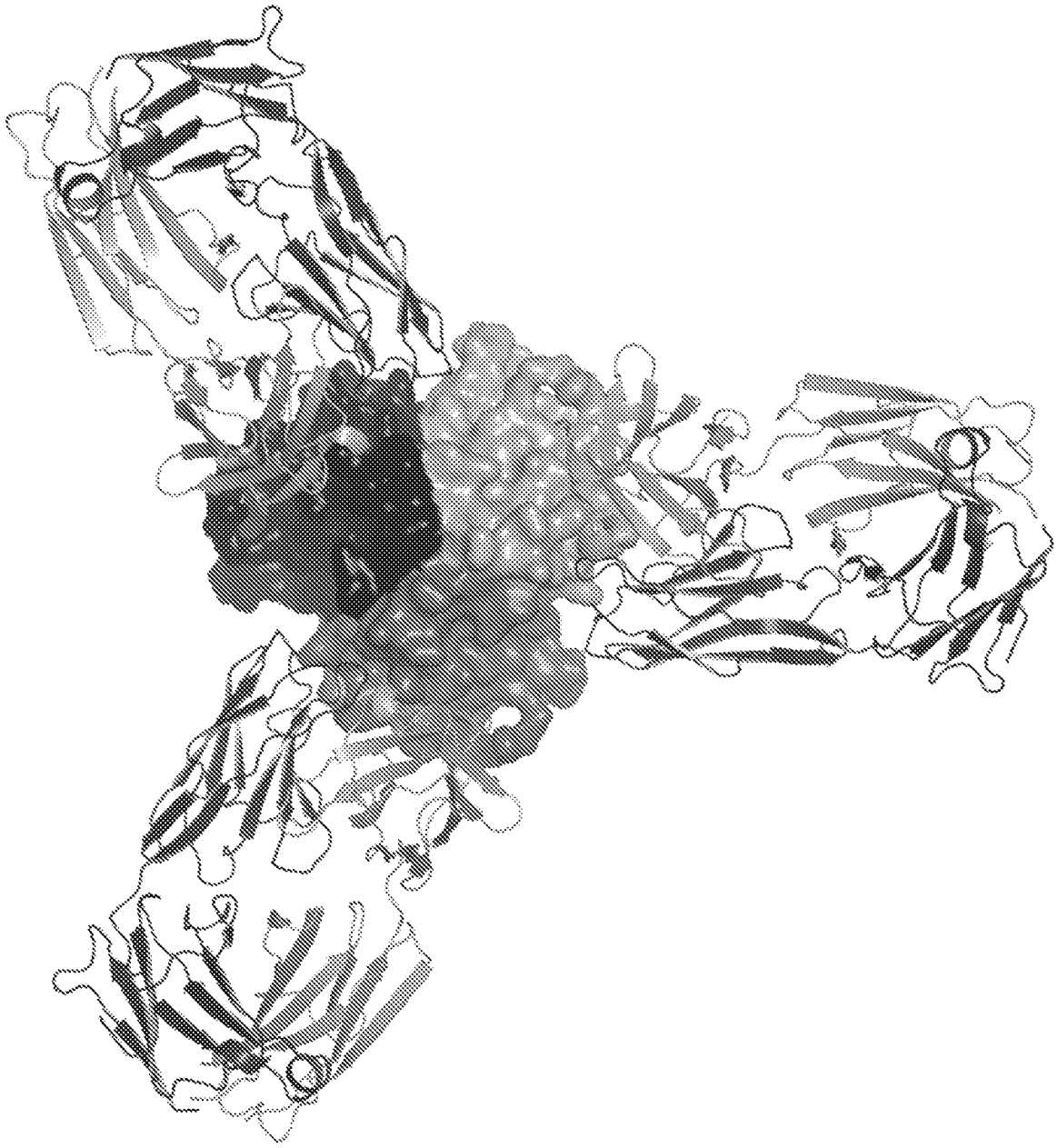


FIG. 9

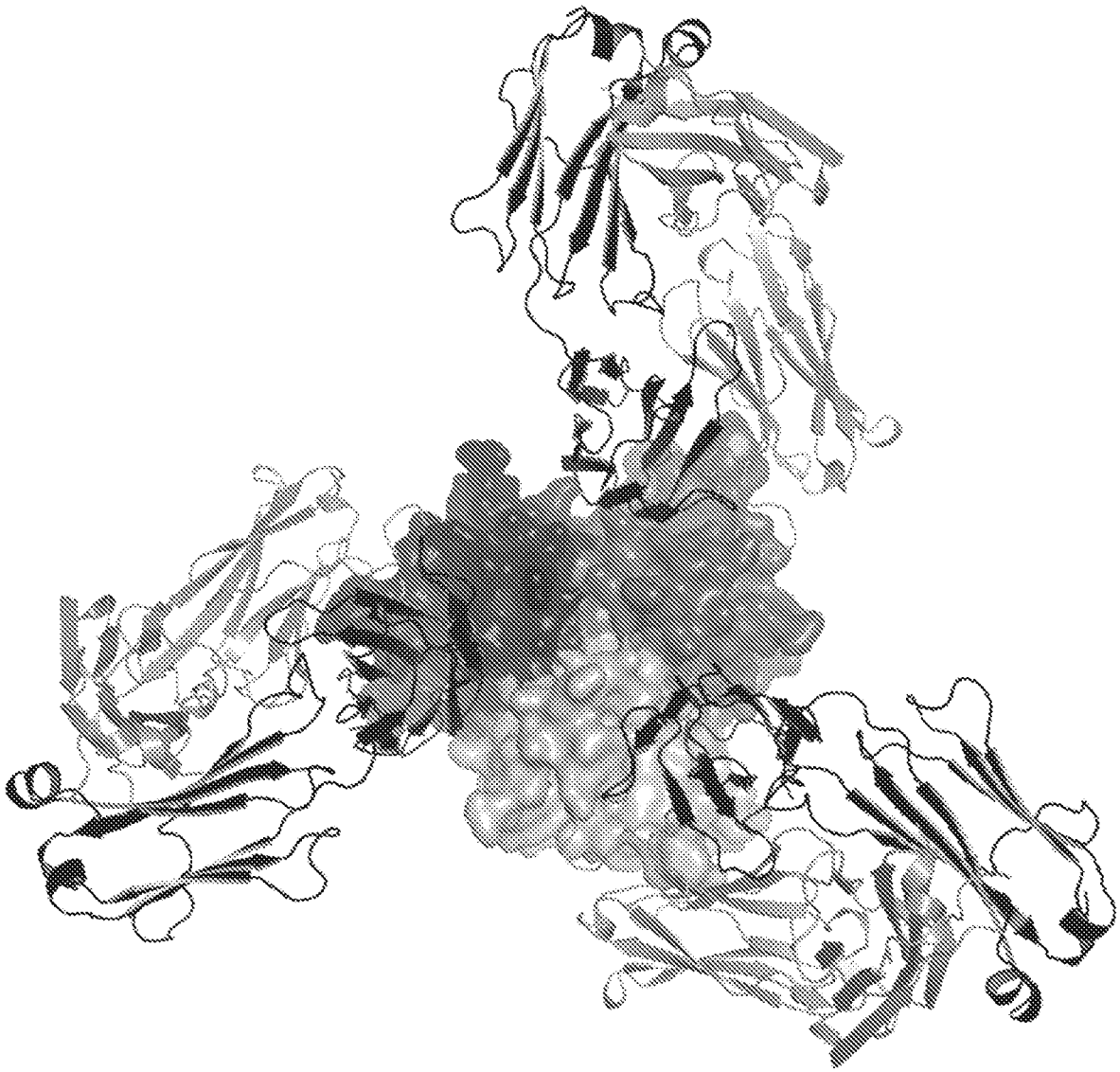


FIG. 10

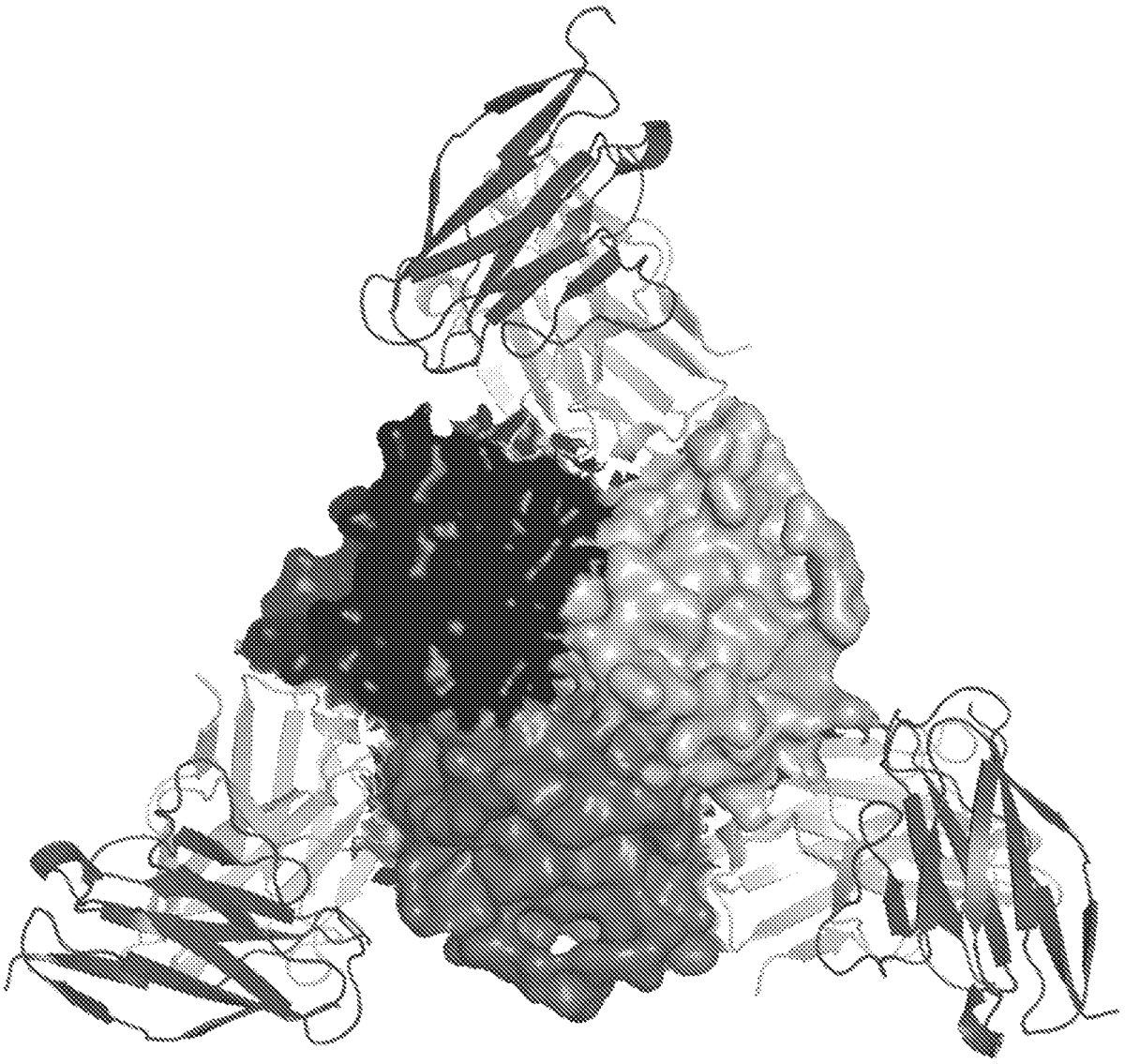


FIG. 11

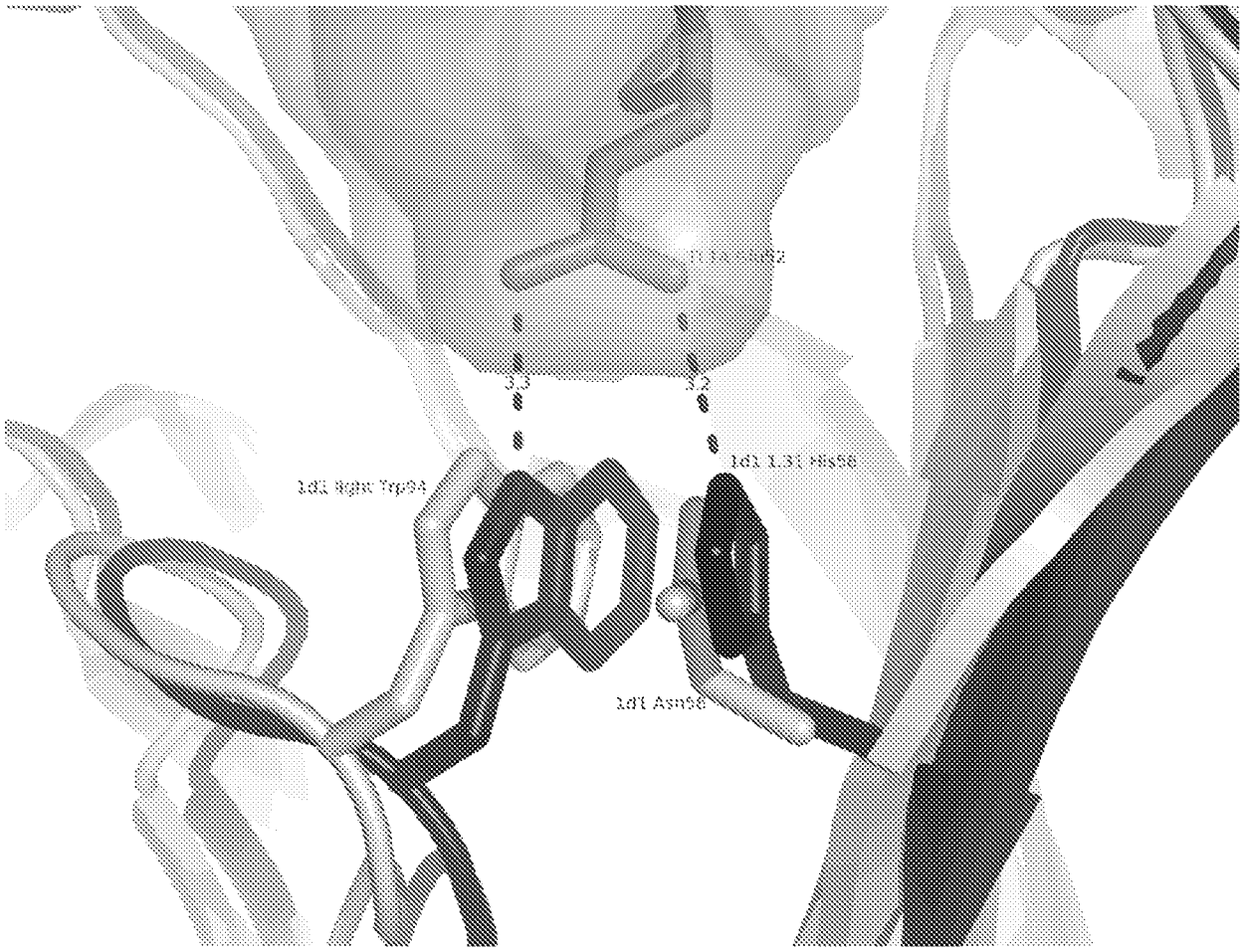


FIG. 12

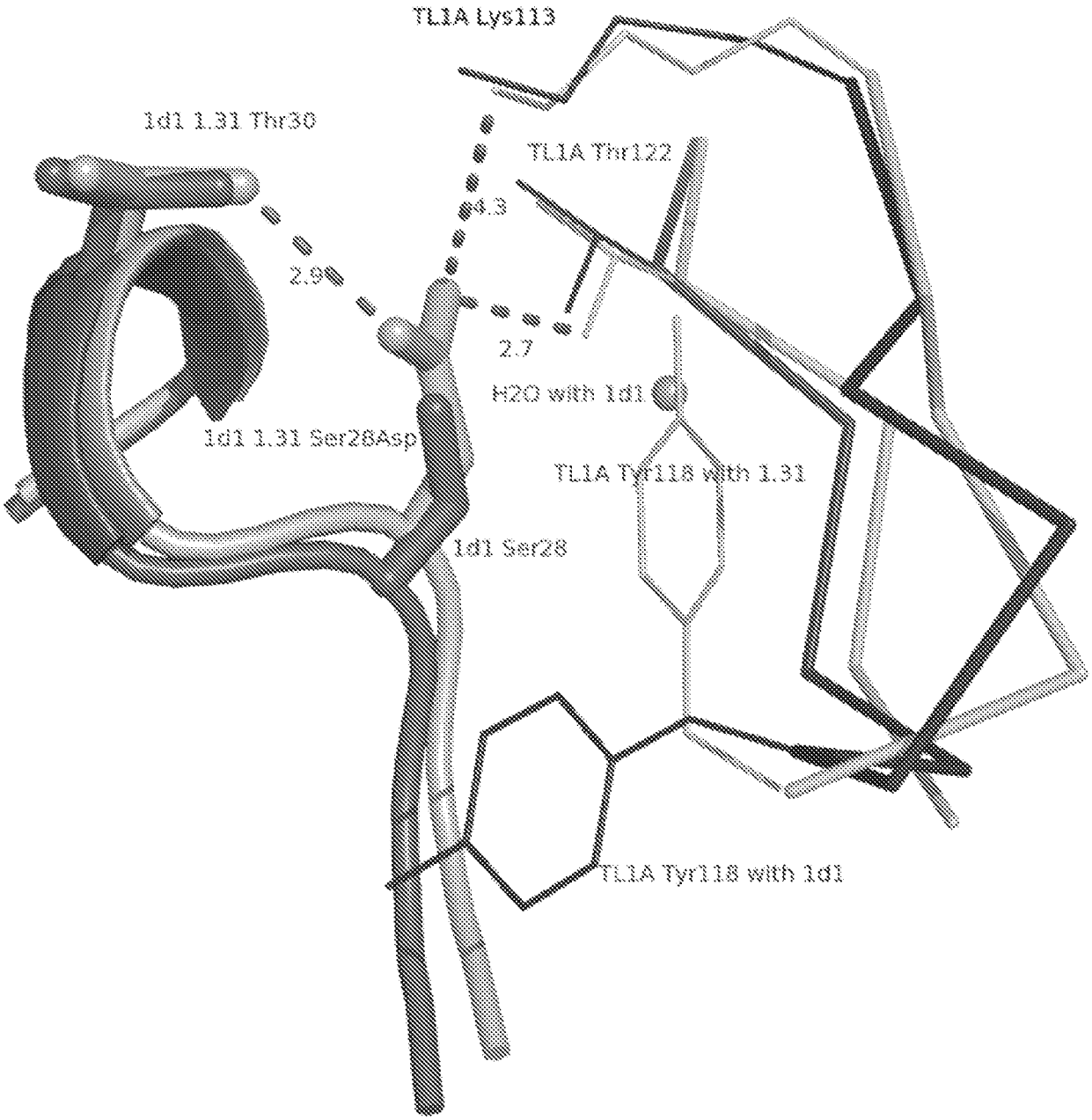

TL1A Lys113
1d1 1.31 Thr30
TL1A Thr122
4.3
2.9
2.7
H2O with 1d1
1d1 1.31 Ser28Asp
TL1A Tyr118 with 1.31
1d1 Ser28
TL1A Tyr118 with 1d1

FIG. 13

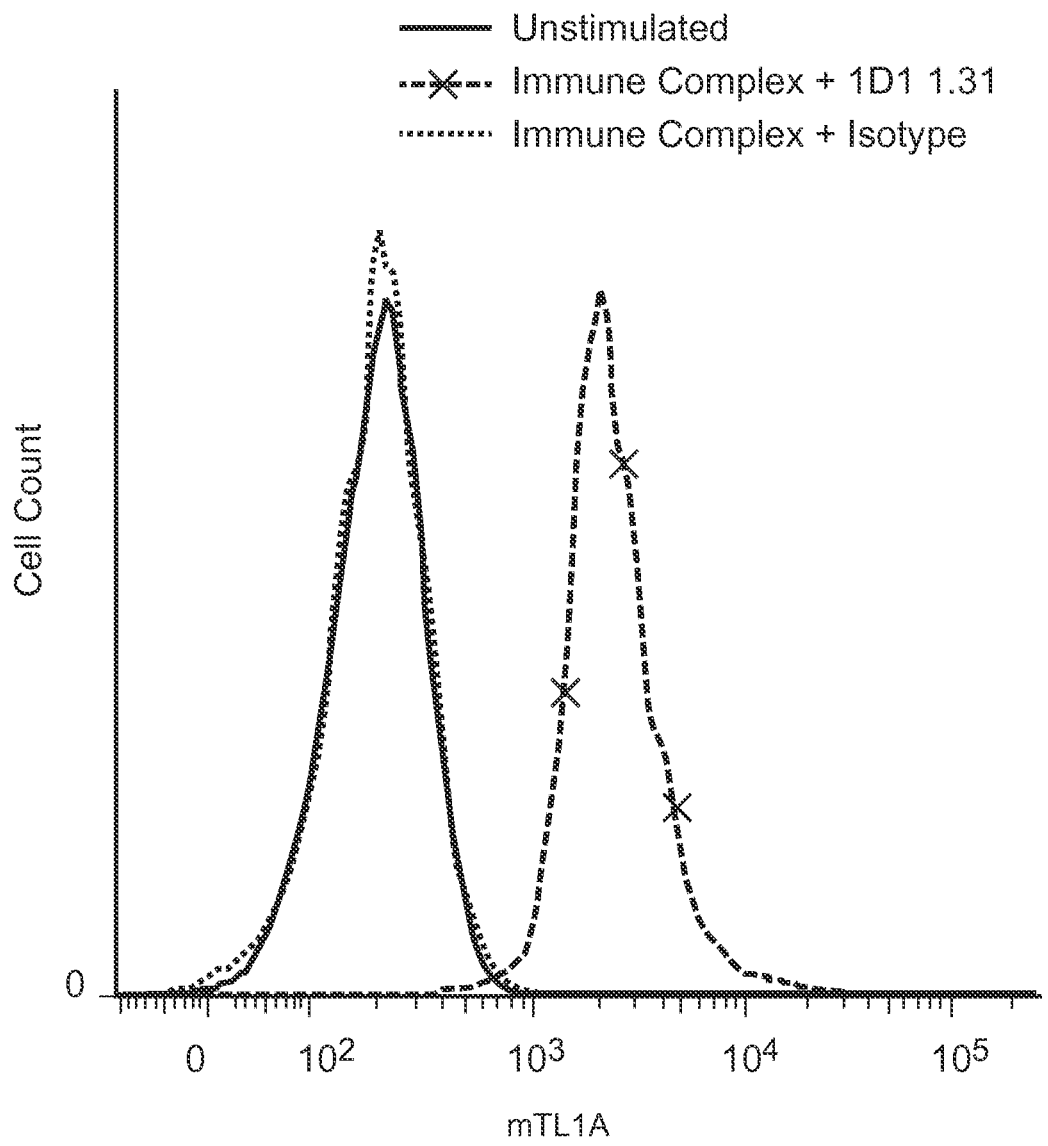

Unstimulated
Immune Complex + 1D1 1.31
Immune Complex + Isotype
Cell Count
0
0
10^2
10^3
10^4
10^5
mTL1A

FIG. 14A

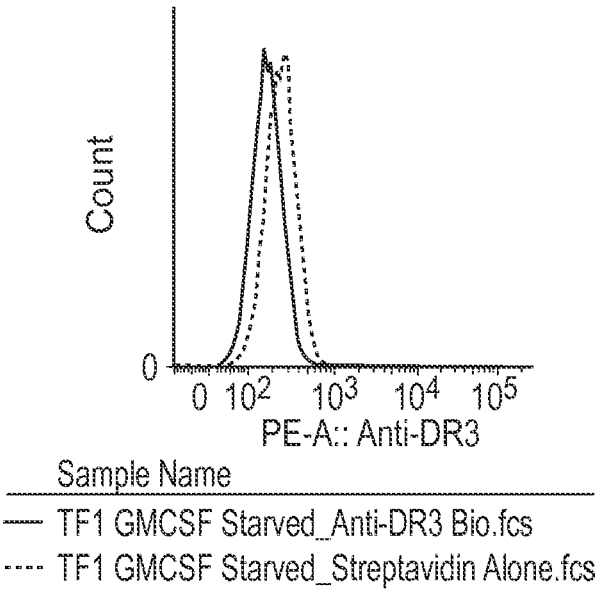


FIG. 14B

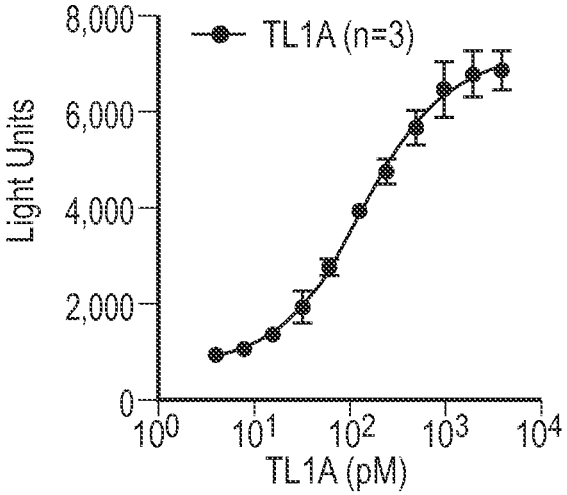


FIG. 14C

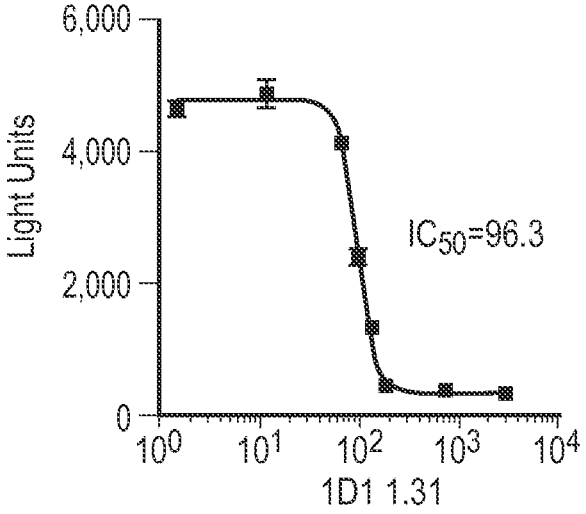
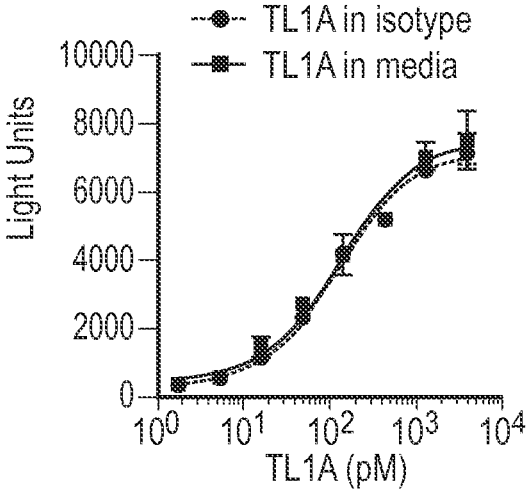


FIG. 14D



	TL1A in isotype	TL1A in media
EC50	124.2	137.1

FIG. 14E

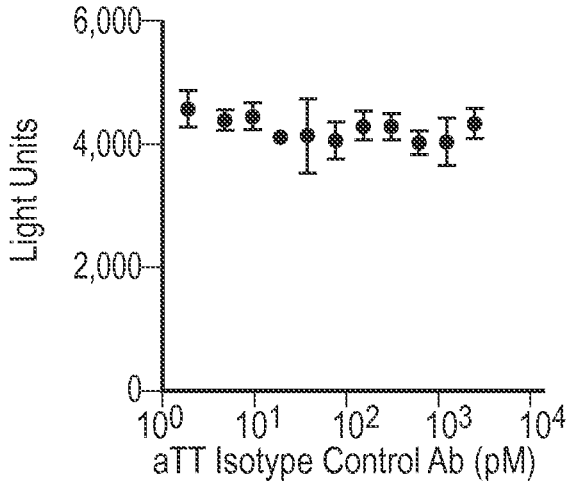


FIG. 15A

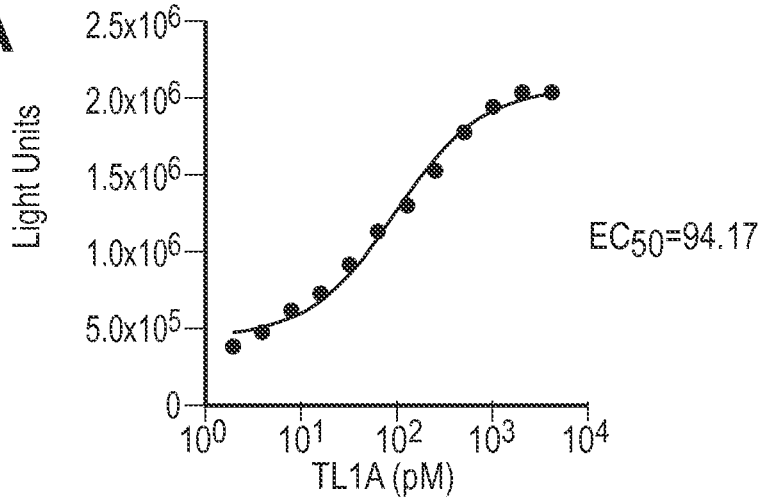


FIG. 15B

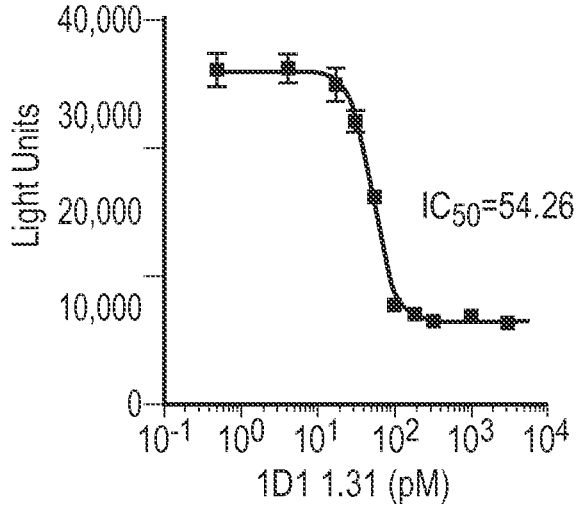


FIG. 16A

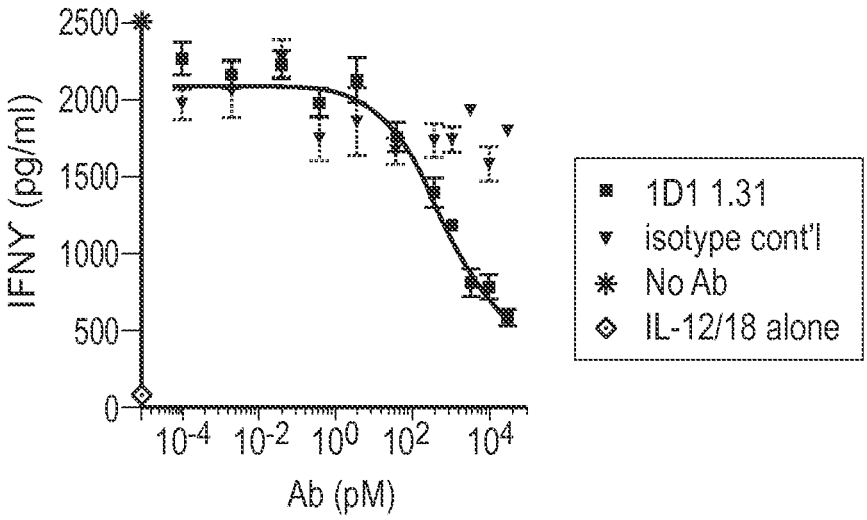


FIG. 16B

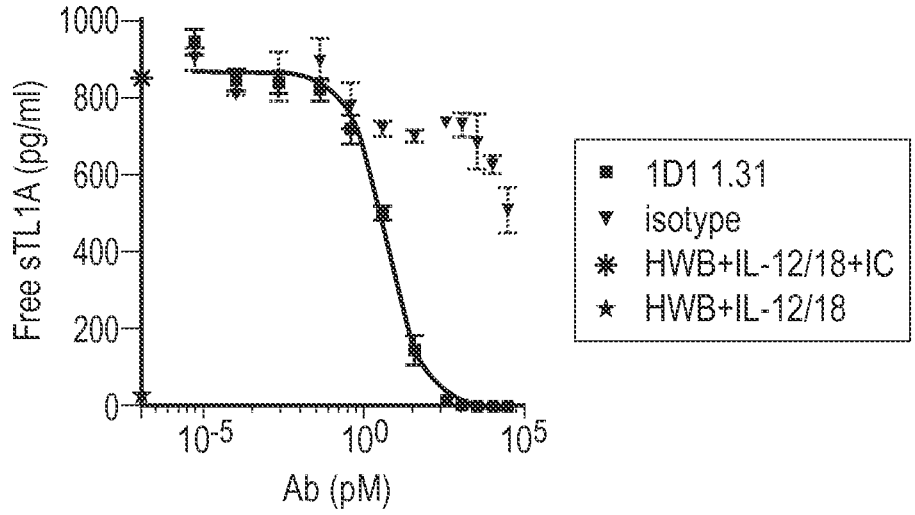


FIG. 17A

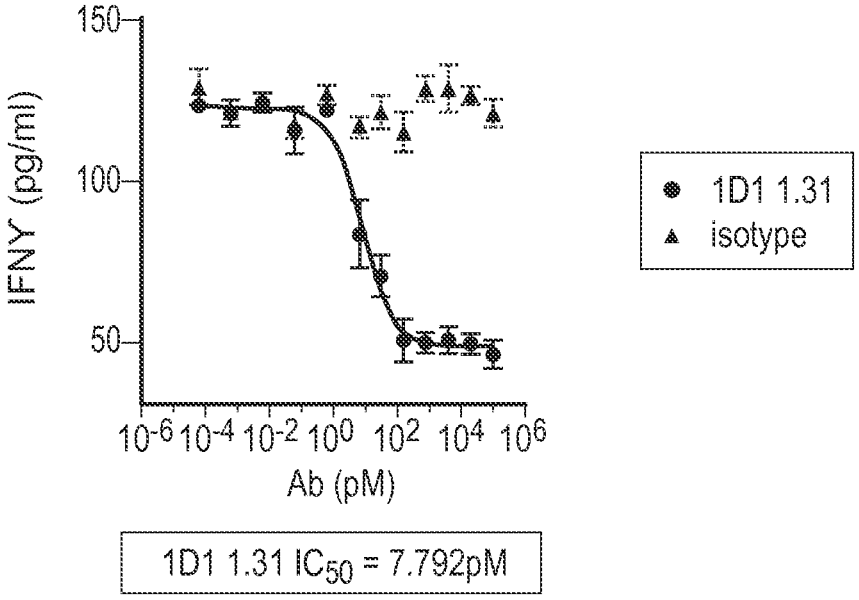


FIG. 17B

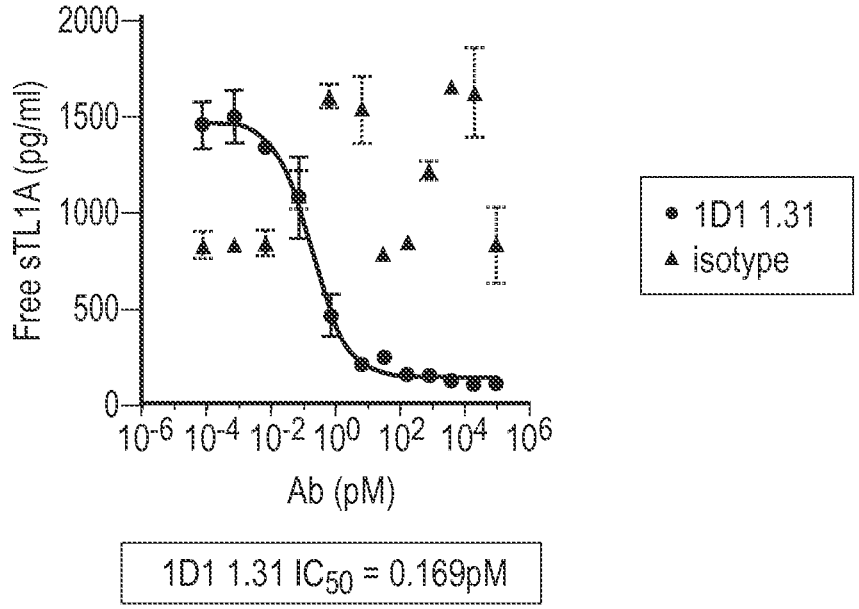


FIG. 18A

	1D1	CDHR H1						CDR H2						
		H S25	H G26	H Y27	H S28	H T30	H Y31	H W50	H S52	H Y53	H N54	H N56	H T57	H N58
TL1A	total	0	23.5	20.2	57.7	33.2	99	28.4	5.5	152.7	58.1	48.2	0.7	13.1
A K113	25				18.8	42.1								
A T115	12.7				28.6									
A Y118	118	15.5	48.8	50.4	36.8									
A P121	7						14.6							
A T122	43.7				28		59.2							
A Q123	16.9						43.5							
A M147	0.2									17.6w				
A F148	5.5									28.3				
A S149	39.1									71.6h				
A Q151	38.8													
B V31	11.8													
B V32	16.3													
B R33	93.4													
B E50	20.4													
B H51	12.2										12.7	26.6		
B E52	111							36.2	15.8		22.4h	33.1	6.4	34.8h
B L53	118							33.4			5.9			
B G54	51.3								9.5	21.9	4.5			
B L55	53.4					21.4	35.6			62.7w				
B A56	11.9									18.7	18.8h			
B F57	26.3									30.7	30.2			
B T58	20.1											33.2		
B E91	6													
B Y168	15.6													
B T169	33													
B K170	46													
B E171	49						22.4							

CONTINUED

FIG. 18B CONTINUED

	FW3		CDR H3							
	H T73	H R76	H Y97	H Y98	H G99	H S100	H G100A	H S100B	H Y100C	H R100D
TL1A	33	22.6	39.2	12.6	45.1	50.1	72.2	79.4	14.4	54
A K113										
A T115		50.5 h								
A Y118										
A P121										
A T122										
A Q123										
A M147										
A F148										
A S149										
A Q151	71.9									
B V31							28.8			
B V32							24.9			
B R33							22.5 w	43.2		
B E50										50.5 S
B H51										
B E52										
B L53			44.7			16.4				55.8
B G54			42.6			19.6				
B L55										
B A56										
B F57										
B T58										
B E91								20.5		
B Y168							14.7	33.6 h		
B T169					3.1	12.1	10.3	27.7	15	
B K170				25.9	40.2	11.8	10	2.1	15.8	
B E171					34.3	36.5	13.8			

CONTINUED

FIG. 18C CONTINUED

	L1			CDR L3	
	L S30	L S31	L Y32	L W94	L W96
TL1A	9.6	15.5	29.7	26.1	6.4
A K113					
A T115					
A Y118					
A P121					
A T122					
A Q123					
A M147					
A F148					
A S149					
A Q151					
B V31					
B V32			7.4		
B R33	23.2	34.7 h	56.8 w		
B E50					
B H51					
B E52				42.7 h	
B L53				21.2	27
B G54					
B L55					
B A56					
B F57					
B T58					
B E91					
B Y168					
B T169					
B K170					
B E171					

FIG. 19A

	1.31	CDHR H1					CDR H2					
TL1A		H G26	H Y27	H D28	H T30	H Y31	H W50	H S52	H Y53	H N54	H N56	H H58
	total	32.8	18	76.3	34.1	88.1	25.2	9.6	151.1	50.5	35.1	11.1
A K113	17.7			29.3 S	18							
A S117	41.9	24.5	7.7									
A Y118	48.9	15.2	37.3	54.2								
A P119	14.2	28.8										
A T122	43.9			37.4 h		50.2						
A Q123	16.5					42.2			7.8			
A M147	0								32.7			
A F148	6.1								71.8 h			
A S149	35.4											
A Q151	49.3			6.6	41.6							
B V31	13.1											
B V32	11.7											
B R33	31.6											
B E50	19.6											
B H51	6.4									14.1		
B E52	110.9						33.3	16.2		25.8 h	56.3	33.3 S
B L53	113.8						33.1					
B G54	51.3							12	23.2	4.1		
B L55	56.3				21.8	38.9			57.8			
B A56	10.7								20.2	17.3 h		
B F57	26.4								30.2	31		
B Y168	25.6											
B T169	43.6											
B K170	15.2											
B E171	51.2					26.4						
B D172	0											

CONTINUED

FIG. 19B CONTINUED

	FW3		CDR H3						
TL1A	H T73	H R76	H Y97	H G99	H S100	H G100A	H S100B	H Y100C	H R100D
	24.7	24	36	38.5	48.2	68	46.9	8.4	41.7
A K113									
A S117		44.5							
A Y118									
A P119									
A T122									
A Q123									
A M147									
A F148									
A S149									
A Q151	47.2								
B V31						32			
B V32						27.6			
B R33						13.2			
B E50									42.0 S
B H51									
B E52									
B L53			43		16				46.3
B G54			40.9		19.8				
B L55									
B A56									
B F57									
B Y168					1.7	15.9	43.2 h		
B T169				5	14.5 h	10.6	28.8 h	21.7	
B K170				25.6	7.1	8.2	2.8		
B E171				30.9 h	36.9	14.3			
B D172				5.9					

CONTINUED

FIG. 19C CONTINUED

	L1	CDR L3	
TL1A	L Y32	L W94	L W96
	20.9	26.3	8.1
A K113			
A S117			
A Y118			
A P119			
A T122			
A Q123			
A M147			
A F148			
A S149			
A Q151			
B V31			
B V32			
B R33	45.5		
B E50			
B H51			
B E52		40.2 h	
B L53		22.5	30.2
B G54			
B L55			
B A56			
B F57			
B Y168			
B T169			
B K170			
B E171			
B D172			

FIG. 20

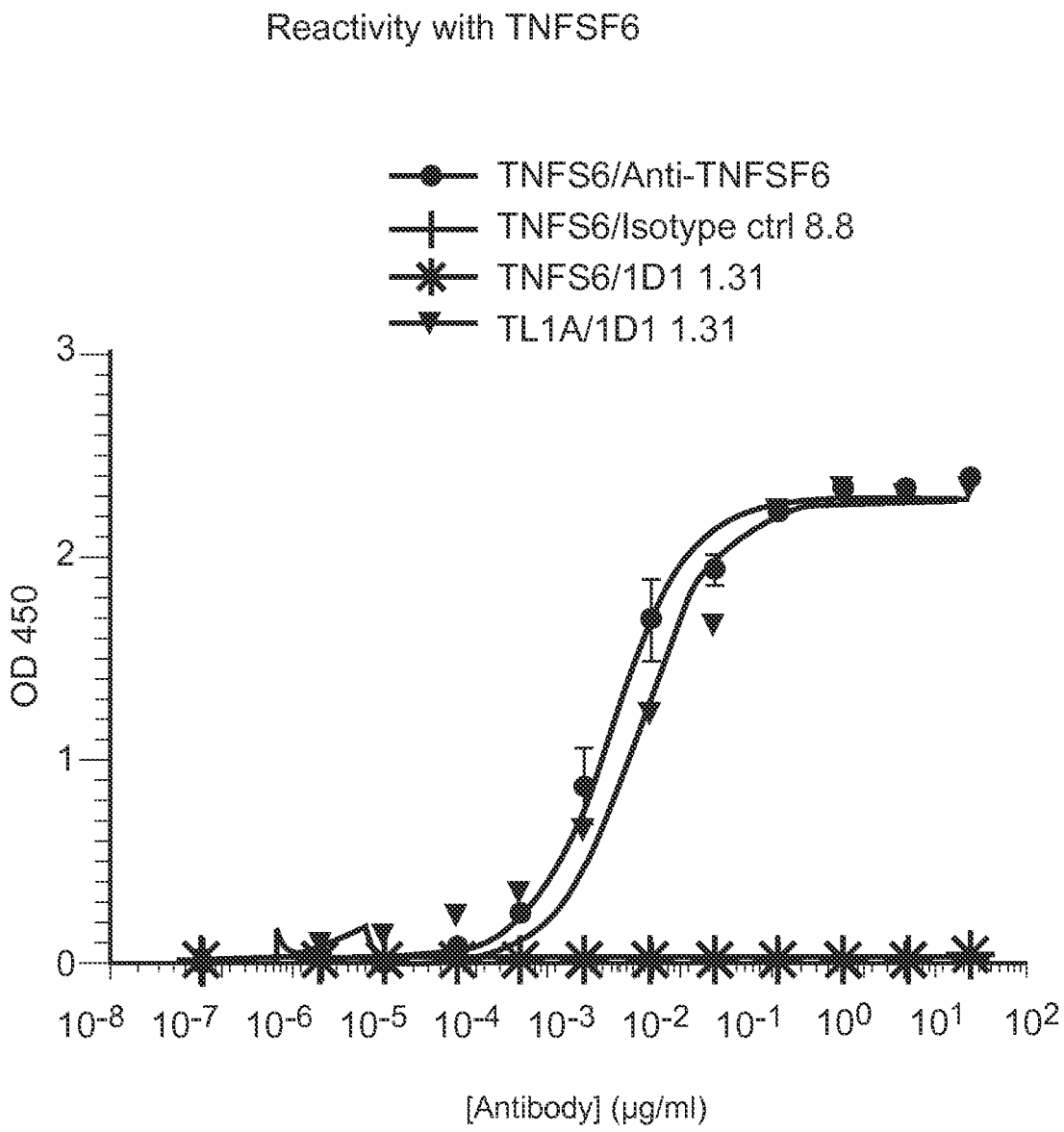

Reactivity with TNFSF6
TNFS6/Anti-TNFSF6
TNFS6/Isotype ctrl 8.8
TNFS6/1D1 1.31
TL1A/1D1 1.31
OD 450
0
1
2
3
10-8 10-7 10-6 10-5 10-4 10-3 10-2 10-1 100 101 102
[Antibody] (µg/ml)

FIG. 21

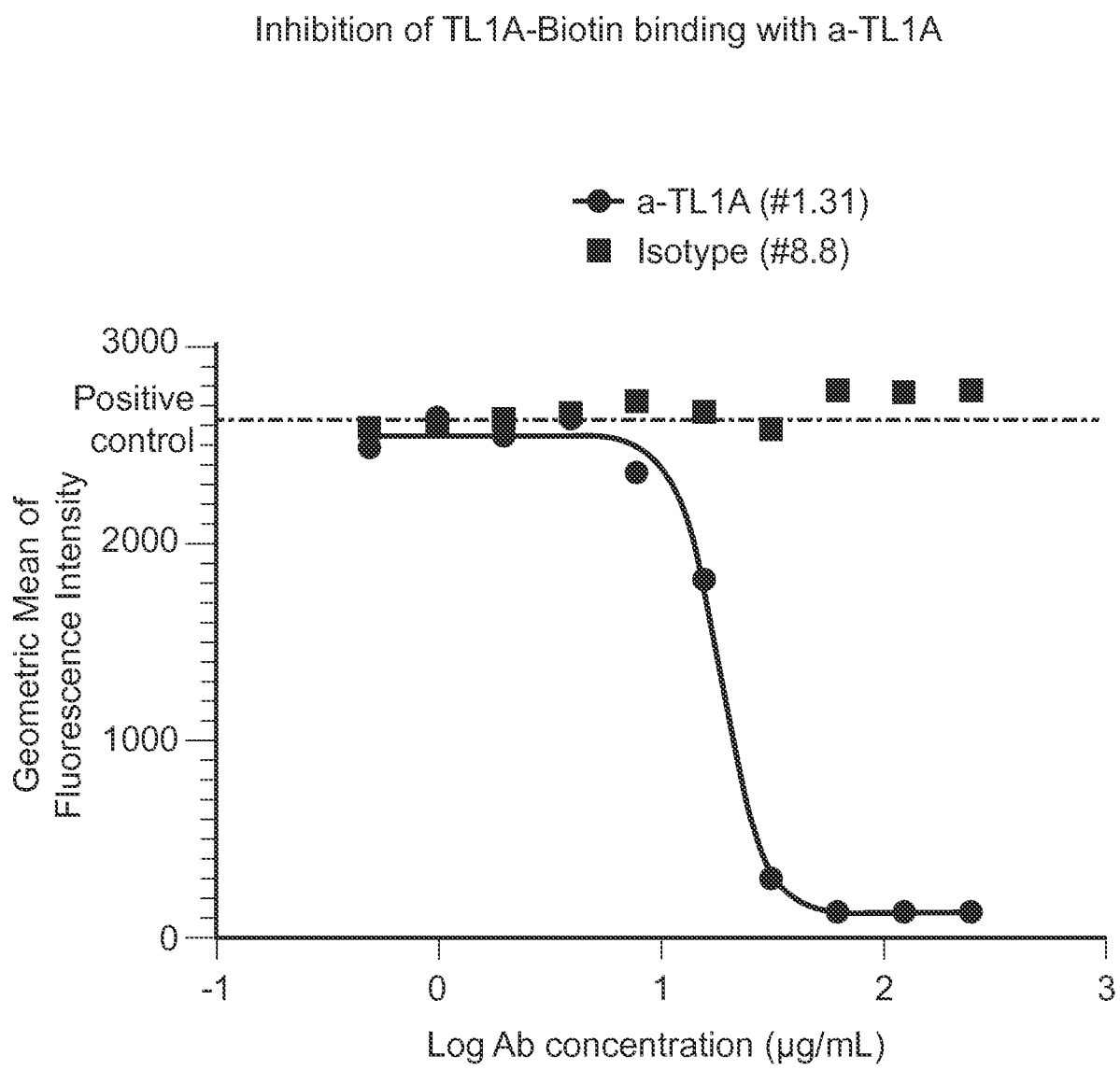

Inhibition of TL1A-Biotin binding with a-TL1A
a-TL1A (#1.31)
Isotype (#8.8)
Geometric Mean of Fluorescence Intensity
3000
Positive control
2000
1000
0
-1
0
1
2
3
Log Ab concentration (µg/mL)

FIG. 22A

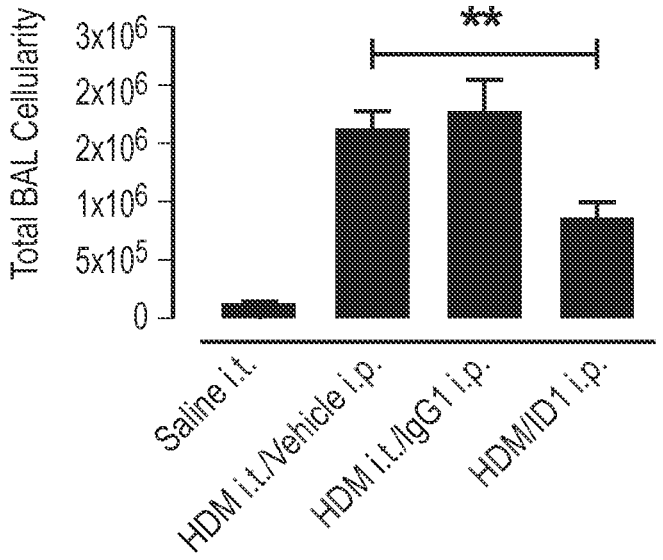


FIG. 22B

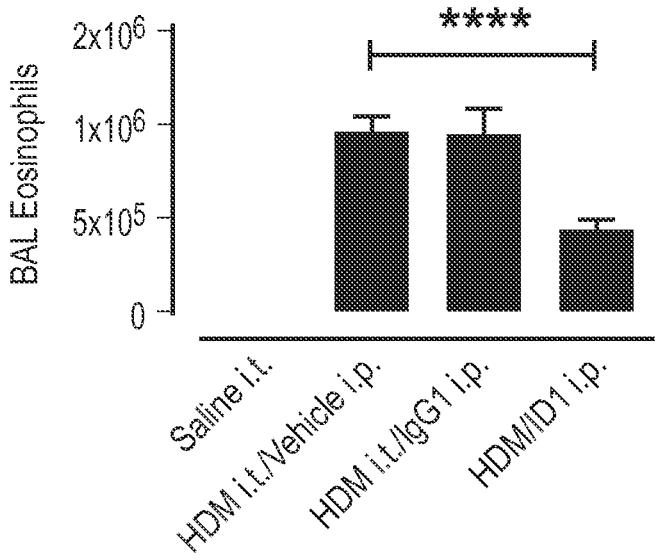


FIG. 22C

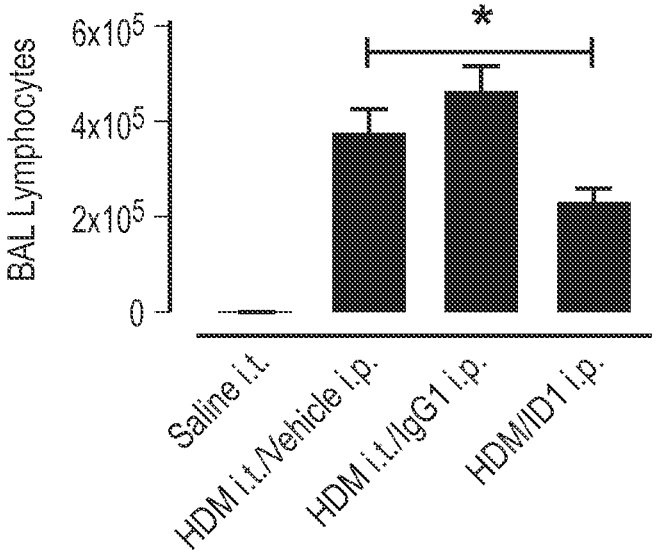


FIG. 22D

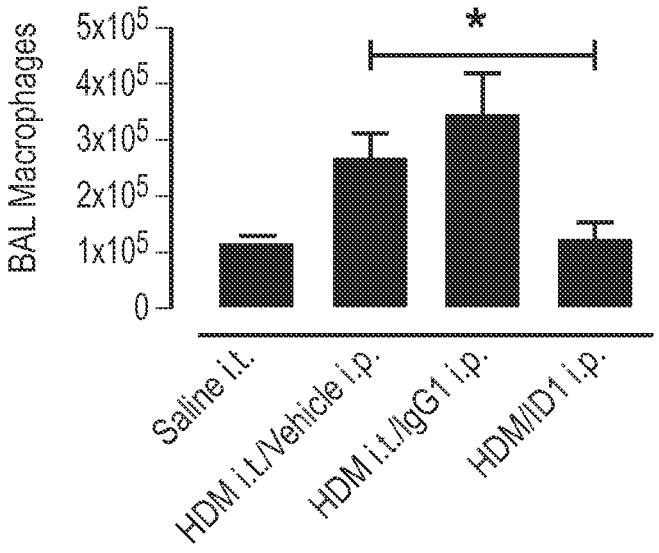


FIG. 22E

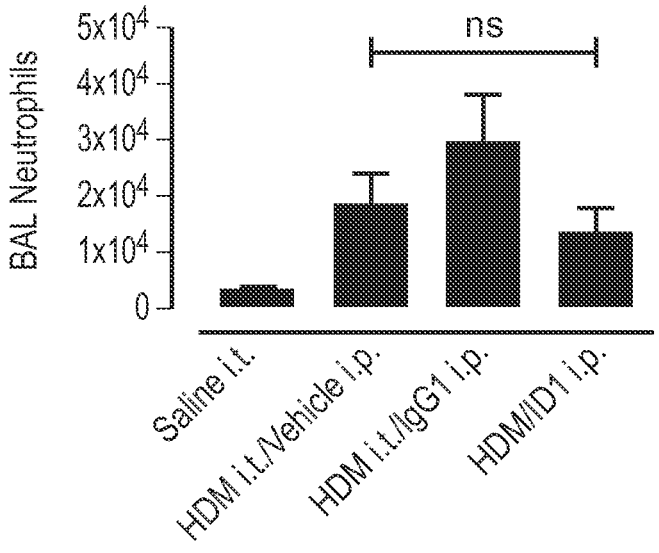


FIG. 23A

7D4		H T28	H T30	H S31	H Y32	H W47	H W50	H S52	H T52A	H Y53	H N54	H N56
	total	19.4	25.3	55.6	21.1	6.7	22.1	3	0.9	143	46.8	12.5
A R103	108.4											
A Q104	35.6			8.2								
A T105	51.3			38.2	50							
A P106	63.5	8	21.7	42.0 h						34.3		
A T107	18.7	24.4		13.4						7.1		
A Q108	25	11.7								38.5		
A H109	93		43.1						12.9	79.6		
A F110	6.5									16.3		
Q113	13.1									28.5		
A F114	0.2									8		
A P115	24.2									52.7		
A R156	100.9											
A G157	6.3											
A M158	144.5					25	39.5					
A T159	47.6											
A S206	26.6											
A N207	58.9											
A S231	10.5										22.6	
A D232	42.5							5			47.2 h	28.6
A I233	22.9											
A S234	91.2						27.6	13.9			13.3	
A L235	8.6											
A V236	8.7											
A D237	3.9											
A Y238	71											
A T239	4.4											

CONTINUED

FIG. 23B CONTINUED

7D4	H N58	H Q61	H Q64	H T73	H H96	H S97	H S98	H S99	H W100	H F100A	H D100B
	53.8	16.8	5.1	13.3	15.2	38.7	67.4	28.5	90.7	106.9	18.1
A R103						41.9	30				28.2 S
A Q104							28.8	31.8 h			
A T105							11.4	4.4			
A P106								17.3			
A T107											
A Q108											
A H109				27.6							
A F110											
Q113											
A F114											
A P115											
A R156									35.0 h	52	
A G157									29.1		
A M158	52.6								66.2		
A T159	51.7	14	10								
A S206		22.2									
A N207									13.6		
A S231											
A D232											
A I233							39.4	13.1			
A S234							27	26.3	23.5	10.8	
A L235								3.7	21	15.3	
A V236								11		19.4	
A D237										27.1	
A Y238						9.5		19.3		37.1 h	23.6
A T239										15.9	

CONTINUED

FIG. 23C CONTINUED

7D4	L Y49	L D50	L F91	L N92	L S93	L Y94
	3.8	24.7	6.4	28.5	13	71.9
A R103	22.1 S	40.2 S	9.7			
A Q104						
A T105						
A P106						
A T107						
A Q108						
A H109						
A F110						
Q113						
A F114						
A P115						
A R156			13.3	64.8 h	7.6	
A G157						
A M158						51.3
A T159						21.5
A S206						33.5
A N207					37.4	46.7 h
A S231						
A D232						
A I233						
A S234						
A L235						
A V236						
A D237						
A Y238			10.7	16		
A T239						

FIG. 24A

26B11		H A33	H L50	H P52	H F52A	H D53	H S55	H Y58	H R96	H N97	H Y99	H S100A
	total	2.4	6.7	4.3	9.6	30.4	26.6	29.4	25.6	14.2	6	32.9
D T105	23.2										16.2	
D P106	40.9					10.9						
D T107	31.6					22.9	35.1					
D Q108	172.9	13.9		26.3	45.2 h	29.1h	18.6			16.5 w		
D H109	61.3											
D F110	150.9		18.1					47				
D K111	126.4									5.4		
D N112	54											
D Q113	15.8							24.7				
D G169	6.7											17.7
D R170	0											
D P171	77.3								30.7 h	17.8		41.4
D N172	66.5								12.7	13.9 h		
D K173	68.8								7.2			
D P174	20.8											
D D175	80											
D S176	13.3											
D S234	29.4											

CONTINUED

FIG. 24B CONTINUED

26B11	H G100B	H S100C	H F100D	H S100E	H F100F	H D100G	L S30	L N31	L W32	L Y49	L A50	L S53
	29	32.2	102.9	56.5	66	9	15.9	45	73.6	31.4	17.6	15.8
D T105			30.3									
D P106			68.6									
D T107			19.3									
D Q108			34.1 h	11.1	37.2							
D H109			33	46.6	38.0 h							
D F110				8.8	47.2							
D K111		0.5		33.1 h	29.0 w	20.3 S			50			
D N112												
D Q113												
D G169												
D R170		6.5										
D P171	11.6	16.6				4.7				9		
D N172		24.6 h		12.5 h		16.4 w			26.9	6.2	12	
D K173								16.7h	14.1	46.5 h	24.1	33
D P174								17.9	35.2			
D D175								48.4			1.3	
D S176							29	4.2				
D S234	44.5	16.7										

CONTINUED

FIG. 24C CONTINUED

26B11	L G66	L S67	L Y91	L N92	L S93	L Y94	L Y96	H D95
	13.4	16.3	11.2	43	28.3	35.6	11.4	0
D T105								
D P106								
D T107								
D Q108								13.3 w
D H109				1.4				
D F110				8.7	10.3	20.7	51.8	29.5
D K111				40.1 w	28.3			2.3
D N112					41.6 h		41	27.1 w
D Q113								5.6
D G169								
D R170								
D P171				2.3				
D N172				9.8 w				
D K173								
D P174								
D D175	41.0 w	41.2						
D S176								
D S234								