```
                1                                                  50
    v1    (1)   EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
    v2    (1)   EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
    v3    (1)   EEELQVIQPDKSVSVAAGESAILLCTVTSLIPVGPIQWFRGAGPARELIY
    v4    (1)   EGLQVIQPDKSVSVAAGESAILHCTATSLIPVGPIQWFRGAGPGRELIY
    v5    (1)   EEELQVIQPDKFVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
    v6    (1)   EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
    v7    (1)   EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
    v8    (1)   EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPARELIY
    v9    (1)   EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
    v10   (1)   EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
                    *   *   *   *   *                          *

                   51                                          100
    v1    (51)  NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSPD
    v2    (51)  NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS-P
    v3    (51)  NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS-P
    v4    (51)  NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSPD
    v5    (51)  NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSPD
    v6    (51)  NQKEGHFPRVTTVSDLTKRNNMDFPIRIGNITPADAGTYYCVKFRKGSPD
    v7    (51)  NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS-P
    v8    (51)  NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS-P
    v9    (51)  NQKEGHFPRVTTVSDLTKRNNMDFSIRISNITPADAGTYYCVKFRKGSPD
    v10   (51)  NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS-P
                                ** *  * * * *                   **

                  101                 119
    v1    (101) DVEFKSGAGTELSVRAKPS
    v2    (100) DTEFKSGAGTELSVRAKPS
    v3    (100) DTEFKSGAGTELSVRAKPS
    v4    (101) DVEFKSGAGTELSVRAKPS
    v5    (101) DVEFKSGAGTELSVRAKPS
    v6    (101) DVEFKSGAGTELSVRAKPS
    v7    (100) DTEFKSGAGTELSVRGKPS
    v8    (100) DTEFKSGAGTELSVRAKPS
    v9    (101) DVEFKSGAGTELSVRAKPS
    v10   (100) DTEFKSGAGTELSVRAKPS
                       *
```

FIG. 1A

```
                1                                                  50
Human_v1    (1) EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
Human_v2    (1) EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
    Cyno    (1) EEELQVIQPEKSVSVAAGESATLNCTATSLIPVGPIQWFRGVGPGRELIY
129mouse    (1) -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGPIKWYRGVGQSRLLIY
                ** * * * *  *  **** * *  *  * * * * ** *
               51                                                 100
Human_v1   (51) NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSP-
Human_v2   (51) NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKIRKGS--
    Cyno   (51) HQKEGHFPRVTPVSDPTKRNNMDFSIRISNITPADAGTYYCVKFRKGS--
129mouse   (50) SFTGEHFPRVTNVSDATKRNNMDFSIRISNVTPEDAGTYYCVKFQKGPSE
                *****    *  **  *    * * * *  *    *  ***
               101                                                120
Human_v1  (100) DDVEFKSGAGTELSVRAKPS
Human_v2   (99) PDTEFKSGAGTELSVRAKPS
    Cyno   (99) PDVELKSGAGTELSVRAKPS
129mouse  (100) PDTEIQSGGGTEVYVLAKPS
                * * **  *   ****
```

FIG. 1B


R1
1 50
Human_v1 (1) EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
Human_v2 (1) EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
129mouse (1) -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGPIKWYRGVGQSRLLIY
NOD (1) -TEVKVIQPEKSVSVAAGDSTVLNCTLTSLLPVGPIRWYRGVGQSRQLIY
BL6 (1) -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGPIRWYRGVGPSRLLIY
BALBc (1) -TEVKVTQPEKSVSVAAGDSTILNCTVTSLLPVGPIRWYRGVGQSRLLIY
51 R2 R3 100
Human_v1 (51) NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSP-
Human_v2 (51) NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS--
129mouse (50) SFTGEHFPRVTNVSDATKRNNMDFSIRISNVTPEDAGTYYCVKFQKGPSE
NOD (50) SFTTEHFPRVTNVSDATKRSNLDFSIRISNVTPEDAGTYYCVKFQRGS--
BL6 (50) SFAGEYVPRIRNVSDTTKRNNMDFSIRISNVTPADAGIYYCVKFQKGSSE
BALBc (50) SFTGEHFPRIRNVSDTTKRNNMDFSIRISNVTPEDAGTYYCVKFQRGSSE
101 120
Human_v1 (100) DDVEFKSGAGTELSVRAKPS
Human_v2 (99) PDTEFKSGAGTELSVRAKPS
129mouse (100) PDTEIQSGGGTEVYVLAKPS
NOD (98) PDTEIQSGGGTEVYVLAK--
BL6 (100) PDTEIQSGGGTEVYVLAK--
BALBc (100) PDTEIQSGGGTEVYVLAK-

FIG.1C

```
                1                                                  50
Human_v1      (1) EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY
Human_v2      (1) EEELQVIQPDKSVSVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY
    Cyno      (1) EEELQVIQPEKSVSVAAGESATLNCTATSLIPVGPIQWFRGVGPGRELIY
129mouse      (1) -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGPIKWYRGVGQSRLLIY
 chicken      (1) --DFKLQQPQSSVVVIKGDTLTLNCTASGSGPIGAVKWVKGWGSDNQTVY
                  ******* **  * ** **** *  ***** * *** ** * ******
                51                                                 100
Human_v1     (51) NQKEGHFPRVTTVSDLTKRNNMDFSIRIGNITPADAGTYYCVKFRKGSP-
Human_v2     (51) NQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGS--
    Cyno     (51) HQKEGHFPRVTPVSDPTKRNNMDFSIRISNITPADAGTYYCVKFRKGS--
129mouse     (50) SFTGEHFPRVTNVSDATKRNNMDFSIRISNVTPEDAGTYYCVKFQKGPSE
 chicken     (49) EHKGSFPRVMRAVPDPTN----DFTIRISNVSLEDAGTYYCVKLRKGIV-
                  ************ *** *****  * * * ****          **  ***
                101               120
Human_v1    (100) DDVEFKSGAGTELSVRAKPS
Human_v2     (99) PDTEFKSGAGTELSVRAKPS
    Cyno     (99) PDVELKSGAGTELSVRAKPS
129mouse    (100) PDTEIQSGGGTEVYVLAKPS
 chicken     (94) DDVVFTRGGGTEVSVHA---
                  * ***** *   ** * ***
```

FIG. 2

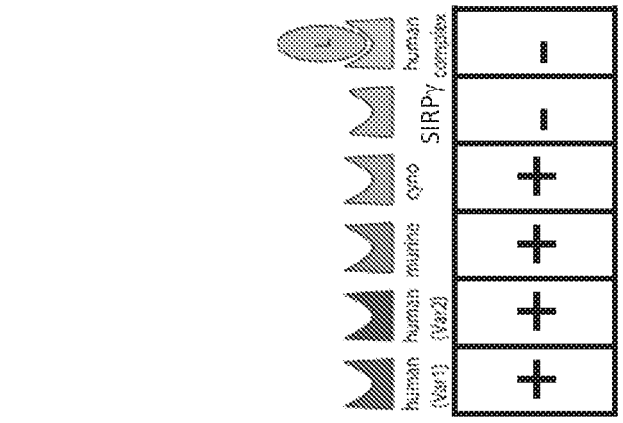

human (Ser1) (Val2)
human murine
cyno
human SIRPγ complex
+ + + + - -

FIG. 3B

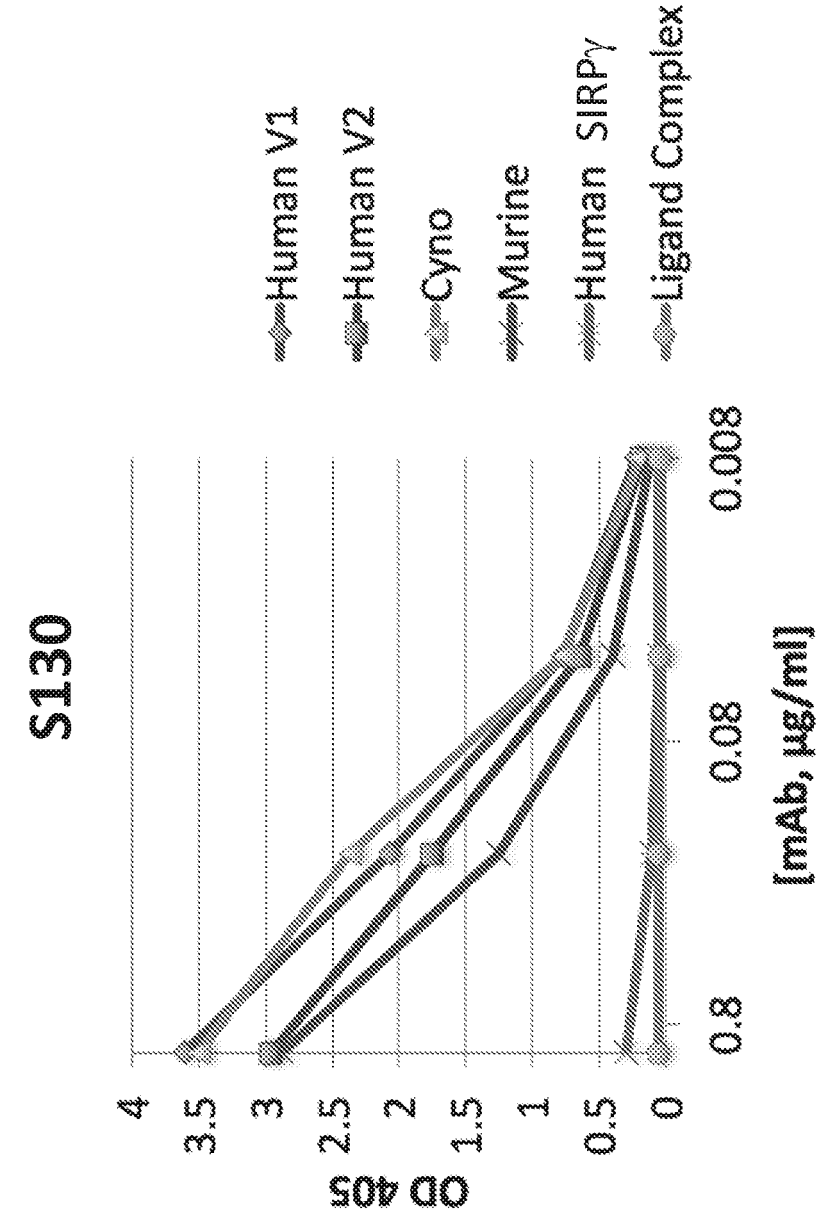

S130
OD 405
4
3.5
3
2.5
2
1.5
1
0.5
0
0.8
0.08
0.008
[mAb, µg/ml]
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex

FIG. 3A

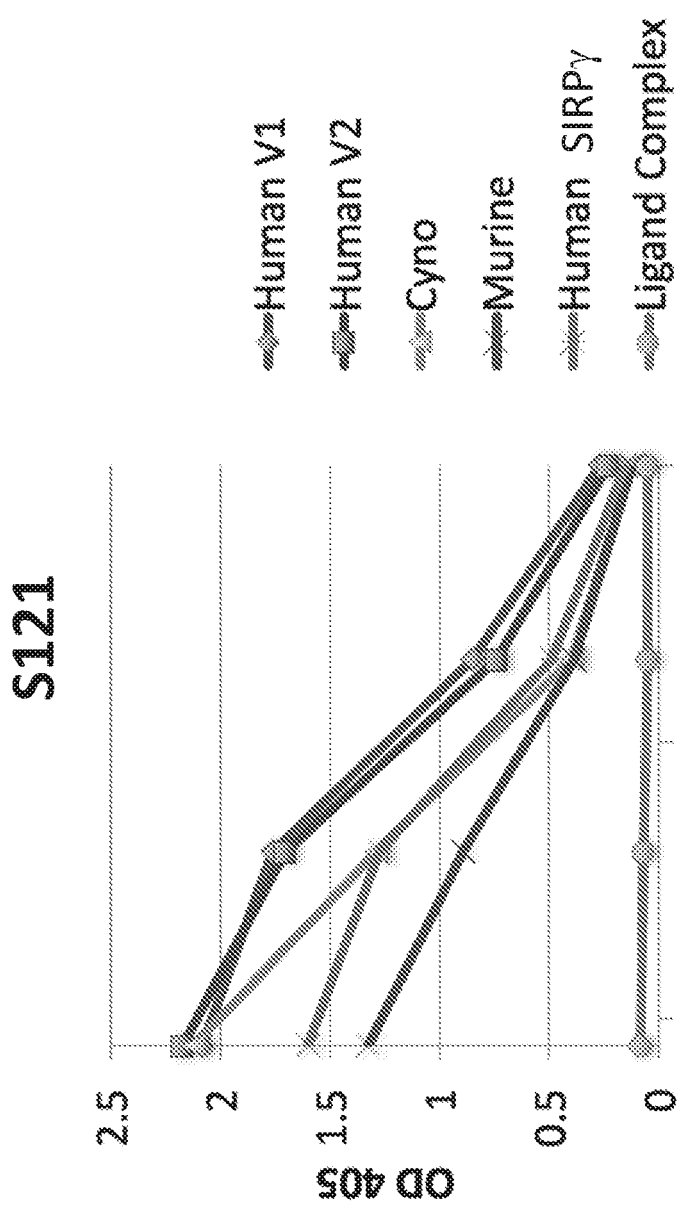

S121
OD 405
2.5
2
1.5
1
0.5
0
0.8
0.08
0.008
[mAb, µg/ml]
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex

FIG. 4A

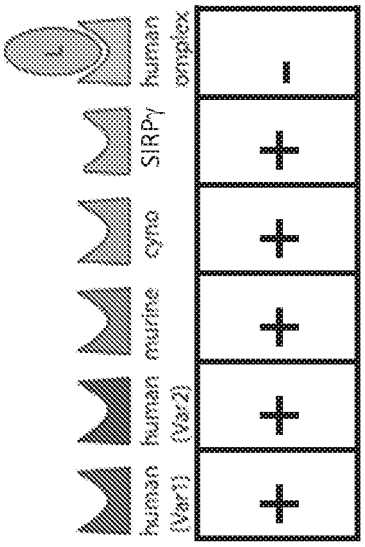

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+
+
+
+
+
+
-

FIG. 4B

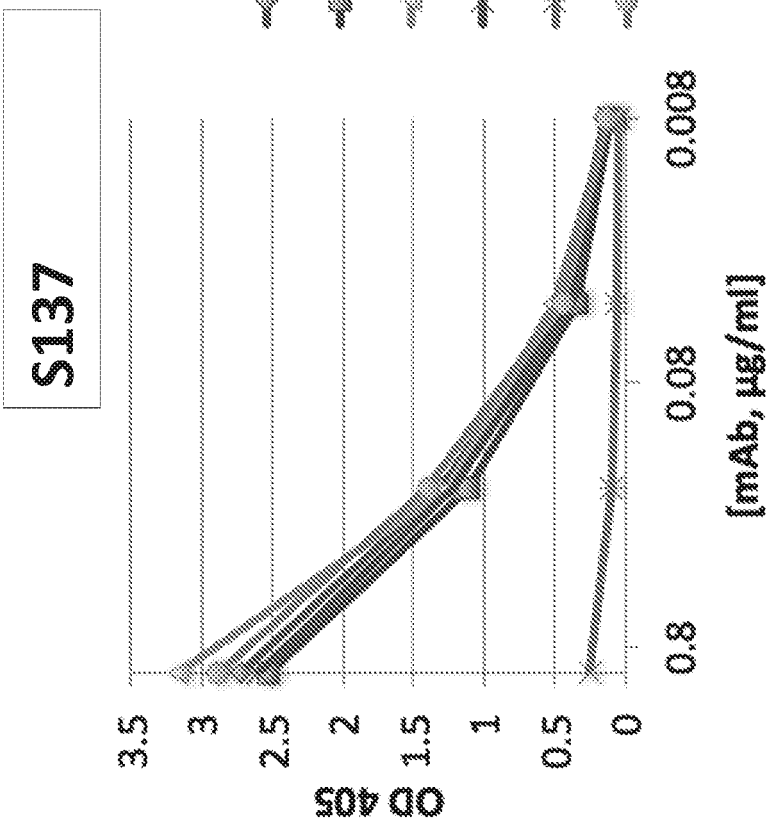

S137
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex
OD 405
[mAb, µg/ml]
3.5
3
2.5
2
1.5
1
0.5
0
0.8
0.08
0.008

FIG. 5A

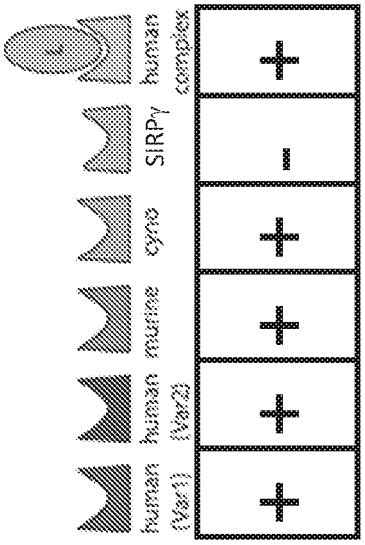

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+
+
+
+
+
-
+

FIG. 5B

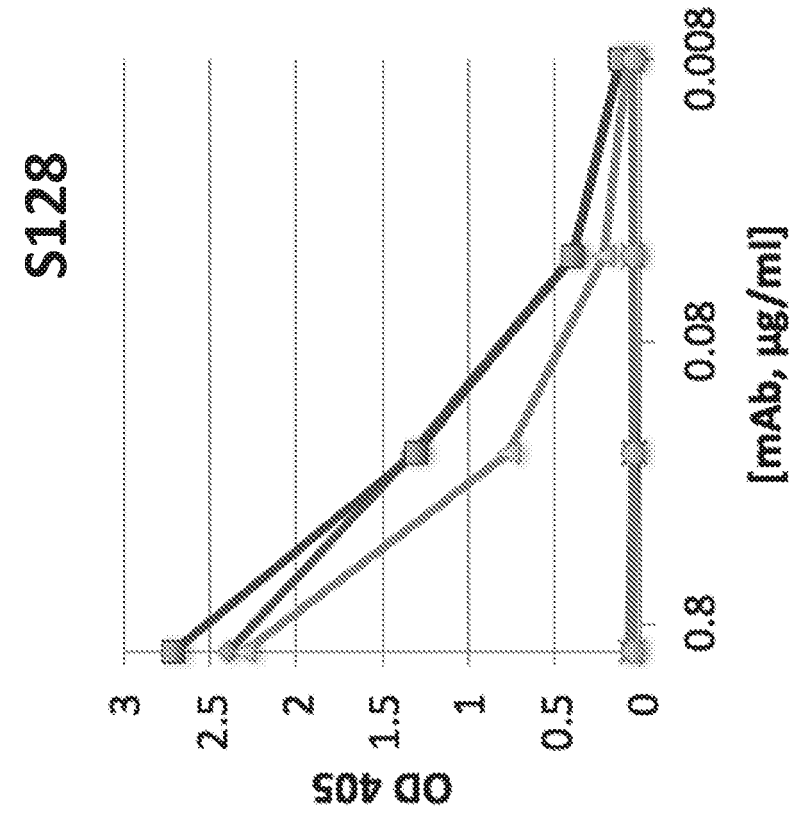

S128
OD 405
3
2.5
2
1.5
1
0.5
0
0.8
0.08
0.008
[mAb, µg/ml]
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex

FIG. 6A

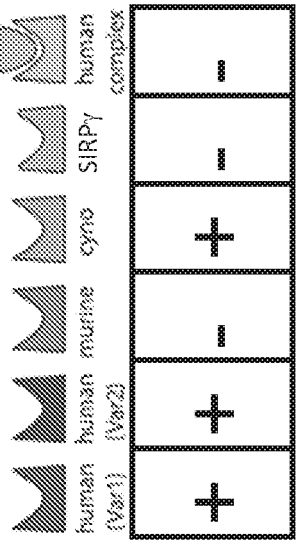

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+ + - - -

FIG. 6B

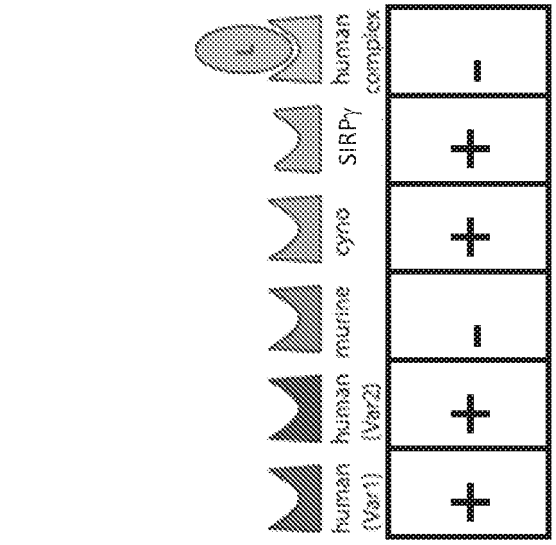

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+ + - + +
+ + - + -

FIG. 7B

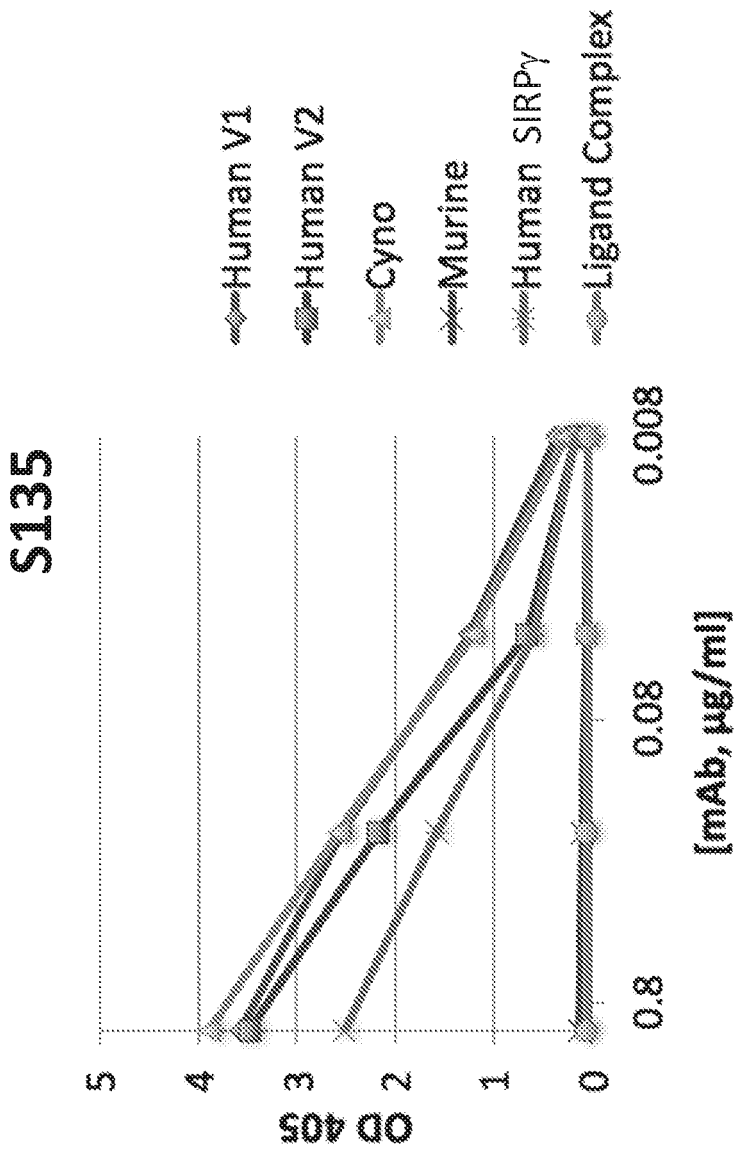

S135
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex
OD 405
5
4
3
2
1
0
0.8
0.08
0.008
[mAb, µg/ml]

FIG. 7A

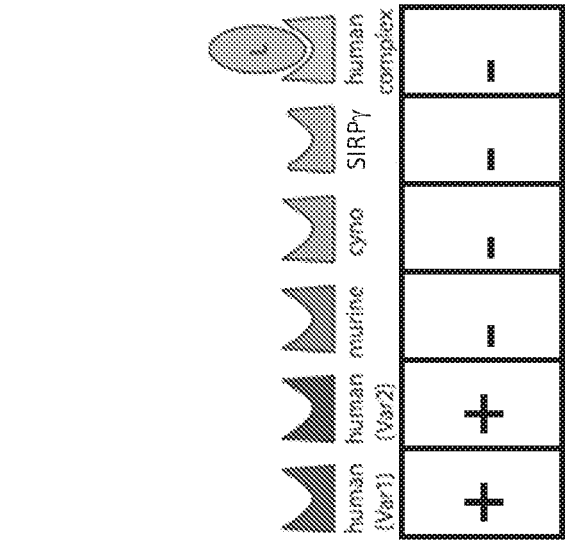

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+
+
-
-
-
-
-
-

FIG. 8B

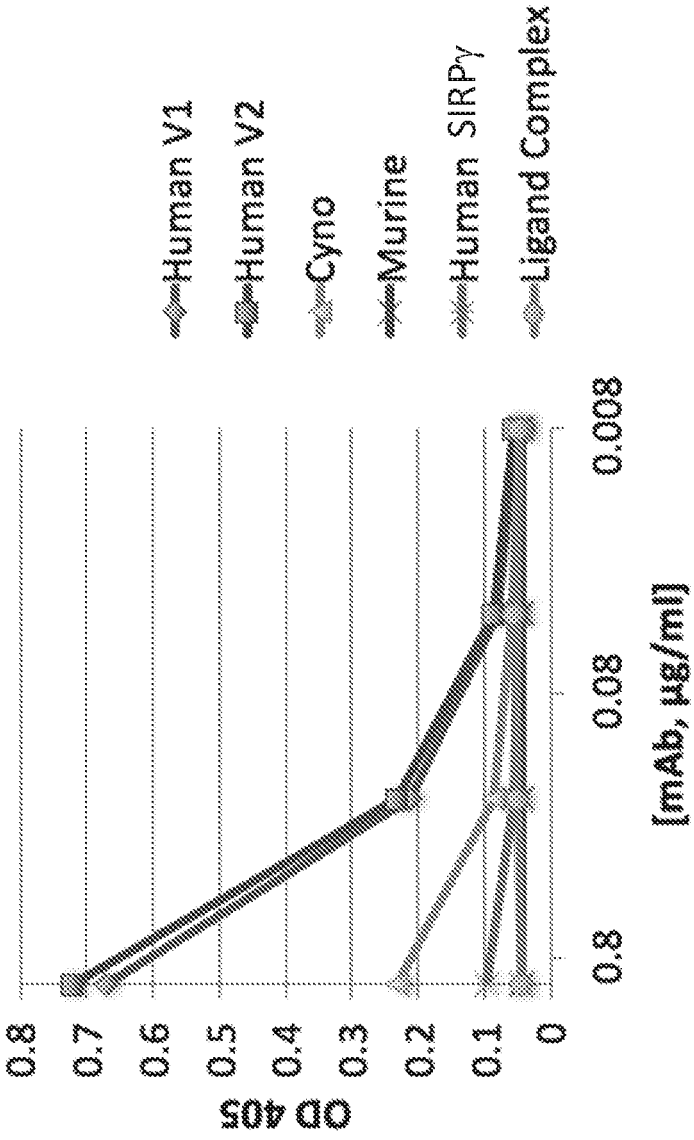

S126
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex
OD 405
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0.8
0.08
0.008
[mAb, µg/ml]

FIG. 8A

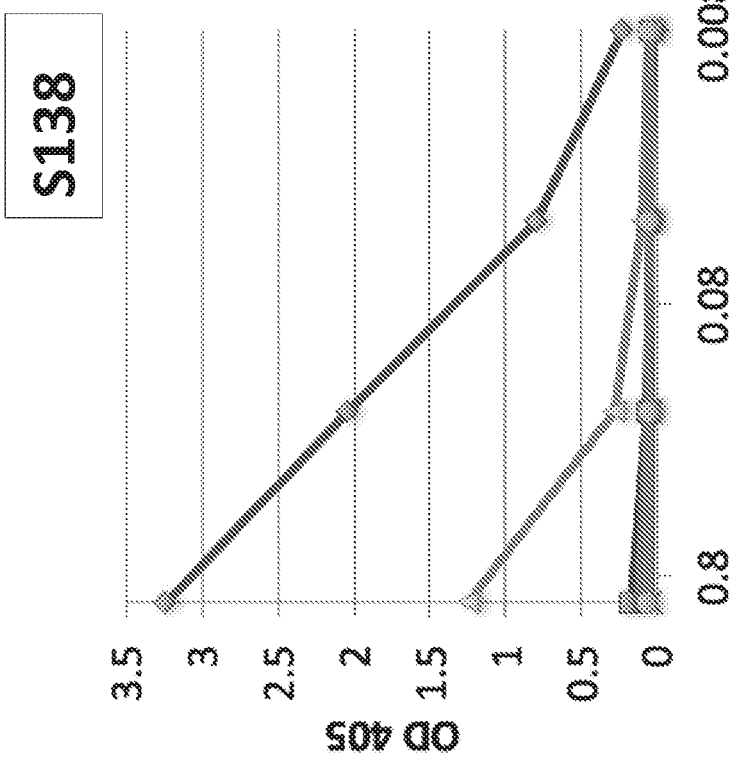

S138
Human V1
Human V2
Cyno
Murine
Human SIRPγ
Ligand Complex
OD 405
3.5
3
2.5
2
1.5
1
0.5
0
0.8
0.08
0.008
[mAb, µg/ml]

FIG. 9A

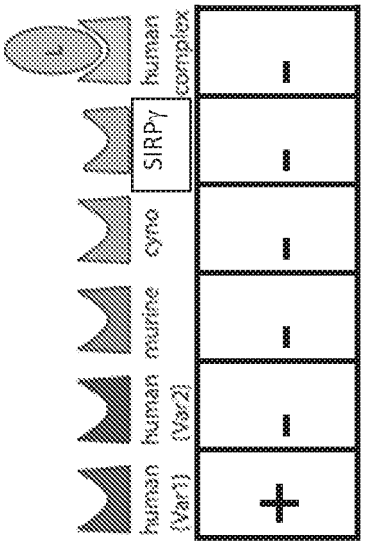

human (Var1)
human (Var2)
murine
cyno
SIRPγ
human complex
+
-
-
-
-
-
-
-

FIG. 9B

```
                1                                  L1                                50
 S1      (1)  ALTQPASVSANPGETVEITCSGG-GSNNAYGWFQQKSPGSAPLTVIYDNG
 S2      (1)  AVTQPASVSANPGETVRITCSG--DSSSYYSWHQQKSPGSAPVSVIYSNT
 S8      (1)  AVTQPSSVSANPGETVEITCSG--SST-YYGWYQQKSPGSAPVTVIYDND
 S9      (1)  ALTQPSSVSANPGETVKITCSGDNSAHYYYGWYQQKSPGSAPVTVIYYND
S11      (1)  AVTQPASVSANPGETVKITCSG--SSSGSYGWYQQKSPGSAPVTLIYETN
S12      (1)  AVTQPASVSANPGETVKITCSG--DSS-YYGWYQQKSPGSAPVTVIYDDN
S13      (1)  AVTQPASVSANPGETVKITCSG--SSS-YYGWYRQKSPGSAPVTLIYDND
S14      (1)  AVTQPASVSANLGETVKITCSG--DSS-YYGWYQQKAPGSAPVTLIYDND
                *   *     *    *      ******* * **  *      ***  ***
                51 L2                                        L3      100
 S1     (50)  KRPSDIPSRFSGSKSDSTGTLTITRVQAEDEAVYYCGSADN-SGAGVFGA
 S2     (49)  DRPSDIPSRFSGSASGSTATLTITGVQAEDEAVYFCGAYDSSSDSDIFGA
 S8     (48)  KRPSDIPSRFSGSKSGSTHTLIITGVQVEDEAVYFCGNEDNN-YVAIFGA
 S9     (51)  KRPSGIPSRFSGSASGSTATLIITGVQVEDEAVYFCGSADSS-NPAIFGA
S11     (49)  KRPSNIPSRFSGSKSGSTATLTITGVQADDEAVYYCGSEDSSTYLSIFGA
S12     (48)  KRPSNIPSRFSGSKSGSTGTLTITGVQADDEAVYFCGNEDNS-YVAIFGA
S13     (48)  KRPSGIPSRFSGSKSGSTNTLTITGVQADDEAVYYCGNEDNS-YVGIFGA
S14     (48)  KRPSNIPSRFSGSKSGSTATLTITGVQADDEAVYYCGNEDMN-YVGIFGA
               *   *         * *  *  *  *  **      *  ** *******
```

FIG. 10A

```
                101                linker                          150
 S1     (99)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
 S2     (99)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGGLSLVCK
 S8     (97)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
 S9    (100)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGRALSLVCR
S11     (99)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
S12     (97)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
S13     (97)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
S14     (97)  GTTLTVLGQSSRSSGGGGSSGGGGSMAAVTLDESGGGLQTPGGALSLVCK
                                                  **      *

                151       H1                    H2          200
 S1    (149)  GSGFTFSSHAMNWVRQAPGKGLEWVAGISS----DGRFTYYGAAVQGRAT
 S2    (149)  ASGFDFSNFNMAWVRQGPGKGLEYVAEISD----TGSTPYYGSAVQGRAT
 S8    (147)  ASGFTFSSYNMGWVRQAPGKGLEFVAGIYASGSSTDTDTTYGPAVAGRAT
 S9    (150)  GSGFSISSYNMGWVRQAPGKGLEFIASIGS----DGSSTHYAPAVKGRAT
S11    (149)  ASGFTFSSFNMGWVRQAPGKGLEFVAAIYS-----GNSAEYGAAVQGRAT
S12    (147)  ASGFTFSSYNMGWVRQAPGKGLEFVAGIYI--ASGDLGTTYGAAVQGRAT
S13    (147)  ASGFTFSSYNMGWVRQAPDKGLEFVAGIYTG-SDAGLSTTYGAAVQGRAT
S14    (147)  ASGFTFNSYNMGWVRQAPGKGLEFVAGIYS--AGGDTSTTYGAAVNGRAT
                *    ****** *     * *     ** * ************ **   *
```

FIG. 10A (cont.'d)

```
                201                                                H3          250
 S1   (195)  ISRDNGQSTVRLQLNNLRAEDTATYYCTKNGG-----CGSGGDLDCIDAW
 S2   (195)  ISRDNGQSTVRLQLNNLRAEDTGTYFCTRN---------FGSSVSSIDAW
 S8   (197)  ISRDNGQSTVRLQLNNLRAEDTGTYYCAKAAGGCSTHTCTAYIADSIDAW
 S9   (196)  ITRDVGQSTVRLQLNNLRAEDTGTYFCAKDAYQCS-YATCNDYLDTIDAW
S11   (194)  ISRDNGQSTVRLQLNNLRAEDTGIYFCAKDAG-SGCYSGVCAGTSSIDAW
S12   (195)  ISRDDGQSTVRLQLNNLRAEDTGTYFCAKSAGGCSAHSCDTYIADSIDAW
S13   (196)  ISRDNGQSTVRLQLNNLGAEDTGIYFCTKSAGGCSDYNCDAYIADSIDAW
S14   (195)  ISRDNGQSTVRLQLNNLRAEDTGIYFCAKAAGGCTAHNCDAYIADSIDAW
                *   *                 *     ** * **********************

                251     261
 S1   (240)  GHGTEVIVSSS
 S2   (236)  GHGTEVIVSSS
 S8   (247)  GHGTEVIVSSS
 S9   (245)  GHGTEVIVSSS
S11   (243)  GHGTEVIVSSS
S12   (245)  GHGTEVIVSSS
S13   (246)  GHGTEVIVSSS
S14   (245)  GHGTEVIVSSS
```

FIG. 10A (cont.'d)

```
                1                    L1                          50
S115     (1)  ETVLTQSPATLSVSPGERATLSCRASQTVG-SKLAWHQQKPGQAPRLLIY
S116     (1)  ETVLTQSPATLSVSPGERATLSCRASQTVG-SKLAWHQQKPGQAPRLLIY
S117     (1)  ETVLTQSPATLSVSPGERATLSCRASQTVG-SKLAWHQQKPGQAPRLLIY
S118     (1)  ETVLTQSPATLSVSPGERATLSCRASQTVG-SKLAWHQQKPGQAPRLLIY
S119     (1)  EIVLTQSPATLSVSPGERATFSCRASQNVK-NDLAWYQQRPGQAPRLLIY
S120     (1)  EIVLTQSPATLSVSPGERATFSCRASQNVK-NDLAWYQQRPGQAPRLLIY
S122     (1)  EIVLTQSPATLSVSPGERATFSCRASQNVK-NDLAWYQQRPGQAPRLLIY
S123     (1)  EIVLTQSPGTLSVSPGERVTLTCRASQGIAG-KIAWYQQKPGQAPRLLIY
S126     (1)  EIVLTQSPGTLTLSPGERATLSCRASQSIGSSYLAWYQQKPGQAPRLLIY
S128     (1)  ETVLTQSPATLSVSPGERATLSCRASQTVG-SKLAWHQQKPGQAPRLLIY
S130     (1)  EIVLTQSPGTLSVSPGERATLSCRASQNVR-SDLAWYQQKLGQAPRLLIY
S135     (1)  EIVLTQSPATLSVSPGERVTFSCRASQNVR-SDIAWYQQKPGQAPRLLIY
S137     (1)  ETVLTQSPGTLTLSPGERATLTCRASQSVY-TYLAWYQEKPGQAPRLLIY
S138     (1)  EIVLTQSPGTLSVSPGERVILTCRASQSVDTYNLAWYQQKPGQAPRLLIY
               *       *  **     ****     *******  * ***
                51 L2                                  L3      100
S115    (50)  DATNRATGISDRFSGSGSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S116    (50)  DATNRATGISDRFSGSRSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S117    (50)  DATNRATGIPDRFSGSGSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S118    (50)  DASRRATGIPDRFSGSGSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S119    (50)  AARIRETGIPERFSGSGSGTEFTLTITSLQSEDFAVYYCQQYYDWPPFTF
S120    (50)  AARIRETGIPERFSGSGSGTEFTLTITSLQSEDFAVYYCQQYYDWPPFTF
S122    (50)  AARIRETGIPERFSGSGSGTEFTLTITSLQSEDFAVYYCQQYYDWPPFTF
S123    (50)  DASSRATGIPGRFSGSGSGTEFTLTITSLQSEDFAVYYCQQHYDWSPLTF
S126    (51)  DATNRATGIPDRFSGSGSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S128    (50)  DASNRATGIPDRFSGSGSGTDFTLTISSLQTEDSAVYYCQQYYYWPPYRF
S130    (50)  DANTRATDIPDRFSGSGSGTEFTLTISSLQSEDFAVYYCQHYYDWPPVTF
S135    (50)  AASSRDTGIPDRFSGSGSGTDFTLTISSLQSEDFGVYYCQQYYDWPPFTF
S137    (50)  GASSRATGIPDRFSGSGSGTVFTLTISSLQSEDFAVYYCQQYYDRPPLTF
S138    (51)  DLSTRATGIPDRFSGSGSGTEFTLTINSLEPEDFAVYYCHQYYDWPPYTF
              **** * * **     *   *     *  **  **    *** *** **
```

FIG. 10B

```
                  101                 linker                          150
S115 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S116 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S117 (100) GGGTKVEIKGQSSRSSGGGGSSRGGGGSDVQLVESGGGVVRPGESLRLSCA
S118 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S119 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLLESGGGVVQPGGSLRLSCA
S120 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVQPGGSLRLSCA
S122 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S123 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGLVQPGGSLRLSCT
S126 (101) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S128 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S130 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S135 (100) GGGTKVEIKGQSSRSSGGGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S137 (100) GGGTKVEIKGQSSRSSGCGGSSGGGGSDVQLVESGGGVVRPGESLRLSCA
S138 (101) GGGTKVEIKGQSSRSSGGGCSSGGGGSDVQLVESGGGVVRPGESLRLSCA
                                *   *       *     *  *  *   *

                  151      H1          H2                 200
S115 (150) ASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDYAESVKGRFTISRD
S116 (150) ASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDYAESVKGRFTISRD
S117 (150) ASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDYAESVKGRFTISRD
S118 (150) ASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDYAESVKGRFTISRD
S119 (150) ASGFSFSNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISRD
S120 (150) ASGFSFSNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISRD
S122 (150) ASGFRFSNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISRD
S123 (150) ASGFTFRNYGMSWVRQAPGEGLEWVSASSG-SGSTYYTDSVKGRFTISRD
S126 (151) ASGFTFSNYDMTWVRQAPGEGLEWVSGISGNGGSTYYADSVKGRFTISRD
S128 (150) ASGFSFRSYAMNWVRQAPGEGLEWVSRIDSGGGGTDYADSVKGRFTISRD
S130 (150) ASGFTFSNYAMSWVRQAPGEGLEWVSLITTNGDGAYYADSVKGRFTISRD
S135 (150) ASGFSFSIYAMSWVRQAPGEGLEWVSTIGAD--DTYYADSVKGRFTISRD
S137 (150) ASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYYADSVKGRFTISRD
S138 (151) ASGFTFSNYAMNWVRQAPGEGLEWVSGISGRGGDTYYADSVKGRFTISRD
                          *  ****  *              ********** **
```

FIG. 10B
(cont'd)

```
                                 201                H3                250
                                                    ___________________
S115 (200) NSENTLYLQMNSLRAEDTAVYYCAKQY-----DWNSFFDYWGLGALVTVSSS
S116 (200) NSENTLYLQMNSLRAEDTAVYYCAKQY-----DWNSFFDYWGLGALVTVSSS
S117 (200) NSENTLYLQMNSLRAEDTAVYYCAKQY-----DWNGFFDYWGLGALVTVSSS
S118 (200) NSENTLYLQMNSLRAEDTAVYYCAKQY-----DWNGFFDYWGLGALVTVSSS
S119 (198) NSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSSS
S120 (198) NSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTRVTVSSS
S122 (198) NSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSSS
S123 (199) NSKNTLYLQMNSLRAEDTAIYYCAKVT-----WNN-FFDYWGLGTLVTVSSS
S126 (201) NSKNTLYLQMNSLRAEDTAVYYCAMN-------RWW--FDYWGLGTLVTVSSS
S128 (200) NSKNTLYLQMNSLRAEDTAVYYCAKQY-----DWNSFFDYWGLGAPVTVSSS
S130 (200) NSKNTLYLQMNSLRAEDTAIYYCAKDGAAHYYDIFFDYWGLGTPVTVSSS
S135 (198) NSKNTLYLQMNSLRAEDTAVYYCAKDSTVGWSGDFFDYWGLGTLVTVSSS
S137 (200) NSKNTLYLQMNSLRAEDTAVYYCAKEN-----NRYRFFDDWGLGTLVTVSSS
S138 (201) NSKNTLYLQMNSLRAEDTAIYYCAKGT-----WNYGSFDYWGLGTLVTVSSS
                                   *     ********** *   *    **
```

FIG. 10B
(cont'd)

FIG. 11A


1
H1
H2
60
S16 (1) DVQLVESGGGVVRPGESLRLSCAVSGFRFSSYAMSWVRQAPGKGLEWVSGISS-GGDTYY
S27 (1) DVQLVESGGGVVRPGESLRLSCAVSGFRFSSYAMSWVRQAPGKGLEWVSGISS-GGDTYY
S55 (1) DVQLVESGGGVVRPGESLRLSCAVSGFRFSSYAMSWVRQAPGKGLEWVSGISS-GGDTYY
S59 (1) DVQLVESGGGVVRPGESLRLSCAVSGFRFSSHAMSWVRQAPGKGLEWVSGISS-GGDTYY
S29 (1) DVQLVESGGGVVRPGESLRLSCAVSGFRFSSYAMSWVRQAPGKGLEWVSGISS-DSDAYY
S201 (1) DVQLVESGGAVVRPGETLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSGISASGSDTYY
S206 (1) DVQLVESGGAVVRPGETLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSGISASGSDTYY
S26 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVSGISASGSGTYY
S25 (1) DVQLVESGGGVVRPGESLRLSCEASGFTFSSNAMSWVRQAPGKGLEWVAGISS-GSDTYY
S73 (1) DVQLVESGGGVVRPGESLRLSCEASGFTFSSNAMSWARQAPGKGLEWVAGISS-GSDTYY
S30 (1) DVQLVESGGGVVRPGESLRLSCEASGFTFSSDAMSWVRQAPGKGLEWVSGISS-GSSTYY
S28 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSNAMSWVRQAPGKGLEWVAGISASG-DTYY
S21 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSNAMSWVRQAPGKGLEWLAGISAGGSDTYY
S24 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSNAMSWVRQAPGKGLEWLAGISAGGSDTYY
S74 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSNAMSWVRQAPGKGLEWLAGISAGDSDTYY
S23 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSHAMSWVRQAPGKGLEWLAGISAGGSDTYY
S17 (1) DVQLVESGGAVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S22 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S66 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S56 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S70 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDAYY
S202 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S60 (1) DVQLVDSGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S65 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S69 (1) DLQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S71 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
S76 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLAGISAGGSDTYY
* * * * ** * ** * ** ******

FIG. 11A (cont'd)

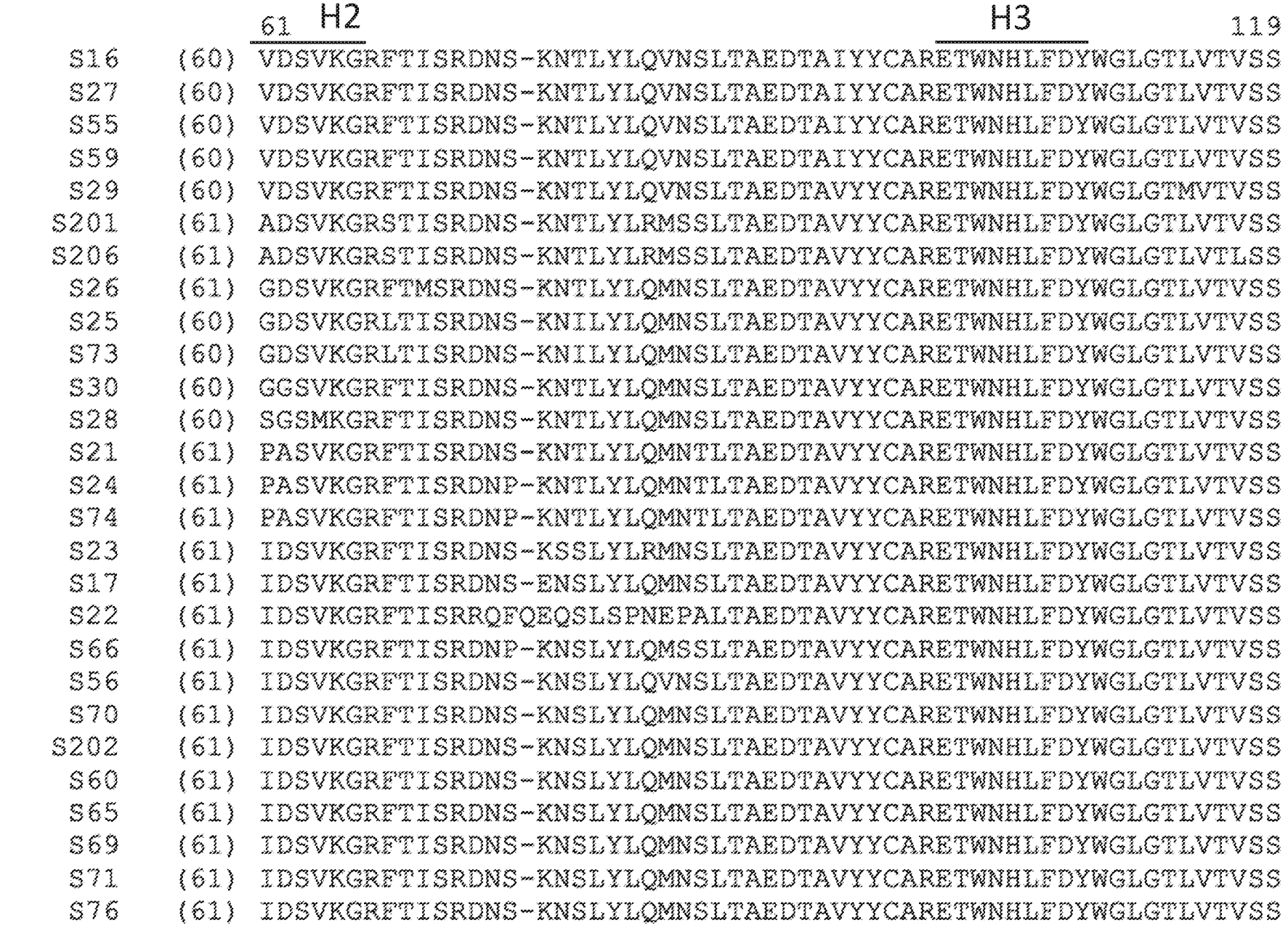


FIG. 11A (cont'd)

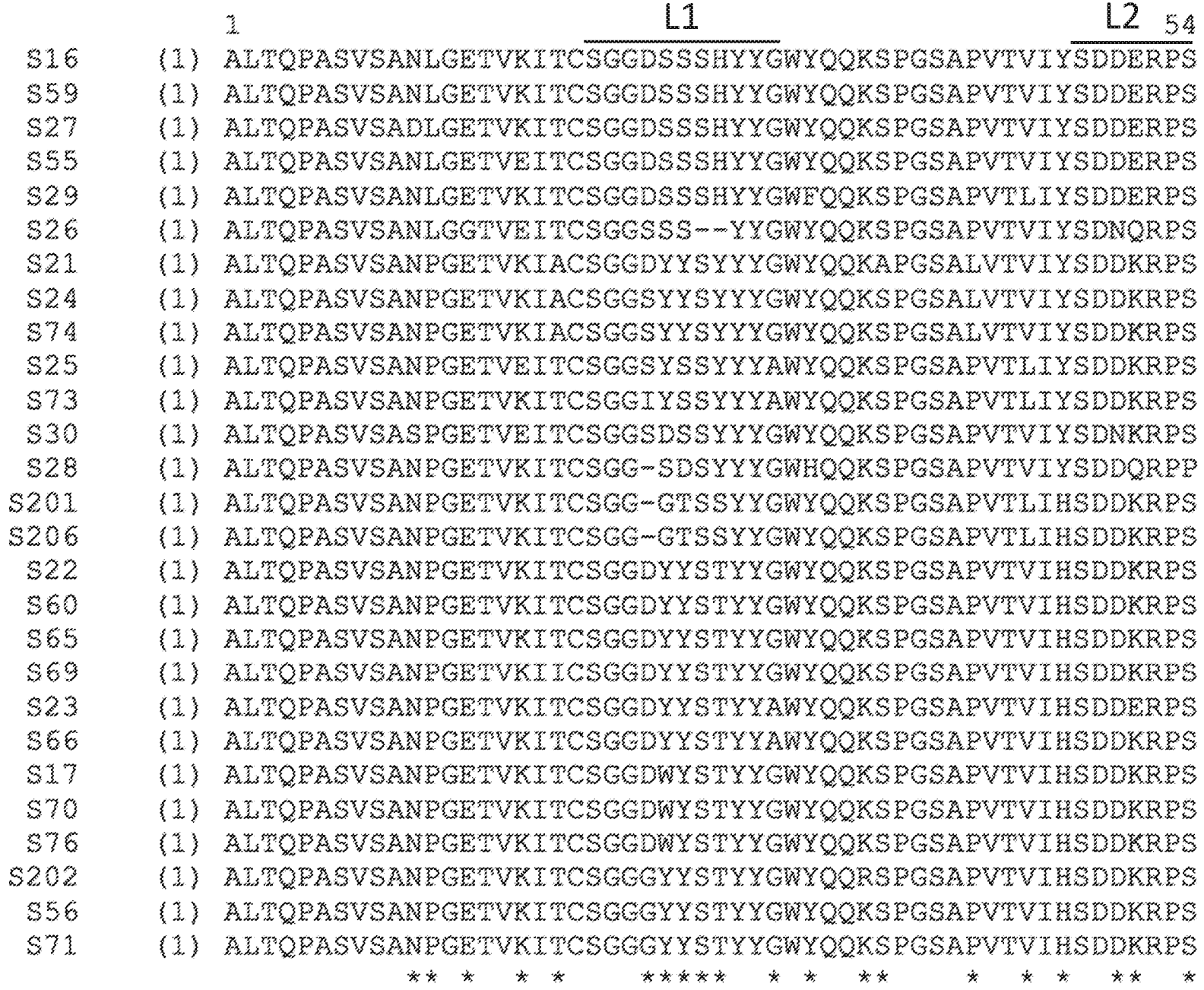


FIG. 11A (cont'd)

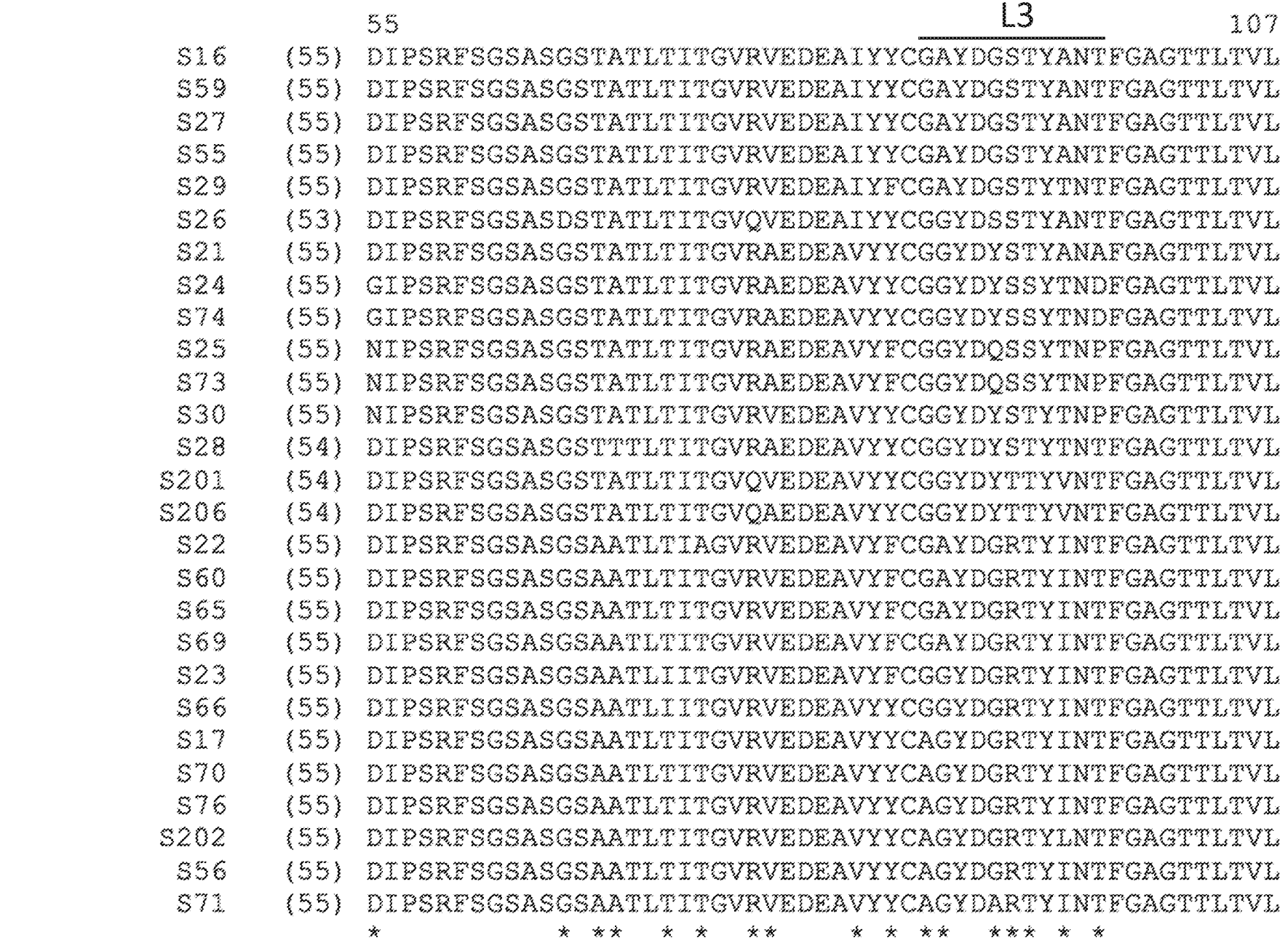


FIG. 11B

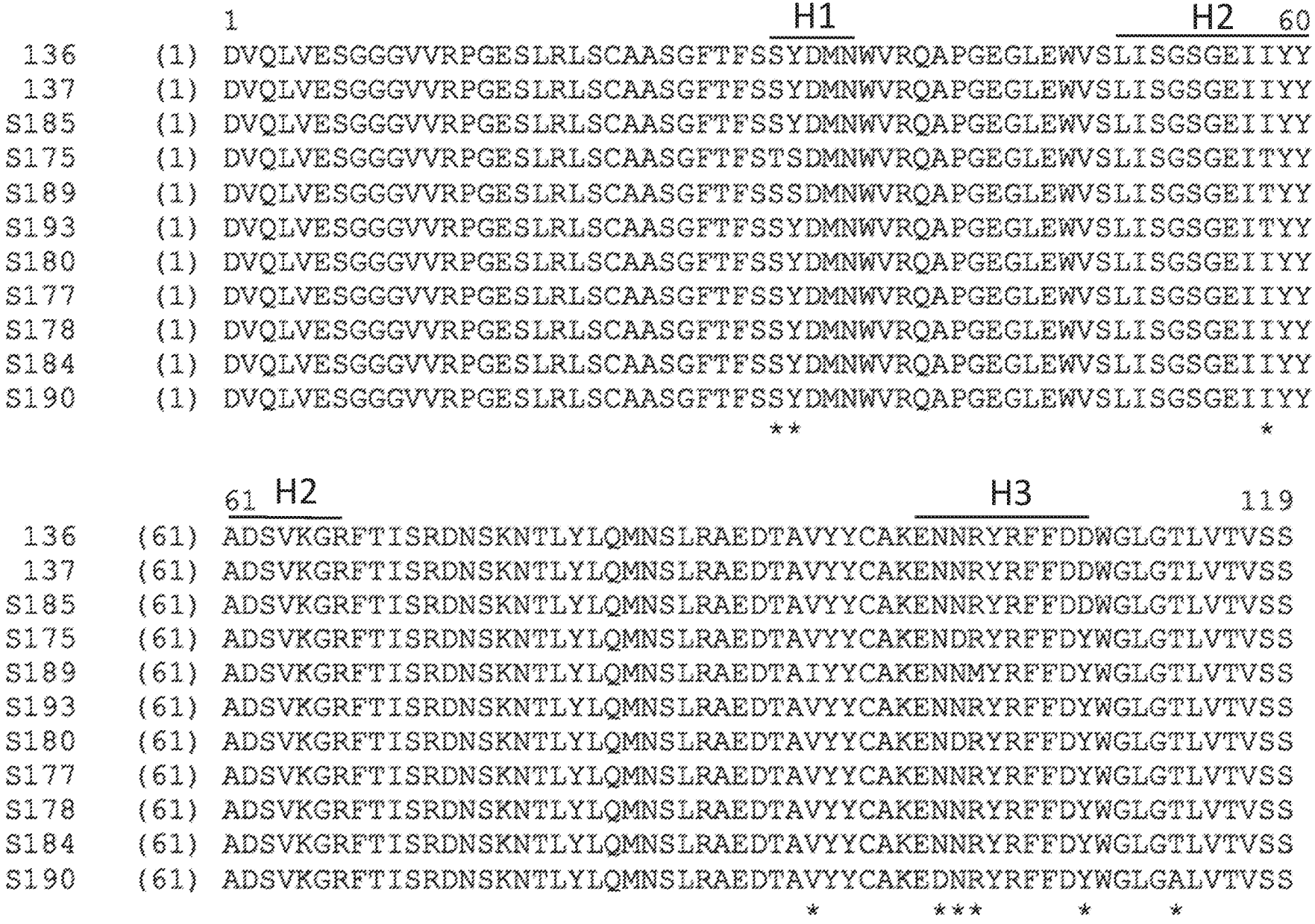

1 H1 H2 60
136 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
137 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S185 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S175 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSTSDMNWVRQAPGEGLEWVSLISGSGEITYY
S189 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSSDMNWVRQAPGEGLEWVSLISGSGEITYY
S193 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEITYY
S180 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S177 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S178 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S184 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
S190 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQAPGEGLEWVSLISGSGEIIYY
** *
61 H2 H3 119
136 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDDWGLGTLVTVSS
137 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDDWGLGTLVTVSS
S185 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDDWGLGTLVTVSS
S175 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENDRYRFFDYWGLGTLVTVSS
S189 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKENNMYRFFDYWGLGTLVTVSS
S193 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDYWGLGTLVTVSS
S180 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENDRYRFFDYWGLGTLVTVSS
S177 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDYWGLGTLVTVSS
S178 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDYWGLGTLVTVSS
S184 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKENNRYRFFDYWGLGTLVTVSS
S190 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEDNRYRFFDYWGLGALVTVSS
* *** * *

FIG. 11B (cont'd)

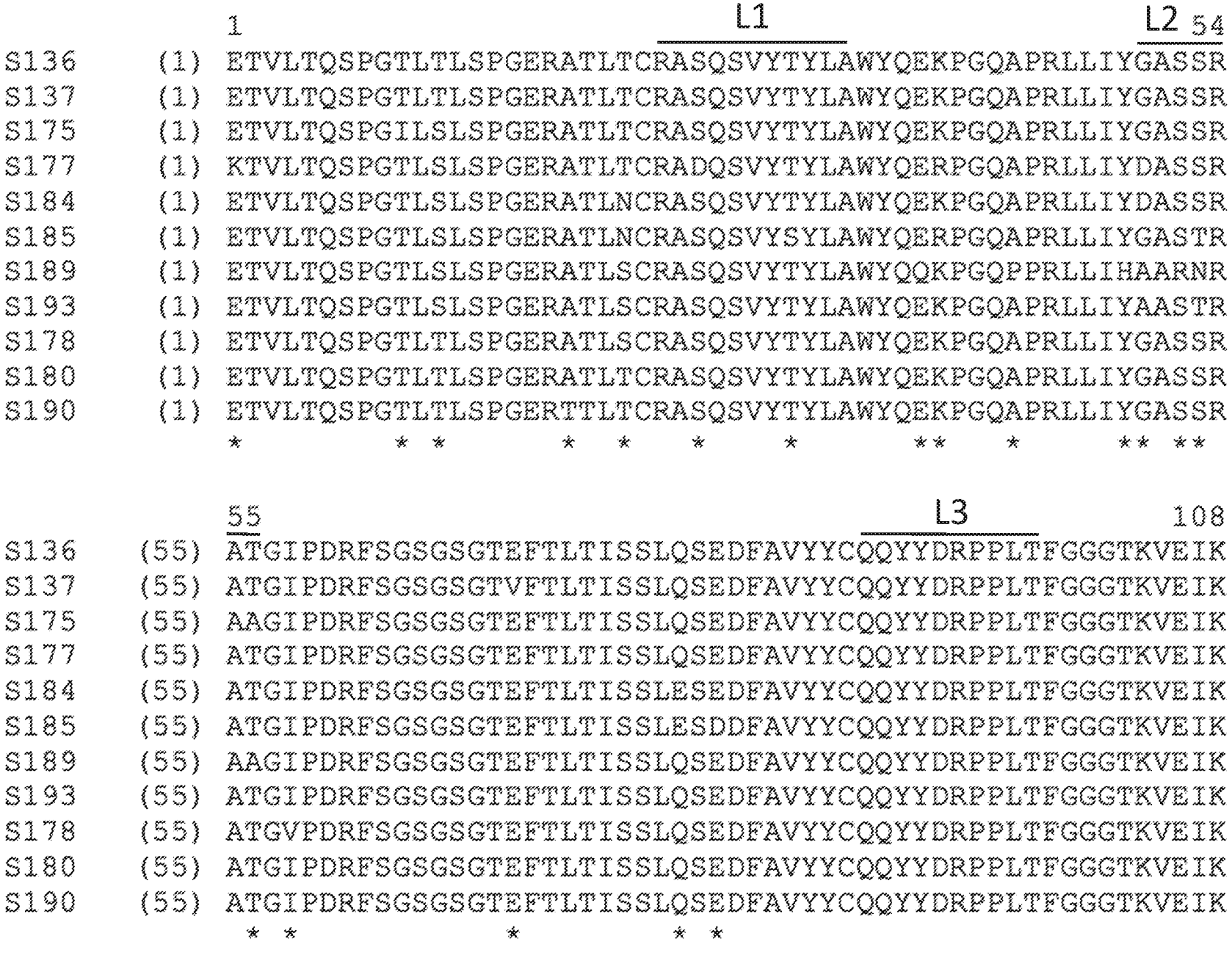


FIG. 11C

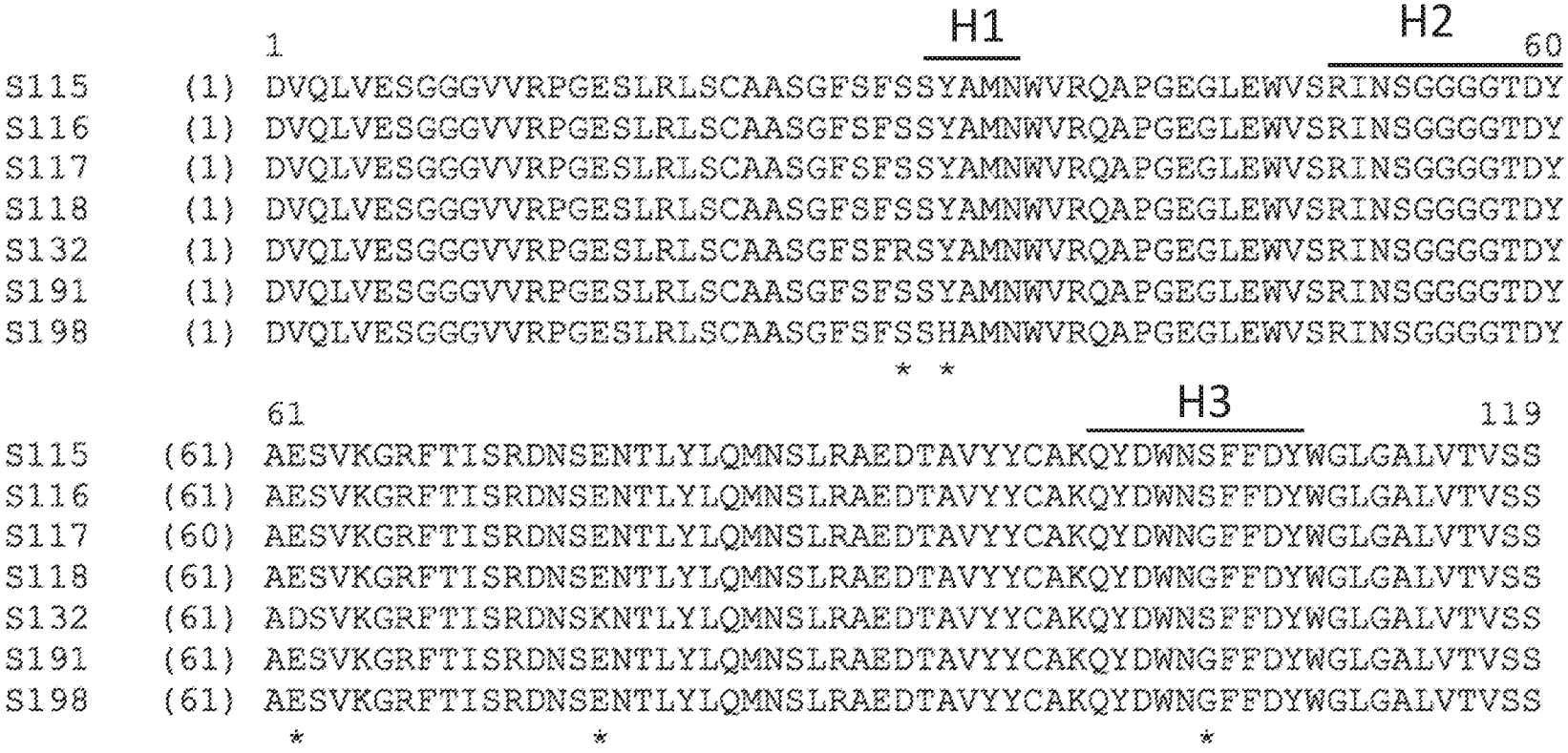

H1
H2
H3
1
60
61
119
S115 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S116 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S117 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S118 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S132 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFRSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S191 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSYAMNWVRQAPGEGLEWVSRINSGGGGTDY
S198 (1) DVQLVESGGGVVRPGESLRLSCAASGFSFSSHAMNWVRQAPGEGLEWVSRINSGGGGTDY
S115 (61) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNSFFDYWGLGALVTVSS
S116 (61) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNSFFDYWGLGALVTVSS
S117 (60) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNGFFDYWGLGALVTVSS
S118 (61) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNGFFDYWGLGALVTVSS
S132 (61) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKQYDWNSFFDYWGLGALVTVSS
S191 (61) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNGFFDYWGLGALVTVSS
S198 (61) AESVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYCAKQYDWNGFFDYWGLGALVTVSS

FIG. 11C (cont'd)

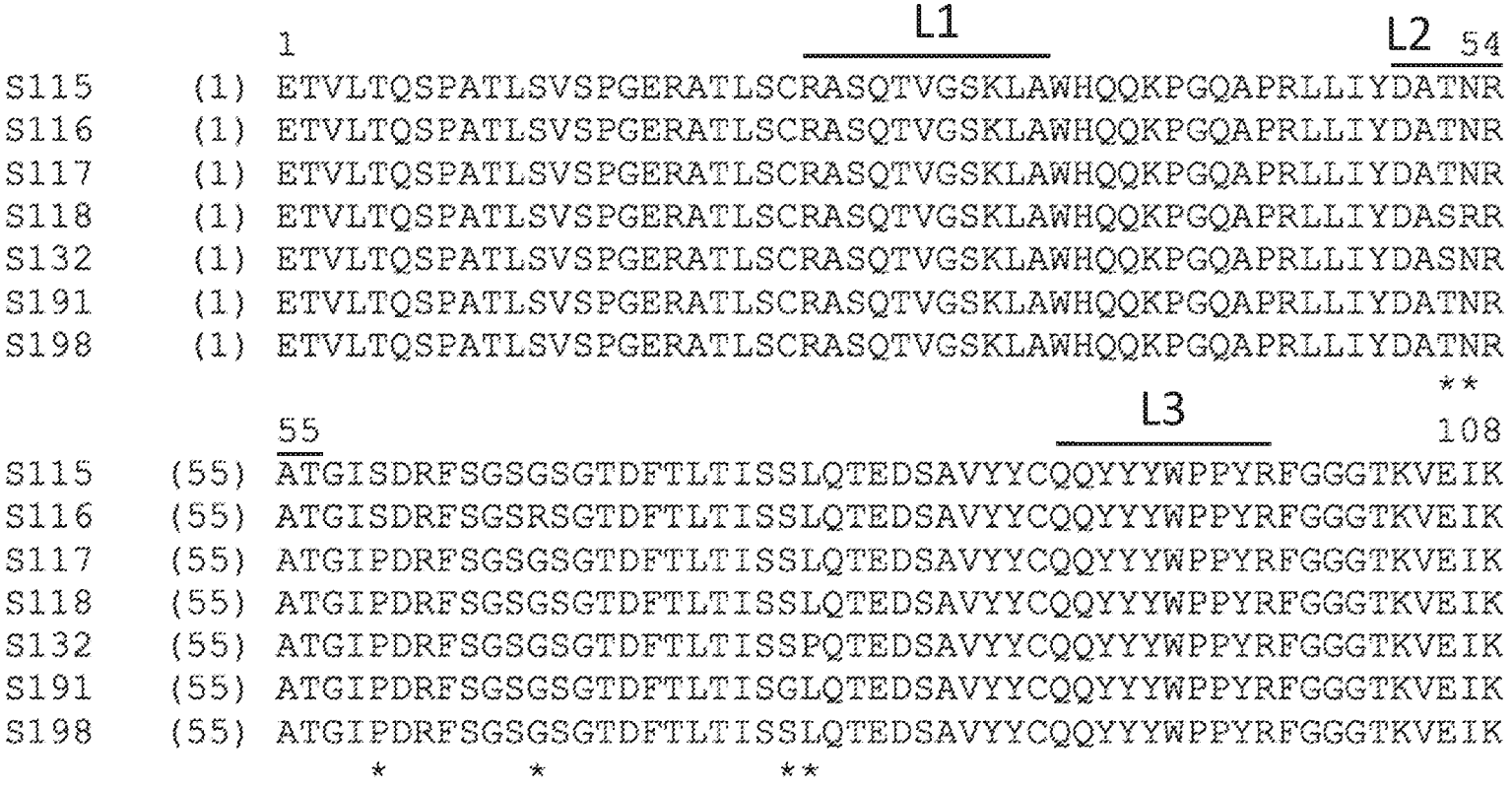


FIG. 11D

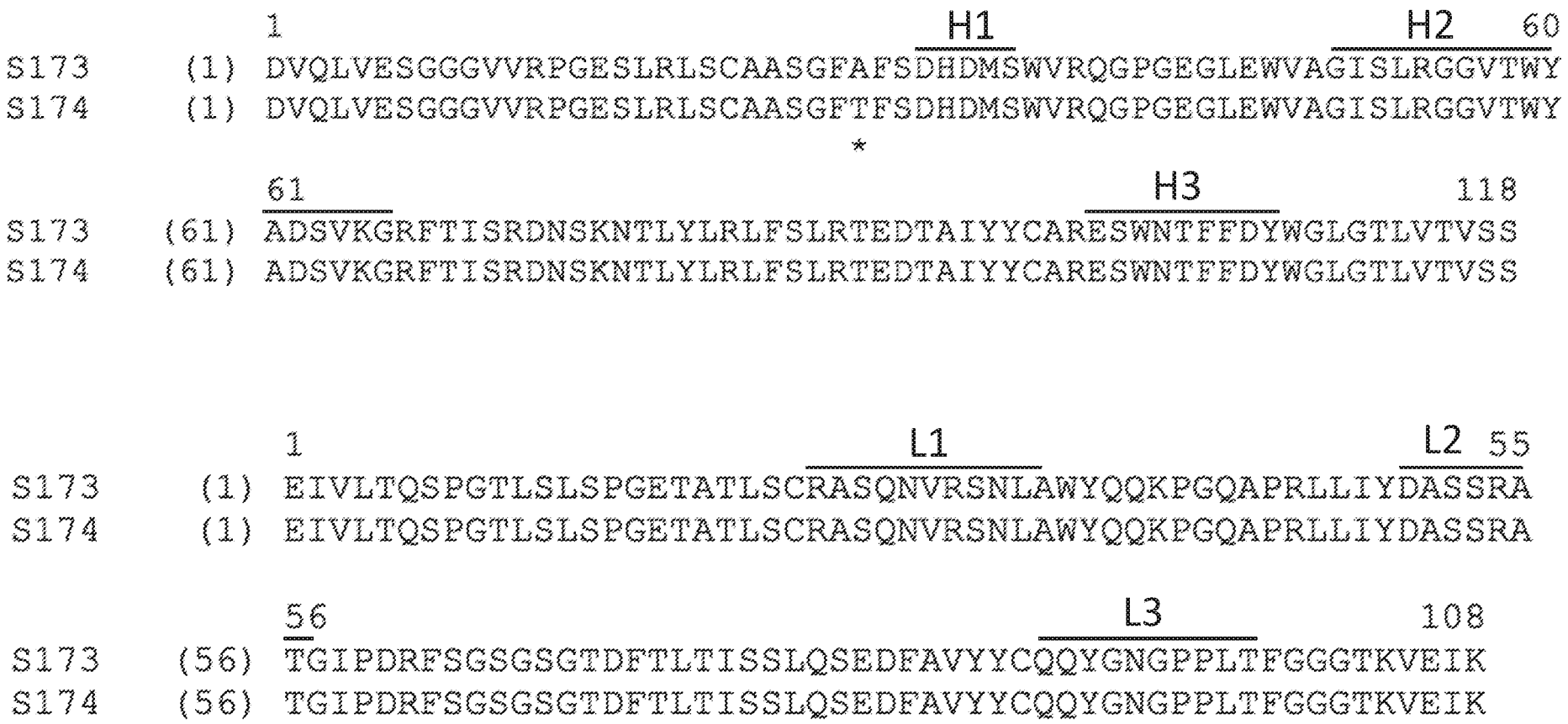

1 H1 H2 60
S173 (1) DVQLVESGGGVVRPGESLRLSCAASGFAFSDHDMSWVRQGPGEGLEWVAGISLRGGVTWY
S174 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSDHDMSWVRQGPGEGLEWVAGISLRGGVTWY
*
61 H3 118
S173 (61) ADSVKGRFTISRDNSKNTLYLRLFSLRTEDTAIYYCARESWNTFFDYWGLGTLVTVSS
S174 (61) ADSVKGRFTISRDNSKNTLYLRLFSLRTEDTAIYYCARESWNTFFDYWGLGTLVTVSS
1 L1 L2 55
S173 (1) EIVLTQSPGTLSLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA
S174 (1) EIVLTQSPGTLSLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA
56 L3 108
S173 (56) TGIPDRFSGSGSGTDFTLTISSLQSEDFAVYYCQQYGNGPPLTFGGGTKVEIK
S174 (56) TGIPDRFSGSGSGTDFTLTISSLQSEDFAVYYCQQYGNGPPLTFGGGTKVEIK

FIG. 11E

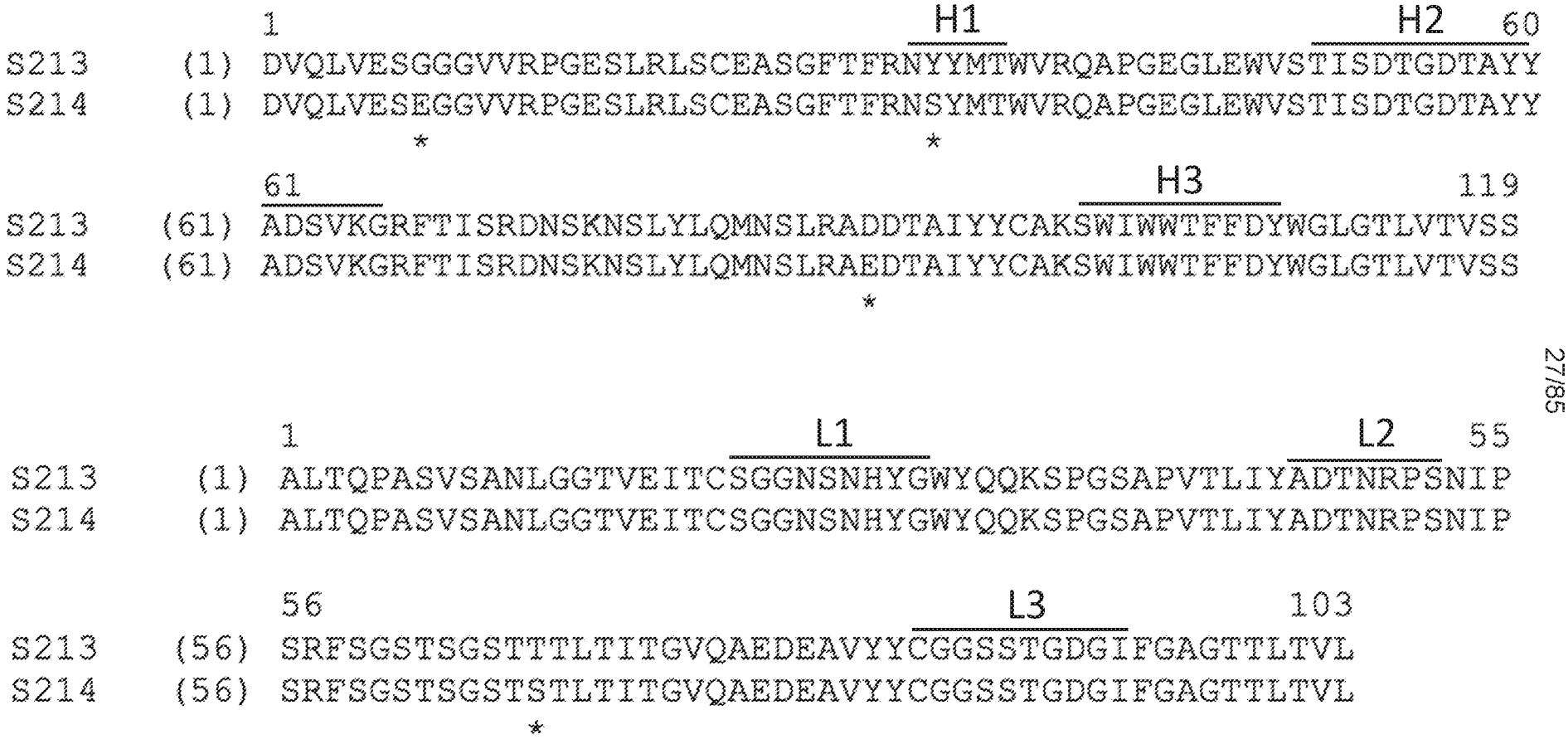

1 H1 H2 60
S213 (1) DVQLVESGGGVVRPGESLRLSCEASGFTFRNYYMTWVRQAPGEGLEWVSTISDTGDTAYY
S214 (1) DVQLVESEGGVVRPGESLRLSCEASGFTFRNSYMTWVRQAPGEGLEWVSTISDTGDTAYY
61 H3 119
S213 (61) ADSVKGRFTISRDNSKNSLYLQMNSLRADDTAIYYCAKSWIWWTFFDYWGLGTLVTVSS
S214 (61) ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTAIYYCAKSWIWWTFFDYWGLGTLVTVSS
1 L1 L2 55
S213 (1) ALTQPASVSANLGGTVEITCSGGNSNHYGWYQQKSPGSAPVTLIYADTNRPSNIP
S214 (1) ALTQPASVSANLGGTVEITCSGGNSNHYGWYQQKSPGSAPVTLIYADTNRPSNIP
56 L3 103
S213 (56) SRFSGSTSGSTTTLTITGVQAEDEAVYYCGGSSTGDGIFGAGTTLTVL
S214 (56) SRFSGSTSGSTSTLTITGVQAEDEAVYYCGGSSTGDGIFGAGTTLTVL

FIG. 11F

>209_VH
DVQLVESGGAVVRPGESLRLSCKASGFTFTNFAMSWVRQAPGEGLEWVSGISGSDDTTYYA
DSVKGRFTISRDNSESTLYLQMNSLRAEDTAVYYCVKDSTVSWNTFFDYWGLGTLVTVSS

>209_VL
ALTQPASVSANLGGTVKITCSGGYGSDDGSSSYYGWYQQKSPGSAPVILIYWDDKRPSDIP
SRFSGSTSGSTTTLTITGVQAEDEAVYFCGTYDTSSGAIFGAGTTLTVL

FIG. 11G

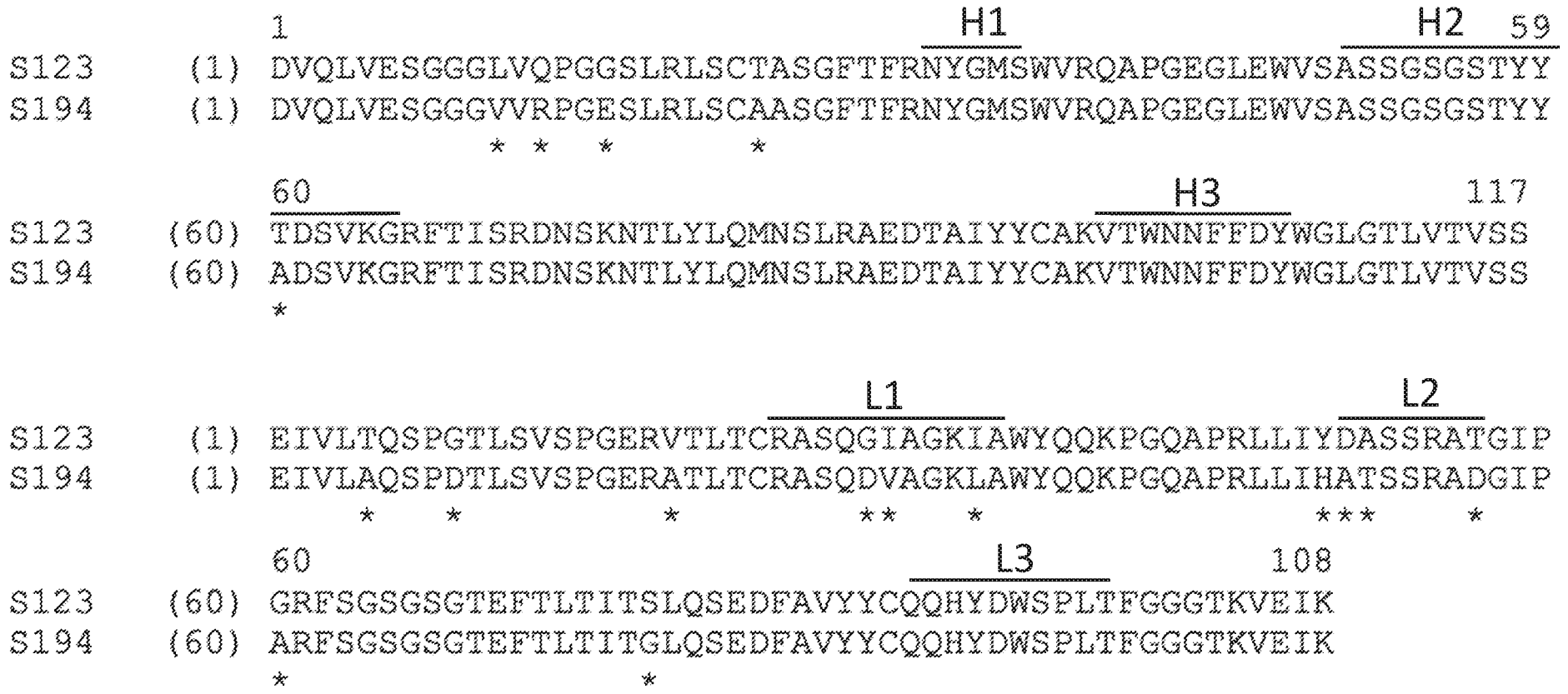

1 H1 H2 59
S123 (1) DVQLVESGGGLVQPGGSLRLSCTASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY
S194 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY
60 H3 117
S123 (60) TDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS
S194 (60) ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS
L1 L2
S123 (1) EIVLTQSPGTLSVSPGERVTLTCRASQGIAGKIAWYQQKPGQAPRLLIYDASSRATGIP
S194 (1) EIVLAQSPDTLSVSPGERATLTCRASQDVAGKLAWYQQKPGQAPRLLIHATSSRADGIP
60 L3 108
S123 (60) GRFSGSGSGTEFTLTITSLQSEDFAVYYCQQHYDWSPLTFGGGTKVEIK
S194 (60) ARFSGSGSGTEFTLTITGLQSEDFAVYYCQQHYDWSPLTFGGGTKVEIK

FIG. 11H

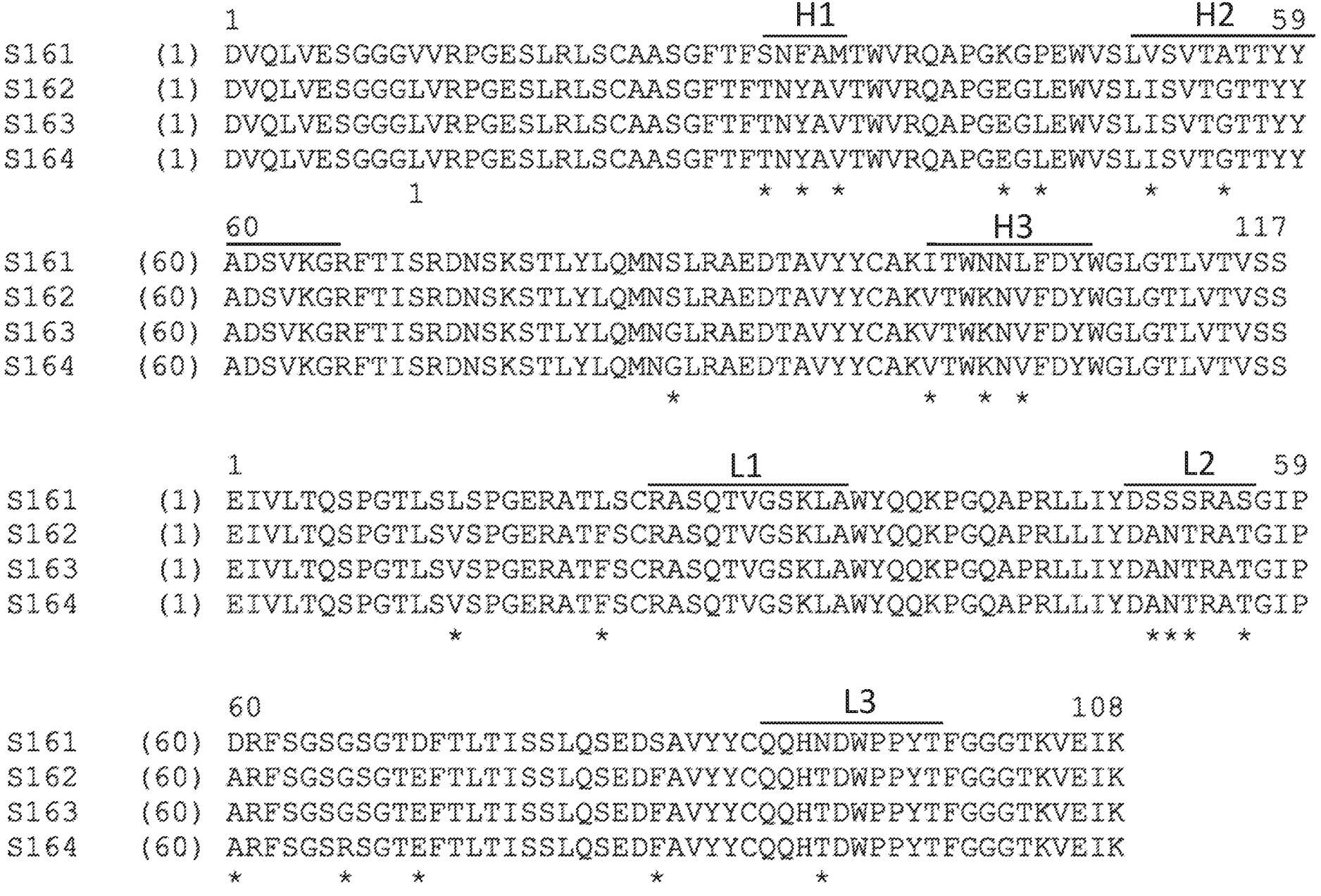

1 H1 H2 59
S161 (1) DVQLVESGGGVVRPGESLRLSCAASGFTFSNFAMTWVRQAPGKGPEWVSLVSVTATTYY
S162 (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTYY
S163 (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTYY
S164 (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTYY
1
60 H3 117
S161 (60) ADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYYCAKITWNNLFDYWGLGTLVTVSS
S162 (60) ADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYYCAKVTWKNVFDYWGLGTLVTVSS
S163 (60) ADSVKGRFTISRDNSKSTLYLQMNGLRAEDTAVYYCAKVTWKNVFDYWGLGTLVTVSS
S164 (60) ADSVKGRFTISRDNSKSTLYLQMNGLRAEDTAVYYCAKVTWKNVFDYWGLGTLVTVSS
1 L1 L2 59
S161 (1) EIVLTQSPGTLSLSPGERATLSCRASQTVGSKLAWYQQKPGQAPRLLIYDSSSRASGIP
S162 (1) EIVLTQSPGTLSVSPGERATFSCRASQTVGSKLAWYQQKPGQAPRLLIYDANTRATGIP
S163 (1) EIVLTQSPGTLSVSPGERATFSCRASQTVGSKLAWYQQKPGQAPRLLIYDANTRATGIP
S164 (1) EIVLTQSPGTLSVSPGERATFSCRASQTVGSKLAWYQQKPGQAPRLLIYDANTRATGIP
60 L3 108
S161 (60) DRFSGSGSGTDFTLTISSLQSEDSAVYYCQQHNDWPPYTFGGGTKVEIK
S162 (60) ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQHTDWPPYTFGGGTKVEIK
S163 (60) ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQHTDWPPYTFGGGTKVEIK
S164 (60) ARFSGSRSGTEFTLTISSLQSEDFAVYYCQQHTDWPPYTFGGGTKVEIK

FIG. 11I

>S149_VH
DVQLVESGGGVVRPGESLRLSCAASGFTFSNFAMNWVRQAPGEGLEWVSLISVTATTYYA
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVTWNNLFDYWGLGTLVTVSS
>S149_VL
EIVLTQSPGTLSLSPGERATLSCRASQPIDSYLAWYQQKPGQAPRLLIYNTVTRATGIPD
RFSGSGSGTDFTLTINRLEPEDFAVYYCQHQYDWPPYIFGGGTKVEIK

>S218_VH
DVQLVESGGGVVRPGESLTLSCTASGFTFTSSTMNWVRQAPGEGLDWVSSISTSGVITYY
ADSVKGRATISRDNSKNTLYLRLFSLRADDTAIYYCATDTFDHWGPGTLVTVSS
>S218_VL
ALTQPASVSANPGETVKITCFGSSGNYGWFQQKSPGSAPVTVIHYNNKRPSDIPSRFSGS
KSGSTGTLTITGVRAEDEAVYFCGAWETGSATFGAGTTLTVL

FIG. 11J

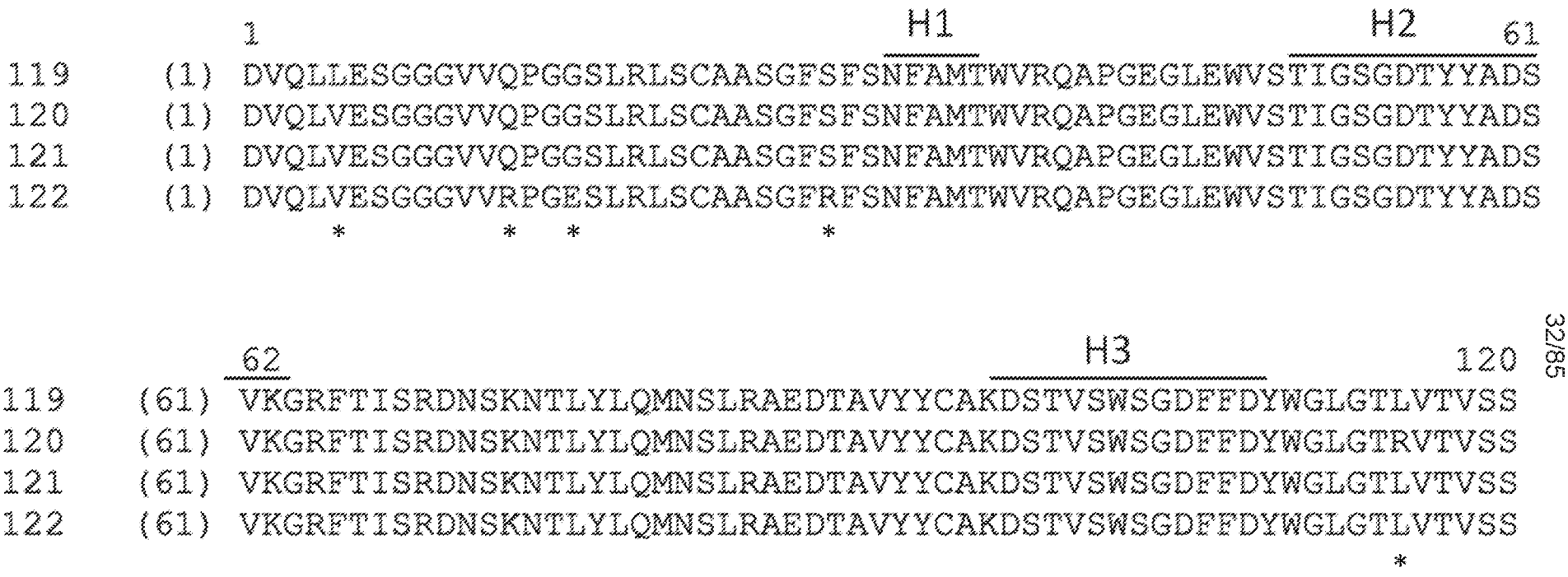
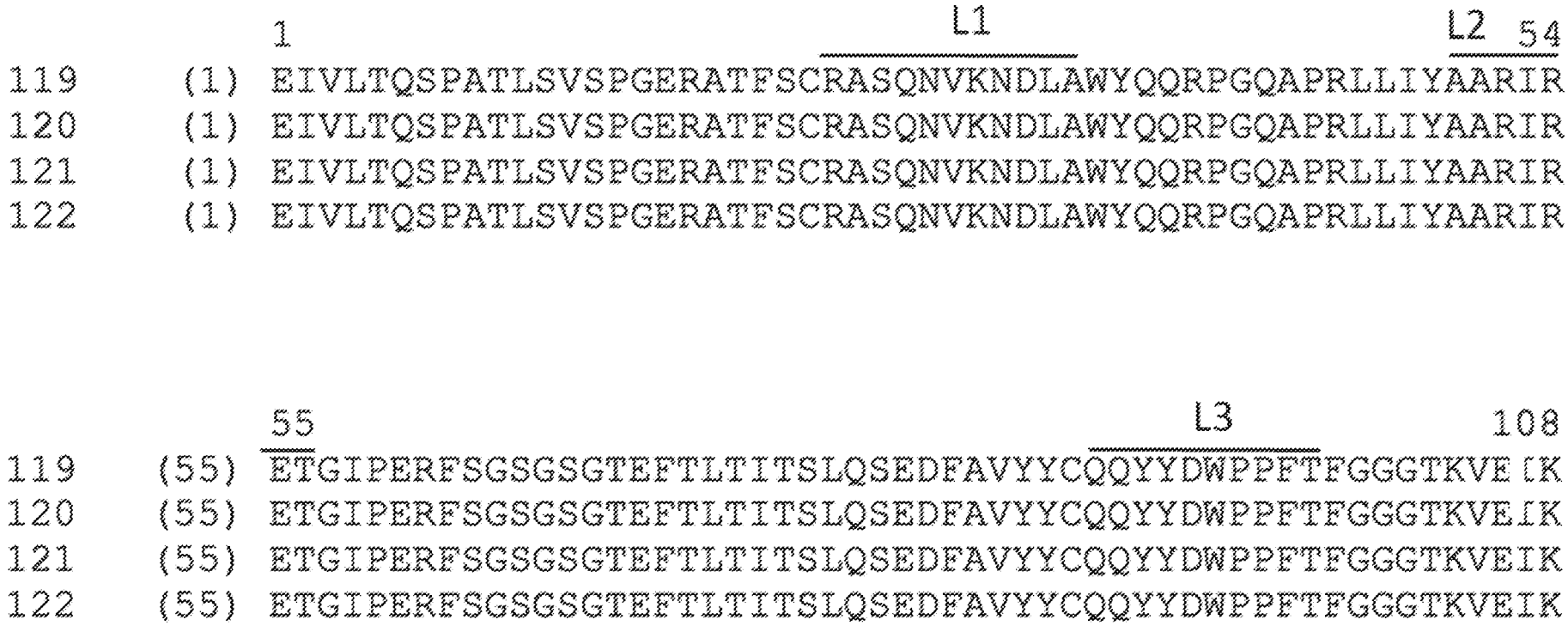

1
H1
H2
61
119 (1) DVQLLESGGGVVQPGGSLRLSCAASGFSFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS
120 (1) DVQLVESGGGVVQPGGSLRLSCAASGFSFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS
121 (1) DVQLVESGGGVVQPGGSLRLSCAASGFSFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS
122 (1) DVQLVESGGGVVRPGESLRLSCAASGFRFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS
62
H3
120
119 (61) VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSS
120 (61) VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTRVTVSS
121 (61) VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSS
122 (61) VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSS

FIG. 11J (cont'd)



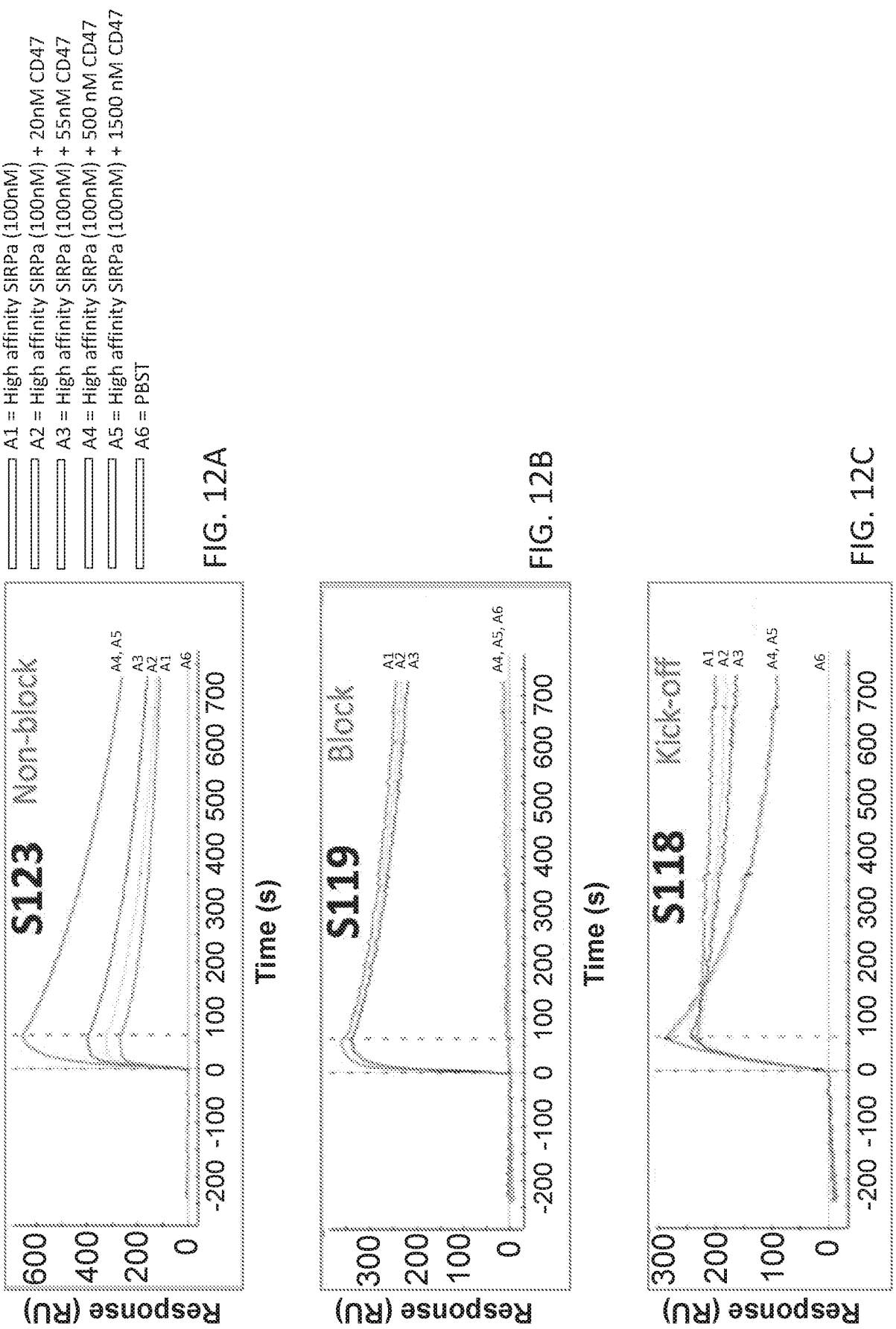


FIG. 12A

FIG. 12B

FIG. 12C

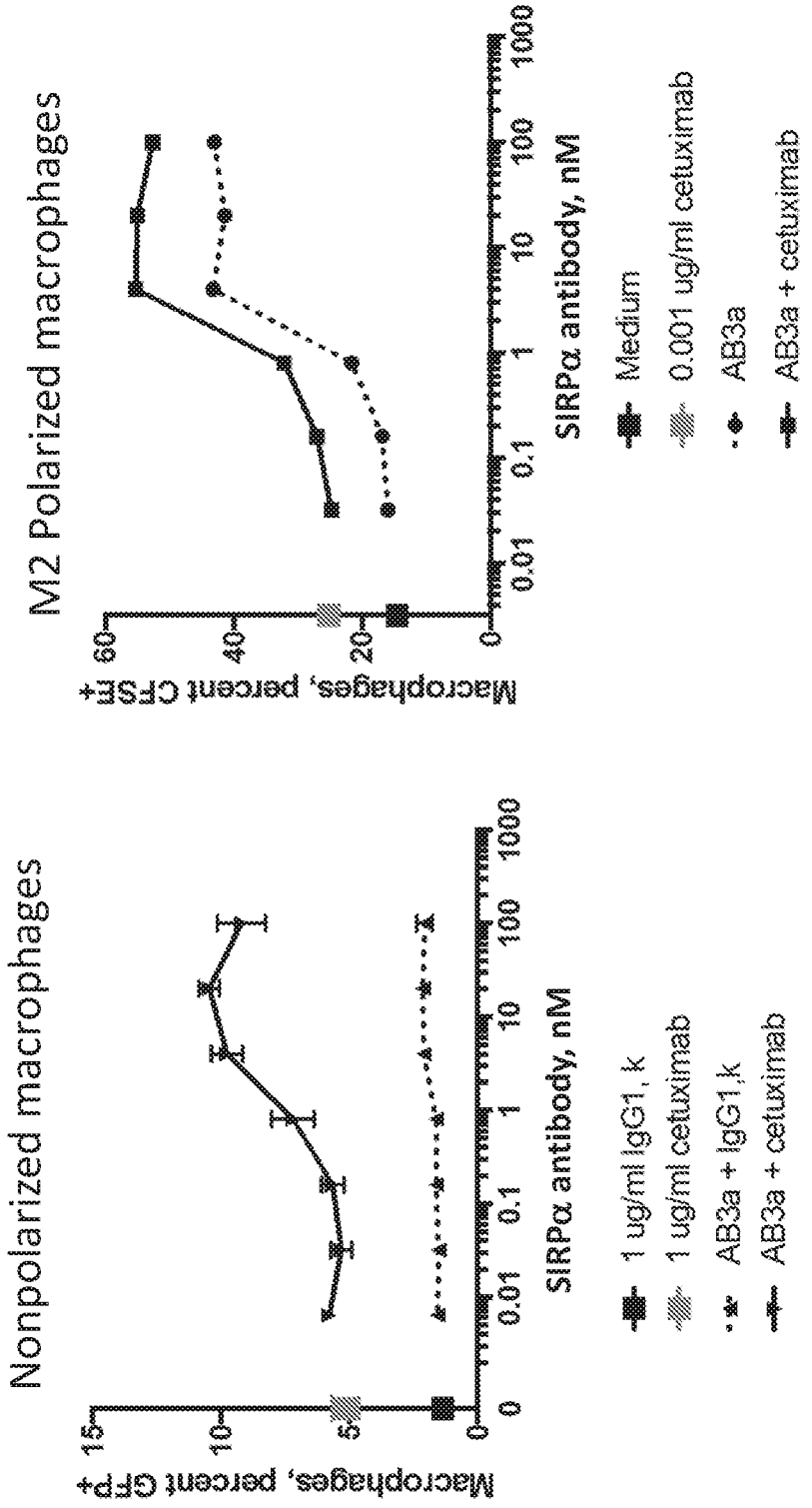


FIG. 13A

FIG. 13B

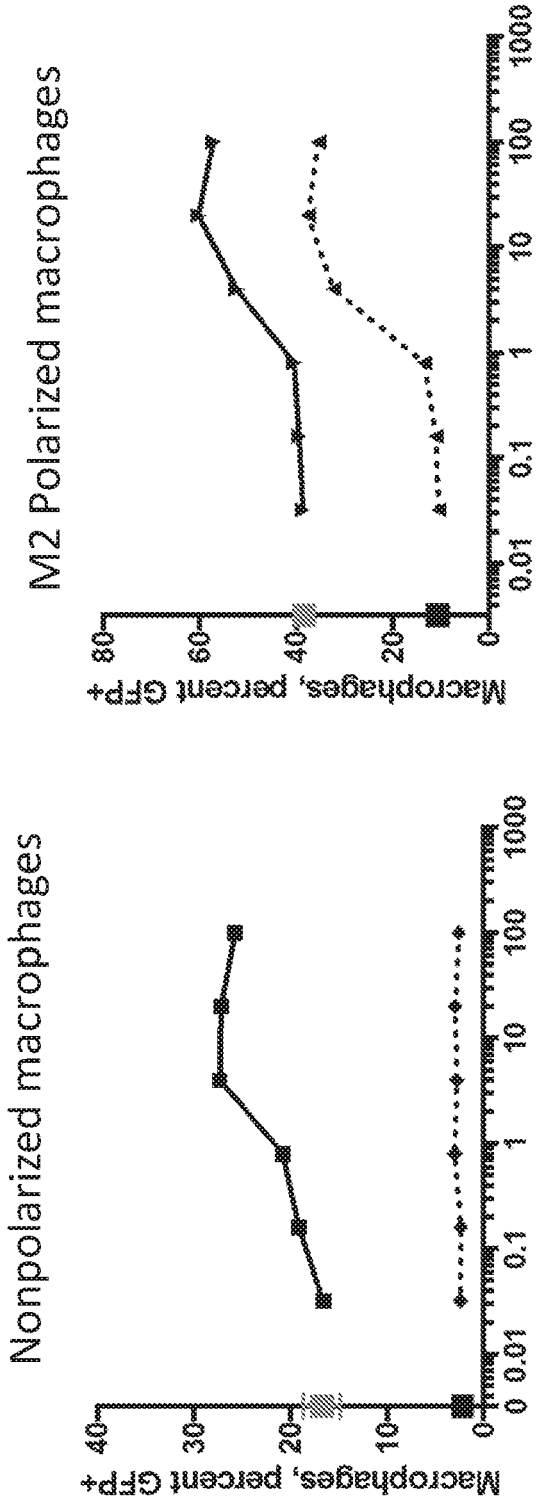


FIG. 13C

FIG. 13D

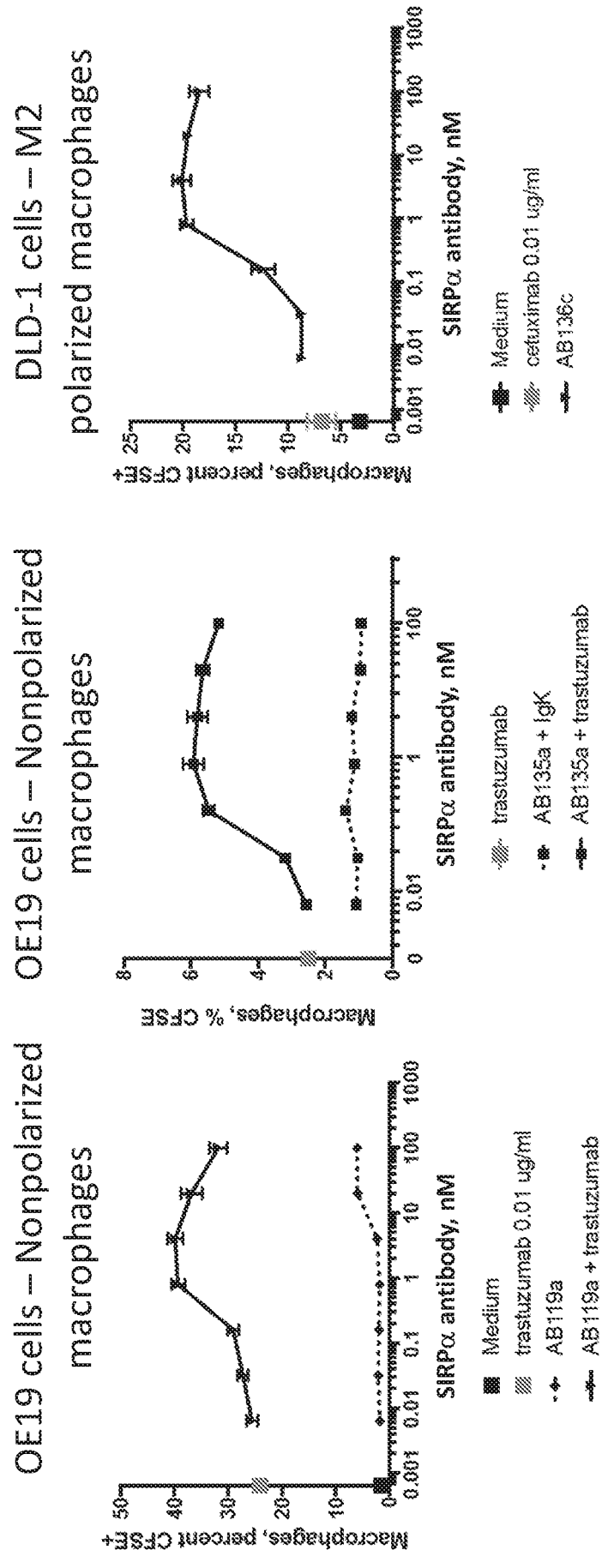


FIG. 13E FIG. 13F FIG. 13G

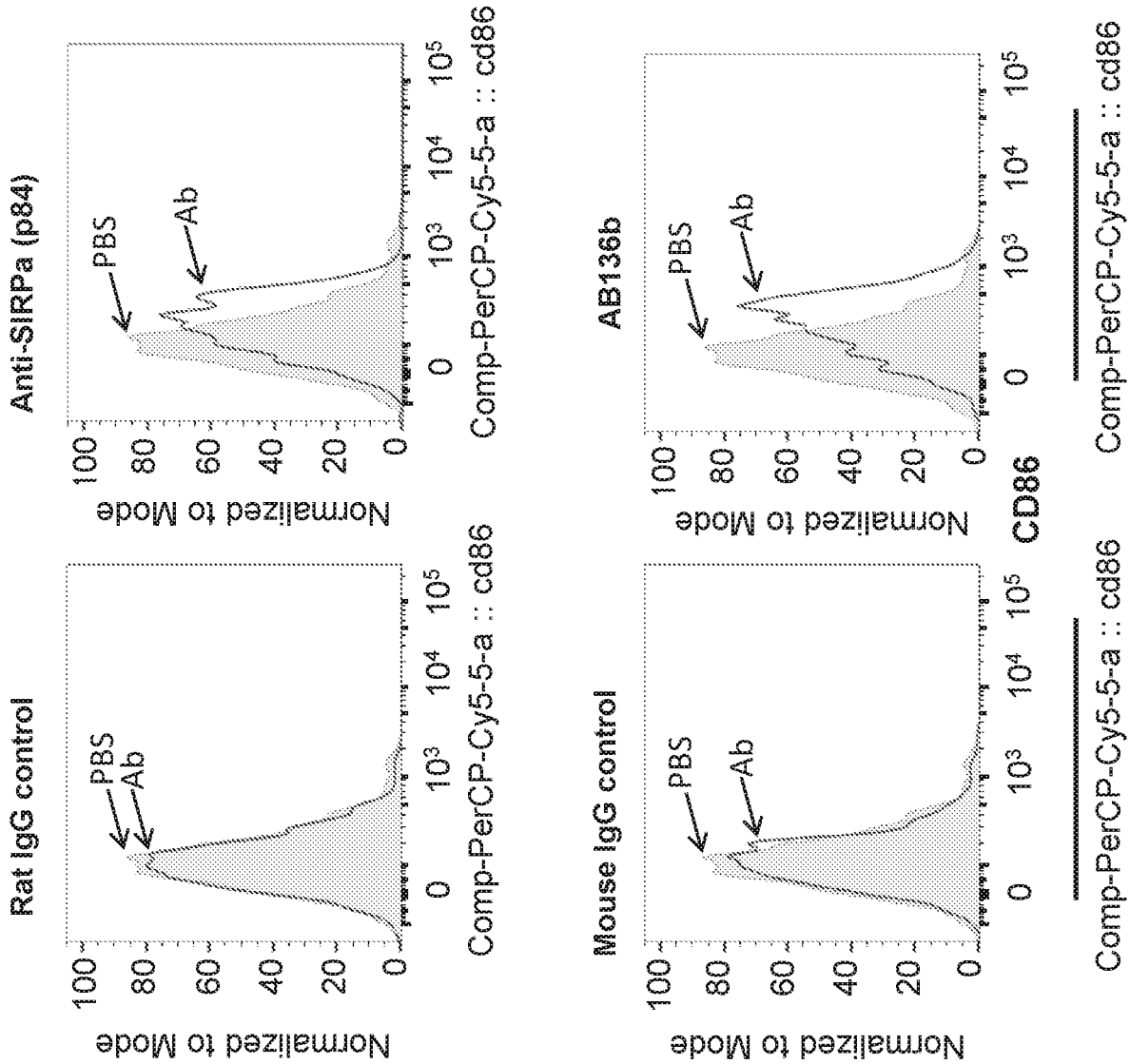
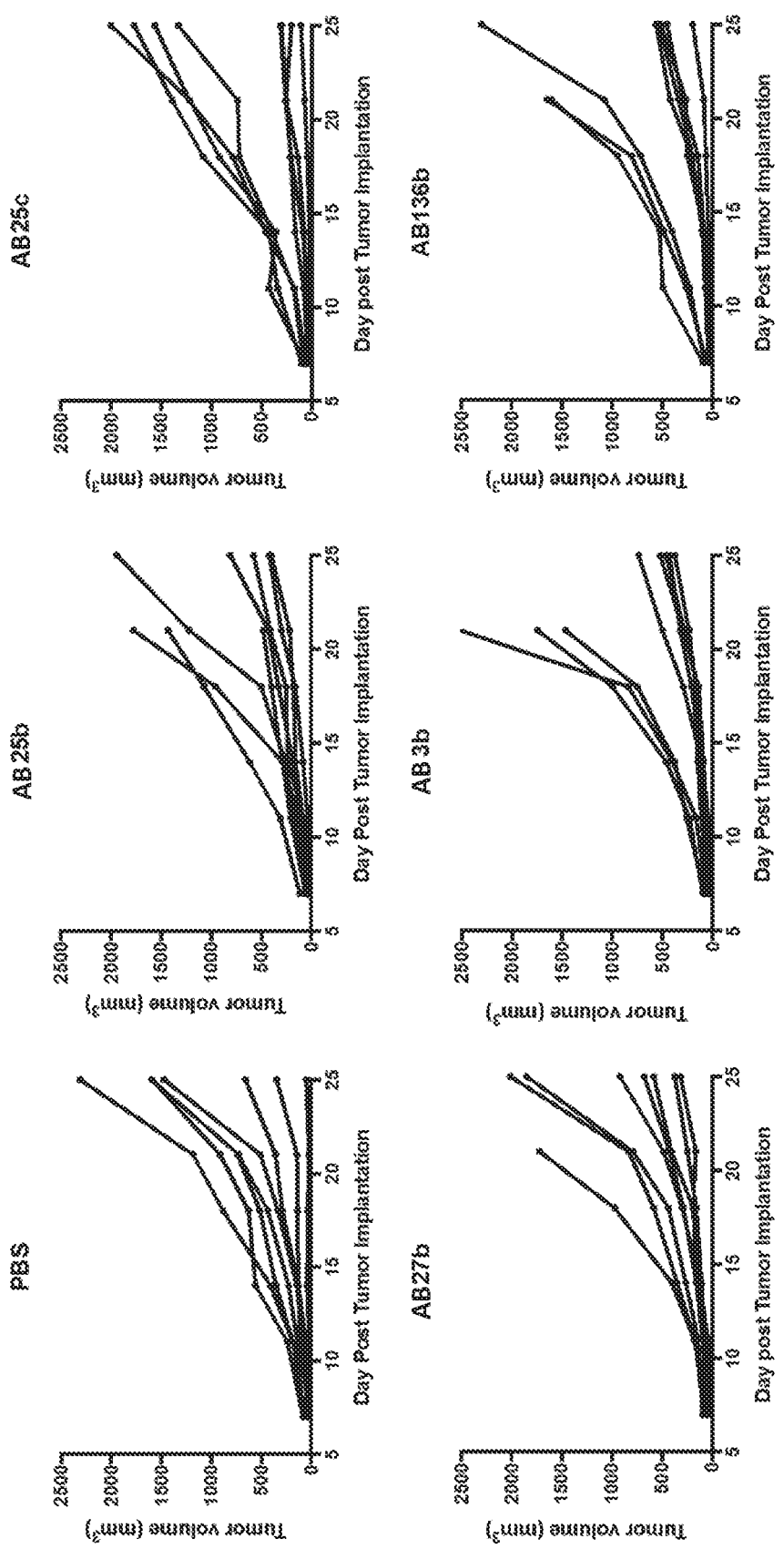

Rat IgG control
Anti-SIRPa (p84)
Mouse IgG control
AB136b
PBS
Ab
Normalized to Mode
Comp-PerCP-Cy5-5-a :: cd86
CD86

FIG. 14



	PBS	AB25b	AB25c	AB27b	AB3b	AB136b
Mice with tumor volume <600 mm^3	2	3	4	3	4	5

FIG. 15

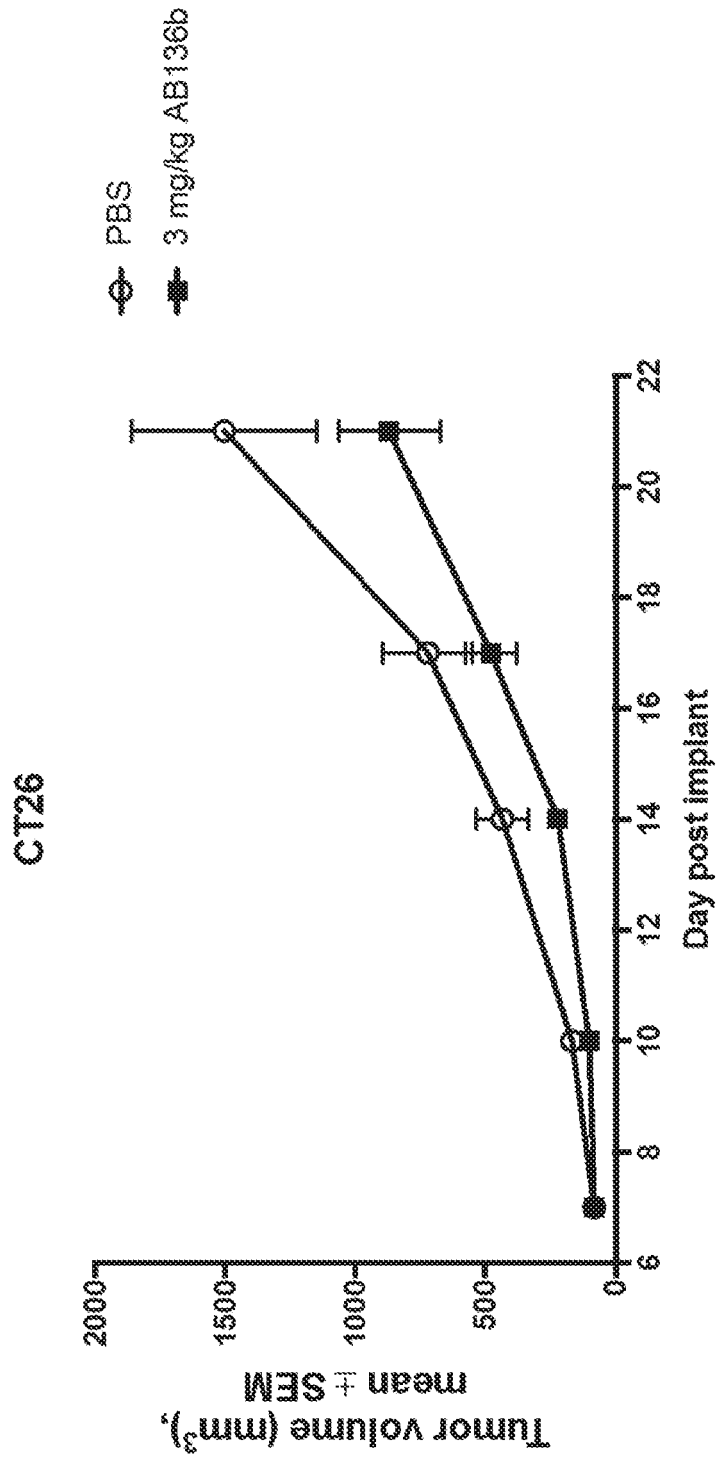

CT26
PBS
3 mg/kg AB136b
Tumor volume (mm³),
mean ± SEM
2000
1500
1000
500
0
6
8
10
12
14
16
18
20
22
Day post implant

FIG. 16

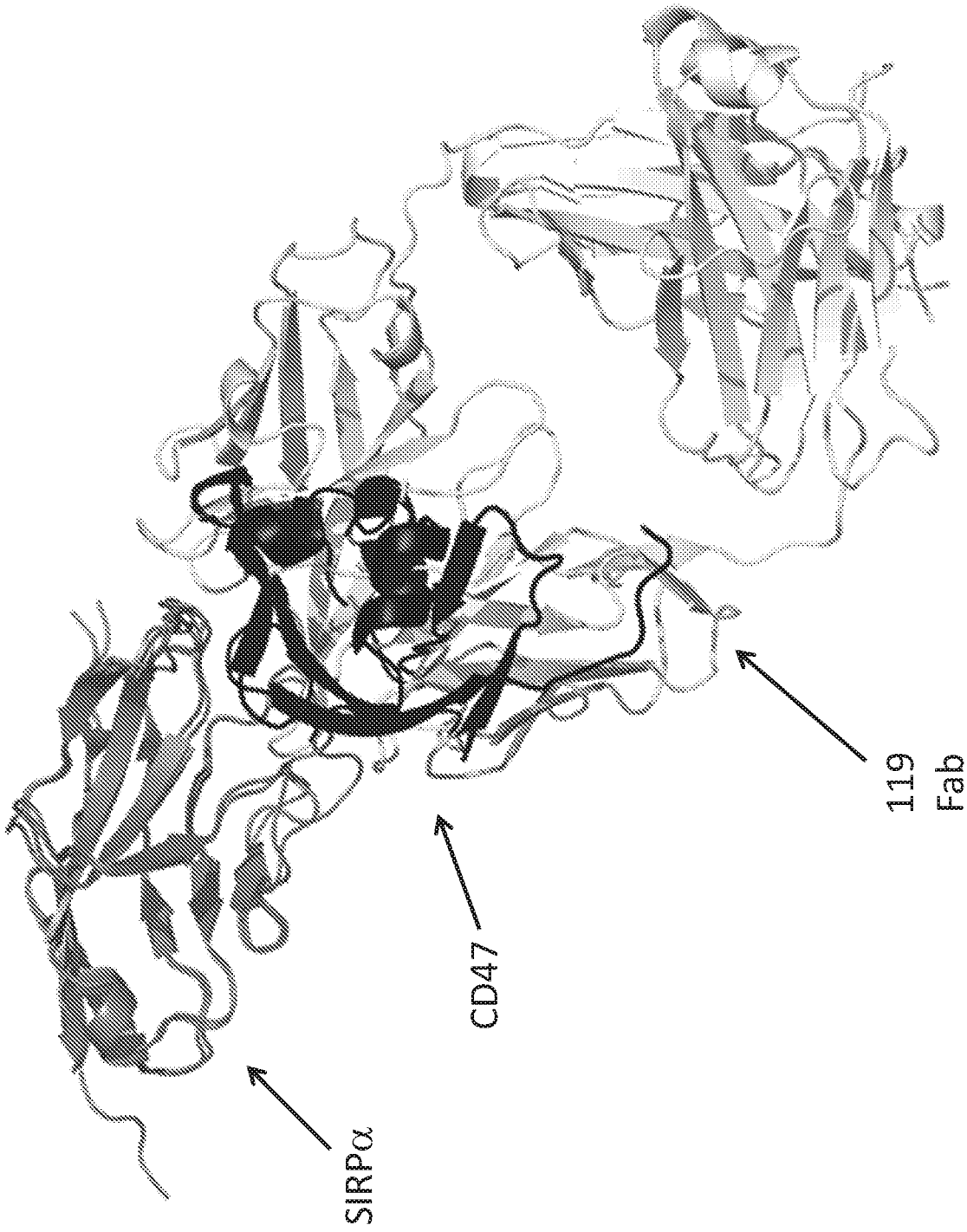


FIG. 17A

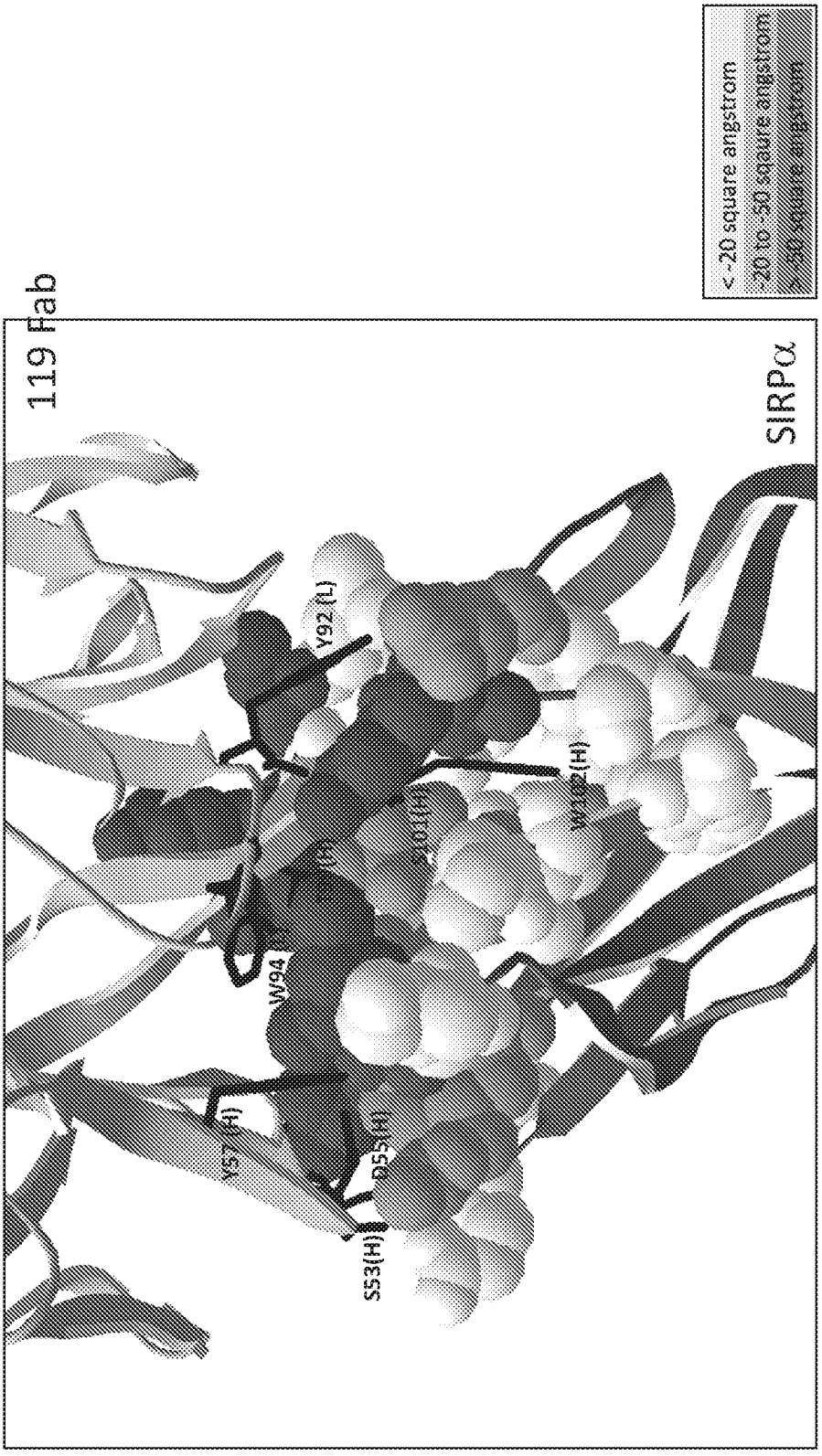

119 Fab
SIRPα
< -20 square angstrom
-20 to -30 square angstrom
> -30 square angstrom
Y92 (L)
W94
Y37 (H)
S53(H)
Q55(H)
S101(H)
W102(H)

FIG. 17B

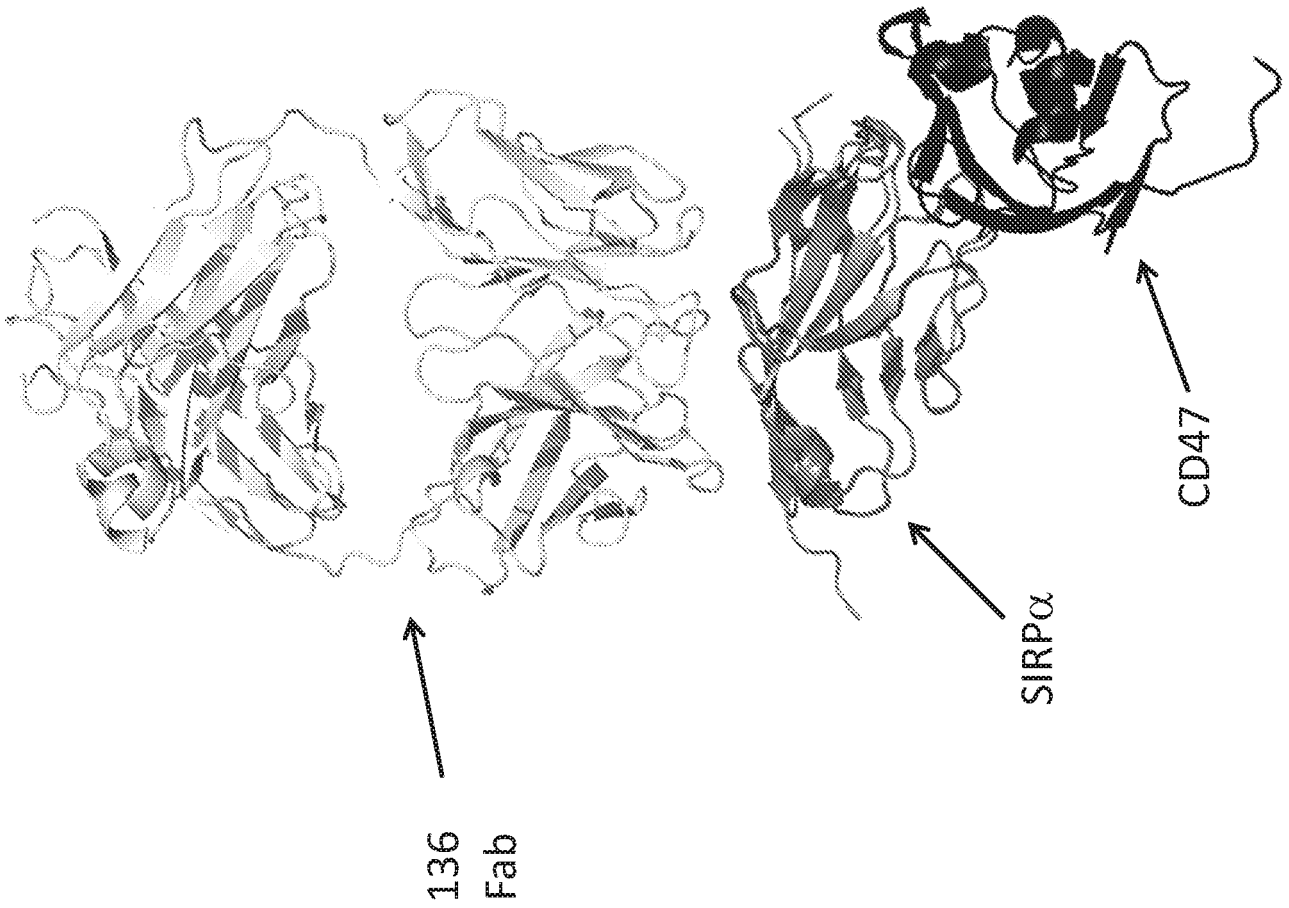


FIG. 18A

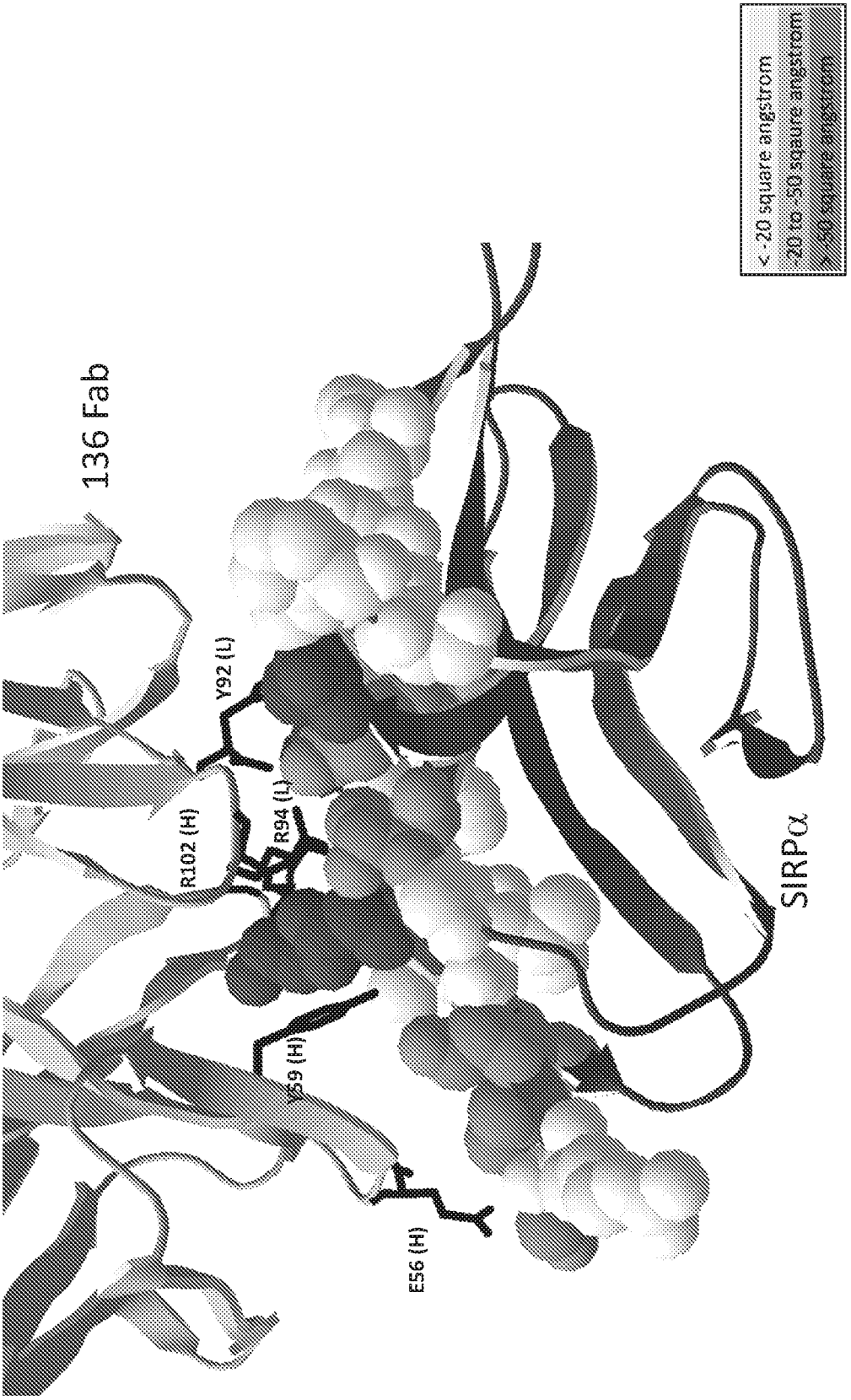

136 Fab
Y92 (L)
R94 (L)
R102 (H)
E59 (H)
E56 (H)
SIRPα
< -20 square angstrom
-20 to -50 square angstrom
> -50 square angstrom

FIG. 18B

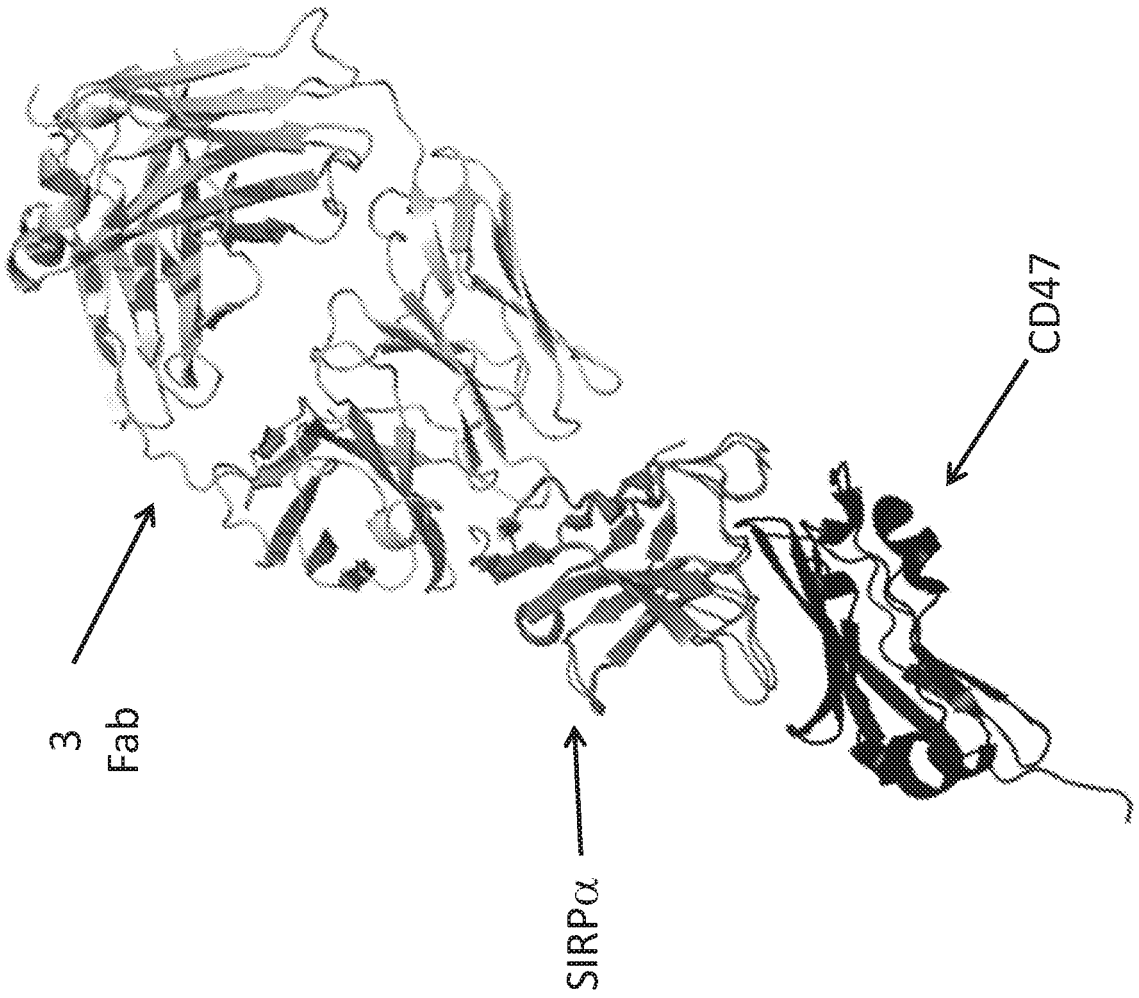


FIG. 19A

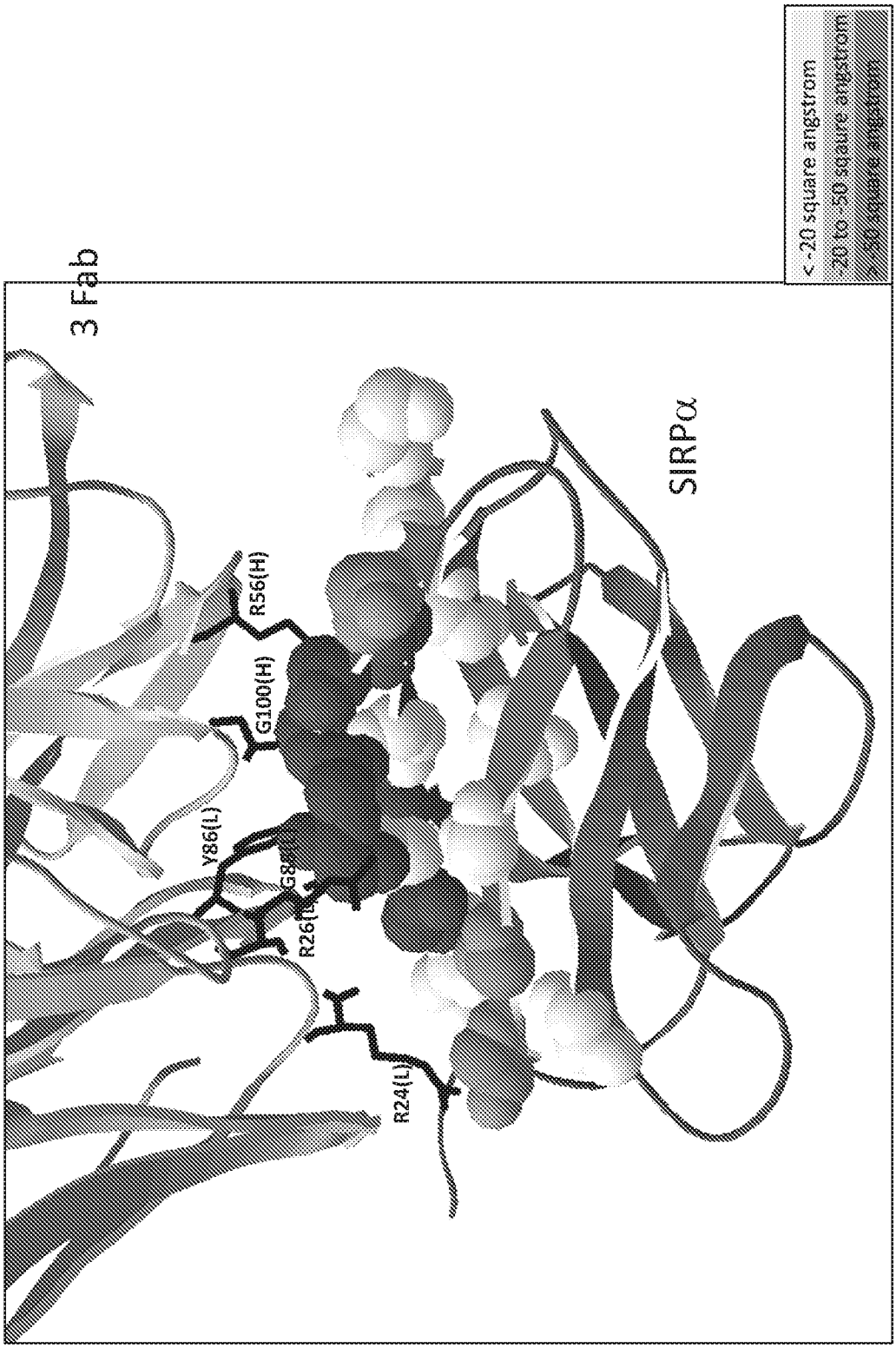

3 Fab
SIRPα
R56(H)
G100(H)
Y86(L)
R24(L)
< -20 square angstrom
-20 to -50 square angstrom
> -50 square angstrom

FIG. 19B

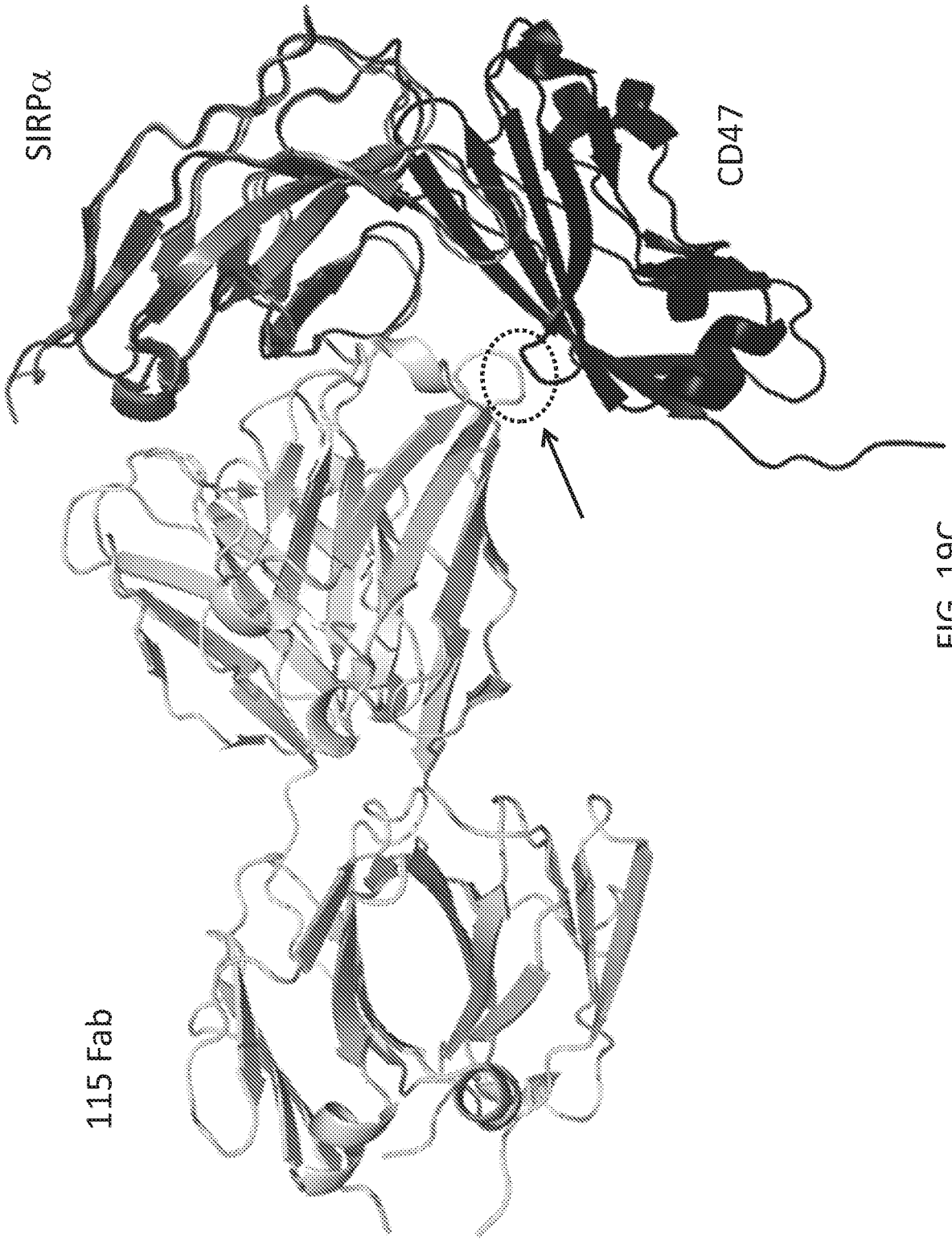


FIG. 19C

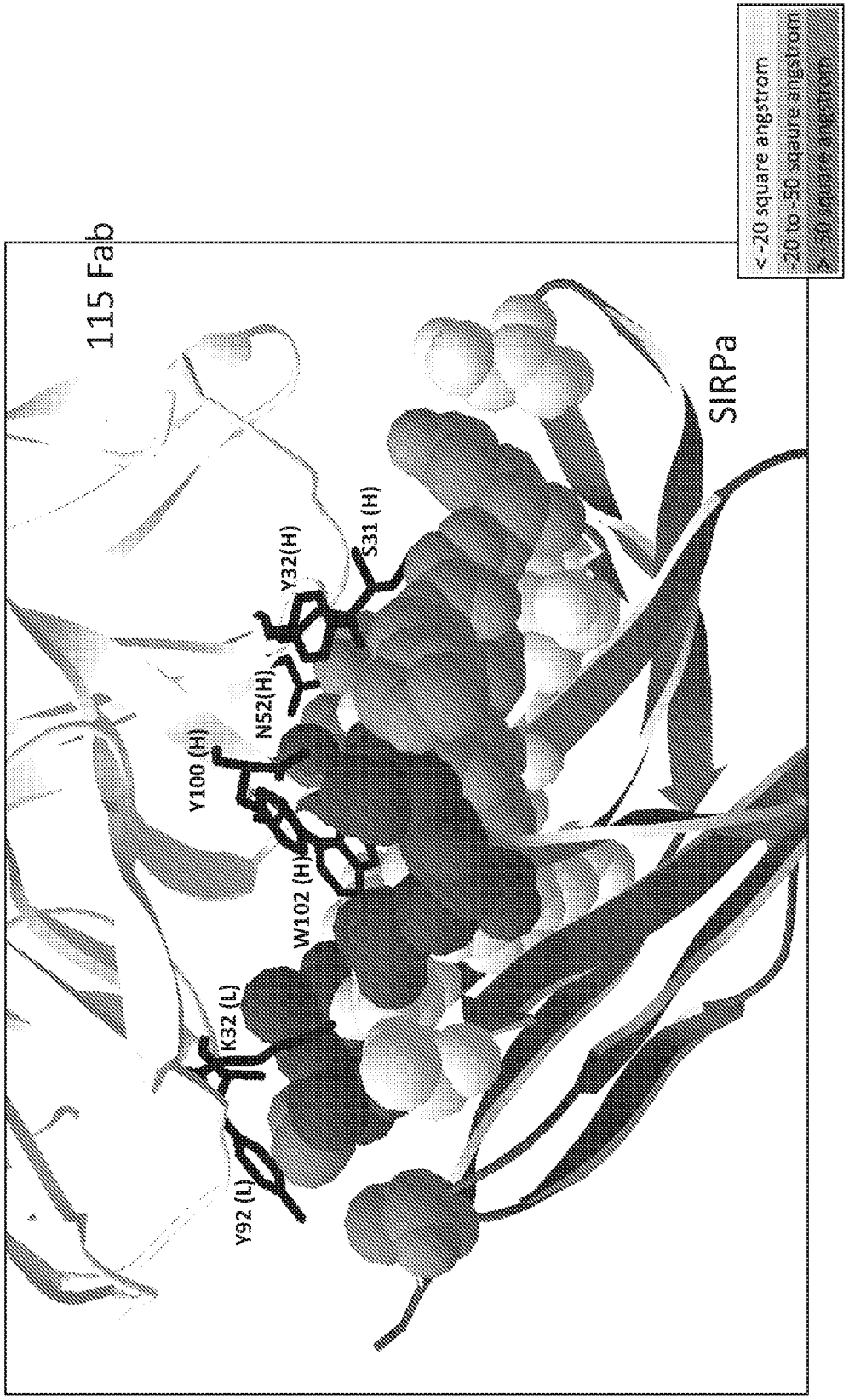

115 Fab
SIRPa
Y92 (L)
K32 (L)
W102 (H)
Y100 (H)
N52(H)
Y32(H)
S31 (H)
< -20 square angstrom
-20 to -50 square angstrom
> -50 square angstrom

FIG. 19D

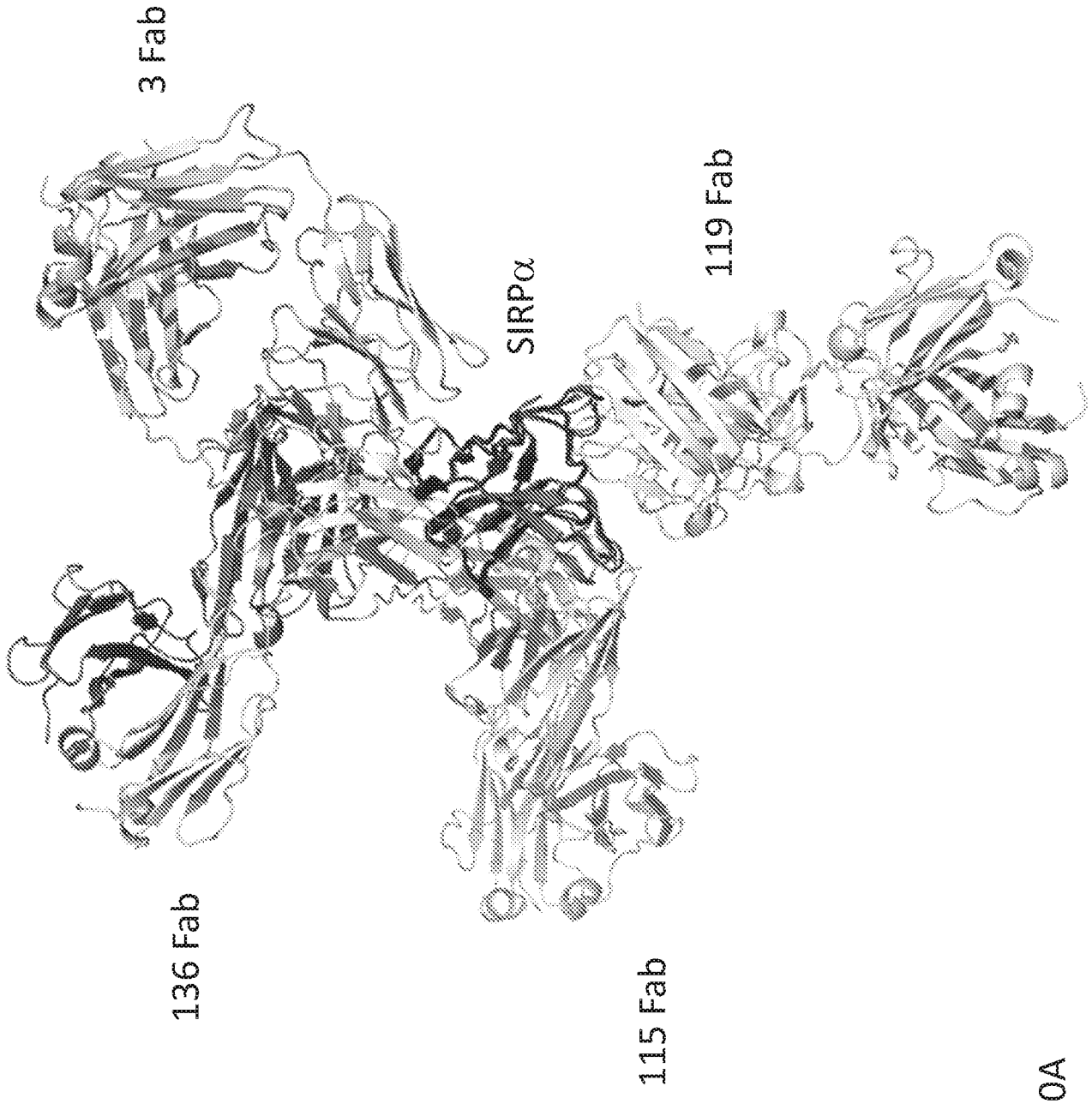


FIG. 20A

FIG. 20B

< -20 square angstrom
-20 to -50 sqaure angstrom
> -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
GLU	3		-13.8			
GLN	5				-11.2	
VAL	6			-5.7	-7.2	
ILE	7				-61.9	
GLN	8			-13.2	-20.1	
PRO	9			-14.6	-72	
ASP	10			-1	-50.3	
LYS	11			-157.6	-159.7	
SER	12			-17.6	-54.5	
LEU	14			-42.2	-29	
ALA	17					-19.7
ARG	24				-15.1	
THR	26				-28.1	
THR	28		-5.9		-33.5	
SER	29	-1.1	-17.3			
LEU	30	-44.3	-39.8			
ILE	31	-15.2	-106.5			
PRO	32		-32.2			
VAL	33	-88.7	-81.4			
GLY	34	-25				
PRO	35	-42	-6.4			
ILE	36	-10	-13.7			

FIG. 20B (cont.'d)

< -20 square angstrom
-20 to -50 sqaure angstrom
> -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
GLN	37	-1.7				
TRP	38		-2.1			
PHE	39					-2
ARG	40					-18.2
ALA	42			-52.9		
GLY	43			-16.8		
PRO	44			-10.9		-44.1
GLY	45					-21.3
ARG	46			-6.8		-15.7
GLU	47					-96.3
LEU	48					-70.3
ILE	49					-20.4
TYR	50	-5.1	-14.2			
ASN	51	-7.3				-3.3
GLN	52	-91.5	-81.9			
LYS	53	-115.8	-114.8			
GLU	54	-57.9	-35.3			-47.7
GLY	55					-19.8
HIS	56					-35.7
PHE	57					-20.6
PRO	58					-69.6
ARG	59					-99

FIG. 20B (cont.'d)

< -20 square angstrom
-20 to -50 sqaure angstrom
> -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
THR	62		-21.5			
SER	64		-5.8			
ASP	65		-7.5			
LEU	66	-20.9	-11.6			
THR	67	-85.8	-62.4			
LYS	68	-24.6	-18.2			
ARG	69	-174	-134.3			
ASN	70		-73.7			
ASN	71		-28.4			
MET	72		-23.4		-12.5	
ASP	73		-1.3			
PHE	74	-11.8	-34.9			
SER	75		-2.2			
ILE	76		-4.5			
ALA	80					-11.2
THR	82					-52
PRO	83					-44.5
ALA	84					-84.6
ASP	85					-16.6
GLY	87			-4.1		
THR	88			-34.1	-12.3	
TYR	89					-1.5

FIG. 20B (cont.'d)

< -20 square angstrom
-20 to -50 sqaure angstrom
> -50 square angstrom

Residue name	Residue number	Buried Surface Area (square angstrom)				
		CD47	Complex 1 (119)	Complex 2 (136)	Complex 3 (3)	Complex 4 (115)
TYR	90			-48.8	-4.7	
LYS	93	-5.2				
ARG	95		-44.5			
LYS	96	-96.8	-88.2			
GLY	97	-22.7	-2.9			
SER	98	-56.1	-14.2			
PRO	99	-19.7				
ASP	100					-12.4
ASP	101	-9.9				
GLU	103			-20.1		
PHE	104			-6.9		
LYS	105			-13.1		
SER	106			-49.9		
GLY	107			-6.9		
ALA	108			-83.6	-54.9	
GLY	109			-12.5	-8.5	
GLU	111			-96.8	-77	
LEU	112			-3		
SER	113			-41.5	-3.7	
ARG	115			-4.9	-4.6	
ALA	116			-23.8		

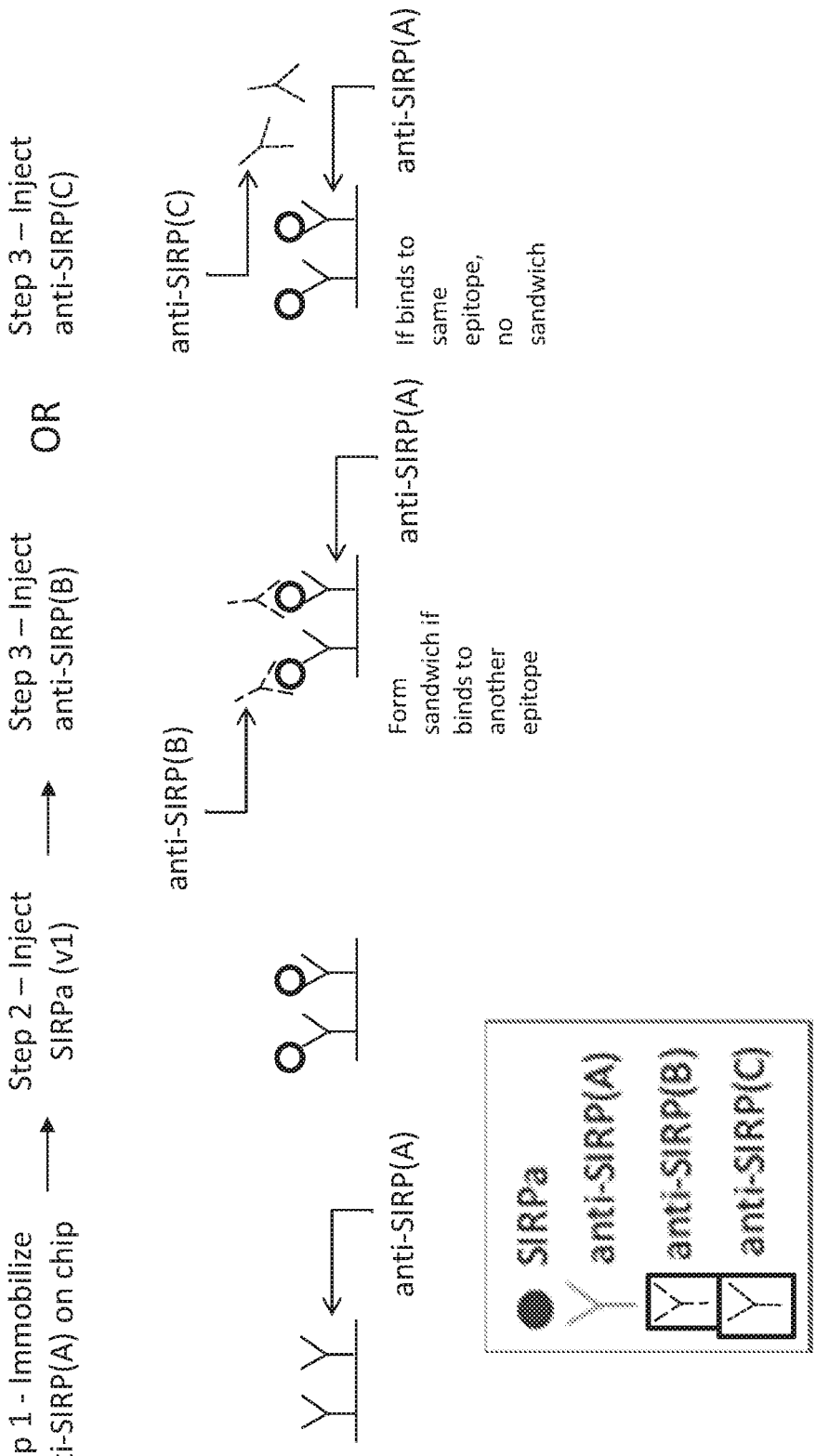

Step 1 - Immobilize anti-SIRP(A) on chip
Step 2 – Inject SIRPa (v1)
Step 3 – Inject anti-SIRP(B)
OR
Step 3 – Inject anti-SIRP(C)
anti-SIRP(A)
anti-SIRP(B)
anti-SIRP(A)
Form sandwich if binds to another epitope
anti-SIRP(C)
anti-SIRP(A)
If binds to same epitope, no sandwich
SIRPa
anti-SIRP(A)
anti-SIRP(B)
anti-SIRP(C)

FIG. 21A

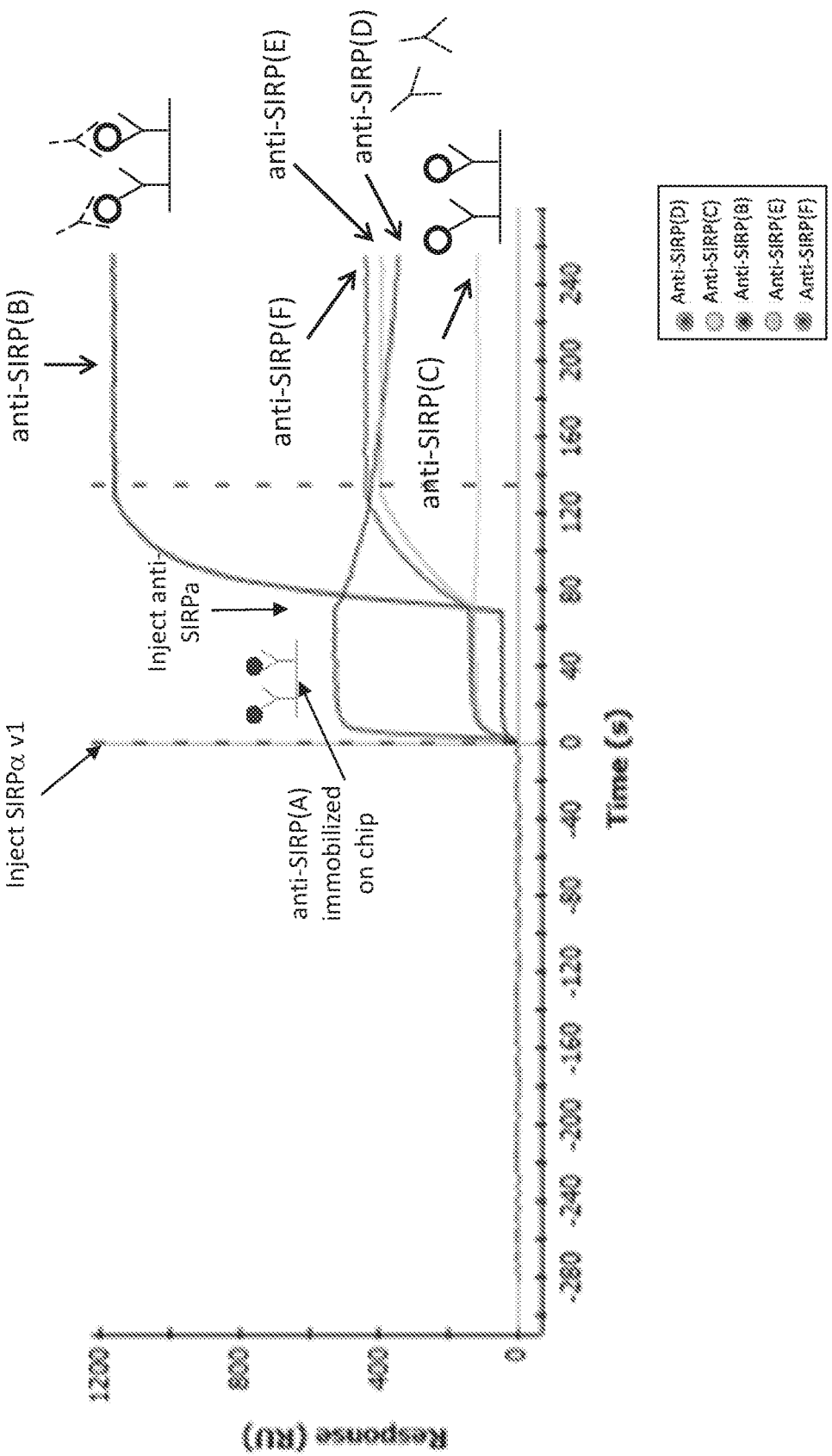

Response (RU)
1200
800
400
0
Time (s)
-260
-240
-200
-160
-120
-80
-40
0
40
80
120
160
200
240
Inject SIRPα v1
anti-SIRP(A) immobilized on chip
Inject anti-SIRPa
anti-SIRP(B)
anti-SIRP(F)
anti-SIRP(C)
anti-SIRP(E)
anti-SIRP(D)
Anti-SIRP(D)
Anti-SIRP(C)
Anti-SIRP(B)
Anti-SIRP(E)
Anti-SIRP(F)

FIG. 21B

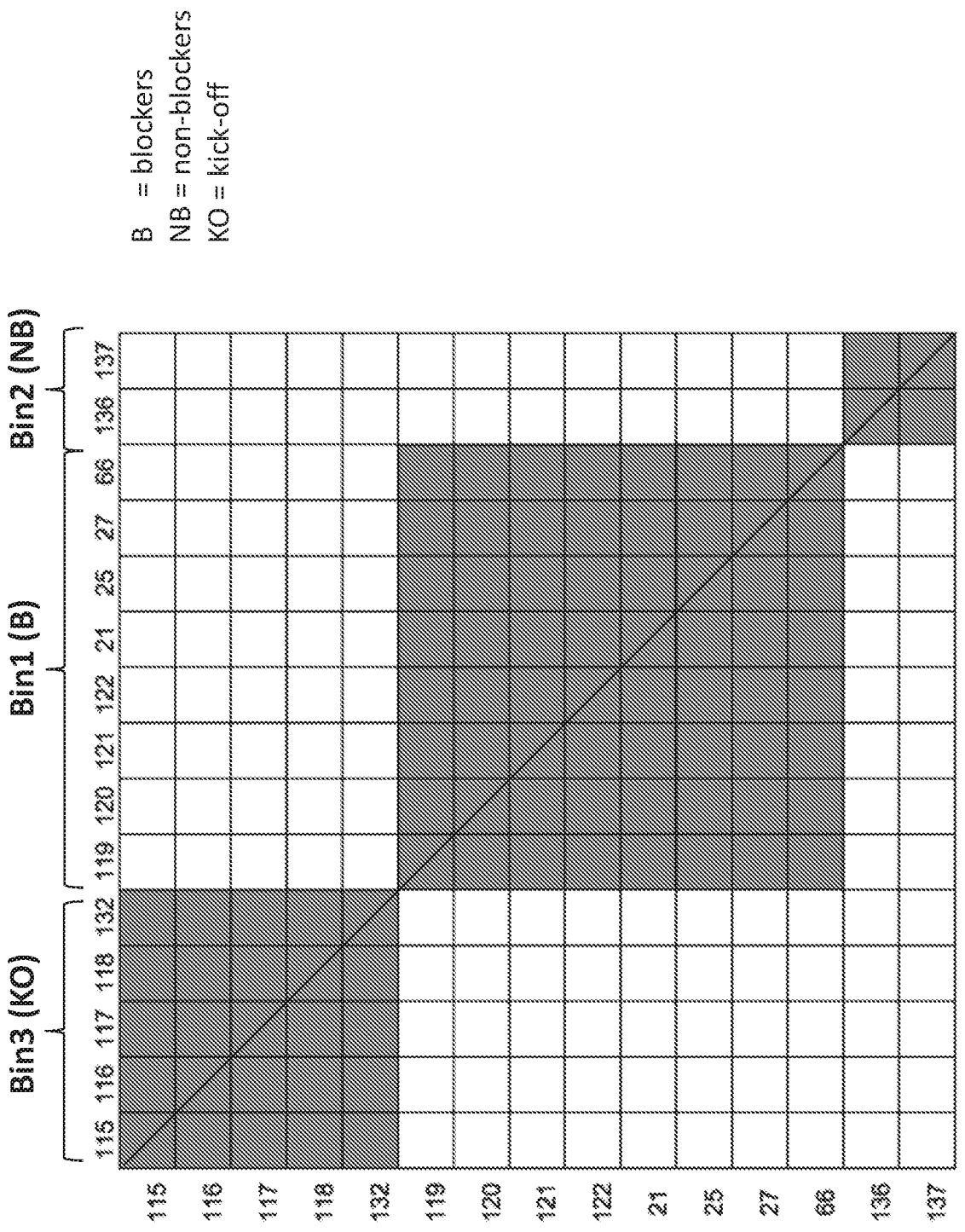

B = blockers
NB = non-blockers
KO = kick-off
Bin3 (KO)
Bin1 (B)
Bin2 (NB)
115
116
117
118
132
119
120
121
122
21
25
27
66
136
137

FIG. 22A

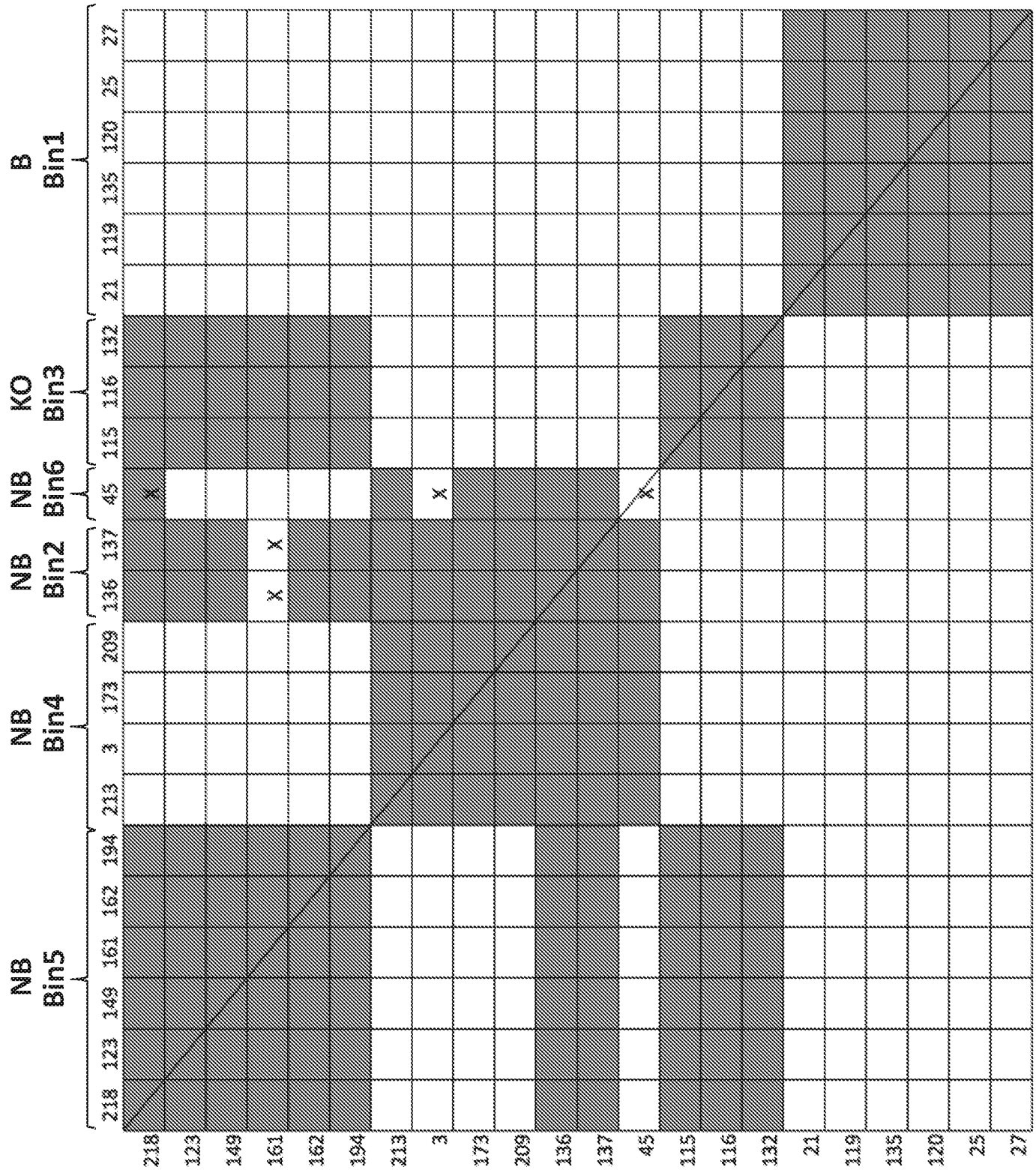

B = blockers
NB = non-blockers
KO = kick-off
NB Bin5
NB Bin4
NB Bin2
NB Bin6
KO Bin3
B Bin1
218 123 149 161 162 194 213 3 173 209 136 137 45 115 116 132 21 119 135 120 25 27

FIG. 22B

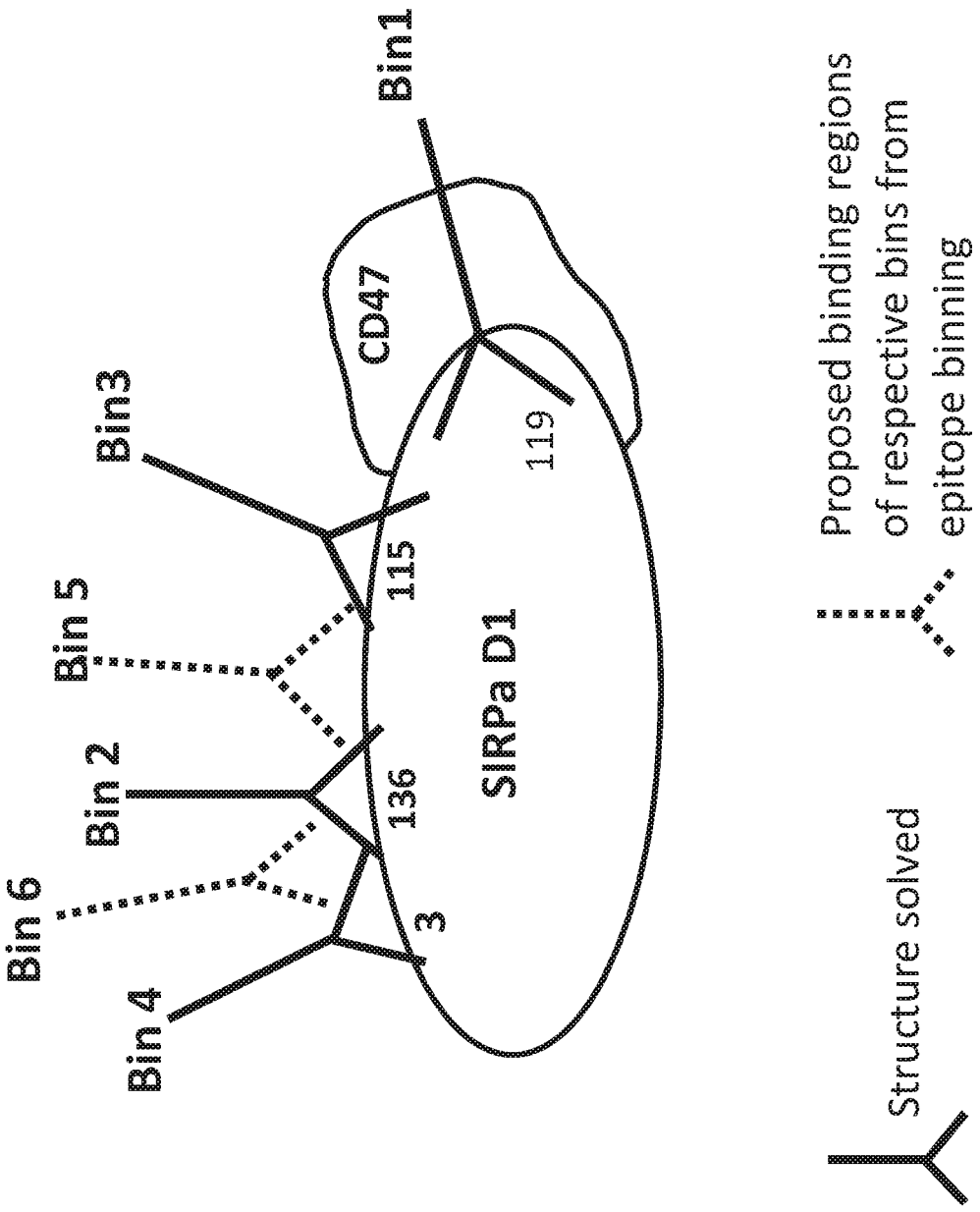

Bin1
CD47
Bin3
119
Bin 5
115
SIRPa D1
Bin 2
136
Bin 6
3
Bin 4
Proposed binding regions
of respective bins from
epitope binning
Structure solved

FIG. 23

```
                          1                                    H1      40
        119_VH_Wt     (1) DVQLLESGGGVVQPGGSLRLSCAASGFSFSNFAMTWVRQA
     119_VH_Mutall    (1) EVQLLESGGGVVQPGGSLRLSCAASGFSFSNFAVTWVRQA
119_VH_MutAll_V34M    (1) EVQLLESGGGVVQPGGSLRLSCAASGFSFSNFAMTWVRQA
119_VH_MutAll_V34L    (1) EVQLLESGGGVVQPGGSLRLSCAASGFSFSNFALTWVRQA
                          *                                    *

                          41            H2                     80
        119_VH_Wt     (41) PGEGLEWVSTIGSGDTYYADSVKGRFTISRDNSKNTLYLQ
     119_VH_Mutall    (41) PGKGLEWVSTIGSGDTYYADSVKGRFTISRDNSKNTLYLQ
119_VH_MutAll_V34M    (41) PGKGLEWVSTIGSGDTYYADSVKGRFTISRDNSKNTLYLQ
119_VH_MutAll_V34L    (41) PGKGLEWVSTIGSGDTYYADSVKGRFTISRDNSKNTLYLQ
                             *

                          81                    H3               120
        119_VH_Wt     (81) MNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGLGTLVTVSS
     119_VH_Mutall    (81) MNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGQGTLVTVSS
119_VH_MutAll_V34M    (81) MNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGQGTLVTVSS
119_VH_MutAll_V34L    (81) MNSLRAEDTAVYYCAKDSTVSWSGDFFDYWGQGTLVTVSS
                                                       *
```

FIG. 24A

```
                                    L1                                  L2
                1                                                       56
119_VL_wt   (1) EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPGQAPRLLIYAARIRET
119_VL_mutAll (1) EIVLTQSPATLSVSPGERATLSCRASQNVKNDLAWYQQKPGQAPRLLIYAARIRET
                                    *                                   *

                57                                                      108
119_VL_wt   (57) GIPERFSGSGSGTEFTLTITSLQSEDFAVYYCQQYYDWPPFTFGGGTKVEIK
119_VL_mutAll (57) GIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYDWPPFTFGGGTKVEIK
                    *                   *                   L3
```

FIG. 24B

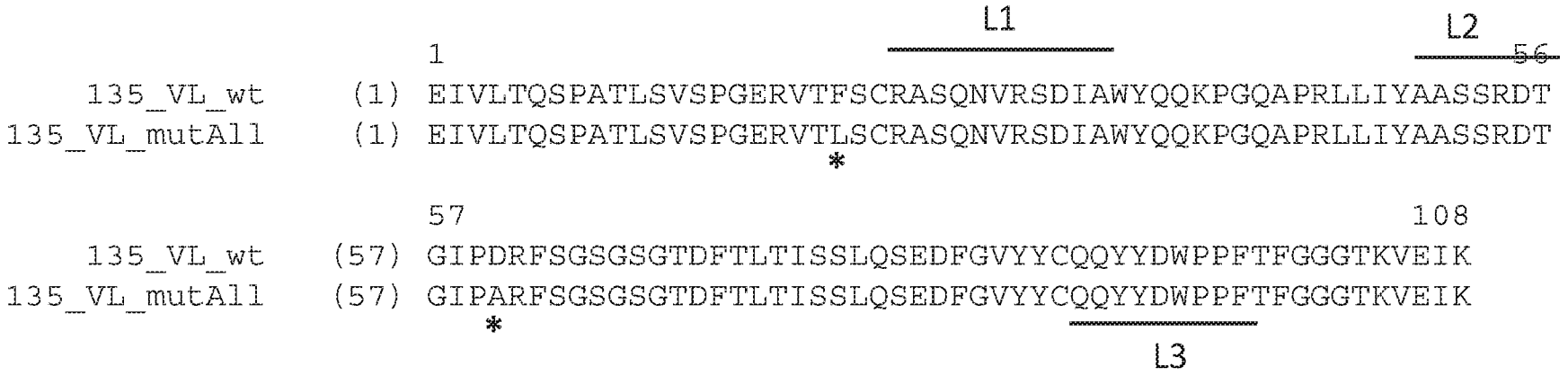

L1
L2
1
56
135_VL_wt (1) EIVLTQSPATLSVSPGERVTFSCRASQNVRSDIAWYQQKPGQAPRLLIYAASSRDT
135_VL_mutAll (1) EIVLTQSPATLSVSPGERVTLSCRASQNVRSDIAWYQQKPGQAPRLLIYAASSRDT
*
57
108
135_VL_wt (57) GIPDRFSGSGSGTDFTLTISSLQSEDFGVYYCQQYYDWPPFTFGGGTKVEIK
135_VL_mutAll (57) GIPARFSGSGSGTDFTLTISSLQSEDFGVYYCQQYYDWPPFTFGGGTKVEIK
*
L3

FIG. 25A

```
                                1                                  H1      40
          135_VH_wt       (1)  DVQLVESGGGVVRPGESLRLSCAASGFSFSIYAMSWVRQA
       135_VH_MutAll      (1)  EVQLVESGGGVVQPGGSLRLSCAASGFSFSIYAVSWVRQA
  135_VH_MutAll_V34M      (1)  EVQLVESGGGVVQPGGSLRLSCAASGFSFSIYAMSWVRQA
  135_VH_MutAll_V34L      (1)  EVQLVESGGGVVQPGGSLRLSCAASGFSFSIYALSWVRQA
                               *           *  *                   *

                               41                 H2                   80
          135_VH_wt       (41) PGEGLEWVSTIGADDTYYADSVKGRFTISRDNSKNTLYLQ
       135_VH_MutAll      (41) PGKGLEWVSTIGADDTYYADSVKGRFTISRDNSKNTLYLQ
  135_VH_MutAll_V34M      (41) PGKGLEWVSTIGADDTYYADSVKGRFTISRDNSKNTLYLQ
  135_VH_MutAll_V34L      (41) PGKGLEWVSTIGADDTYYADSVKGRFTISRDNSKNTLYLQ
                                 *

                               81                       H3              120
          135_VH_wt       (81) MNSLRAEDTAVYYCAKDSTVGWSGDFFDYWGLGTLVTVSS
       135_VH_MutAll      (81) MNSLRAEDTAVYYCAKDSTVGWSGDFFDYWGQGTLVTVSS
  135_VH_MutAll_V34M      (81) MNSLRAEDTAVYYCAKDSTVGWSGDFFDYWGQGTLVTVSS
  135_VH_MutAll_V34L      (81) MNSLRAEDTAVYYCAKDSTVGWSGDFFDYWGQGTLVTVSS
                                                           *
```

FIG. 25B


L1
L2
1
56
136_VL_wt (1) ETVLTQSPGTLTLSPGERATLTCRASQSVYTYLAWYQEKPGQAPRLLIYGASSRAT
136_VL_mutall (1) EIVLTQSPGTLSLSPGERATLSCRASQSVYTYLAWYQQKPGQAPRLLIYGASSRAT
136_VL_Mutall_I2T (1) ETVLTQSPGTLSLSPGERATLSCRASQSVYTYLAWYQQKPGQAPRLLIYGASSRAT
57
108
136_VL_wt (57) GIPDRFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYDRPPLTFGGGTKVEIK
136_VL_mutall (57) GIPDRFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYDRPPLTFGGGTKVEIK
136_VL_Mutall_I2T (57) GIPDRFSGSGSGTEFTLTISSLQSEDFAVYYCQQYYDRPPLTFGGGTKVEIK
L3

FIG. 26A

```
                                1                                  H1     40
          136_VH_wt       (1)   DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWVRQA
       136_VH_mutall      (1)   EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDVNWVRQA
136_VH_Mutall_V34M        (1)   EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMNWVRQA
136_VH_Mutall_V34L        (1)   EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDLNWVRQA
                                *             *  *                   *

                               41                H2                  80
          136_VH_wt       (41)  PGEGLEWVSLISGSGEIIYYADSVKGRFTISRDNSKNTLY
       136_VH_mutall      (41)  PGKGLEWVSLISGSGEIIYYADSVKGRFTISRDNSKNTLY
136_VH_Mutall_V34M        (41)  PGKGLEWVSLISGSGEIIYYADSVKGRFTISRDNSKNTLY
136_VH_Mutall_V34L        (41)  PGKGLEWVSLISGSGEIIYYADSVKGRFTISRDNSKNTLY
                                  *

                               81                      H3            119
          136_VH_wt       (81)  LQMNSLRAEDTAVYYCAKENNRYRFFDDWGLGTLVTVSS
       136_VH_mutall      (81)  LQMNSLRAEDTAVYYCAKENNRYRFFDDWGQGTLVTVSS
136_VH_Mutall_V34M        (81)  LQMNSLRAEDTAVYYCAKENNRYRFFDDWGQGTLVTVSS
136_VH_Mutall_V34L        (81)  LQMNSLRAEDTAVYYCAKENNRYRFFDDWGQGTLVTVSS
                                                              *
```

FIG. 26B

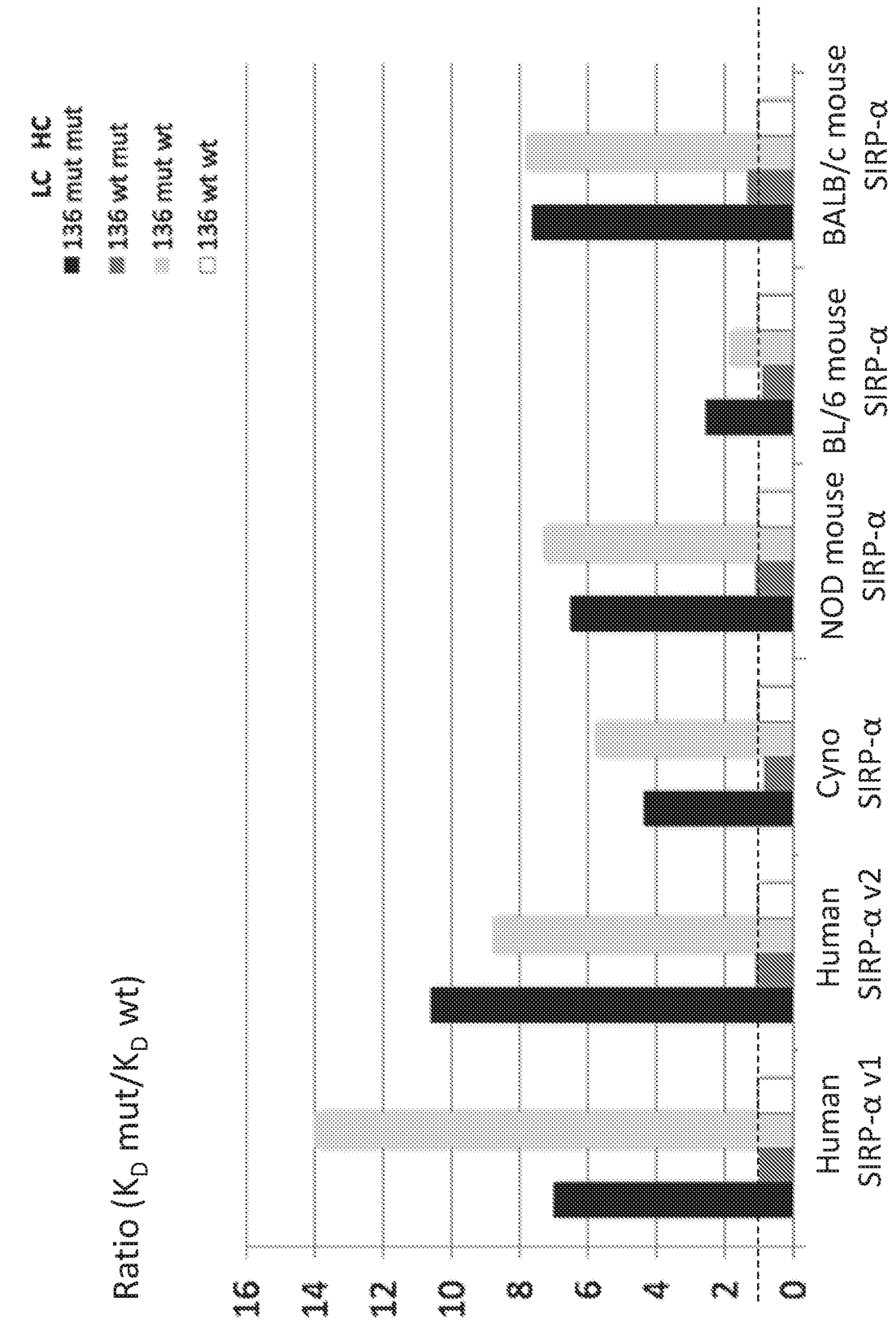

LC HC
136 mut mut
136 wt mut
136 mut wt
136 wt wt
Ratio (K_D mut/K_D wt)
16
14
12
10
8
6
4
2
0
Human SIRP-α v1
Human SIRP-α v2
Cyno SIRP-α
NOD mouse SIRP-α
BL/6 mouse SIRP-α
BALB/c mouse SIRP-α

FIG. 27A

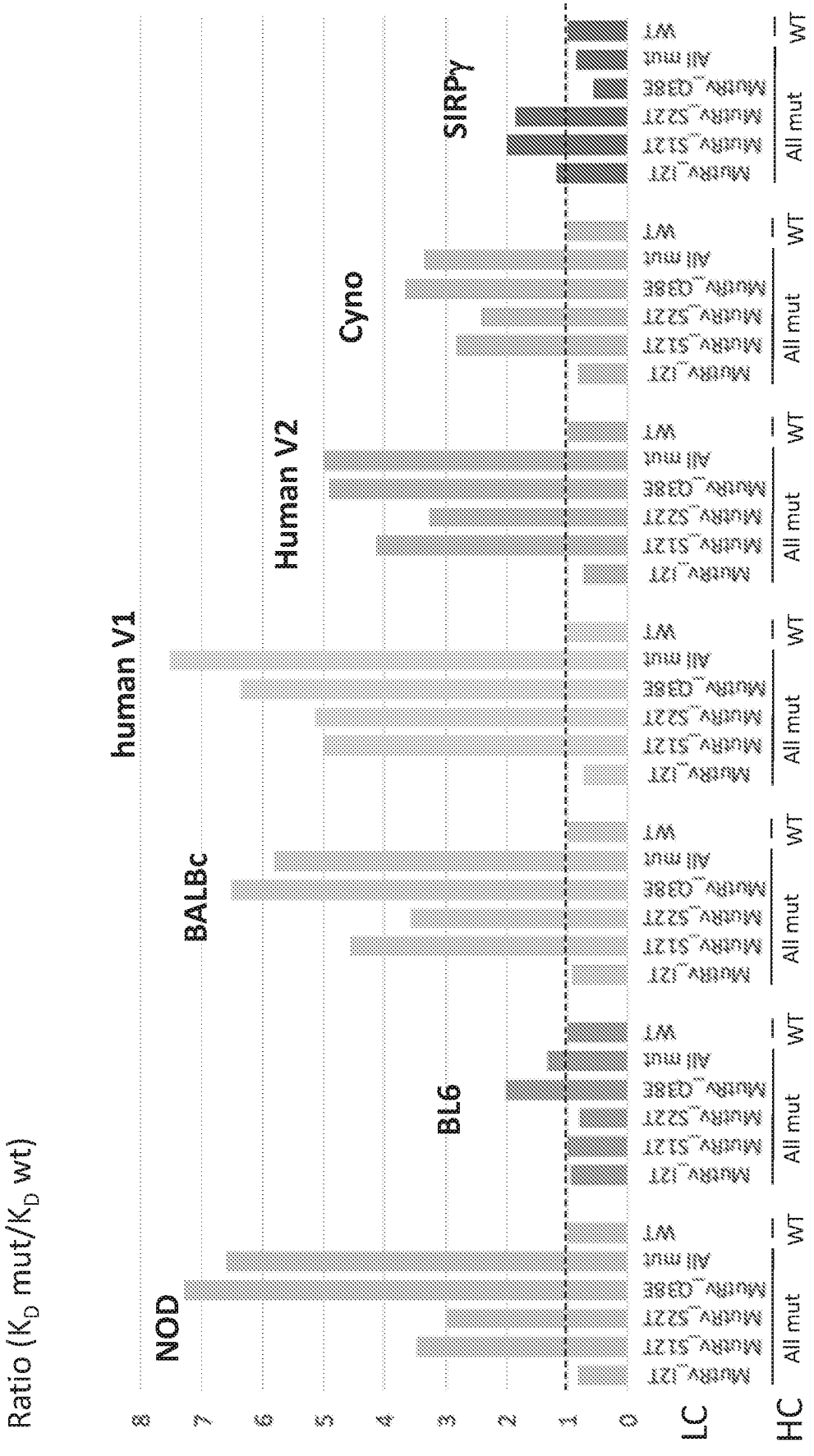

Ratio (K_D mut/K_D wt)
8
7
6
5
4
3
2
1
0
NOD
BALBc
BL6
human V1
Human V2
Cyno
SIRPγ
LC
HC
All mut
WT
All mut
WT
MuRRv_I27T
MuRRv_S12T
MuRRv_S22T
MuRRv_Q38E
All mut
WT

FIG. 27B

Parental VL	AB21_Heavy Chain							AB25_heavy chain							AB27 Heavy Chain							AB66 Heavy Chain						
Human framework	25	25	66	66	25	21		25	25	66	66	25	21		25	25	66	66	25	21		25	25	66	66	25	21	
	IGLV3	IGLV2	IGLV3	IGLV1	IGLV2	IGLV1		IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1		IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1		IGLV3	IGLV1	IGLV3	IGLV1	IGLV2	IGLV1	
	Hum1	Hum2	Hum3	Hum4	Hum5	Hum6		Hum1	Hum2	Hum3	Hum4	Hum5	Hum6		Hum1	Hum2	Hum3	Hum4	Hum5	Hum6		Hum1	Hum2	Hum3	Hum4	Hum5	Hum6	
Protein yield	+	-	+	-	+	-		+	-	+	-	+	-		+	-	+	-	+	-		+	+	+	+	+	+	
Human v1																												
Human v2																												
Cyno SIRPa																												
BALBc SIRPa																												
Human SIRPg																												

Protein Yield (mg/mL)

"+" – no change

"-" – reduced expression

Binding affinity (Koff 1/s)

- No change
- Reduced by 1-2log

FIG. 28

```
                                  1                   L1                  L2  54
Hum1      (1)  SYELTQPPSVSVSPGQTARITCSGGSYSSYYYAWYQQKPGQAPVTLIYSDDKRP
Hum8      (1)  SYELTQPPSVSVSPGQTARITCSGGAYSSYYYAWYQQKPGQAPVLVIYSDSKRP
hum9      (1)  SYELTQPPSVSVSPGQTARITCSGGAYSSYYYAWYQQKPGQAPVLVIYSDDKRP
                                           *                  **    *

                                  55                        L3    108
Hum1      (55) SNIPERFSGSSSGTTVTLTISGVQAEDEADYYCGGYDQSSYTNPFGGGTKLTVL
Hum8      (55) SGIPERFSGSSSGTTVTLTISGVQAEDEADYYCGGYDQSSYTNPFGGGTKLTVL
hum9      (55) SGIPERFSGSSSGTTVTLTISGVQAEDEADYYCGGYDQSSYTNPFGGGTKLTVL
                    *
```

FIG. 29

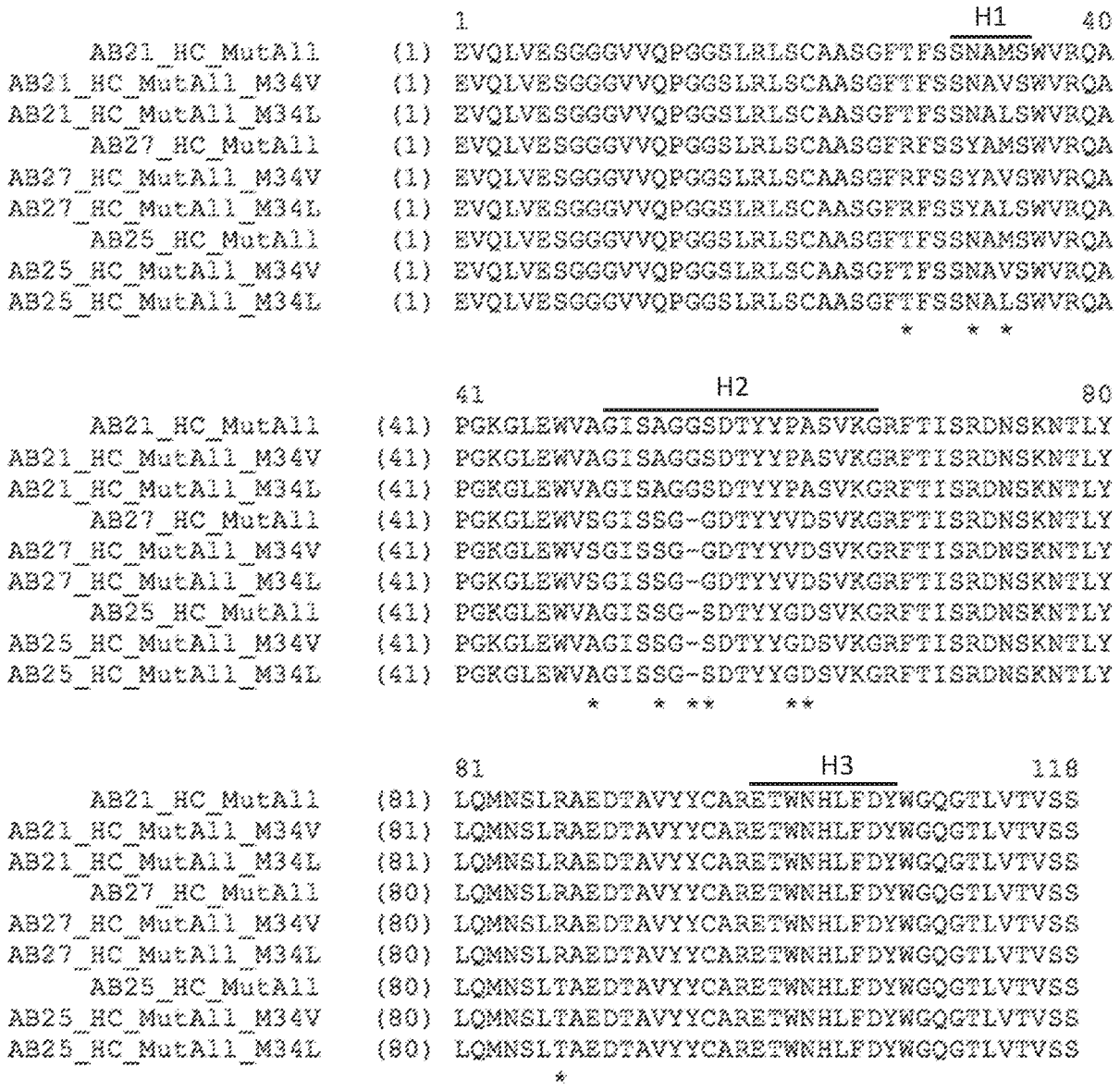

1 H1 40
AB21_HC_MutAll (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAMSWVRQA
AB21_HC_MutAll_M34V (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAVSWVRQA
AB21_HC_MutAll_M34L (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNALSWVRQA
AB27_HC_MutAll (1) EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYAMSWVRQA
AB27_HC_MutAll_M34V (1) EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYAVSWVRQA
AB27_HC_MutAll_M34L (1) EVQLVESGGGVVQPGGSLRLSCAASGFRFSSYALSWVRQA
AB25_HC_MutAll (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAMSWVRQA
AB25_HC_MutAll_M34V (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNAVSWVRQA
AB25_HC_MutAll_M34L (1) EVQLVESGGGVVQPGGSLRLSCAASGFTFSSNALSWVRQA
41 H2 80
AB21_HC_MutAll (41) PGKGLEWVAGISAGGSDTYYPASVKGRFTISRDNSKNTLY
AB21_HC_MutAll_M34V (41) PGKGLEWVAGISAGGSDTYYPASVKGRFTISRDNSKNTLY
AB21_HC_MutAll_M34L (41) PGKGLEWVAGISAGGSDTYYPASVKGRFTISRDNSKNTLY
AB27_HC_MutAll (41) PGKGLEWVSGISSG-GDTYYVDSVKGRFTISRDNSKNTLY
AB27_HC_MutAll_M34V (41) PGKGLEWVSGISSG-GDTYYVDSVKGRFTISRDNSKNTLY
AB27_HC_MutAll_M34L (41) PGKGLEWVSGISSG-GDTYYVDSVKGRFTISRDNSKNTLY
AB25_HC_MutAll (41) PGKGLEWVAGISSG-SDTYYGDSVKGRFTISRDNSKNTLY
AB25_HC_MutAll_M34V (41) PGKGLEWVAGISSG-SDTYYGDSVKGRFTISRDNSKNTLY
AB25_HC_MutAll_M34L (41) PGKGLEWVAGISSG-SDTYYGDSVKGRFTISRDNSKNTLY
81 H3 110
AB21_HC_MutAll (81) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB21_HC_MutAll_M34V (81) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB21_HC_MutAll_M34L (81) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB27_HC_MutAll (80) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB27_HC_MutAll_M34V (80) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB27_HC_MutAll_M34L (80) LQMNSLRAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB25_HC_MutAll (80) LQMNSLTAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB25_HC_MutAll_M34V (80) LQMNSLTAEDTAVYYCARETWNHLFDYWGQGTLVTVSS
AB25_HC_MutAll_M34L (80) LQMNSLTAEDTAVYYCARETWNHLFDYWGQGTLVTVSS

FIG. 30

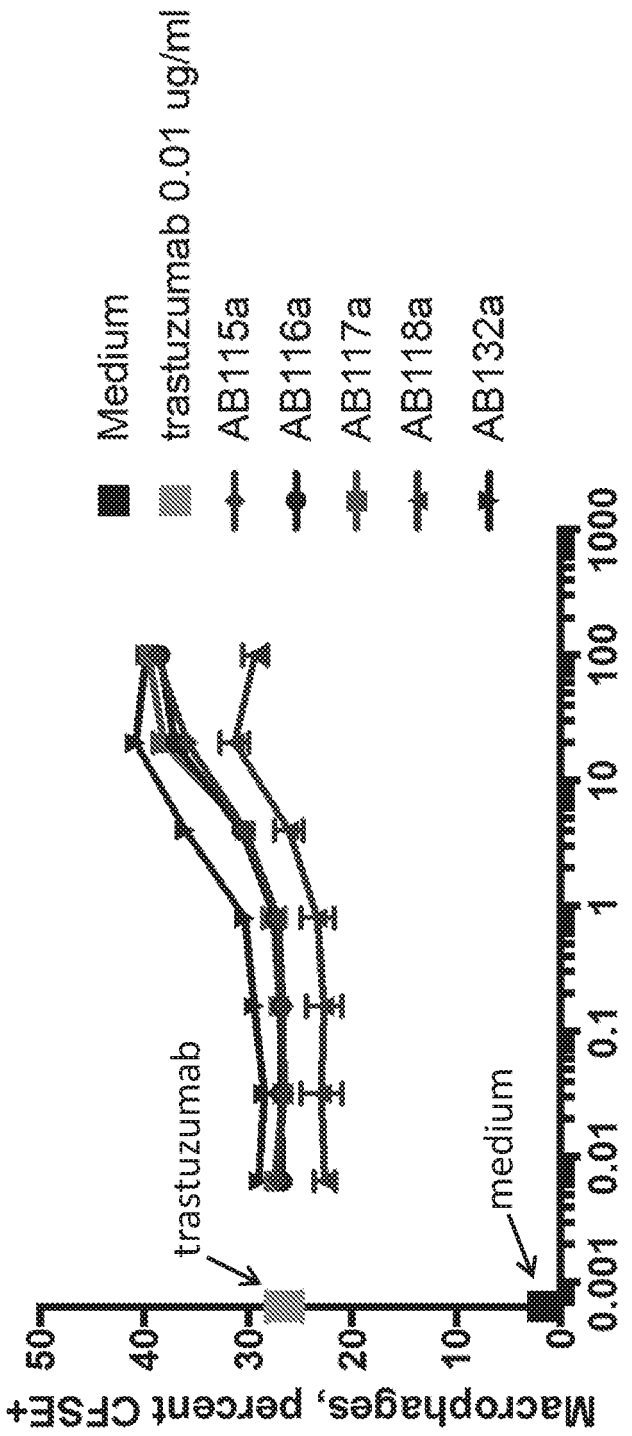

Macrophages, percent CFSE+
50
40
30
20
10
0
trastuzumab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
trastuzumab 0.01 ug/ml
AB115a
AB116a
AB117a
AB118a
AB132a

FIG. 31

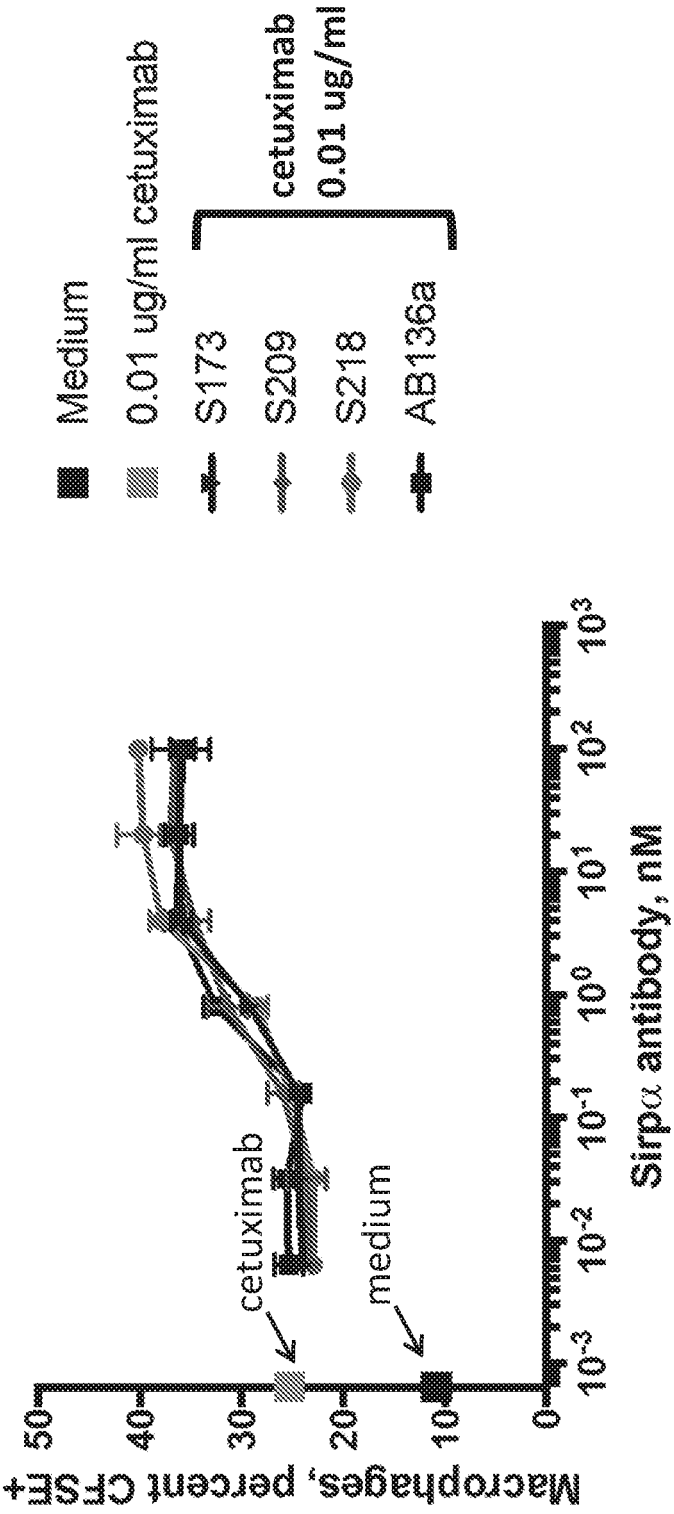

Medium
0.01 ug/ml cetuximab
S173
S209
S218
AB136a
cetuximab 0.01 ug/ml
Macrophages, percent CFSE+
0
10
20
30
40
50
cetuximab
medium
10-3
10-2
10-1
100
101
102
103
Sirpα antibody, nM

FIG. 32

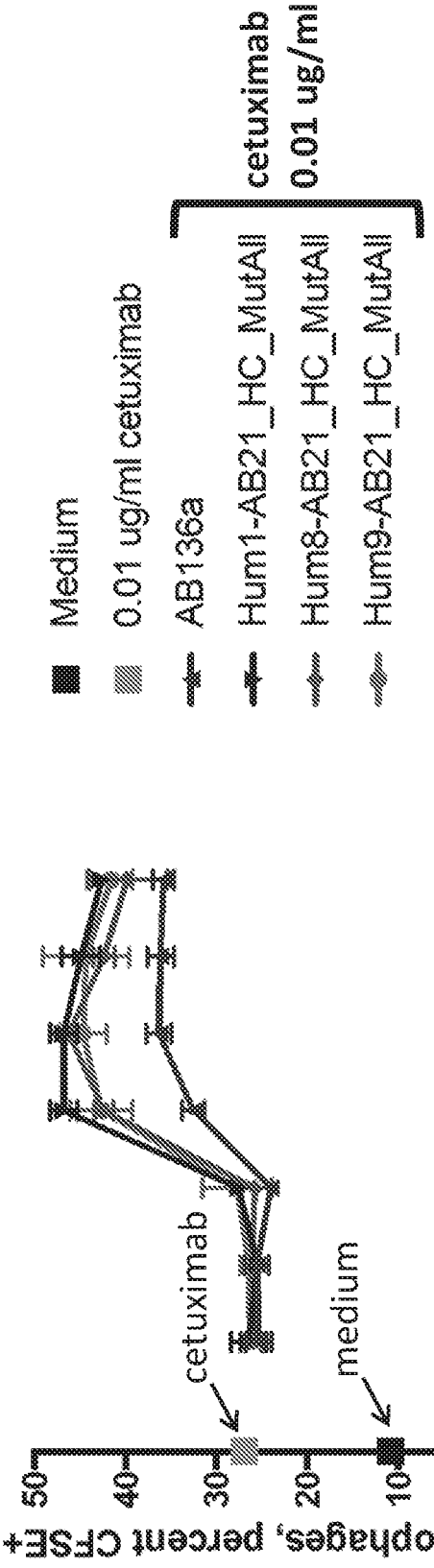

Macrophages, percent CFSE+
50
40
30
20
10
0
cetuximab
medium
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
Sirpα antibody, nM
Medium
0.01 ug/ml cetuximab
AB136a
Hum1-AB21_HC_MutAll
Hum8-AB21_HC_MutAll
Hum9-AB21_HC_MutAll
cetuximab 0.01 ug/ml

FIG. 33A

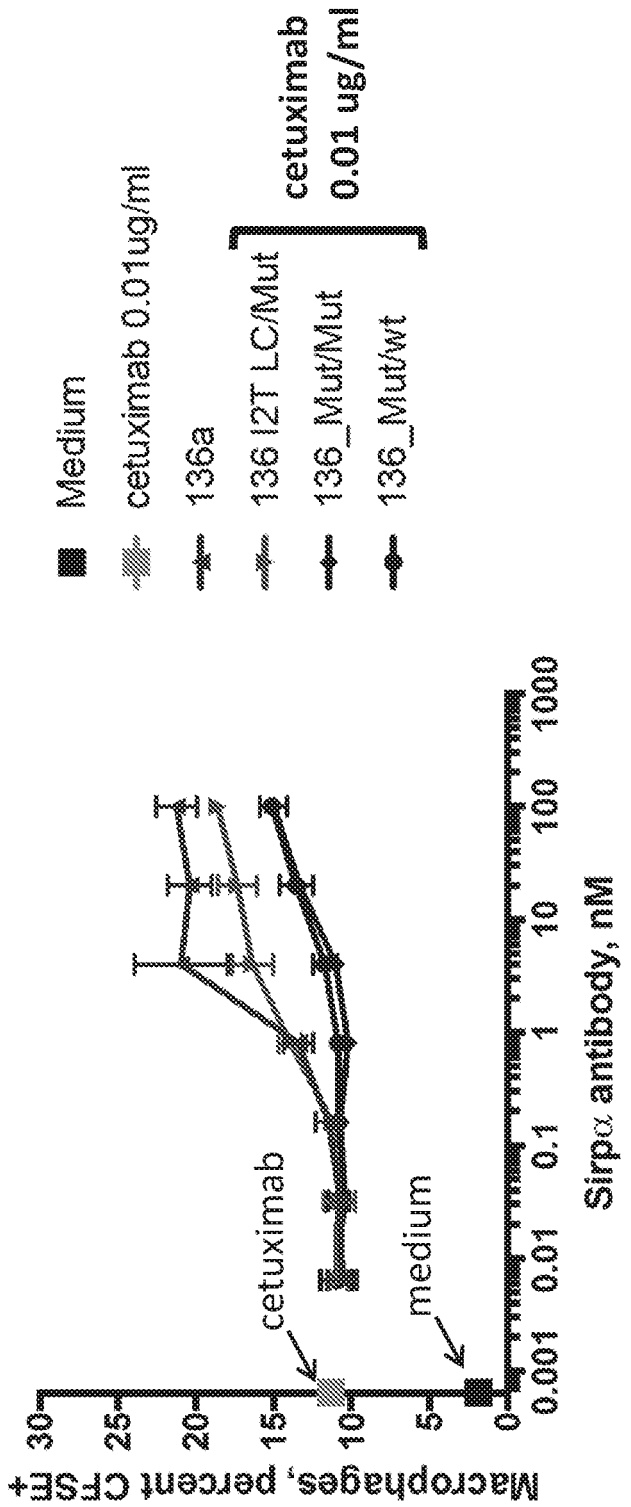

Medium
cetuximab 0.01ug/ml
136a
136 I2T LC/Mut
136_Mut/Mut
136_Mut/wt
cetuximab 0.01 ug/ml
Macrophages, percent CFSE+
30
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM

FIG. 33B

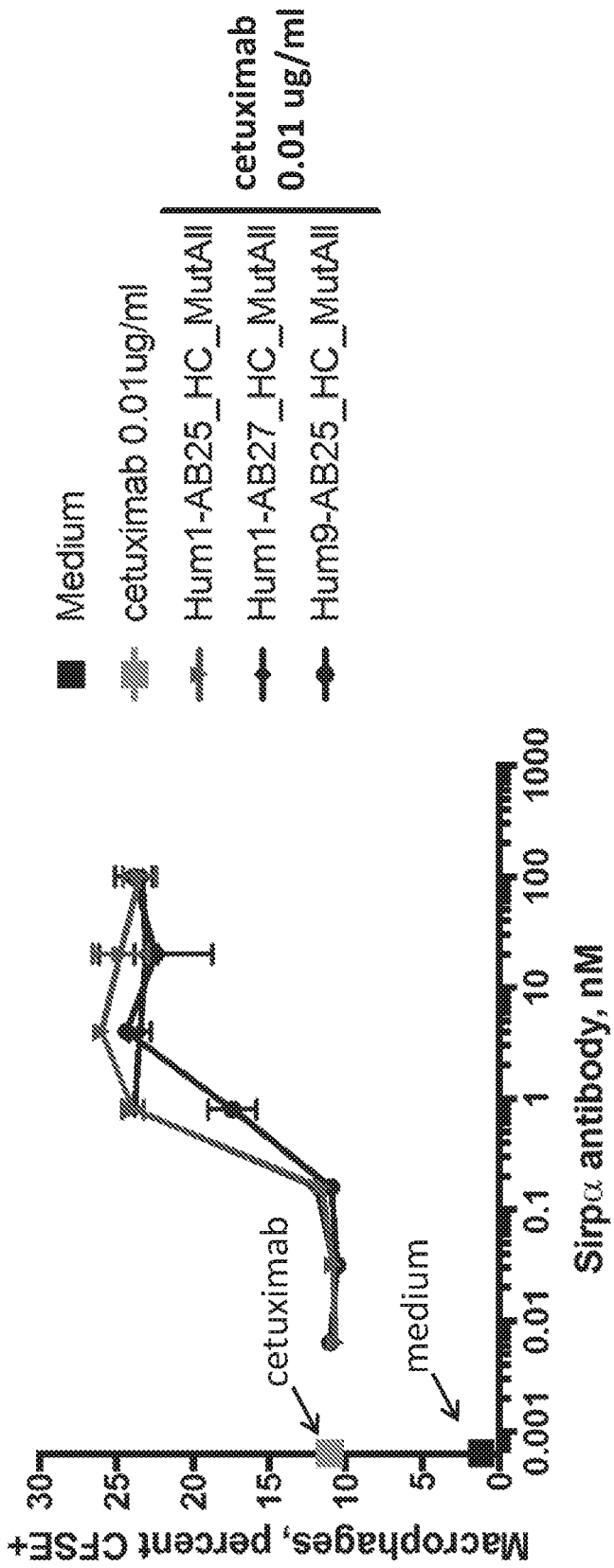

Macrophages, percent CFSE+
30
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
cetuximab 0.01ug/ml
Hum1-AB25_HC_MutAll
Hum1-AB27_HC_MutAll
Hum9-AB25_HC_MutAll
cetuximab
0.01 ug/ml

FIG. 33C

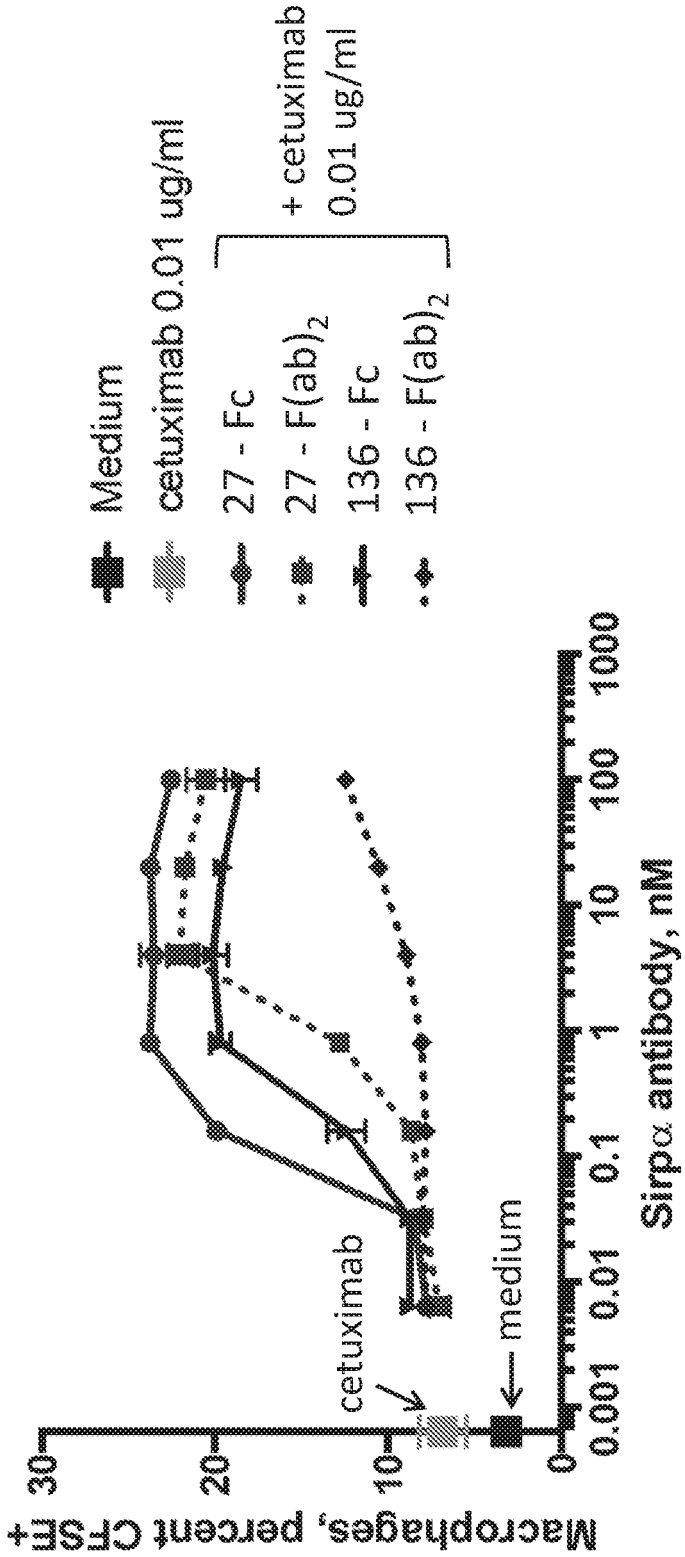

Macrophages, percent CFSE+
30
20
10
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
cetuximab 0.01 ug/ml
27 - Fc
27 - F(ab)2
136 - Fc
136 - F(ab)2
+ cetuximab
0.01 ug/ml

FIG. 34

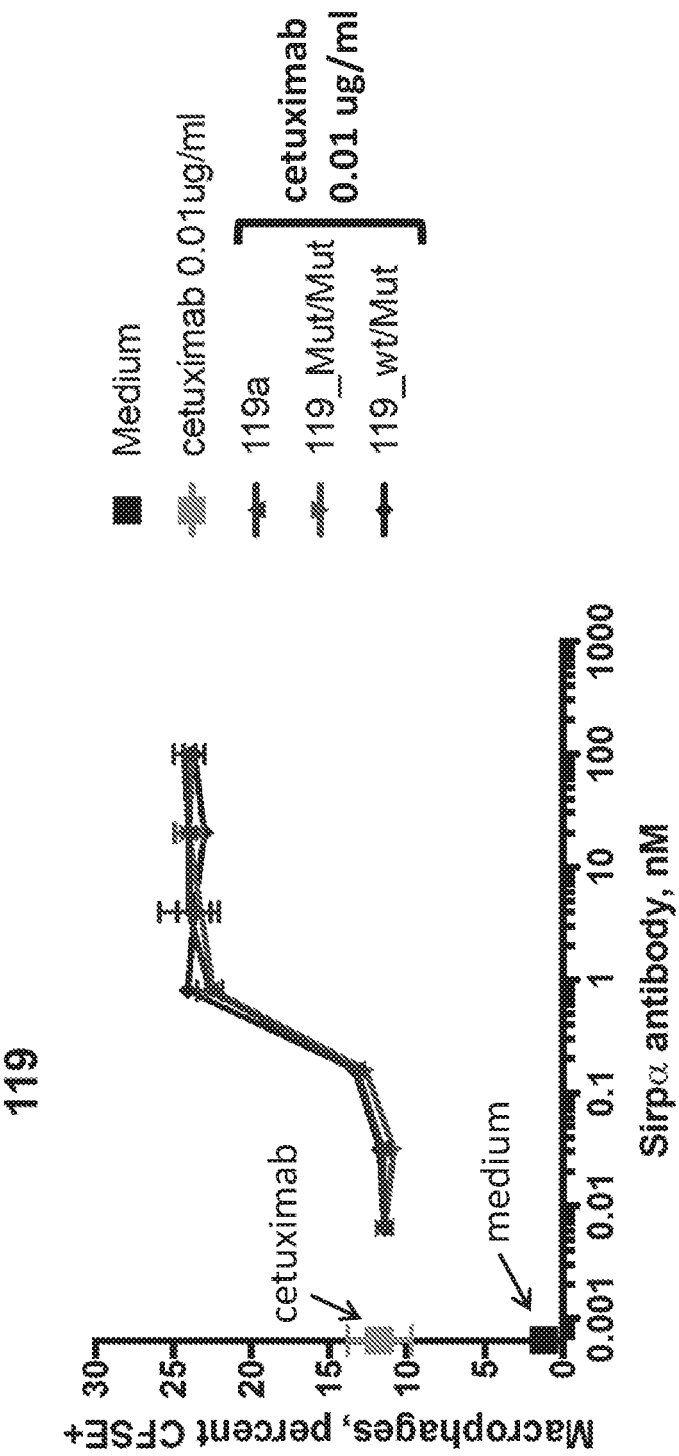

119
Macrophages, percent CFSE+
30
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
cetuximab 0.01ug/ml
119a
119_Mut/Mut
119_wt/Mut
cetuximab
0.01 ug/ml

FIG. 35

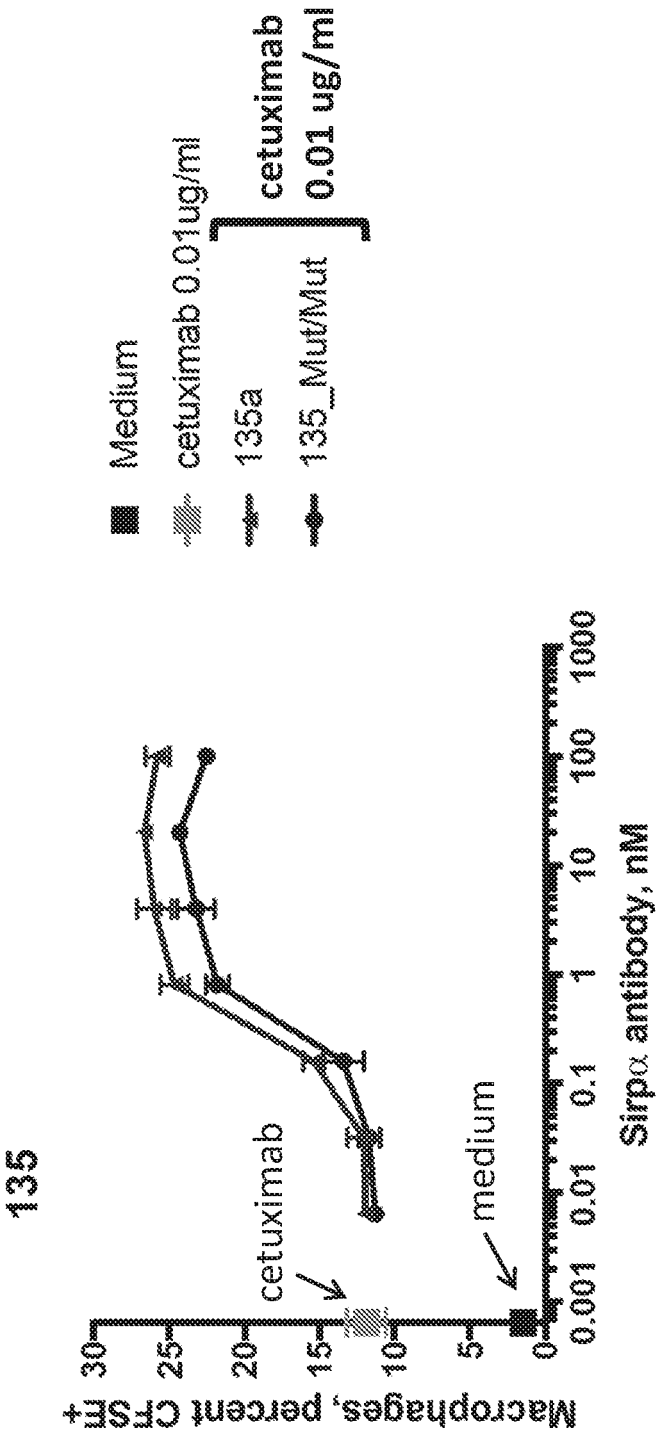

135
Macrophages, percent CFSE+
30
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
cetuximab 0.01ug/ml
135a
135_Mut/Mut
cetuximab
0.01 ug/ml

FIG. 36

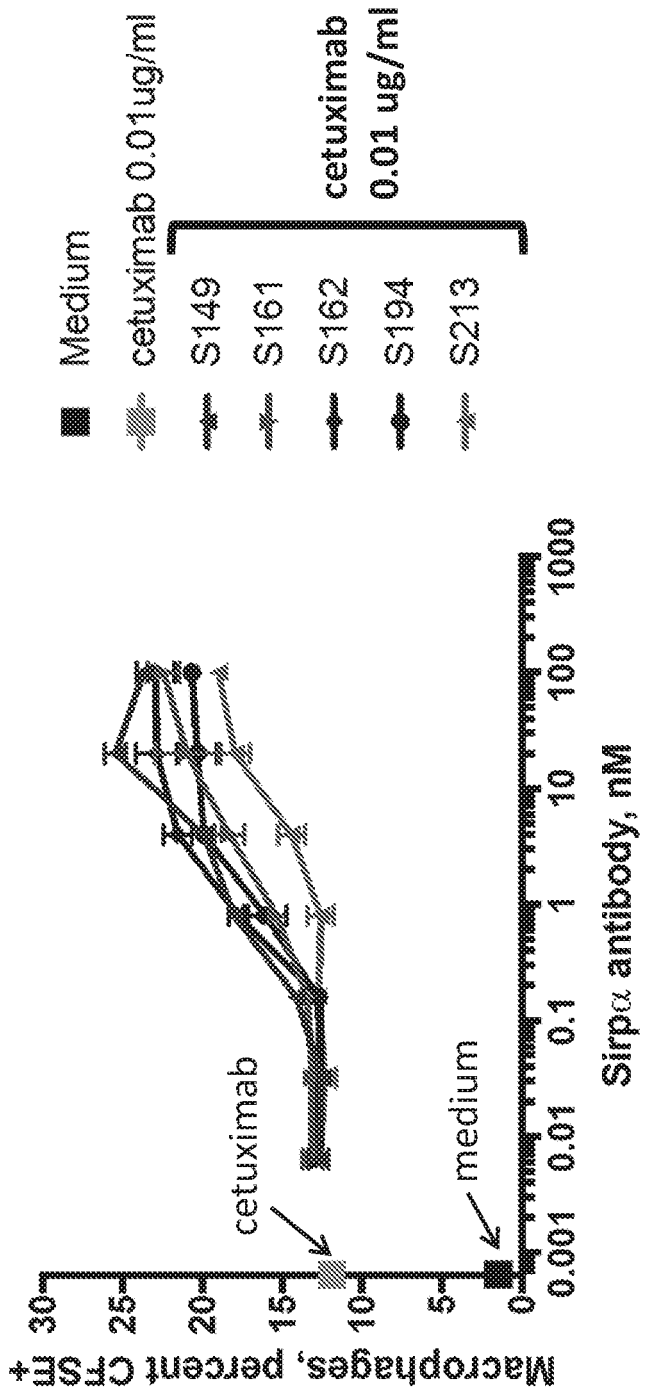

Medium
cetuximab 0.01ug/ml
S149
S161
S162
S194
S213
cetuximab 0.01 ug/ml
Macrophages, percent CFSE+
30
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM

FIG. 37

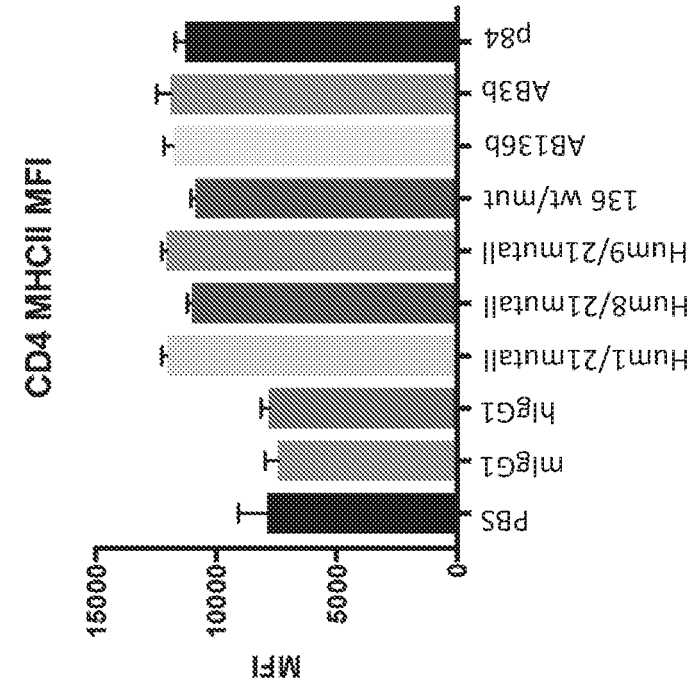


FIG. 38B

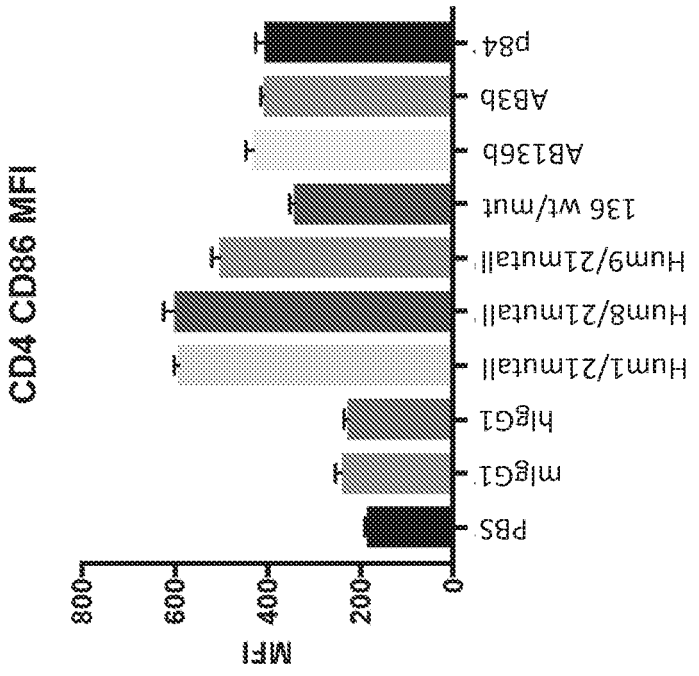


FIG. 38A

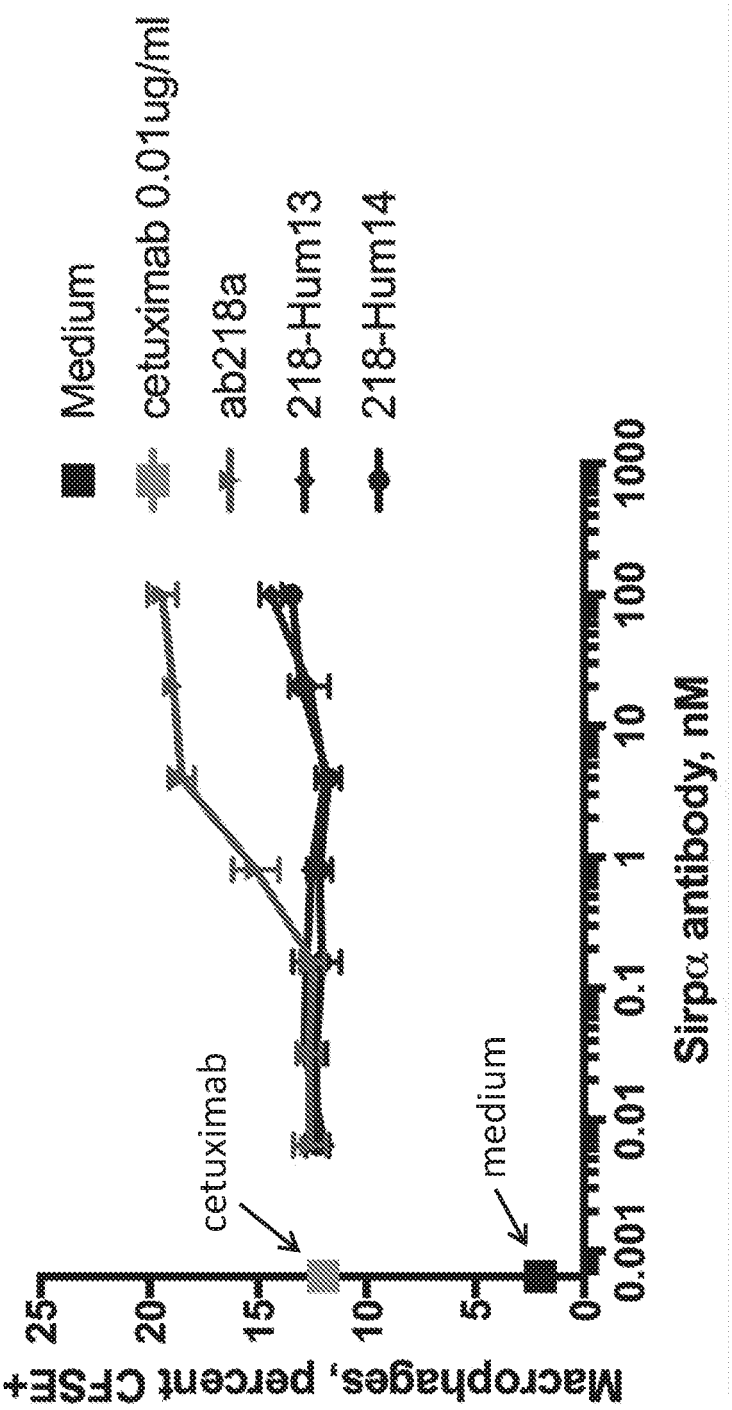

Macrophages, percent CFSE+
25
20
15
10
5
0
cetuximab
medium
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM
Medium
cetuximab 0.01ug/ml
ab218a
218-Hum13
218-Hum14

FIG. 39A

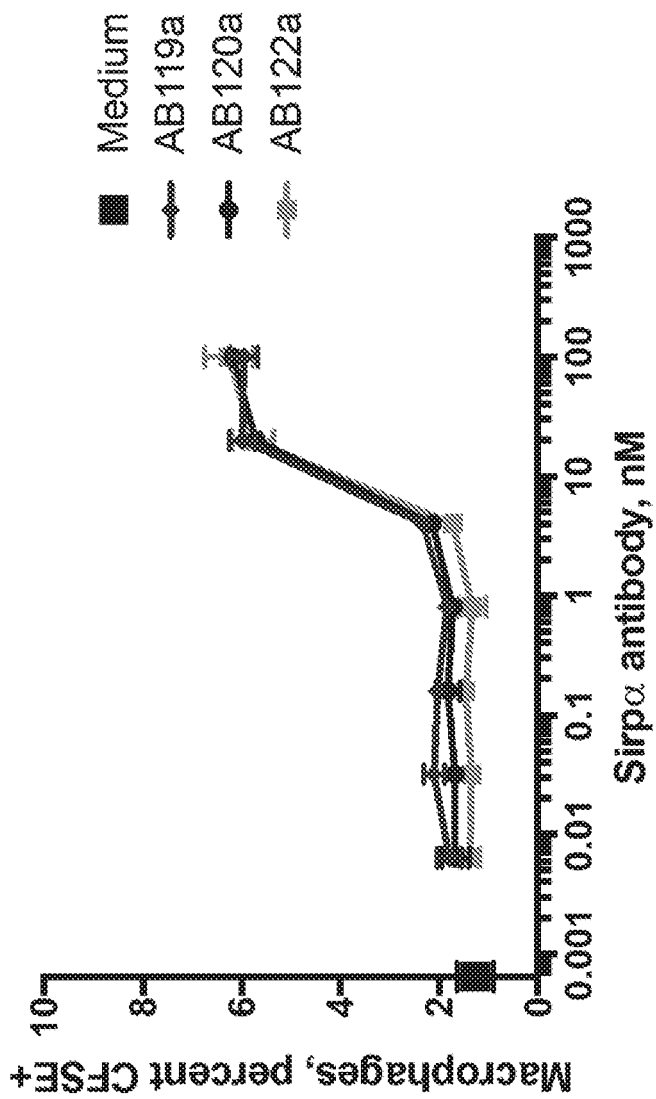

Blockers Single Agent
Medium
AB119a
AB120a
AB122a
Macrophages, percent CFSE+
0
2
4
6
8
10
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM

FIG. 39B

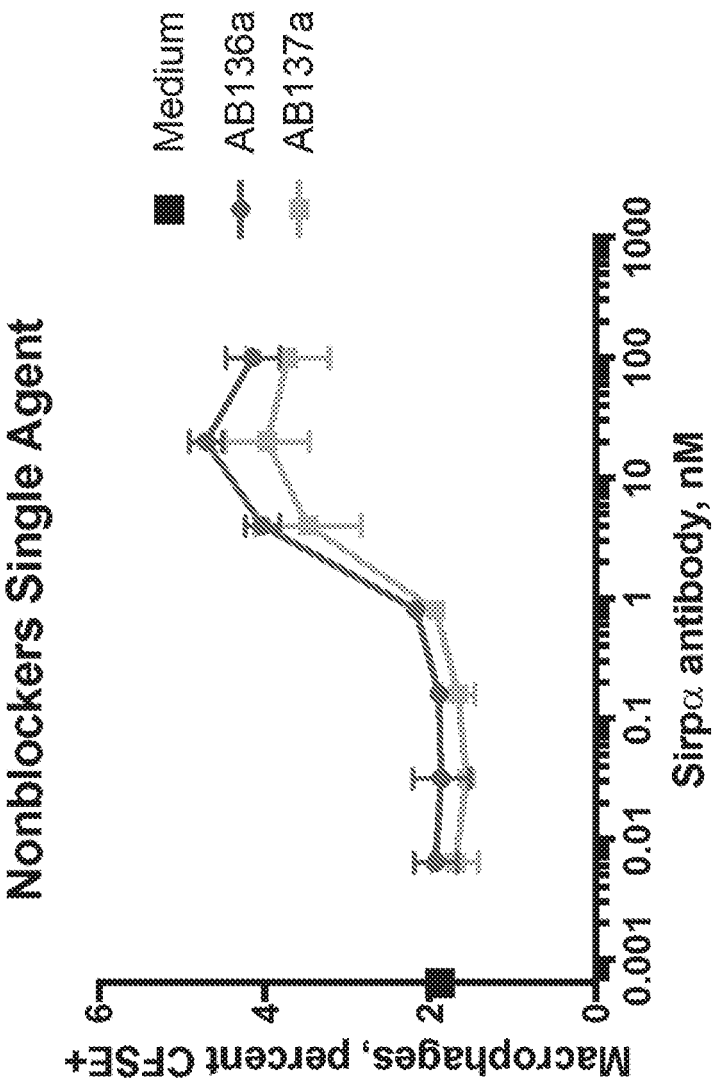

Nonblockers Single Agent
Medium
AB136a
AB137a
Macrophages, percent CFSE+
0
2
4
6
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM

FIG. 39C

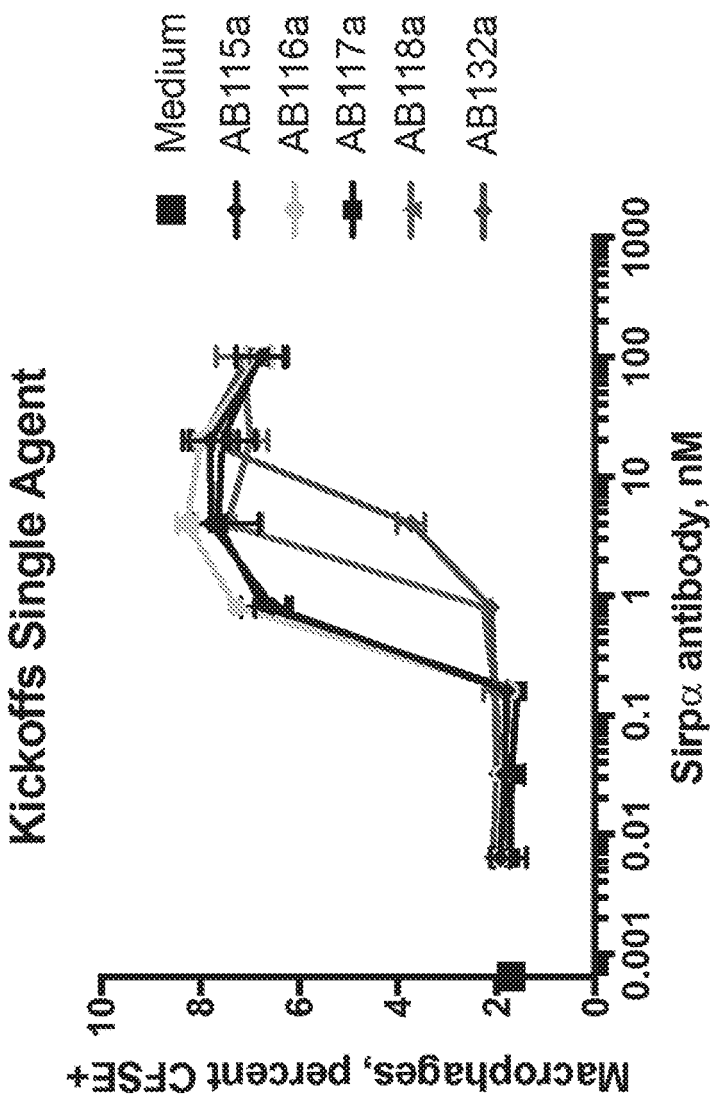
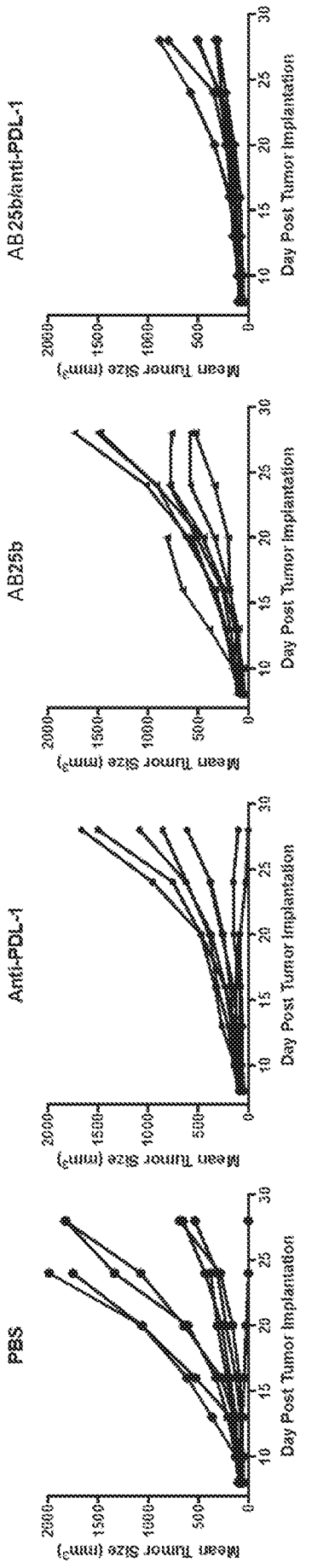
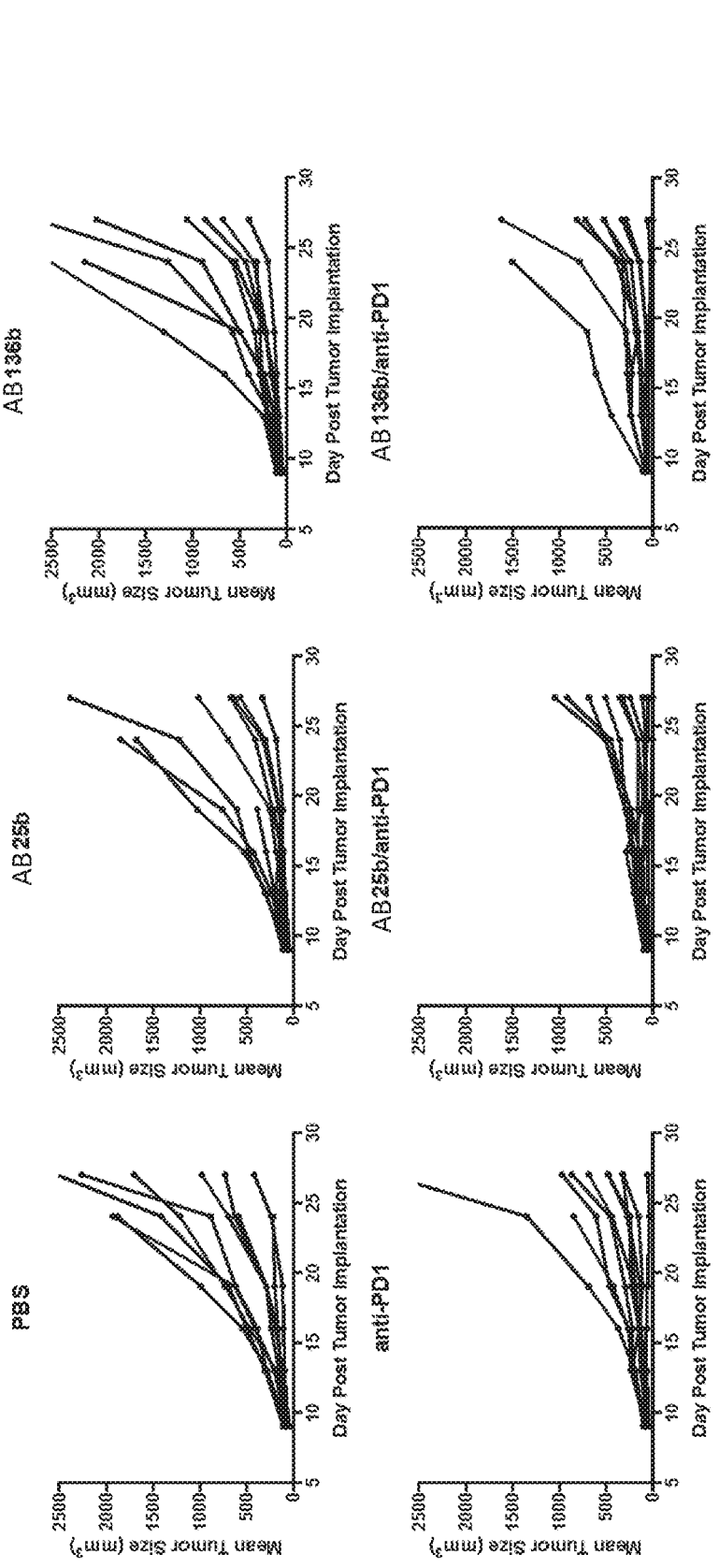

Kickoffs Single Agent
Medium
AB115a
AB116a
AB117a
AB118a
AB132a
Macrophages, percent CFSE+
0
2
4
6
8
10
0.001
0.01
0.1
1
10
100
1000
Sirpα antibody, nM

FIG. 39D



	PBS	Anti-PDL1	AB25b	AB25b/anti-PDL1
Mice with tumor volume <600 mm3	2	2	2	6

FIG. 40



	PBS	Anti-PD1	AB25b	AB25b/anti-PD1	AB136b	AB136b/anti-PD1
Mice with tumor volume <600 mm3	1	5	2	7	1	6

FIG. 41