

|     |       |                                                    |     |  |     |
|-----|-------|----------------------------------------------------|-----|--|-----|
|     |       |                                                    | 1   |  | 50  |
| v1  | (1)   | EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v2  | (1)   | EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v3  | (1)   | EEELQVIQPKSVSVAAGESAILLCTVTSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v4  | (1)   | EEGLQVIQPKSVSVAAGESAILHCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v5  | (1)   | EEELQVIQPKFVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v6  | (1)   | EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v7  | (1)   | EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v8  | (1)   | EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v9  | (1)   | EEELQVIQPKSVLVAAGETATLRCTATSLIPVGPIONFRGAGPARELIY  |     |  |     |
| v10 | (1)   | EEELQVIQPKSVSVAAGESAILHCTVTSLIPVGPIONFRGAGPARELIY  |     |  |     |
|     |       | * * * * *                                          |     |  | *   |
|     |       |                                                    | 51  |  | 100 |
| v1  | (51)  | NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P |     |  |     |
| v2  | (51)  | NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P |     |  |     |
| v3  | (51)  | NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P |     |  |     |
| v4  | (51)  | NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P |     |  |     |
| v5  | (51)  | NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P |     |  |     |
| v6  | (51)  | NOKEGHFFRVTTVSDLTKRNNMDFSIRIGNITPADAGTYVCVKFRKGS-P |     |  |     |
| v7  | (51)  | NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P |     |  |     |
| v8  | (51)  | NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-P |     |  |     |
| v9  | (51)  | NOKEGHFFRVTTVSDLTKRNNMDFSIRISNITPADAGTYVCVKFRKGS-P |     |  |     |
| v10 | (51)  | NOKEGHFFRVTTVSESTKRENMDFSISISNITPADAGTYVCVKFRKGS-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

|          |       |                            |                     |        |   |     |
|----------|-------|----------------------------|---------------------|--------|---|-----|
| Human_v1 | (1)   | EEELQVIQPDKSVLVAAGETATLRC  | TATSLIPVGPIQWFRGAGP | CRELIY | 1 | 50  |
| Human_v2 | (1)   | EEELQVIQPDKSVVAAGESAILHCTV | TSLIPVGPIQWFRGAGP   | ARELIY |   |     |
| Cyno     | (1)   | EEELQVIQPEKSVVAAGESATLNC   | TATSLIPVGPIQWFRGVGP | GRELIY |   |     |
| 129mouse | (1)   | -KELKVTQPEKSVVAAGDSTVLNCT  | LSLLPVGPIKWYRGVGS   | RLLIY  |   |     |
|          |       | ** * * *                   | * * * * *           | * * *  |   |     |
|          | 51    |                            |                     |        |   | 100 |
| Human_v1 | (51)  | NQKEGHEPRVTVSDLT           | KRNNMDFSIRIGNITP    | ADAGTY |   |     |
| Human_v2 | (51)  | NQKEGHEPRVTVSE             | TKRNNMDFSISISNITP   | ADAGTY |   |     |
| Cyno     | (51)  | HQKEGHEPRVTPVSDPT          | KRNNMDFSIRISNITP    | ADAGTY |   |     |
| 129mouse | (50)  | SFTGEHFRVTVNSD             | ATKRNNMDFSIRISNVT   | PE     |   |     |
|          |       | *****                      | * * *               | * * *  |   |     |
|          | 101   |                            |                     |        |   | 120 |
| Human_v1 | (100) | DDVEFKSGAGTE               | LSVR                | AKPS   |   |     |
| Human_v2 | (99)  | PDTEFKSGAGTE               | LSVR                | AKPS   |   |     |
| Cyno     | (99)  | PDVELKSGAGTE               | LSVR                | AKPS   |   |     |
| 129mouse | (100) | PDTEIQSGGTE                | VYVL                | AKPS   |   |     |
|          |       | * * *                      | * * *               | *****  |   |     |

FIG. 1B

|          |       |  | <u>R1</u>                           |                        |                  |
|----------|-------|--|-------------------------------------|------------------------|------------------|
|          |       |  | 1                                   |                        | 50               |
| Human_v1 | (1)   |  | EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGP | IQWFRGAGPGRELIY        |                  |
| Human_v2 | (1)   |  | EEELQVIQPDKSVVAAGESAILHCTVTSLIPVGP  | IQWFRGAGPARELIY        |                  |
| 129mouse | (1)   |  | -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGP | IKWYRGVGSRLLIY         |                  |
| NOD      | (1)   |  | -TEVKVIQPEKSVSVAAGDSTVLNCTLTSLLPVGP | IRWYRGVGSRLLIY         |                  |
| BL6      | (1)   |  | -KELKVTQPEKSVSVAAGDSTVLNCTLTSLLPVGP | IRWYRGVGSRLLIY         |                  |
| BALBC    | (1)   |  | -TEVKVTQPEKSVSVAAGDSTILNCTVTSLLPVGP | IRWYRGVGSRLLIY         |                  |
|          |       |  | ** ** *                             | ** ** *                | ** ** *          |
|          |       |  | 51                                  |                        |                  |
|          |       |  |                                     | <u>R2</u>              | <u>R3</u> 100    |
| Human_v1 | (51)  |  | NQKEGHFPRVTTVSDLT                   | KRNNMDFSIRIGNITPADAGTY | YCVKFKGSP-       |
| Human_v2 | (51)  |  | NQKEGHFPRVTTVSEST                   | KRENMDFSISISNITPADAGTY | YCVKFKGS--       |
| 129mouse | (50)  |  | SFTGEHFPRVTNVSDAT                   | KRNNMDFSIRISNVTPE      | DAGTYCVKFKGPSE   |
| NOD      | (50)  |  | SFTTEHFPRVTNVSDAT                   | KRSNLDIFSIRISNVTPE     | DAGTYCVKFKQSGS-- |
| BL6      | (50)  |  | SFACEYVPRIRNVSDTT                   | KRNNMDFSIRISNVTPADAGI  | YCVKFKQKSSE      |
| BALBC    | (50)  |  | SFTGEHFPRIRNVSDTT                   | KRNNMDFSIRISNVTPE      | DAGTYCVKFKQKSSE  |
|          |       |  | *****                               | ***                    | ***              |
|          |       |  | 101                                 |                        |                  |
|          |       |  |                                     | <u>120</u>             |                  |
| Human_v1 | (100) |  | DDVEFKSGAGTELSV                     | RAKPS                  |                  |
| Human_v2 | (99)  |  | PDTEFKSGAGTELSV                     | RAKPS                  |                  |
| 129mouse | (100) |  | PDTEIQSGGGTEVYV                     | LAKPS                  |                  |
| NOD      | (98)  |  | PDTEIQSGGGTEVYV                     | LAK--                  |                  |
| BL6      | (100) |  | PDTEIQSGGGTEVYV                     | LAK--                  |                  |
| BALBC    | (100) |  | PDTEIQSGGGTEVYV                     | LAK-                   |                  |
|          |       |  | * * *                               | * * *                  | * * *            |

FIG.1C

|          |       |                                                     |     |
|----------|-------|-----------------------------------------------------|-----|
|          | 1     |                                                     | 50  |
| Human_v1 | (1)   | EEELQVIQPDKSVLVAAGETATLRCTATSLIPVGPIQWFRGAGPGRELIY  |     |
| Human_v2 | (1)   | EEELQVIQPDKSVVAAGESAILHCTVTSLIPVGPIQWFRGAGPARELIY   |     |
| Cyno     | (1)   | EEELQVIQPEKSVVAAGESATLNCTATSLIPVGPIQWFRGVGPARELIY   |     |
| 129mouse | (1)   | -KELKVTQPEKSVVAAGDSTVLNCTLTSLIPVGPIKWYRGVGSRLLIY    |     |
| chicken  | (1)   | --DFKLQQPQSSVVVIKGDTLNCTASGCPICAVKWVKWVGSDNQTVY     |     |
|          |       | ***** ** * ** * ** * ** * ** * ** * ** *            |     |
|          | 51    |                                                     | 100 |
| Human_v1 | (51)  | NQKEGHFPRVTVSDLTKRNNMDFESIRIGNITPADAGTYCVKFRKGS-    |     |
| Human_v2 | (51)  | NQKEGHFPRVTVSESTKRNNMDFESISINITPADAGTYCVKFRKGS--    |     |
| Cyno     | (51)  | HQKEGHFPRVTPVSDPTKRNNMDFESIRISNITPADAGTYCVKFRKGS--  |     |
| 129mouse | (50)  | SFTGEHFPRVTNVSDATKRNNMDFESIRISNVTPEADAGTYCVKFKQGPSE |     |
| chicken  | (49)  | EHKGSFPRVMRAVDPDN---DFTIRISNVSLDAGTYCVKLRKGIV-      |     |
|          |       | ***** ** * ** * ** * ** * ** * ** * ** *            |     |
|          | 101   |                                                     | 120 |
| Human_v1 | (100) | DDVEFKSGAGTELSVRAKPS                                |     |
| Human_v2 | (99)  | PDTEFKSGAGTELSVRAKPS                                |     |
| Cyno     | (99)  | PDVELKSGAGTELSVRAKPS                                |     |
| 129mouse | (100) | PDTEIQSGGGTEVYVLAKPS                                |     |
| chicken  | (94)  | DDVVFTRGGGTEVSVHA---                                |     |
|          |       | * **** * ** * ** *                                  |     |

FIG. 2

S130

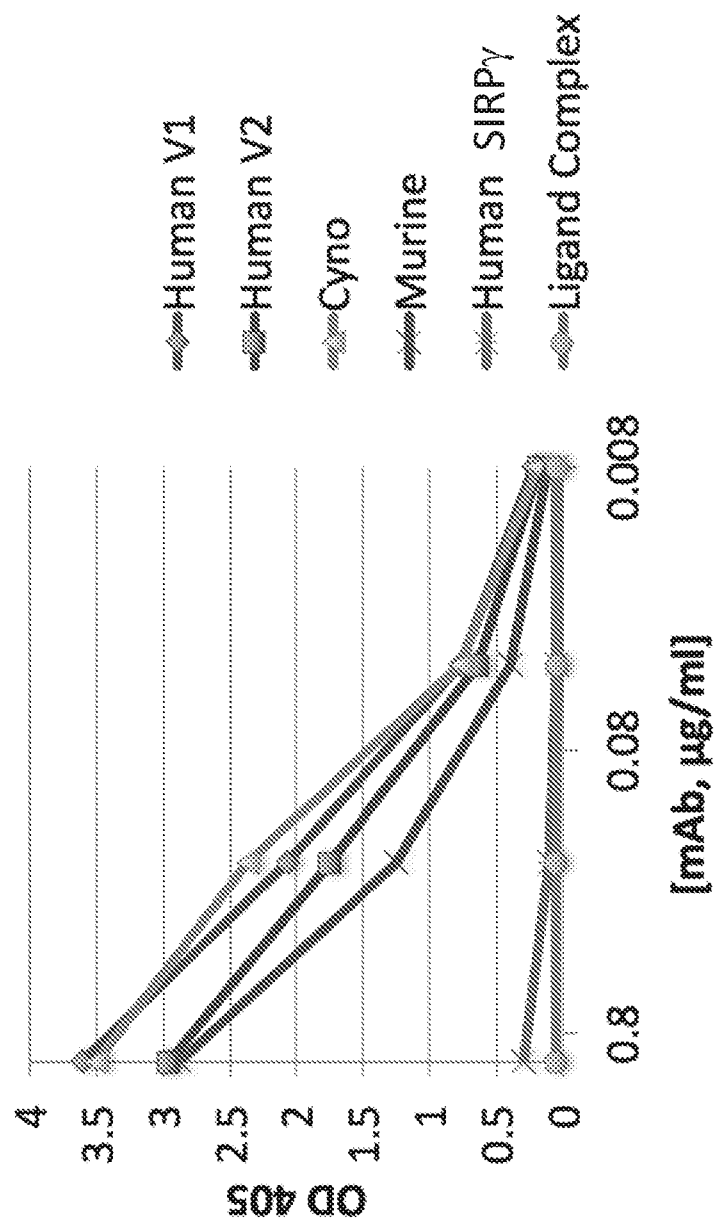


FIG. 3A

|            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Human (V1) | Human (V2) | Human (V2) | Human (V2) | Human (V2) | Human (V2) | Human (V2) | Human (V2) | Human (V2) | Human (V2) |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |
| +          | +          | +          | +          | +          | +          | +          | +          | +          | +          |

FIG. 3B

# S121

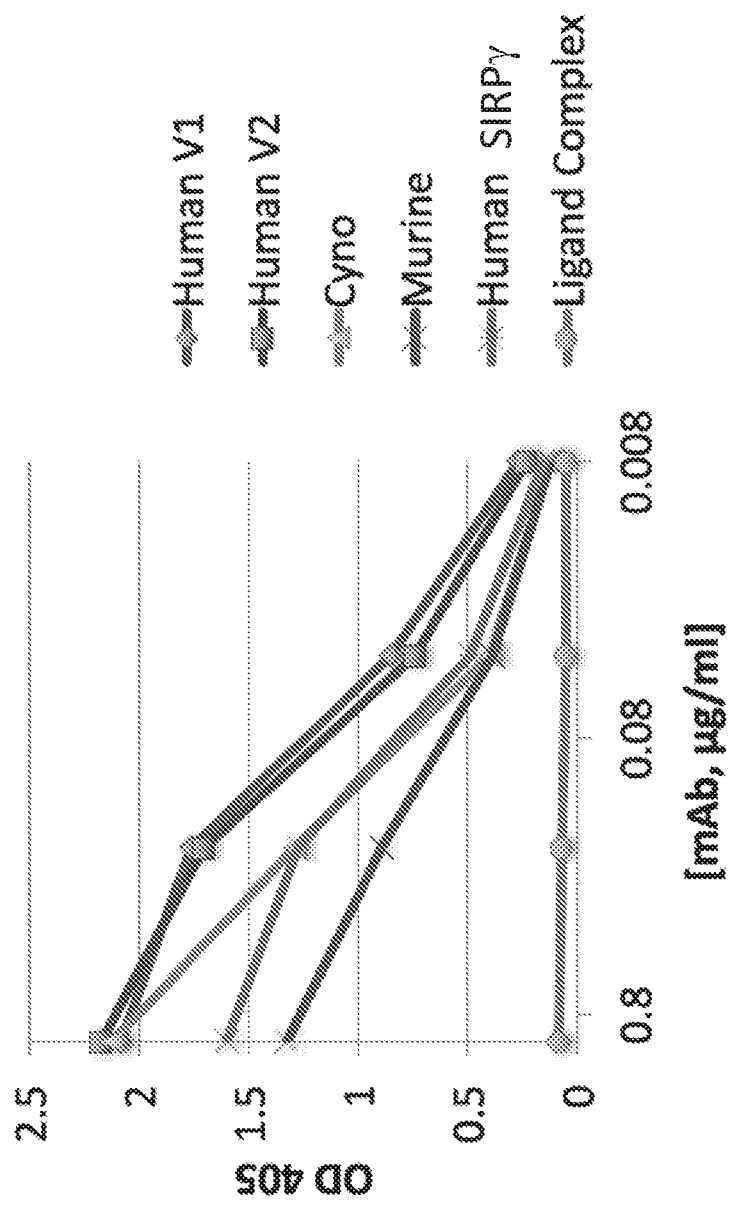


FIG. 4A

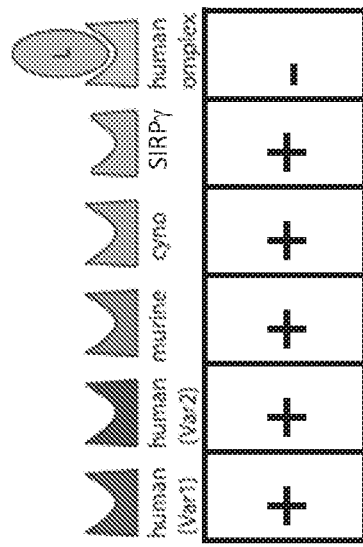


FIG. 4B

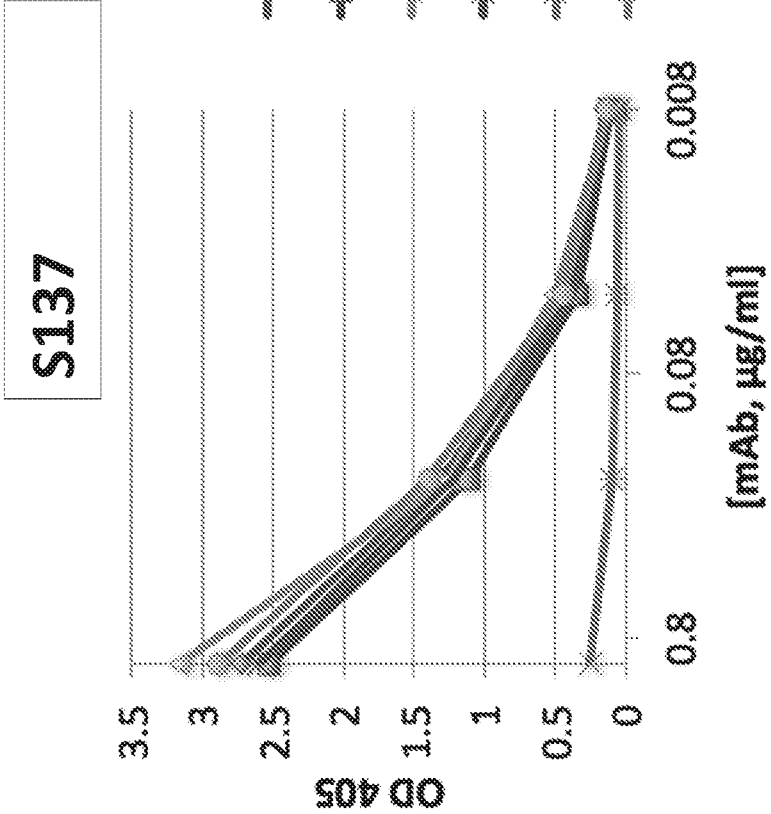


FIG. 5A

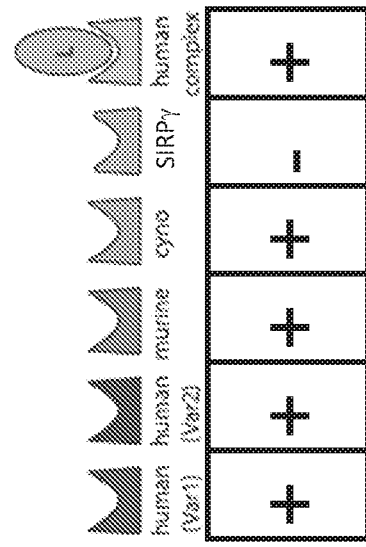


FIG. 5B

S128

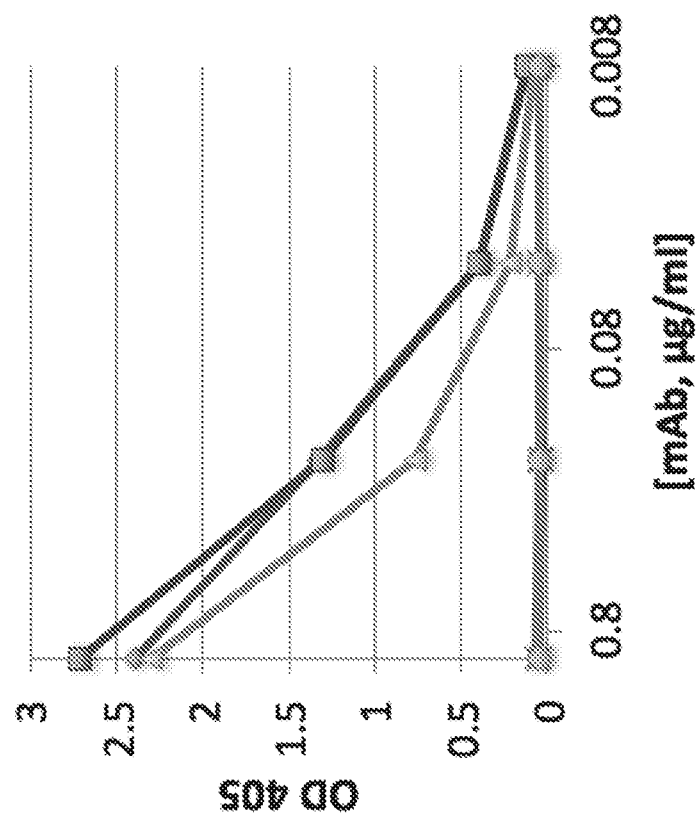


FIG. 6A

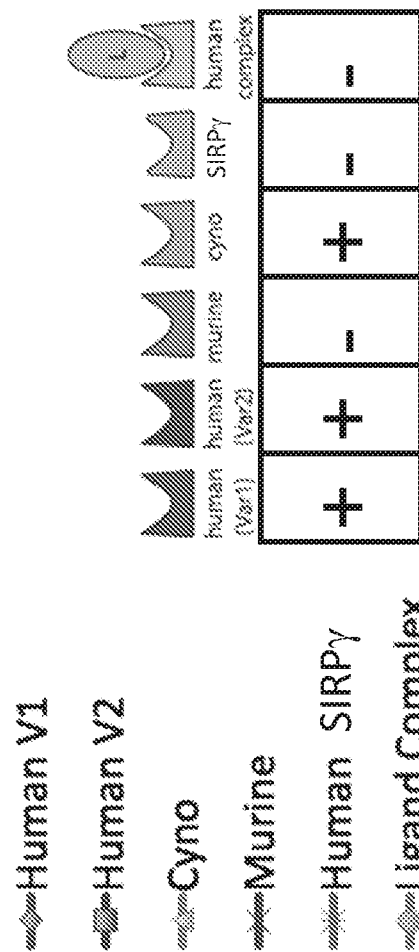


FIG. 6B

S135

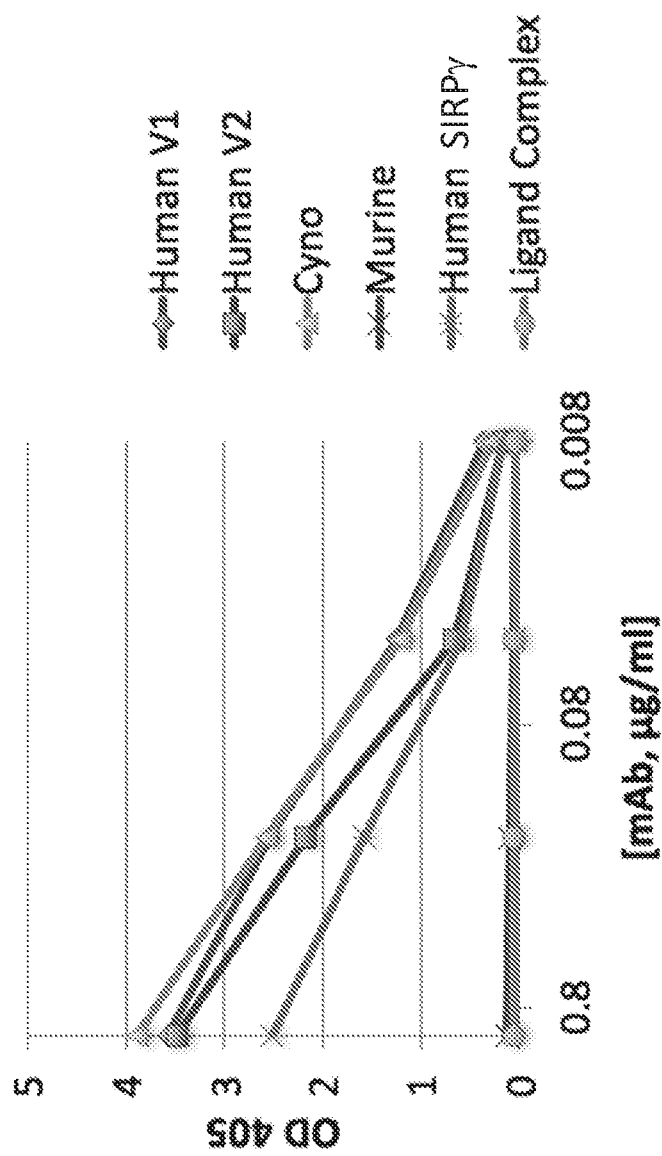


FIG. 7A

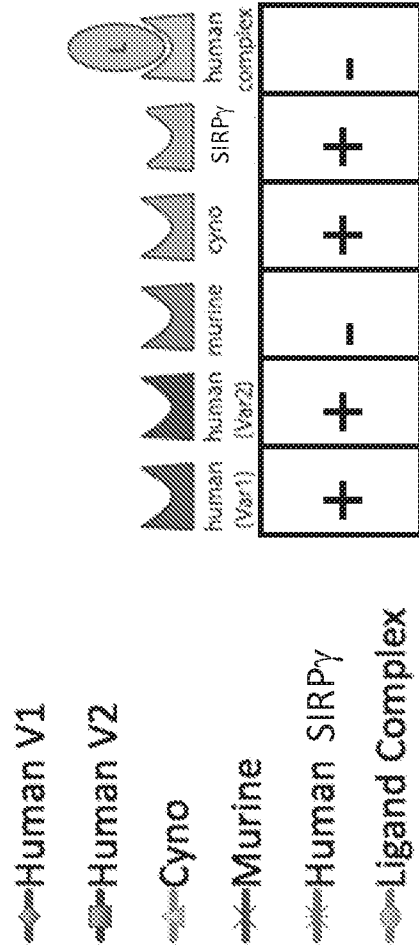


FIG. 7B

S126

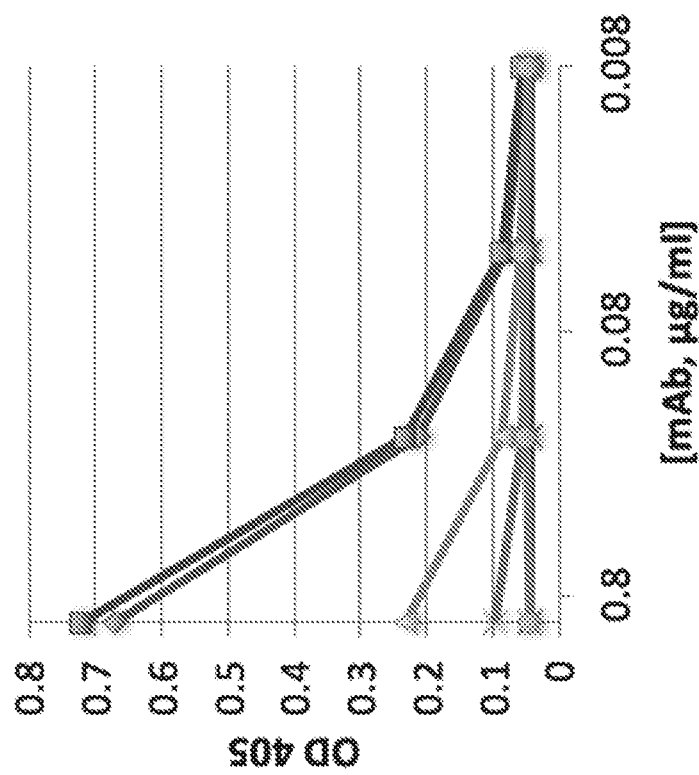


FIG. 8A

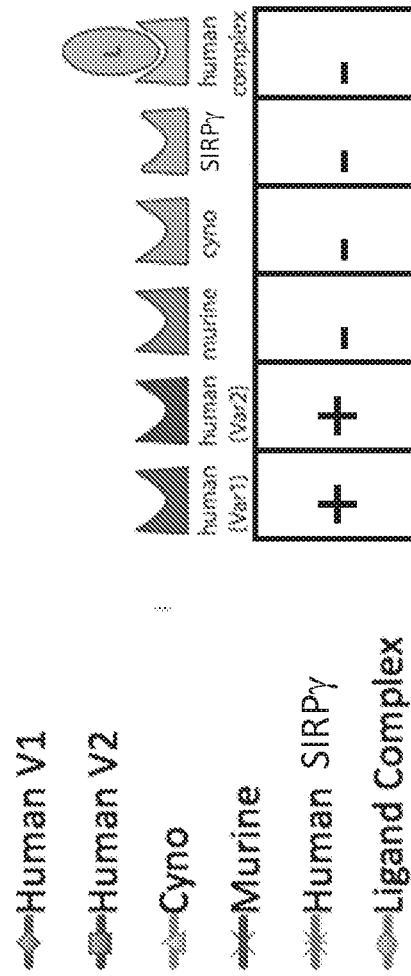


FIG. 8B

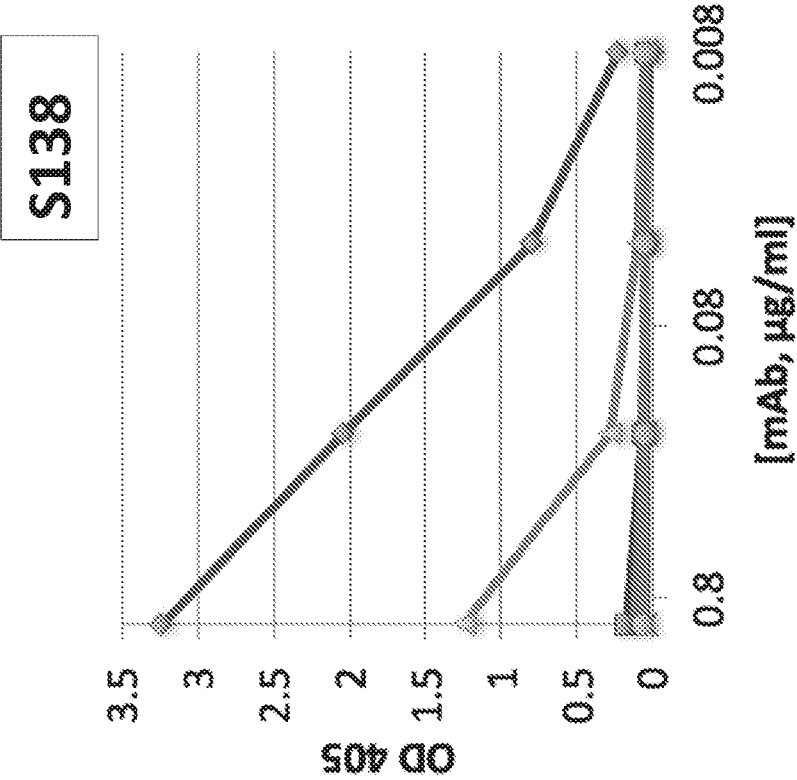


FIG. 9A

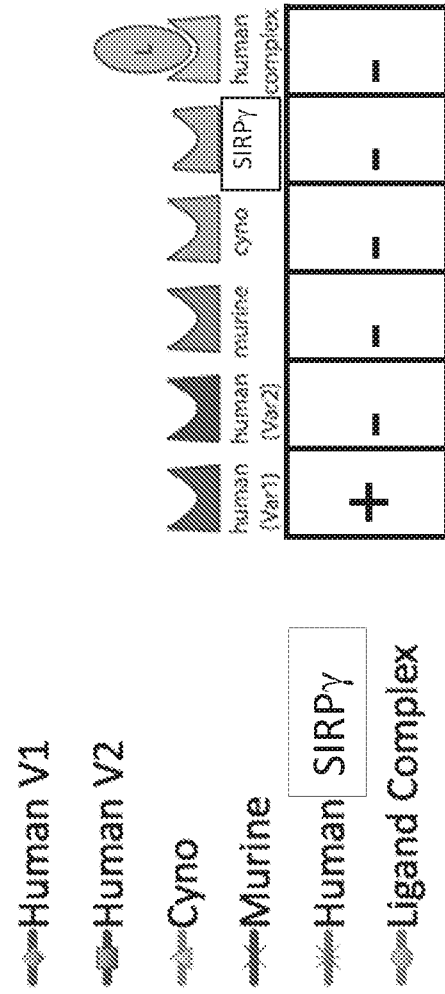


FIG. 9B





|     |       | H3                                                 | 250   |
|-----|-------|----------------------------------------------------|-------|
| 201 |       |                                                    |       |
| S1  | (195) | ISRDNGQSTVRLQLNNLRAEDTATYYCTKNGG-----CGSGGLDCIDAW  |       |
| S2  | (195) | ISRDNGQSTVRLQLNNLRAEDTGTYFCTRN-----FGSSVSSIDAW     |       |
| S8  | (197) | ISRDNGQSTVRLQLNNLRAEDTGTYCAKAAGCSTHTCTAYIADSIDAW   |       |
| S9  | (196) | ITRDVGQSTVRLQLNNLRAEDTGTYFCAKDAYQCS-YATCNDYLDTIDAW |       |
| S11 | (194) | ISRDNGQSTVRLQLNNLRAEDTGTYFCAKDAG-SGCYSGVCAGTSSIDAW |       |
| S12 | (195) | ISRDDGQSTVRLQLNNLRAEDTGTYFCAKSAGGCSAHSCDTYIADSIDAW |       |
| S13 | (196) | ISRDNGQSTVRLQLNNLGAEDTGTYFCKSAGGCSDYNCDAYIADSIDAW  |       |
| S14 | (195) | ISRDNGQSTVRLQLNNLRAEDTGTYFCAKAAGGCTAHNCDAYIADSIDAW |       |
|     |       | * * *                                              | ***** |
|     |       | 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)



|      |       |       |                                              |     |
|------|-------|-------|----------------------------------------------|-----|
|      |       |       | linker                                       |     |
| 101  |       |       |                                              | 150 |
| S115 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S116 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S117 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S118 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S119 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S120 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S122 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S123 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCT             |     |
| S126 | (101) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S128 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S130 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S135 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S137 | (100) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
| S138 | (101) | GGG   | GGGSSGGGSDVQLVESGGGVVRPGESLRLSCA             |     |
|      |       | *     | *                                            | *   |
|      |       | *     | *                                            | *   |
| 151  |       |       |                                              | 200 |
|      |       | H1    | H2                                           |     |
| S115 | (150) | ASGFS | SSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR    |     |
| S116 | (150) | ASGFS | SSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR    |     |
| S117 | (150) | ASGFS | SSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR    |     |
| S118 | (150) | ASGFS | SSYAMNWRQAPGEGLEWVSRINSGGGTDYAESVKGRFTISR    |     |
| S119 | (150) | ASGFS | SNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR  |     |
| S120 | (150) | ASGFS | SNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR  |     |
| S122 | (150) | ASGFS | SNFAMTWVRQAPGEGLEWVSTIGSG--DTYYADSVKGRFTISR  |     |
| S123 | (150) | ASGFT | ERNYGMWVRQAPGEGLEWVSASSG--SGSTYYTDSVKGRFTISR |     |
| S126 | (151) | ASGFT | SNYDMTWVRQAPGEGLEWVSGISGNGGSTYYADSVKGRFTISR  |     |
| S128 | (150) | ASGFS | RSYAMNWRQAPGEGLEWVSRIDSGGGTDYADSVKGRFTISR    |     |
| S130 | (150) | ASGFT | FSNYAMSWVRQAPGEGLEWVSLITNCGDGYADSVKGRFTISR   |     |
| S135 | (150) | ASGFS | FSIYAMSWVRQAPGEGLEWVSTIGAD--DTYYADSVKGRFTISR |     |
| S137 | (150) | ASGFT | FSYDMNWRQAPGEGLEWVSLISGSEIIYYADSVKGRFTISR    |     |
| S138 | (151) | ASGFT | FSNYAMNWRQAPGEGLEWVSGISGRGGDTYYADSVKGRFTISR  |     |
|      |       | *     | *****                                        | **  |

FIG. 10B  
(cont'd)

|      |       |     | H3                                                 | 250 |
|------|-------|-----|----------------------------------------------------|-----|
| S115 | (200) | 201 | NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS |     |
| S116 | (200) |     | NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS |     |
| S117 | (200) |     | NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS |     |
| S118 | (200) |     | NSENTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGALVTVSSS |     |
| S119 | (198) |     | NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS  |     |
| S120 | (198) |     | NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS  |     |
| S122 | (198) |     | NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS  |     |
| S123 | (199) |     | NSKNTLYLQMNSLRAEDTAIYYCAKVT---WNN-FFDYWGLGTLVTVSSS |     |
| S126 | (201) |     | NSKNTLYLQMNSLRAEDTAVYYCAMN---RWW--FDYWGLGTLVTVSSS  |     |
| S128 | (200) |     | NSKNTLYLQMNSLRAEDTAVYYCAKQY---DWNSEFDYWGLGAPVTVSSS |     |
| S130 | (200) |     | NSKNTLYLQMNSLRAEDTAIYYCAKDGAHYYDIFFDYWGLGTPVTVSSS  |     |
| S135 | (198) |     | NSKNTLYLQMNSLRAEDTAVYYCAKDSVSWSGDFFDYWGLGTLVTVSSS  |     |
| S137 | (200) |     | NSKNTLYLQMNSLRAEDTAVYYCAKEN---NRYRFFDDWGLGTLVTVSSS |     |
| S138 | (201) |     | NSKNTLYLQMNSLRAEDTAIYYCAKGT---WNYGSFDYWGLGTLVTVSSS |     |
|      |       | *   | *****                                              | **  |

FIG. 10B  
(cont.'d)

FIG. 11A

|      | H1                                                               | H2                                           | G0 |
|------|------------------------------------------------------------------|----------------------------------------------|----|
| S16  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAVSGCFESSYAMSWVRQAPCKGLEWVSGISS-GGDTYY |    |
| S27  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAVSGCFESSYAMSWVRQAPCKGLEWVSGISS-GGDTYY |    |
| S55  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAVSGCFESSYAMSWVRQAPCKGLEWVSGISS-GGDTYY |    |
| S59  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAVSGCFESSHAMSWVRQAPCKGLEWVSGISS-GGDTYY |    |
| S29  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAVSGCFESSYAMSWVRQAPCKGLEWVSGISS-DSDAYY |    |
| S201 | (1) DVQLVESGGAVRPPGETLRLSCTASGFTFSSYAMSWVRQAPCKGLEWVSGISASGSDDTY |                                              |    |
| S206 | (1) DVQLVESGGAVRPPGETLRLSCTASGFTFSSYAMSWVRQAPCKGLEWVSGISASGSDDTY |                                              |    |
| S26  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASCFTFSTYAMSWVRQAPCKGLEWVSGISASCSGTYY |    |
| S25  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCEASGFTFSSNAMSVRQAPCKGLEWVAGISS-GSDTTY  |    |
| S73  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCEASGFTFSSNAMSWARQAPCKGLEWVAGISS-GSDTTY |    |
| S30  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCEASGFTFSSDAMSWVRQAPCKGLEWVSGISS-GSSTYY |    |
| S28  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFSSSNAMSWVRQAPCKGLEWVAGISASG-DTYY  |    |
| S21  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSNAMSVRQAPCKGLEWLAGISAGGSDDTY  |    |
| S24  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSNAMSVRQAPCKGLEWLAGISAGGSDDTY  |    |
| S74  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSNAMSVRQAPCKGLEWLAGISAGDSDDTY  |    |
| S23  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSHAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S17  | (1) DVQLVESGGAVRPPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S22  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S66  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S56  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S70  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDAY |    |
| S202 | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S60  | (1) DVQLVDGGGVRRPGE                                              | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S65  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S69  | (1) DLQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S71  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |
| S76  | (1) DVQLVESGGGVRRPGE                                             | SLRLSCAASGFTFSSYAMSWVRQAPCKGLEWLAGISAGGSDDTY |    |

FIG. 11A (cont'd)

|      | 61   | H2             | H3                                             | 119 |
|------|------|----------------|------------------------------------------------|-----|
| S16  | (60) | VDSVKGRFTISRDN | -KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S27  | (60) | VDSVKGRFTISRDN | -KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S55  | (60) | VDSVKGRFTISRDN | -KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S59  | (60) | VDSVKGRFTISRDN | -KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S29  | (60) | VDSVKGRFTISRDN | -KNTLYLQVNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S201 | (61) | ADSVKGRSTISRDN | -KNTLYLRMSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S206 | (61) | ADSVKGRSTISRDN | -KNTLYLRMSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S26  | (61) | GDSVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S25  | (60) | GDSVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S73  | (60) | GDSVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S30  | (60) | GDSVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S28  | (60) | SGSMKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S21  | (61) | PASVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S24  | (61) | PASVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S74  | (61) | PASVKGRFTISRDN | -KNTLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S23  | (61) | IDSVKGRFTISRDN | -KSSLYLRMNSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS  |     |
| S17  | (61) | IDSVKGRFTISRDN | -ENSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S22  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S66  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S56  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S70  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S202 | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S60  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S65  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S69  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S71  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |
| S76  | (61) | IDSVKGRFTISRDN | -KNSLYLQMNSSLTAEDTAIYYCARETNHLEFDYWGGLGLTLVTSS |     |

\*\* \* \* \* \* \*\*\*\*\* \*

\* \*

FIG. 11A (cont'd)

|      |     | 1                                                      | L1 | L2 | 54 |
|------|-----|--------------------------------------------------------|----|----|----|
| S16  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S59  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S27  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S55  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S29  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S26  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDNQRPS |    |    |    |
| S21  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S24  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S74  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S25  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S73  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S30  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDNKRPS |    |    |    |
| S28  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S201 | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S206 | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S22  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S60  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S65  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S69  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S23  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDERPS |    |    |    |
| S66  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S17  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S70  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S76  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S202 | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S56  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |
| S71  | (1) | ALTQPASVSANLGETVKITCSGGDSSSHYYGWYQQKSPGSAPVTVIYSDDKRPS |    |    |    |

FIG. 11A (cont'd)

|      | 55   | L3                                                     | 107 |
|------|------|--------------------------------------------------------|-----|
| S16  | (55) | DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL |     |
| S59  | (55) | DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL |     |
| S27  | (55) | DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL |     |
| S55  | (55) | DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL |     |
| S29  | (55) | DIPSRFSGSASGSTATLTTITGVRVEDEAIYCCAYDGSSTYANTFCAGTTLTVL |     |
| S26  | (53) | DIPSRFSGSASDSTATLTTITGVQVEDEAIYCCGYDSSSTYANTFCAGTTLTVL |     |
| S21  | (55) | DIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYANAFGAGTTLTVL  |     |
| S24  | (55) | GIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSSYTNDGAGTTLTVL   |     |
| S74  | (55) | GIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSSYTNDGAGTTLTVL   |     |
| S25  | (55) | NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDQSSYTNPFCAGTTLTVL  |     |
| S73  | (55) | NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDQSSYTNPFCAGTTLTVL  |     |
| S30  | (55) | NIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYTNPFAGTTLTVL   |     |
| S28  | (54) | DIPSRFSGSASGSTATLTTITGVRAEDEAVYCCGYDYSTYTNPFAGTTLTVL   |     |
| S201 | (54) | DIPSRFSGSASGSTATLTTITGVQVEDEAVYCCGYDYTYVNTFCAGTTLTVL   |     |
| S206 | (54) | DIPSRFSGSASGSTATLTTITGVQAEDEAVYCCGYDYTYVNTFCAGTTLTVL   |     |
| S22  | (55) | DIPSRFSGSASGSAATLTTIAGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL  |     |
| S60  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL  |     |
| S65  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL  |     |
| S69  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCAYDGRTYINTFCAGTTLTVL  |     |
| S23  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S66  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S17  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S70  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S76  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S202 | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S56  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDGRTYINTFCAGTTLTVL  |     |
| S71  | (55) | DIPSRFSGSASGSAATLTTITGVRVEDEAVYCCGYDARTYINTFCAGTTLTVL  |     |
|      | *    | * * * * *                                              | *   |

FIG. 11B

|      |      | <u>H1</u>                                                     | <u>H2</u> | 60  |
|------|------|---------------------------------------------------------------|-----------|-----|
| 1    |      |                                                               |           |     |
| 136  | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| 137  | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S185 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S175 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S189 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S193 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S180 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S177 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S178 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S184 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
| S190 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSSYDMNWRQAPGEGLEWVSLISGSGEIYY    |           |     |
|      |      | **                                                            |           | *   |
|      |      |                                                               |           |     |
|      |      |                                                               | <u>H3</u> | 119 |
| 136  | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| 137  | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S185 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S175 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S189 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S193 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S180 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S177 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S178 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S184 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
| S190 | (61) | ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKENNRYRFFDDWGLGLTLVTSS |           |     |
|      |      | *                                                             | **        | *   |



FIG. 11C

|      |      | <u>H1</u>         | <u>H2</u>     | <u>60</u>                        |
|------|------|-------------------|---------------|----------------------------------|
|      | 1    |                   |               |                                  |
| S115 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S116 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S117 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S118 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S132 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S191 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSYAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
| S198 | (1)  | DVQLVESGGGVVRPGE  | SLRLSCAASGFS  | SSHAMNWWVRQAPGEGLEWVSRINSGGGGTDY |
|      |      |                   | *             | *                                |
|      | 61   |                   | <u>H3</u>     | <u>119</u>                       |
| S115 | (61) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S116 | (61) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S117 | (60) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S118 | (61) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S132 | (61) | ADSVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S191 | (61) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
| S198 | (61) | AESVKGRFTISRDNSEN | TLYLQMNSLRAED | TAVYYCAKQYDWNSEFFDYWGLGALVTVSS   |
|      |      |                   | *             | *                                |

FIG. 11C (cont'd)

|      |      | <u>L1</u>                                             | <u>L2</u> | <u>54</u>  |
|------|------|-------------------------------------------------------|-----------|------------|
|      | 1    |                                                       |           |            |
| S115 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDATNR |           |            |
| S116 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDATNR |           |            |
| S117 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDATNR |           |            |
| S118 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDASRR |           |            |
| S132 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDASNR |           |            |
| S191 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDATNR |           |            |
| S198 | (1)  | ETVLTQSPATLSVSPGERATLSCRASQTVGSKLAWHQKPGQAPRLLIYDATNR |           |            |
|      |      |                                                       |           | **         |
|      | 55   |                                                       | <u>L3</u> | <u>108</u> |
| S115 | (55) | ATGISDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
| S116 | (55) | ATGISDRFSGSRSGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK     |           |            |
| S117 | (55) | ATGIPDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
| S118 | (55) | ATGIPDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
| S132 | (55) | ATGIPDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
| S191 | (55) | ATGIPDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
| S198 | (55) | ATGIPDRFSGSGGTDFTLTISLQTEDSAVYCCQYYWPPYRFGGKVEIK      |           |            |
|      |      | *                                                     | *         | *          |
|      |      | *                                                     | *         | *          |

FIG. 11D

|      |      | H1                                                           | H2 | 60    |
|------|------|--------------------------------------------------------------|----|-------|
| S173 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFAFSDHDMSWVRQQGPGEGLWVAGISLRGGVTWY |    |       |
| S174 | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFTFSDHDMSWVRQQGPGEGLWVAGISLRGGVTWY |    |       |
|      |      | *                                                            |    |       |
|      |      |                                                              | H3 | 118   |
| S173 | (61) | ADSVKGRFTISRDN SKNTLYLRFLSLRTEDTAIYYCARESWNTFFDYWGGLGLTVTVSS |    |       |
| S174 | (61) | ADSVKGRFTISRDN SKNTLYLRFLSLRTEDTAIYYCARESWNTFFDYWGGLGLTVTVSS |    |       |
|      |      |                                                              |    |       |
|      |      |                                                              | L1 | L2 55 |
| S173 | (1)  | EIVLTQSPGTLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA        |    |       |
| S174 | (1)  | EIVLTQSPGTLSPGETATLSCRASQNVRSNLAWYQQKPGQAPRLLIYDASSRA        |    |       |
|      |      |                                                              |    |       |
|      |      |                                                              | L3 | 108   |
| S173 | (56) | TGIPDRFSGSGGTDFTLTISSLSQSEDFAVYCCQQYGNPPLTFGGGKVEIK          |    |       |
| S174 | (56) | TGIPDRFSGSGGTDFTLTISSLSQSEDFAVYCCQQYGNPPLTFGGGKVEIK          |    |       |

FIG. 11E

|      |      |                                                              |                  |     |    |
|------|------|--------------------------------------------------------------|------------------|-----|----|
|      |      | H1                                                           | H2               | 60  |    |
| 1    |      |                                                              |                  |     |    |
| S213 | (1)  | DVQLVESGGVVRPGESLRLSCEASGFTFRNYYMTWVRQAPGEGLEWVSTISDTGDTAYY  |                  |     |    |
| S214 | (1)  | DVQLVESEGGVVRPGESLRLSCEASGFTFRNSYMTWVRQAPGEGLEWVSTISDTGDTAYY |                  |     |    |
|      |      | *                                                            |                  |     |    |
|      |      |                                                              | H3               | 119 |    |
| 61   |      |                                                              |                  |     |    |
| S213 | (61) | ADSVKGRFTISRDNKNSLYLQMNSLRADDTAIYYCAKSWIWNWTFEDYWGLGLTVTVSS  |                  |     |    |
| S214 | (61) | ADSVKGRFTISRDNKNSLYLQMNSLRAEDTAIYYCAKSWIWNWTFEDYWGLGLTVTVSS  |                  |     |    |
|      |      | *                                                            |                  |     |    |
|      |      |                                                              | L1               | L2  | 55 |
| 1    |      |                                                              |                  |     |    |
| S213 | (1)  | ALTQPASVSANLGGTVEITCSGGNSNHYGWYQQKSPGSA                      | PVTLIYADTNRPSNIP |     |    |
| S214 | (1)  | ALTQPASVSANLGGTVEITCSGGNSNHYGWYQQKSPGSA                      | PVTLIYADTNRPSNIP |     |    |
|      |      |                                                              |                  |     |    |
|      |      |                                                              | L3               | 103 |    |
| 56   |      |                                                              |                  |     |    |
| S213 | (56) | SREFSGTSGSTTLTITGVQAEDEAVYCGGSSTGDGIFGAGTTLTVL               |                  |     |    |
| S214 | (56) | SREFSGTSGSTTLTITGVQAEDEAVYCGGSSTGDGIFGAGTTLTVL               |                  |     |    |
|      |      | *                                                            |                  |     |    |

FIG. 11F

>209\_VH  
DVQLVESGAVVRPGESLRLSCKASGFTFTNFAMSWVRQAPGEGLEWVSGISGSDDTTYA  
DSVKGRFTISRDNSESTLYLQMNSLRAEDTAVYYCVKDS TVSWNTFFDYWGLGLTLTVSS  
>209\_VL  
ALTQPASVSNLGGTVKITCSGGYGSDDGSSSYYGWYQQKSPGSAFVILIYWDDKRPSDIP  
SRFSGSTGTTTLTITGVQAEDEAVYFCGTYDTSSGAI FGAGTTLTVL

FIG. 11G

|      |      | <u>H1</u>                                                    | <u>H2</u> | <u>59</u> |
|------|------|--------------------------------------------------------------|-----------|-----------|
| 1    |      |                                                              |           |           |
| S123 | (1)  | DVQLVESGGGLVQPGGSLRLSCTASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY  |           |           |
| S194 | (1)  | DVQLVESGGGVVRPGESLRLSCTASGFTFRNYGMSWVRQAPGEGLEWVSASSGSGSTYY  |           |           |
|      |      | * * * *                                                      |           |           |
| 60   |      |                                                              | <u>H3</u> | 117       |
| S123 | (60) | TDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS  |           |           |
| S194 | (60) | ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCAKVTWNNFFDYWGLGTLVTVSS  |           |           |
|      |      | *                                                            |           |           |
|      |      |                                                              | <u>L1</u> | <u>L2</u> |
| S123 | (1)  | EIVLTQSPGTLSPGERVTLTCSRASQGIAGKIAWYQQKPGQAPRLLIYDASSRATGIP   |           |           |
| S194 | (1)  | EIVLAQSPDTLSVSPGERATLTCSRASQDVAGKLAWYQQKPGQAPRLLIHATSSRADGIP |           |           |
|      |      | * * *                                                        | * * *     | *         |
| 60   |      |                                                              | <u>L3</u> | 108       |
| S123 | (60) | GRFSGSGSGTEFTLTITSLQSEDFAVYYCQOHYDWSPLTFEGGGTKVEIK           |           |           |
| S194 | (60) | ARFSGSGSGTEFTLTITGLQSEDFAVYYCQOHYDWSPLTFEGGGTKVEIK           |           |           |
|      |      | *                                                            |           |           |

FIG. 11H

|      | H1                                                             | H2 | 59  |
|------|----------------------------------------------------------------|----|-----|
| 1    |                                                                |    |     |
| S161 | (1) DVQLVESGGVVRPGESLRLSCAASGFTFSNFAMTWVRQAPGKGPENVSLVSVTATTYY |    |     |
| S162 | (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTY |    |     |
| S163 | (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTY |    |     |
| S164 | (1) DVQLVESGGGLVRPGESLRLSCAASGFTFTNYAVTWVRQAPGEGLEWVSLISVTGTTY |    |     |
|      | 1                                                              | *  | *   |
|      |                                                                | *  | *   |
| 60   |                                                                |    |     |
| S161 | (60) ADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKITWNNLFDYWGLGLTVTVSS | H3 | 117 |
| S162 | (60) ADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKVTWKNVFDYWGLGLTVTVSS |    |     |
| S163 | (60) ADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKVTWKNVFDYWGLGLTVTVSS |    |     |
| S164 | (60) ADSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKVTWKNVFDYWGLGLTVTVSS |    |     |
|      | *                                                              | *  | *   |
|      |                                                                | *  | *   |
| 1    |                                                                |    |     |
| S161 | (1) EIVLTQSPGTLSPGERATLSCRASQTVGSKLAWYQQKPKGQAPRLLIYDSSSRASGIP | L1 | 59  |
| S162 | (1) EIVLTQSPGTLSPGERATLSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP |    |     |
| S163 | (1) EIVLTQSPGTLSPGERATLSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP |    |     |
| S164 | (1) EIVLTQSPGTLSPGERATLSCRASQTVGSKLAWYQQKPKGQAPRLLIYDANTRATGIP |    |     |
|      | *                                                              | *  | *   |
|      | *                                                              | *  | *   |
| 60   |                                                                |    |     |
| S161 | (60) DRFSGSGGTDFTLTISSLQSEDSAVYYCQQHNDWPPYTFGGGKVEIK           | L3 | 108 |
| S162 | (60) ARFSGSGGTEFTLTISSLQSEDFAVYYCQQHTDWPYPYTFGGGKVEIK          |    |     |
| S163 | (60) ARFSGSGGTEFTLTISSLQSEDFAVYYCQQHTDWPYPYTFGGGKVEIK          |    |     |
| S164 | (60) ARFSGSRSGTEFTLTISSLQSEDFAVYYCQQHTDWPYPYTFGGGKVEIK         |    |     |
|      | *                                                              | *  | *   |
|      | *                                                              | *  | *   |

FIG. 11I

>S149\_VH  
DVQLVESGGVVRPGEISRLSCAASGFTFSNFAMNWVRQAPGEGLEWVSLISVTATTYYA  
DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVTWNNLFDYWGLGLTLVTVSS  
>S149\_VL  
EIVLTQSPGTLSLSPGERATLSCRASQPIDSYLAWYQQKPGQAPRLLIYNTVTRATGIPD  
RFSGSGSGTDFTLTINRLEPEDFAVYYCQHQQHQQYDWPPIYIFGGGTKVEIK

>S218\_VH  
DVQLVESGGVVRPGEISLTLSCTASGFTFTSSTMNWVRQAPGEGLDWVSSISTSGVITYY  
ADSVKGRATISRDNSKNTLYLRLFLSLRADDTAIYYCATDTEFDHWGPGTLVTVSS  
>S218\_VL  
ALTQPASVSANGETVKITCFGSSGNYGWFQQKSPGSAPVTVIHYYNNKRPSDIPSRFSGS  
KSGSTGTLTITGVRAEDEAVYFCGAWETGSATFGAGTTLTVL

ע"פ

|      | 1   | H1                                                          | H2 | 61 |
|------|-----|-------------------------------------------------------------|----|----|
| 1119 | (1) | DVQLLESGGVVQPCGSLRLSCAASGFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS  |    |    |
| 1120 | (1) | DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS |    |    |
| 1121 | (1) | DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS |    |    |
| 1122 | (1) | DVQLVESGGGVVQPCGSLRLSCAASGFSNFAMTWVRQAPGEGLEWVSTIGSGDTYYADS |    |    |

|      |      |                                                               |     |
|------|------|---------------------------------------------------------------|-----|
|      |      | H3                                                            | 120 |
|      |      | <u>62</u>                                                     |     |
| 1119 | (61) | VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDSTVSWSGDEFDYWGLGTLVTVSS |     |
| 1120 | (61) | VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDSTVSWSGDEFDYWGLGTRVTVSS |     |
| 1121 | (61) | VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDSTVSWSGDEFDYWGLGTLVTVSS |     |
| 1122 | (61) | VKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDSTVSWSGDEFDYWGLGTLVTVSS | *   |

FIG. 11J (cont'd)

|     |      | L1                                                     |    | L2 | 54  |
|-----|------|--------------------------------------------------------|----|----|-----|
| 119 | (1)  | EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR |    |    |     |
| 120 | (1)  | EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR |    |    |     |
| 121 | (1)  | EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR |    |    |     |
| 122 | (1)  | EIVLTQSPATLSVSPGERATFSCRASQNVKNDLAWYQQRPQQAPRLLIYAARIR |    |    |     |
|     |      |                                                        |    |    |     |
|     |      |                                                        | L3 |    | 108 |
| 119 | (55) | ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP                |    |    |     |
| 120 | (55) | ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP                |    |    |     |
| 121 | (55) | ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP                |    |    |     |
| 122 | (55) | ETGIPERFSGSGTEFTLTITSLQSEDFAVYYCQQYYDWP                |    |    |     |

- ▬ A1 = High affinity SIRPa (100nM)
- ▬ A2 = High affinity SIRPa (100nM) + 20nM CD47
- ▬ A3 = High affinity SIRPa (100nM) + 55nM CD47
- ▬ A4 = High affinity SIRPa (100nM) + 500 nM CD47
- ▬ A5 = High affinity SIRPa (100nM) + 1500 nM CD47
- ▬ A6 = PBST

FIG. 12A

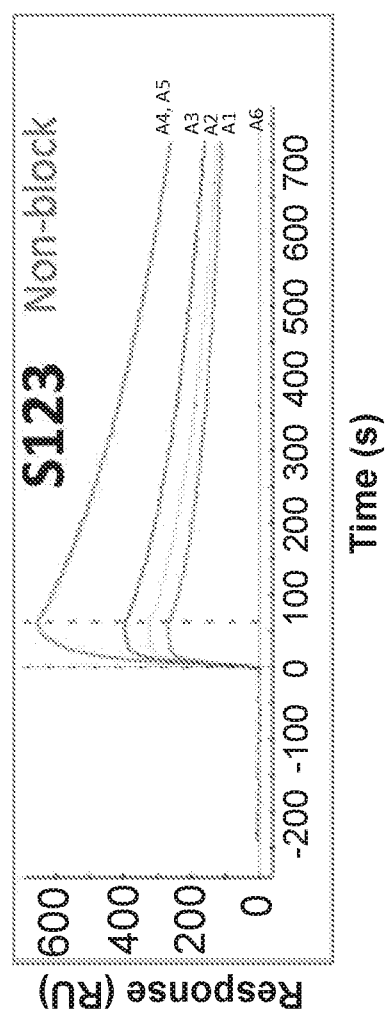
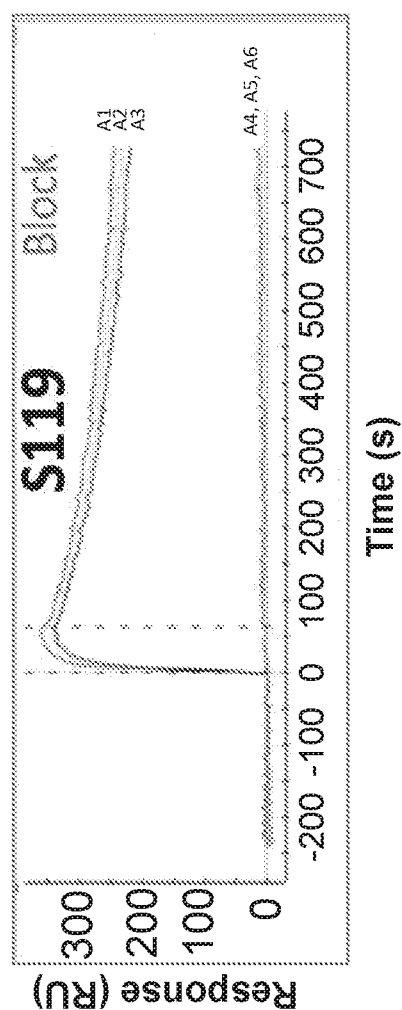


FIG. 12B

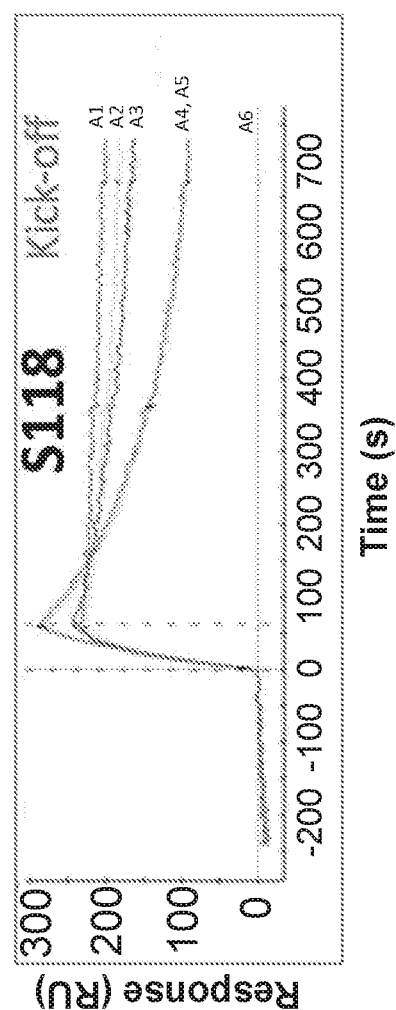


FIG. 12C

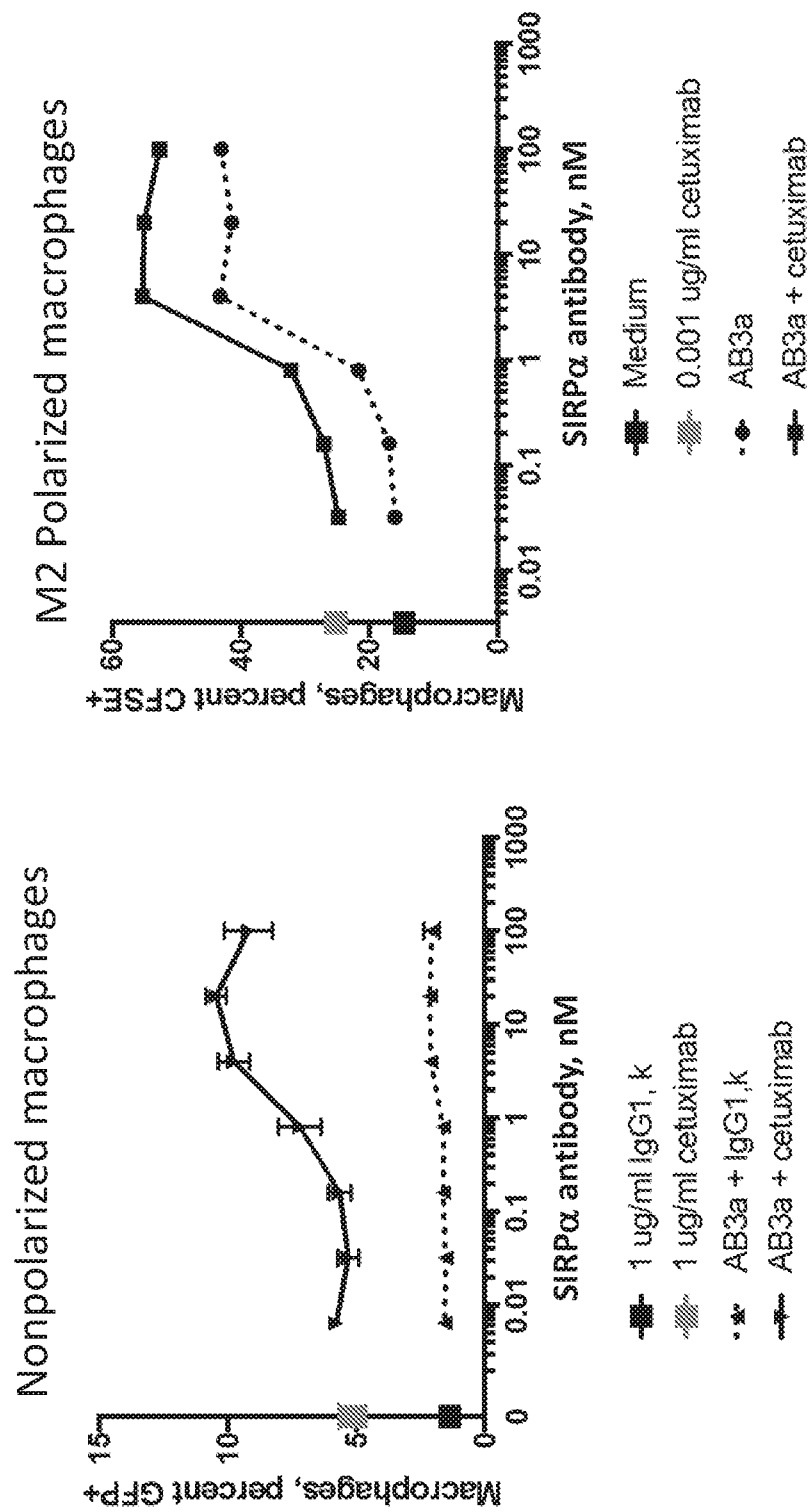


FIG. 13A

FIG. 13B

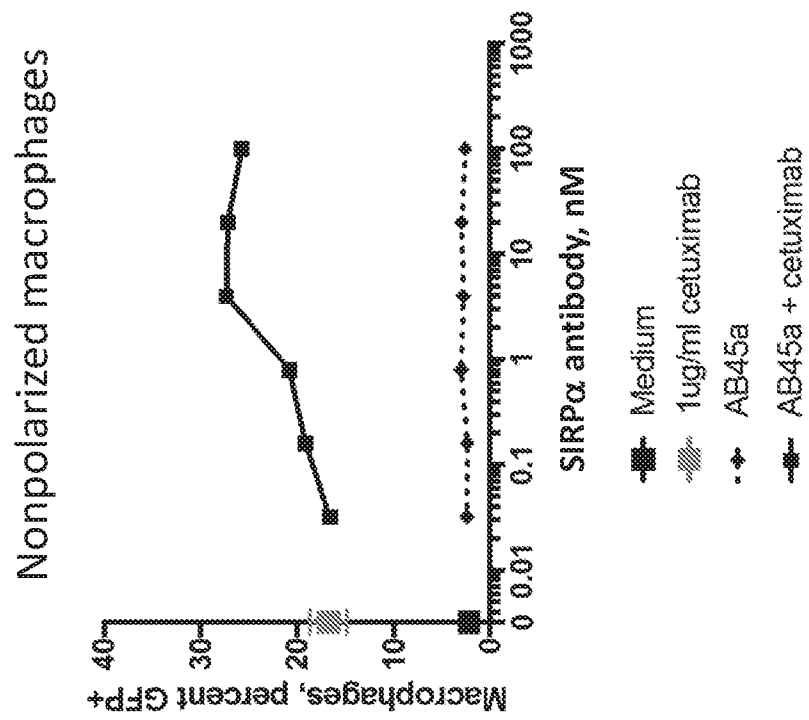


FIG. 13C

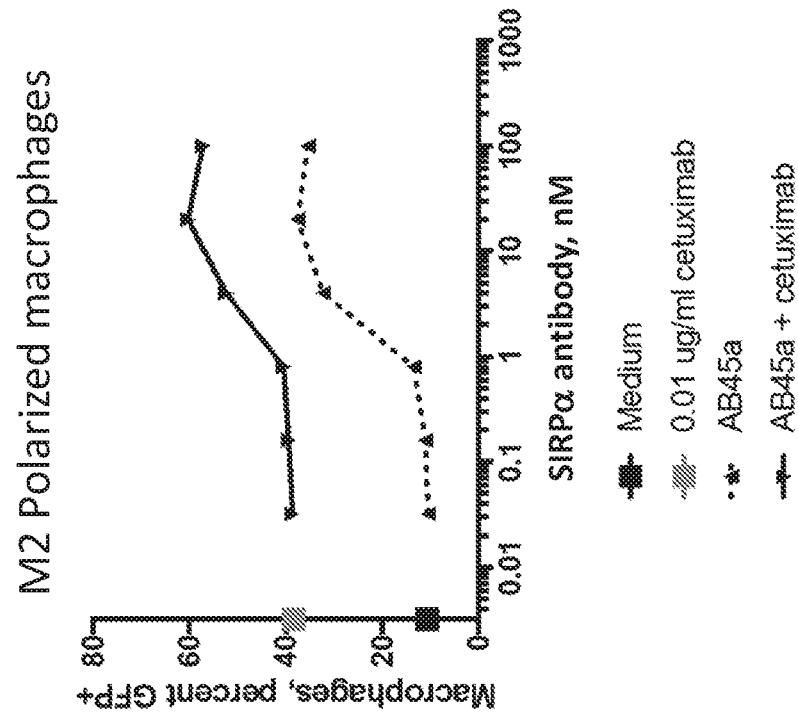


FIG. 13D

OE19 cells – Nonpolarized  
macrophages

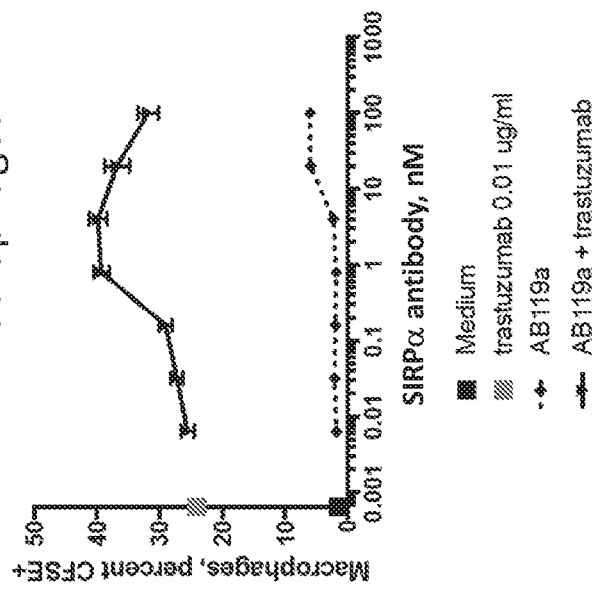


FIG. 13E

OE19 cells – Nonpolarized  
macrophages

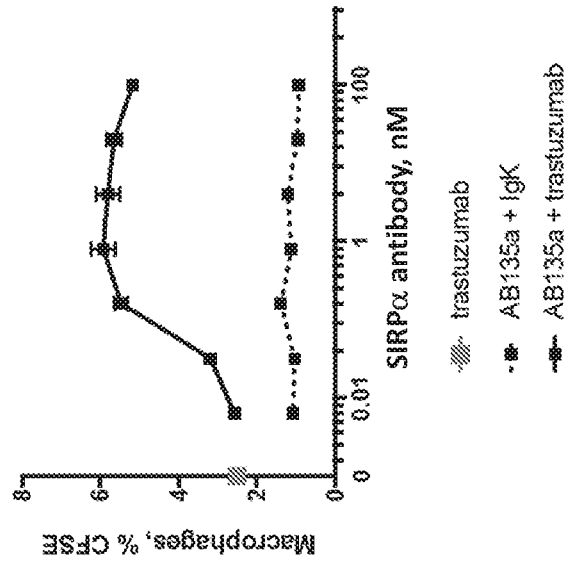


FIG. 13F

DLD-1 cells – M2  
polarized macrophages

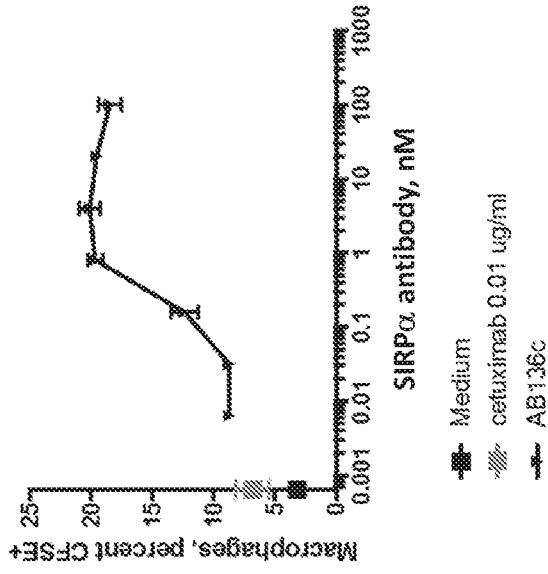
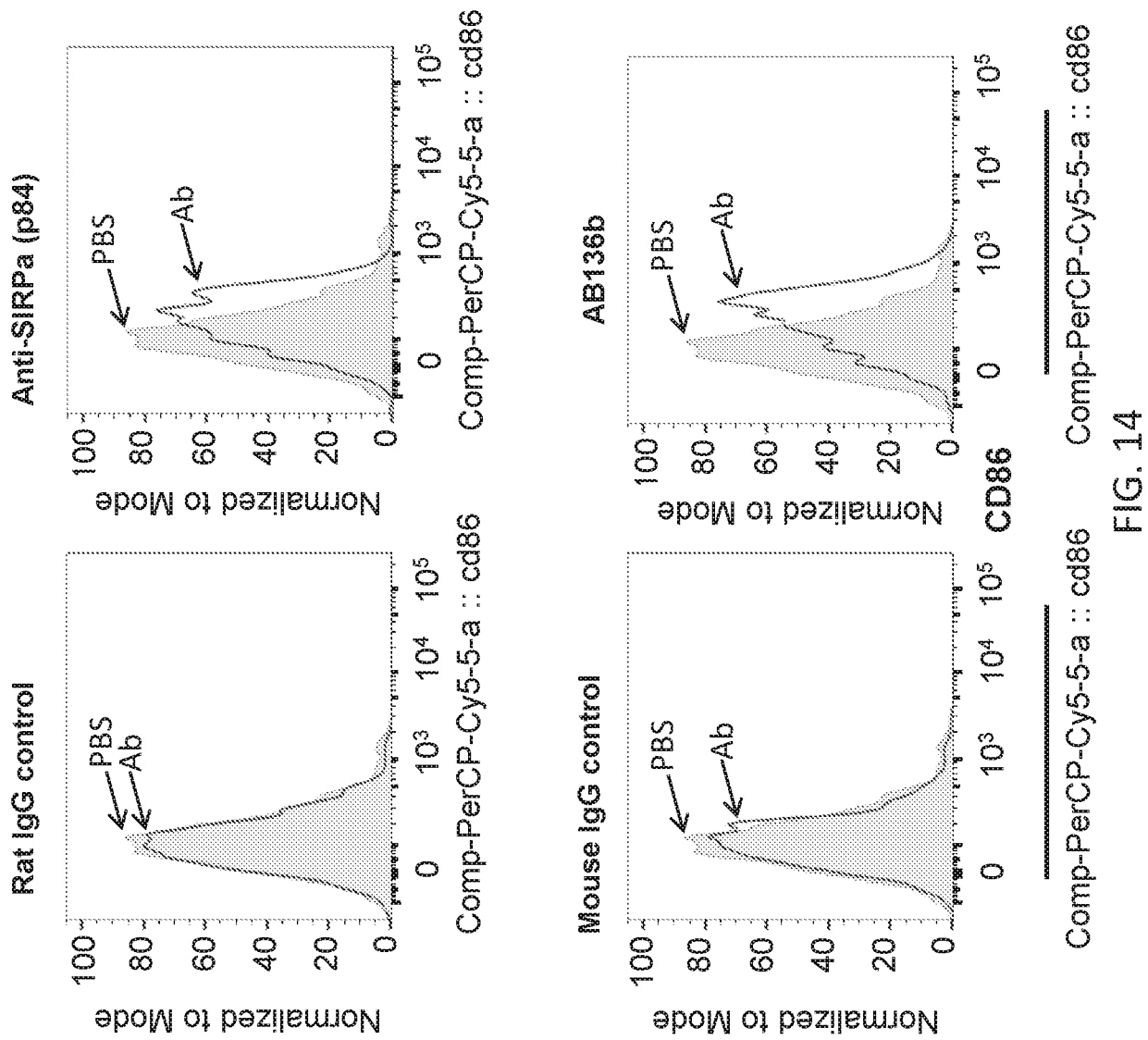
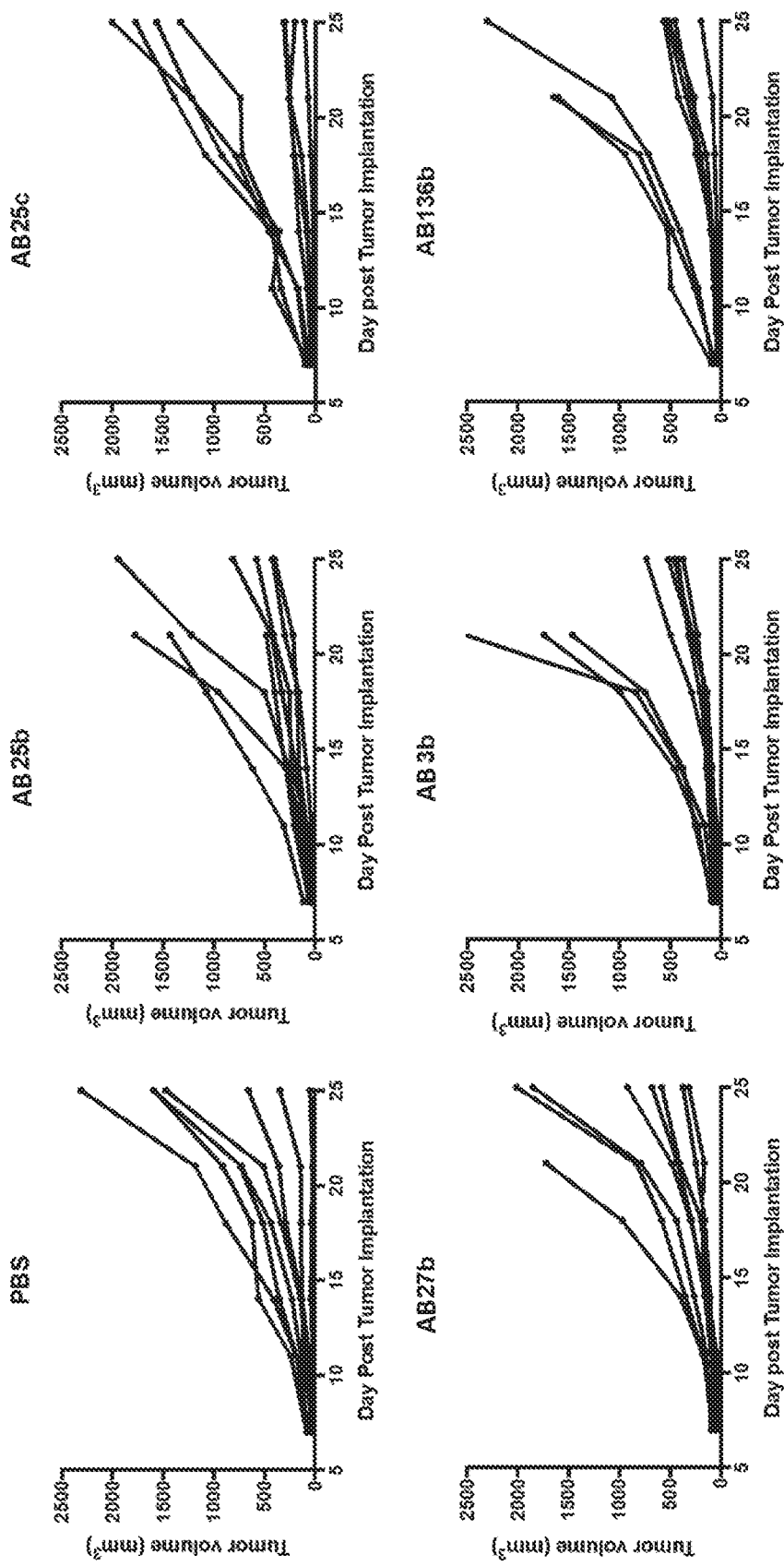


FIG. 13G





|                                             | PBS | AB25b | AB25c | AB27b | AB3b | AB136b |
|---------------------------------------------|-----|-------|-------|-------|------|--------|
| Mice with tumor volume <600 mm <sup>3</sup> | 2   | 3     | 4     | 3     | 4    | 5      |

FIG. 15

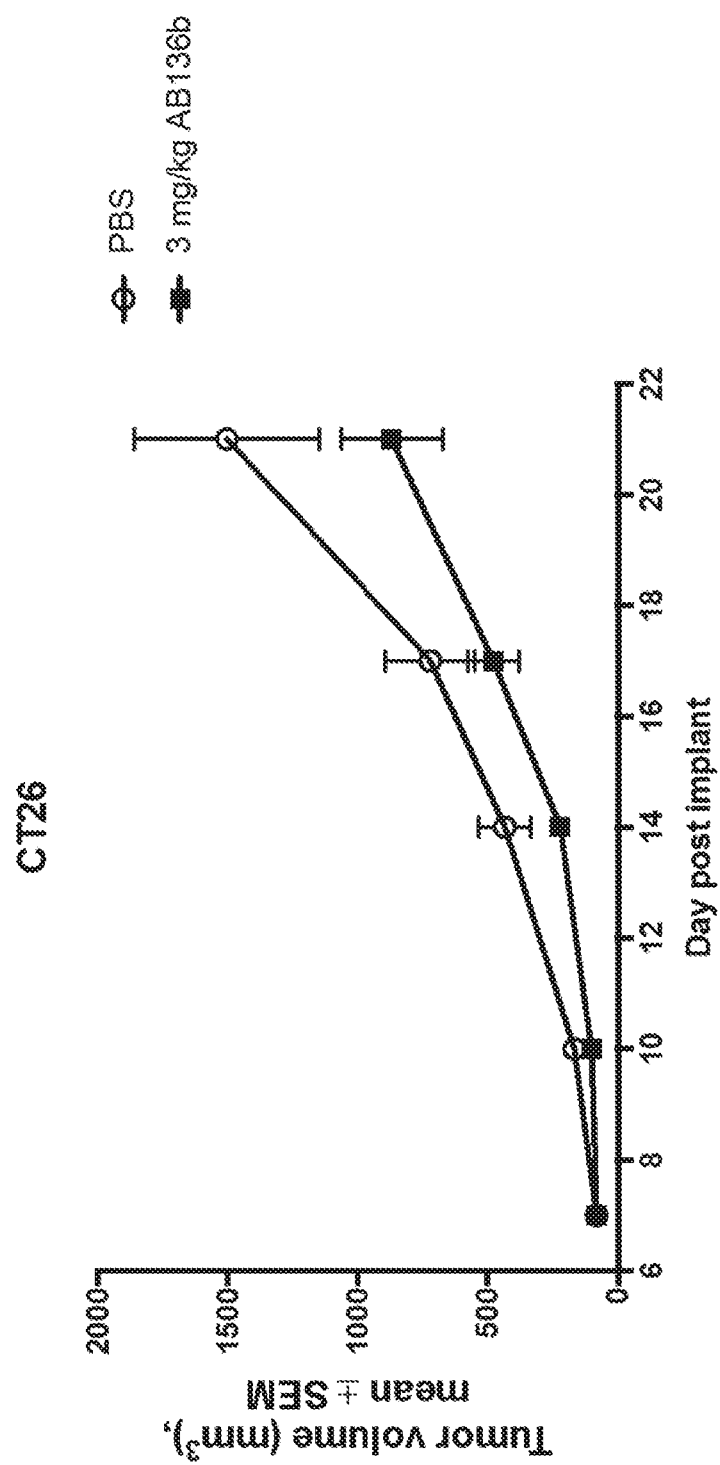


FIG. 16

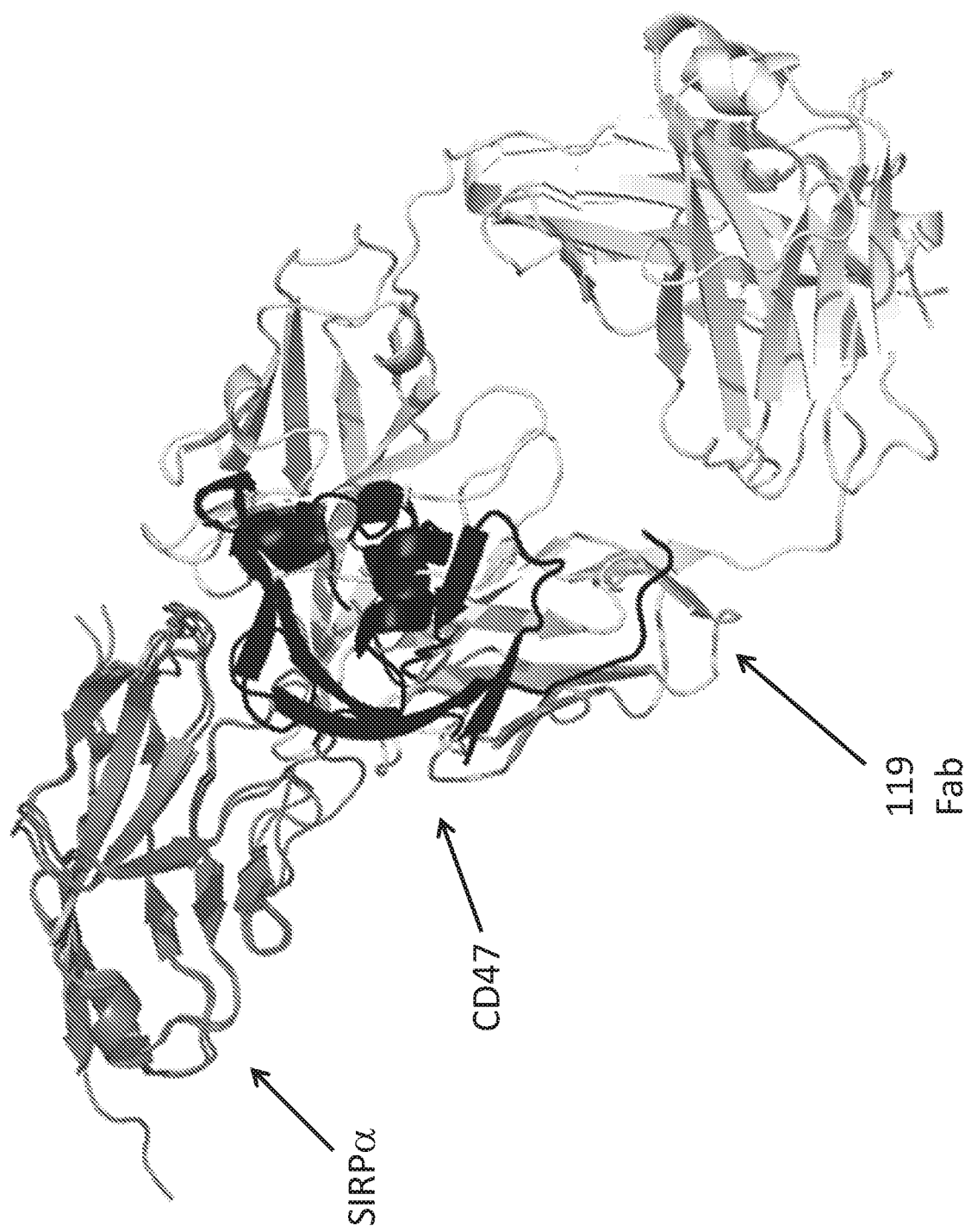


FIG. 17A

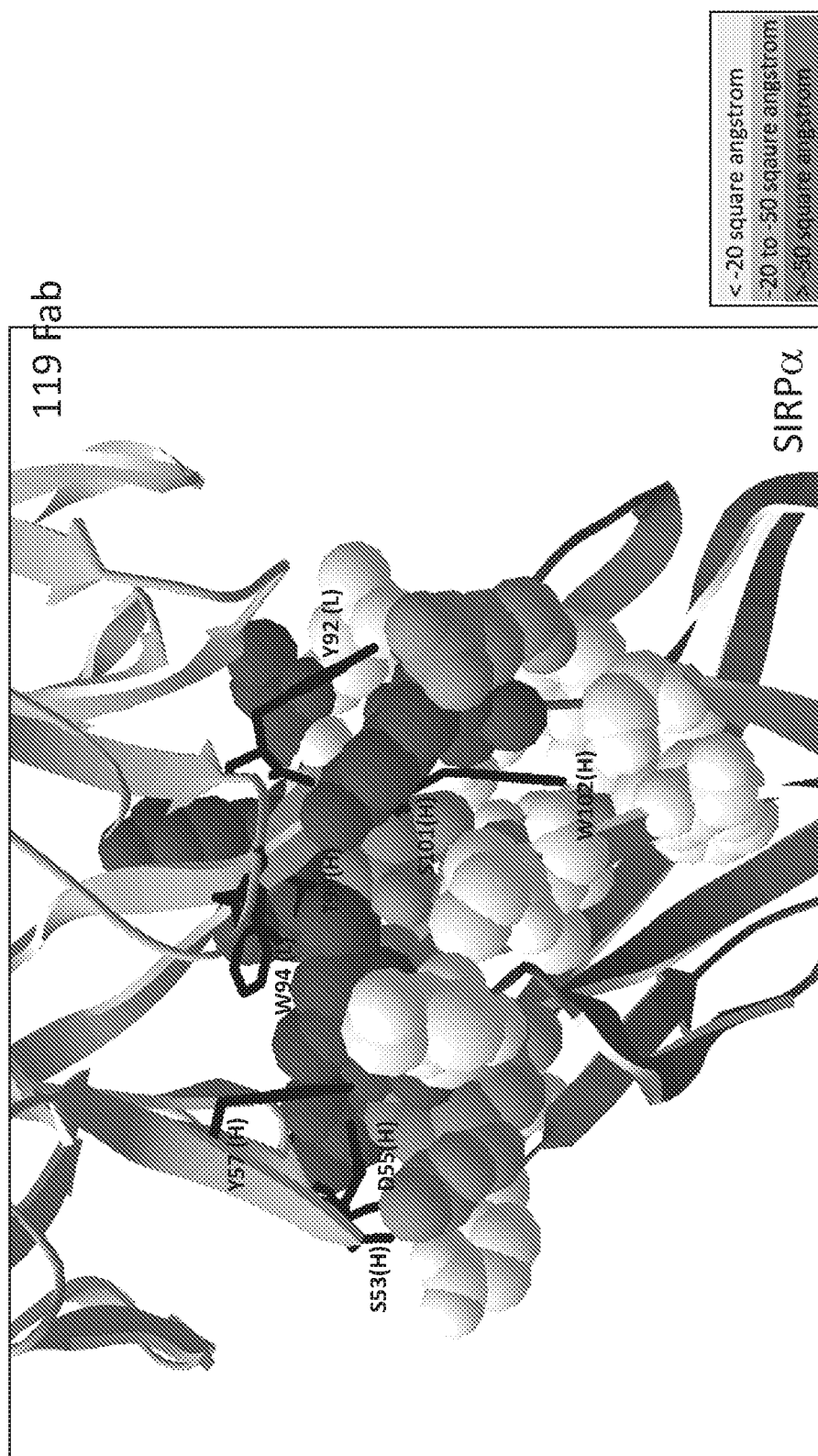


FIG. 17B

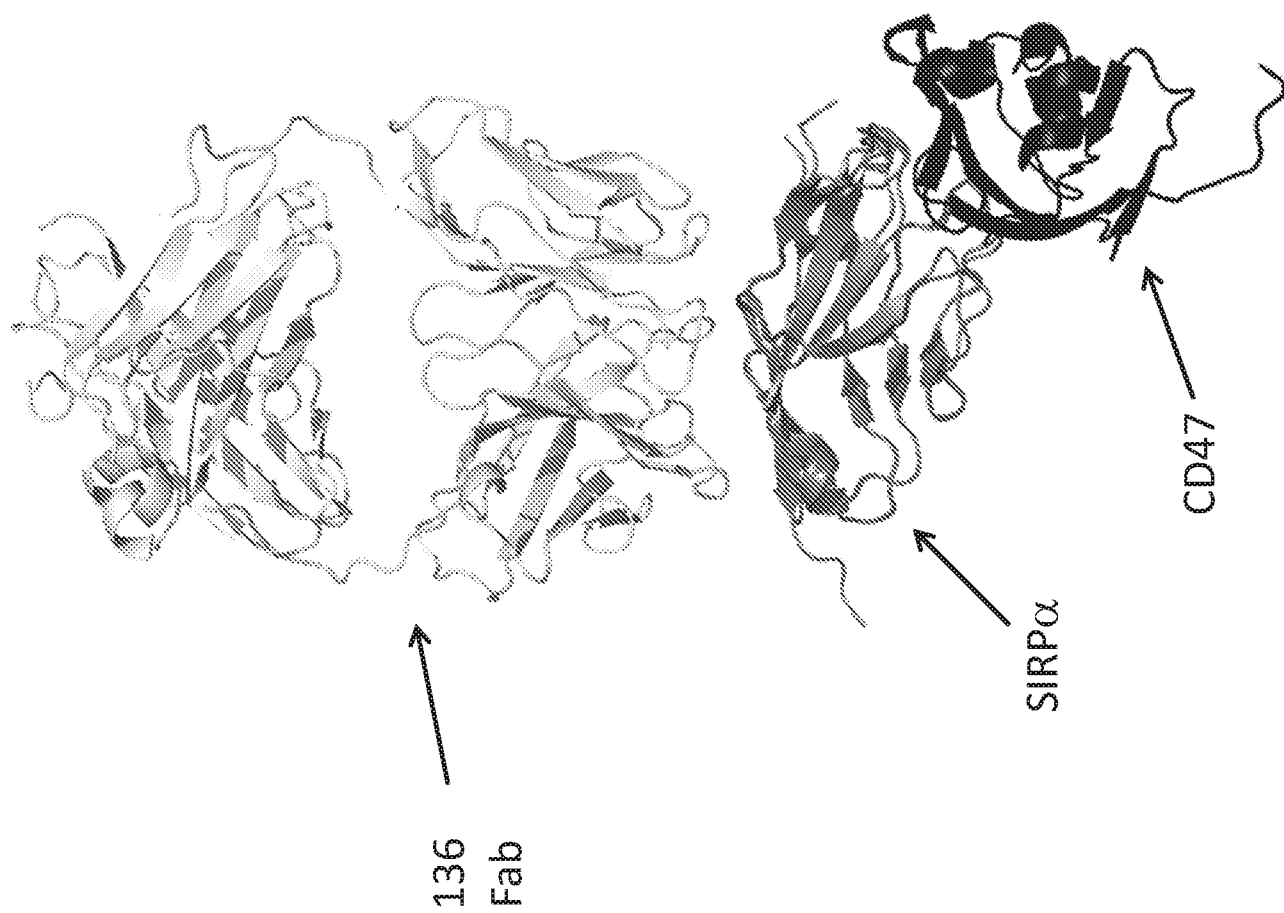


FIG. 18A

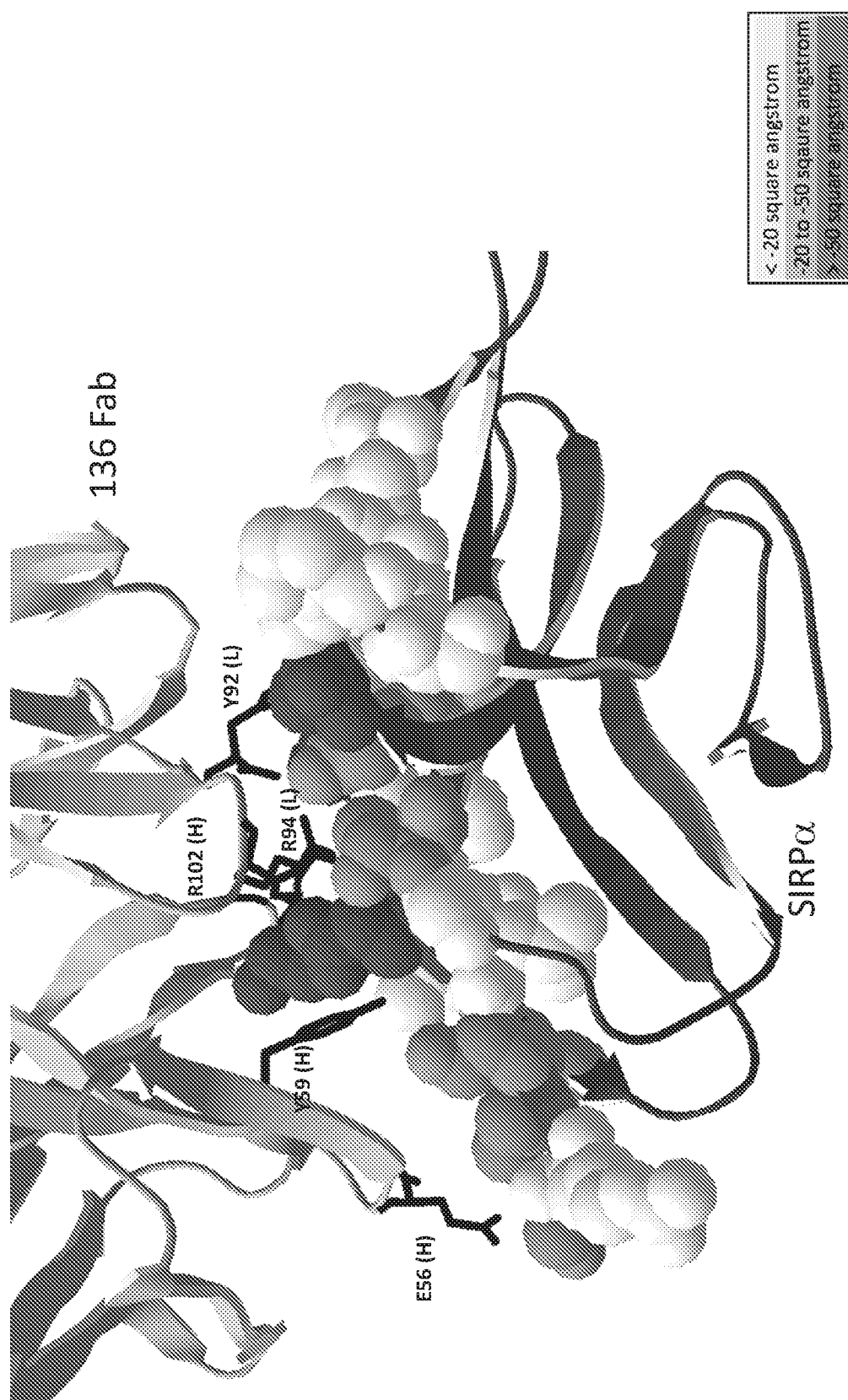


FIG. 18B

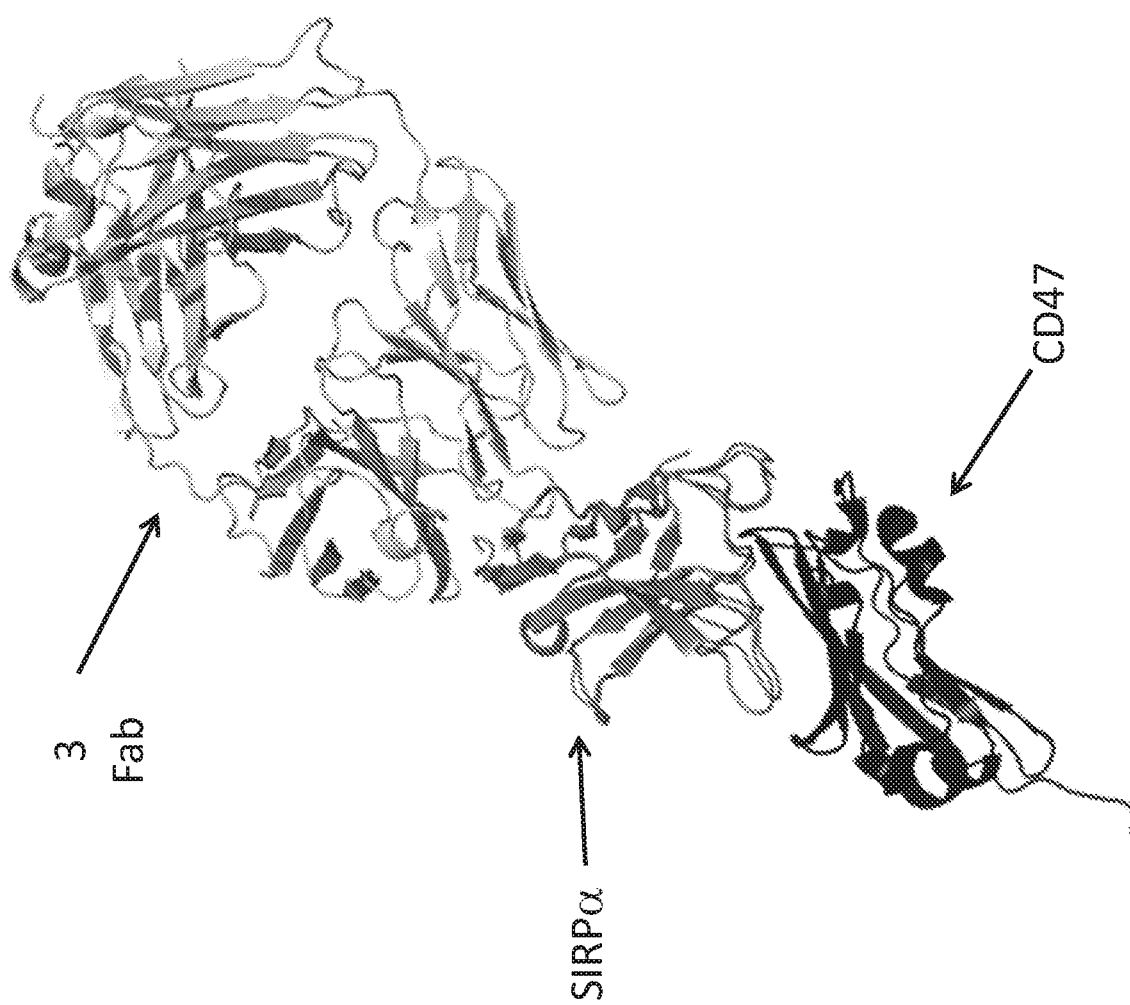


FIG. 19A

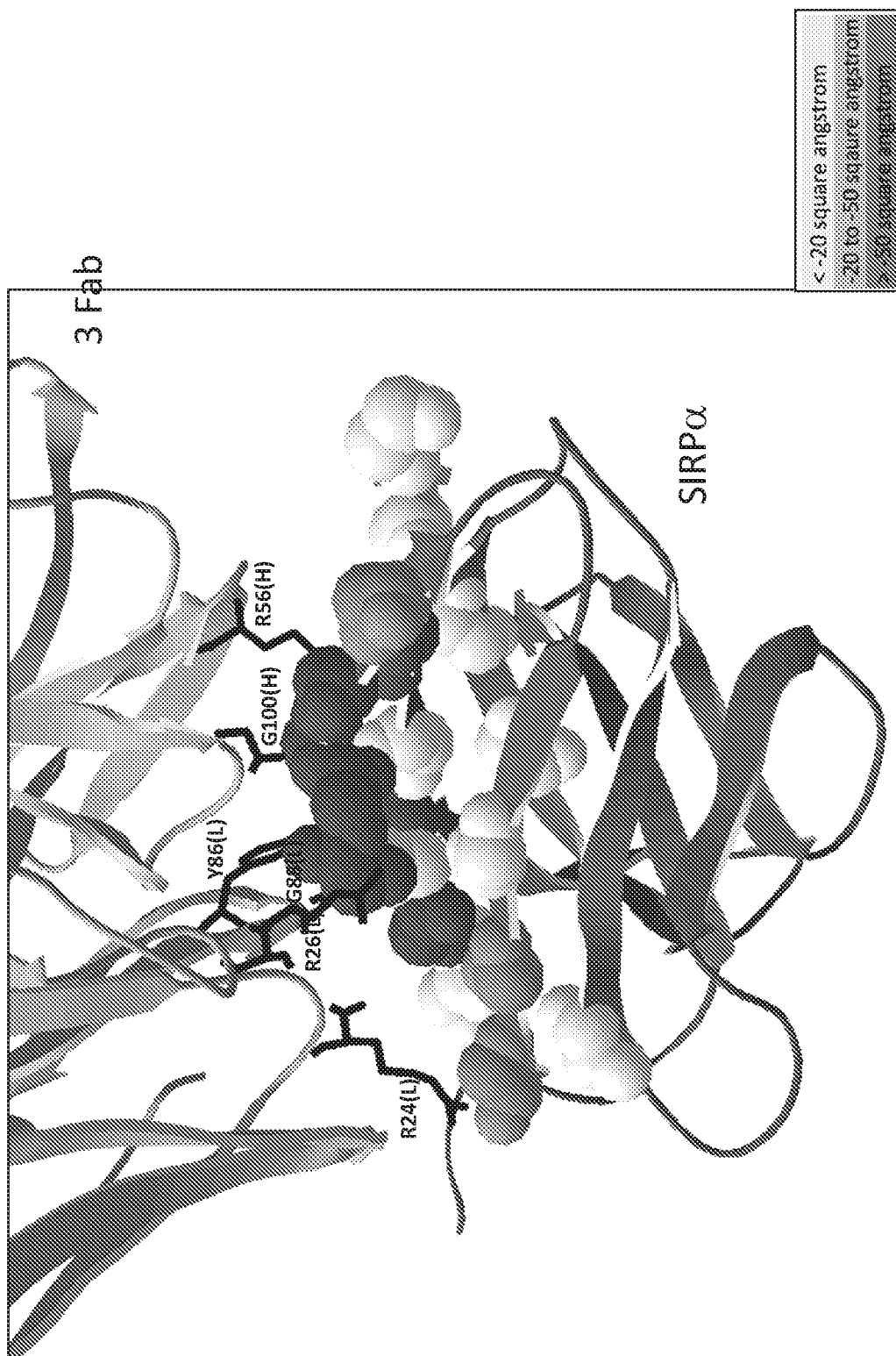


FIG. 19B

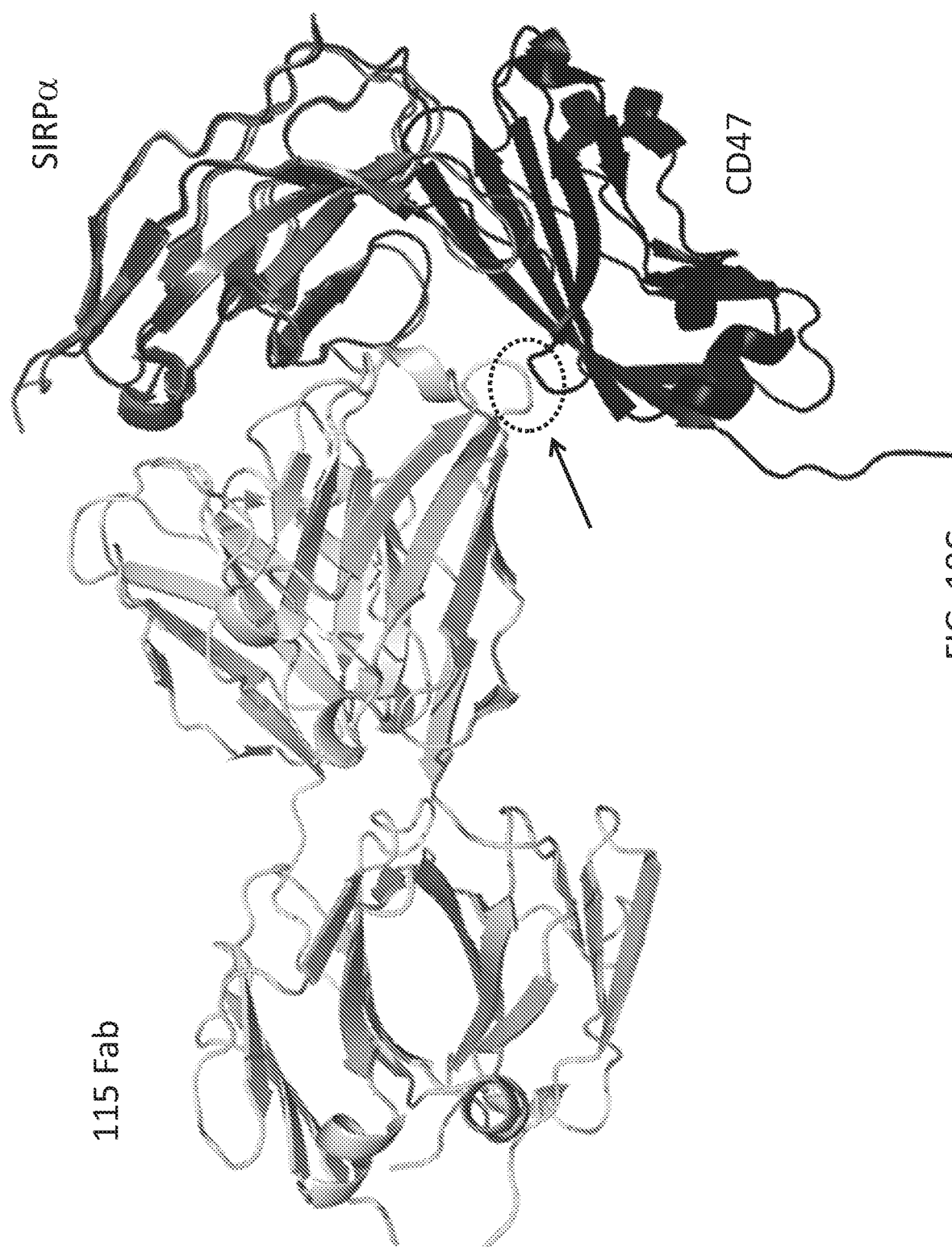


FIG. 19C

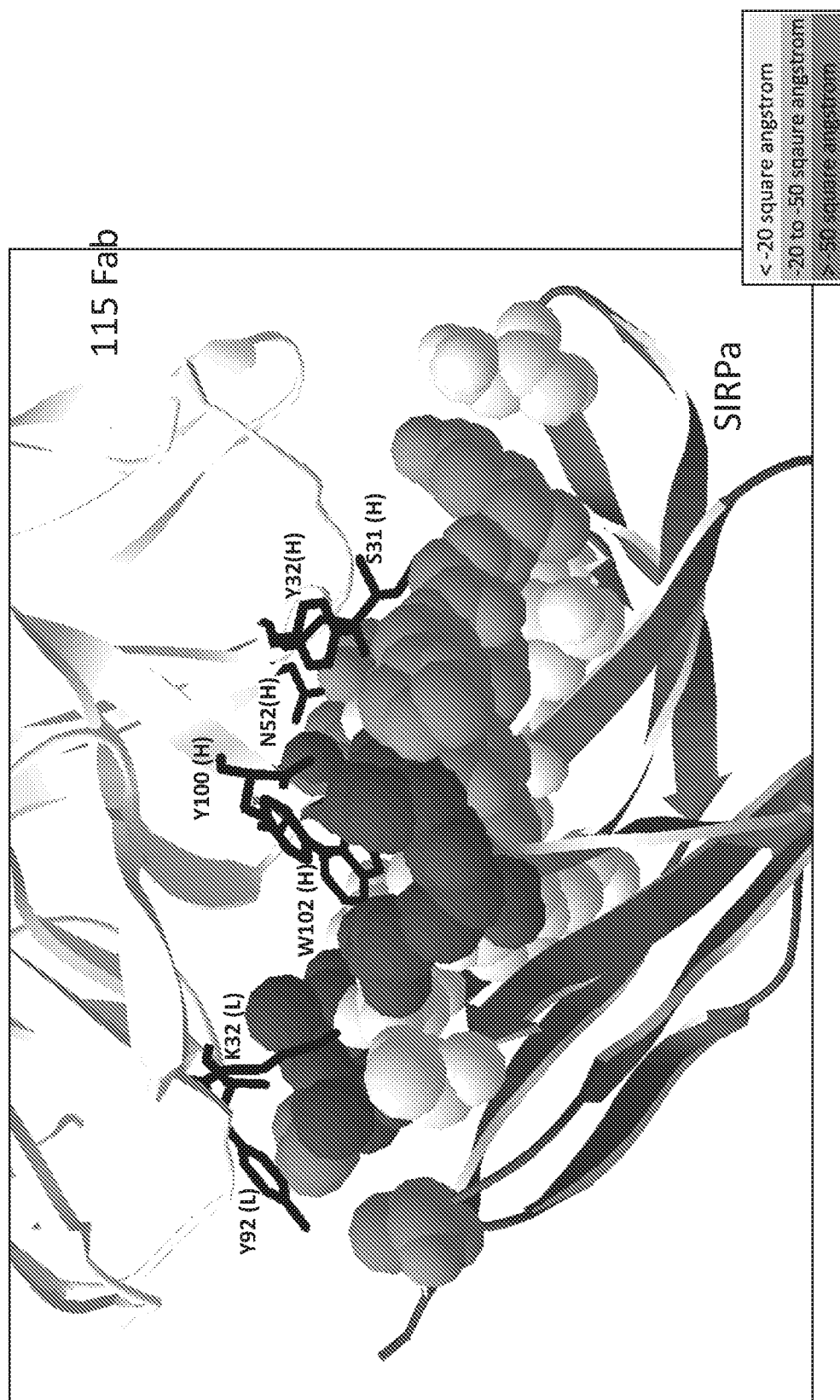


FIG. 19D

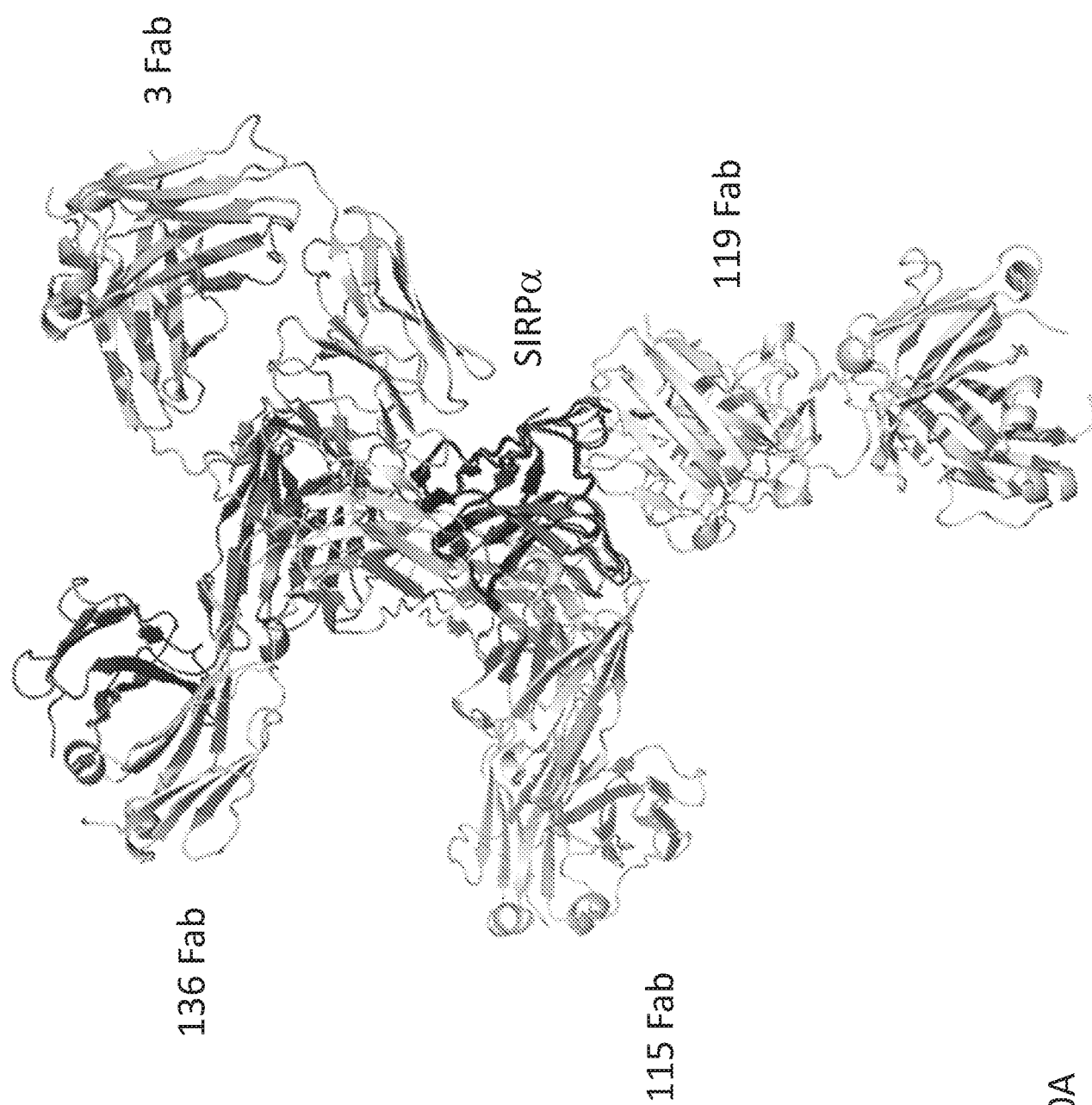


FIG. 20A

FIG. 20B

< -20 square angstrom  
 -20 to -50 square 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           | -7.2          |                 |
| 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 square 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             |                                       |                 |                 |               | -69             |

FIG. 20B (cont.'d)

< -20 square angstrom  
 -20 to -50 square 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 square 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           |               |                 |

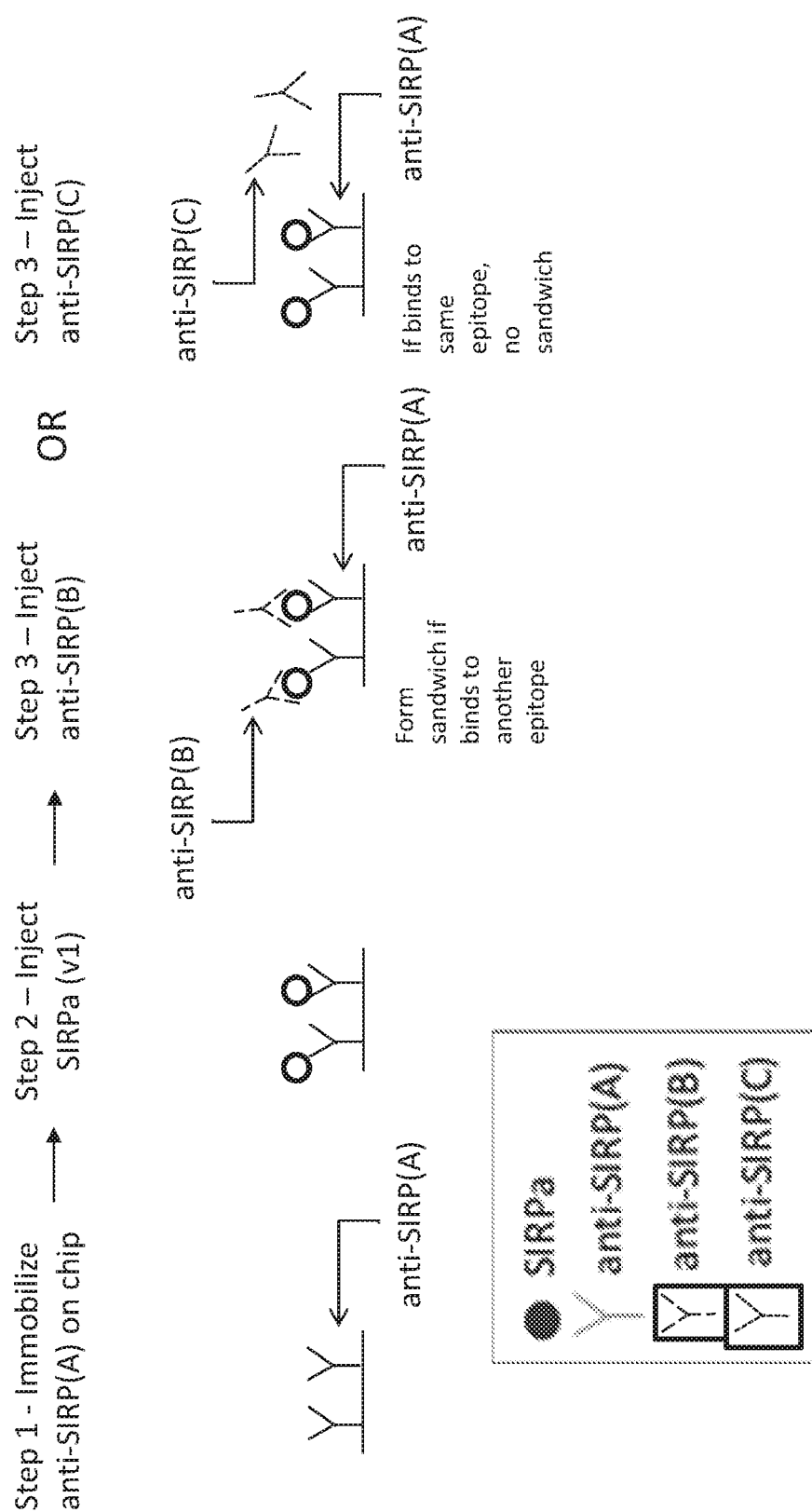


FIG. 21A

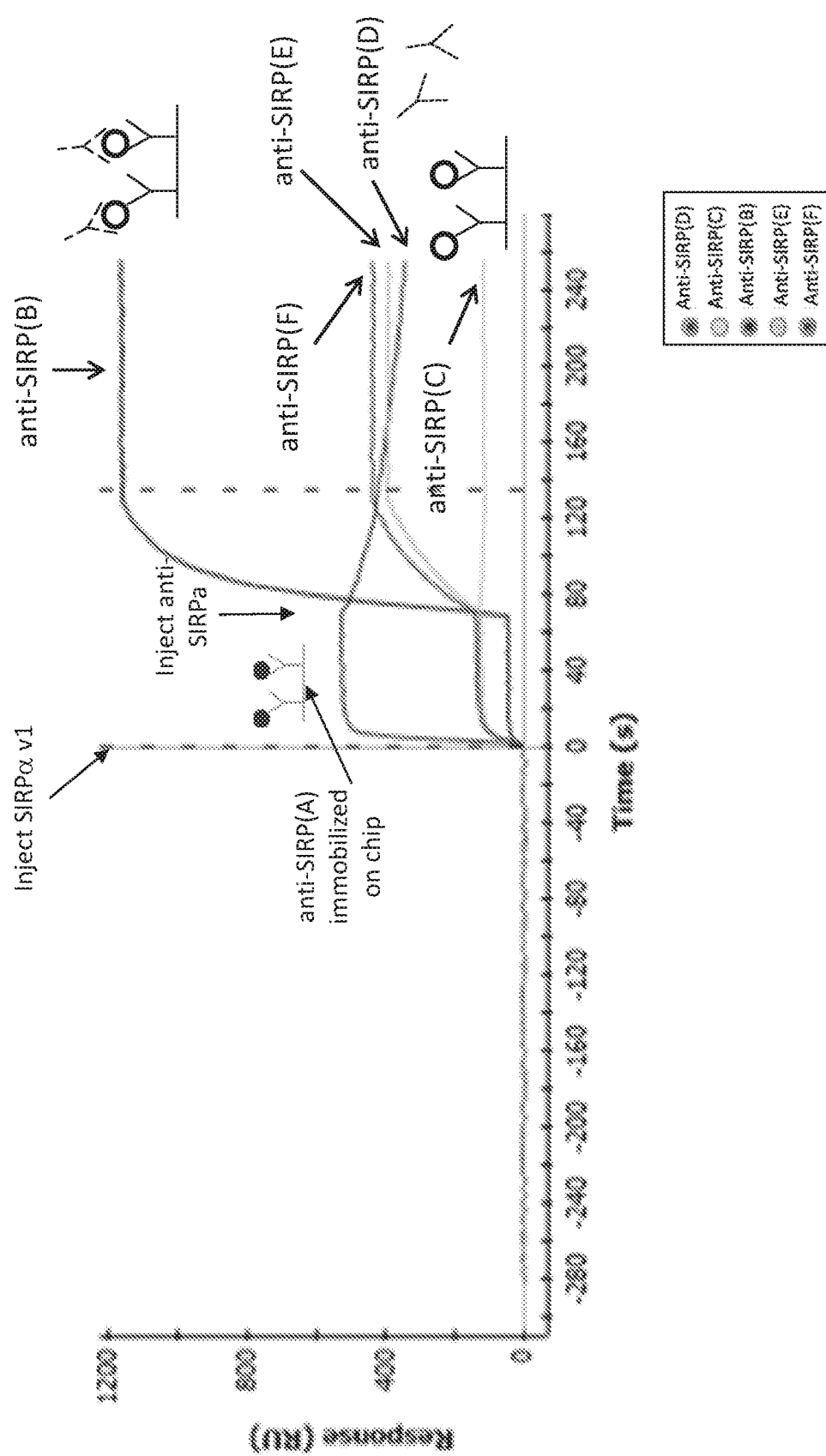


FIG. 21B

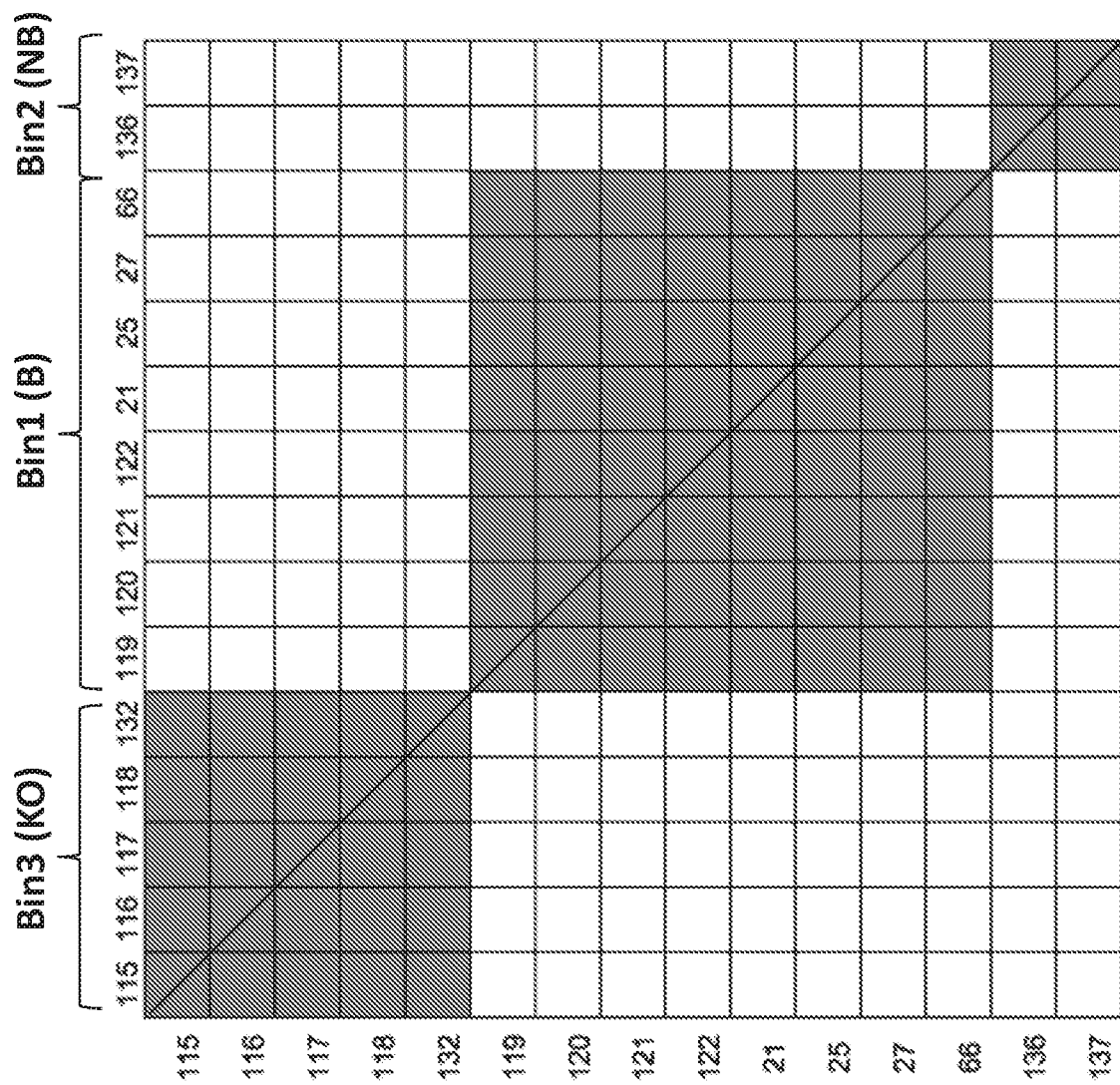


FIG. 22A

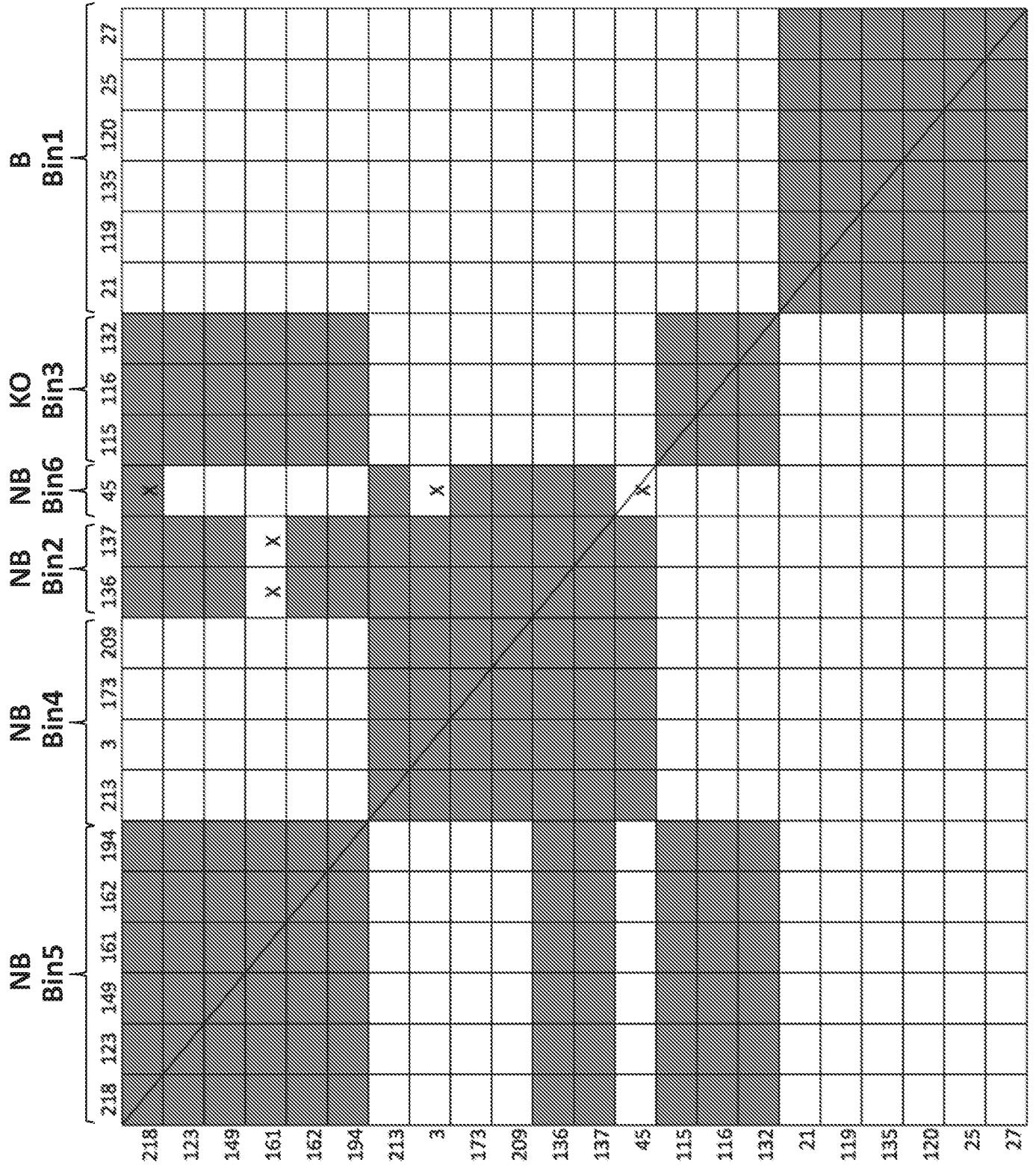


FIG. 22B

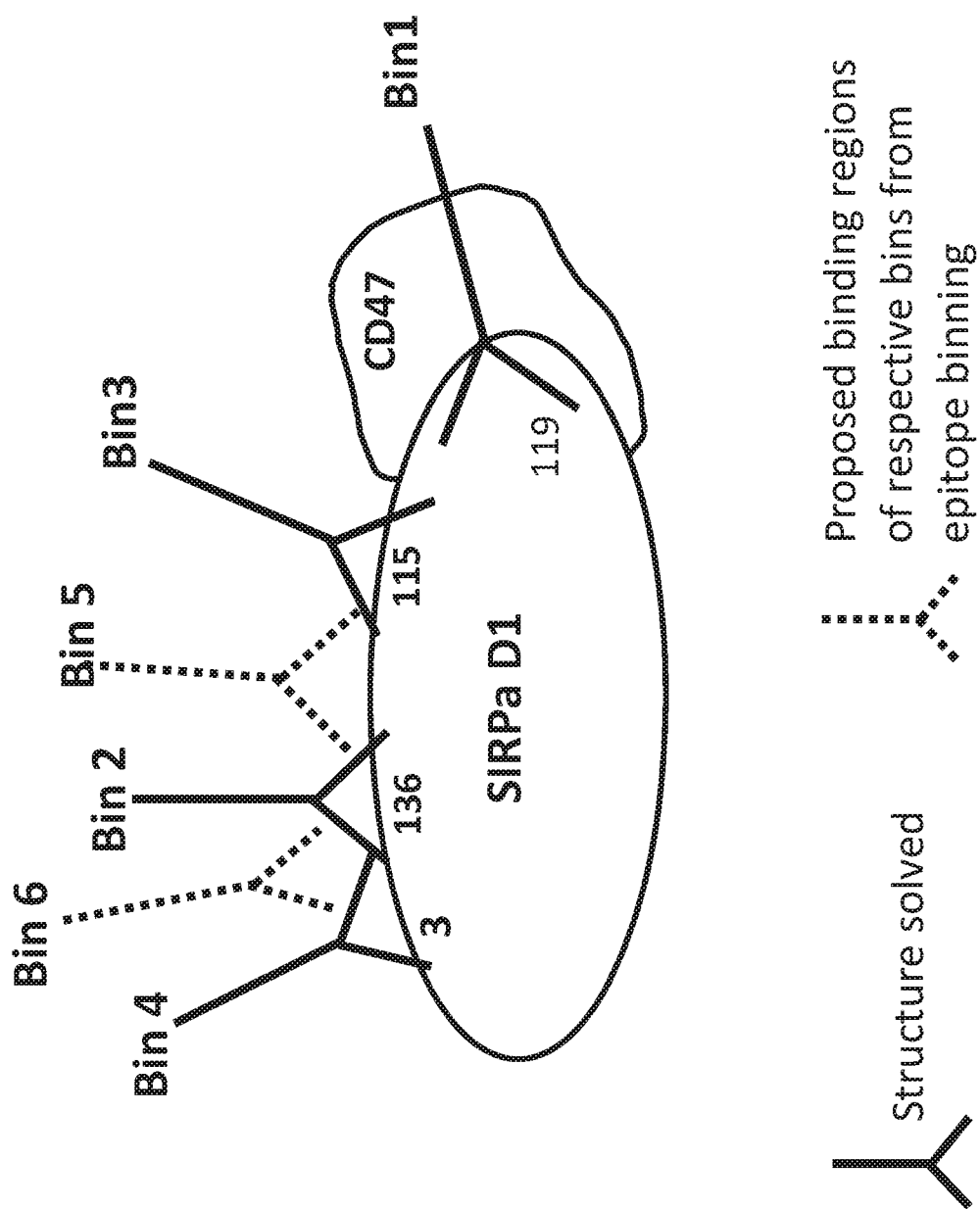


FIG. 23







|    |                    |      | H1                                               | 40  |
|----|--------------------|------|--------------------------------------------------|-----|
| 1  |                    |      |                                                  |     |
|    | 135_VH_wt          | (1)  | DVQLVESGGGVVRPGESLRLSCAASGFSFIYAMSWVRQA          |     |
|    | 135_VH_MutAll      | (1)  | EVQLVESGGGVVQPGGSLRLSCAASGFSFIYAVSWVRQA          |     |
|    | 135_VH_MutAll_V34M | (1)  | EVQLVESGGGVVQPGGSLRLSCAASGFSFIYAMSWVRQA          |     |
|    | 135_VH_MutAll_V34L | (1)  | EVQLVESGGGVVQPGGSLRLSCAASGFSFIYALSWVRQA          |     |
|    |                    | *    | *                                                | *   |
| 41 |                    |      |                                                  | 80  |
|    | 135_VH_wt          | (41) | PGEGLWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ         |     |
|    | 135_VH_MutAll      | (41) | PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ        |     |
|    | 135_VH_MutAll_V34M | (41) | PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ        |     |
|    | 135_VH_MutAll_V34L | (41) | PGKGLEWVSTIGADDTYYADSVKGRFTISRDN SKNTLYLQ        |     |
|    |                    | *    |                                                  |     |
| 81 |                    |      |                                                  | 120 |
|    | 135_VH_wt          | (81) | MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> GLTLVTVSS |     |
|    | 135_VH_MutAll      | (81) | MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> GLTLVTVSS |     |
|    | 135_VH_MutAll_V34M | (81) | MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> GLTLVTVSS |     |
|    | 135_VH_MutAll_V34L | (81) | MNSLRAEDTAVYCAKDS <u>TVGWSGDFFDYWG</u> GLTLVTVSS |     |
|    |                    | *    |                                                  |     |

FIG. 25B





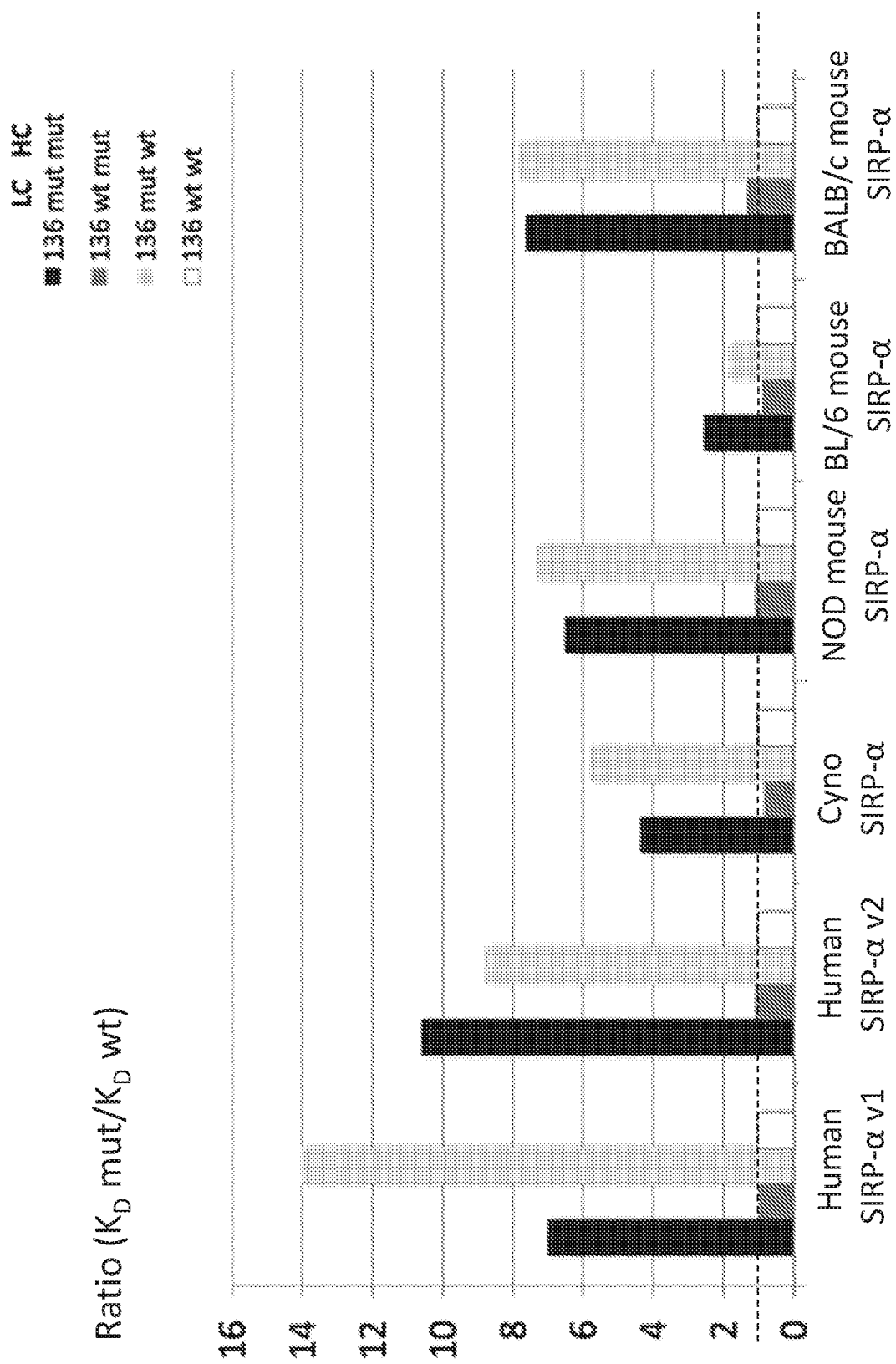
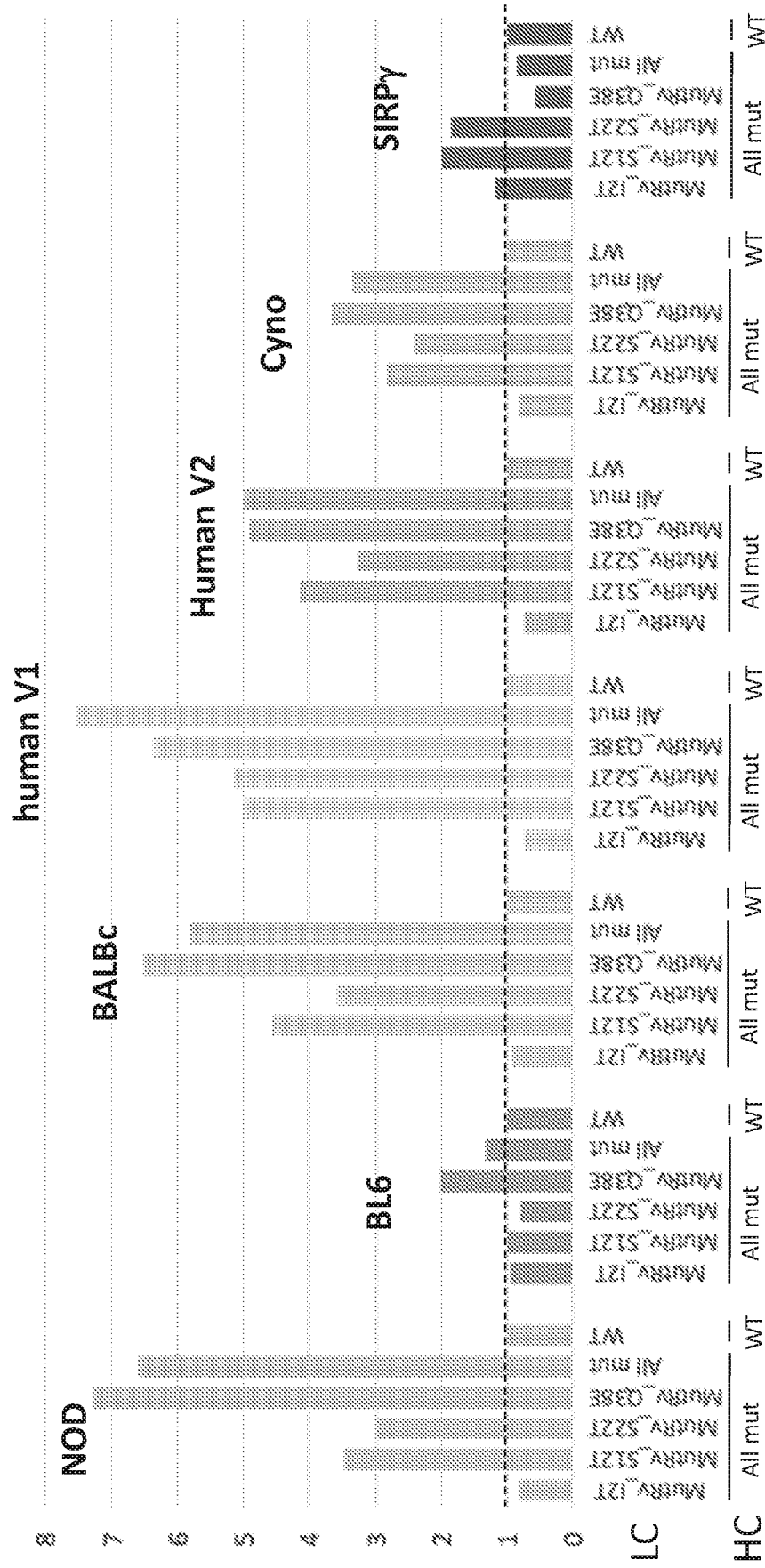


FIG. 27A



|                 | AB21_Heavy Chain |       |       |       |       |       |       |       |       |       | AB25_heavy chain |       |       |       |       |       |       |       |       |       | AB27 Heavy Chain |       |       |       |       |       |       |       |       |       | AB66 Heavy Chain |       |       |       |       |  |  |  |  |  |
|-----------------|------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|--|--|--|--|--|
|                 | 25               | 25    | 66    | 66    | 25    | 25    | 25    | 25    | 66    | 66    | 25               | 25    | 25    | 66    | 66    | 25    | 25    | 25    | 66    | 66    | 25               | 25    | 25    | 66    | 66    | 25    | 25    | 25    | 66    | 66    | 25               | 25    | 25    | 66    | 66    |  |  |  |  |  |
|                 | IGLV3            | IGLV1 | IGLV3 | IGLV1 | IGLV2 | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3            | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3            | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3 | IGLV1 | IGLV3            | IGLV1 | IGLV3 | IGLV1 | IGLV3 |  |  |  |  |  |
| Parental VL     |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |  |  |  |  |  |
| Human framework |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |       |       |       |       |       |                  |       |       |       |       |  |  |  |  |  |
| 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

Protein Yield (mg/mL)      Binding affinity (Koff 1/s)

"+" – no change      • No change

"-" – reduced expression      • Reduced by 1-2log

FIG. 28

|      |      | <u>L1</u>                                                | <u>L2</u> | <u>54</u>  |
|------|------|----------------------------------------------------------|-----------|------------|
| Hum1 | (1)  | SYELTQPPSVSVSPGQTARITCSGGSSSSYYYAWYQQKPGQAPVTLIYSDDKRP   |           |            |
| Hum8 | (1)  | SYELTQPPSVSVSPGQTARITCSGGAYSSSSYYYAWYQQKPGQAPVLVIYSDSKRP |           |            |
| hum9 | (1)  | SYELTQPPSVSVSPGQTARITCSGGAYSSSSYYYAWYQQKPGQAPVLVIYSDDKRP |           |            |
|      |      | *                                                        | **        | *          |
|      |      |                                                          |           |            |
|      |      |                                                          | <u>L3</u> | <u>108</u> |
| Hum1 | (55) | SNIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL     |           |            |
| Hum8 | (55) | SGIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL     |           |            |
| hum9 | (55) | SGIPERFSGSSSGTTVTLTISGVQAEDEADYCGGYDQSSYTNPFGGGKLTVL     |           |            |
|      |      | *                                                        |           |            |

FIG. 29

|                     | 1   | H1             | 40                    |
|---------------------|-----|----------------|-----------------------|
| AB21_HC_MutA11      | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAMS |
| AB21_HC_MutA11_M34V | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAV  |
| AB21_HC_MutA11_M34L | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAL  |
| AB27_HC_MutA11      | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFRFSSYAM  |
| AB27_HC_MutA11_M34V | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFRFSSYAV  |
| AB27_HC_MutA11_M34L | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFRFSSYAL  |
| AB25_HC_MutA11      | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAMS |
| AB25_HC_MutA11_M34V | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAV  |
| AB25_HC_MutA11_M34L | (1) | EVQLVESGGGVVQP | GGSLRLSCAASGFTFSSNAL  |

|                     | 41   | H2                      | 80           |
|---------------------|------|-------------------------|--------------|
| AB21_HC_MutA11      | (41) | PKGLEWVAGISAGGSDTYYPASV | KGRFTISRDN   |
| AB21_HC_MutA11_M34V | (41) | PKGLEWVAGISAGGSDTYYPASV | KGRFTISRDN   |
| AB21_HC_MutA11_M34L | (41) | PKGLEWVAGISAGGSDTYYPASV | KGRFTISRDN   |
| AB27_HC_MutA11      | (41) | PKGLEWVSGISSG-GDTYYVD   | SVKGRFTISRDN |
| AB27_HC_MutA11_M34V | (41) | PKGLEWVSGISSG-GDTYYVD   | SVKGRFTISRDN |
| AB27_HC_MutA11_M34L | (41) | PKGLEWVSGISSG-GDTYYVD   | SVKGRFTISRDN |
| AB25_HC_MutA11      | (41) | PKGLEWVAGISSG-SDTYYGDS  | VKGRFTISRDN  |
| AB25_HC_MutA11_M34V | (41) | PKGLEWVAGISSG-SDTYYGDS  | VKGRFTISRDN  |
| AB25_HC_MutA11_M34L | (41) | PKGLEWVAGISSG-SDTYYGDS  | VKGRFTISRDN  |

|                     | 81   | H3                      | 118         |
|---------------------|------|-------------------------|-------------|
| AB21_HC_MutA11      | (81) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB21_HC_MutA11_M34V | (81) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB21_HC_MutA11_M34L | (81) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB27_HC_MutA11      | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB27_HC_MutA11_M34V | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB27_HC_MutA11_M34L | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB25_HC_MutA11      | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB25_HC_MutA11_M34V | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |
| AB25_HC_MutA11_M34L | (80) | LQMNSLRAEDTAVYICARETWNH | LFDYWGQGLTV |

FIG. 30

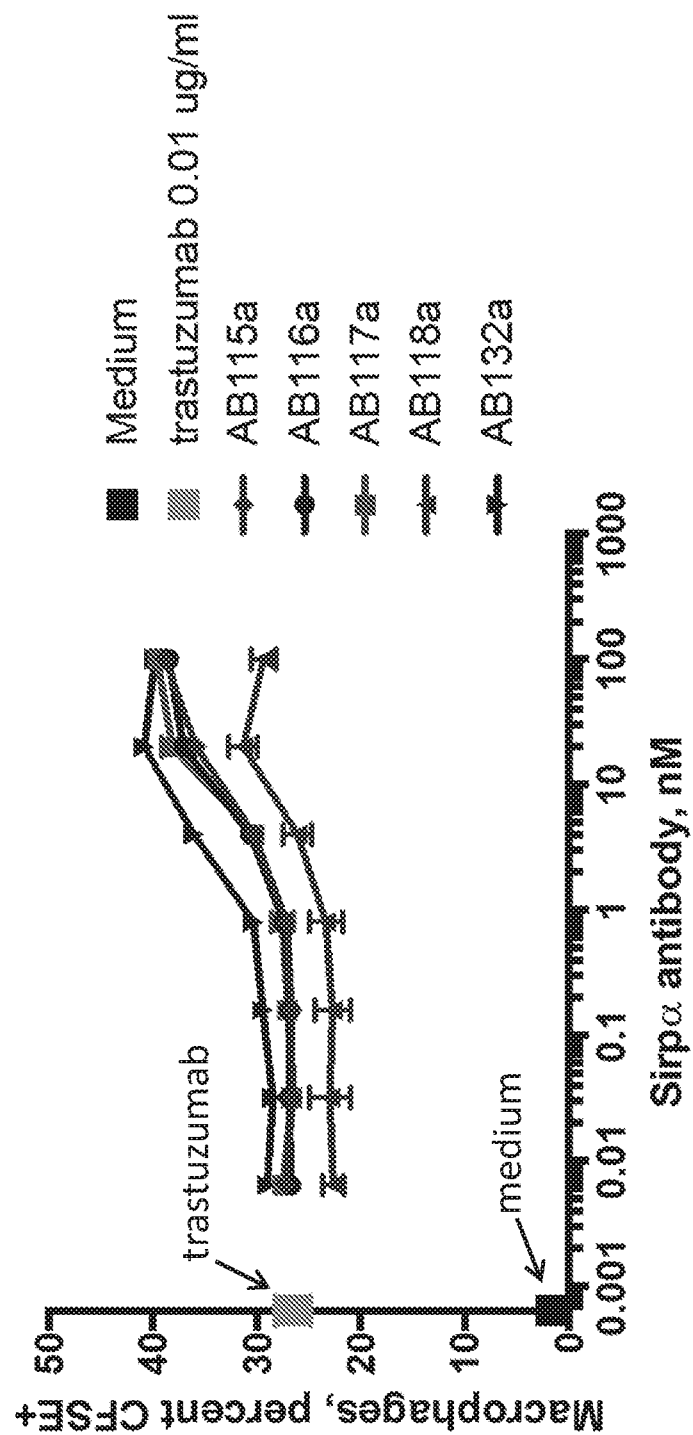


FIG. 31

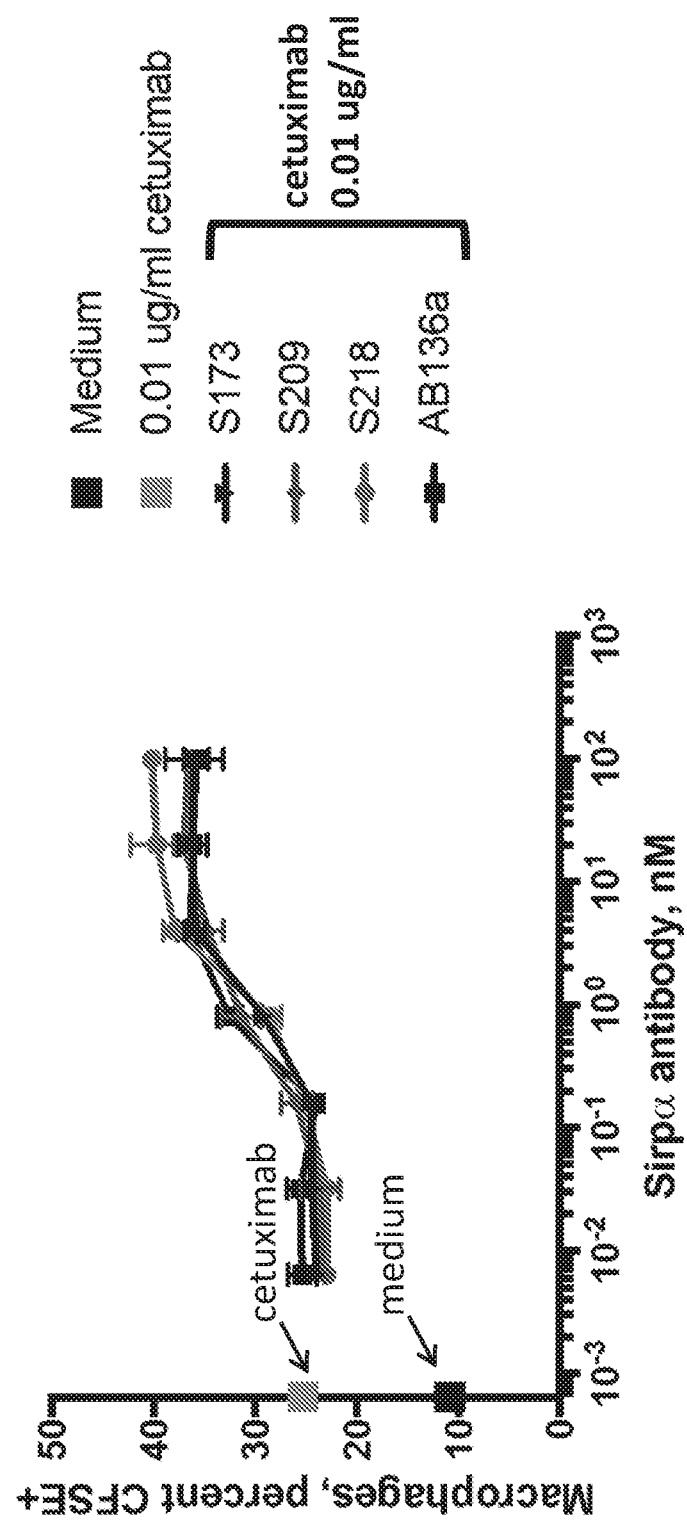


FIG. 32

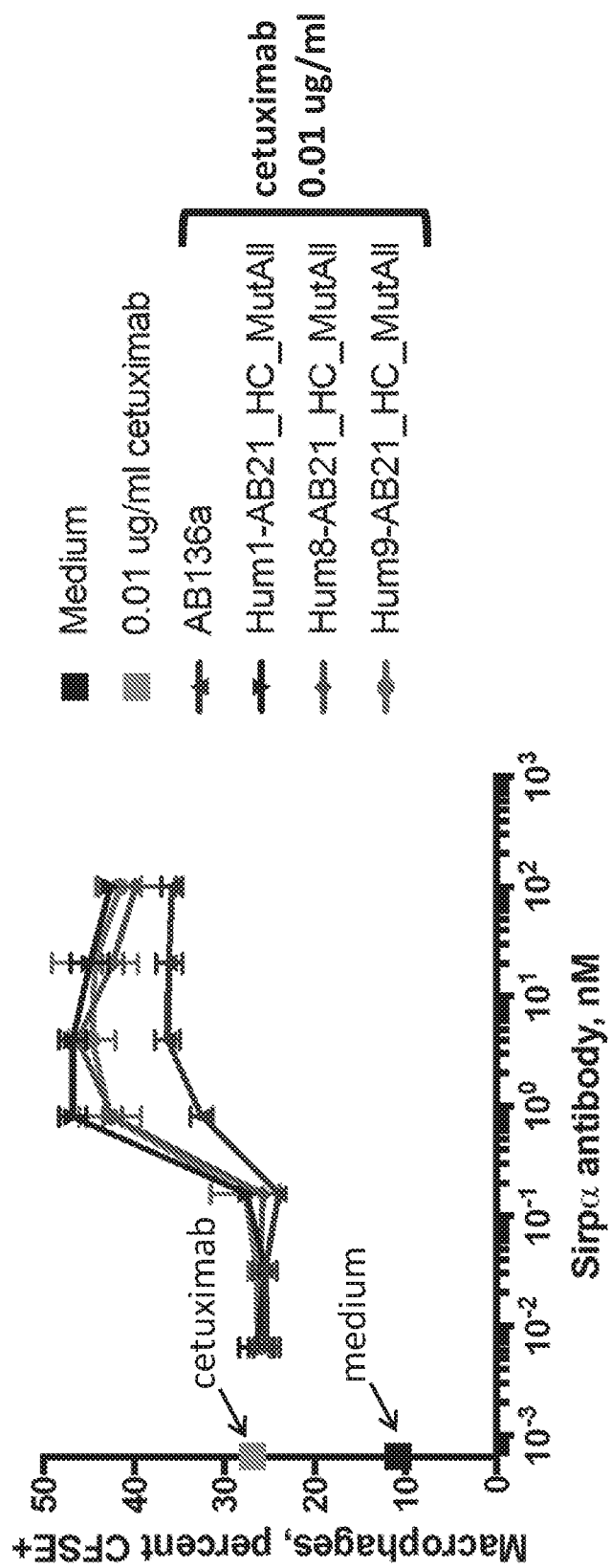


FIG. 33A

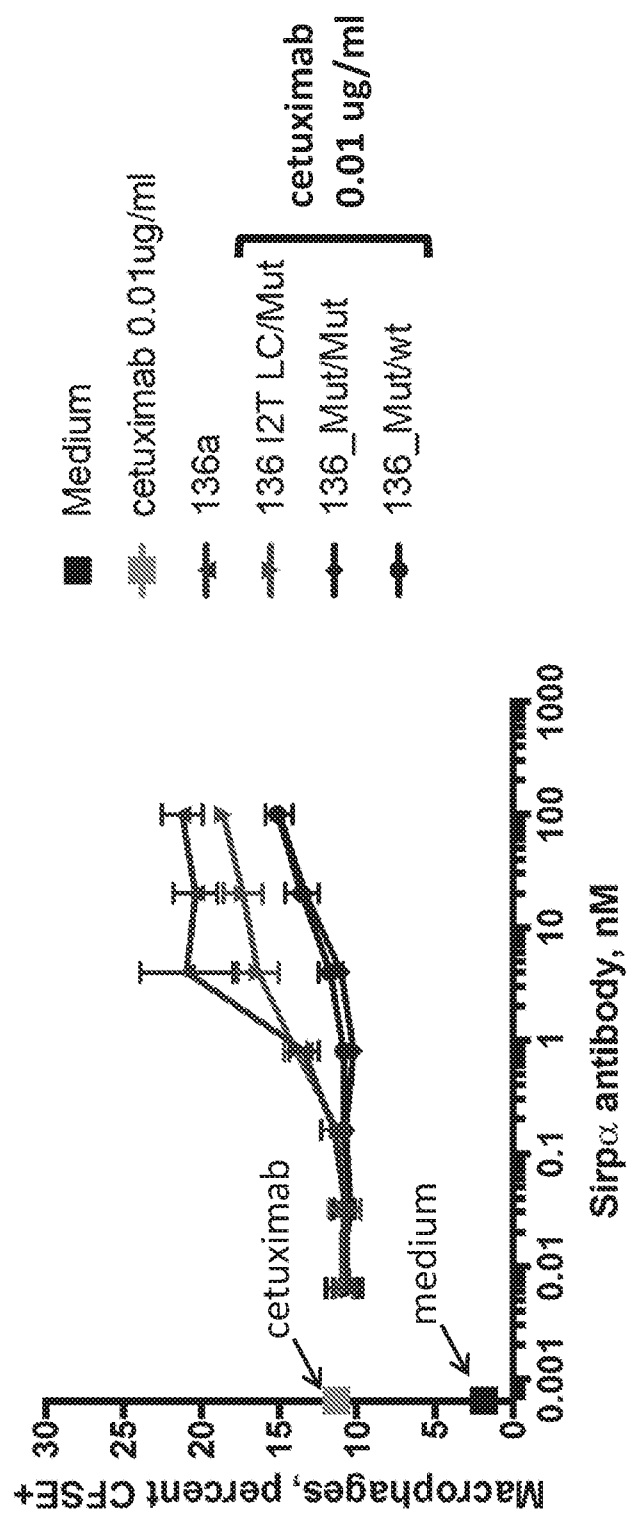


FIG. 33B

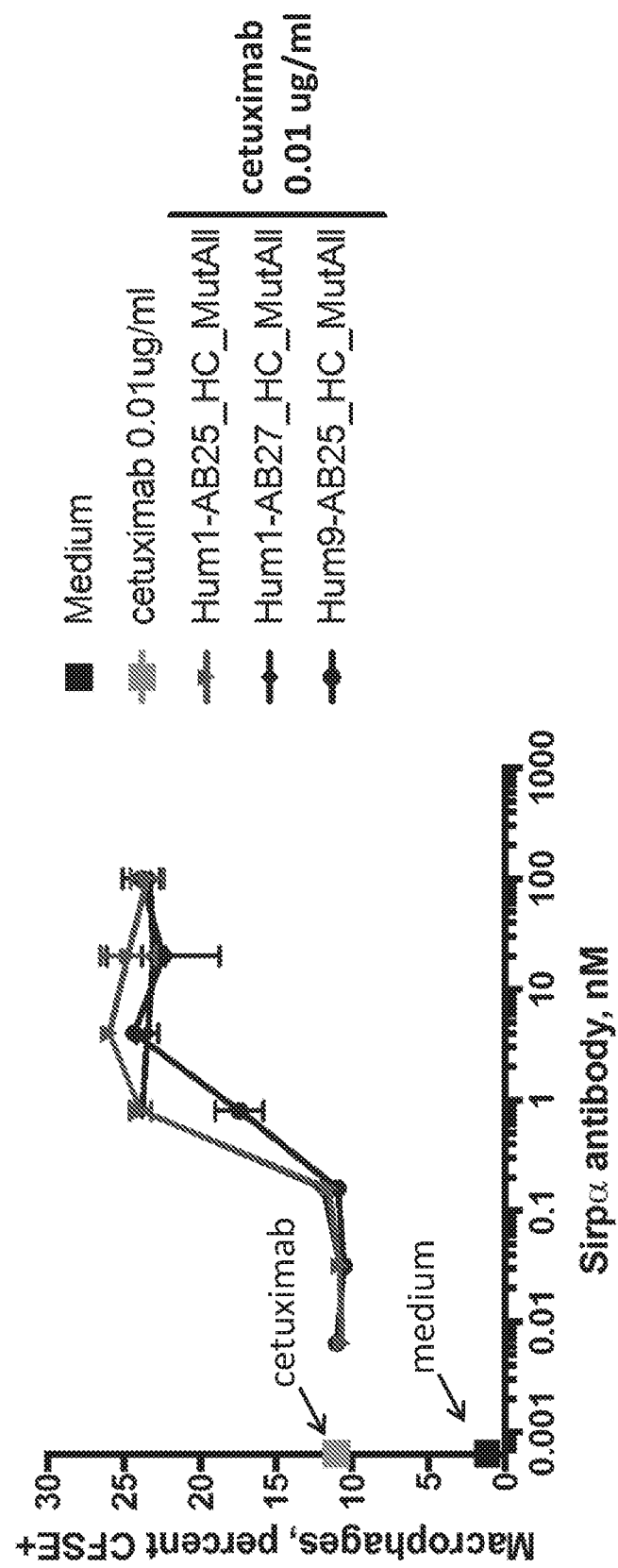


FIG. 33C

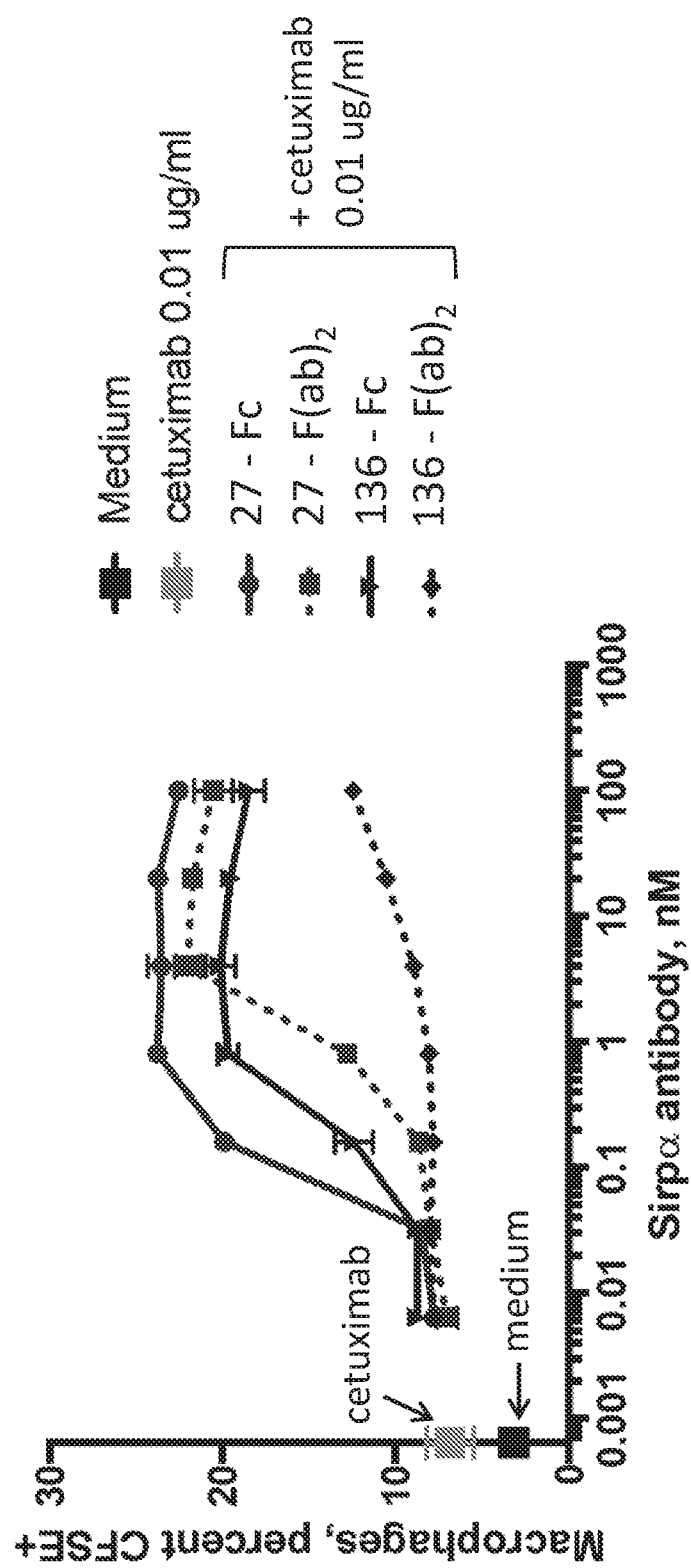


FIG. 34

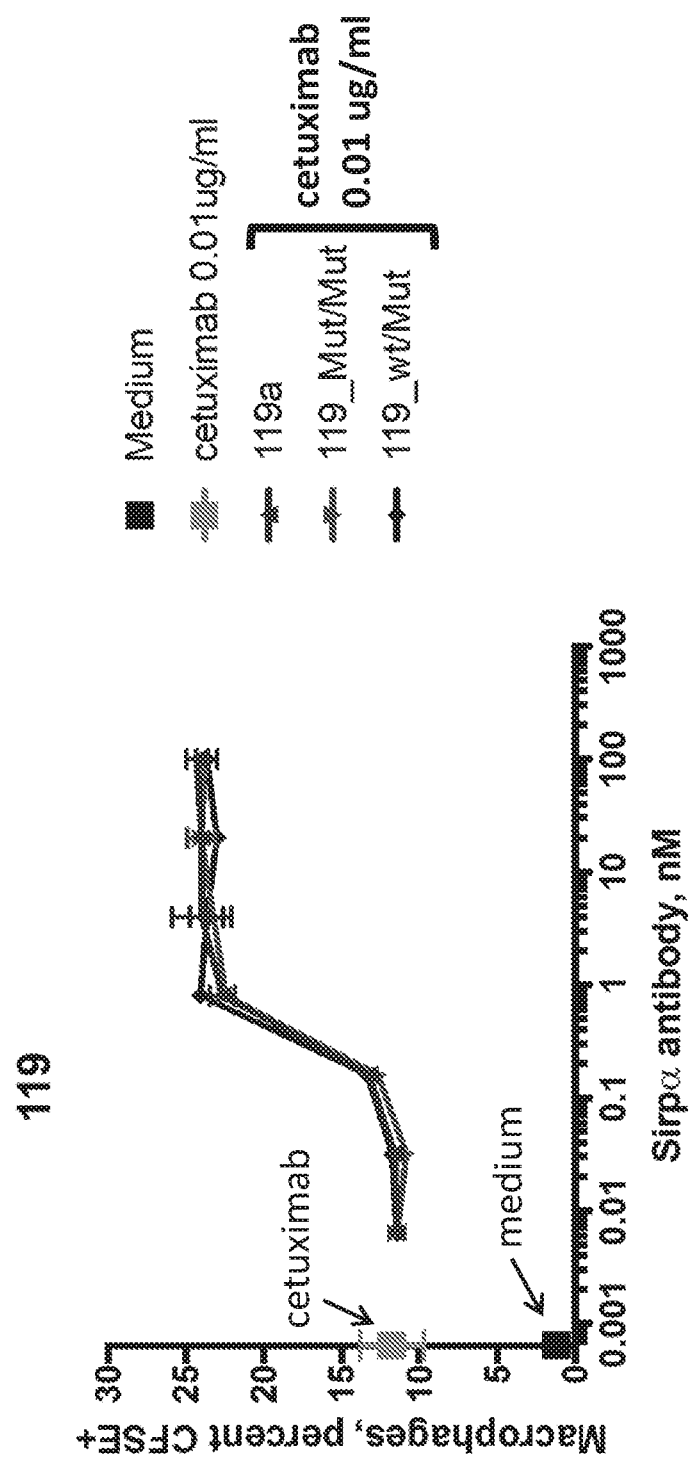


FIG. 35

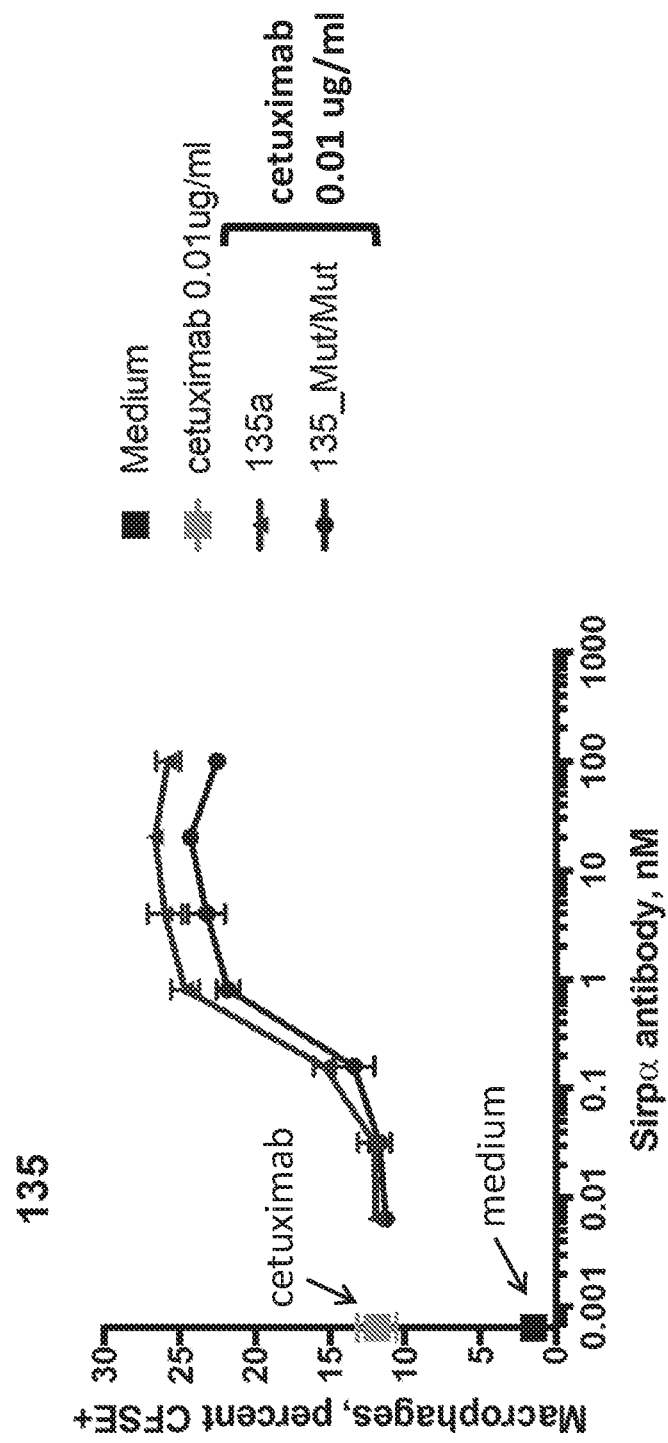


FIG. 36

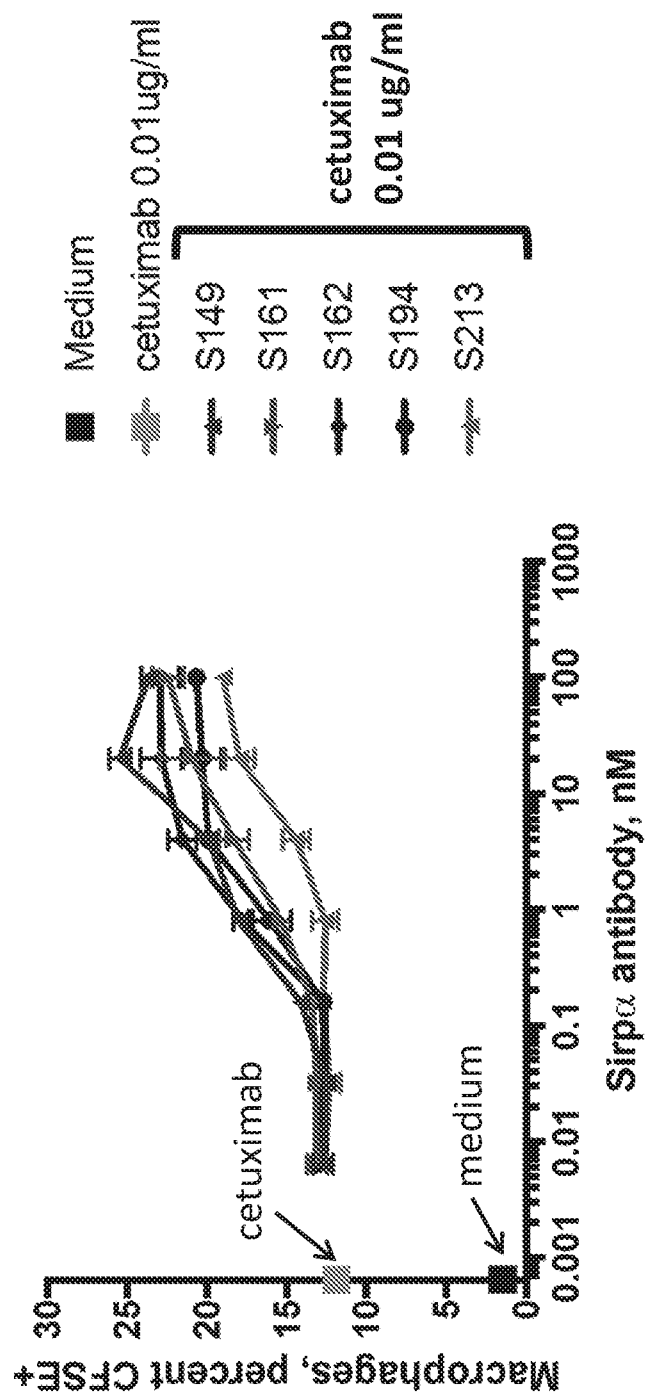


FIG. 37

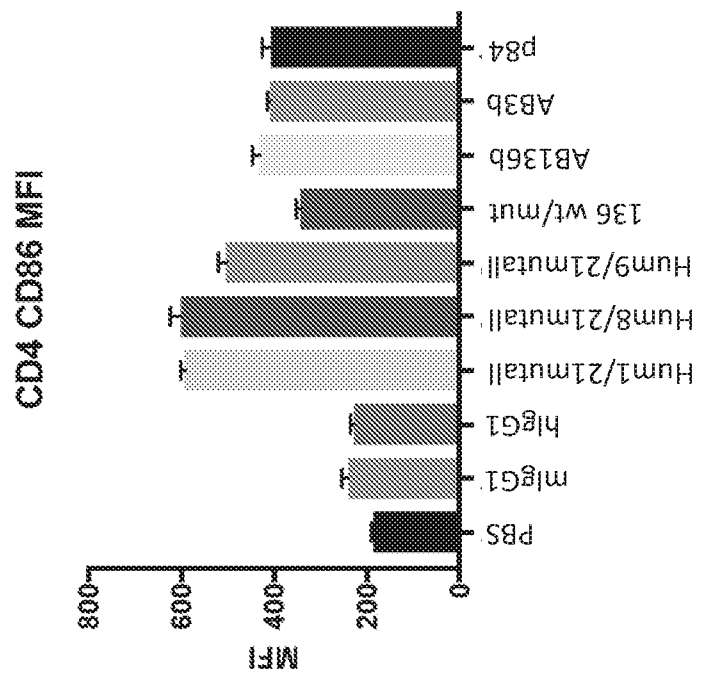


FIG. 38A

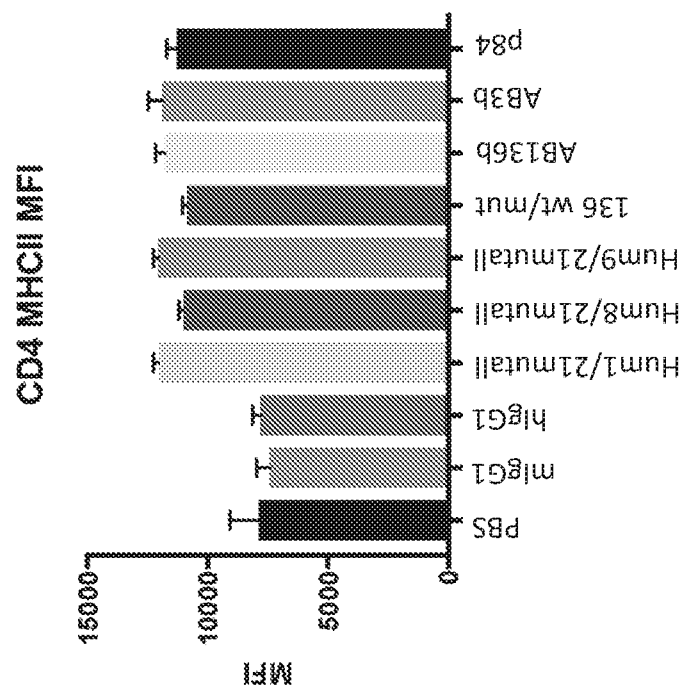


FIG. 38B

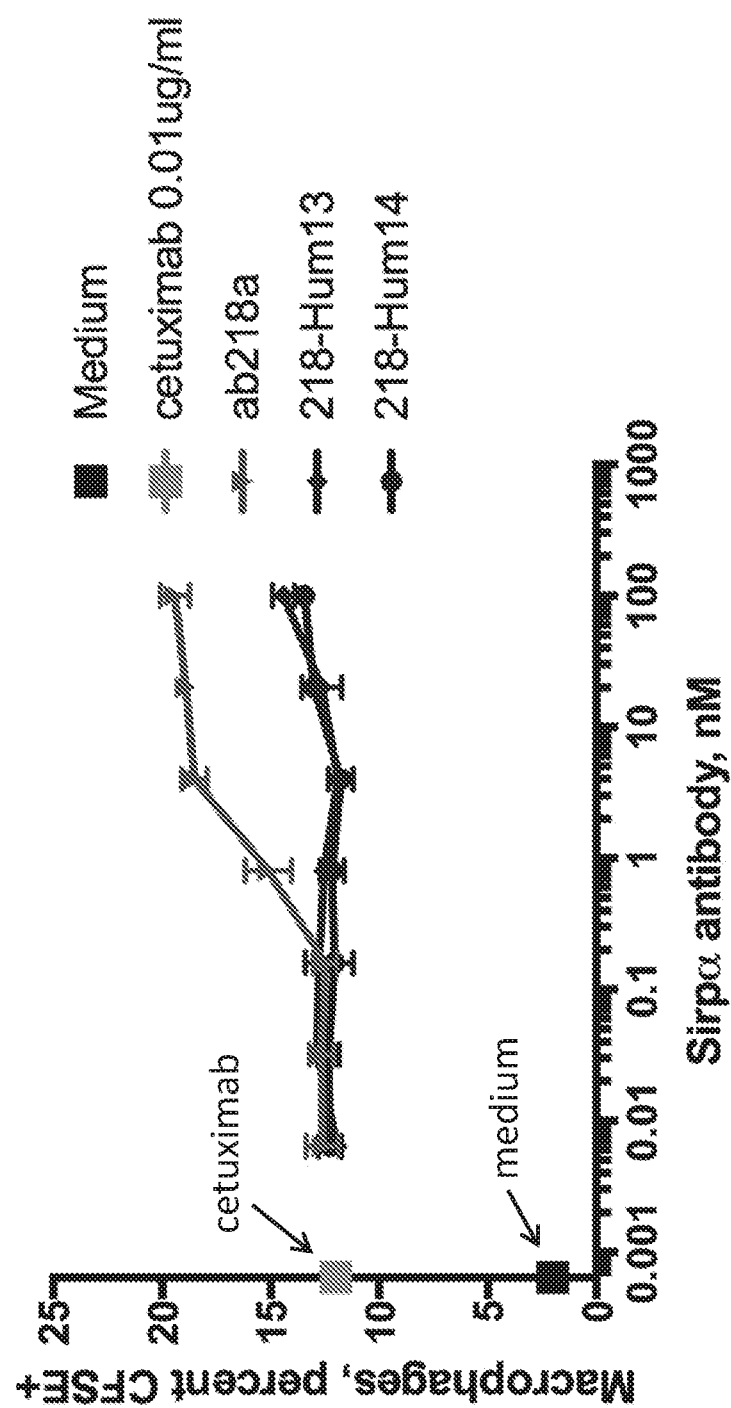


FIG. 39A

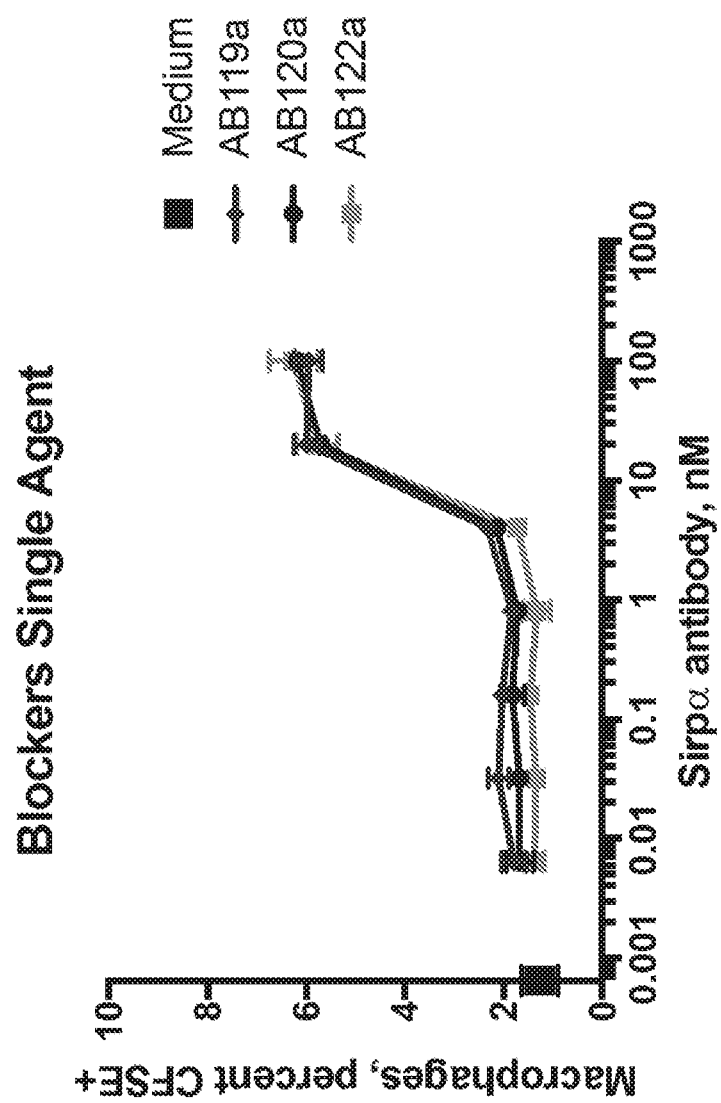


FIG. 39B

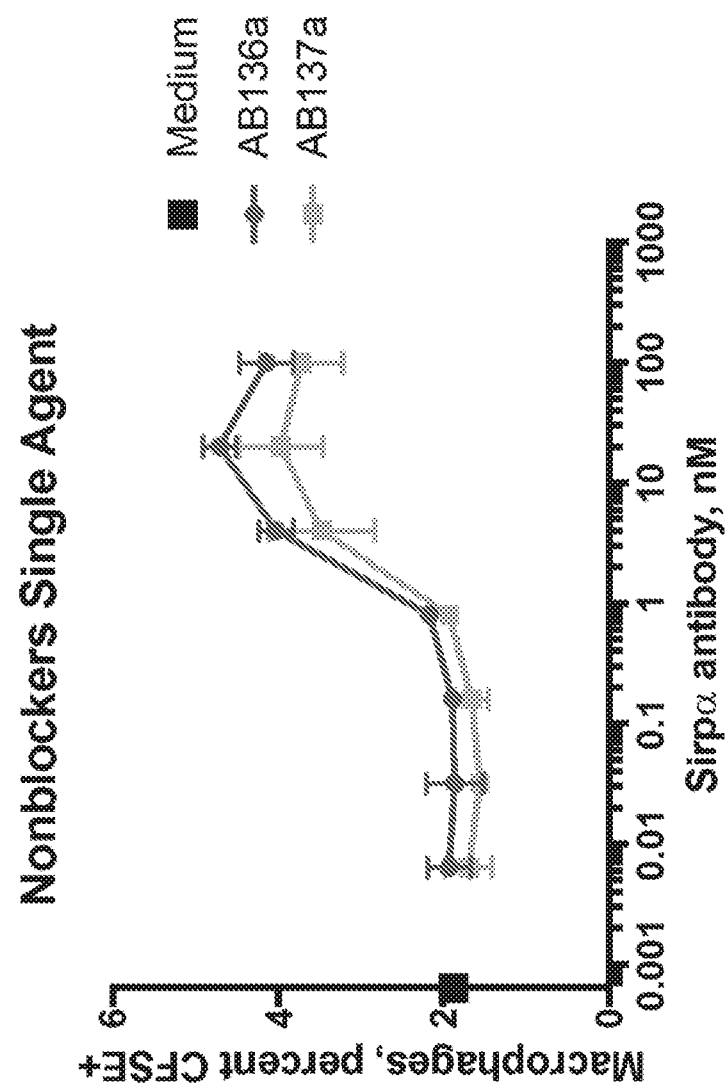


FIG. 39C

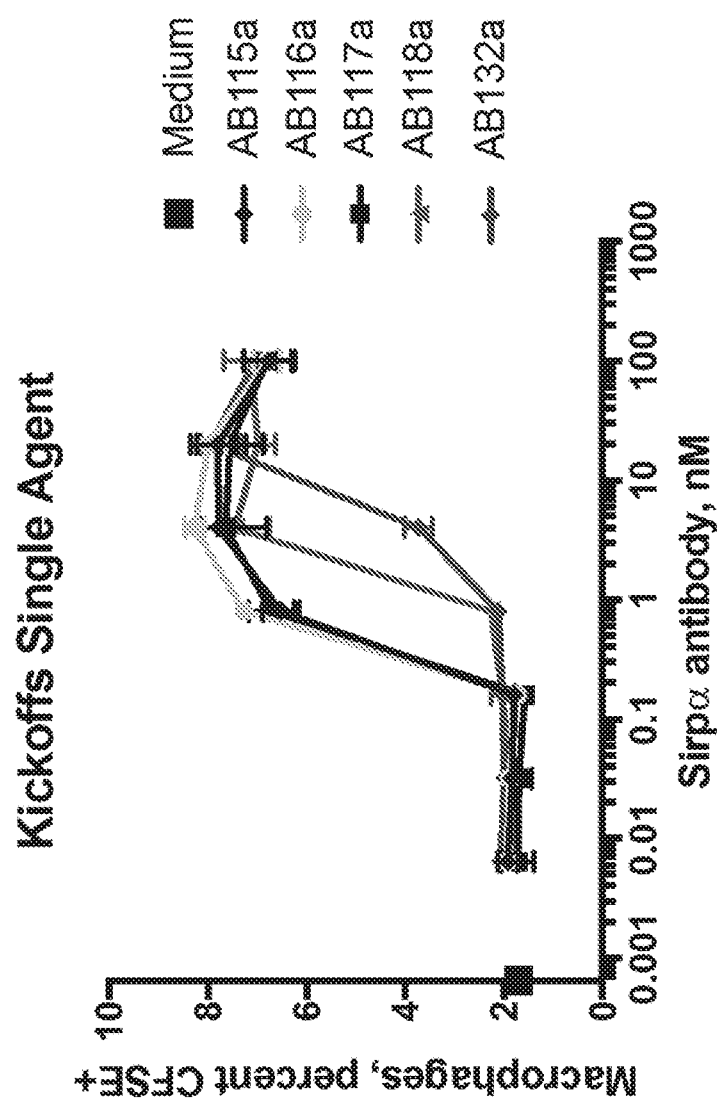
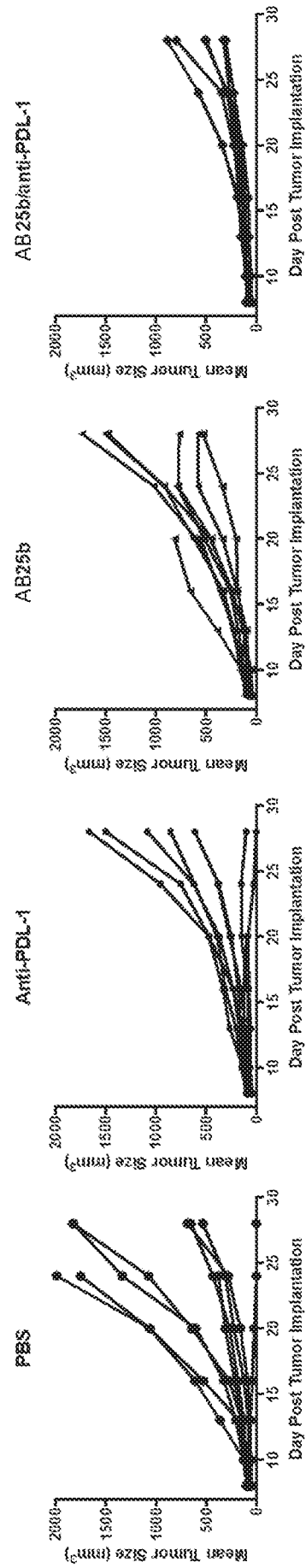
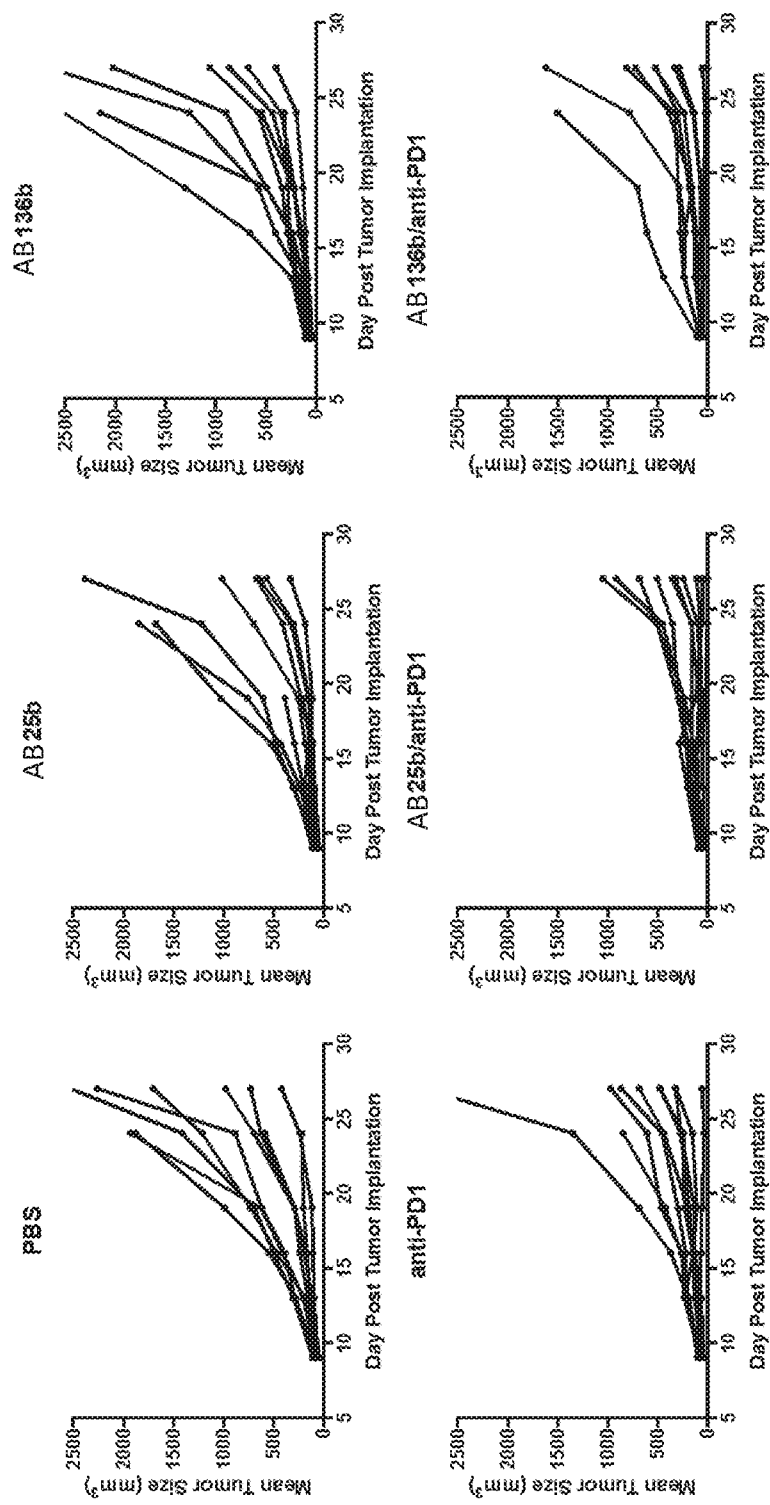


FIG. 39D



|                                                | PBS | Anti-PDL1 | AB25b | AB25b/anti-PDL1 |
|------------------------------------------------|-----|-----------|-------|-----------------|
| Mice with tumor<br>volume <600 mm <sup>3</sup> | 2   | 2         | 2     | 6               |

FIG. 40



|                                             | PBS | Anti-PD1 | AB25b | AB25b/anti-PD1 | AB136b | AB136b/anti-PD1 |
|---------------------------------------------|-----|----------|-------|----------------|--------|-----------------|
| Mice with tumor volume <600 mm <sup>3</sup> | 1   | 5        | 2     | 7              | 1      | 6               |

FIG. 41