FIG. 1A

SEQ ID NO:1

QEDEDGDYEELVLALRSEEDGLAEAPEHGTTATFHRCAKDPWRLPGTYVVVLKEE
THLSQSERTARRLQAQAARRGYLTKILHVFHGLLPGFLVKMSGDLLELALKLPHV
DYIEEDSSVFAQSIPWNLERITPPRYRADEYQPPDGGSLVEVYLLDTSIQSDHRE
IEGRVMVTDFENVPEEDGTRFHRQASKCDSHGTHLAGVVSGRDAGVAKGASMRSL
RVLNCQGKGTVSGTLIGLEFIRKSQLVQPVGPLVVLLPLAGGYSRVLNAACQRLA
RAGVVLVTAAGNFRDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVD
LFAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEPELTLAELRQRL
IHFSAKDVINEAWFPEDQRVLTPNLVAALPPSTHGAGWQLFCRTVWSAHSGPTRM
ATAIARCAPDEELLSCSSFSRSGKRRGERMEAQGGKLVCRAHNAFGGEGVYAIAR
CCLLPQANCSVHTAPPAEASMGTRVHCHQQGHVLTGCSSHWEVEDLGTHKPPVLR
PRGQPNQCVGHREASIHASCCHAPGLECKVKEHGIPAPQGQVTVACEEGWTLTGC
SALPGTSHVLGAYAVDNTCVVRSRDVSTTGSTSEEAVTAVAICCRSRHLAQASQE
LQ

FIG. 1B-1

```
                10        20        30        40        50
          ---------|---------|---------|---------|---------|
Query   : atgggcaccgtcagctccaggcggtcctggtggccgctgccactgctgct  SEQ ID NO:2
Frame1  : M  G  T  V  S  S  R  R  S  W  W  P  L  P  L  L  L   SEQ ID NO:3

                60        70        80        90        100
          ---------|---------|---------|---------|---------|
Query   : gctgctgctgctgctcctgggtcccgcgggcgcccgtgcgcaggaggacg
Frame1  :  L  L  L  L  L  L  G  P  A  G  A  R  A  Q  E  D  E

                110       120       130       140       150
          ---------|---------|---------|---------|---------|
Query   : aggacggcgactacgaggagctggtgctagccttgcgctccgaggaggac
Frame1  :    D  G  D  Y  E  E  L  V  L  A  L  R  S  E  E  D

          50    160       170       180       190       200
          ---------|---------|---------|---------|---------|
Query   : ggcctggccgaagcacccgagcacggaaccacagccacctttccaccgctg
Frame1  : G  L  A  E  A  P  E  H  G  T  T  A  T  F  H  R  C

                210       220       230       240       250
          ---------|---------|---------|---------|---------|
Query   : cgccaaggatccgtggaggttgcctggcacctacgtggtggtgctgaagg
Frame1  :  A  K  D  P  W  R  L  P  G  T  Y  V  V  V  L  K  E

          50    260       270       280       290       300
          ---------|---------|---------|---------|---------|
Query   : aggagacccacctctcgcagtcagagcgcactgcccgccgcctgcaggcc
Frame1  :    E  T  H  L  S  Q  S  E  R  T  A  R  R  L  Q  A

                310       320       330       340       350
          ---------|---------|---------|---------|---------|
Query   : caggctgcccgccggggatacctcaccaagatcctgcatgtcttccatgg
Frame1  : Q  A  A  R  R  G  Y  L  T  K  I  L  H  V  F  H  G

          50    360       370       380       390       400
          ---------|---------|---------|---------|---------|
Query   : ccttcttcctggcttcctggtgaagatgagtggcgacctgctggagctgg
Frame1  :  L  L  P  G  F  L  V  K  M  S  G  D  L  L  E  L  A

                410       420       430       440       450
          ---------|---------|---------|---------|---------|
Query   : ccttgaagttgccccatgtcgactacatcgaggaggactcctctgtcttt
Frame1  :    L  K  L  P  H  V  D  Y  I  E  E  D  S  S  V  F

          50    460       470       480       490       500
          ---------|---------|---------|---------|---------|
Query   : gcccagagcatcccgtggaacctggagcggattacccctccgcggtaccg
Frame1  : A  Q  S  I  P  W  N  L  E  R  I  T  P  P  R  Y  R

                510       520       530       540       550
          ---------|---------|---------|---------|---------|
Query   : ggcggatgaataccagccccccgacggaggcagcctggtggaggtgtatc
Frame1  :  A  D  E  Y  Q  P  P  D  G  G  S  L  V  E  V  Y  L
```

FIG. 1B-2

```
          50        560       570       580       590       600
          ---------|---------|---------|---------|---------|
Query   : tcctagacaccagcatacagagtgaccaccgggaaatcgagggcagggtc
Frame1  :   L  D  T  S  I  Q  S  D  H  R  E  I  E  G  R  V

                    610       620       630       640       650
          ---------|---------|---------|---------|---------|
Query   : atggtcaccgacttcgagaatgtgcccgaggaggacgggacccgcttcca
Frame1  : M  V  T  D  F  E  N  V  P  E  E  D  G  T  R  F  H

          50        660       670       680       690       700
          ---------|---------|---------|---------|---------|
Query   : cagacaggccagcaagtgtgacagtcatggcacccacctggcaggggtgg
Frame1  :  R  Q  A  S  K  C  D  S  H  G  T  H  L  A  G  V  V

                    710       720       730       740       750
          ---------|---------|---------|---------|---------|
Query   : tcagcggccgggatgccggcgtggccaagggtgccagcatgcgcagcctg
Frame1  :   S  G  R  D  A  G  V  A  K  G  A  S  M  R  S  L

          50        760       770       780       790       800
          ---------|---------|---------|---------|---------|
Query   : cgcgtgctcaactgccaagggaagggcacggttagcggcaccctcatagg
Frame1  : R  V  L  N  C  Q  G  K  G  T  V  S  G  T  L  I  G

                    810       820       830       840       850
          ---------|---------|---------|---------|---------|
Query   : cctggagtttattcggaaaagccagctggtccagcctgtggggccactgg
Frame1  :  L  E  F  I  R  K  S  Q  L  V  Q  P  V  G  P  L  V

          50        860       870       880       890       900
          ---------|---------|---------|---------|---------|
Query   : tggtgctgctgcccctggcgggtgggtacagccgcgtcctcaacgccgcc
Frame1  :   V  L  L  P  L  A  G  G  Y  S  R  V  L  N  A  A

                    910       920       930       940       950
          ---------|---------|---------|---------|---------|
Query   : tgccagcgcctggcgagggctggggtcgtgctggtcaccgctgccggcaa
Frame1  : C  Q  R  L  A  R  A  G  V  V  L  V  T  A  A  G  N

          50        960       970       980       990       1000
          ---------|---------|---------|---------|---------|
Query   : cttccgggacgatgcctgcctctactccccagcctcagctcccgaggtca
Frame1  :  F  R  D  D  A  C  L  Y  S  P  A  S  A  P  E  V  I

                    1010      1020      1030      1040      1050
          ---------|---------|---------|---------|---------|
Query   : tcacagttggggccaccaatgcccaggaccagccggtgaccctggggact
Frame1  :   T  V  G  A  T  N  A  Q  D  Q  P  V  T  L  G  T

           50       1060      1070      1080      1090      1100
          ---------|---------|---------|---------|---------|
Query   : ttggggaccaactttggccgctgtgtggacctctttgccccaggggagga
Frame1  : L  G  T  N  F  G  R  C  V  D  L  F  A  P  G  E  D
```

FIG. 1B-3

```
          100       1110      1120      1130      1140      1150
          ----------|---------|---------|---------|---------|
Query   : catcattggtgcctccagcgactgcagcacctgctttgtgtcacagagtg
Frame1  :  I  I  G  A  S  S  D  C  S  T  C  F  V  S  Q  S  G

          150       1160      1170      1180      1190      1200
          ----------|---------|---------|---------|---------|
Query   : ggacatcacaggctgctgcccacgtggctggcattgcagccatgatgctg
Frame1  :   T  S  Q  A  A  A  H  V  A  G  I  A  A  M  M  L

          200       1210      1220      1230      1240      1250
          ----------|---------|---------|---------|---------|
Query   : tctgccgagccggagctcaccctggccgagttgaggcagagactgatcca
Frame1  : S  A  E  P  E  L  T  L  A  E  L  R  Q  R  L  I  H

          250       1260      1270      1280      1290      1300
          ----------|---------|---------|---------|---------|
Query   : cttctctgccaaagatgtcatcaatgaggcctggttcccctgaggaccagc
Frame1  :  F  S  A  K  D  V  I  N  E  A  W  F  P  E  D  Q  R

          300       1310      1320      1330      1340      1350
          ----------|---------|---------|---------|---------|
Query   : gggtactgacccccaacctggtggccgccctgccccccagcacccatggg
Frame1  :   V  L  T  P  N  L  V  A  A  L  P  P  S  T  H  G

          350       1360      1370      1380      1390      1400
          ----------|---------|---------|---------|---------|
Query   : gcaggttggcagctgttttgcaggactgtgtggtcagcacactcggggcc
Frame1  : A  G  W  Q  L  F  C  R  T  V  W  S  A  H  S  G  P

          400       1410      1420      1430      1440      1450
          ----------|---------|---------|---------|---------|
Query   : tacacggatggccacagccatcgcccgctgcgccccagatgaggagctgc
Frame1  :  T  R  M  A  T  A  I  A  R  C  A  P  D  E  E  L  L

          450       1460      1470      1480      1490      1500
          ----------|---------|---------|---------|---------|
Query   : tgagctgctccagtttctccaggagtgggaagcggcggggcgagcgcatg
Frame1  :   S  C  S  S  F  S  R  S  G  K  R  R  G  E  R  M

          500       1510      1520      1530      1540      1550
          ----------|---------|---------|---------|---------|
Query   : gaggcccaaggggcaagctggtctgccgggcccacaacgcttttggggg
Frame1  : E  A  Q  G  G  K  L  V  C  R  A  H  N  A  F  G  G

          550       1560      1570      1580      1590      1600
          ----------|---------|---------|---------|---------|
Query   : tgagggtgtctacgccattgccaggtgctgcctgctaccccaggccaact
Frame1  :  E  G  V  Y  A  I  A  R  C  C  L  L  P  Q  A  N  C

          600       1610      1620      1630      1640      1650
          ----------|---------|---------|---------|---------|
Query   : gcagcgtccacacagctccaccagctgaggccagcatggggacccgtgtc
Frame1  :   S  V  H  T  A  P  P  A  E  A  S  M  G  T  R  V
```

FIG. 1B-4

```
          650       1660       1670       1680       1690       1700
          ---------|---------|---------|---------|---------|
Query   : cactgccaccaacagggccacgtcctcacaggctgcagctcccactggga
Frame1  : H  C  H  Q  Q  G  H  V  L  T  G  C  S  S  H  W  E

          700       1710       1720       1730       1740       1750
          ---------|---------|---------|---------|---------|
Query   : ggtggaggaccttggcacccacaagccgcctgtgctgaggccacgaggtc
Frame1  :  V  E  D  L  G  T  H  K  P  P  V  L  R  P  R  G  Q

          750       1760       1770       1780       1790       1800
          ---------|---------|---------|---------|---------|
Query   : agcccaaccagtgcgtgggccacagggaggccagcatccacgcttcctgc
Frame1  :    P  N  Q  C  V  G  H  R  E  A  S  I  H  A  S  C

          800       1810       1820       1830       1840       1850
          ---------|---------|---------|---------|---------|
Query   : tgccatgccccaggtctggaatgcaaagtcaaggagcatggaatcccggc
Frame1  : C  H  A  P  G  L  E  C  K  V  K  E  H  G  I  P  A

          850       1860       1870       1880       1890       1900
          ---------|---------|---------|---------|---------|
Query   : ccctcaggggcaggtgaccgtggcctgcgaggagggctggaccctgactg
Frame1  :  P  Q  G  Q  V  T  V  A  C  E  E  G  W  T  L  T  G

          900       1910       1920       1930       1940       1950
          ---------|---------|---------|---------|---------|
Query   : gctgcagcgccctccctgggacctcccacgtcctgggggcctacgccgta
Frame1  :    C  S  A  L  P  G  T  S  H  V  L  G  A  Y  A  V

          950       1960       1970       1980       1990       2000
          ---------|---------|---------|---------|---------|
Query   : gacaacacgtgtgtagtcaggagccgggacgtcagcactacaggcagcac
Frame1  : D  N  T  C  V  V  R  S  R  D  V  S  T  T  G  S  T

                    2010       2020       2030       2040       2050
          ---------|---------|---------|---------|---------|
Query   : cagcgaagaggccgtgacagccgttgccatctgctgccggagccggcacc
Frame1  :  S  E  E  A  V  T  A  V  A  I  C  C  R  S  R  H  L

           50       2060       2070       2080       2090       2100
          ---------|---------|---------|---------|---------|
Query   : tggcgcaggcctcccaggagctccag
Frame1  :    A  Q  A  S  Q  E  L  Q
```

FIG. 2A

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
4		Germline			DIVMTQSPLSLPVTPGEPASISC	RSSQSLLHSNGYNYLD	WYLQKPGQSPQLLIY
5	30A4	A3		JK3	----------S----------P-----	----------F-N	----------
6		Germline			DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY
7	3C4	O2		JK4	----------	----R--N--S	--L-----I-------
8		Germline			DIQMTQSPSSLSASVGDRVTITC	RASQSISSYLN	WYQQKPGKAPKLLIY
9	23B5	O2		JK5	--L---------------------	----------	----------V---
10	25G4	O2		JK5	----------	--------I---	----------Y-----
11		Germline			QSVLTQPPSVSGAPGQRVTISC	TGSSSNIGAGYDVH	WYQQLPGTAPKLLIY
12	31H4	V1-13		JL2	----------	----------	----------S
13	27B2	V1-13		JL2	----------	----------H-----	----V----------
14		Germline			QSALTQPASVSGSPGQSITISC	TGTSSDVGGYNYVS	WYQQHPGKAPKLMIY
15	25A7	V1-4		JL2	----------	--------R--S--	---H--------V---
16	27H5	V1-4		JL2	----------	----------S--	----------P-------
17	26H5	V1-4		JL2	----------	----------S--	----------P-------
18	31D1	V1-4		JL2	----------	----------S--	----------P-------
19	20D10	V1-4		JL2	----------	----------S--	----Y---P---K--
20	27E7	V1-4		JL2	----------	----------S--	----------P-------
21	30B9	V1-4		JL2	----------	----------S--	----------P-------
22	19H9	V1-4		JL2	----------	--N--------S--	----------P-------
23	26E10	V1-4		JL2	----------	----------S--	----------
23	21B12	V1-4		JL2	----------	----------S--	----------
24	17C2	V1-4		JL2	----------	--------A--S--	----------R---

FIG. 2B

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
25		Germline			QSALTQPASVSGSPGQSITISC	TGTSSDVGGYNYVS	WYQQHPGKAPKLMIY
26	23G1	V1-4		JL3	----------S---	----------S--	----------
27		Germline			QSALTQPASVSGSPGQSITISC	TGTSSDVGSYNLVS	WYQQHPGKAPKLMIY
28	13H1	V1-7		JL3	L---------N-----	----------N-----	----YS----------
29		Germline			QSVLTQPPSASGTPGQRVTISC	SGSSSNIGSNTVN	WYQQLPGTAPKLLIY
30	9C9	V1-16		JL3	----------K---	----------K---	----V----------
31	9H6	V1-16		JL3	----------P-----------	----------------	----------
32	31A4	V1-16		JL3	----------------------	----------------	----------
33	1A12	V1-16		JL3	----------------------	----------K-----	----F----------
34		Germline			QSVLTQPPSVSAAPGQKVTISC	SGSSSNIGNNYVS	WYQQLPGTAPKLLIY
35	16F12	V1-19		JL1	----------------------	----------F---	----------
36	22E2	V1-19		JL1	----------------------	----------F---	----------
37	27A6	V1-19		JL1	----------------------	----------F---	----F----------
38	28B12	V1-19		JL1	----------------------	----------F---	----------
39	28D6	V1-19		JL1	----------T-----------	----------F---	----------
40	31G11	V1-19		JL1	----------------------	----------F---	----------
41		Germline			QSVLTQPPSVSAAPGQKVTISC	SGSSSNIGNNYVS	WYQQLPGTAPKLLIY
42	13B5	V1-19		JL2	----------------------	---N----------	----------
43		Germline			SYELTQPPSVSVSPGQTASITC	SGDKLGDKYAC	WYQQKPGQSPVLVIY
44	31B12	V2-1		JL2	----------------------R---	----------	----------
45		Germline			QPVLTQPPSASASLGASVTLTC	TLSSGYSNYKVD	WYQQRPGKGPRFVMR
46	3B6	V5-2		JL2	----------LF----------	----------S-E---	----------

FIG. 2C

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
4		LGSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	MQALQTPFT	FGPGTKVDIK
5	30A4	---H---	----------E----------	--V------	----------
6		AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQSYSTPLT	FGGGTKVEIK
7	3C4	-------	----------S----------	-------I-	----------
8		AASSLQS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQSYSTPIT	FGQGTRLEIK
9	23B5	-------	----------N----------	-----S---	----------
10	25G4	--A----	----------	-----A---	----------
11		GNSNRPS	GVPDRFSGSKSGTSASLAITGLQAEDEADYYC	QSYDSSLSGSV	FGGGTKLTVL
12	31H4	-------	----------	----------	----------
13	27B2	--TY---	----------	----N----V-	----------
14		EVSNRPS	GVSNRFSGSKSGNTASLTISGLQAEDEADYYC	SSYTSSSVV	FGGGTKLTVL
15	25A7	-------	---T----------	----------	----------
286	25A7v1	-------	---T----------	----------	----------
16	27H5	-------	---I----------	-----T-M-	----------
287	27H5v1	-------	---I----------	-----T-M-	----------
17	26H5	-------	---I----------	-----T-M-	----------
18	31D1	-------	----------	-----T-M-	---------A-
19	20D10	-------	----------	-----T-M-	----------
20	27E7	-------	----------	-----T-M-	----------
21	30B9	-------	----------	-----T-M-	----------
22	19H9	-------	-I----------	-----T-M-	----------
287	19H9v1	-------	-I----------	-----T-M-	----------
23	26E10	-------	----------	N----T-M-	----------
23	21B12	-------	----------	N----T-M-	----------
24	17C2	-------	----------	-----TNM-	----------

FIG. 2D

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
25		EVSNRPS	GVSNRFSGSKSGNTASLTISGLQAEDEADYYC	SSYTSSS V	FGGGTKLTVL
26	23G1	--T-----	----------	N----T-M-	----------
27		EGSKRPS	GVSNRFSGSKSGNTASLTISGLQAEDEADYYC	CSYAGSST	FGGGTKLTVL
28	13H1	-V------	----------	---------LV	----------
29		SNNQRPS	GVPDRFSGSKSGTSASLAISGLQSEDEADYYC	AAWDDSLN V	FGGGTKLTVL
30	9C9	R-----L	----------	---------W-	----------
31	9H6	---R---	----------	--------W-	----------
32	31A4	-------	----------	-V-------GWV	----------
33	1A12	---R----	----------	---------W-	--A-------
34		DNNKRPS	GIPDRFSGSKSGTSATLGITGLQTGDEADYYC	GTWDSSLSAYV	FGTGTKVTVL
35	16F12	-Y------	----------	----------	-----R----
36	22E2	-Y------	----------	---------G-	-----R----
37	27A6	-Y------	----------	---------S-	-----R----
38	28B12	-Y------	----------	---------G-	-----R----
39	28D6	-Y------	----------	---------G-	-----R----
40	31G11	-S------	----------D-----------	----------	----------
41		DNNKRPS	GIPDRFSGSKSGTSATLGITGLQTGDEADYYC	GTWDSSLSAVV	FGGGTKLTVL
42	13B5	-------	----------N-----------	----------	----------
43		QDSKRPS	GIPERFSGSNSGNTATLTISGTQAMDEADYYC	QAWDSSTAVV	FGGGTKLTVL
44	31B12	--NT--W--L	----------K-----V----------	---------- V--	----------
45		VGTGGIVGSKGD	GIPDRFSVLGSGLNRYLTIKNIQEEDESDYHC	GADHGSGSNFVVV	FGGGTKLTVL
46	3B6	-D----------E	----------	--------T-----	----------
45		VGTGGIV	GSKGDGIPDRFSVLGSGLNRYLTIKNIQEEDE	SDYHCGADHGSGSNFVVV	FGGGTKLTVL
46	3B6v1	-D------	----E-----------	----------T-----	----------

FIG. 3A

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
47		**Germline**			QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYGIS	WVRQAPGQGLEWMG
48	20D10	VH1-18		JH6B	-I----------	--PL------	----------
49	26E10	VH1-18		JH6B	----------	---L------	----------
49	21B12	VH1-18		JH6B	----------	---L------	----------
50	23G1	VH1-18		JH6B	----------	---L------	----------
51	26H5	VH1-18		JH6B	----------	---L------	----------
52	27H5	VH1-18		JH6B	----------R-	---L------	----------
53	31D1	VH1-18		JH6B	-I----------	---L------	----------
54	27E7	VH1-18		JH6B	----------L-	--SL------	----------
55	30B9	VH1-18		JH6B	----------	--PL------	----------
56	19H9	VH1-18		JH6B	----------	--AL------	----------
57	17C2	VH1-18		JH6B	----------	--S-------	----------
58	25A7	VH1-18		JH6B	----------	----P-----	----------
59		**Germline**			QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYGIS	WVRQAPGQGLEWMG
60	3B6	VH1-18		JH4B	----------	----------	----------
61		**Germline**			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWMS	WVRQAPGKGLEWVA
62	9H6	VH3-7	D7-27	JH3A	----------	-----R----	----------
63		**Germline**			EVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYWMS	WVRQAPGKGLEWVA
64	9C9	VH3-7	D7-27	JH3B	----------VV-	----------	----------
65	1A12	VH3-7	D7-27	JH3B	----------	-L---NF---	----------
66		**Germline**			EVQLVESGGGLVKPGGSLRLSCAAS	GFTFSSYSMN	WVRQAPGKGLEWVS
67	31H4	VH3-21	D3-3	JH3A	----------	----------	----------
68		**Germline**			EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPGKGLEWVS
69	13B5	VH3-23		JH4B	----------	----------	----------

FIG. 3B

Seq ID No.	LINE	V	D	J	FR1	CDR1	FR2
70		Germline			EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYAMS	WVRQAPGKGLEWVS
71	23B5	VH3-23	D2-8	JH4B	----------	---------N	----------
72	25G4	VH3-23	D2-8	JH4B	----------	---------N	----------
73		Germline			QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
74	30A4	VH3-33		JH6B	----------	----------	----------
75		Germline			QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
76	27A6	VH3-33	D6-6	JH6B	---H------	-----N-F--	----------
77	28B12	VH3-33	D6-6	JH6B	----------	------F---	----------
289	28B12v1	VH3-33	D6-6	JH6B	---H------	------F---	----------
78	28D6	VH3-33	D6-6	JH6B	----------	------F---	----------
79	16F12	VH3-33	D6-6	JH6B	---H------	----N-F---	----------
80	22E2	VH3-33	D6-6	JH6B	----------	------F---	----------
81	31B12	VH3-33	D6-6	JH6B	----------	----------	----------
290	31B12v1	VH3-33	D6-6	JH6B	----------	----------	---------C--
82		Germline			QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
83	31G11	VH3-33	D6-19	JH6B	----------	----R-----	----------
84		Germline			QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
85	3C4	VH4-31		JH6B	----------	------SD----	----------
86		Germline			QVQLQESGPGLVKPSQTLSLTCTVS	GGSISSGGYYWS	WIRQHPGKGLEWIG
87	27B2	VH4-31	D5-5	JH4B	----------	----------	----------
88		Germline			QVQLQQWGAGLLKPSETLSLTCAVY	GGSFSGYYWS	WIRQPPGKGLEWIG
89	31A4	VH4-34	D6-6	JH4B	----------	-----A---N	----------
90		Germline			QVQLQQSGPGLVKPSQTLSLTCAIS	GDSVSSNSAAWN	WIRQSPSRGLEWLG
91	13H1	VH6-1		JH4B	----------	----------	----------

FIG. 3C

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
47		WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	YGMDV	WGQGTTVTVSS
48	20D10	----------V--	S----------V----------	G-----	----------
49	26E10	-V-F----------	-G-----P----------	G-----	----------
49	21B12	-V-F----------	-G-----P----------	G-----	----------
50	23G1	-V-F----------	-G-----P----------	G-----	----------
51	26H5	---F----------V--	----------V----------	G-----	----------
52	27H5	---V----------V--	----------V-------S----------	G-----	----------
53	31D1	---F----------V--	----------V----------F---	G-----	----------
54	27E7	----------V--	----------V---V----------	G-----	----------
55	30B9	----------V--	----------V----------	G-----	----------
56	19H9	----------V--	----------V----------	G-----	----------
57	17C2	-V----------F--	----------	G-V---	----------
58	25A7	----------E-----	----------V----------F-----	G-V---	----------
59		WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	GY DY	WGQGTLVTVSS
60	3B6	---T----------V--	----------	--TR--	----------
61		NIKQDGSEKYYVDSVKG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	NWG AFDV	WGQGTMVTVSS
62	9H6	---H----------	----------	ES---F-----	--H-------
63		NIKQDGSEKYYVDSVKG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	NWG AFDI	WGQGTMVTVSS
64	9C9	----------	----------	ES---F-----	----------
65	1A12	----------	----------S-T-	ES---F-----	----------
66		SISSSSSYIYYADSVKG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	DYDFWSGYYTAFDV	WGQGTMVTVSS
67	31H4	----------S-------	----------F----	-------A--D----	----------
68		AISGSGGSTYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	FDY	WGQGTLVTVSS
69	13B5	T----------R----------	----------	EVGSP----	----------

FIG. 3D

Seq ID No.	LINE	CDR2	FR3	CDR3	FR4
70		AISGSGGSTYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	VLMVYA DY	WGQGTLVTVSS
71	23B5	T------DN----------	----------------------------------	KF-------ML--	----------
72	25G4	T---------N--------	----------------------------------	KF-------ML--	----------
73		VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	YYYGMDV	WGQGTTVTVSS
74	30A4	--------D----------	----------------------------------	ETGPLKL--------	----------
75		VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	IAA GMDV	WGQGTTVTVSS
76	27A6	L---S----D----------	----------------------------------	AIAALYYYY----	----------
77	28B12	L---N----------------	----------------------------------	AIAALYYYY----	--H-------
78	28D6	L---N----------------	----------------------------------	AIAALYYYY----	----------
79	16F12	L---S----DE----------	----------------------------------	AIAALYYYY----	----------
80	22E2	L---N----------------	----------------------------------	AIAALYYYY----	----------
291	22E2v1	L---N----------------	----------------------------------	AIAALYYYY----	----------
81	31B12	I----------------------	----------------------------------	RGGLAARPG----	----------
292	31B12v1	I----------------------	----------------------------------	RGGL----PG----	----------
82		VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	GIAVAYYYYGMDV	WGQGTTVTVSS
83	31G11	L---E----T---V------	----------------------------------	----------	----------
84		YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	YYYGMDV	WGQGTTVTVSS
85	3C4	----------------------	-I----------L----------------------	GGVTT----A----	----------
86		YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	EDTAMV YFDY	WGQGTLVTVSS
87	27B2	---N----------------	----------------------------------	-------P------	----------
88		EINHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	GQLV FDY	WGQGTLVTVSS
89	31A4	------R-D----------	----------K---------N----------	----P-----	----------
90		RTYYRSKWYNDYAVSVKS	RITINPDTSKNQFSLQLNSVTPEDTAVYYCAR	FDY	WGQGTLVTVSS
91	13H1	----------KN-S------	----------G----------	GGPTAA----	----------

FIG. 3E

31H4

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGA
GACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCC
GCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGT
TACATTTCCTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCC
AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTA
TTTCTGTGCGAGAGATTACGATTTTTGGAGTGCTTACTATGATGCTTTTGATGTCTGG
GGCCAAGGGACAATGGTCACCGTCTCTTCA3' **(SEQ ID NO: 152)**

Amino acid sequence of heavy chain variable region:
EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYISY
ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYFCARDYDFWSAYYDAFDVWGQGT
MVTVSS **(SEQ ID NO: 67)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCA
CCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGT
ACCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTCTGGTAACAGCAATCGGC
CCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACA
GCAGCCTGAGTGGTTCGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 153)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLISGNSNRPSGV
PDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGSVFGGGTKLTVL **(SEQ ID NO: 12)**

FIG. 3F

20D10

Nucleotide sequence of heavy chain variable region:
5'CAGATTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACCCCTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGCGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' **(SEQ ID NO: 92)**

Amino acid sequence of heavy chain variable region:
QIQLVQSGAEVKKPGASVKVSCKASGYPLTSYGISWVRQAPGQGLEWMG
WISAYNGNTNYAQKVQGSVTMTTDTSTSTVYMELRSLRSDDTAVYYCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 48)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGTACCCAGGCAAACCCCCCAAACTCAA
GATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 93)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQYPGKPPKLKIYE
VSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGG
TKLTVL **(SEQ ID NO: 19)**

FIG. 3G

26E10

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTAACCAGCTATGGTATCAG
CTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGGTCAGT
TTTTATAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGGCACCA
TGACCACAGACCCATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGGCTACGGTATGGACGTC
TGGGGCCAAGGGACCACGGTCACCGTCTCCTCT3' **(SEQ ID NO: 94)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMGWVS
FYNGNTNYAQKLQGRGTMTTDPSTSTAYMELRSLRSDDTAVYYCARGYGMDV
WGQGTTVTVSS **(SEQ ID NO: 49)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGA
TCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTCTGTC
TCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGG
TCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGC
AACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT
ATTACTGCAATTCATATACAAGCACCAGCATGGTATTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' **(SEQ ID NO: 95)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPKLMIYEVSN
RPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCNSYTSTSMVFGGGTKLTVL
(SEQ ID NO: 23)

Alternative Nucleotide sequence of light chain variable region (26E10v1):
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGA
TCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTCTGTC
TCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACTCATGATTTATGAGG
TCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGC
AACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT
ATTACTGCAACTCATATACAAGCACCAGCATGGTATTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' **(SEQ ID NO: 293)**

FIG. 3H

26H5

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAAGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCTTTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCT3' **(SEQ ID NO: 96)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMG
WISFYNGNTNYAQKVQGRVTMTTDTSTSTVYMELRSLRSDDTAVYYCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 51)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCAT
GATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTATTCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 97)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIY
EVSNRPSGVSIRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGG
TKLTVL **(SEQ ID NO: 17)**

FIG. 3I

31D1

Nucleotide sequence of heavy chain variable region:
5'CAGATTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCTTTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTTCTGT
GCGAGAGGTTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 98)**

Amino acid sequence of heavy chain variable region:
QIQLVQSGAEVKKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMG
WISFYNGNTNYAQKVQGRVTMTTDTSTSTVYMELRSLRSDDTAVYFCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 53)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCGTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCAT
GATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGGCCGTCCTA3' **(SEQ ID NO: 99)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIY
EVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGG
GTKLAVL **(SEQ ID NO: 18)**

FIG. 3J

23G1

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTAACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGGTCAGTTTTTATAATGGTAACACAAACTATGCACAGAAGCTC
CAGGGCAGAGGCACCATGACCACAGACCCATCCACGAGCACAGCCTAC
ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 100)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMG
WVSFYNGNTNYAQKLQGRGTMTTDPSTSTAYMELRSLRSDDTAVYYCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 50)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACTCAT
GATTTATGAGGTCACTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTACTGCAACTCATATACAAGCACCAGCA
TGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 101)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPKLMIY
EVTNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCNSYTSTSMVFGG
GTKLTVL **(SEQ ID NO: 26)**

FIG. 3K

27B2

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACA
GACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGT
GGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAG
TGGATTGGGTACATATATAACAGTGGGAGCACCTACTACAACCCGTCC
CTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCT
CCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTG
TGCGAGAGAGGATACAGCTATGGTTCCTTACTTTGACTACTGGGGCCAG
GGAACCCTGGTCACCGTCTCCTCA3' **(SEQ ID NO: 102)**

Amino acid sequence of heavy chain variable region:
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG
YIYNSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREDT
AMVPYFDYWGQGTLVTVSS **(SEQ ID NO: 87)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTACTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCA
GAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGGCACA
TTATGATGTGCACTGGTACCAGCAGGTTCCAGGAACAGCCCCCAAACT
CCTCATCTATGGTAACACCTATCGGCCCTCAGGGGTCCCTGACCGATTC
TCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCC
AGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAACAGCC
TGAGTGGTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA3'
(SEQ ID NO: 103)

Amino acid sequence of light chain variable region:
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAHYDVHWYQQVPGTAPKLLIY
GNTYRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDNSLSGVVF
GGGTKLTVL **(SEQ ID NO: 13)**

FIG. 3L

16F12

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAACAGCTTT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCACTTATCTGGTCTGATGGAAGTGATGAATACTATGCAGACTCCGTGA
AGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTG
CGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGGG
GCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 104)**

Amino acid sequence of heavy chain variable region:
QVHLVESGGGVVQPGRSLRLSCAASGFTFNSFGMHWVRQAPGKGLEWVA
LIWSDGSDEYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARA
IAALYYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 79)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTTTGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACTATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGA
GTGCTTATGTCTTCGGAACTGGGACCAGGGTCACCGTCCTA3' **(SEQ ID NO: 105)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDY
NKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAYVFGT
GTRVTVL **(SEQ ID NO: 35)**

FIG. 3M

22E2

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGCAGCTTT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCACTTATATGGAATGATGGAAGTAATAAATACTATGCAGACTCCGTG
AAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGT
GCGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGG
GGCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 106)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVA
LIWNDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
AIAALYYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 80)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTTTGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACTATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGTCTGA
GTGGTTATGTCTTCGGAACTGGGACCAGGGTCACCGTCCTA3' **(SEQ ID NO: 107)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDY
NKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGYVFGT
GTRVTVL **(SEQ ID NO: 36)**

FIG. 3N

27A6

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCACCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAACAGCTTT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCACTTATATGGTCTGATGGAAGTGATAAATACTATGCAGACTCCGTGA
AGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTG
CGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGGG
GCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 108)**

Amino acid sequence of heavy chain variable region:
QVHLVESGGGVVQPGRSLRLSCAASGFTFNSFGMHWVRQAPGKGLEWVA
LIWSDGSDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARA
IAALYYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 76)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGTTCCAACATTGGGAATAAT
TTTGTATCCTGGTACCAGCAGTTCCCAGGAACAGCCCCCAAACTCCTCA
TTTATGACTATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGG
CTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGACT
GGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGT
TCTTATGTCTTCGGAACTGGGACCAGGGTCACCGTCCTA3' **(SEQ ID NO: 109)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQFPGTAPKLLIYDY
NKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSSYVFGT
GTRVTVL **(SEQ ID NO: 37)**

FIG. 3O

28B12

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGCAGCTTT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCACTTATATGGAATGATGGAAGTAATAAATACTATGCAGACTCCGTG
AAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGT
GCGAGAGCCATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGG
GGCCACGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 110)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVA
LIWNDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
AIAALYYYYGMDVWGHGTTVTVSS **(SEQ ID NO: 77)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTTTGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACTATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGA
GTGGTTATGTCTTCGGAACTGGGACCAGGGTCACCGTCCTA3' **(SEQ ID NO: 111)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDY
NKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGYVFGT
GTRVTVL **(SEQ ID NO: 38)**

FIG. 3P

28D6

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGA
GACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGCAGCTTTGGCATGCA
CTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCACTTAT
ATGGAATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCG
ATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATG
AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCC
ATAGCAGCCCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 112)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFGMHWVRQAPGKGLEWVA
LIWNDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
AIAALYYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 78)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCACAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTTTGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACTATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTACTACTGCGGAACATGGGATAGCAGCCTGA
GTGGTTATGTCTTCGGAACTGGGACCAGGGTCACCGTCCTA3' **(SEQ ID NO: 113)**

Amino acid sequence of light chain variable region:
QSVLTQPPTVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDY
NKRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGYVFGT
GTRVTVL **(SEQ ID NO: 39)**

FIG. 3Q

31G11

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGGAGCTAT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCACTTATATGGCATGATGGAAGTAATACATACTATGTAGACTCCGTGA
AGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTG
CGAGAGGTATAGCAGTGGCTTACTACTACTACGGTATGGACGTCTGGG
GCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 114)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEWV
ALIWHDGSNTYYVDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA
RGIAVAYYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 83)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAA
TTTTGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACAGTAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACGTCAGCCACCCTGGACATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGA
GTGCTTATGTTTTCGGAACTGGGACCAAGGTCACCGTCCTA3' **(SEQ ID NO: 115)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDS
NKRPSGIPDRFSGSKSGTSATLDITGLQTGDEADYYCGTWDSSLSAYVFGT
GTKVTVL **(SEQ ID NO: 40)**

FIG. 3R

23B5

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTAT
GCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCAACTATTAGTGGTAGTGGTGATAACACATACTACGCAGACTCCGTGA
AGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTG
CGAAAAAGTTTGTACTAATGGTGTATGCTATGCTTGACTACTGGGGCCA
GGGAACCCTGGTCACCGTCTCCTCA3' **(SEQ ID NO: 116)**

Amino acid sequence of heavy chain variable region:
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVS
TISGSGDNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKK
FVLMVYAMLDYWGQGTLVTVSS **(SEQ ID NO: 71)**

Nucleotide sequence of light chain variable region:
5'GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGA
GACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGTTAT
TTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGGTCCTGATC
TATGCTGCCTCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCA
GTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCTGA
AGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTCCCCCATCACC
TTCGGCCAAGGGACACGACTGGAGATTAAA3' **(SEQ ID NO: 117)**

Amino acid sequence of light chain variable region:
DILMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKVLIYAAS
SLQSGVPSRFSGSGSGTDFTLTINSLQPEDFATYYCQQSYSSPITFGQGTRLE
IK **(SEQ ID NO: 9)**

FIG. 3S

25G4

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCGGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTAT
GCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCAACTATTAGTGGTAGTGGTGGTAACACATACTACGCAGACTCCGTGA
AGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTG
CGAAAAAGTTTGTACTAATGGTGTATGCTATGCTTGACTACTGGGGCCA
GGGAACCCTGGTCACCGTCTCCTCA3' **(SEQ ID NO: 118)**

Amino acid sequence of heavy chain variable region:
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVS
TISGSGGNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKK
FVLMVYAMLDYWGQGTLVTVSS **(SEQ ID NO: 72)**

Nucleotide sequence of light chain variable region:
5'GACATCCAGATGACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGA
GACAGAGTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCATCTAT
TTAAATTGGTATCAGCAGAAGCCAGGGAAAGCCCCTTACCTCCTGATCT
ATGCTGCAGCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGTGGCA
GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGA
AGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTGCCCCCATCACC
TTCGGCCAAGGGACACGACTGGAGATTAAA3' **(SEQ ID NO: 119)**

Amino acid sequence of light chain variable region:
DIQMTQSPSSLSASVGDRVTITCRASQSISIYLNWYQQKPGKAPYLLIYAAA
SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSAPITFGQGTRLE
IK **(SEQ ID NO: 10)**

FIG. 3T

27E7

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCACTGAAGGTCTCCTGCAAGGCTTCTGGTTACAGTTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGGTGAGGAGTCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 120)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASLKVSCKASGYSLTSYGISWVRQAPGQGLEWMG
WISAYNGNTNYAQKVQGRVTMTTDTSTSTVYMEVRSLRSDDTAVYYCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 54)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCAT
GATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAATACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 121)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIY
EVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGG
GTKLTVL **(SEQ ID NO: 20)**

FIG. 3U

27H5

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAGGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCGTTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGCTGAGGAGCCTGAGCTCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 122)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKRPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEWMG
WISVYNGNTNYAQKVQGRVTMTTDTSTSTVYMELRSLSSDDTAVYYCAR
GYGMDVWGQGTTVTVSS **(SEQ ID NO: 52)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCAT
GATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTATTCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 123)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIY
EVSNRPSGVSIRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGG
TKLTVL **(SEQ ID NO: 16)**

FIG. 3V

30B9

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTCA
GTGAAGGTCTCCTGCAAGGCTTCTGGTTACCCCTTGACCAGCTATGGTATCAG
CTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGATCAGC
GCTTACAATGGTAACACAAACTATGCACAGAAGGTCCAGGGCAGAGTCACCA
TGACCACAGACACATCCACGAGCACAGTCTACATGGAGTTGAGGAGCCTGAG
ATCTGACGACACGGCCGTGTATTACTGTGCGAGAGGCTACGGTATGGACGTC
TGGGGCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 124)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYPLTSYGISWVRQAPGQGLEWMGWISA
YNGNTNYAQKVQGRVTMTTDTSTSTVYMELRSLRSDDTAVYYCARGYGMDV
WGQGTTVTVSS **(SEQ ID NO: 55)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGA
TCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTCTGTC
TCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCATGATTTATGAGG
TCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGC
AATACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT
ATTTCTGCAGCTCATATACAAGCACCAGCATGGTCTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' **(SEQ ID NO: 125)**

Alternative Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGA
TCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTCTGTC
TCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCATGATTTATGAGG
TCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGC
AACACGGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT
ATTTCTGCAGCTCATATACAAGCACCAGCATGGTCTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' **(SEQ ID NO: 294)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPKLMIYEVSN
RPSGVSNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGGTKLTVL
(SEQ ID NO: 21)

FIG. 3W

19H9

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGTTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACGCCTTGACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGATCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGGTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGTCTAC
ATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 126)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYALTSYGISWVRQAPGQGLEWM
GWISAYNGNTNYAQKVQGRVTMTTDTSTSTVYMELRSLRSDDTAVYYCA
RGYGMDVWGQGTTVTVSS **(SEQ ID NO: 56)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAACAGTGACGTTGGTGGTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAACCCCCCAAACTCAT
GATTTATGAGGTCAGTAATCGGCCCTCAGGGATTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTTCTGCAGCTCATATACAAGCACCAGCAT
GGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 127)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTNSDVGGYNSVSWYQQHPGKPPKLMIY
EVSNRPSGISNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTSTSMVFGGG
TKLTVL **(SEQ ID NO: 22)**

FIG. 3X

17C2

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGC
CTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACAGCTTTACCAGCTAT
GGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATG
GGATGGGTCAGCGCTTACAATGGTAACACAAACTATGCACAGAAGTTC
CAGGGCAGAGTCACCATGACCACAGACACATCCACGAGCACAGCCTAC
ATGGAACTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGT
GCGAGAGGCTACGTTATGGACGTCTGGGGCCAAGGGACCACGGTCACC
GTCTCCTCA3' **(SEQ ID NO: 128)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYGISWVRQAPGQGLEWMG
WVSAYNGNTNYAQKFQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCA
RGYVMDVWGQGTTVTVSS **(SEQ ID NO: 57)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTTTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGCTTATA
ACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAAACGCA
TGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTC
TGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCACCAAC
ATGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 129)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGAYNSVSWYQQHPGKAPKRMIY
EVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSTNMVFGG
GTKLTVL **(SEQ ID NO: 24)**

FIG. 3Y

13H1

Nucleotide sequence of heavy chain variable region:
5'CAGGTACAGTTGCAGCAGTCAGGTCCAGGACTGGTGAAGCCCTCGCA
GACCCTCTCACTCACCTGTGCCATCTCCGGGGACAGTGTCTCTAGCAAC
AGTGCTGCTTGGAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAG
TGGCTGGGAAGGACATACTACAGGTCCAAGTGGTATAAAAATTATTCA
GTATCTGTGAAAAGTCGAATAACCATCAACCCAGACACATCCAAGAAC
CAGTTCTCTCTGCAACTGAACTCTGTGACTCCCGGGGACACGGCTGTGT
ATTACTGTGCAAGAGGGGGGCCAACTGCTGCTTTTGACTACTGGGGCC
AGGGAACCCTGGTCACCGTCTCCTCA3' **(SEQ ID NO: 130)**

Amino acid sequence of heavy chain variable region:
QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLG
RTYYRSKWYKNYSVSVKSRITINPDTSKNQFSLQLNSVTPGDTAVYYCAR
GGPTAAFDYWGQGTLVTVSS **(SEQ ID NO: 91)**

Nucleotide sequence of light chain variable region:
5'CTTTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAG
TCGATCACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGGAATTATA
ACCTTGTCTCCTGGTACCAACAGTATTCAGGCAAAGCCCCCAAACTCAT
GATTTATGAGGTCAGTAAGCGGCCCTCAGGGGTTTCTAATCGCTTCTCT
GGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTCCAGG
CTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGCAC
TTTGGTTTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 131)**

Amino acid sequence of light chain variable region:
LSALTQPASVSGSPGQSITISCTGTSSDVGNYNLVSWYQQYSGKAPKLMIY
EVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTLVFG
GGTKLTVL **(SEQ ID NO: 28)**

FIG. 3Z

9C9

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGTTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGTAGTCTCTGGATTCACCTTTAGTAGCTATT
GGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG
CCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGA
AGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTG
CGAGAGAGTCAAACTGGGGATTTGCTTTTGATATCTGGGGCCAAGGGA
CAATGGTCACCGTCTCTTCA3' **(SEQ ID NO: 132)**

Amino acid sequence of heavy chain variable region:
EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVA
NIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARE
SNWGFAFDIWGQGTMVTVSS **(SEQ ID NO: 64)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCA
GAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAA
GACTGTAAACTGGTACCAACAGGTCCCAGGAACGGCCCCCAAACTCCT
CATCTATAGGAATAATCAGCGGCCCTTAGGGGTCCCTGACCGATTCTCT
GGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGT
CTGAGGATGAGGCTGATTATTATTGTGCAGCATGGGATGACAGCCTGA
ATTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 133)**

Amino acid sequence of light chain variable region:
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQVPGTAPKLLIYRN
NQRPLGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGG
GTKLTVL **(SEQ ID NO: 30)**

FIG. 3AA

9H6

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTCGCTATT
GGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG
CCAACATAAAGCATGATGGAAGTGAGAAATACTATGTGGACTCTGTGA
AGGGCCGATTCACCATTTCCAGAGACAACGCCAAGAACTCACTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTG
CGAGAGAGTCAAACTGGGGATTTGCTTTTGATGTCTGGGGCCACGGGA
CAATGGTCACCGTCTCTTCA3' **(SEQ ID NO: 134)**

Amino acid sequence of heavy chain variable region:
EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVA
NIKHDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARE
SNWGFAFDVWGHGTMVTVSS **(SEQ ID NO: 62)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGCCCCCCGGACA
GAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAAT
ACTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTC
ATCTATAGTAATAATCGGCGGCCCTCAGGGGTCCCTGACCGATTCTCTG
GCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTC
TGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAA
TTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 135)**

Amino acid sequence of light chain variable region:
QSVLTQPPSASGPPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSN
NRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWVFGG
GTKLTVL **(SEQ ID NO: 31)**

FIG. 3BB

13B5

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG
GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTAT
GCCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTC
TCAACTATTAGTGGTAGTGGTGGTAGGACATATTACGCAGACTCCGTGA
AGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC
TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTG
CGAAAGAAGTTGGCAGTCCCTTTGACTACTGGGGCCAGGGAACCCTGG
TCACCGTCTCCTCA3' **(SEQ ID NO: 136)**

Amino acid sequence of heavy chain variable region:
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVST
ISGSGGRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEV
GSPFDYWGQGTLVTVSS **(SEQ ID NO: 69)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACA
GAAGGTCACCATCTCCTGCTCTGGAAGCAACTCCAACATTGGGAATAA
TTATGTATCCTGGTACCAGCAGCTCCCAGGAACAGCCCCCAAACTCCTC
ATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTG
GCTCCAACTCTGGCACGTCAGCCACCCTGGGCATCACCGGACTCCAGA
CTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGA
GTGCTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 137)**

Amino acid sequence of light chain variable region:
QSVLTQPPSVSAAPGQKVTISCSGSNSNIGNNYVSWYQQLPGTAPKLLIYD
NNKRPSGIPDRFSGSNSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFG
GGTKLTVL **(SEQ ID NO: 42)**

FIG. 3CC

31B12

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTC
CCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGC
ACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAATTATATG
GTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACC
ATCTCCAGAGACAATTCCAAGAACACACTGTATCTTCAAATGAACAGCCTGA
GAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGAGGGGGGGTCTGGCAGC
TCGTCCGGGCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
TCA3' **(SEQ ID NO: 138)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAIIWY
DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRGGLAARP
GGMDVWGQGTTVTVSS **(SEQ ID NO: 81)**

Nucleotide sequence of light chain variable region:
5'TCCTATGAGCTGACTCAGCCACCCTCAGTGTCTGTGTCCCCAGGACAGACA
GCCAGAATCACCTGCTCTGGAGATAAATTGGGGGATAAATATGCTTGCTGGT
ATCAGCAGAAACCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAAATACCAA
GTGGCCCTTAGGGATCCCTGAGCGATTCTCTGGCTCCAAGTCTGGGAACACA
GTCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACT
GTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGAC
CGTCCTA3' **(SEQ ID NO: 139)**

Amino acid sequence of light chain variable region:
SYELTQPPSVSVSPGQTARITCSGDKLGDKYACWYQQKPGQSPVLVIYQNTKWP
LGIPERFSGSKSGNTVTLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
(SEQ ID NO: 44)

Alternative Nucleotide sequence of light chain variable region:
5'TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACA
GCCAGAATCACCTGCTCTGGAGATAAATTGGGGGATAAATATGCTTGCTGGT
ATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAAATACCAA
GTGGCCCTTAGGGATCCCTGAGCGATTCTCTGGCTCCAAGTCTGGGAACACA
GTCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACT
GTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGAC
CGTCCTA3' **(SEQ ID NO: 295)**

FIG. 3DD

3C4

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACA
GACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGT
GATTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAG
TGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCC
TCAAGAGTCGAATTACCATATCAGTAGACACGTCTAAGAACCTGTTCTC
CCTGAAGTTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGT
GCGAGAGGGGGGGGTGACTACGTACTACTACGCTATGGACGTCTGGGGC
CAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 140)**

Amino acid sequence of heavy chain variable region:
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSDYYWSWIRQHPGKGLEWIG
YIYYSGSTYYNPSLKSRITISVDTSKNLFSLKLSSVTAADTAVYYCARGGVT
TYYYAMDVWGQGTTVTVSS **(SEQ ID NO: 85)**

Nucleotide sequence of light chain variable region:
5'GACATACAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGA
GACAGAGTCACCATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTAT
TTAAGTTGGTATCTGCAGAAACCAGGGATTGCCCCTAAGCTCCTGATCT
ATGCTGCATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTTCAGTGGCA
GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAATCTGA
AGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCATT
TTCGGCGGAGGGACCAAGGTGGAGATCAAA3' **(SEQ ID NO: 141)**

Amino acid sequence of light chain variable region:
DIQMTQSPSSLSASVGDRVTITCRASQRISNYLSWYLQKPGIAPKLLIYAAS
SLQSGVPSRFSGSGSGTDFTLTISSLQSEDFATYYCQQSYSTPLIFGGGTKVE
IK **(SEQ ID NO: 7)**

FIG. 3EE

30A4

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG
GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTAT
GGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG
GCAGTTATATGGTATGATGGAAGTGATAAATACTATGCAGACTCCGTG
AAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGT
GCGAGAGAGACTGGTCCCTTGAAACTCTACTACTACGGTATGGACGTCT
GGGGCCAAGGGACCACGGTCACCGTCTCCTCA3' **(SEQ ID NO: 142)**

Amino acid sequence of heavy chain variable region:
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA
VIWYDGSDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
ETGPLKLYYYGMDVWGQGTTVTVSS **(SEQ ID NO: 74)**

Nucleotide sequence of light chain variable region:
5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGTCCGTCACCCCTGGA
GAGCCGCCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTA
ATGGATACAACTTTTTGAATTGGTACCTGCAGAAGCCAGGGCAGTCTCC
ACAACTCCTGATCTATTTGGGTTCTCATCGGGCCTCCGGGGTCCCTGAC
AGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGGAAATCAGC
AGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGTTCTAC
AAACTCCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA3'
(SEQ ID NO: 143)

Amino acid sequence of light chain variable region:
DIVMTQSPLSLSVTPGEPPSISCRSSQSLLHSNGYNFLNWYLQKPGQSPQLLI
YLGSHRASGVPDRFSGSGSGTDFTLEISRVEAEDVGVYYCMQVLQTPFTFG
PGTKVDIK **(SEQ ID NO: 5)**

FIG. 3FF

1A12

Nucleotide sequence of heavy chain variable region:
5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGG
GGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGACTCACCTTTAGTAA
CTTTTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAG
TGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGG
ACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAA
TTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCT
GTGTATTCCTGTACGAGAGAGTCAAACTGGGGATTTGCTTTTGATAT
CTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA3' **(SEQ ID NO: 144)**

Amino acid sequence of heavy chain variable region:
EVQLVESGGGLVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGLEW
VANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYS
CTRESNWGFAFDIWGQGTMVTVSS **(SEQ ID NO: 65)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC
AGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGT
AAAACTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCCCCAAAC
TCCTCATCTATAGTAATAATCGGCGGCCCTCAGGGGTCCCTGACCGA
TTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGG
GCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATG
ACAGCCTGAATTGGGTGTTCGGCGCAGGGACCAAGCTGACCGTCCTA
3' **(SEQ ID NO: 145)**

Amino acid sequence of light chain variable region:
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLLIYS
NNRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNWV
FGAGTKLTVL **(SEQ ID NO: 33)**

FIG. 3GG

3B6

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGG
GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAG
CTATGGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGT
GGATGGGATGGATCAGCACTTACAATGGTAACACAAACTATGCACA
GAAGGTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGC
ACAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCG
TTTATTACTGTGCGAGAGGGTATACTCGGGACTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCA3' **(SEQ ID NO: 146)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW
MGWISTYNGNTNYAQKVQGRVTMTTDTSTSTAYMELRSLRSDDTAVY
YCARGYTRDYWGQGTLVTVSS **(SEQ ID NO: 60)**

Nucleotide sequence of light chain variable region:
5'CAGCCTGTGCTGACTCAGCCACTTTTTGCATCAGCCTCCCTGGGAG
CCTCGGTCACACTCACCTGCACCCTGAGCAGCGGCTACAGTAGTTAT
GAAGTGGACTGGTATCAGCAGAGACCAGGGAAGGGCCCCCGGTTTG
TCATGCGAGTGGACACTGGTGGGATTGTGGGATCCAAGGGGGAAGG
CATCCCTGATCGCTTCTCAGTTTTGGGCTCAGGCCTGAATCGGTATCT
GACCATCAAGAACATCCAGGAAGAGGATGAGAGTGACTACCACTGT
GGGGCAGACCATGGCAGTGGGACCAACTTCGTGGTGGTATTCGGCG
GAGGGACCAAGCTGACCGTCCTA3' **(SEQ ID NO: 147)**

Amino acid sequence of light chain variable region:
QPVLTQPLFASASLGASVTLTCTLSSGYSSYEVDWYQQRPGKGPRFVM
RVDTGGIVGSKGEGIPDRFSVLGSGLNRYLTIKNIQEEDESDYHCGADH
GSGTNFVVVFGGGTKLTVL **(SEQ ID NO: 46)**

FIG. 3HH

31A4

Nucleotide sequence of heavy chain variable region:
5'CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCG
GAGACCCTGTCCCTCACCTGCGCTGTCTATGGTGGGTCCTTCAGTGC
GTACTACTGGAACTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAG
TGGATTGGGGAAATCAATCATAGTGGAAGAACCGACTACAACCCGT
CCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAAGCA
GTTCTCCCTGAAGCTGAACTCTGTGACCGCCGCGGACACGGCTGTGT
ATTACTGTGCGAGAGGGCAGCTCGTCCCCTTTGACTACTGGGGCCAG
GGAACCCTGGTCACCGTCTCTTCA3' **(SEQ ID NO: 148)**

Amino acid sequence of heavy chain variable region:
QVQLQQWGAGLLKPSETLSLTCAVYGGSFSAYYWNWIRQPPGKGLEWI
GEINHSGRTDYNPSLKSRVTISVDTSKKQFSLKLNSVTAADTAVYYCAR
GQLVPFDYWGQGTLVTVSS **(SEQ ID NO: 89)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGC
AGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGT
AATACTGTAAATTGGTATCAGCAACTCCCAGGAACGGCCCCCAAACT
CCTCATCTATAGTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGAT
TCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG
CTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGA
CAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTC
CTA3' **(SEQ ID NO: 149)**

Amino acid sequence of light chain variable region:
QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIY
SNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNG
WVFGGGTKLTVL **(SEQ ID NO: 32)**

FIG. 3II

25A7

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGG
GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTCCCAG
CTATGGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGT
GGATGGGATGGATCAGCGCTTACAATGGTAACACAAACTATGCAGA
GAAGCTCCAGGGCAGAGTCACCATGACCACAGACACATCCACGAGC
ACAGCCTACATGGAGGTGAGGAGCCTGAGATCTGACGACACGGCCG
TGTTTTACTGTGCGAGAGGCTACGTTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCCTCT3' **(SEQ ID NO: 150)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTFPSYGISWVRQAPGQGLEW
MGWISAYNGNTNYAEKLQGRVTMTTDTSTSTAYMEVRSLRSDDTAVF
YCARGYVMDVWGQGTTVTVSS **(SEQ ID NO: 58)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGAC
AGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTCGT
TATAATTCTGTCTCCTGGTACCAACACCACCCAGGCAAAGCCCCCAA
AGTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTACTC
GCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCT
GGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATAC
AAGCAGCAGCGTTGTATTCGGCGGAGGGACCAAACTGACCGTCCTA
3' **(SEQ ID NO: 151)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGRYNSVSWYQHHPGKAPKVM
IYEVSNRPSGVSTRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSVVF
GGGTKLTVL **(SEQ ID NO: 15)**

FIG. 3JJ

21B12

Nucleotide sequence of heavy chain variable region:
5'CAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCTGGG
GCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTAACCAG
CTATGGTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGT
GGATGGGATGGGTCAGTTTTTATAATGGTAACACAAACTATGCACAG
AAGCTCCAGGGCAGAGGCACCATGACCACAGACCCATCCACGAGCA
CAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGACACGGCCGT
GTATTACTGTGCGAGAGGCTACGGTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCCTCT3' **(SEQ ID NO: 94)**

Amino acid sequence of heavy chain variable region:
QVQLVQSGAEVKKPGASVKVSCKASGYTLTSYGISWVRQAPGQGLEW
MGWVSFYNGNTNYAQKLQGRGTMTTDPSTSTAYMELRSLRSDDTAVY
YCARGYGMDVWGQGTTVTVSS **(SEQ ID NO: 49)**

Nucleotide sequence of light chain variable region:
5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGAC
AGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGT
TATAACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAAGCCCCCAA
ACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATC
GCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCT
GGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAATTCATATAC
AAGCACCAGCATGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
3' **(SEQ ID NO: 296)**

Amino acid sequence of light chain variable region:
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKAPKLM
IYEVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCNSYTSTSMV
FGGGTKLTVL **(SEQ ID NO: 23)**

FIG. 3KK

Constant Domains

Human IgG2:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV
ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNG
KEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 154)

Human IgG4:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRV
ESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQ
EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD
KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 155)

Human lambda:

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK
AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT
VAPTECS (SEQ ID NO: 156)

Human kappa:

TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC (SEQ ID NO: 157)

FIG. 3LL

5H5.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGGTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTG
GGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCA
CCGGCTACTATATACACTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGATGGATCAACCCTCACAGTGGTGGCGCAAA
CTATGCACAGAAGTTTCAGGGCAGGGTCACCATGACCAGGGACA
CGTCCATCAGCACAGCCTACATGGAGCTGAGCAGGCTGAGATCT
GACGACACGGCCGTGTATTACTGTGCGAGAGGCAACTGGAACTA
CGACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCA3' (SEQ ID NO:418)

Amino acid sequence of heavy chain variable region:

QVQVVQSGAEVKKPGASVKVSCKASGYTFTGYYIHWVRQAPGQGL
EWMGWINPHSGGANYAQKFQGRVTMTRDTSISTAYMELSRLRSDD
TAVYYCARGNWNYDYYGMDVWGQGTTVTVSS (SEQ ID NO:419)

Nucleotide sequence of light chain variable region:

5'GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGT
AGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGACATTA
GCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTA
AGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCAT
CTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA
TCAGCAGCCTACAGCCTGAAGATGTTGCAACTTATTTCTGTCAAA
GGTATCAGATTGCCCCATTCACTTTCGGCCCTGGGACCAAGGTGG
ATATCAAA3' (SEQ ID NO:420)

Amino acid sequence of light chain variable region:

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLAWYQQKPGKVPKLL
IYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYFCQRYQIAPF
TFGPGTKVDIK (SEQ ID NO:421)

FIG. 3MM

24F7.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATCTGGTATGATGGAAGTACTAAATAC
TATGCAGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGA
GGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCA3' (SEQ ID NO:422)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGL
EWVAVIWYDGSTKYYADSVKGRSTISRDNSKNTLYLQMNSLRAED
TAVYYCARSVAGYHYYYGMDVWGQGTTVTVSS (SEQ ID NO: 423)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCT
ATTATGCAACCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTATGGTAAAAACTACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTCC
CGGGACAGCATTGGTAACCATCTGGTGTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:424)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRGYYATWYQQKPRQAPVLV
IYGKNYRPSGIPDRFSGSTSGNTASLTITGAQAEDEADYYCNSRDSIG
NHLVFGGGTKLTVL (SEQ ID NO:425)

FIG. 3NN

22B11.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAGCTATGGCTTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTTAGATGGAAGTAATAAATA
CTATGCAGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACA
ATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTAC
CACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCA3' (SEQ ID NO:426)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGLHWVRQAPGKGLE
WVAVIWLDGSNKYYADSVKGRSTISRDNSKNTLYLQMNSLRAEDT
AVYYCARSVAGYHYYYGMDVWGQGTTVTVSS (SEQ ID NO:427)

Nucleotide sequence of light chain variable region:
5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGTT
ATTATGGAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTTTGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTC
ACGGGACATCATTGGTGACCATCTGCTGTTCGGCGGAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:428)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRSYYGSWYQQKPRQAPVLVI
FGKNNRPSGIPDRFSGSTSGNTASLTITGAQAEDEADYYCNSRDIIGD
HLLFGGGTKLTVL (SEQ ID NO:429)

FIG. 3OO

30F1.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGTCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GGAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTTTGATGGAAGTAATAAATAC
TATGCAGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCCGA
GGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCA3'(SEQ ID NO:430)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQSGRSLRLSCAASGFTFRNYGMHWVRQAPGKGL
EWVAVIWFDGSNKYYADSVKGRSTISRDNSKNTLYLLMNSLRAEDT
AVYYCARSVAGYHYYYGMDVWGQGTTVTVSS (SEQ ID NO:431)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAGGGAGACAGCCTCAGAAGCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGAATCTCTGGCTCCACCTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAAATC
CCGGGACATCATTGGTGACCATCTGGTGTTCGGCGGAGGGACCA
AACTGACCGTCCTA3' (SEQ ID NO:432)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPRQAPVLVI
YGKNNRPSGIPDRISGSTSGNTASLTITGAQAEDEADYYCKSRDIIGD
HLVFGGGTKLTVL (SEQ ID NO:433)

FIG. 3PP

24B9.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATA
CTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAA
TTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGTGAGAGATCGGGGACTGGAC
TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3' (SEQ ID
NO:434)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGL
EWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAED
TAVYYCVRDRGLDWGQGTLVTVSS (SEQ ID NO:435)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAAGTC
CCGGGACAGCAGTGGTGACCATCTGGTGTTCGGCGGAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:436)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRGYYASWYQQKPRQAPVLV
IYGKNNRPSGIPDRFSGSTSGNTASLTITGAQAEDEADYYCKSRDSSG
DHLVFGGGTKLTVL (SEQ ID NO:437)

FIG. 3QQ

24B9.2

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATTTGGTATGATGGAAGTAGTAAATAC
TATGCAGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAAT
TCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCCGA
GGACACGGCTGTGTATTACTGTGCGAGGTCAGTGGCTGGTTACCA
CTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCTCCTCA3'(SEQ ID NO:438)

Amino acid sequence of heavy chain variable region:

QVQVVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGKGL
EWVAVIWYDGSSKYYADSVKGRSTISRDNSKNTVYLQMNSLRAED
TAVYYCARSVAGYHYYYGMDVWGQGTTVTVSS (SEQ ID NO:439)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAAGTC
CCGGGACAGCAGTGGTGACCATCTGGTGTTCGGCGGAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:440)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRGYYASWYQQKPRQAPVLV
IYGKNNRPSGIPDRFSGSTSGNTASLTITGAQAEDEADYYCKSRDSSG
DHLVFGGGTKLTVL (SEQ ID NO:441)

FIG. 3RR

20A5.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGTCTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTTATAAAGA
CTATGCAGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACA
ACTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTATTGTGCGAGGTCAGTGGCTGGTTAC
CACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT
CACCGTCTCCTCA3' (SEQ ID NO:442)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVVQPGRSLSLSCAASGFTFSSYGMHWVRQAPGKGLE
WVAVIWYDGSYKDYADSVKGRSTISRDNSKNTLYLQMNSLRAEDT
AVYYCARSVAGYHYYYGMDVWGQGTTVTVSS (SEQ ID NO:443)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAACCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTATT
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAATCACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAAATC
CCGGGACATCATTGGTAACCATCTGCTGTTCGGCGGAGGGACTAA
GCTGACCGTCCTA3' (SEQ ID NO:444)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPRQAPILVI
YGKNNRPSGIPDRFSGSTSGITASLTITGAQAEDEADYYCKSRDIIGN
HLLFGGGTKLTVL (SEQ ID NO:445)

FIG. 3SS

20A5.2

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGCGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCCTCA
GTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCCAGGGG
CTGGAGTGGGTGGCAGTCATATGGTATGATGGAAGTAACAAATA
CTATGCAGCCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAA
TTCCAAGAACACGCTGTATCTGCAAATGAACAGTCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGAGAGGGGGTGGTTCGGGG
AGTCATCGCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG
ACCACGGTCACCGTCTCCTCA3' (SEQ ID NO:446)

Amino acid sequence of heavy chain variable region:

QVQLVASGGGVVQPGRSLRLSCAASGFTLSSYGMHWVRQAPGQGL
EWVAVIWYDGSNKYYAASVKGRFTISRDNSKNTLYLQMNSLRAED
TAVYYCARGGGSGSHRYYYYGMDVWGQGTTVTVSS (SEQ ID
NO:447)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAACCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTATT
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACCTCAGGAATCACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAAATC
CCGGGACATCATTGGTAACCATCTGCTGTTCGGCGGAGGGACTAA
GCTGACCGTCCTA3' (SEQ ID NO:448)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRTYYASWYQQKPRQAPILVI
YGKNNRPSGIPDRFSGSTSGITASLTITGAQAEDEADYYCKSRDIIGN
HLLFGGGTKLTVL (SEQ ID NO:449)

FIG. 3TT

20E5.1 – version1 (v1)

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAGGTAATAAATA
CTATGCAGACTCCGTGAAGGGCCGATCCATCATCTCCAGAGACAA
TTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTTTATTATTGTGCGAGGTCAGTGGCTGGTTACC
ATTATTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCGCCTCA3' (SEQ ID NO:450)

Amino acid sequence of heavy chain variable region:

QVQVVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGL
EWVAVIWYDGGNKYYADSVKGRSIISRDNSKSTLYLQMNSLRAEDT
AVYYCARSVAGYHYYYGMDVWGQGTTVTVAS (SEQ ID NO:451)

Nucleotide sequence of light chain variable region:

5'CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGG
ACAGTCGATCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGG
TGGTTATAACTCTGTCTCCTGGTACCAACAGCACCCAGGCAAACC
CCCCAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGAT
TTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTG
ACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTTCTGC
AGCTCATATACAAGCACCAGCATGGTCTTCGGCGGAGGGACCAA
GCTGGCCGTCCTA3' (SEQ ID NO:452)

Amino acid sequence of light chain variable region:

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNSVSWYQQHPGKPPK
LMIYEVSNRPSGISNRFSGSKSGNTASLTISGLQAEDEADYFCSSYTST
SMVFGGGTKLAVL (SEQ ID NO:453)

FIG. 3UU

20E5.1 – version2 (v2)

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAAGTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAACTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATGGTATGATGGAGGTAATAAATA
CTATGCAGACTCCGTGAAGGGCCGATCCATCATCTCCAGAGACAA
TTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTTTATTATTGTGCCGAGGTCAGTGGCTGGTTACC
ATTATTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCA
CCGTCGCCTCA3' (SEQ ID NO:454)

Amino acid sequence of heavy chain variable region:

QVQVVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGL
EWVAVIWYDGGNKYYADSVKGRSIISRDNSKSTLYLQMNSLRAEDT
AVYYCARSVAGYHYYYGMDVWGQGTTVTVAS (SEQ ID NO:455)

Nucleotide sequence of light chain variable region:

5'TCTTCTGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCCTTGGG
ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAGGCT
ATTATGCAAGCTGGTACCAGCAGAAGCCAAGACAGGCCCCTGTA
CTTGTCATCTATGGTAAAAACAACCGGCCCTCAGGGATCCCAGAC
CGATTCTCTGGCTCCACGTCAGGAAACACAGCTTCCTTGACCATC
ACTGGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTAACTCC
CGGGACAACATTGGTGACCATCTGGTGTTCGGCGGAGGGACCAA
GCTGACCGTCCTA3' (SEQ ID NO:456)

Amino acid sequence of light chain variable region:

SSELTQDPAVSVALGQTVRITCQGDSLRGYYASWYQQKPRQAPVLV
IYGKNNRPSGIPDRFSGSTSGNTASLTITGAQAEDEADYYCNSRDNIG
DHLVFGGGTKLTVL (SEQ ID NO:457)

FIG. 3VV

8A3.1

Nucleotide sequence of heavy chain variable region:

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCCGGATTCACCTTTA
GTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTGGCCAGCATAAAACAAGATGGAAGTGAGAAATA
CTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAA
CGCCAGGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGAGAGATCTTGTATTAATGG
TGTATGATATAGACTACTACTACTACGGTATGGACGTCTGGGGCC
AAGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO:458)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLE
WVASIKQDGSEKYYVDSVKGRFTISRDNARNSLYLQMNSLRAEDTA
VYYCARDLVLMVYDIDYYYYGMDVWGQGTTVTVSS (SEQ ID
NO:459)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCC
TGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCT
GCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCC
AGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGC
CTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAG
ATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGG
GTTTATTACTGCATGCAAGCTCTACAAACTCCGCTCACTTTCGGC
GGAGGGACCAAGGTAGAGATCAAA3' (SEQ ID NO:460)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQS
PQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
ALQTPLTFGGGTKVEIK (SEQ ID NO:461)

FIG. 3WW

11F1.1

Nucleotide sequence of heavy chain variable region:

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCCGGATTCACCTTTA
GTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTGGCCAGCATAAAACAAGATGGAAGTGAGAAATA
CTATGTGGACTCTGTGAAGGGCCGATTCGCCATCTCCAGAGACAA
CGCCAAGAACTCACTGTTTCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGAGAGATCTTGTACTAATGG
TGTATGATATAGACTACTACTACTACGGTATGGACGTCTGGGGCC
AAGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO:462)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMSWVRQAPGKGL
EWVASIKQDGSEKYYVDSVKGRFAISRDNAKNSLFLQMNSLRAEDT
AVYYCARDLVLMVYDIDYYYYGMDVWGQGTTVTVSS (SEQ ID
NO:463)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCTGTCACCCCT
GGAGAGCCGGCCTCCATCTCTTGCAGGTCTAGTCAGAGCCTCCTG
CATAGTAATGGGTACAACTATTTGGATTGGTACCTGCAGAAGCCA
GGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCC
TCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACACAT
CTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGAGT
TTATTACTGCATGCAAACTCTACAAACTCCGCTCACTTTCGGCGG
AGGGACCAAGGTGGAGATCAAA3' (SEQ ID NO:464)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQS
PQLLIYLGSNRASGVPDRFSGSGSGTHLTLKISRVEAEDVGVYYCMQ
TLQTPLTFGGGTKVEIK (SEQ ID NO:465)

FIG. 3XX

12H11.1

Nucleotide sequence of heavy chain variable region:

5'CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGCCCAGCCTG
GGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCA
GTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCAGTTATATACTATGATGGAATTAATAAACAC
TATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGA
GGACACGGCTGTGTATTACTGTGCGAGAGATCGGGGACTGGACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCA3' (SEQ ID NO:466)

Amino acid sequence of heavy chain variable region:

QVQLVESGGGVAQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGL
EWVAVIYYDGINKHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDT
AVYYCARDRGLDWGQGTLVTVSS (SEQ ID NO:467)

Nucleotide sequence of light chain variable region:

5'GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCT
GGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTT
TATACAGCTCCAACAGTAAGAACTACTTAGTTTGGTACCAGCAGA
AACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCCTCTACCC
GGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTG
GCAGTTTATTACTGTCAACAATATTATAGTACTCCGTGGACGTTC
GGCCAAGGGACCAAGGTGGAAATCAAA3' (SEQ ID NO:468)

Amino acid sequence of light chain variable region:

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLVWYQQKPG
QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQ
QYYSTPWTFGQGTKVEIK (SEQ ID NO:469)

FIG. 3YY

11H4.1

Nucleotide sequence of heavy chain variable region:

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGACTCACCTTTA
GTAACTTTTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAATGATAAATA
CTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAA
CGCCAAGAATTCACTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGAGAGAGTCAAACTGGGGA
TTTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT
TCA3' (SEQ ID NO:470)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGL
EWVANIKQDGNDKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAED
TAVYYCARESNWGFAFDIWGQGTMVTVSS (SEQ ID NO:471)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGG
GCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGG
AAGTAAAACTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCC
CCAAACTCCTCATCTATAGTAATAATCGGCGGCCCTCAGGGGTCC
CTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTG
CAGCATGGGATGACAGCCTGAATTGGGTGTTCGGCGCAGGGACC
AAGCTGACCGTCCTA3' (SEQ ID NO:472)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLL
IYSNNRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDS
LNWVFGAGTKLTVL (SEQ ID NO:473)

FIG. 3ZZ

11H8.1

Nucleotide sequence of heavy chain variable region:

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGTTTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGACTCACCTTTA
GTAACTTTTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATA
CTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAA
CGCCAAGAATTCACTGTATCTGCAAATGAACAGCCTGAGAGCCG
AGGACACGGCTGTGTATTACTGTGCGAGAGAGTCAAACTGGGGA
TTTGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT
TCA3' (SEQ ID NO:474)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGLTFSNFWMSWVRQAPGKGL
EWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDT
AVYYCARESNWGFAFDIWGQGTMVTVSS (SEQ ID NO:475)

Nucleotide sequence of light chain variable region:

5'CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGG
GCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGG
AAGTAAAACTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCC
CCAAACTCCTCATCTATAGTAATAATCGGCGGCCCTCAGGGGTCC
CTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGG
CCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTG
CAACATGGGATGACAGACTGAATTGGGTGTTCGGCGCAGGGACC
AAGCTGACCGTCCTA3' (SEQ ID NO:476)

Amino acid sequence of light chain variable region:

QSVLTQPPSASGTPGQRVTISCSGSSSNIGSKTVNWYQQFPGTAPKLL
IYSNNRRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDR
LNWVFGAGTKLTVL (SEQ ID NO:477)

FIG. 3AAA

11G1.5

Nucleotide sequence of heavy chain variable region:

5'CAGGTCACCTTGAAGGAGTCTGGTCCTGTGCTGGTGAAACCCAC
AGAGACCCTCACGCTGACCTGCACCGTCTCTGGGTTCTCACTCAG
CAATGTTAGAATGGGTGTGAGCTGGATCCGTCAGCCCCCAGGGA
AGGCCCTGGAGTGGCTTGCACACATTTTTTCGAATGACGAAAATT
CCTACAGAACATCTCTGAAGAGCAGGCTCACCATCTCCAAGGAC
ACCTCCAAAAGCCAGGTGGTCCTTACCATGACCAACATGGACCCT
GTGGACACAGCCACATATTACTGTGCACGGATAGTGGGAGCTAC
AACGGATGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCAC
CGTCTCTTCA3' (SEQ ID NO:478)

Amino acid sequence of heavy chain variable region:

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNVRMGVSWIRQPPGKAL
EWLAHIFSNDENSYRTSLKSRLTISKDTSKSQVVLTMTNMDPVDTAT
YYCARIVGATTDDAFDIWGQGTMVTVSS (SEQ ID NO:479)

Nucleotide sequence of light chain variable region:

5'TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGG
ACAGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTA
AAAGTGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTGTG
CTGGTCGTCTATGATGATAGCGACCGGCCCTCAGGGATCCCTGAG
CGATTCTCTGGCTCCAACTCTGGGAACACGGCCACCCTGACCATC
AGCAGGGTCGAAGCCGGGGATGAGGCCGACTTTTACTGTCAGGT
GTGGGATAGTAGTAGTGATCCTGTGGTATTCGGCGGAGGGACCA
AGCTGACCGTCCTA3' (SEQ ID NO:480)

Amino acid sequence of light chain variable region:

SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLV
VYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEADFYCQVWDSS
SDPVVFGGGTKLTVL (SEQ ID NO:481)

FIG. 3BBB

8A1.2

Nucleotide sequence of heavy chain variable region:

5'GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTG
GGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTA
GTAACTATTGGATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTGGCCAGCATAAAGCAAGATGGAAGTGAGAGATA
CTATGTGGACTCTGTGAAGGGCCGATTCACCATCTCCCGAGACAC
CGCCAAGAACTCTCTGTATCTCCAAATGAACAGCCTGCGAGCCGA
GGACACGGCTGTGTATTACTGTGCGAGACCTCTTGTACTAATGGT
GTATGCTCTACACTACTACTACTACGGTATGGACGTCTGGGGCCA
CGGGACCACGGTCACCGTCTCCTCA3' (SEQ ID NO:482)

Amino acid sequence of heavy chain variable region:

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMTWVRQAPGKGL
EWVASIKQDGSERYYVDSVKGRFTISRDTAKNSLYLQMNSLRAEDT
AVYYCARPLVLMVYALHYYYYGMDVWGHGTTVTVSS (SEQ ID
NO:483)

Nucleotide sequence of light chain variable region:

5'GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCC
TGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCT
GCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGAAGCC
AGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGC
CTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAG
ATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGG
GTTTATTACTGCATGCAAGCTCTACAAACTCCGCTCACTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA3' (SEQ ID NO:484)

Amino acid sequence of light chain variable region:

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQS
PQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ
ALQTPLTFGGGTKVEIK (SEQ ID NO:485)

FIG. 3CCC

Heavy variable	SEQ ID NO:	Germline	Germline	FR1	CDR1	FR2
	493	VH1|1-02		QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTGYYMH	WVRQAPGQGLEWMG
5H5.1G	419	VH1|1-02	JH6	---V----------	--------I-	----------
		Germline	Germline	FR1	CDR1	FR2
	494	VH3|3-33		QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
24B9.1G	435	VH3|3-33	JH4	----------	----------	----------
		Germline	Germline	FR1	CDR1	FR2
	495	VH3|3-33		QVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYGMH	WVRQAPGKGLEWVA
24F7.1G	423	VH3|3-33	JH6	----------	----------	----------
22B11.1G	427	VH3|3-33	JH6	----------	--------L-	----------
20A5.1G	443	VH3|3-33	JH6	----------S-	----------	----------
20A5.2G	447	VH3|3-33	JH6	----A-----------	---L------	-------Q--
30F1.1G	431	VH3|3-33	JH6	----------S-	----RN----	----------
20E5.1G	451	VH3|3-33	JH6	---V----------	-----N----	----------
24B9.2G	439	VH3|3-33	JH6	---V----------G-	-----N----	----------

FIG. 3DDD

Heavy variable	SEQ ID NO:	CDR2	FR3	CDR3	FR4
	493	WINPNSGGTNYAQKFQG	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAR		
5H5.1G	419	----H---A--------	----------	GNWNYDYYGMDV	WGQGTTVTVSS
		CDR2	FR3	CDR3	FR4
	494	VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR		
24B9.1G	435	----------	----------	DRGLD	WGQGTLVTVSS
		CDR2	FR3	CDR3	FR4
	495	VIWYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR		
24F7.1G	423	-------T----------	-S----------	SVAGYHYYYGMDV	WGQGTTVTVSS
22B11.1G	427	---L----------	-S----------	SVAGYHYYYGMDV	WGQGTTVTVSS
20A5.1G	443	-------Y-D-------	-S----------	SVAGYHYYYGMDV	WGQGTTVTVSS
20A5.2G	447	----------A-----	----------	GGGSGSHRYYYYGMDV	WGQGTTVTVSS
30F1.1G	431	---F----------	-S----------L----------	SVAGYHYYYGMDV	WGQGTTVTVSS
20E5.1G	451	------G----------	-SI---------S----------	SVAGYHYYYGMDV	WGQGTTVTVAS
24B9.2G	439	------S----------	-S----------V----------	SVAGYHYYYGMDV	WGQGTTVTVSS

FIG. 3EEE

Kappa variable	SEQ ID NO:			FR1	CDR1	FR2
		Germline	Germline			
	496	VK1|A20		DIQMTQSPSSLSASVGDRVTITC	RASQGISNYLA	WYQQKPGKVPKLLIY
5H5.1K	421	VK1|A20	JK3	----------D----------	----------D----------	----------
Lambda variable						
		Germline	Germline	FR1	CDR1	FR2
	497	VL2|2a2		QSALTQPASVSGSPGQSITISC	TGTSSDVGGYNYVS	WYQQHPGKAPKLMIY
20E5.1L v1	453	VL2|2a2	JL2	----------	----------S--	----------P----------

		Germline	Germline	FR1	CDR1	FR2
	498	VL3|3l		SSELTQDPAVSVALGQTVRITC	QGDSLRSYYAS	WYQQKPGQAPVLVIY
30F1.1L	433	VL3|3l	JL2	----------	----------	----------R----------
22B11.1L	429	VL3|3l	JL2	----------	----------G-	----------R----------F
24B9.1L	437	VL3|3l	JL2	----------	------G----	----------R----------
24B9.2L	441	VL3|3l	JL2	----------	------G----	----------R----------
20E5.1L v2	457	VL3|3l	JL2	----------	------G----	----------R----------
24F7.1L	425	VL3|3l	JL2	----------	------G---T	----------R----------
20A5.1L	445	VL3|3l	JL2	----------	------T----	----------R---I----
20A5.2L	449	VL3|3l	JL2	----------	------T----	----------R---I----

FIG. 3FF

Kappa variable	SEQ ID NO:	CDR2	FR3	CDR3	FR4
	496	AASTLQS	GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC		
5H5.1K	421	-------	----------F-	QRYQIAPFT	FGPGTKVDIK
Lambda_variable					
		CDR2	FR3	CDR3	FR4
	497	EVSNRPS	GVSNRFSGSKSGNTASLTISGLQAEDEADYYC		
20E5.1L v1	453	-------	-I----------F-	SSYTSTSMV	FGGGTKLAVL

		CDR2	FR3	CDR3	FR4
	498	GKNNRPS	GIPDRFSGSSSGNTASLTITGAQAEDEADYYC		
30F1.1L	433	-------	-----I---T----------	KSRDIIGDHLV	FGGGTKLTVL
22B11.1L	429	-------	----------T----------	NSRDIIGDHLL	FGGGTKLTVL
24B9.1L	437	-------	----------T----------	KSRDSSGDHLV	FGGGTKLTVL
24B9.2L	441	-------	----------T----------	KSRDSSGDHLV	FGGGTKLTVL
20E5.1L v2	457	-------	----------T----------	NSRDNIGDHLV	FGGGTKLTVL
24F7.1L	425	---Y---	----------T----------	NSRDSIGNHLV	FGGGTKLTVL
20A5.1L	445	-------	----------T--I-------	KSRDIIGNHLL	FGGGTKLTVL
20A5.2L	449	-------	----------T--I-------	KSRDIIGNHLL	FGGGTKLTVL

FIG. 3GGG

	SEQ ID NO:					SEQ ID NO:			SEQ ID NO:		SEQ ID NO:
				FR1			CDR1			FR2	
		Germline	Germline								
	486	VH2|226		QVTLKESGPVLVKPTETLTLTCTVS		506	GFSLSNARMGVS		507	WIRQPPGKALEWLA	509
11G1.5	479	VH2|226	JH3	----------		506	-----V-----		508	----------	509
		Germline	Germline	FR1			CDR1			FR2	
	487	VH3|307		EVQLVESGGGLVQPGGSLRLSCAAS		510	GFTFSSYWMS		511	WVRQAPGKGLEWVA	514
11H8.1	475	VH3|307	JH3	----------		510	-L---NF---		512	----------	514
11H4.1	471	VH3|307	JH3	----------		510	-L---NF---		512	----------	514
8A3.1	459	VH3|307	JH6	----------		510	----------		511	----------	514
11F1.1	463	VH3|307	JH6	----------		510	-----N----		500	----------	514
8A1.2	483	VH3|307	JH6	----------		510	-----N---T		513	----------	514
		Germline	Germline	FR1			CDR1			FR2	
	488	VH3|3-33		QVQLVESGGGVVQPGRSLRLSCAAS		515	GFTFSSYGMH		517	WVRQAPGKGLEWVA	518
12H11.1	467	VH3|3-33	JH4	----------A----------		516	----------		517	----------	518

FIG. 3HH

	SEQ ID NO:		SEQ ID NO:		SEQ ID NO:		SEQ ID NO:		SEQ ID NO:
		CDR2		FR3		CDR3		FR4	
	486	HIFSNDEKSYSTSLKS	519	RLTISKDTSKSQVVLTMTNMDPVDTATYYCARI	521		522		
11G1.5	479	-------N--R-----	520	----------	521	VGATTDIAFDI		WGQGTMVTVSS	523
		CDR2		FR3		CDR3		FR4	
	487	NIKQDGSEKYYVDSVKG	526	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	529				
11H8.1	475	----------	526	----------	529	ESNWGFAFDI	533	WGQGTMVTVSS	523
11H4.1	471	------ND-------	527	----------	529	ESNWGFAFDI	533	WGQGTMVTVSS	523
8A3.1	459	S---------------	501	---------R----------	530	DLVLMVYDIDYYYYGMDV	502	WGQGTTVTVSS	524
11F1.1	463	S---------------	501	--A---------F----------	531	DLVLMVYDIDYYYYGMDV	502	WGQGTTVTVSS	524
8A1.2	483	S-------R-------	528	------T----------	532	PLVLMVYALHYYYYGMDV	534	WGHGTTVTVSS	525
		CDR2		FR3		CDR3		FR4	
	488	VIWYDGSNKYYADSVKG	535	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	537				
12H11.1	467	--Y---I--H------	536	----------	537	DRGLD	538	WGQGTLVTVSS	539

FIG. 3III

	SEQ ID NO:				SEQ ID NO:		SEQ ID NO:		SEQ ID NO:
		Germline	Germline	FR1		CDR1		FR2	
	489	VK2|A19		DIVMTQSPLSLPVTPGEPASISC	540	RSSQSLLHSNGYNYLD	503	WYLQKPGQSPQLLIY	541
8A1.2	485	VK2|A19	JK4	-------------------------	540	-------------------	503	----------------	541
8A3.1	461	VK2|A19	JK4	-------------------------	540	-------------------	503	----------------	541
11F1.1	465	VK2|A19	JK4	-------------------------	540	-------------------	503	----------------	541
		Germline	Germline	FR1		CDR1		FR2	
	490	VK4|B3		DIVMTQSPDSLAVSLGERATINC	542	KSSQSVLYSSNNKNYLA	543	WYQQKPGQPPKLLIY	545
12H11.1	469	VK4|B3	JK1	-------------------------	542	----------S----V	544	----------------	545
		Germline	Germline	FR1		CDR1		FR2	
	491	VL1|1c		QSVLTQPPSASGTPGQRVTISC	546	SGSSSNIGSNTVN	547	WYQQLPGTAPKLLIY	549
11H4.1	473	VL1|1c	JL3b	-------------------------	546	----------K---	548	----F----------	550
11H8.1	477	VL1|1c	JL3b	-------------------------	546	----------K---	548	----F----------	550
		Germline	Germline	FR1		CDR1		FR2	
	492	VL3|3h		SYVLTQPPSVSVAPGKTARITC	551	GGNNIGSKSVH	553	WYQQKPGQAPVLVIY	554
11G1.5	481	VL3|3h	JL2	----------Q------	552	----------	553	----------V-	555

FIG. 3JJ

	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
	489	LGSNRAS	504	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	556				
8A1.2	485	-------	504	----------	556	MQALQTPLT	558	FGGGTKVEIK	559
8A3.1	461	-------	504	----------	556	MQALQTPLT	558	FGGGTKVEIK	559
11F1.1	465	-------	504	----------HL----------	567	MQTLQTPLT	505	FGGGTKVEIK	559
		CDR2		FR3		CDR3		FR4	
	490	WASTRES	560	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	561				
12H11.1	469	-------	560	----------	561	QQYYSTPWT	562	FGQGTKVEIK	563
		CDR2		FR3		CDR3		FR4	
	491	SNNQRPS	564	GVPDRFSGSKSGTSASLAISGLQSEDEADYYC	566				
11H4.1	473	---R---	565	----------	566	AAWDDSLNWV	567	FGAGTKLTVL	569
11H8.1	477	---R---	565	----------	566	ATWDDRLNWV	568	FGAGTKLTVL	569
		CDR2		FR3		CDR3		FR4	
	492	YDSDRPS	570	GIPERFSGSNSGNTATLTISRVEAGDEADYYC	572				
11G1.5	481	D------	571	----------F--	573	QVWDSSSDPVV	574	FGGGTKLTVL	575

FIG. 4A

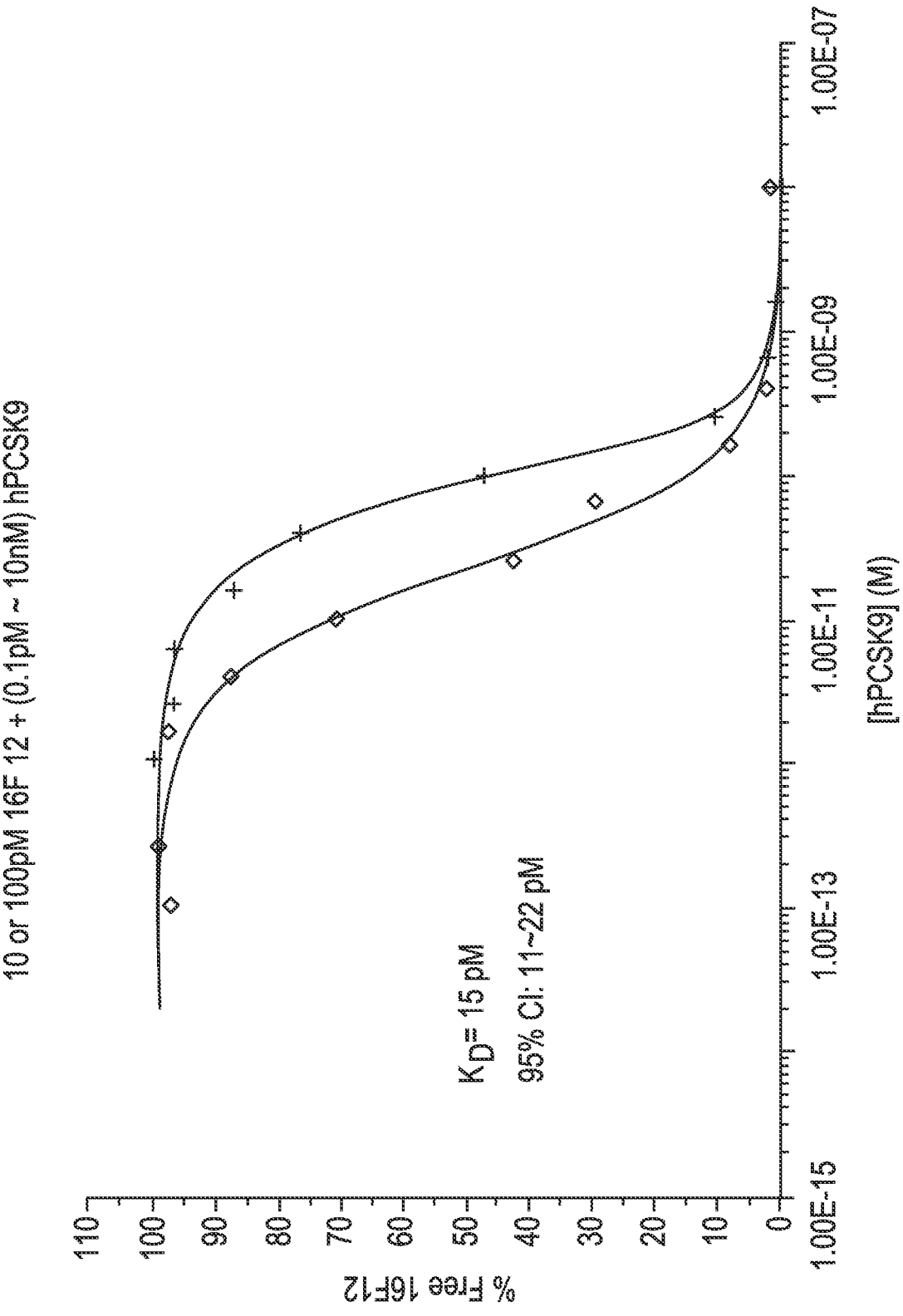

10 or 100pM 16F 12 + (0.1pM ~ 10nM) hPCSK9
% Free 16F12
110
100
90
80
70
60
50
40
30
20
10
0
1.00E-15
1.00E-13
1.00E-11
1.00E-09
1.00E-07
[hPCSK9] (M)
KD= 15 pM
95% CI: 11~22 pM

FIG. 4B

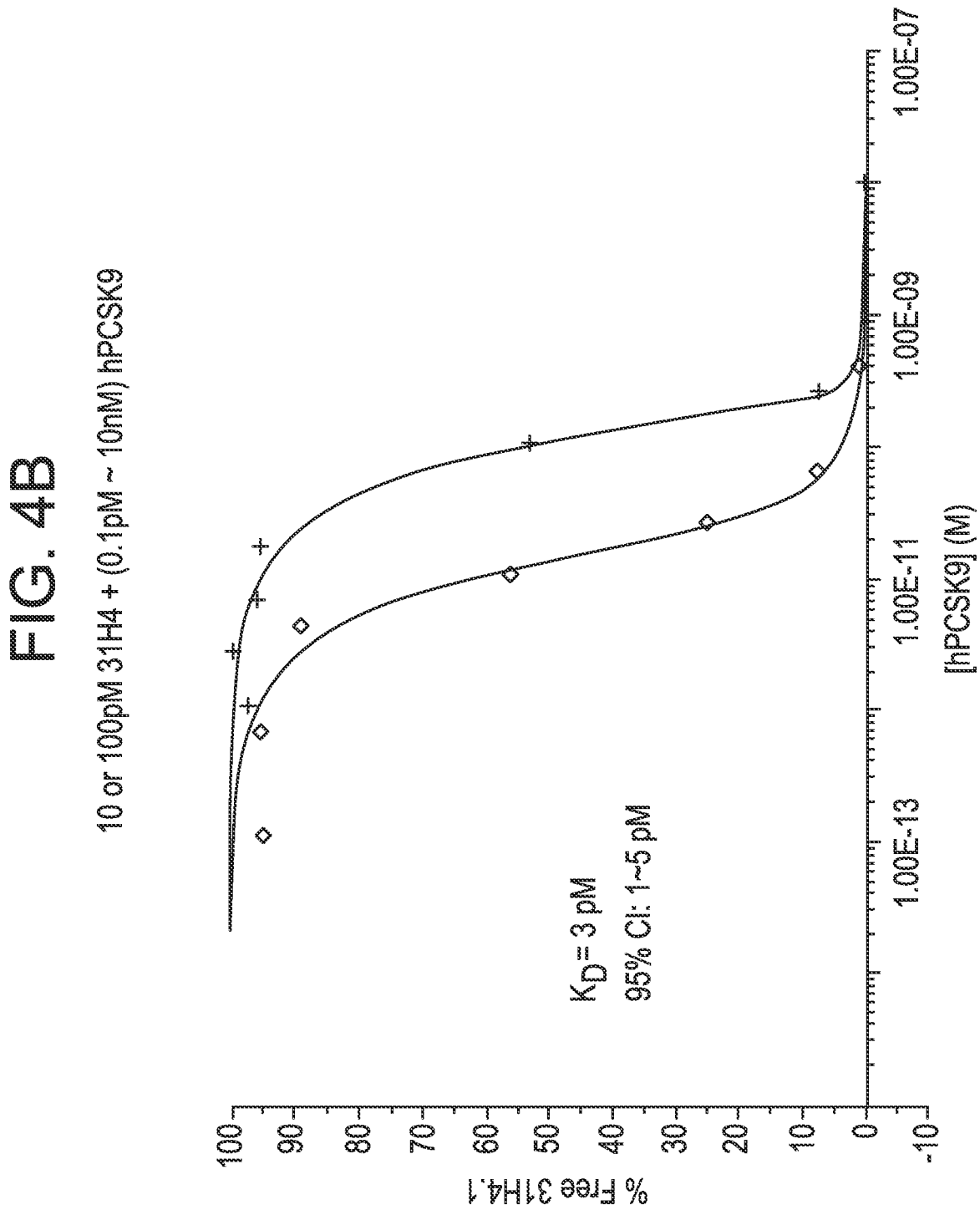

10 or 100pM 31H4 + (0.1pM ~ 10nM) hPCSK9
% Free 31H4.1
100
90
80
70
60
50
40
30
20
10
0
-10
1.00E-13
1.00E-11
1.00E-09
1.00E-07
[hPCSK9] (M)
KD= 3 pM
95% CI: 1~5 pM

FIG. 4C

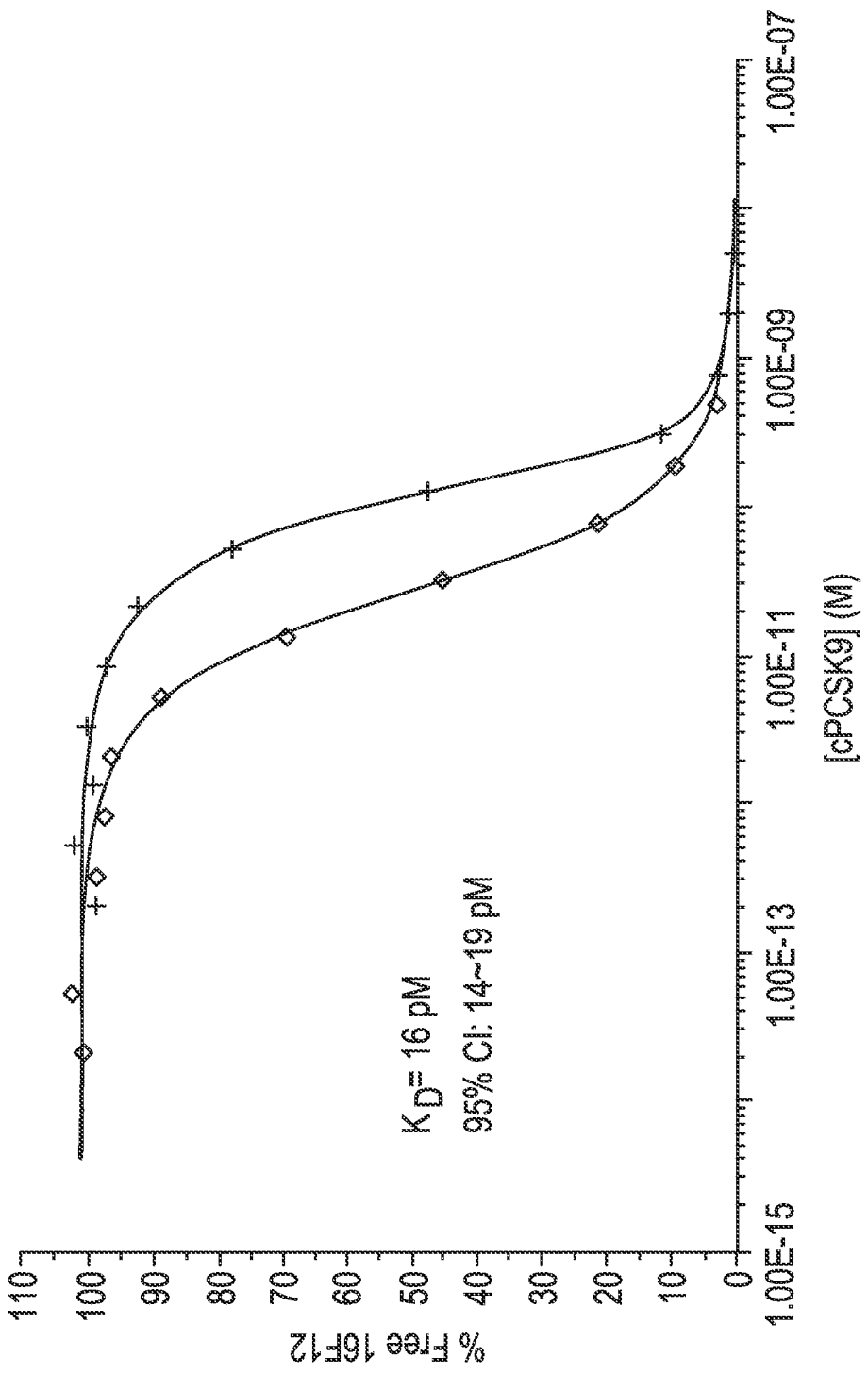

10 or 100pM 16F12 + (0.05pM ~ 5nM) cPCSK9
% Free 16F12
110
100
90
80
70
60
50
40
30
20
10
0
1.00E-15
1.00E-13
1.00E-11
1.00E-09
1.00E-07
[cPCSK9] (M)
K_D= 16 pM
95% CI: 14~19 pM

FIG. 4D

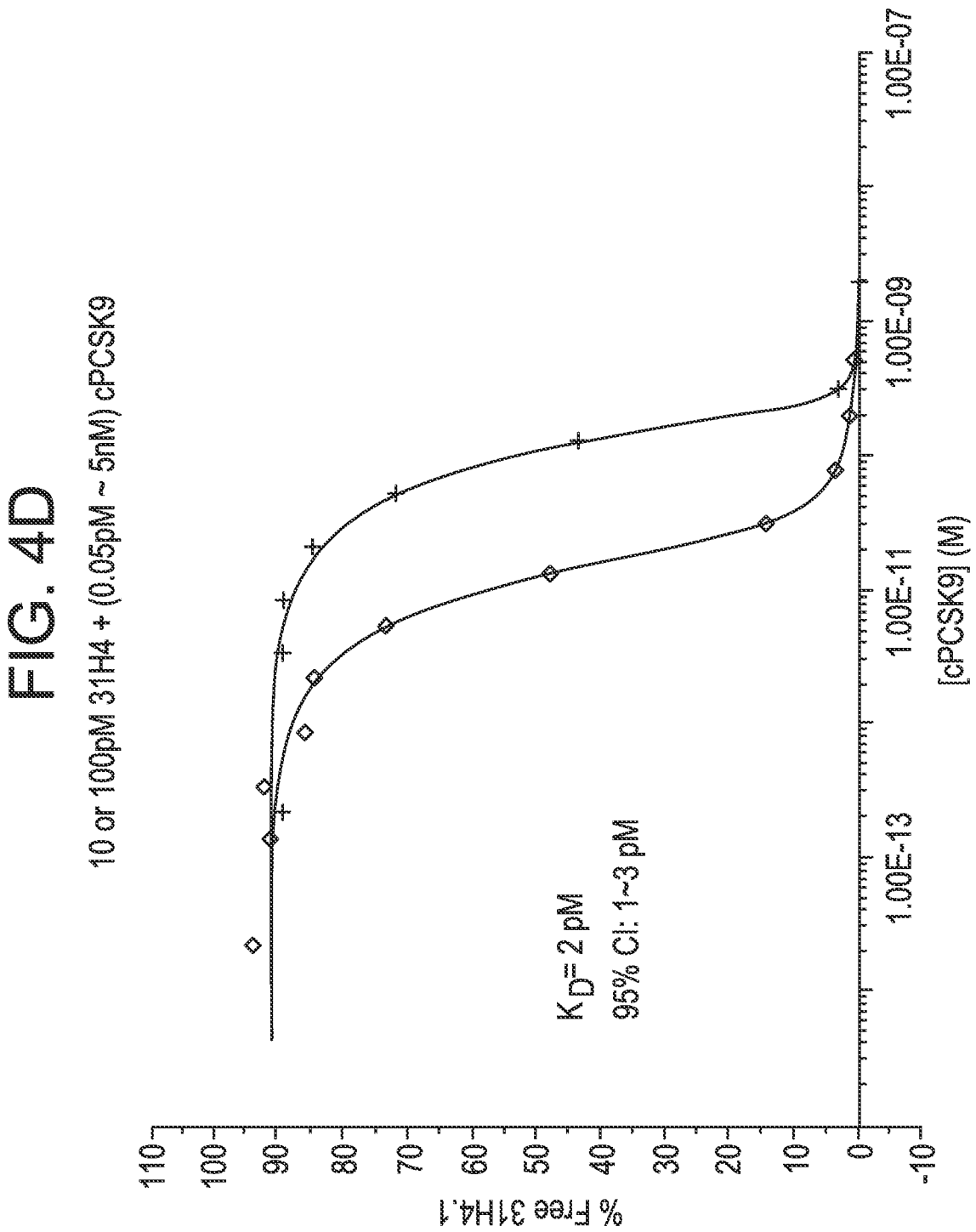

10 or 100pM 31H4 + (0.05pM ~ 5nM) cPCSK9
% Free 31H4.1
110
100
90
80
70
60
50
40
30
20
10
0
-10
1.00E-13
1.00E-11
1.00E-09
1.00E-07
[cPCSK9] (M)
K_D= 2 pM
95% CI: 1~3 pM

FIG. 4E

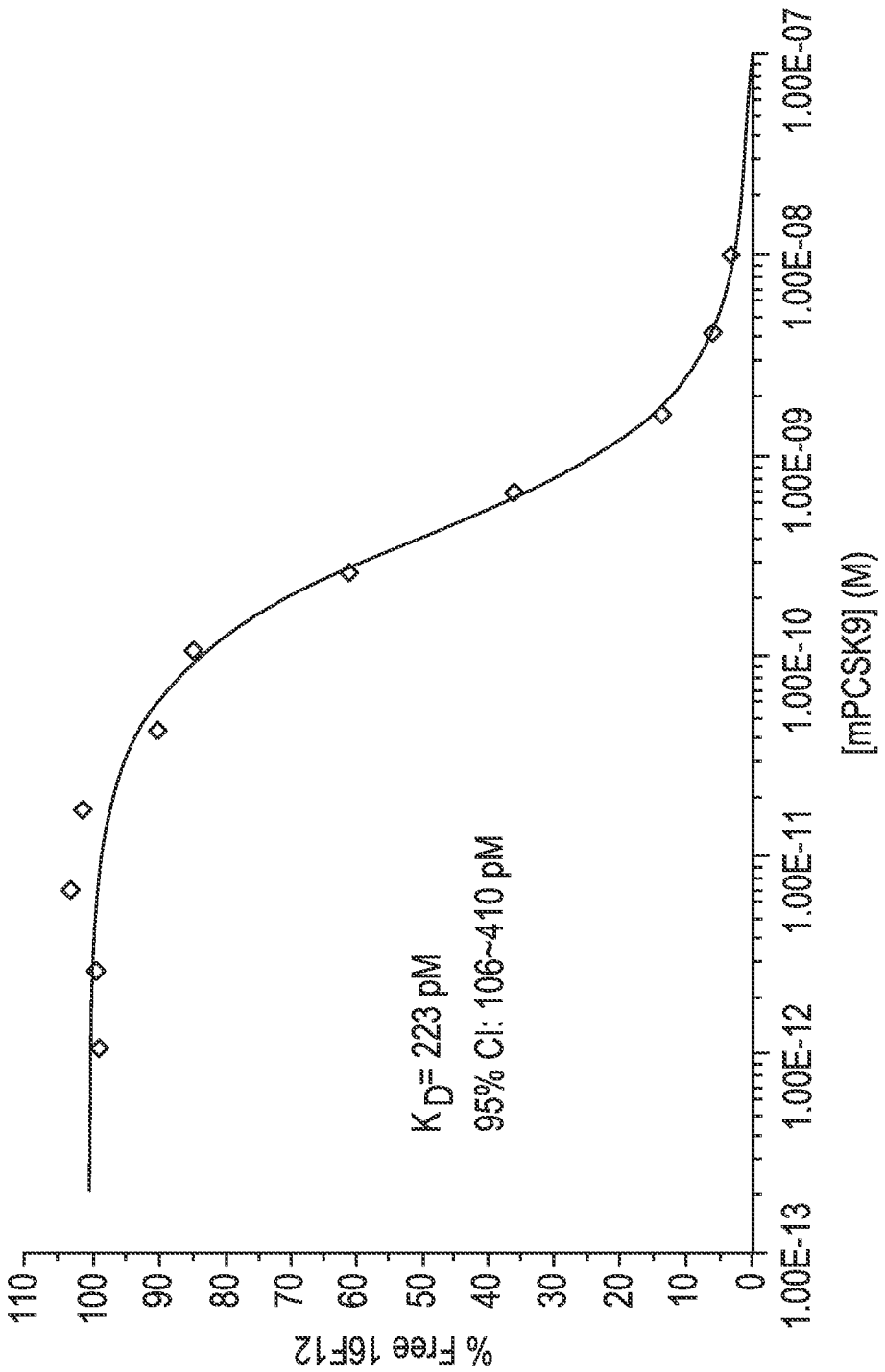

100pM 16F12 + (1pM ~ 10nM) mPCSK9
% Free 16F12
110
100
90
80
70
60
50
40
30
20
10
0
1.00E-13
1.00E-12
1.00E-11
1.00E-10
1.00E-09
1.00E-08
1.00E-07
[mPCSK9] (M)
K_D= 223 pM
95% CI: 106~410 pM

FIG. 4F

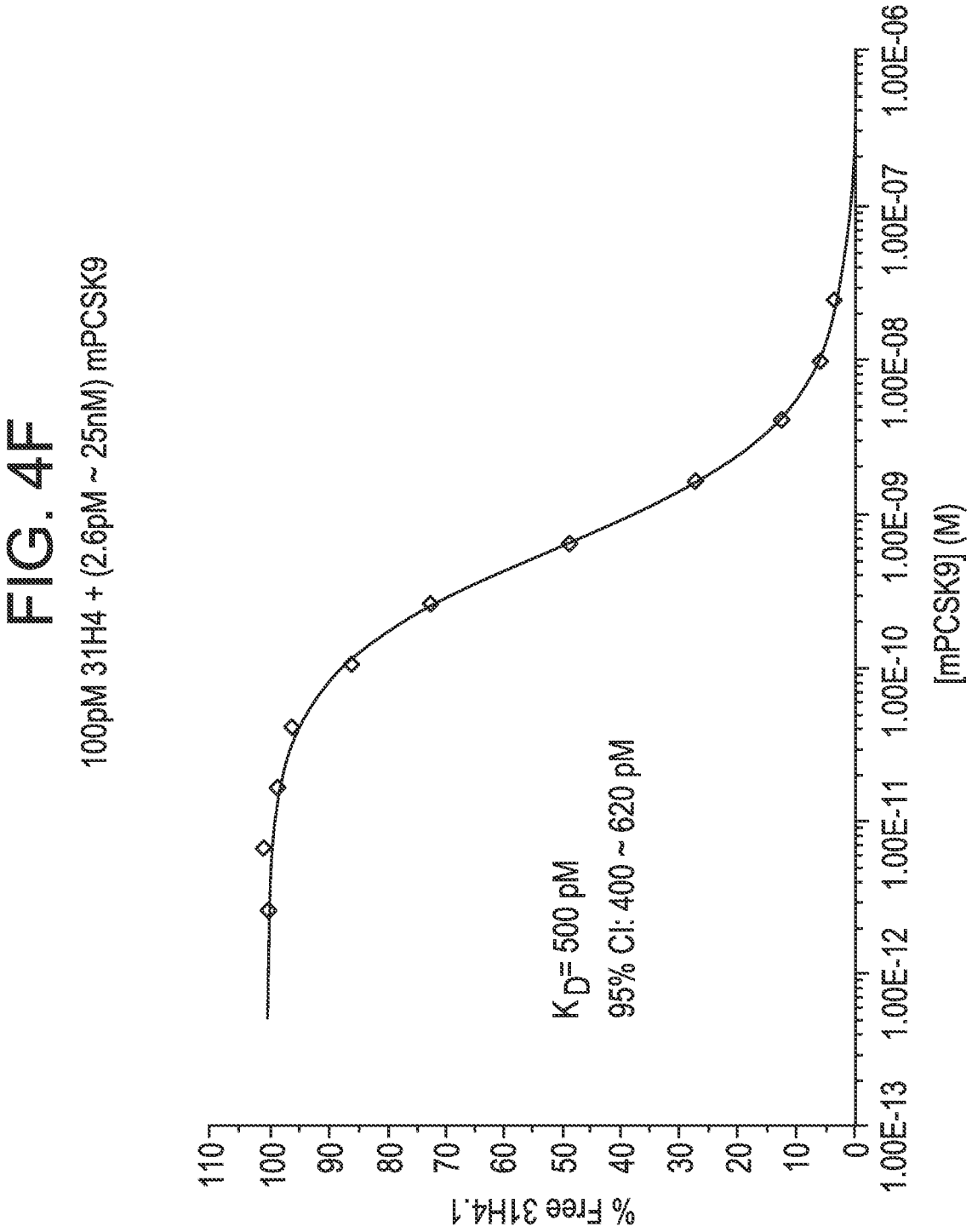

100pM 31H4 + (2.6pM ~ 25nM) mPCSK9
% Free 31H4.1
110
100
90
80
70
60
50
40
30
20
10
0
1.00E-13
1.00E-12
1.00E-11
1.00E-10
1.00E-09
1.00E-08
1.00E-07
1.00E-06
[mPCSK9] (M)
K_D= 500 pM
95% CI: 400 ~ 620 pM

FIG. 5A

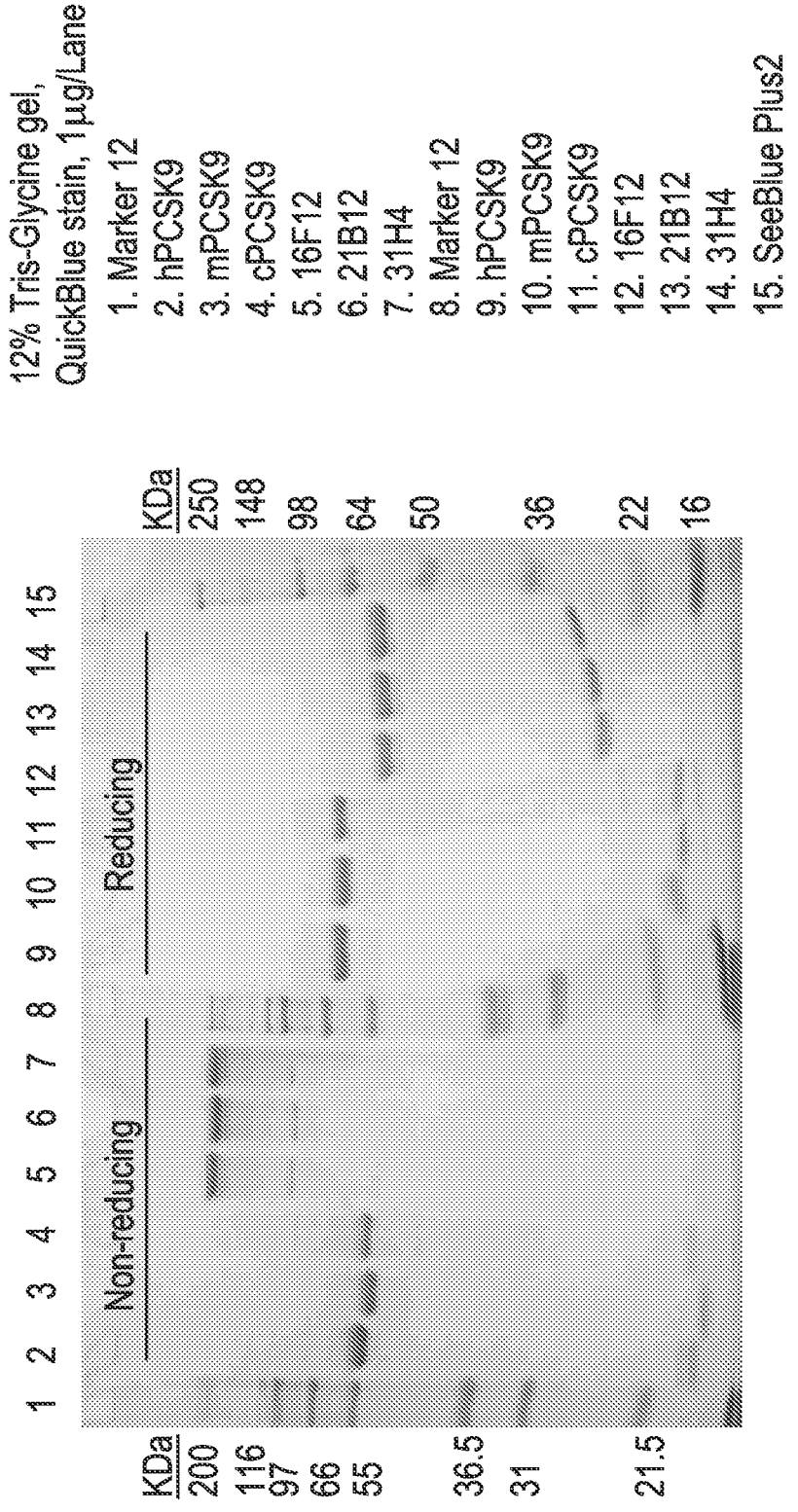

12% Tris-Glycine gel,
QuickBlue stain, 1µg/Lane
1. Marker 12
2. hPCSK9
3. mPCSK9
4. cPCSK9
5. 16F12
6. 21B12
7. 31H4
8. Marker 12
9. hPCSK9
10. mPCSK9
11. cPCSK9
12. 16F12
13. 21B12
14. 31H4
15. SeeBlue Plus2
Non-reducing
Reducing
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
KDa
200
116
97
66
55
36.5
31
21.5
KDa
250
148
98
64
50
36
22
16

FIG. 5B

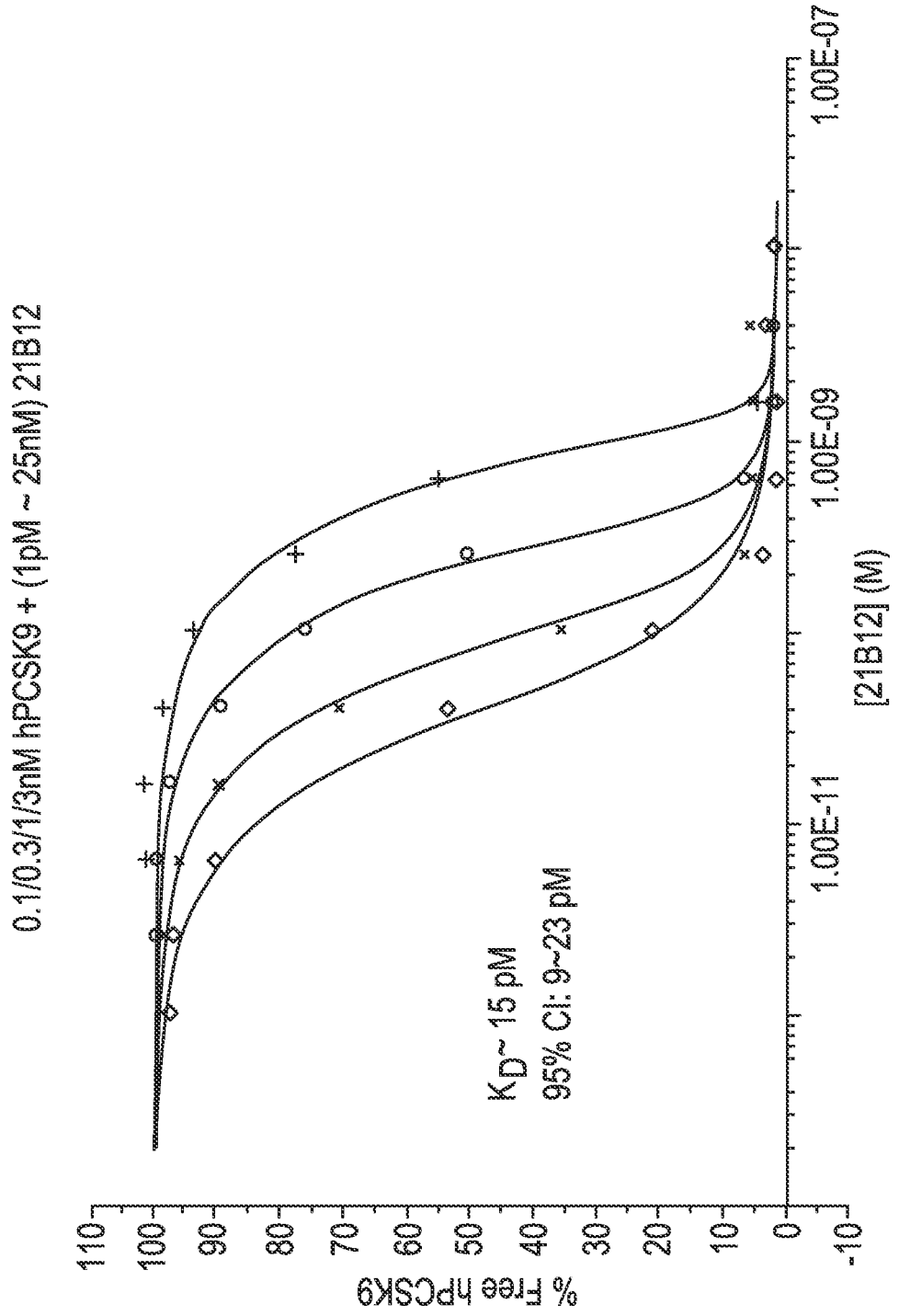

0.1/0.3/1/3nM hPCSK9 + (1pM ~ 25nM) 21B12
% Free hPCSK9
110
100
90
80
70
60
50
40
30
20
10
0
-10
1.00E-11
1.00E-09
1.00E-07
[21B12] (M)
KD~ 15 pM
95% CI: 9~23 pM

FIG. 5C

0.1/0.3/1/3nM cPCSK9 + (1pM ~ 25nM) 21B12

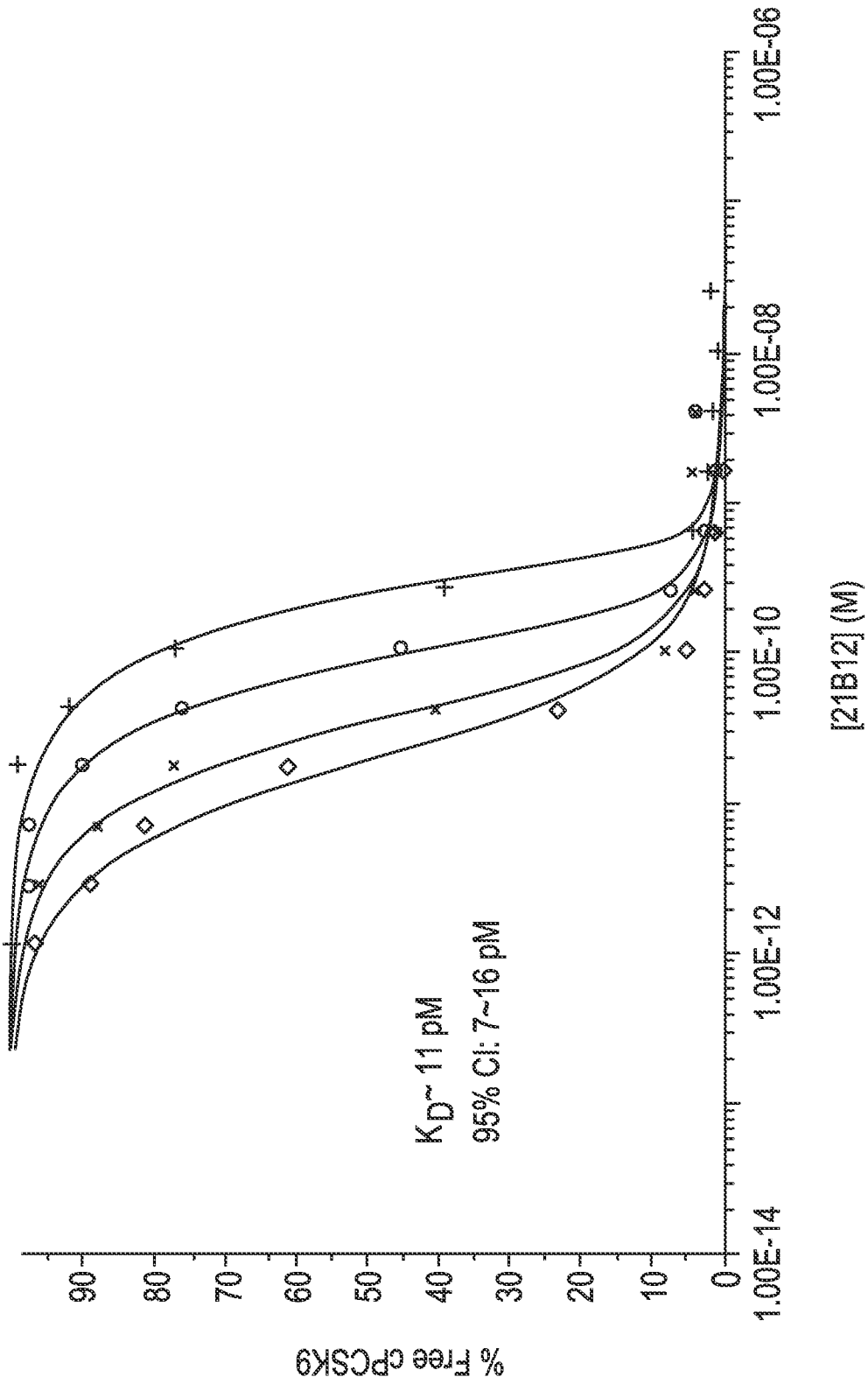


FIG. 5D

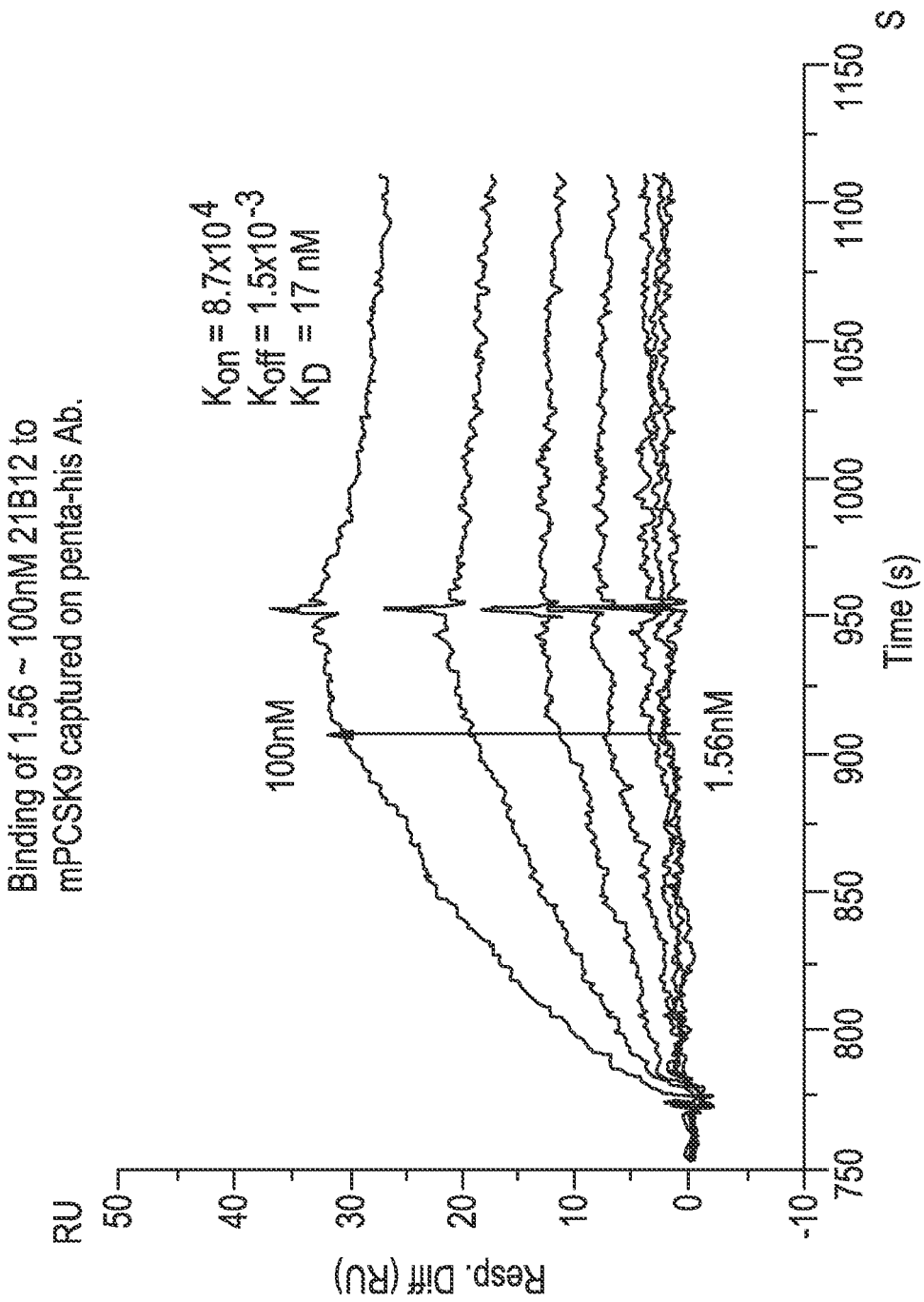

Binding of 1.56 ~ 100nM 21B12 to
mPCSK9 captured on penta-his Ab.
K_{on} = 8.7x10^{4}
K_{off} = 1.5x10^{-3}
K_D = 17 nM
100nM
1.56nM
RU
Resp. Diff (RU)
Time (s)
S
50
40
30
20
10
0
-10
750
800
850
900
950
1000
1050
1100
1150

FIG. 5E

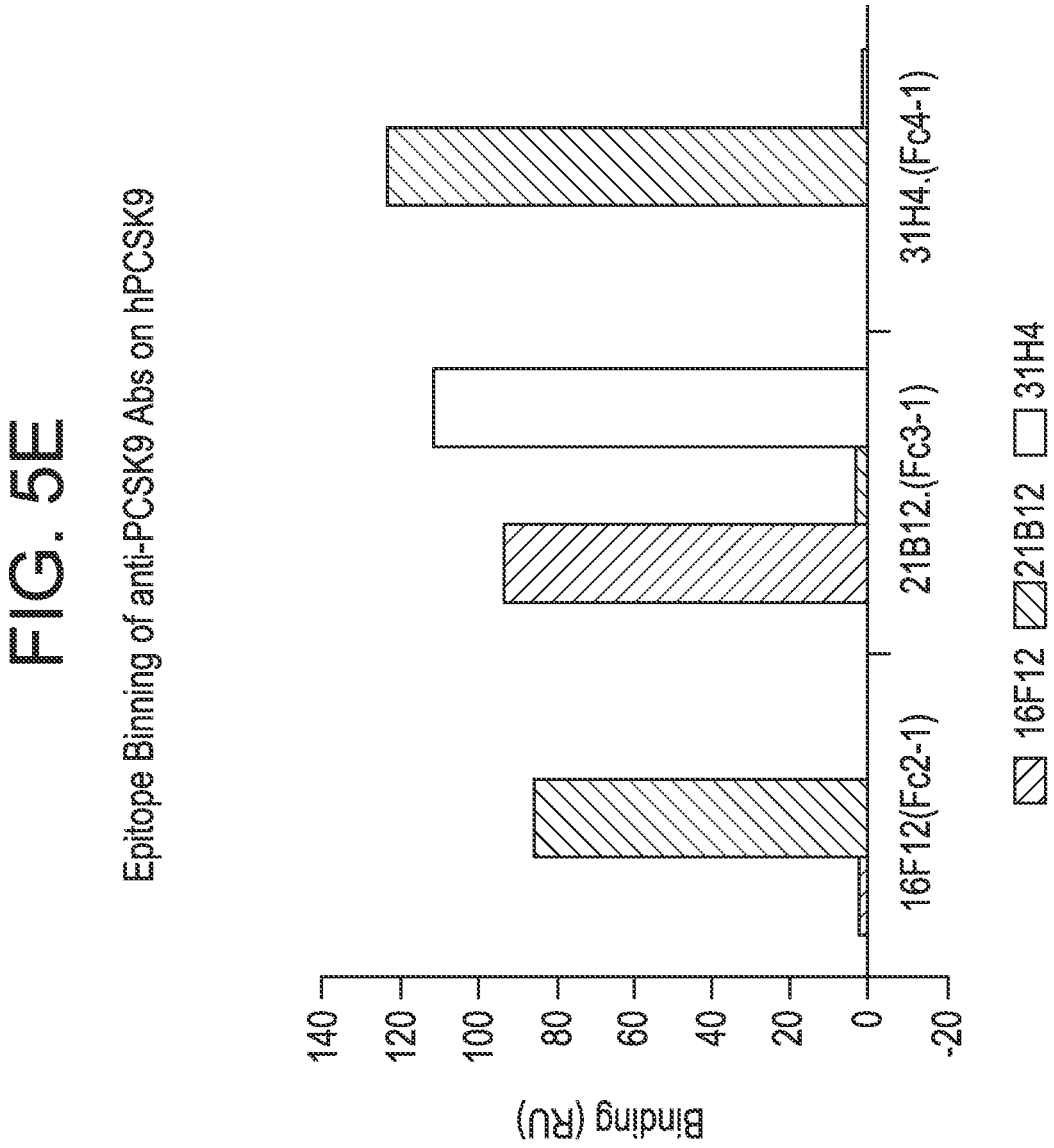

Epitope Binning of anti-PCSK9 Abs on hPCSK9
Binding (RU)
140
120
100
80
60
40
20
0
-20
16F12(Fc2-1)
21B12.(Fc3-1)
31H4.(Fc4-1)
16F12
21B12
31H4

FIG. 6A

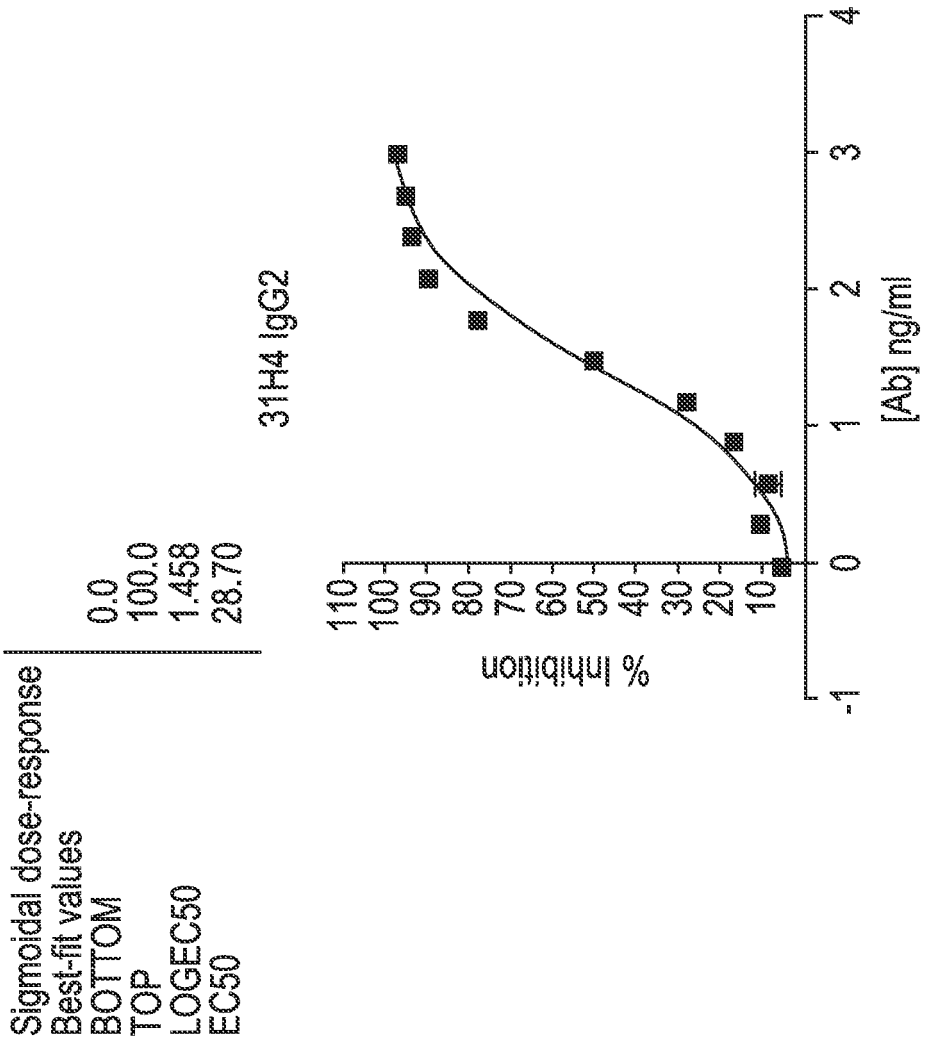

Sigmoidal dose-response
Best-fit values
BOTTOM
TOP
LOGEC50
EC50
0.0
100.0
1.458
28.70
31H4 IgG2
% Inhibition
110
100
90
80
70
60
50
40
30
20
10
-1
0
1
2
3
4
[Ab] ng/ml

FIG. 6B

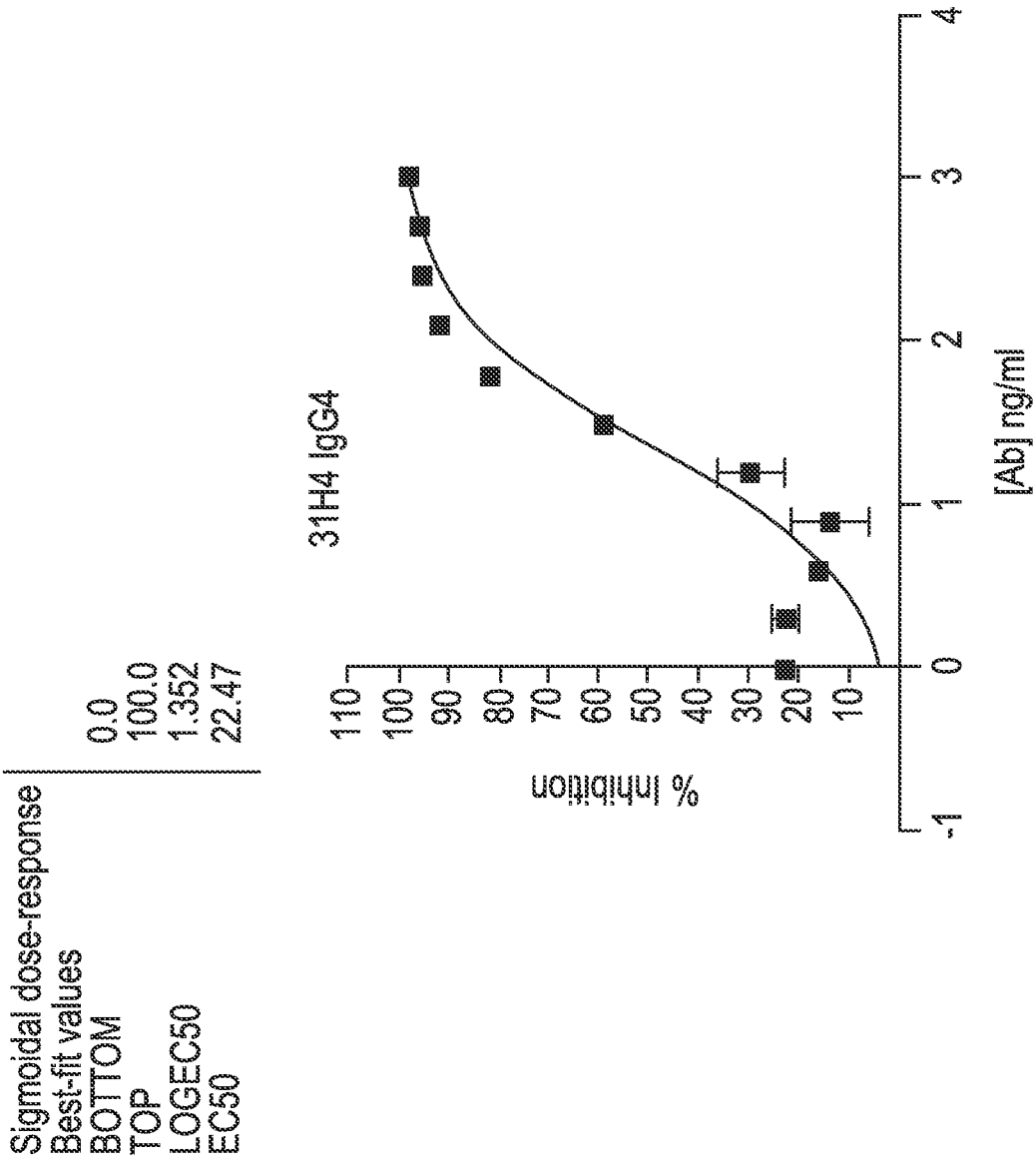

Sigmoidal dose-response
Best-fit values
BOTTOM 0.0
TOP 100.0
LOGEC50 1.352
EC50 22.47
31H4 IgG4
% Inhibition
110
100
90
80
70
60
50
40
30
20
10
-1
0
1
2
3
4
[Ab] ng/ml

FIG. 6C

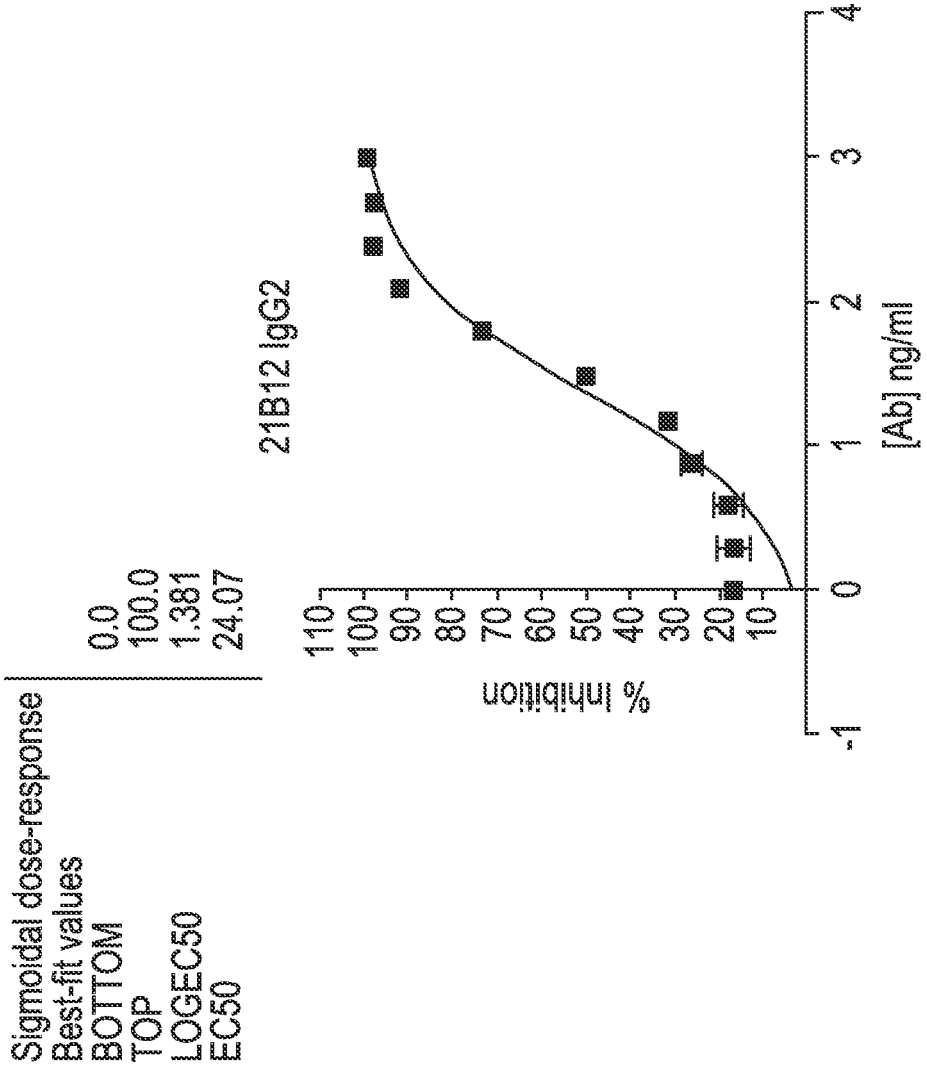

Sigmoidal dose-response
Best-fit values
BOTTOM
TOP
LOGEC50
EC50
0.0
100.0
1.381
24.07
21B12 IgG2
% inhibition
110
100
90
80
70
60
50
40
30
20
10
-1
0
1
2
3
4
[Ab] ng/ml

FIG. 6D

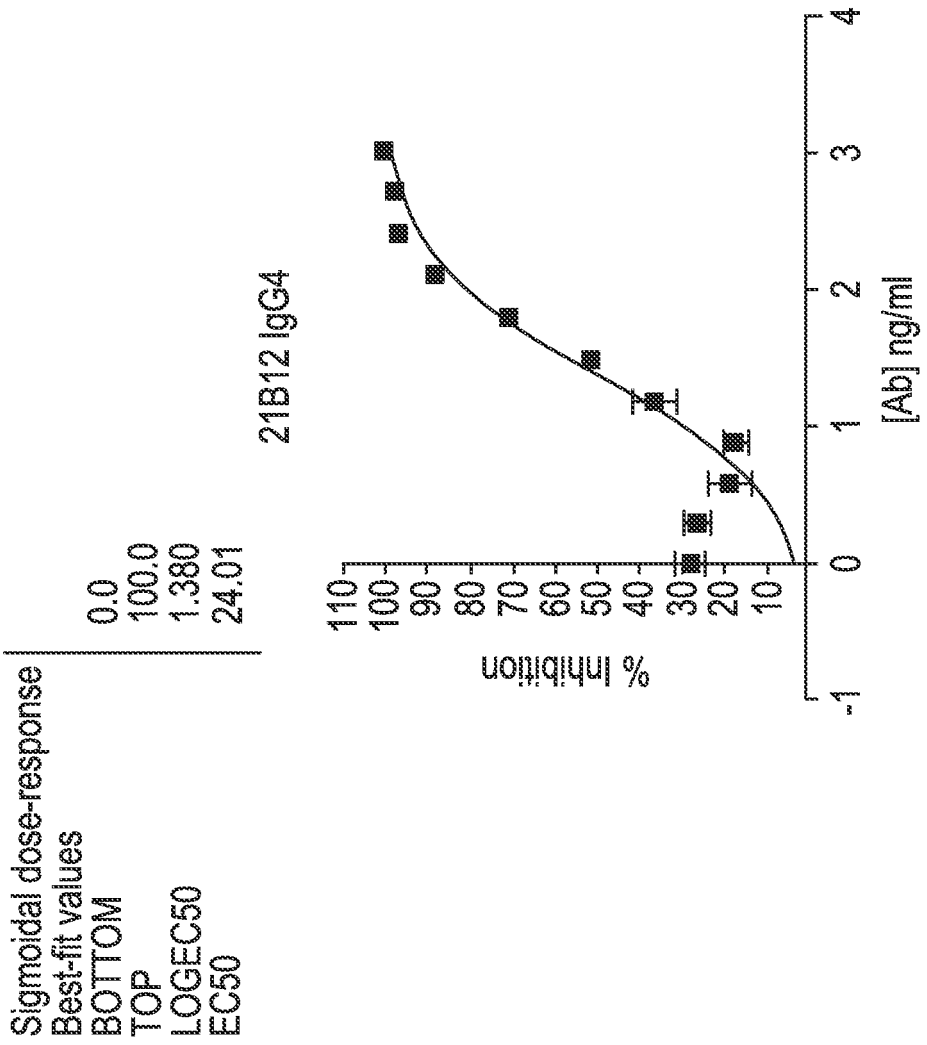

Sigmoidal dose-response
Best-fit values
BOTTOM
TOP
LOGEC50
EC50
0.0
100.0
1.380
24.01
21B12 IgG4
% Inhibition
110
100
90
80
70
60
50
40
30
20
10
-1
0
1
2
3
4
[Ab] ng/ml

FIG. 7A

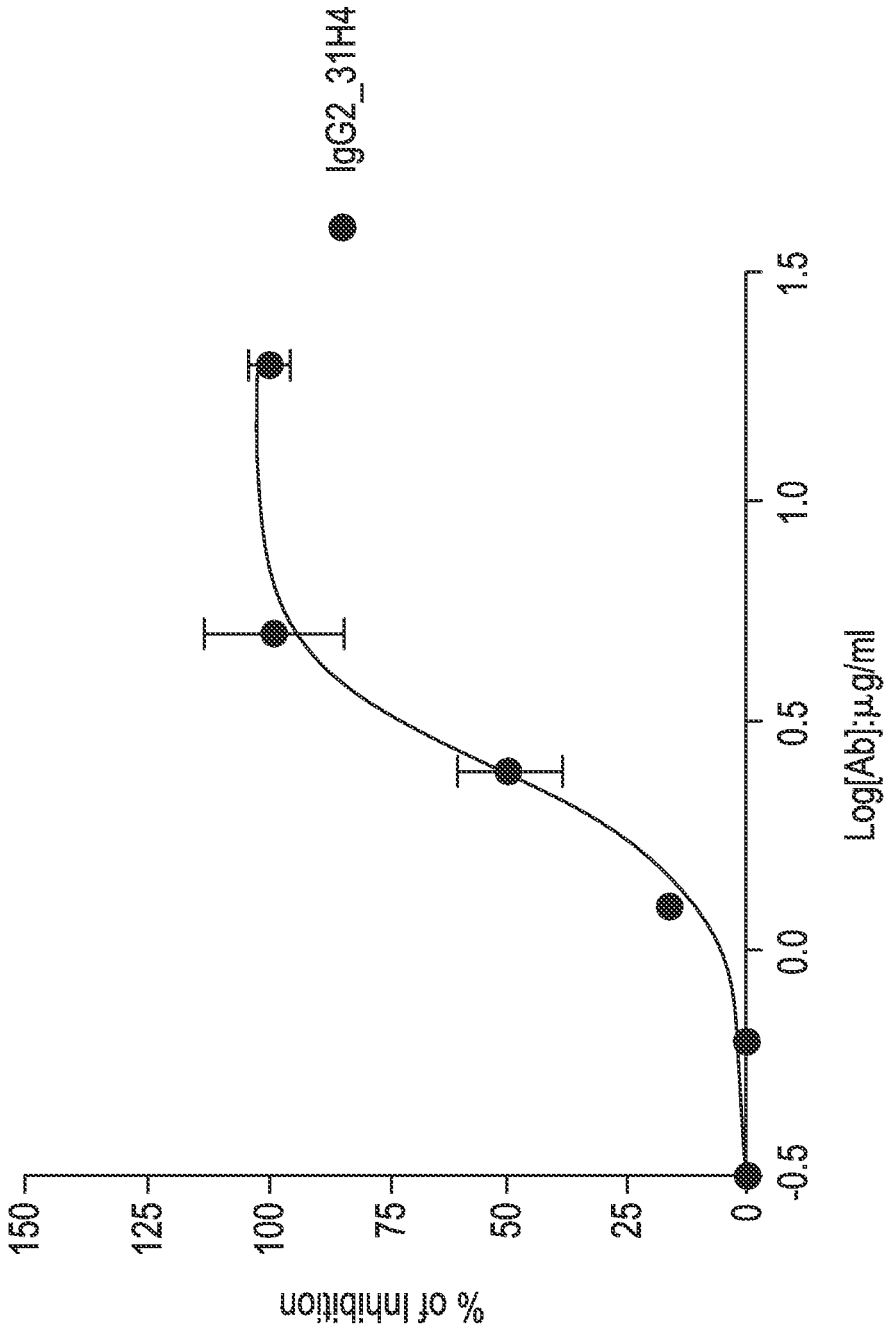

IgG2_31H4
% of Inhibition
150
125
100
75
50
25
0
-0.5
0.0
0.5
1.0
1.5
Log[Ab]:µg/ml

FIG. 7B

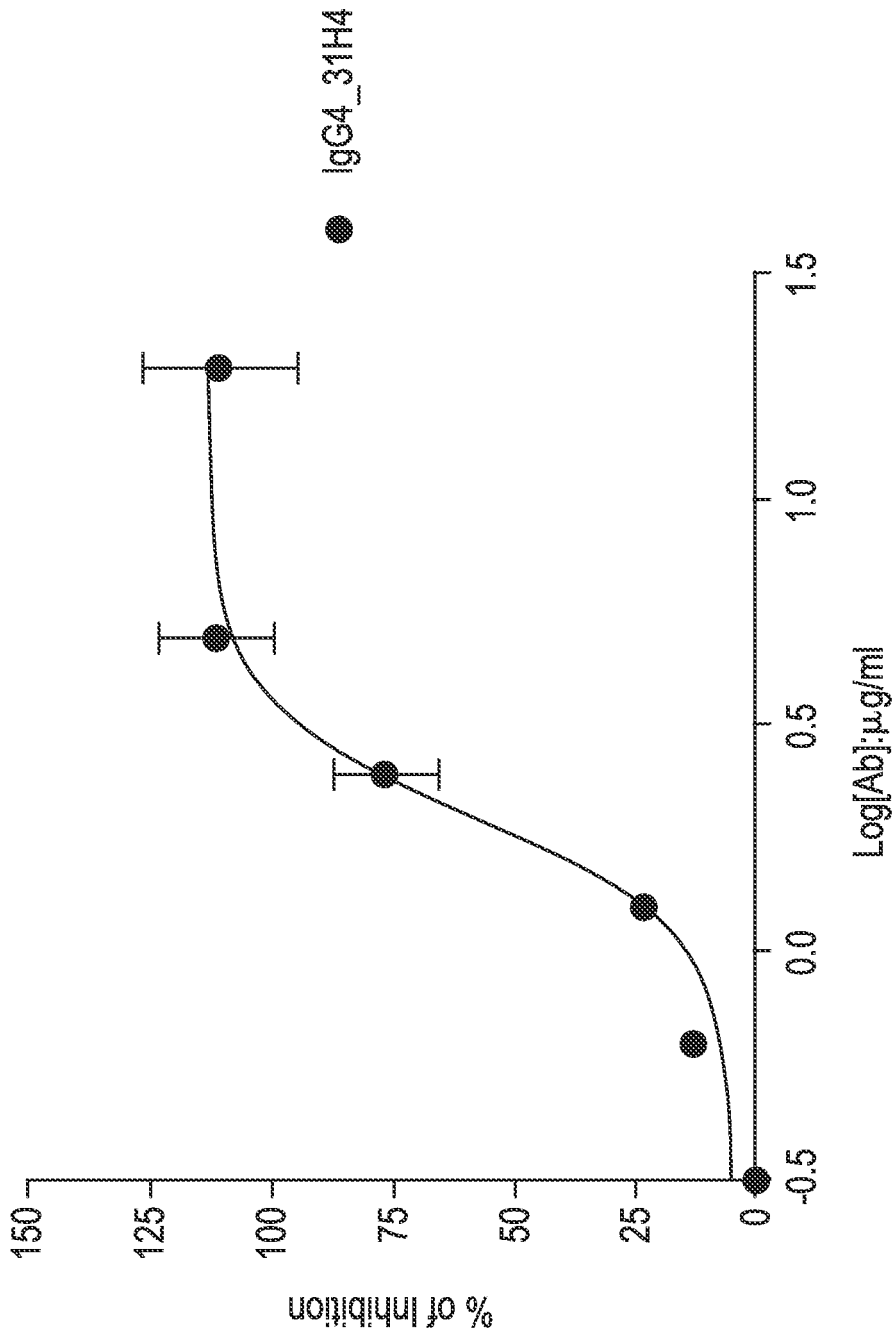

IgG4_31H4
% of Inhibition
150
125
100
75
50
25
0
-0.5
0.0
0.5
1.0
1.5
Log[Ab]:µg/ml

FIG. 7C

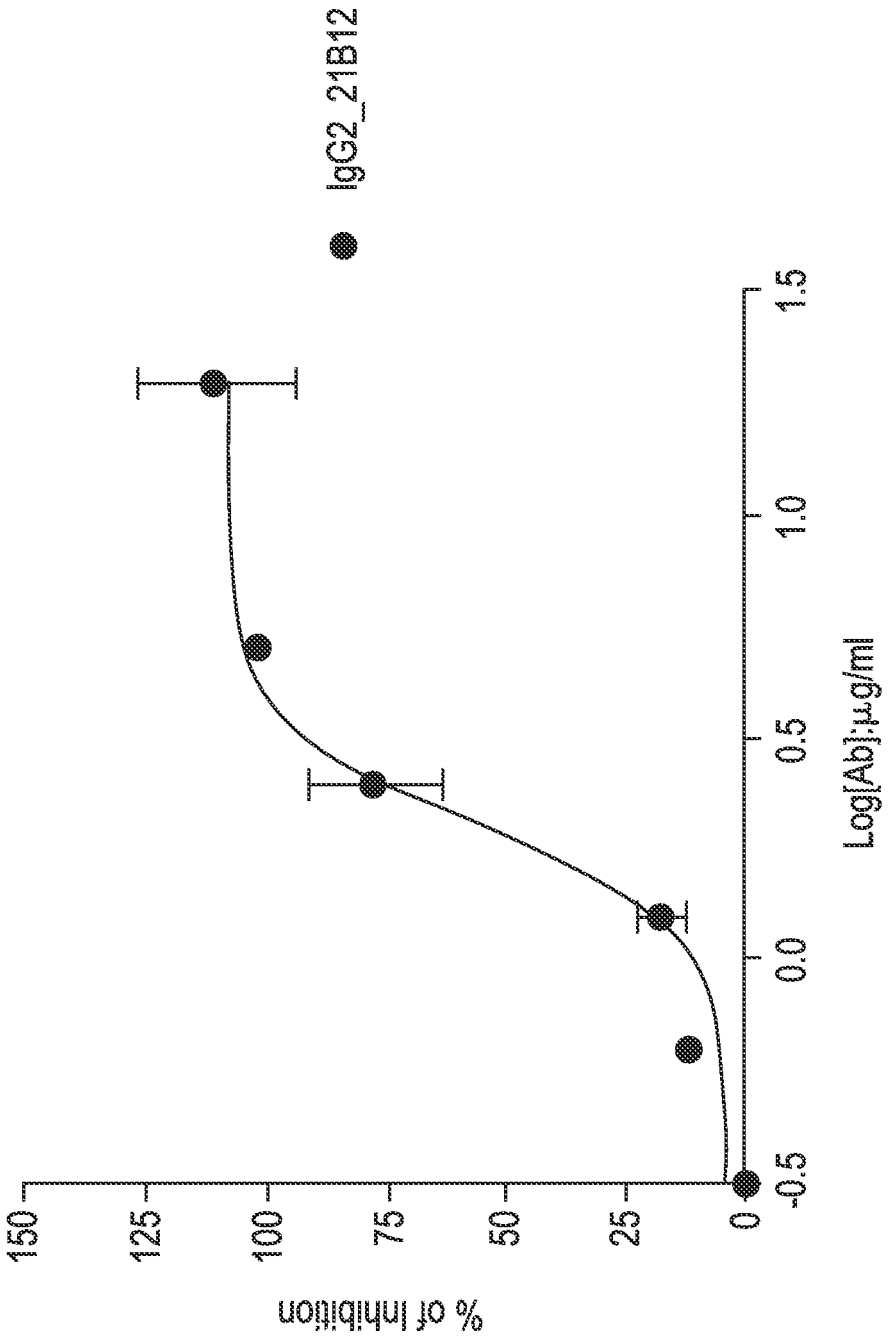

IgG2_21B12
% of Inhibition
150
125
100
75
50
25
0
-0.5
0.0
0.5
1.0
1.5
Log[Ab];µg/ml

FIG. 7D

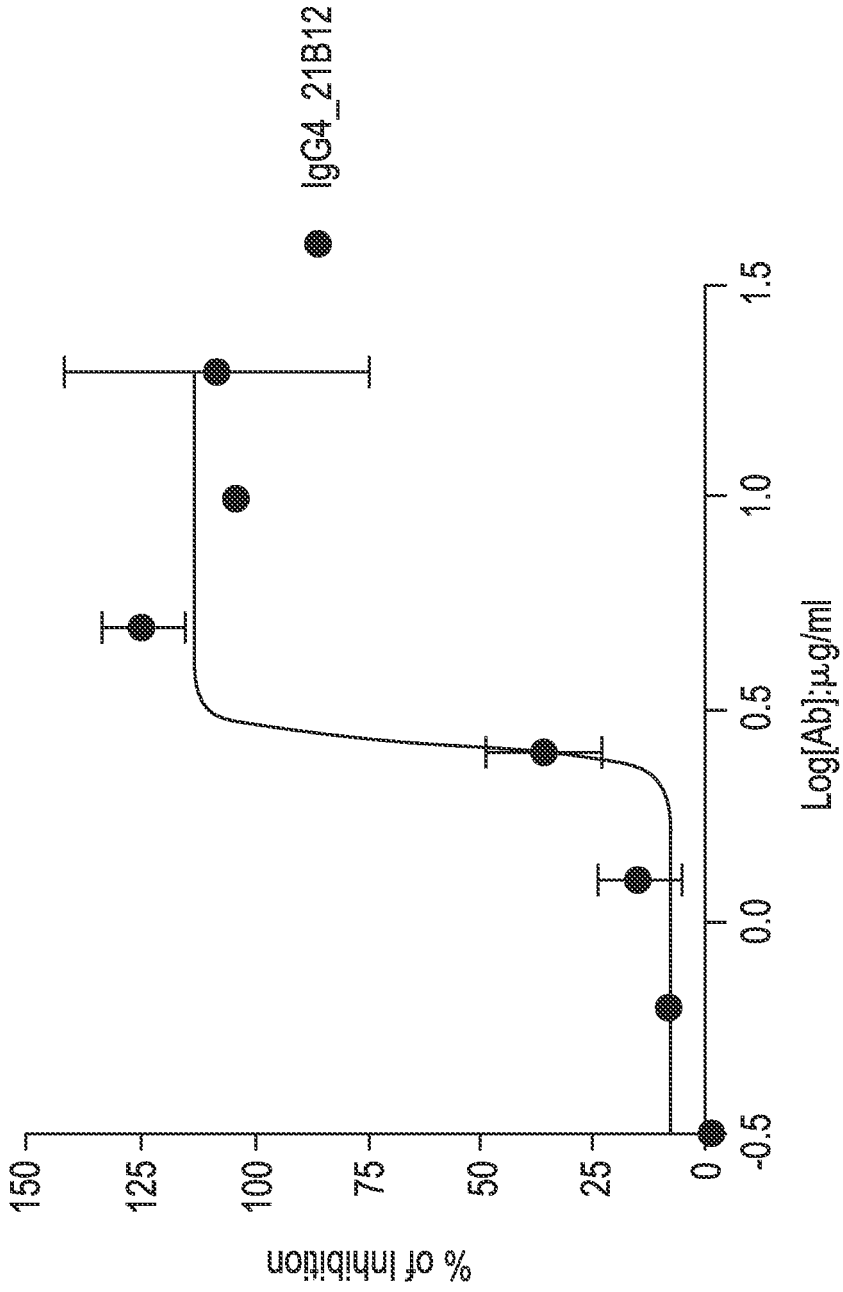

IgG4_21B12
% of Inhibition
150
125
100
75
50
25
0
-0.5
0.0
0.5
1.0
1.5
Log[Ab]:µg/ml

FIG. 8A

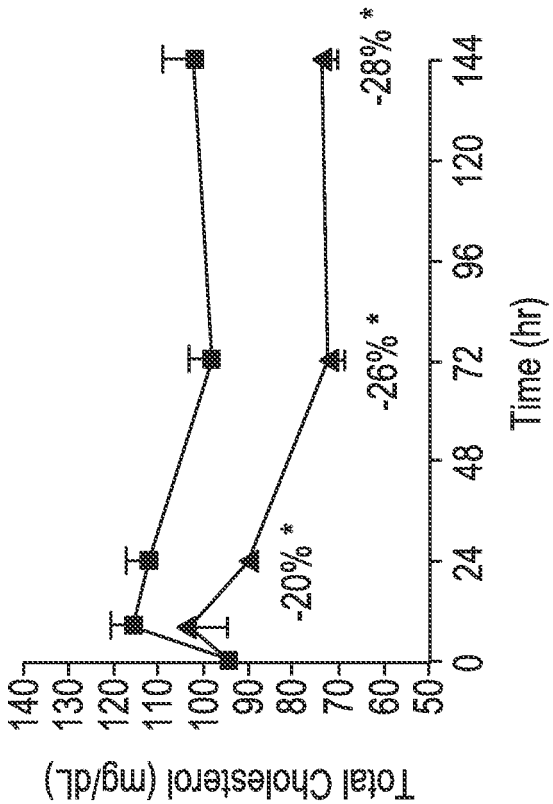

Total Cholesterol
Total Cholesterol (mg/dL)
140
130
120
110
100
90
80
70
60
50
0
24
48
72
96
120
144
Time (hr)
-20% *
-26% *
-28% *

FIG. 8B

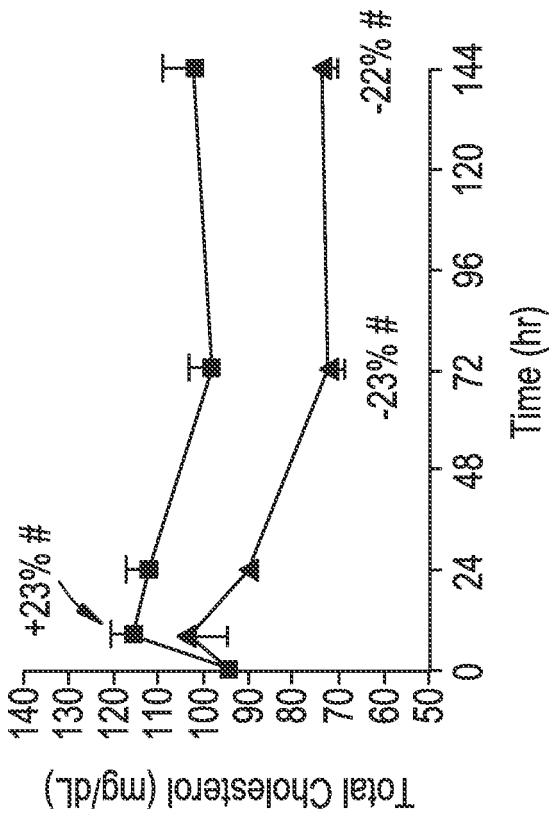

Total Cholesterol
Total Cholesterol (mg/dL)
140
130
120
110
100
90
80
70
60
50
0
24
48
72
96
120
144
Time (hr)
+23% #
-23% #
-22% #

FIG. 8D

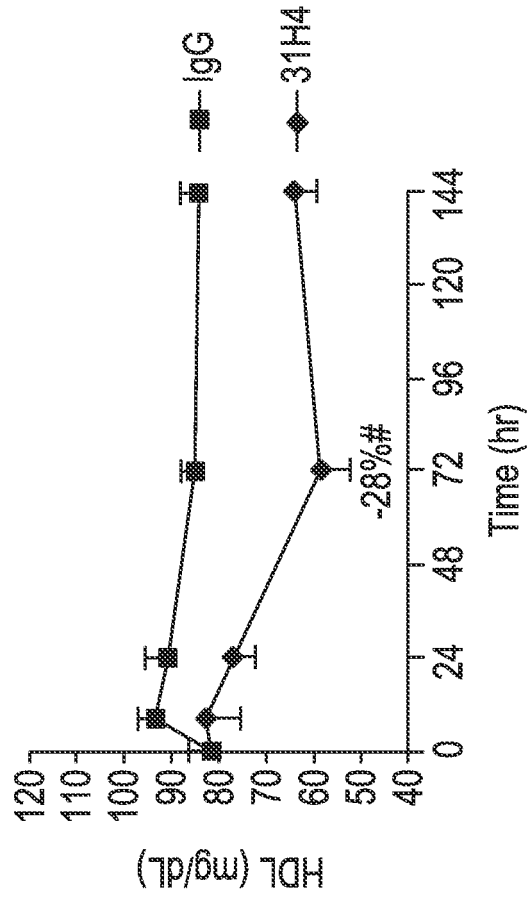

HDL
IgG
31H4
-28%#
HDL (mg/dL)
Time (hr)
120
110
100
90
80
70
60
50
40
0
24
48
72
96
120
144

FIG. 8C

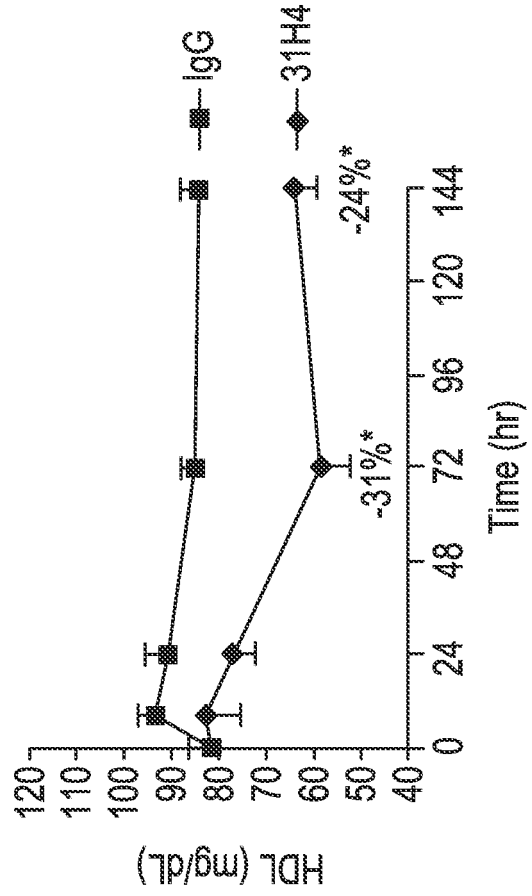

HDL
IgG
31H4
-24%*
-31%*
HDL (mg/dL)
Time (hr)
120
110
100
90
80
70
60
50
40
0
24
48
72
96
120
144

FIG. 9

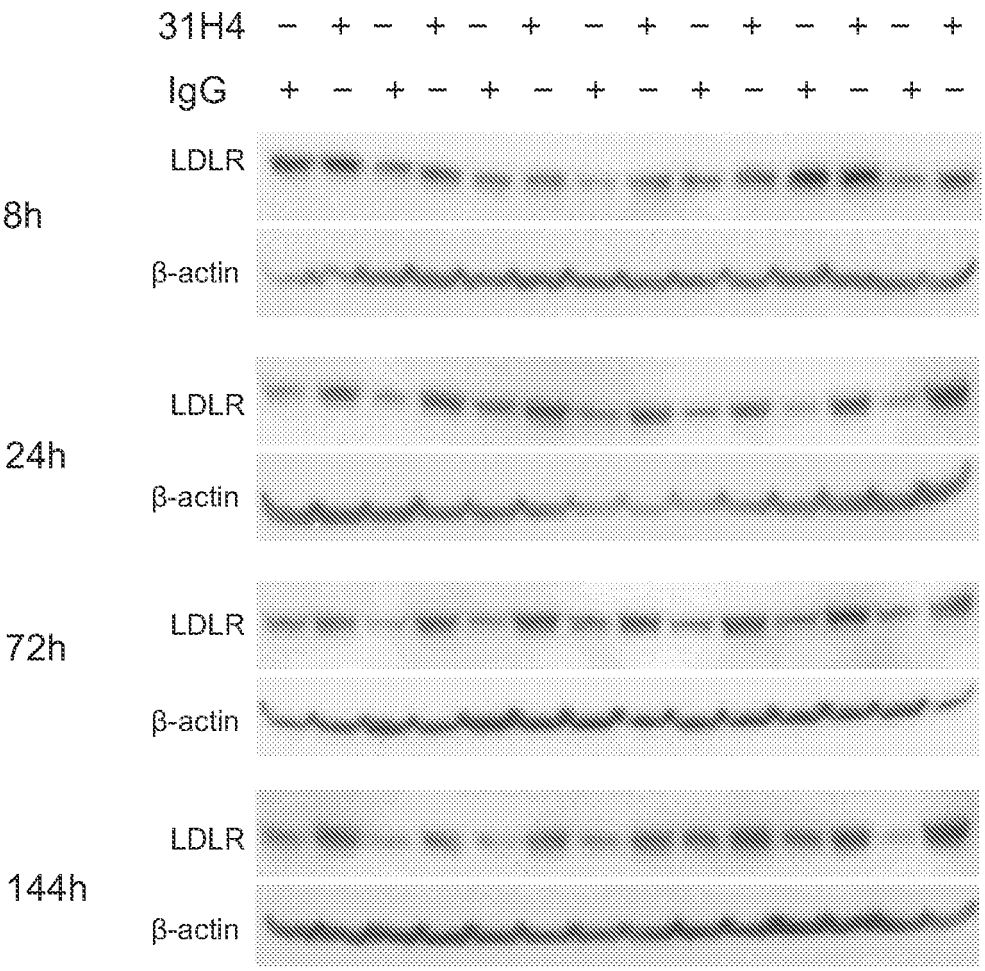

31H4 − + − + − + − + − + − + − +
IgG + − + − + − + − + − + − + −
8h
LDLR
β-actin
24h
LDLR
β-actin
72h
LDLR
β-actin
144h
LDLR
β-actin

FIG. 10A

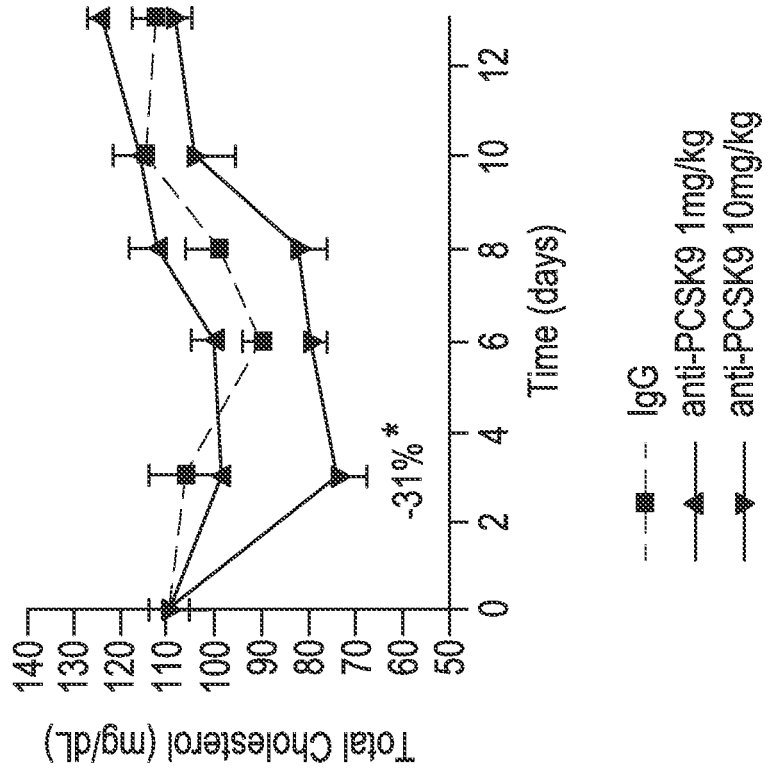


FIG. 10B

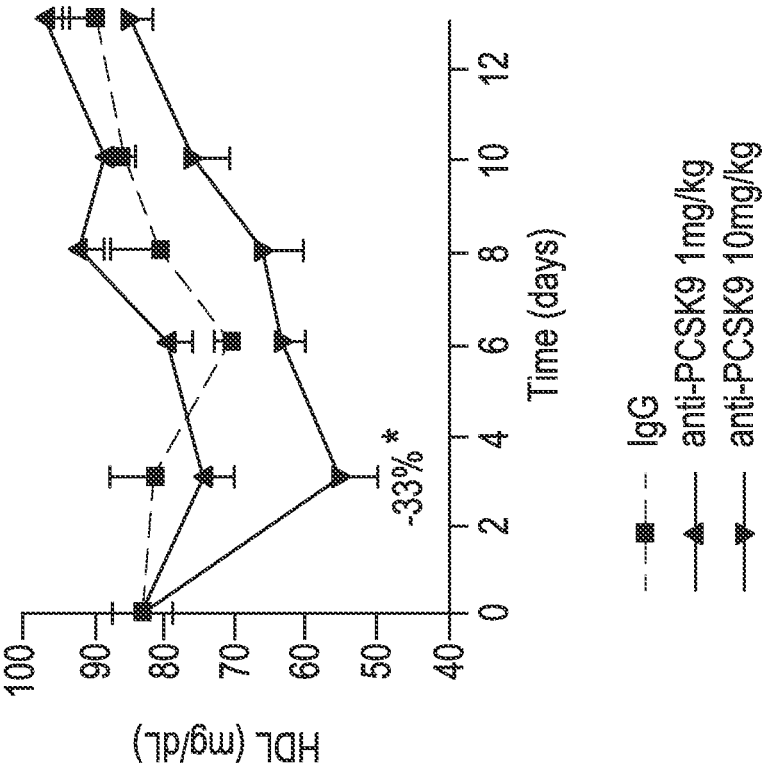


FIG. 10C

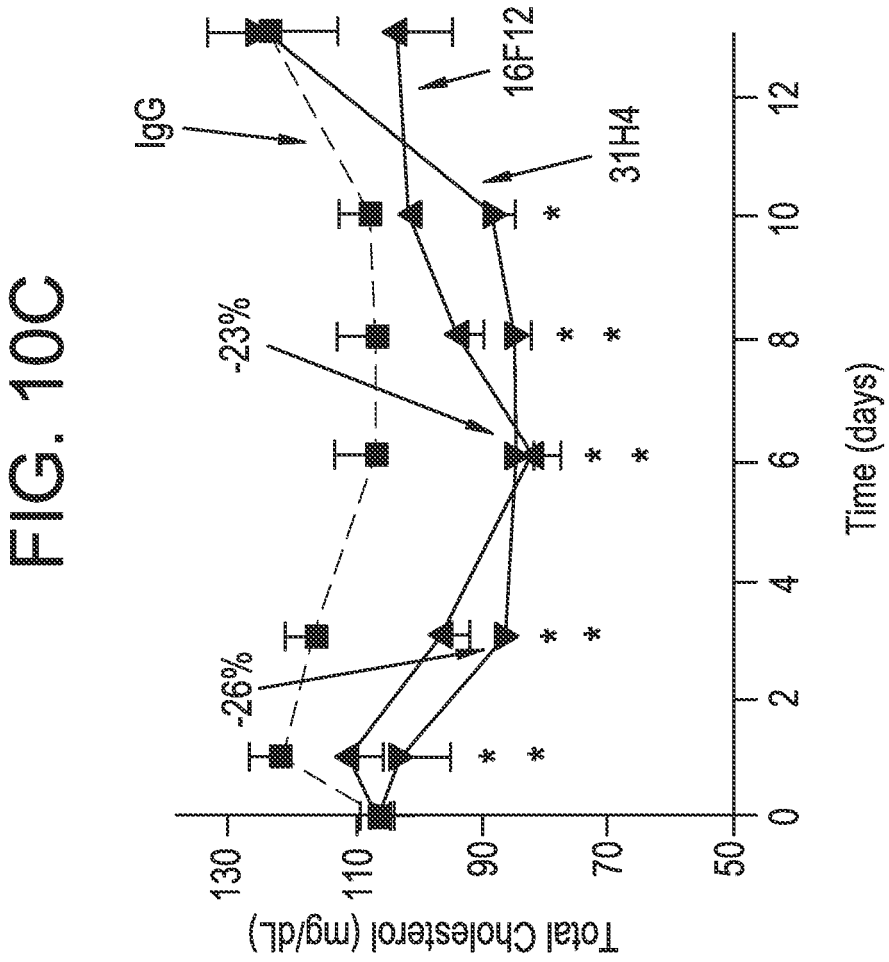

IgG
16F12
31H4
-23%
-26%
Total Cholesterol (mg/dL)
130
110
90
70
50
0
2
4
6
8
10
12
Time (days)

FIG. 11A

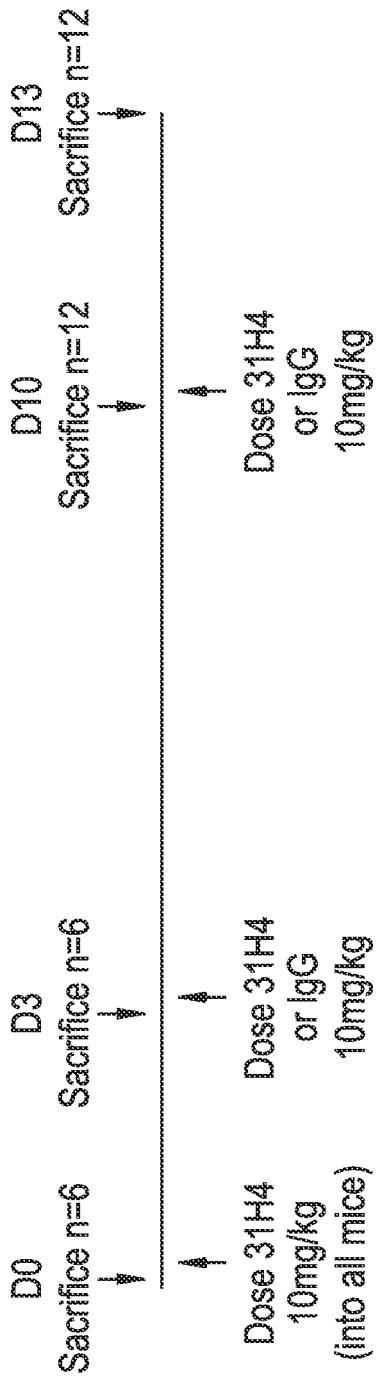

D0
Sacrifice n=6
D3
Sacrifice n=6
D10
Sacrifice n=12
D13
Sacrifice n=12
Dose 31H4
10mg/kg
(into all mice)
Dose 31H4
or IgG
10mg/kg
Dose 31H4
or IgG
10mg/kg

FIG. 11B

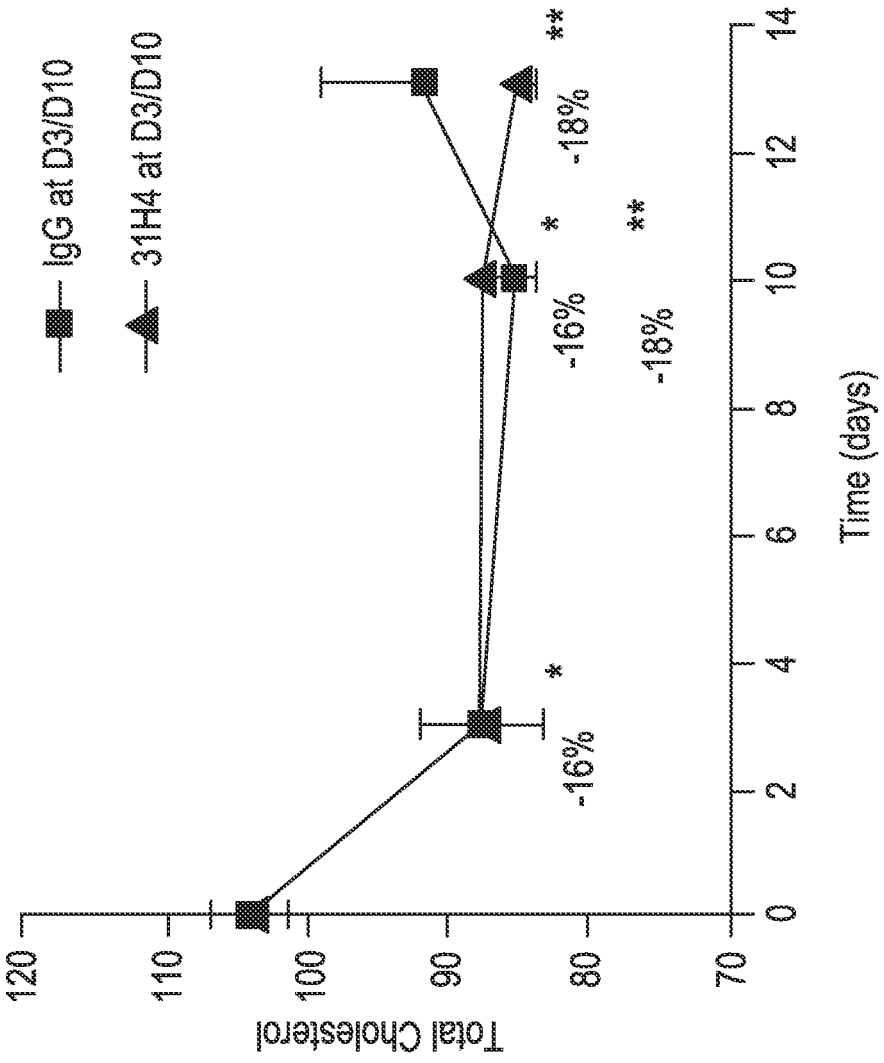

IgG at D3/D10
31H4 at D3/D10
Total Cholesterol
Time (days)
120
110
100
90
80
70
0
2
4
6
8
10
12
14
-16%
-18%
-16%
-18%
*
*
**
**

FIG. 12A

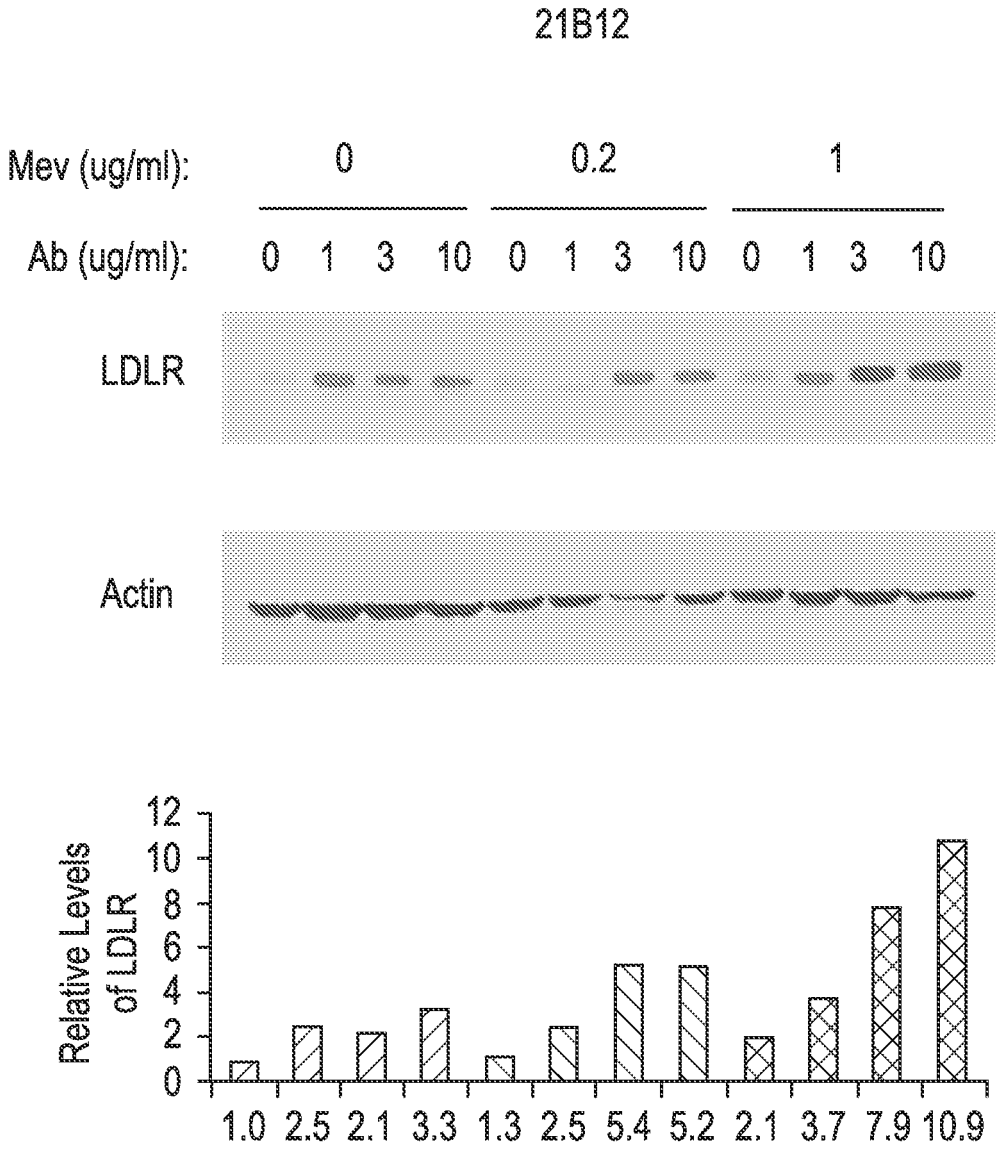

21B12
Mev (ug/ml):
0
0.2
1
Ab (ug/ml):
0 1 3 10 0 1 3 10 0 1 3 10
LDLR
Actin
Relative Levels of LDLR
0
2
4
6
8
10
12
1.0 2.5 2.1 3.3 1.3 2.5 5.4 5.2 2.1 3.7 7.9 10.9

FIG. 12B

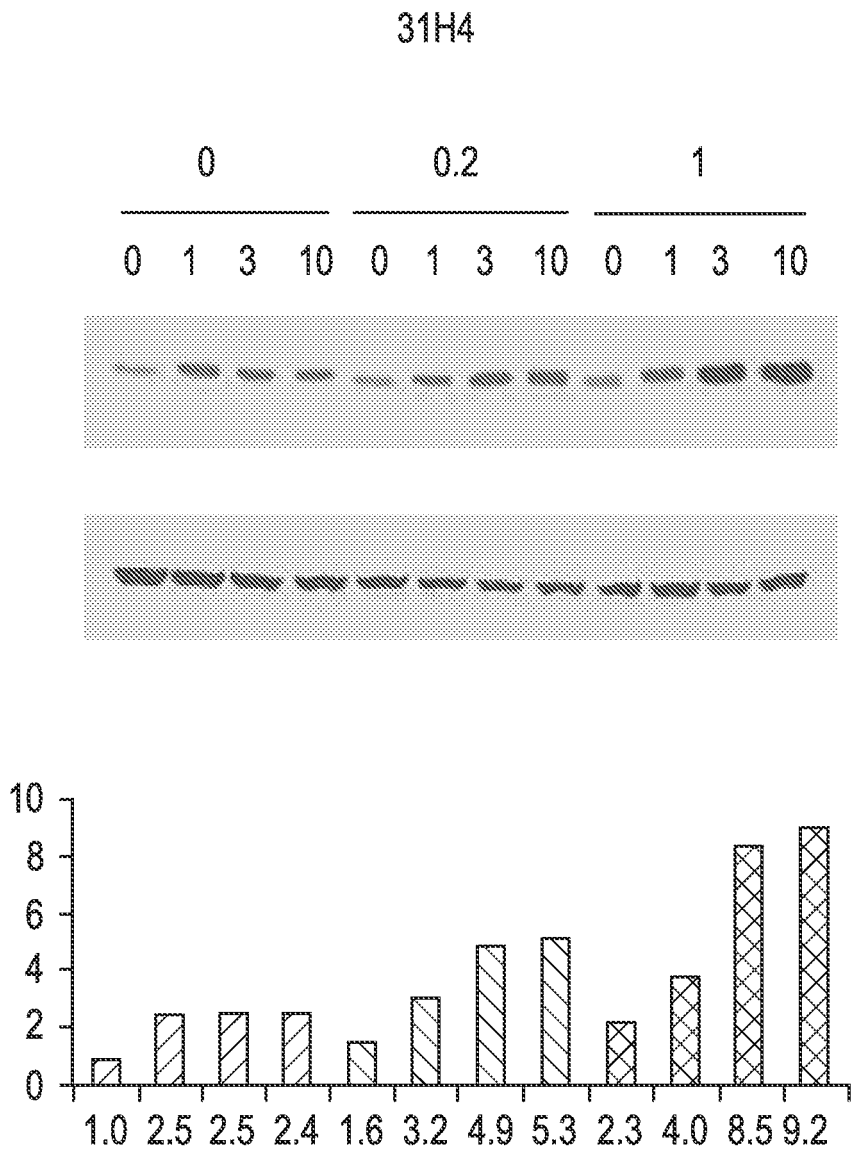

31H4
0
0.2
1
0 1 3 10 0 1 3 10 0 1 3 10
10
8
6
4
2
0
1.0 2.5 2.5 2.4 1.6 3.2 4.9 5.3 2.3 4.0 8.5 9.2

FIG. 12C

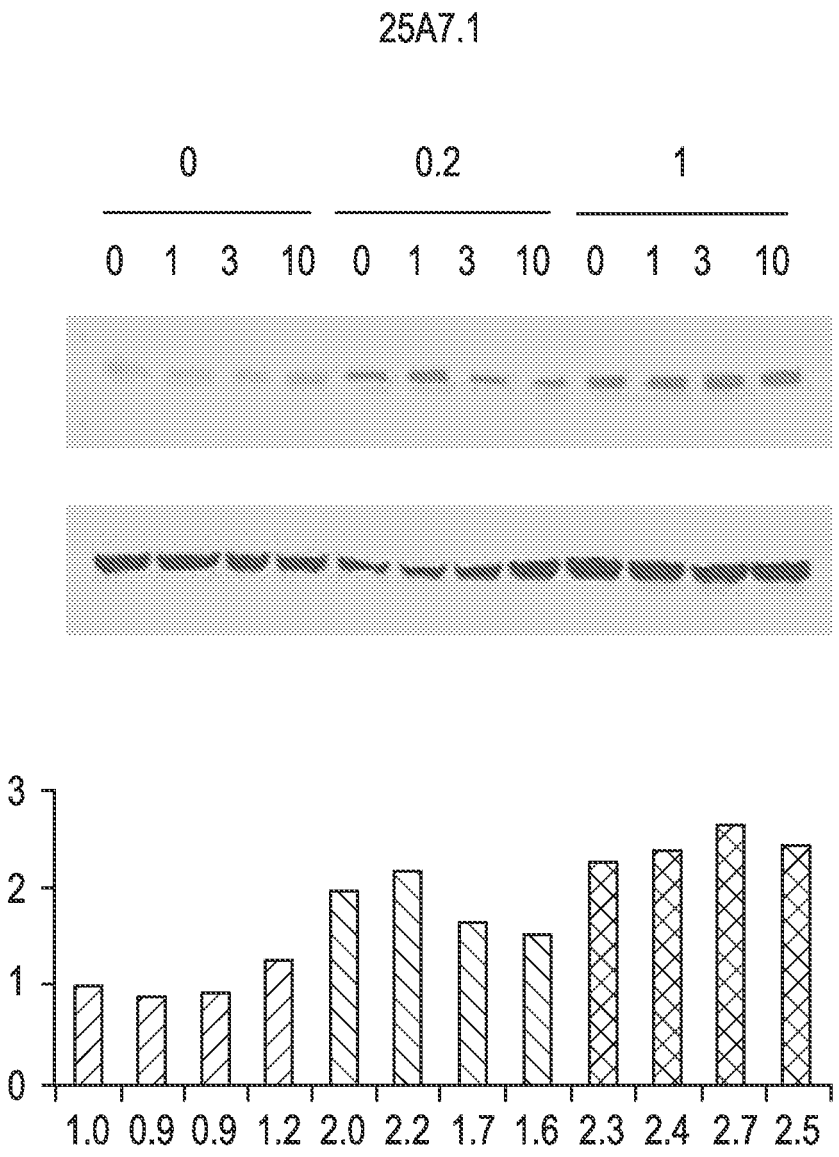

25A7.1
0
0.2
1
0 1 3 10 0 1 3 10 0 1 3 10
3
2
1
0
1.0 0.9 0.9 1.2 2.0 2.2 1.7 1.6 2.3 2.4 2.7 2.5

FIG. 12D

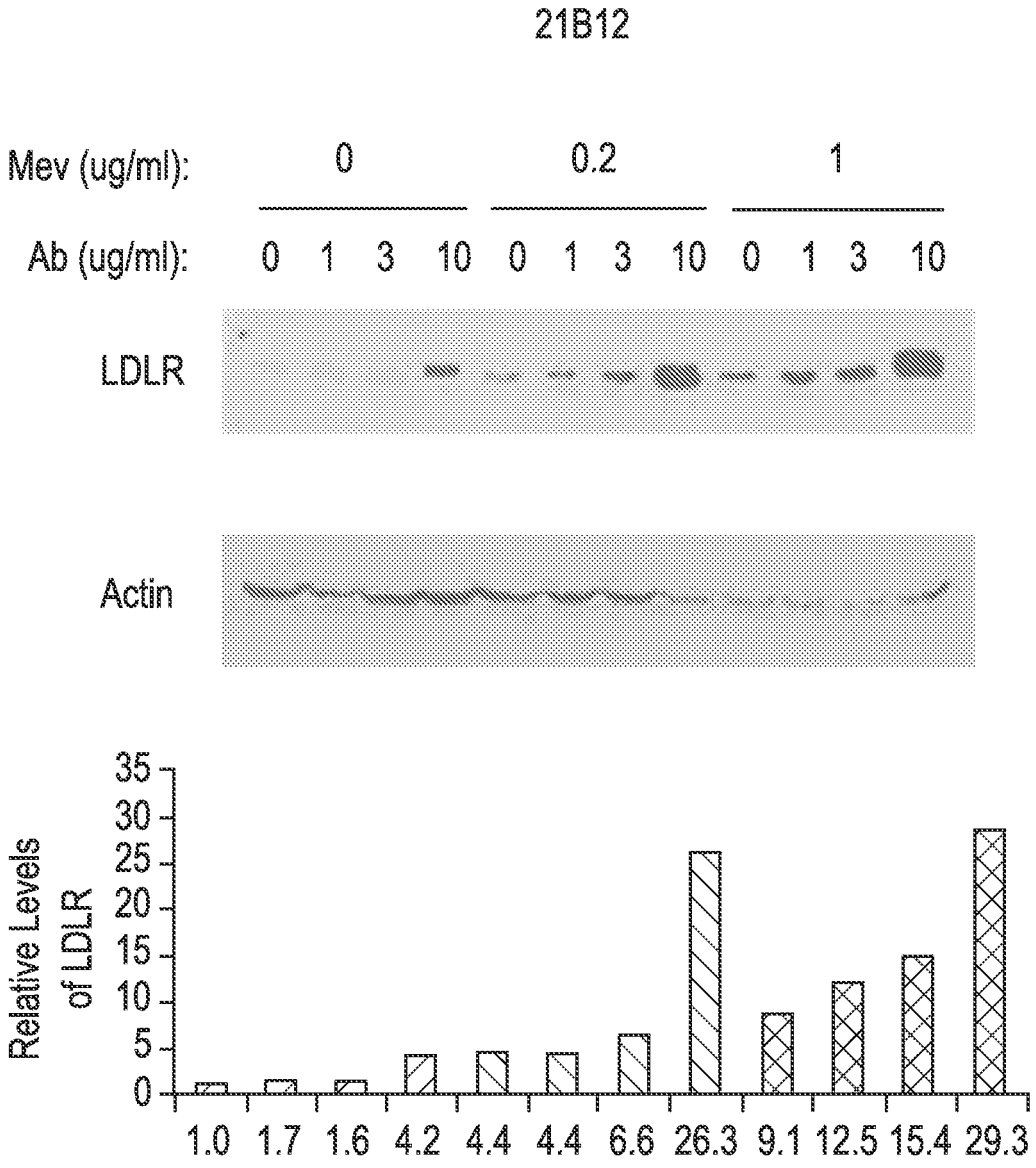

21B12
Mev (ug/ml):
0
0.2
1
Ab (ug/ml):
0 1 3 10 0 1 3 10 0 1 3 10
LDLR
Actin
Relative Levels of LDLR
35
30
25
20
15
10
5
0
1.0 1.7 1.6 4.2 4.4 4.4 6.6 26.3 9.1 12.5 15.4 29.3

FIG. 12E

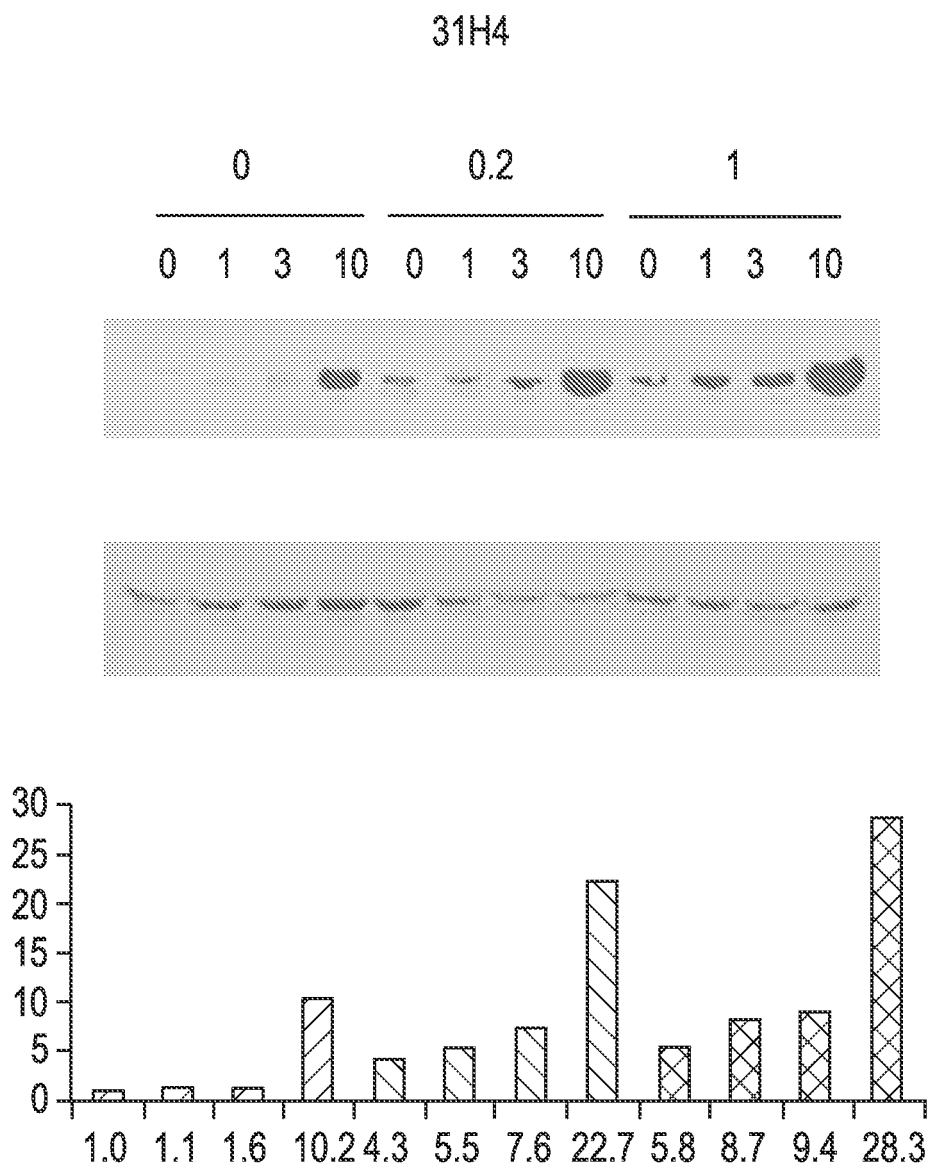

31H4
0
0.2
1
0 1 3 10 0 1 3 10 0 1 3 10
30
25
20
15
10
5
0
1.0 1.1 1.6 10.2 4.3 5.5 7.6 22.7 5.8 8.7 9.4 28.3

FIG. 12F

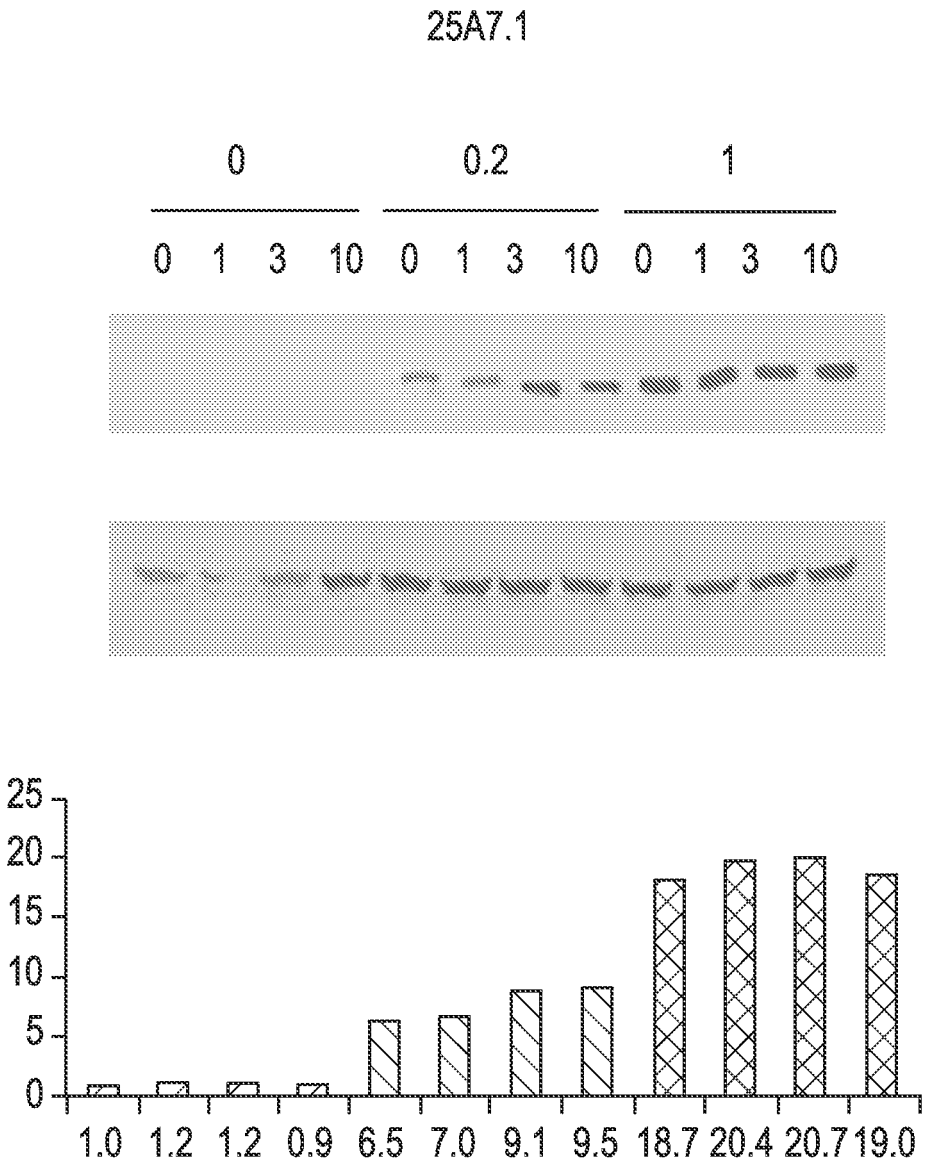

25A7.1
0
0.2
1
0 1 3 10 0 1 3 10 0 1 3 10
25
20
15
10
5
0
1.0 1.2 1.2 0.9 6.5 7.0 9.1 9.5 18.7 20.4 20.7 19.0

FIG. 13A

Light Chain:

```
23B5_light_cdr    RASQSI.....SSYLN (SEQ ID NO:209)  AASSLQS (SEQ ID NO:211)  QQSYSSPIT~~~~~~~~~ (SEQ ID NO:213)
25G4_light_cdr    RASQSI.....SIYLN (SEQ ID NO:388)  AAASLQS (SEQ ID NO:393)  QQSYSAPIT~~~~~~~~~ (SEQ ID NO:394)
3C4_light_cdr     RASQRI.....SNYLS (SEQ ID NO:219)  AASSLQS (SEQ ID NO:211)  QQSYSTPLI~~~~~~~~~ (SEQ ID NO:235)
30A4_light_cdr    RSSQSLLHSNGYNFLN (SEQ ID NO:220)  LGSHRAS (SEQ ID NO:227)  MQVLQTPFT~~~~~~~~~ (SEQ ID NO:236)
21B12_light_cdr   ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  NSYTSTSMV~~~~~~~~~ (SEQ ID NO:395)
23G1_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVTNRPS (SEQ ID NO:162)  NSYTSTSMV~~~~~~~~~ (SEQ ID NO:395)
20D10_light_cdr   ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~ (SEQ ID NO:164)
26H5_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~ (SEQ ID NO:164)
31D1_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~(SEQ ID NO:164)
27E7_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~(SEQ ID NO:164)
27H5_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~ (SEQ ID NO:164)
30B9_light_cdr    ~~TGTSSDVGGYNSVS (SEQ ID NO:158)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~ (SEQ ID NO:164)
19H9_light_cdr    ~~TGTNSDVGGYNSVS (SEQ ID NO:389)  EVSNRPS (SEQ ID NO:162)  SSYTSTSMV~~~~~~~~~(SEQ ID NO:164)
17C2_light_cdr    ~~TGTSSDVGAYNSVS (SEQ ID NO:390)  EVSNRPS (SEQ ID NO:162)  SSYTSTNMV~~~~~~~~~(SEQ ID NO:164)
25A7_light_cdr    ~~TGTSSDVGRYNSVS (SEQ ID NO:391)  EVSNRPS (SEQ ID NO:162)  SSYTSSSVV~~~~~~~~~(SEQ ID NO:396)
13H1_light_cdr    ~~TGTSSDVGNYNLVS (SEQ ID NO:221)  EVSKRPS (SEQ ID NO:228)  CSYAGSSTLV~~~~~~~~ (SEQ ID NO:237)
31H4_light_cdr    ~~TGSSSNIGAGYDVH (SEQ ID NO:222)  GNSNRPS (SEQ ID NO:229)  QSYDSSLSGSV~~~~~~~ (SEQ ID NO:238)
27B2_light_cdr    ~~TGSSSNIGAHYDVH (SEQ ID NO:223)  GNTYRPS (SEQ ID NO:230)  QSYDNSLSGVV~~~~~~~ (SEQ ID NO:239)
9H6_light_cdr     ~~SGSSSNIGSNT.VN (SEQ ID NO:197)  SNNYRPS (SEQ ID NO:199)  AAWDDSLN.WV~~~~~~~ (SEQ ID NO:397)
1A12_light_cdr    ~~SGSSSNIGSKT.VN (SEQ ID NO:381)  SNNYRPS (SEQ ID NO:199)  AAWDDSLN.WV~~~~~~~ (SEQ ID NO:397)
9C9_light_cdr     ~~SGSSSNIGSKT.VN (SEQ ID NO:381)  RNNQRPL (SEQ ID NO:392)  AAWDDSLN.WV~~~~~~~ (SEQ ID NO:397)
31A4_light_cdr    ~~SGSSSNIGSNT.VN (SEQ ID NO:197)  SNNQRPS (SEQ ID NO:231)  AVWDDSLNGWV~~~~~~~ (SEQ ID NO:240)
22E2_light_cdr    ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DYNKRPS (SEQ ID NO:183)  GTWDSSLSGYV~~~~~~~ (SEQ ID NO:185)
28B12_light_cdr   ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DYNKRPS (SEQ ID NO:183)  GTWDSSLSGYV~~~~~~~ (SEQ ID NO:185)
28D6_light_cdr    ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DYNKRPS (SEQ ID NO:183)  GTWDSSLSGYV~~~~~~~ (SEQ ID NO:185)
16F12_light_cdr   ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DYNKRPS (SEQ ID NO:183)  GTWDSSLSAYV~~~~~~~ (SEQ ID NO:185)
27A6_light_cdr    ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DYNKRPS (SEQ ID NO:183)  GTWDSSLSSYV~~~~~~~ (SEQ ID NO:398)
31G11_light_cdr   ~~SGSSSNIGNNF.VS (SEQ ID NO:182)  DSNKRPS (SEQ ID NO:184)  GTWDSSLSAYV~~~~~~~ (SEQ ID NO:399)
13B5_light_cdr    ~~SGSNSNIGNNY.VS (SEQ ID NO:224)  DNNKRPS (SEQ ID NO:232)  GTWDSSLSAVV~~~~~~~ (SEQ ID NO:241)
31B12_light_cdr   ~~~~~SGDKLGDKYAC. (SEQ ID NO:225)  QNTKWPL (SEQ ID NO:233)  QAWDSSTVV~~~~~~~~~ (SEQ ID NO:242)
3B6_light_cdr     ~~~~TLSSGYSSYEVD (SEQ ID NO:226)  VDTGGIV (SEQ ID NO:234)  SDYHCGADHGSGTNFVVV (SEQ ID NO:243)
Consensus
```

FIG. 13B

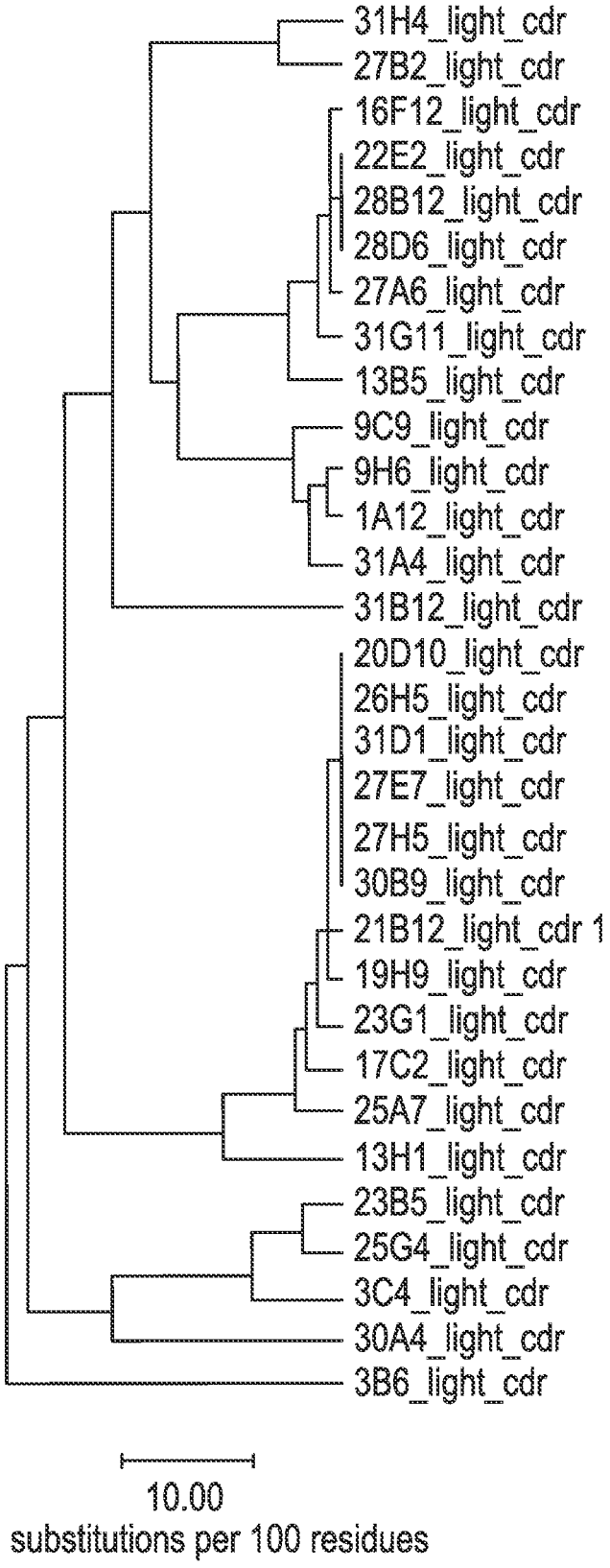

31H4_light_cdr
27B2_light_cdr
16F12_light_cdr
22E2_light_cdr
28B12_light_cdr
28D6_light_cdr
27A6_light_cdr
31G11_light_cdr
13B5_light_cdr
9C9_light_cdr
9H6_light_cdr
1A12_light_cdr
31A4_light_cdr
31B12_light_cdr
20D10_light_cdr
26H5_light_cdr
31D1_light_cdr
27E7_light_cdr
27H5_light_cdr
30B9_light_cdr
21B12_light_cdr 1
19H9_light_cdr
23G1_light_cdr
17C2_light_cdr
25A7_light_cdr
13H1_light_cdr
23B5_light_cdr
25G4_light_cdr
3C4_light_cdr
30A4_light_cdr
3B6_light_cdr
10.00
substitutions per 100 residues

FIG. 13C

Heavy Chain:

```
20D10_heavy_cdr  ~~GYPLTSYGIS (SEQ ID NO:168) WISAYNG.NTNYAQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
30B9_heavy_cdr   ~~GYPLTSYGIS (SEQ ID NO:168) WISAYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
27E7_heavy_cdr   ~~GYSLTSYGIS (SEQ ID NO:366) WISAYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
19H9_heavy_cdr   ~~GYALTSYGIS (SEQ ID NO:367) WISAYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
21B12_heavy_cdr  ~~GYTLTSYGIS (SEQ ID NO:368) WVSFYNG.NTN AQKLQG (SEQ ID NO:175) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
23G1_heavy_cdr   ~~GYTLTSYGIS (SEQ ID NO:368) WVSFYNG.NTN AQKLQG (SEQ ID NO:175) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
26H5_heavy_cdr   ~~GYTLTSYGIS (SEQ ID NO:368) WISFYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
31D1_heavy_cdr   ~~GYTLTSYGIS (SEQ ID NO:368) WISFYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
27H5_heavy_cdr   ~~GYTLTSYGIS (SEQ ID NO:368) WISVYNG.NTN AQKVQG (SEQ ID NO:174) GYGMDV~~~~~~~~~~(SEQ ID NO:180)
17C2_heavy_cdr   ~~GYSFTSYGIS (SEQ ID NO:369) WVSAYNG.NTN AQKFQG (SEQ ID NO:178) GYVMDV~~~~~~~~~~(SEQ ID NO:387)
25A7_heavy_cdr   ~~GYTFPSYGIS (SEQ ID NO:370) WISAYNG.NTN AEKLQG (SEQ ID NO:179) GYVMDV~~~~~~~~~~(SEQ ID NO:387)
3B6_heavy_cdr    ~~GYTFTSYGIS (SEQ ID NO:244) WISTYNG.NTN AQKVQG (SEQ ID NO:252) GYTRDY~~~~~~~~~~(SEQ ID NO:261)
9C9_heavy_cdr    ~~GFTFSSYWMS (SEQ ID NO:371) NIKQDGS.EKY VDSVKG (SEQ ID NO:377) E....SNWGFAFDI (SEQ ID NO:385)
9H6_heavy_cdr    ~~GFTFSRYWMS (SEQ ID NO:372) NIKHDGS.EKY VDSVKG (SEQ ID NO:378) E....SNWGFAFDV (SEQ ID NO:386)
1A12_heavy_cdr   ~~GLTFSNFWMS (SEQ ID NO:373) NIKQDGS.EKY VDSVKG (SEQ ID NO:377) E....SNWGFAFDI (SEQ ID NO:385)
23B5_heavy_cdr   ~~GFTFSSYAMN (SEQ ID NO:374) TISGSGD.NTY ADSVKG (SEQ ID NO:379) KFVLMVYAMLDY~~ (SEQ ID NO:218)
25G4_heavy_cdr   ~~GFTFSSYAMN (SEQ ID NO:374) TISGSGG.NTY ADSVKG (SEQ ID NO:380) KFVLMVYAMLDY~~ (SEQ ID NO:218)
13B5_heavy_cdr   ~~GFTFSSYAMS (SEQ ID NO:245) TISGSGG.RTY ADSVKG (SEQ ID NO:253) E....VGSPFDY~~ (SEQ ID NO:262)
22E2_heavy_cdr   ~~GFTFSSFGMH (SEQ ID NO:188) LIWNDGS.NKY ADSVKG (SEQ ID NO:381) AIAAL.YYYYGMDV (SEQ ID NO:195)
28B12_heavy_cdr  ~~GFTFSSFGMH (SEQ ID NO:188) LIWNDGS.NKY ADSVKG (SEQ ID NO:381) AIAAL.YYYYGMDV (SEQ ID NO:195)
28D6_heavy_cdr   ~~GFTFSSFGMH (SEQ ID NO:188) LIWNDGS.NKY ADSVKG (SEQ ID NO:381) AIAAL.YYYYGMDV (SEQ ID NO:195)
16F12_heavy_cdr  ~~GFTFNSFGMH (SEQ ID NO:375) LIWSDGS.DEY ADSVKG (SEQ ID NO:382) AIAAL.YYYYGMDV (SEQ ID NO:195)
27A6_heavy_cdr   ~~GFTFNSFGMH (SEQ ID NO:375) LIWSDGS.DKY ADSVKG (SEQ ID NO:383) AIAAL.YYYYGMDV (SEQ ID NO:195)
31G11_heavy_cdr  ~~GFTFRSYGMH (SEQ ID NO:376) LIWHDGS.NTY VDSVKG (SEQ ID NO:384) GIAVA.YYYYGMDV (SEQ ID NO:196)
30A4_heavy_cdr   ~~GFTFSSYGMH (SEQ ID NO:246) VIWYDGS.DKY ADSVKG (SEQ ID NO:254) ETGPLKLYYYGMDV (SEQ ID NO:263)
31B12_heavy_cdr  ~~GFTFSSYGMH (SEQ ID NO:246) IIWYDGS.NKY ADSVKG (SEQ ID NO:255) R.GGLAARPGGMDV (SEQ ID NO:264)
31H4_heavy_cdr   ~~GFTFSSYSMN (SEQ ID NO:247) SISSSSS.YIS ADSVKG (SEQ ID NO:256) DYDFWSAYYDAFDV (SEQ ID NO:265)
27B2_heavy_cdr   GGSISSGGYYWS (SEQ ID NO:248) YIYNSGSTY.. NPSLKS (SEQ ID NO:257) ED.TAMVPY.FDY~ (SEQ ID NO:266)
3C4_heavy_cdr    GGSISSSDYYWS (SEQ ID NO:249) YIYYSGSTY.. NPSLKS (SEQ ID NO:258) GG.VTTYYYAMDV~ (SEQ ID NO:267)
31A4_heavy_cdr   GGSFSA..YYWN (SEQ ID NO:250) EINHSGRTD.. NPSLKS (SEQ ID NO:259) GQ.LVPFDY~~~~~ (SEQ ID NO:268)
13H1_heavy_cdr   GDSVSSNSAAWN (SEQ ID NO:251) RTYYRSKWYKN SVSVKS (SEQ ID NO:260) GGPTAAFDY~~~~~ (SEQ ID NO:269)
Consensus                                                    *
```

FIG. 13D

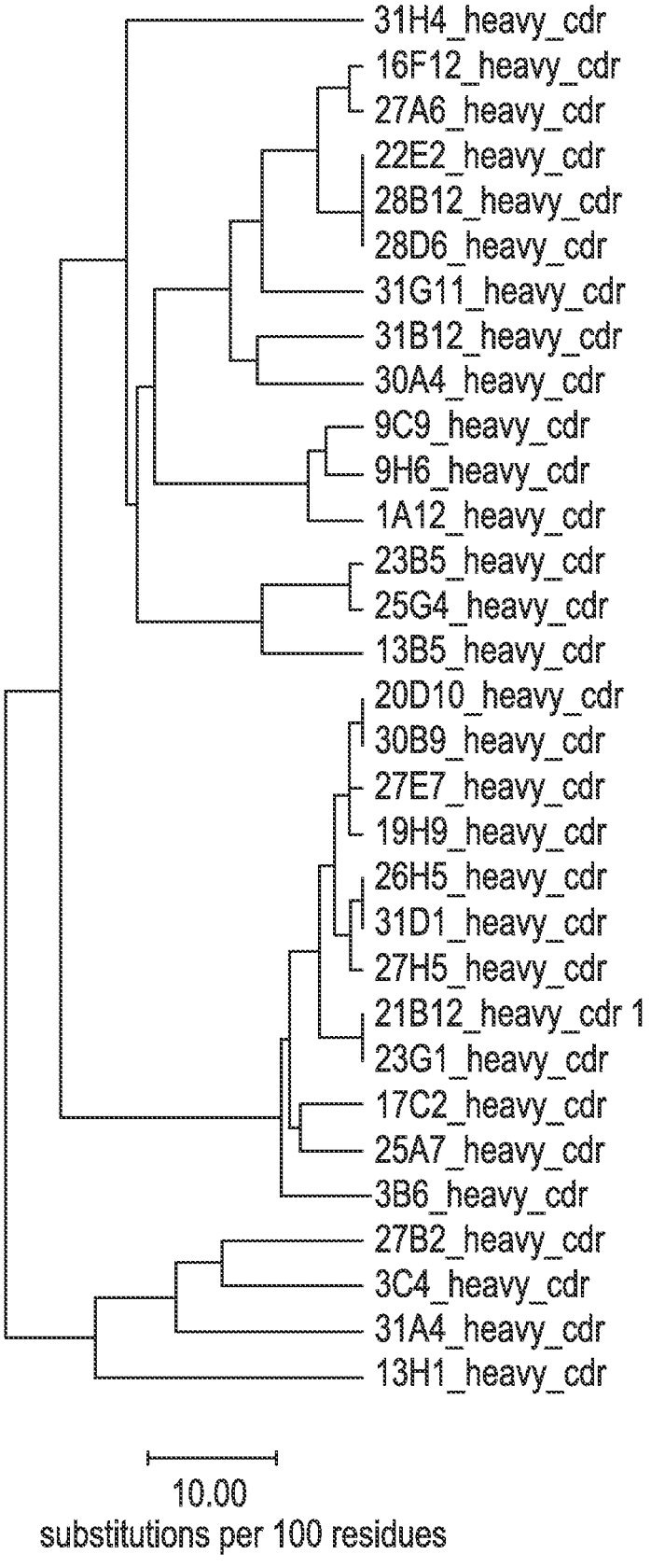

31H4_heavy_cdr
16F12_heavy_cdr
27A6_heavy_cdr
22E2_heavy_cdr
28B12_heavy_cdr
28D6_heavy_cdr
31G11_heavy_cdr
31B12_heavy_cdr
30A4_heavy_cdr
9C9_heavy_cdr
9H6_heavy_cdr
1A12_heavy_cdr
23B5_heavy_cdr
25G4_heavy_cdr
13B5_heavy_cdr
20D10_heavy_cdr
30B9_heavy_cdr
27E7_heavy_cdr
19H9_heavy_cdr
26H5_heavy_cdr
31D1_heavy_cdr
27H5_heavy_cdr
21B12_heavy_cdr 1
23G1_heavy_cdr
17C2_heavy_cdr
25A7_heavy_cdr
3B6_heavy_cdr
27B2_heavy_cdr
3C4_heavy_cdr
31A4_heavy_cdr
13H1_heavy_cdr
10.00
substitutions per 100 residues

FIG. 13E

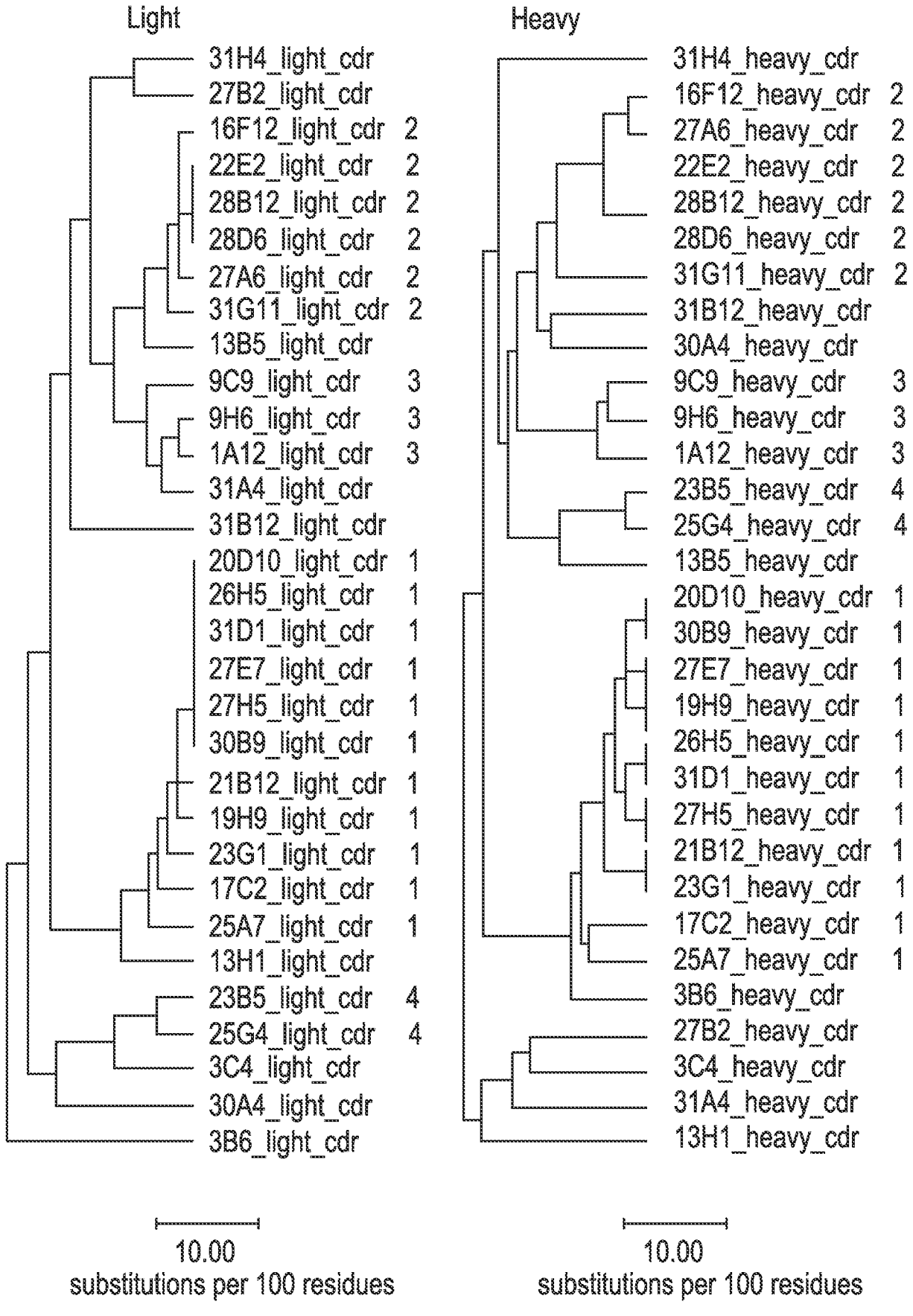

Light
31H4_light_cdr
27B2_light_cdr
16F12_light_cdr 2
22E2_light_cdr 2
28B12_light_cdr 2
28D6_light_cdr 2
27A6_light_cdr 2
31G11_light_cdr 2
13B5_light_cdr
9C9_light_cdr 3
9H6_light_cdr 3
1A12_light_cdr 3
31A4_light_cdr
31B12_light_cdr
20D10_light_cdr 1
26H5_light_cdr 1
31D1_light_cdr 1
27E7_light_cdr 1
27H5_light_cdr 1
30B9_light_cdr 1
21B12_light_cdr 1
19H9_light_cdr 1
23G1_light_cdr 1
17C2_light_cdr 1
25A7_light_cdr 1
13H1_light_cdr
23B5_light_cdr 4
25G4_light_cdr 4
3C4_light_cdr
30A4_light_cdr
3B6_light_cdr
10.00
substitutions per 100 residues
Heavy
31H4_heavy_cdr
16F12_heavy_cdr 2
27A6_heavy_cdr 2
22E2_heavy_cdr 2
28B12_heavy_cdr 2
28D6_heavy_cdr 2
31G11_heavy_cdr 2
31B12_heavy_cdr
30A4_heavy_cdr
9C9_heavy_cdr 3
9H6_heavy_cdr 3
1A12_heavy_cdr 3
23B5_heavy_cdr 4
25G4_heavy_cdr 4
13B5_heavy_cdr
20D10_heavy_cdr 1
30B9_heavy_cdr 1
27E7_heavy_cdr 1
19H9_heavy_cdr 1
26H5_heavy_cdr 1
31D1_heavy_cdr 1
27H5_heavy_cdr 1
21B12_heavy_cdr 1
23G1_heavy_cdr 1
17C2_heavy_cdr 1
25A7_heavy_cdr 1
3B6_heavy_cdr
27B2_heavy_cdr
3C4_heavy_cdr
31A4_heavy_cdr
13H1_heavy_cdr
10.00
substitutions per 100 residues

FIG. 13F

Consensus for Group 1:

```
20D10_light_heavy_cdr  TGTSSDVGGYNSVS  (SEQ ID NO:158)  SYSNRPS  (SEQ ID NO:162)  SSYTSTSTWV  (SEQ ID NO:164)
30B9_light_heavy_cdr     S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     S   TSM   (SEQ ID NO:164)
27E7_light_heavy_cdr     S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     S   ISM   (SEQ ID NO:164)
19H9_light_heavy_cdr     N   G         (SEQ ID NO:159)     S     (SEQ ID NO:162)     S   TSM   (SEQ ID NO:164)
21B12_light_heavy_cdr    S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     N   TSM   (SEQ ID NO:165)
23G1_light_heavy_cdr     S   G         (SEQ ID NO:158)     T     (SEQ ID NO:163)     N   ISM   (SEQ ID NO:165)
26H5_light_heavy_cdr     S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     S   TSM   (SEQ ID NO:164)
31D1_light_heavy_cdr     S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     S   TSM   (SEQ ID NO:164)
27H5_light_heavy_cdr     S   G         (SEQ ID NO:158)     S     (SEQ ID NO:162)     S   ISM   (SEQ ID NO:164)
17C2_light_heavy_cdr     S   A         (SEQ ID NO:160)     S     (SEQ ID NO:162)     S   TNM   (SEQ ID NO:166)
25A7_light_heavy_cdr     S   R         (SEQ ID NO:161)     S     (SEQ ID NO:162)     S   SSV   (SEQ ID NO:167)
                         *** ***** ******                ** *****                 ***** *

20D10_light_heavy_cdr  GYPLTSYGIS  (SEQ ID NO:168)  WISAYNGNTNYAQKVQG  (SEQ ID NO:174)  GYGMDV  (SEQ ID NO:180)
30B9_light_heavy_cdr     PLT       (SEQ ID NO:168)     I A     Q V    (SEQ ID NO:174)     G     (SEQ ID NO:180)
27E7_light_heavy_cdr     SLT       (SEQ ID NO:169)     I A     Q V    (SEQ ID NO:174)     G     (SEQ ID NO:180)
19H9_light_heavy_cdr     ALT       (SEQ ID NO:170)     I A     Q V    (SEQ ID NO:174)     G     (SEQ ID NO:180)
21B12_light_heavy_cdr    TLT       (SEQ ID NO:171)     V F     Q L    (SEQ ID NO:175)     G     (SEQ ID NO:180)
23G1_light_heavy_cdr     TLT       (SEQ ID NO:171)     V F     Q L    (SEQ ID NO:175)     G     (SEQ ID NO:180)
26H5_light_heavy_cdr     TLT       (SEQ ID NO:171)     I F     Q V    (SEQ ID NO:176)     G     (SEQ ID NO:180)
31D1_light_heavy_cdr     TLT       (SEQ ID NO:171)     I F     Q V    (SEQ ID NO:176)     G     (SEQ ID NO:180)
27H5_light_heavy_cdr     TLT       (SEQ ID NO:171)     I V     Q V    (SEQ ID NO:177)     G     (SEQ ID NO:180)
17C2_light_heavy_cdr     SFT       (SEQ ID NO:172)     V A     Q F    (SEQ ID NO:178)     V     (SEQ ID NO:181)
25A7_light_heavy_cdr     TFP       (SEQ ID NO:173)     I A     E L    (SEQ ID NO:179)     V     (SEQ ID NO:181)
                         **  *****                   * * ********* * **                  ** ***
```

Consensus for Group 2:

```
22E2_light_heavy_cdr   SGSSSNIGNNFVS  (SEQ ID NO:182)  DVNERPS  (SEQ ID NO:183)  GTWDSSLSGYV  (SEQ ID NO:185)
28B12_light_heavy_cdr                 (SEQ ID NO:182)     Y     (SEQ ID NO:183)     G     (SEQ ID NO:185)
28D6_light_heavy_cdr                  (SEQ ID NO:182)     Y     (SEQ ID NO:183)     G     (SEQ ID NO:185)
16F12_light_heavy_cdr                 (SEQ ID NO:182)     Y     (SEQ ID NO:183)     A     (SEQ ID NO:186)
27A6_light_heavy_cdr                  (SEQ ID NO:182)     Y     (SEQ ID NO:183)     S     (SEQ ID NO:187)
31G11_light_heavy_cdr                 (SEQ ID NO:182)     S     (SEQ ID NO:184)     A     (SEQ ID NO:186)
                       **************                     * ******                  ********* **

22E2_light_heavy_cdr   GFTFSSFGMH  (SEQ ID NO:188)  LIWNDGSNKYYADSVEG  (SEQ ID NO:191)  ARAALYYYGMDV  (SEQ ID NO:195)
28B12_light_heavy_cdr     S F      (SEQ ID NO:188)     N   NK  A      (SEQ ID NO:191)     A   AL        (SEQ ID NO:195)
28D6_light_heavy_cdr      S F      (SEQ ID NO:188)     N   NK  A      (SEQ ID NO:191)     A   AL        (SEQ ID NO:195)
16F12_light_heavy_cdr     N F      (SEQ ID NO:189)     S   DE  A      (SEQ ID NO:192)     A   AI        (SEQ ID NO:195)
27A6_light_heavy_cdr      N F      (SEQ ID NO:188)     S   DK  A      (SEQ ID NO:193)     A   AI        (SEQ ID NO:195)
31G11_light_heavy_cdr     R Y      (SEQ ID NO:190)     H   NT  V      (SEQ ID NO:194)     G   VA        (SEQ ID NO:196)
                          **** * ***                  *** ***  **  ******                  **  *********
```

FIG. 13G

Consensus for Group 3:

```
9H6_light_heavy_cdr   SGSSSNIGSNTVN (SEQ ID NO:197)      SNNRRPS (SEQ ID NO:199)   AAWDDSLNGV (SEQ ID NO:201)
1A12_light_heavy_cdr        K       (SEQ ID NO:198)      S  R  S (SEQ ID NO:199)
9C9_light_heavy_cdr         K       (SEQ ID NO:198)      R  Q  L (SEQ ID NO:200)
                      ********** ***                      ** **                  **********

9H6_light_heavy_cdr   GFTFSRYAMS (SEQ ID NO:202)  NIKHDGSEKYYVDSVKG (SEQ ID NO:205)  ESWGFAEDV (SEQ ID NO:207)
1A12_light_heavy_cdr  L  NF      (SEQ ID NO:203)       Q            (SEQ ID NO:206)          I  (SEQ ID NO:208)
9C9_light_heavy_cdr   F  SY      (SEQ ID NO:204)       Q            (SEQ ID NO:206)          I  (SEQ ID NO:208)
                      * ***  ***                  **** ****************                **********
```

Consensus for Group 4:

```
23B5_light_heavy_cdr  RASQSISSYLN (SEQ ID NO:209)  AASSLQS (SEQ ID NO:211)   QQSYSSPIT (SEQ ID NO:213)
25G4_light_heavy_cdr        I   (SEQ ID NO:210)       A  (SEQ ID NO:212)          A  (SEQ ID NO:214)
                      ******** ***                  ** ****                  ***** ***

23B5_light_heavy_cdr  GFTFSSYAMH (SEQ ID NO:215)  TISGSGDNTYYADSVKG (SEQ ID NO:216)  EYYLWYFAMLDY (SEQ ID NO:218)
25G4_light_heavy_cdr                                    G           (SEQ ID NO:217)
                      **********                  ****** ************             ************
```

FIG. 13H

Group 1 (11 members)

	LV_CDR1	SEQ ID NO:	LV_CDR2	SEQ ID NO:	LV_CDR3	SEQ ID NO:	H_CDR1	SEQ ID NO:	H_CDR2	SEQ ID NO:	H_CDR3	SEQ ID NO:
	1										58	
CONSENSUS	TGTSSDVGGYNSVS	305	EVSNRPS	306	SSYTSTSMV	307	SYGIS	308	WISAYNGNTNYAQKVQG	309	GYGMDV	310
25A7	.....R.....	311	.....	312	.....S.V.	313	.....	308	.....E.L..	314	..V...	315
17C2	.....A.....	316	.....	312	.....N..	317	.....	308	.V.....F..	318	..V...	315
21B12	.....	305	.....	312	N.....	319	.....	308	.V.F.....L..	320	.....	310
23G1	.....	305	..T....	321	N.....	319	.....	308	.V.F.....L..	320	.....	310
19H9	...N.....	322	.....	312	.....	307	.....	308	.....	309	.....	310
27H5	.....	305	.....	312	.....	307	.....	308	...V.....	323	.....	310
26H5	.....	305	.....	312	.....	307	.....	308	...F.....	324	.....	310
31D1	.....	305	.....	312	.....	307	.....	308	...F.....	324	.....	310
27E7	.....	305	.....	312	.....	307	.....	308	.....	309	.....	310
20D10	.....	305	.....	312	.....	307	.....	308	.....	309	.....	310
30B9	.....	305	.....	312	.....	307	.....	308	.....	309	.....	310

Group 2 (6 members)

Light chain:

	LV_CDR1	SEQ ID NO:	LV_CDR2	SEQ ID NO:	LV_CDR3	SEQ ID NO:
	1					
CONSENSUS	SGSSSNIGNNFVS	325	DYNKRPS	326	GTWDSSLSGYV	327
31G11	.....	325	.S.....	331	.....A..	332
28D6	.....	325	.....	326	.....	327
28B12	.....	325	.....	326	.....	327
22E2	.....	325	.....	326	.....	327
16F12	.....	325	.....	326	.....A..	332
27A6	.....	325	.....	326	.....S..	337

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FIG. 13I

Group 2, continued

Heavy chain:

	H_CDR1 SEQ ID NO:		H_CDR2	SEQ ID NO:	H_CDR3	SEQ ID NO: 66
CONSENSUS	SFGMH	328	LIWNDGSNKYYADSVKG	329	AIAALYYYGMDV	330
31G11	.Y...	333	...H....T..V.....	334	G..VA.....	335
28D6	.....	328	.....	329	.....	330
28B12	.....	328	.....	329	.....	330
22E2	.....	328	.....	329	.....	330
16F12	.....	328	...S...DE.....	336	.....	330
27A6	.....	328	...S...D.....	338	.....	330

FIG. 13J

```
Group 3 (3 members)
          LV_CDR1   SEQ ID NO:  LV_CDR2  SEQ ID NO:  LV_CDR3   SEQ ID NO:  H_CDR1  SEQ ID NO:  H_CDR2                          SEQ ID NO:  H_CDR3   SEQ ID NO:
                                                                                                                                    62
CONSENSUS SGSSSNIGSKTVN  339  SNNRRPS  340  AAWDDSLNWV  341  YWMS  342  NIKQDGSEKYYVDSVKG  343  ESNWGFAFDI  344
      9H6 ..........N... 345  ....... 340  .......... 341  R.... 346  ...H.............. 347  .........V 348
      9C9 .............. 339  R..Q..L 349  .......... 341  S.... 350  .................. 343  .......... 344
     1A12 .............. 339  ....... 340  .......... 341  NT... 351  .................. 343  .......... 344

Group 4 (2 members)
          KV_CDR1   SEQ ID NO:  KV_CDR2  SEQ ID NO:  KV_CDR3   SEQ ID NO:
                                                                                                                                    1
CONSENSUS RASQSIS YLN 352  AA SLQS 353  QQSYS PIT 354
      25G4 .....I... 355  ..A.... 356  .....A... 357
      23B5 .....S... 358  ..S.... 359  .....S... 360

          H_CDR1  SEQ ID NO:  H_CDR2          SEQ ID NO:  H_CDR3          SEQ ID NO:
                                                                                                                                    71
CONSENSUS SYAMN   361  TISGSG NTYYADSVKG  362  KFVLMVYAMLDY  363
      25G4 .....  361  .......G.......... 364  ............ 363
      23B5 .....  361  .......D.......... 365  ............ 363
```

FIG. 14

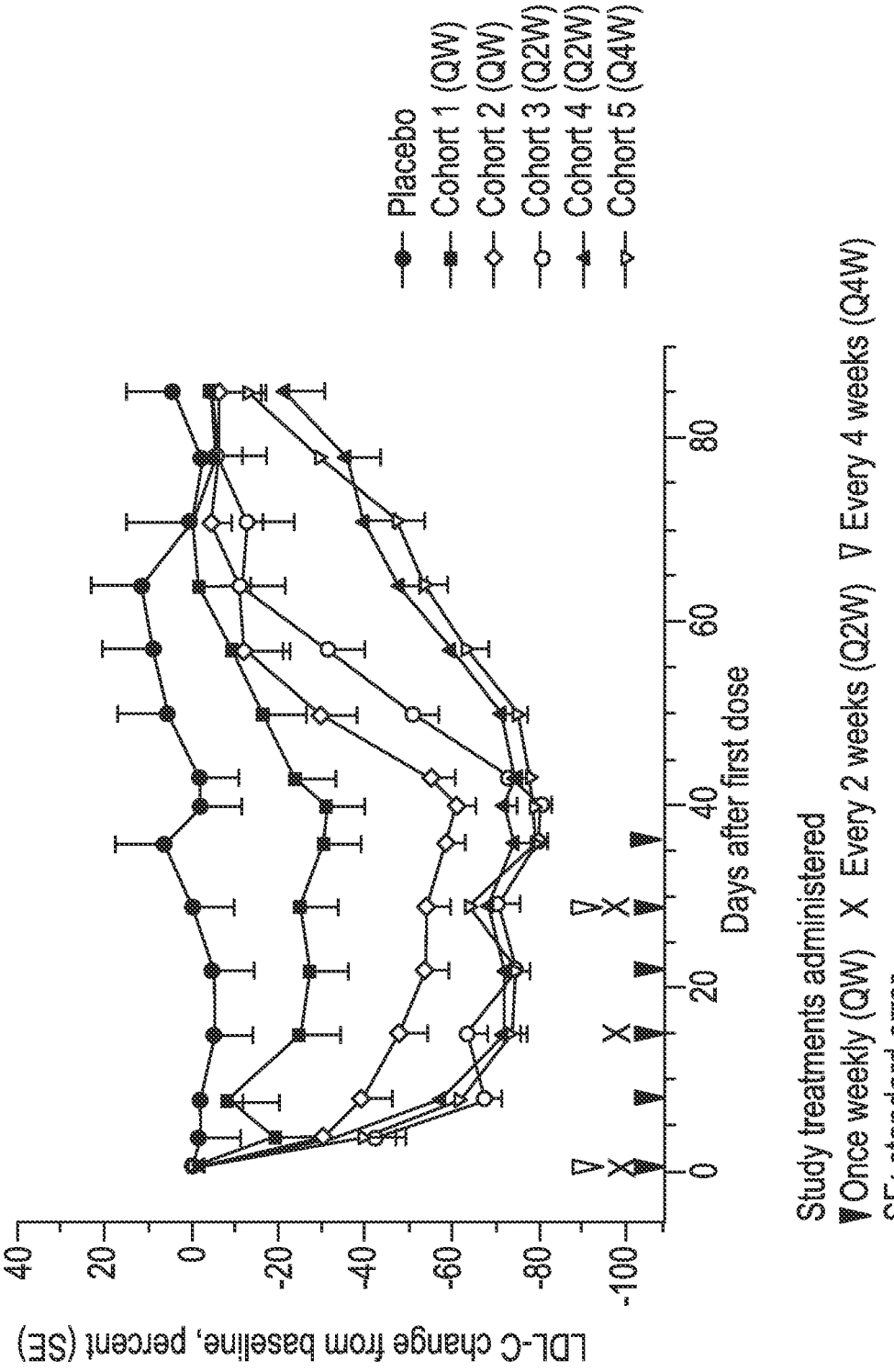

Placebo
Cohort 1 (QW)
Cohort 2 (QW)
Cohort 3 (Q2W)
Cohort 4 (Q2W)
Cohort 5 (Q4W)
LDL-C change from baseline, percent (SE)
40
20
0
-20
-40
-60
-80
-100
0
20
40
60
80
Days after first dose
Study treatments administered
▼Once weekly (QW) X Every 2 weeks (Q2W) ▽ Every 4 weeks (Q4W)
SE: standard error

FIG. 15

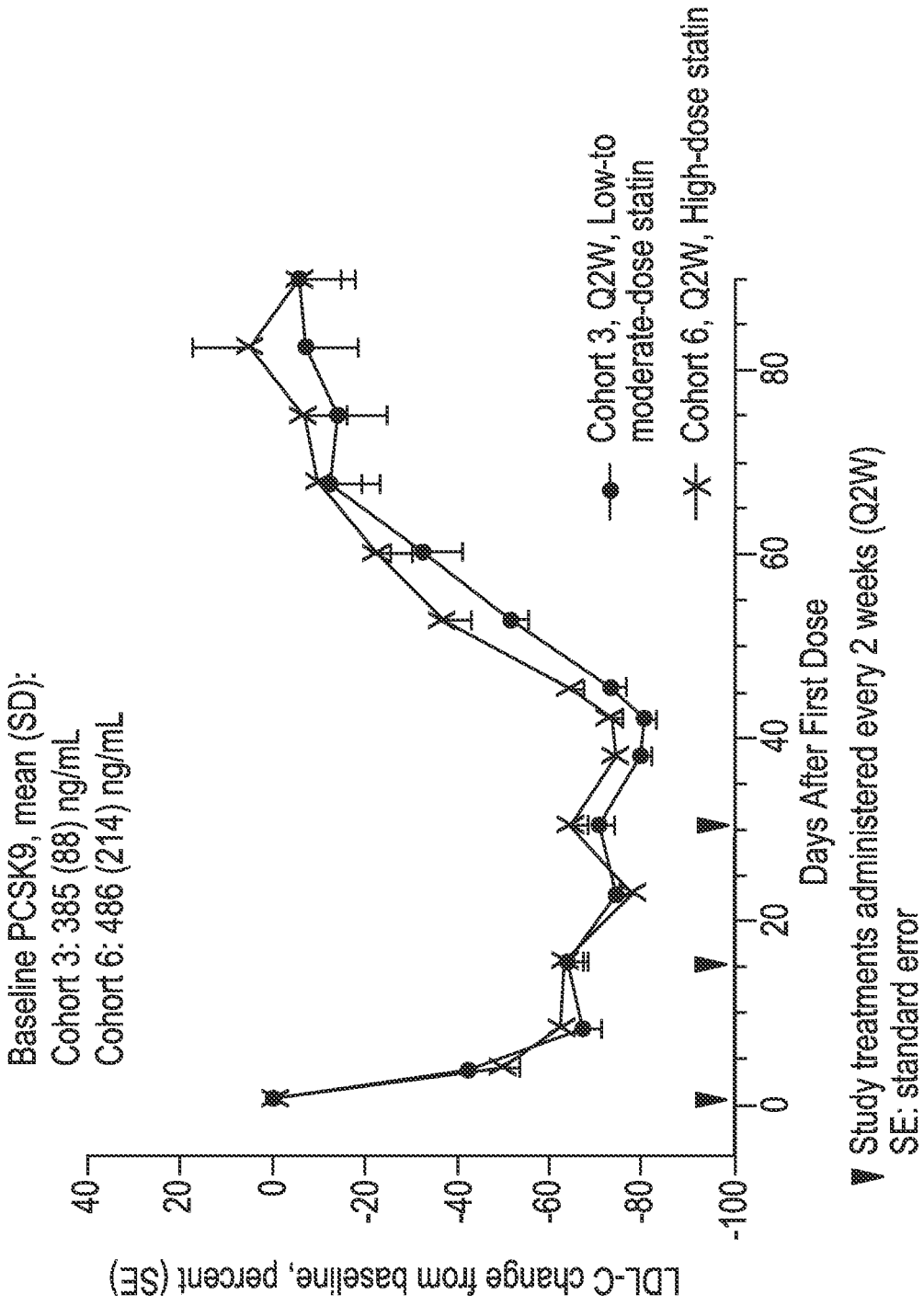

Baseline PCSK9, mean (SD):
Cohort 3: 385 (88) ng/mL
Cohort 6: 486 (214) ng/mL
Cohort 3, Q2W, Low-to moderate-dose statin
Cohort 6, Q2W, High-dose statin
LDL-C change from baseline, percent (SE)
40
20
0
-20
-40
-60
-80
-100
0
20
40
60
80
Days After First Dose
Study treatments administered every 2 weeks (Q2W)
SE: standard error

FIG. 16

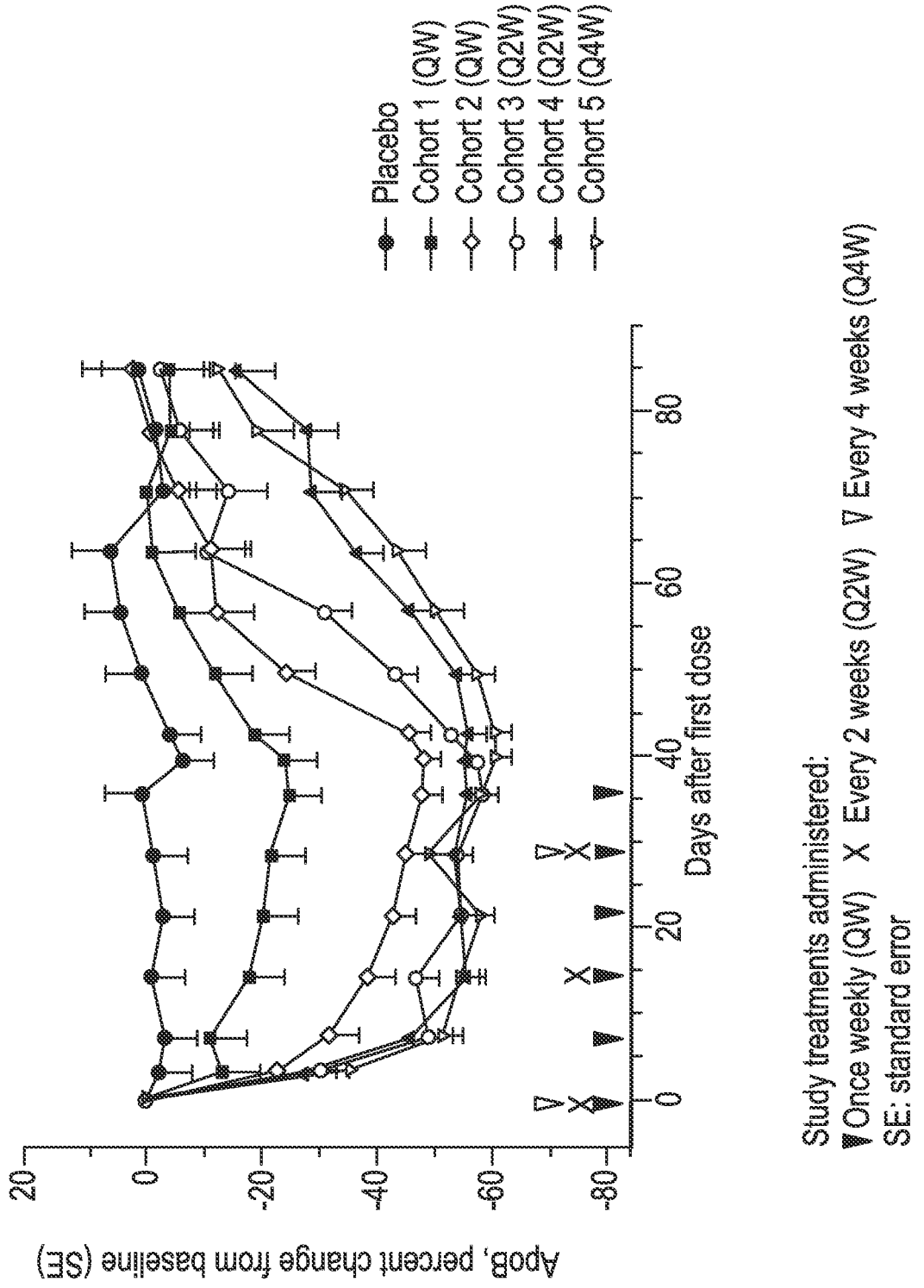
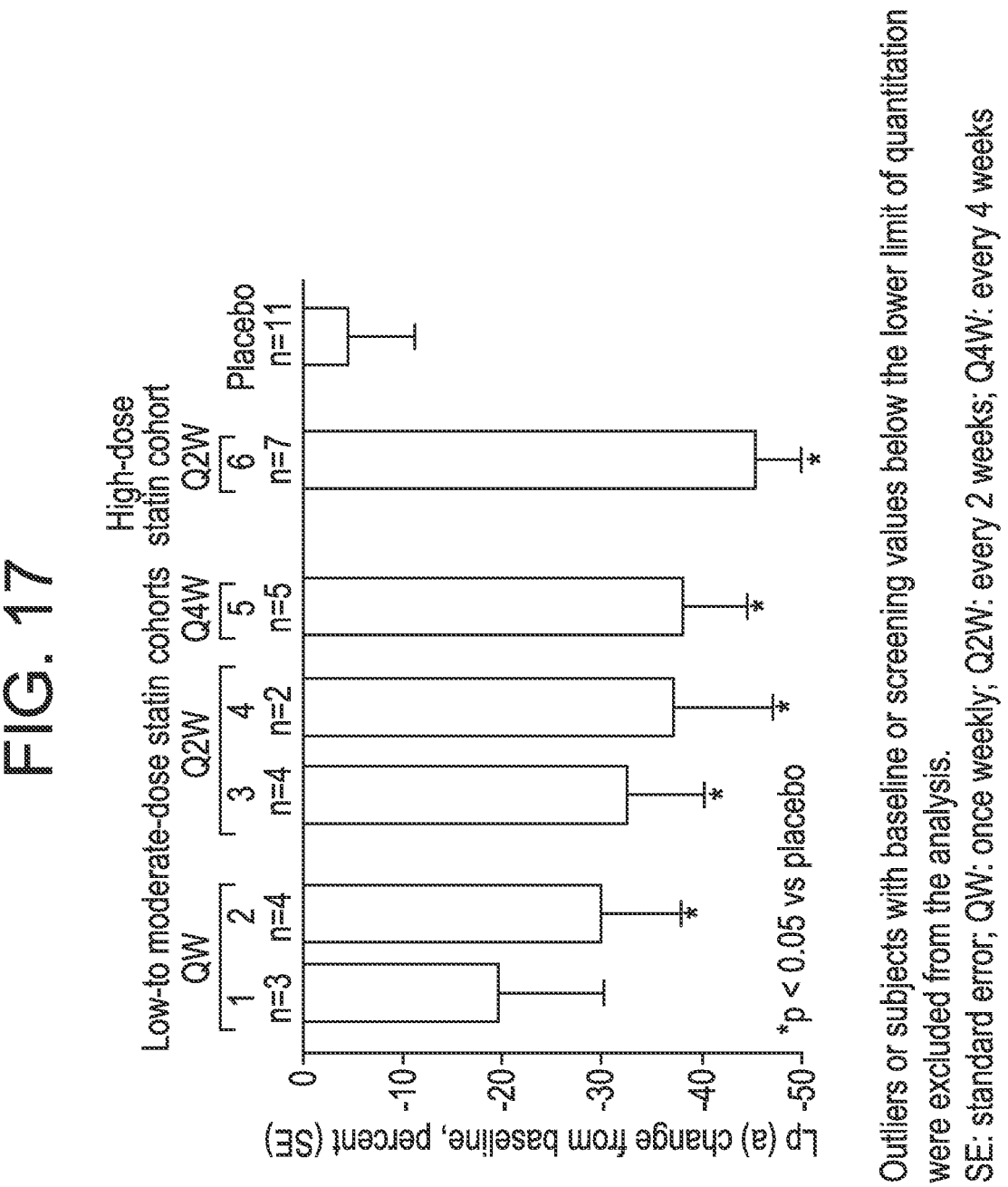

Placebo
Cohort 1 (QW)
Cohort 2 (QW)
Cohort 3 (Q2W)
Cohort 4 (Q2W)
Cohort 5 (Q4W)
ApoB, percent change from baseline (SE)
20
0
-20
-40
-60
-80
0
20
40
60
80
Days after first dose
Study treatments administered:
▼Once weekly (QW) X Every 2 weeks (Q2W) ▽ Every 4 weeks (Q4W)
SE: standard error

FIG. 17



Outliers or subjects with baseline or screening values below the lower limit of quantitation were excluded from the analysis.
SE: standard error; QW: once weekly; Q2W: every 2 weeks; Q4W: every 4 weeks

FIG. 18

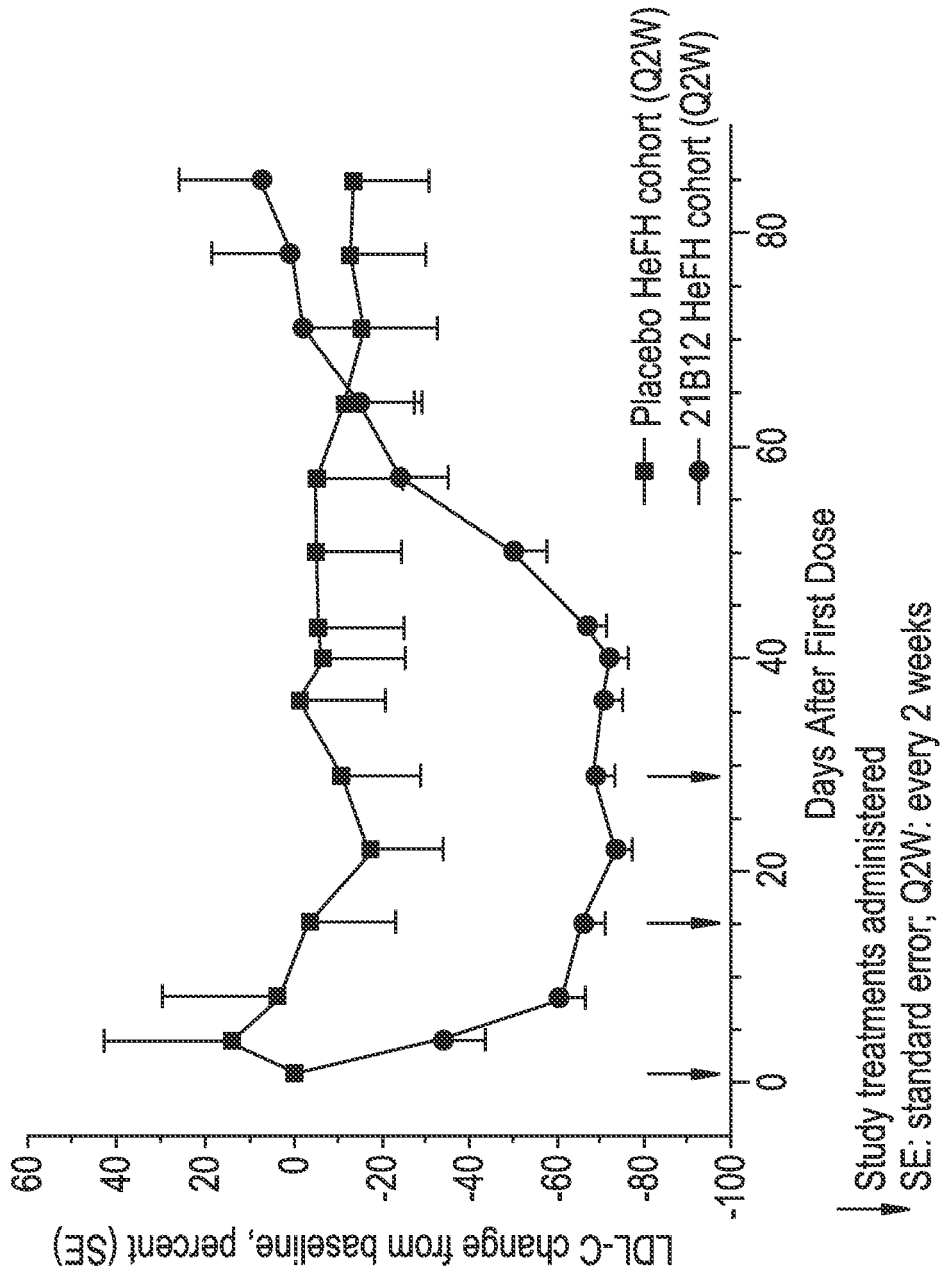

LDL-C change from baseline, percent (SE)
60
40
20
0
-20
-40
-60
-80
-100
0
20
40
60
80
Days After First Dose
Placebo HeFH cohort (Q2W)
21B12 HeFH cohort (Q2W)
Study treatments administered
SE: standard error; Q2W: every 2 weeks

FIG. 19

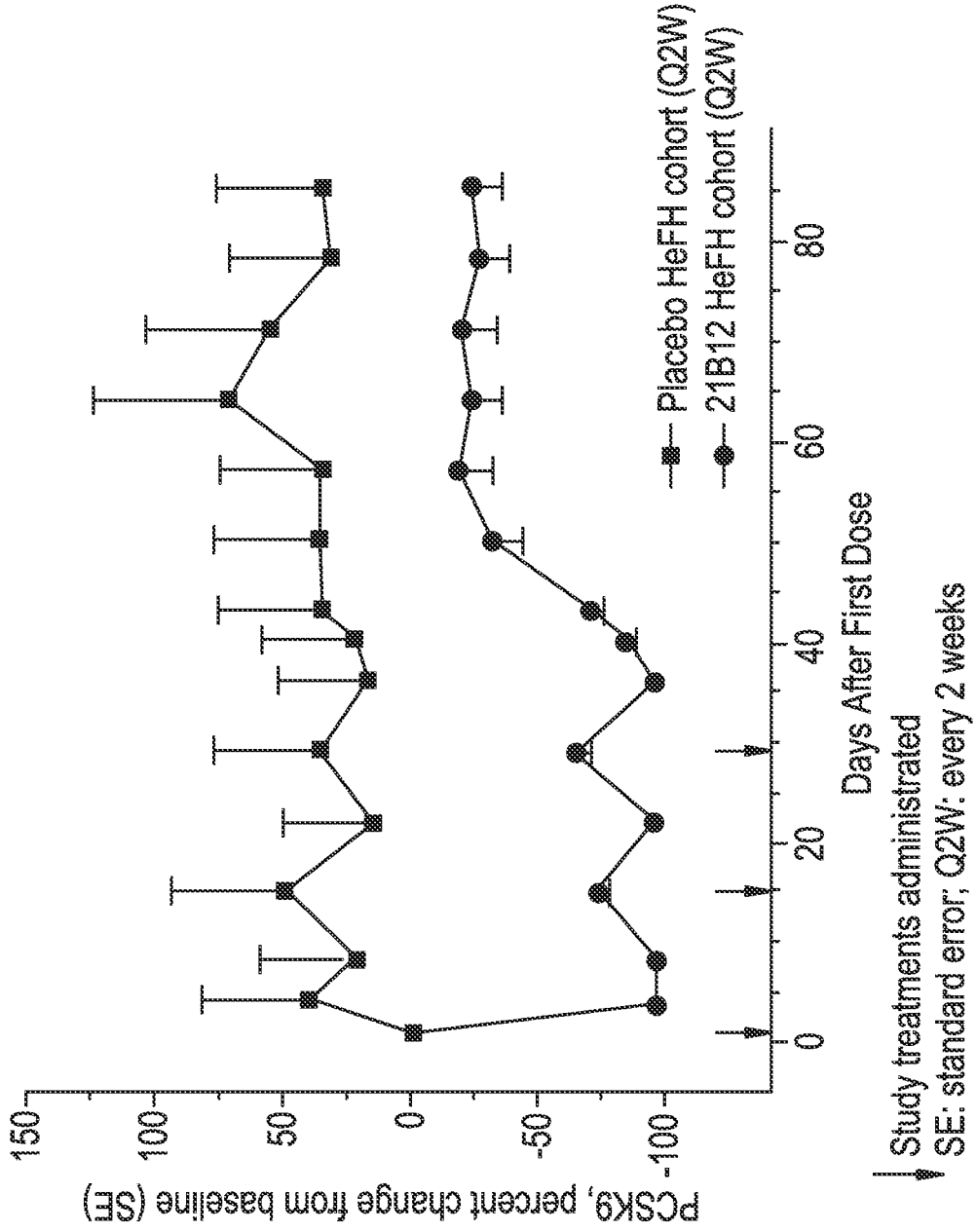

PCSK9, percent change from baseline (SE)
150
100
50
0
-50
-100
0
20
40
60
80
Days After First Dose
Placebo HeFH cohort (Q2W)
21B12 HeFH cohort (Q2W)
Study treatments administrated
SE: standard error; Q2W: every 2 weeks

FIG. 20

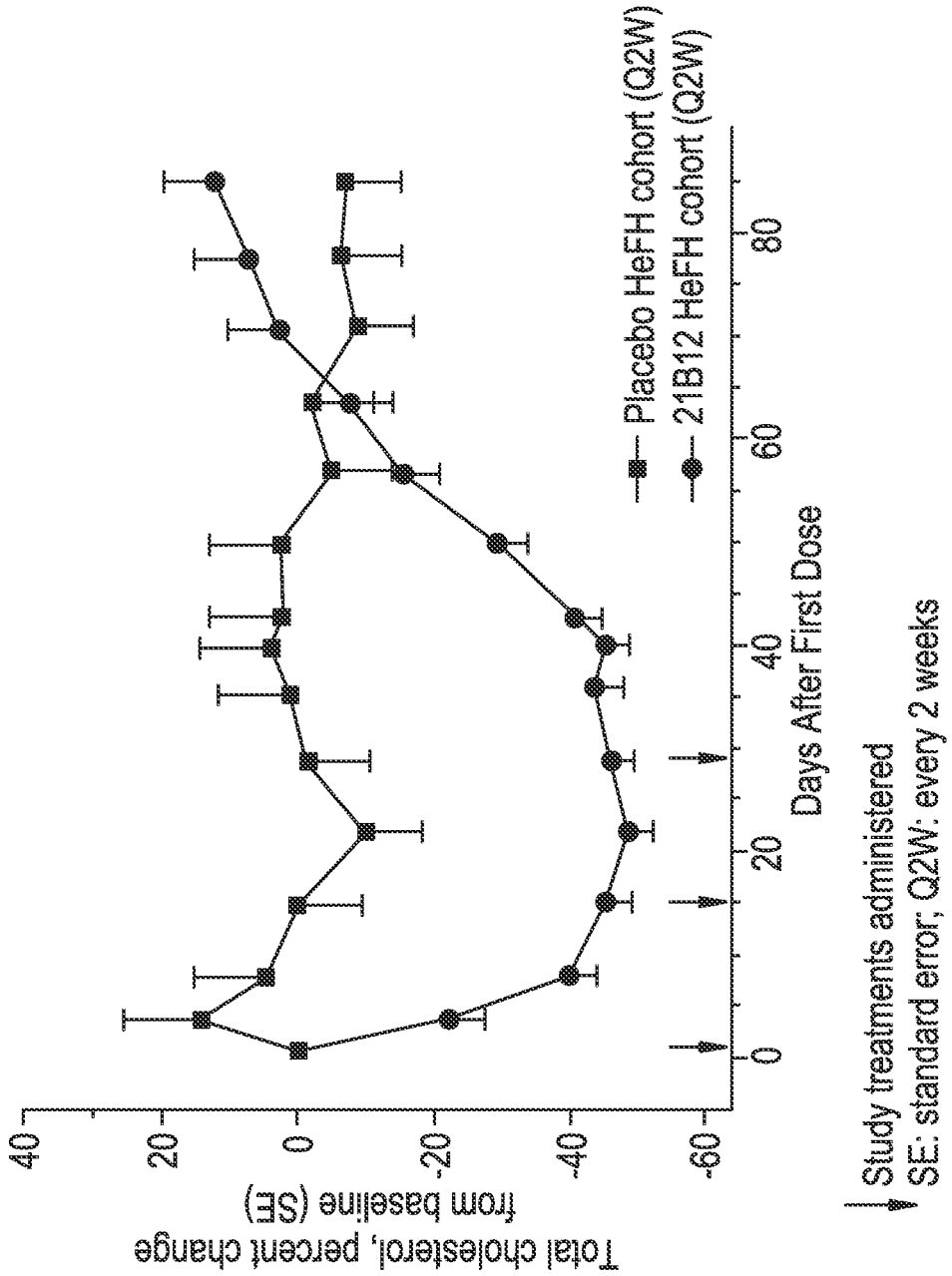

Total cholesterol, percent change from baseline (SE)
40
20
0
-20
-40
-60
0
20
40
60
80
Days After First Dose
Placebo HeFH cohort (Q2W)
21B12 HeFH cohort (Q2W)
Study treatments administered
SE: standard error; Q2W: every 2 weeks

FIG. 21

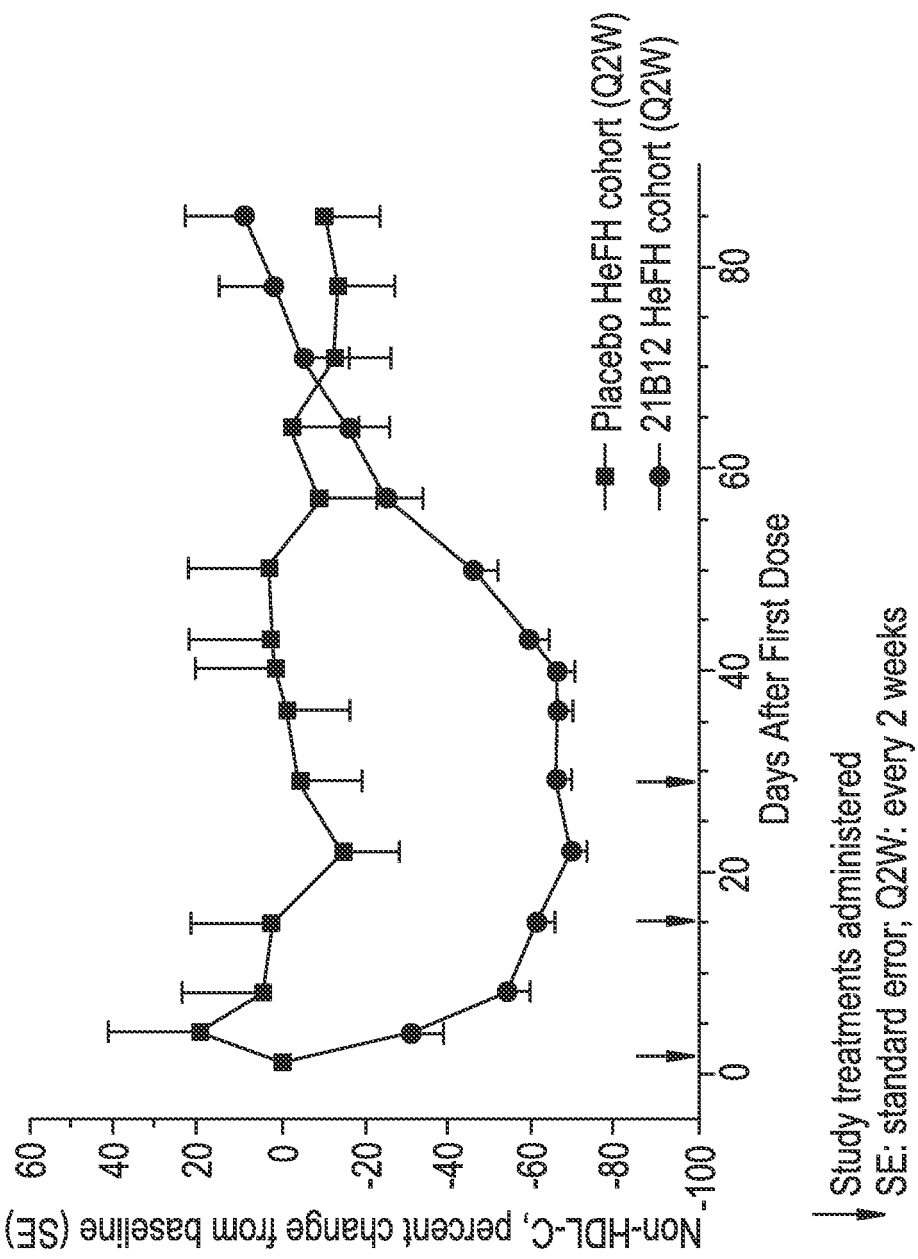

Non-HDL-C, percent change from baseline (SE)
60
40
20
0
-20
-40
-60
-80
-100
0
20
40
60
80
Days After First Dose
Placebo HeFH cohort (Q2W)
21B12 HeFH cohort (Q2W)
Study treatments administered
SE: standard error; Q2W: every 2 weeks

FIG. 22

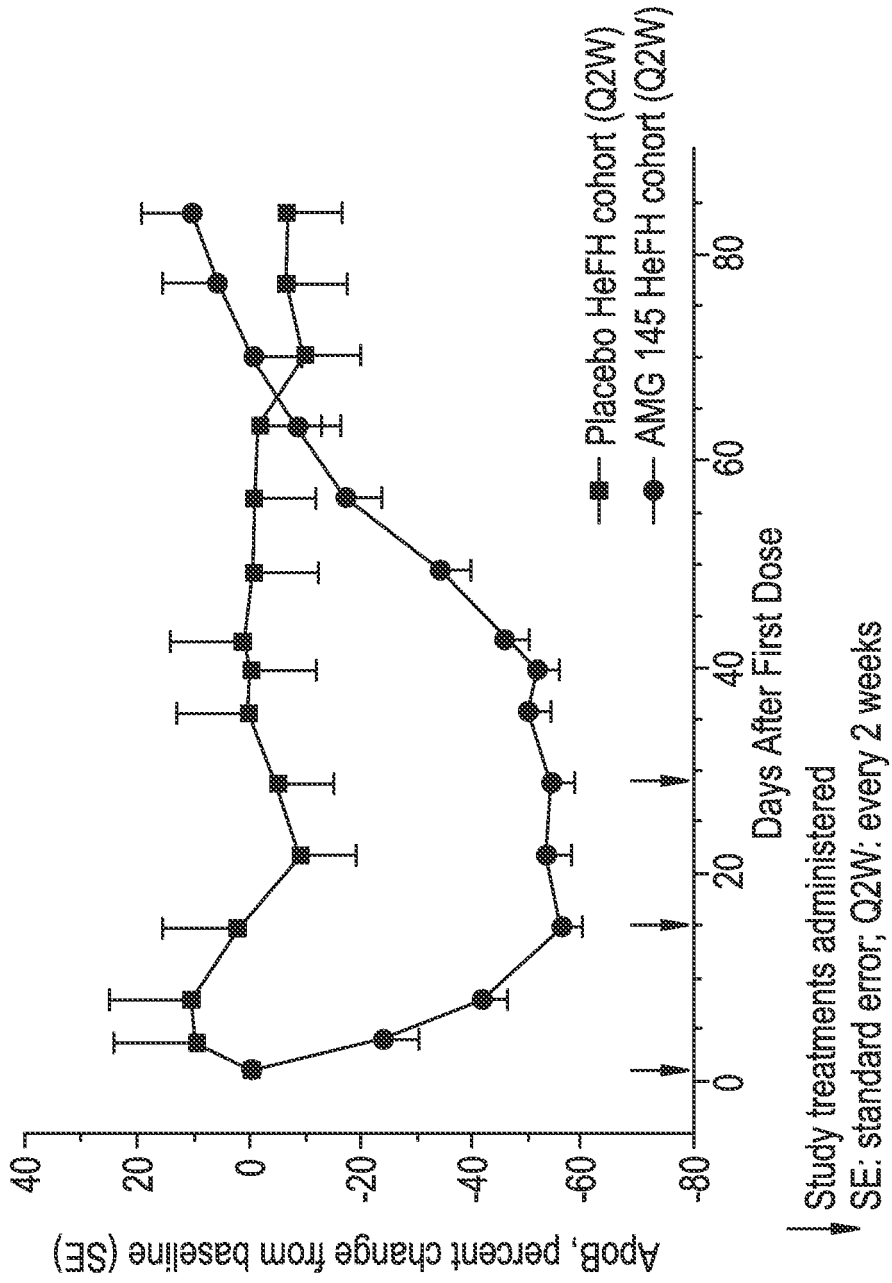

ApoB, percent change from baseline (SE)
40
20
0
-20
-40
-60
-80
0
20
40
60
80
Days After First Dose
Placebo HeFH cohort (Q2W)
AMG 145 HeFH cohort (Q2W)
Study treatments administered
SE: standard error; Q2W: every 2 weeks

FIG. 23

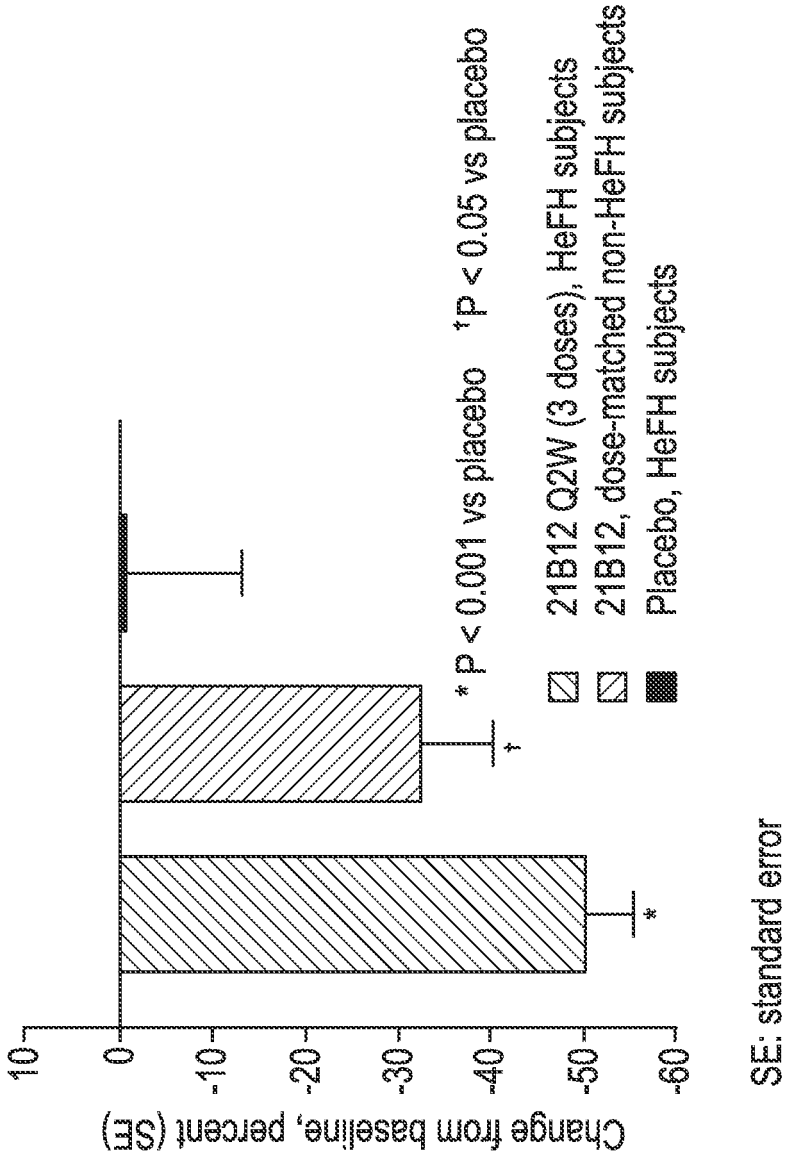

Change from baseline, percent (SE)
10
0
-10
-20
-30
-40
-50
-60
* P < 0.001 vs placebo
† P < 0.05 vs placebo
21B12 Q2W (3 doses), HeFH subjects
21B12, dose-matched non-HeFH subjects
Placebo, HeFH subjects
SE: standard error

FIG. 24B

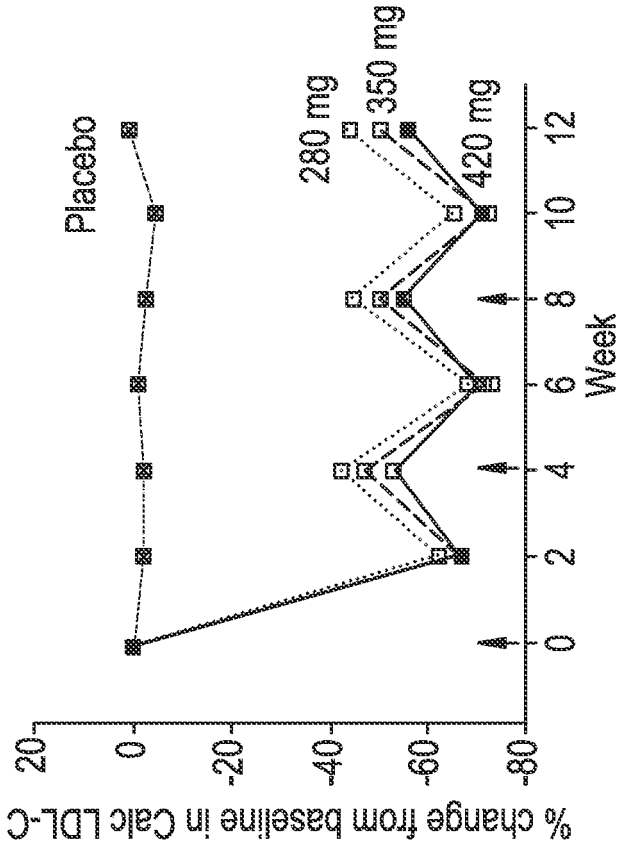


FIG. 24A

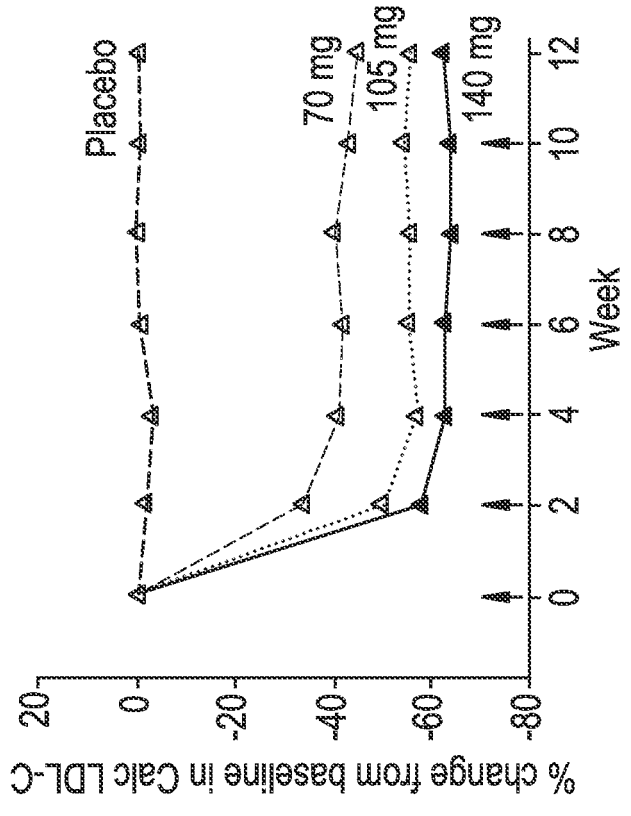


FIG. 25B

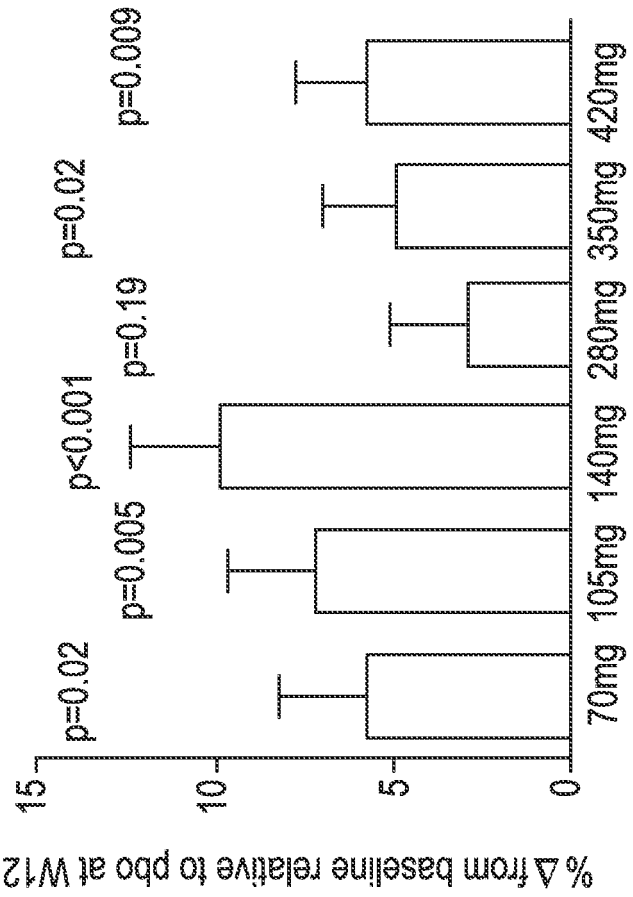


FIG. 25A

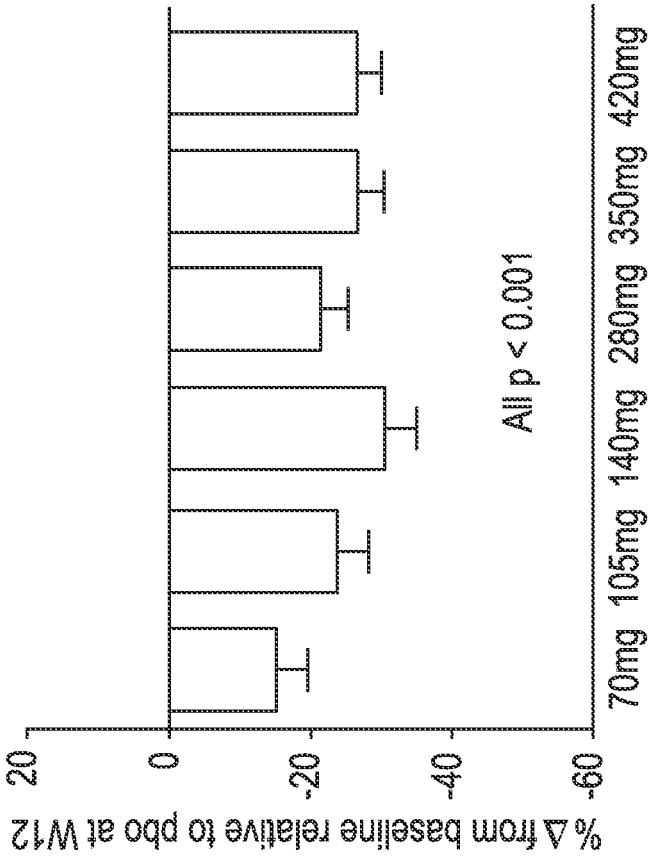


FIG. 25D

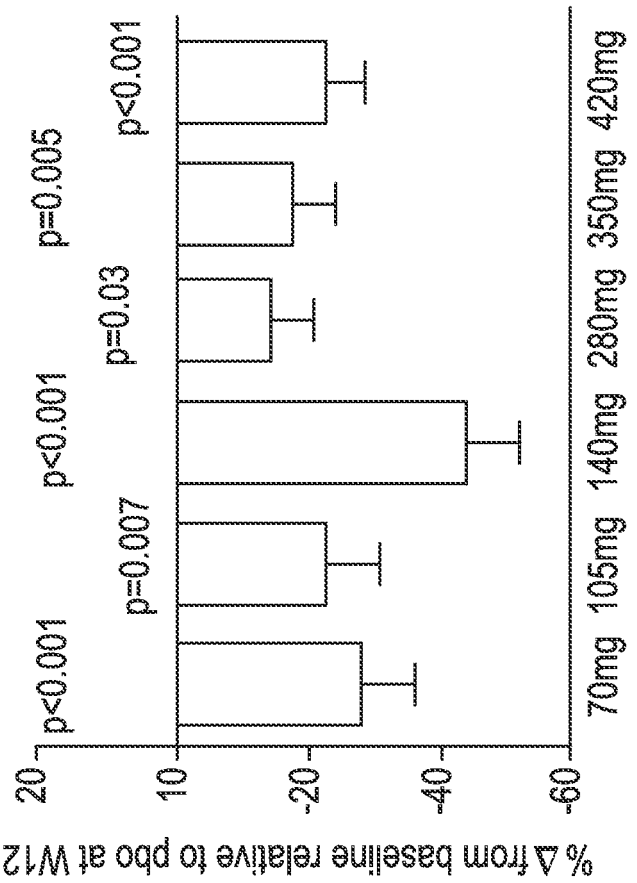


FIG. 25C

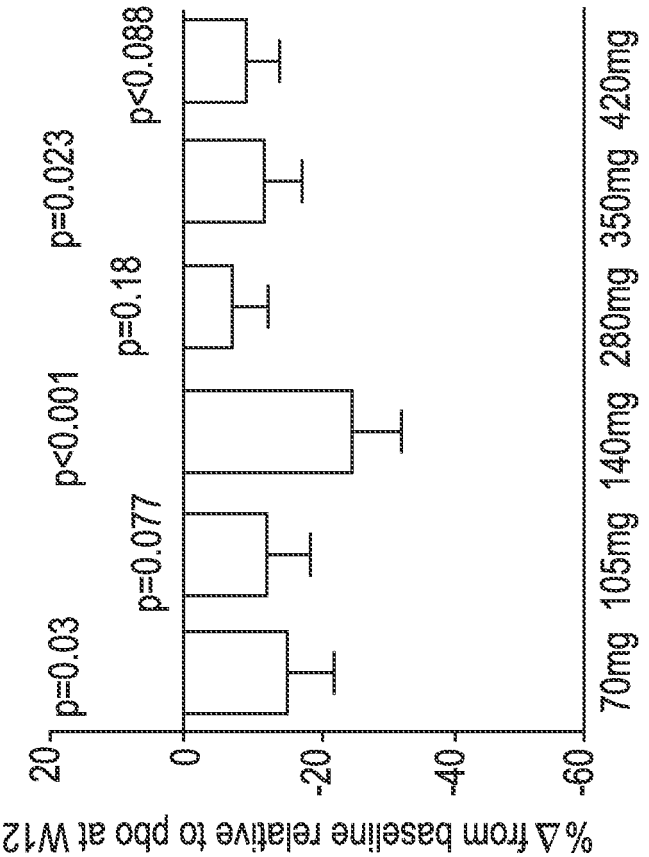


FIG. 26

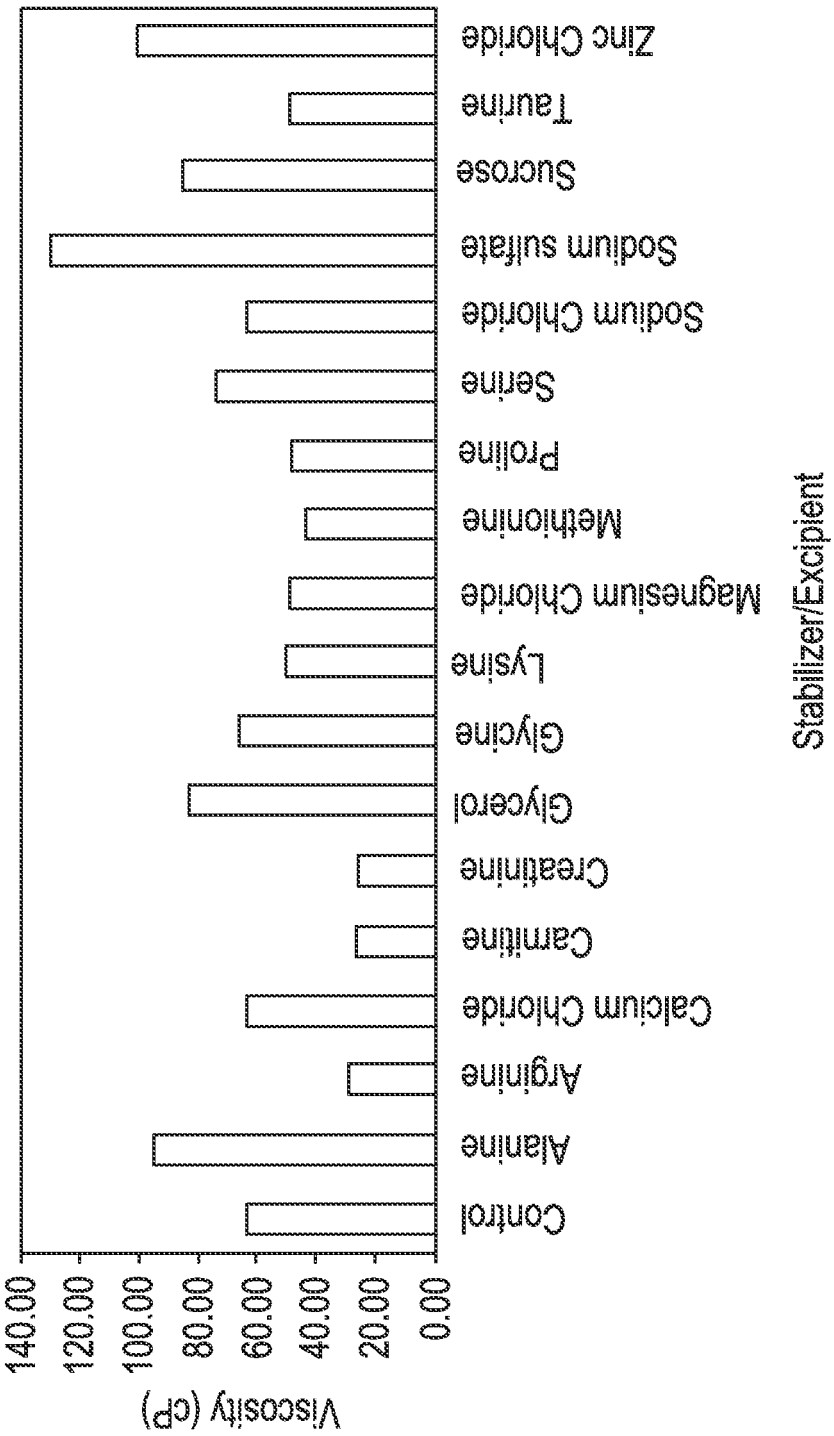

Viscosity (cP)
140.00
120.00
100.00
80.00
60.00
40.00
20.00
0.00
Stabilizer/Excipient
Control
Alanine
Arginine
Calcium Chloride
Carnitine
Creatinine
Glycerol
Glycine
Lysine
Magnesium Chloride
Methionine
Proline
Serine
Sodium Chloride
Sodium sulfate
Sucrose
Taurine
Zinc Chloride

FIG. 27

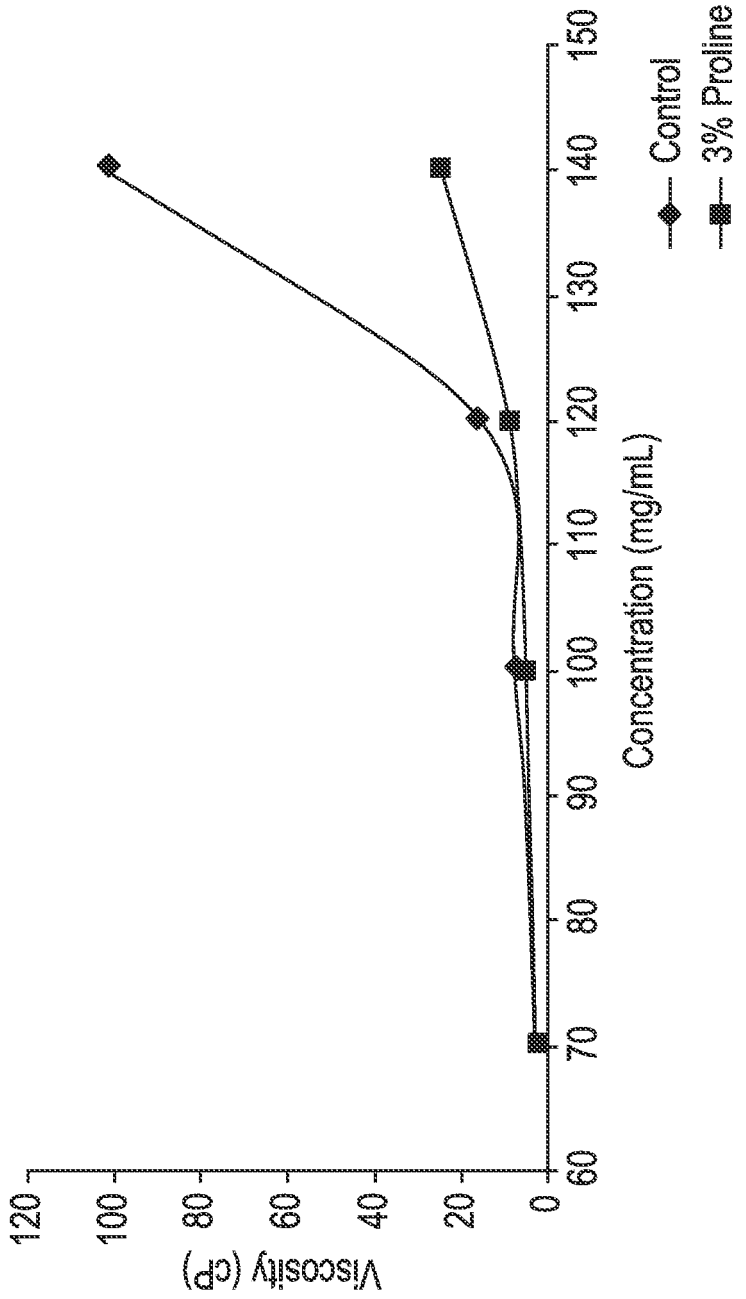

Viscosity (cP)
120
100
80
60
40
20
0
60
70
80
90
100
110
120
130
140
150
Concentration (mg/mL)
Control
3% Proline

FIG. 28A

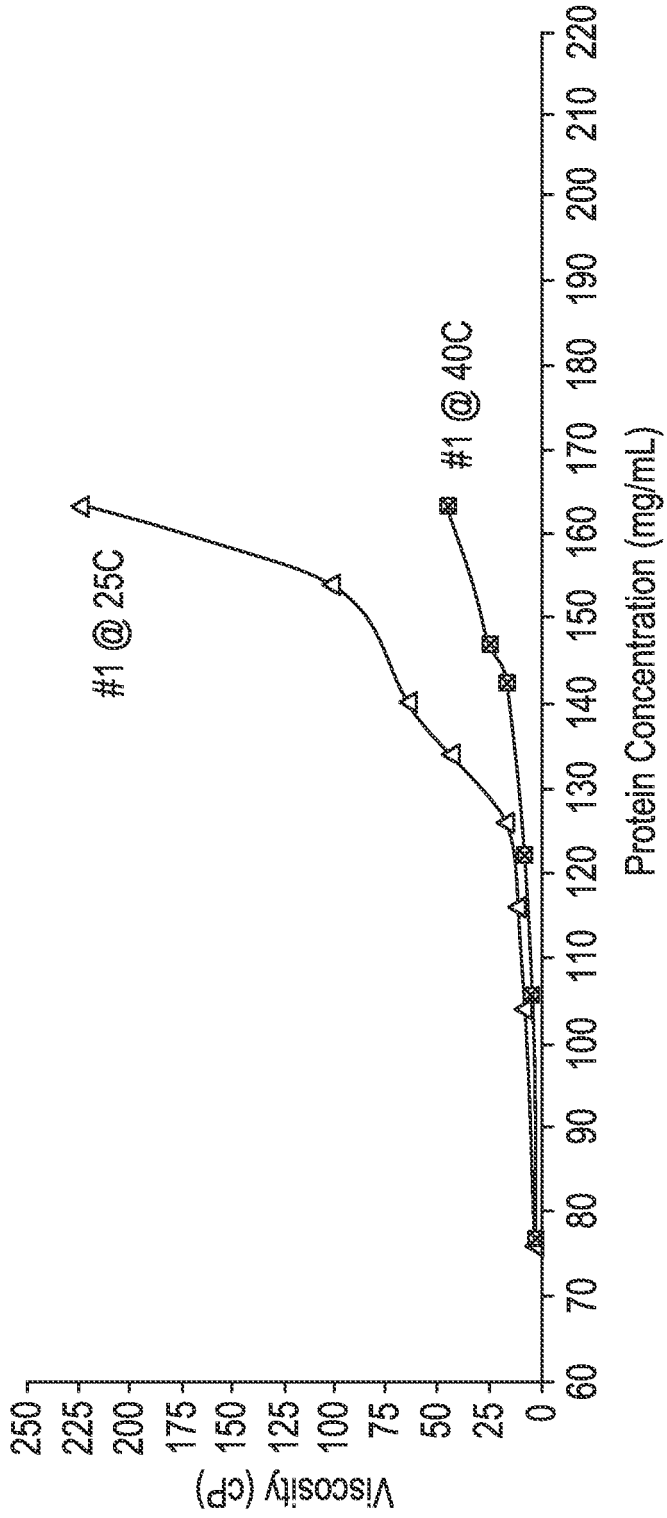

#1 @ 25C
#1 @ 40C
Viscosity (cP)
Protein Concentration (mg/mL)
0
25
50
75
100
125
150
175
200
225
250
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220

FIG. 28B

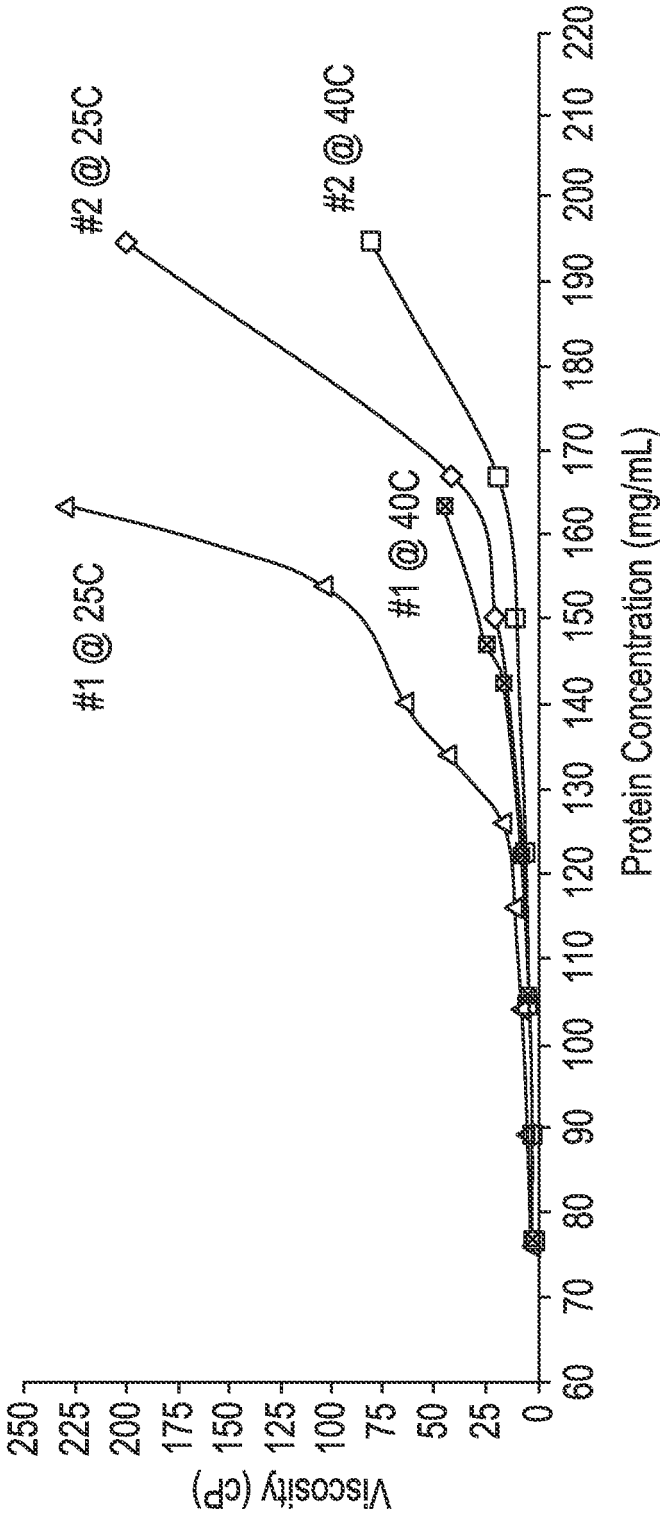

#2 @ 25C
#2 @ 40C
#1 @ 25C
#1 @ 40C
Viscosity (cP)
Protein Concentration (mg/mL)
250
225
200
175
150
125
100
75
50
25
0
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220

FIG. 28C

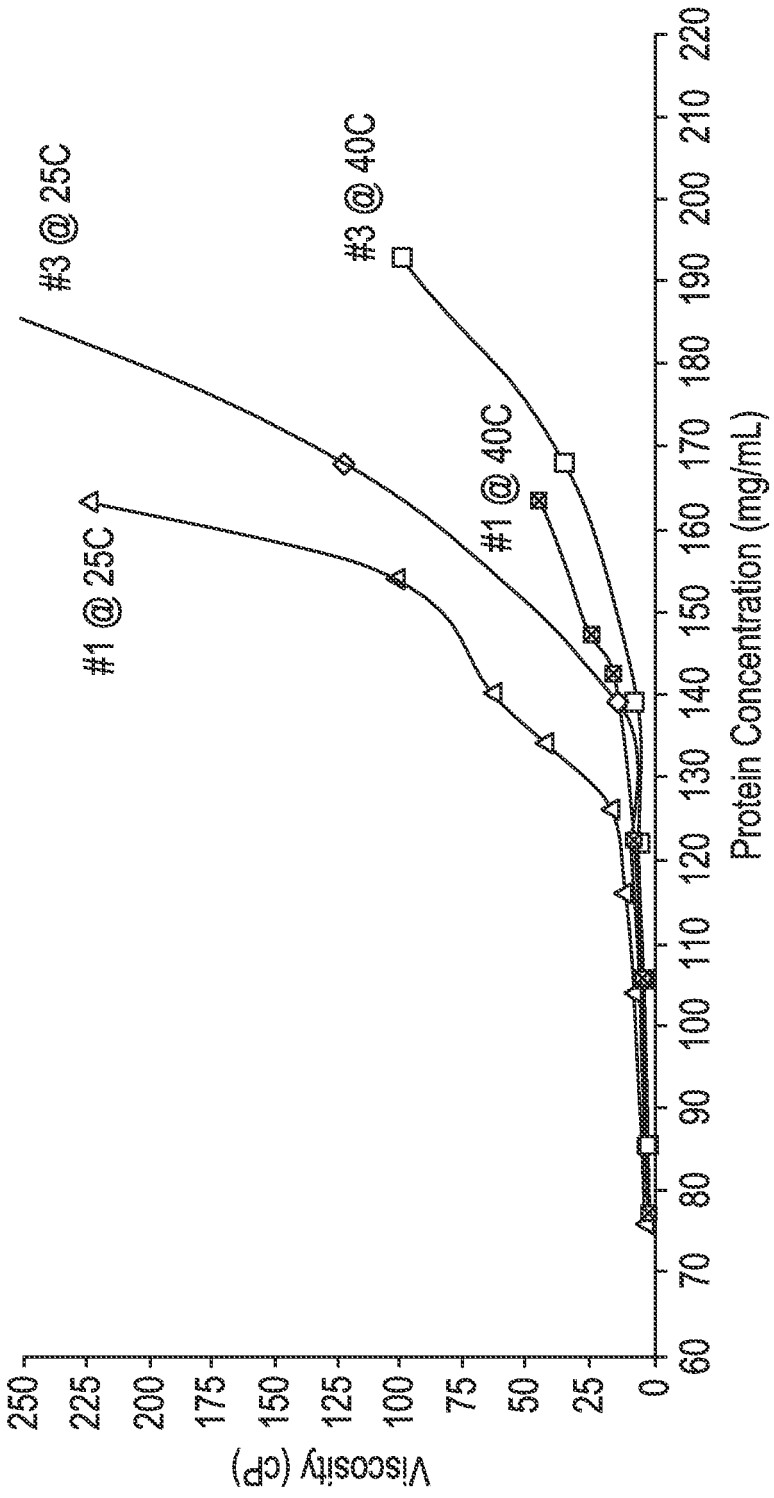

#3 @ 25C
#3 @ 40C
#1 @ 40C
#1 @ 25C
Viscosity (cP)
Protein Concentration (mg/mL)
0
25
50
75
100
125
150
175
200
225
250
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220

FIG. 28D

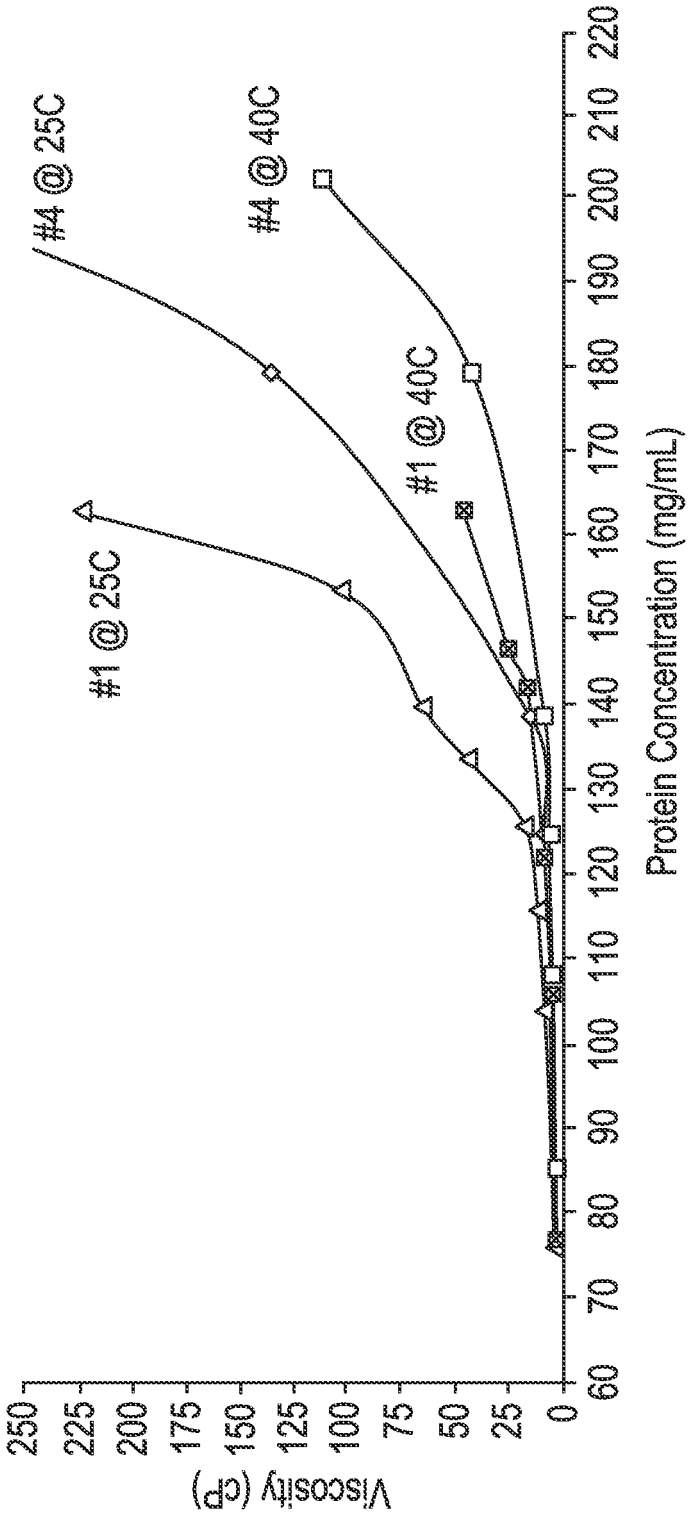
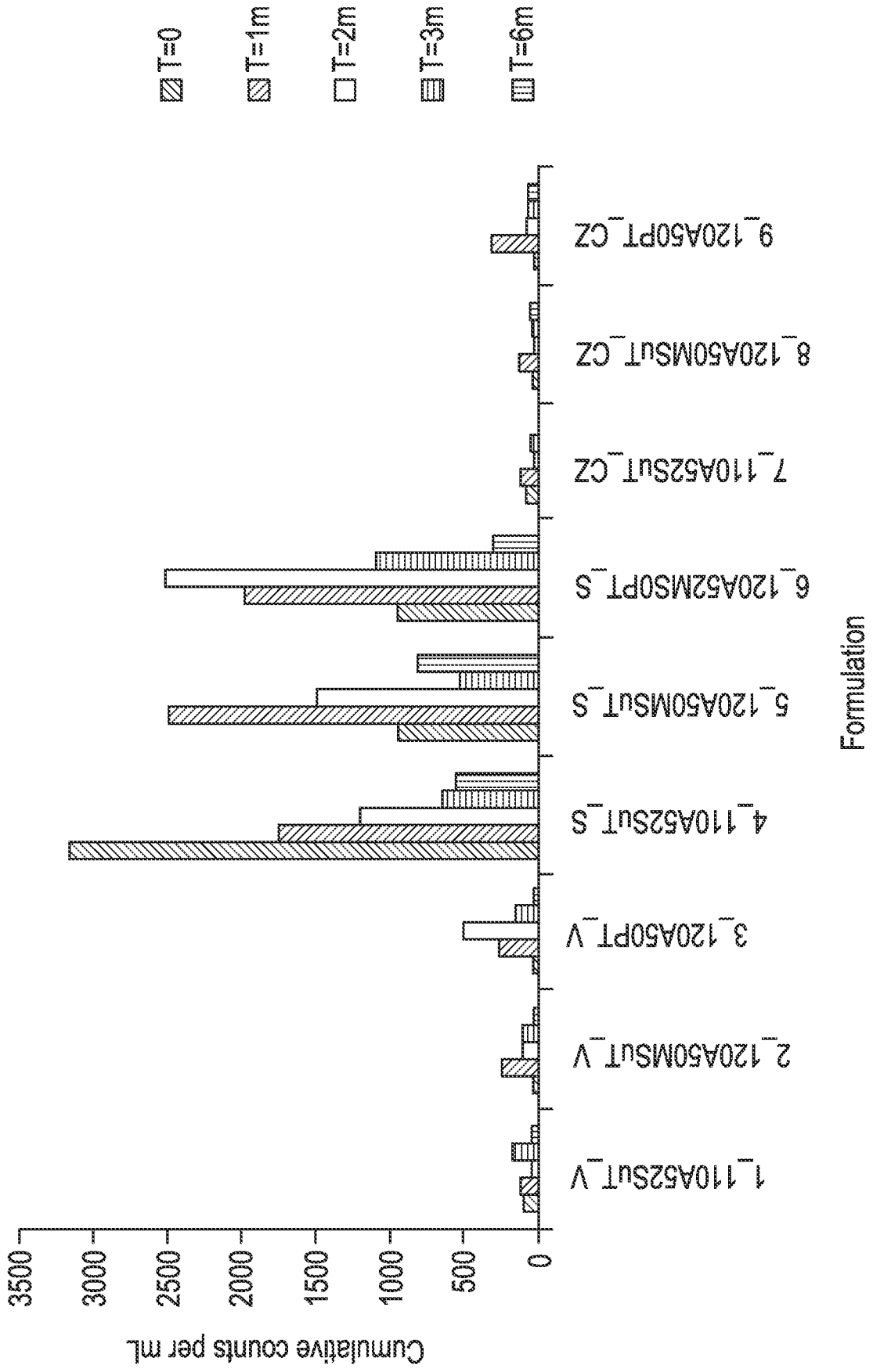

#4 @ 25C
#4 @ 40C
#1 @ 40C
#1 @ 25C
Viscosity (cP)
250
225
200
175
150
125
100
75
50
25
0
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
Protein Concentration (mg/mL)

FIG. 29A


T=0
T=1m
T=2m
T=3m
T=6m
Cumulative counts per mL
3500
3000
2500
2000
1500
1000
500
0
1_110A52SuT_V
2_120A50MSuT_V
3_120A50PT_V
4_110A52SuT_S
5_120A50MSuT_S
6_120A52MS0PT_S
7_110A52SuT_CZ
8_120A50MSuT_CZ
9_120A50PT_CZ
Formulation

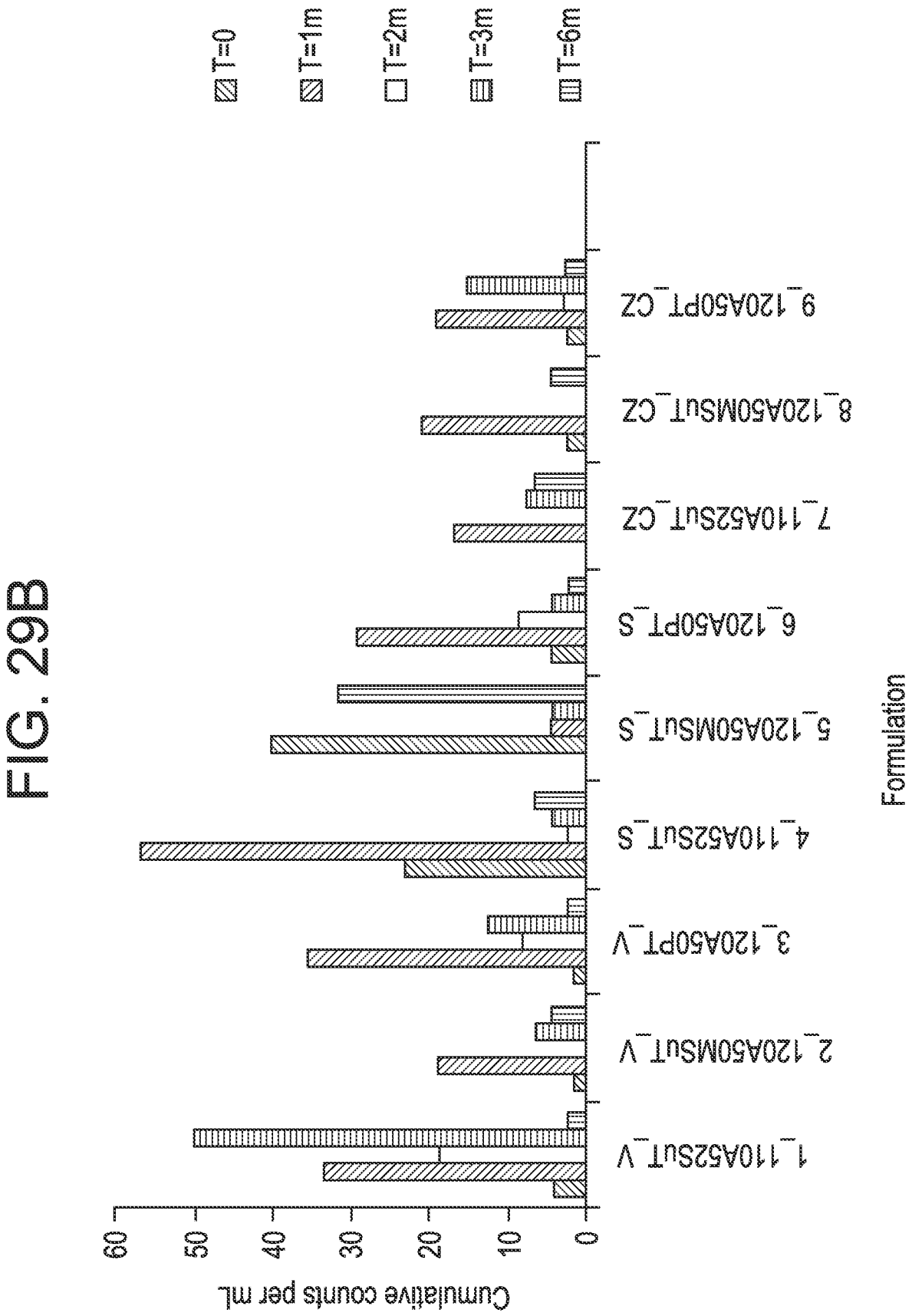

T=0
T=1m
T=2m
T=3m
T=6m
Cumulative counts per mL
0
10
20
30
40
50
60
1_110A52SuT_V
2_120A50MSuT_V
3_120A50PT_V
4_110A52SuT_S
5_120A50MSuT_S
6_120A50PT_S
7_110A52SuT_CZ
8_120A50MSuT_CZ
9_120A50PT_CZ
Formulation

FIG. 29B

FIG. 30A

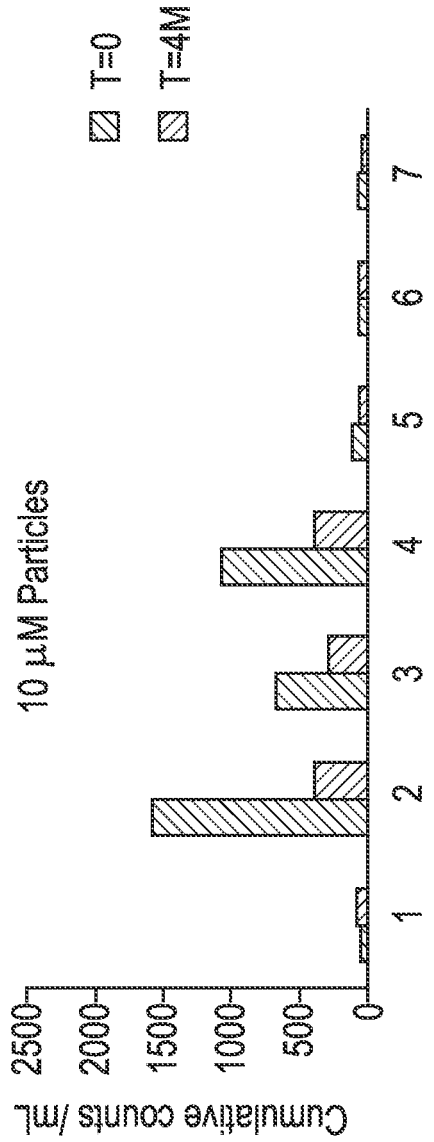

T=0
T=4M
10 µM Particles
Cumulative counts /mL
2500
2000
1500
1000
500
0
1
2
3
4
5
6
7

FIG. 30B

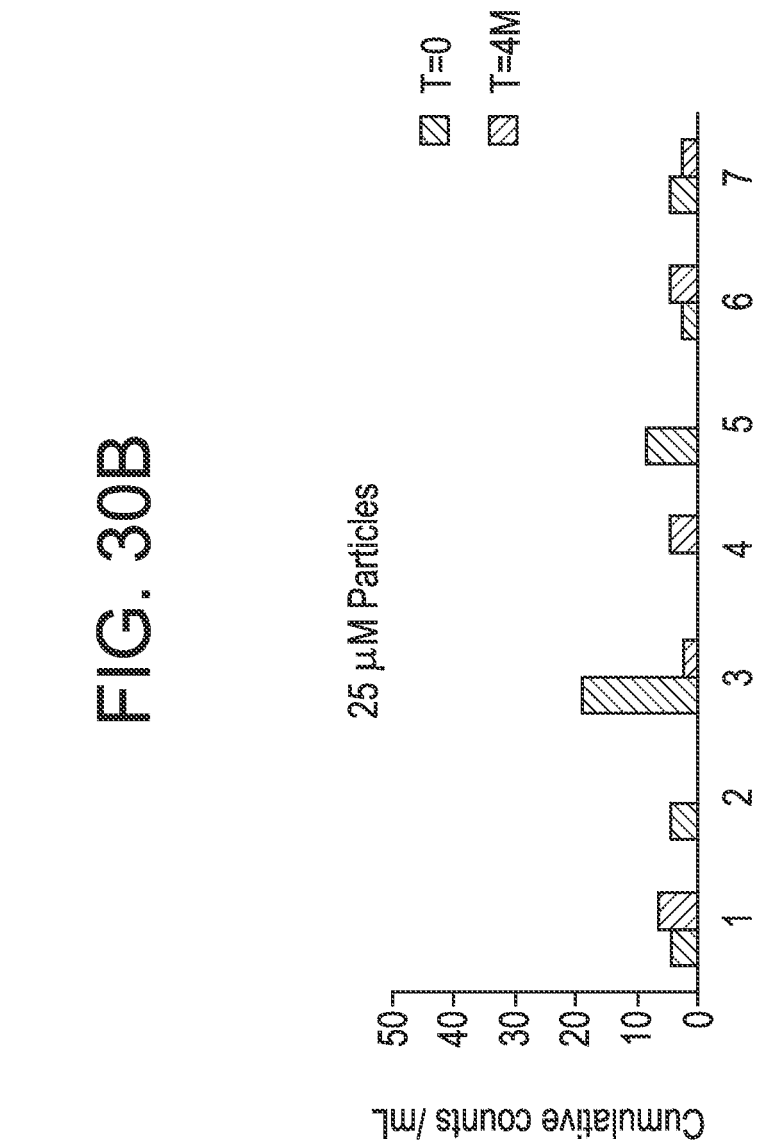

T=0
T=4M
25 µM Particles
Cumulative counts /mL
0
10
20
30
40
50
1
2
3
4
5
6
7

FIG. 31

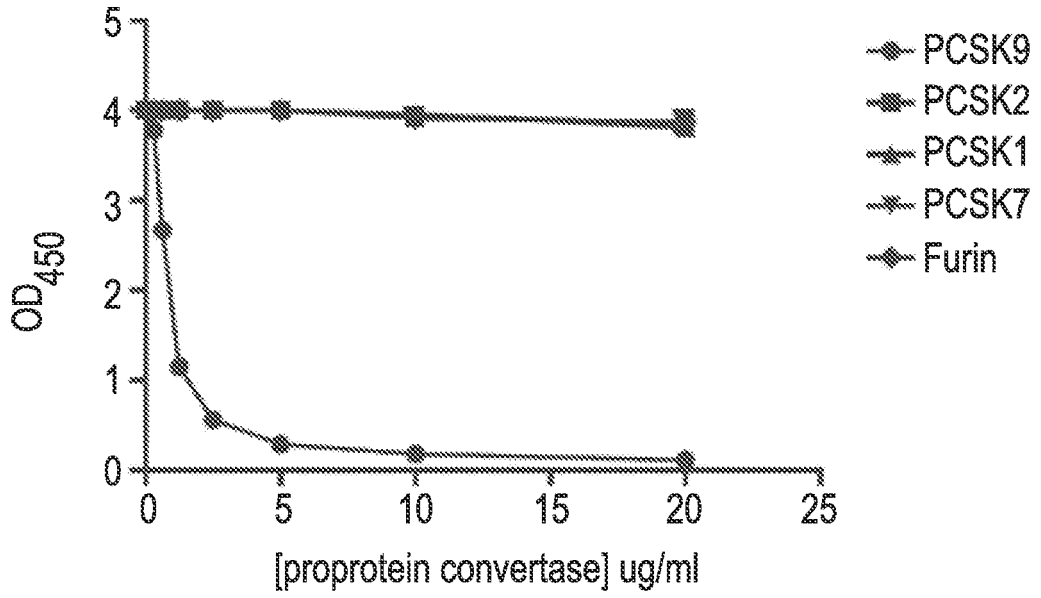

5
4
3
2
1
0
OD_{450}
0
5
10
15
20
25
[proprotein convertase] ug/ml
PCSK9
PCSK2
PCSK1
PCSK7
Furin

FIG. 32

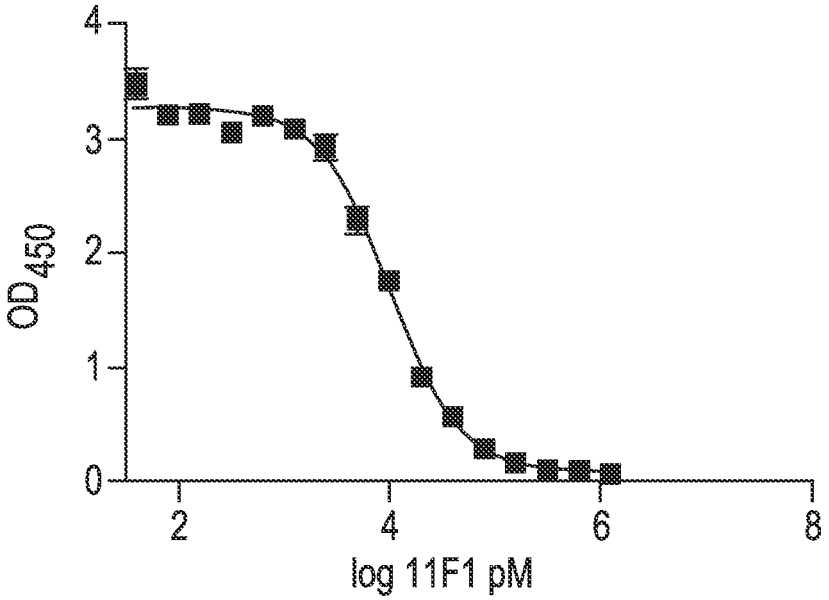


FIG. 33

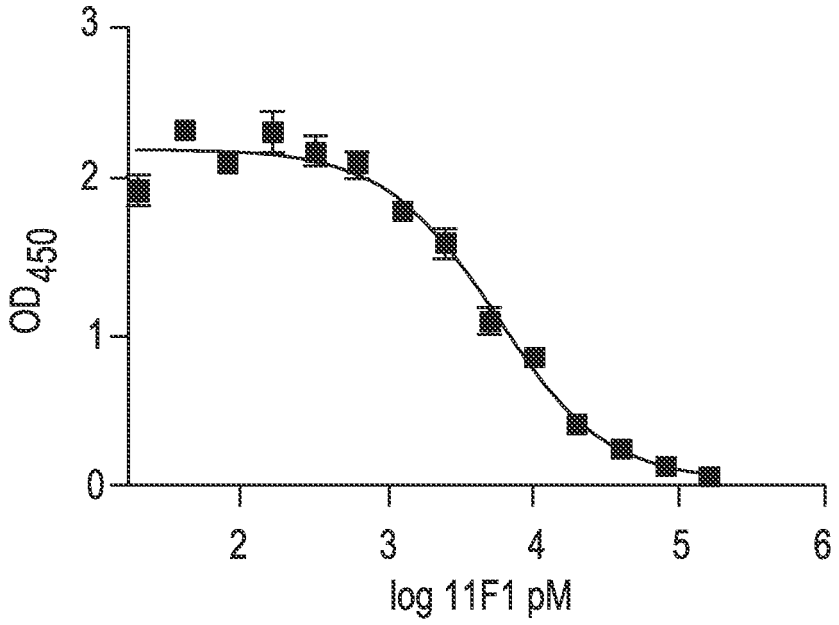


FIG. 34

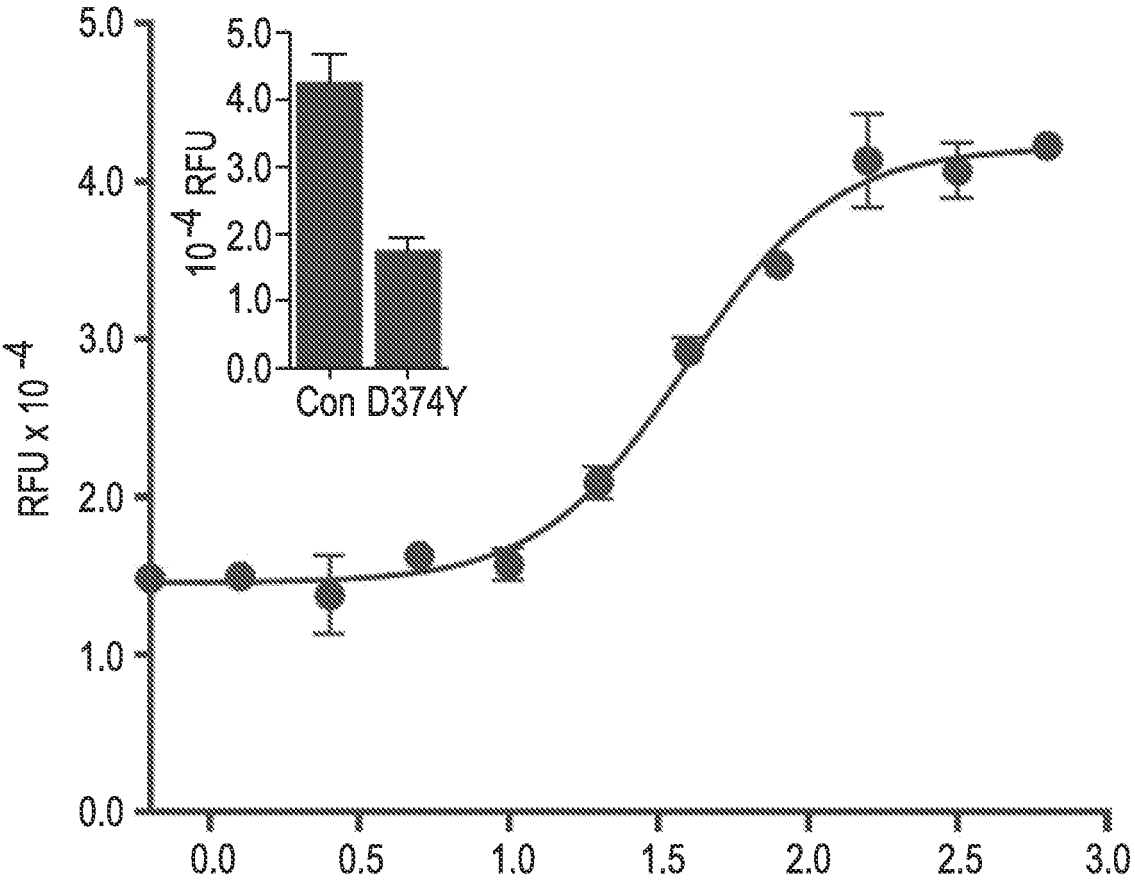

RFU x 10 -4
5.0
4.0
3.0
2.0
1.0
0.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
10-4 RFU
5.0
4.0
3.0
2.0
1.0
0.0
Con
D374Y

FIG. 35

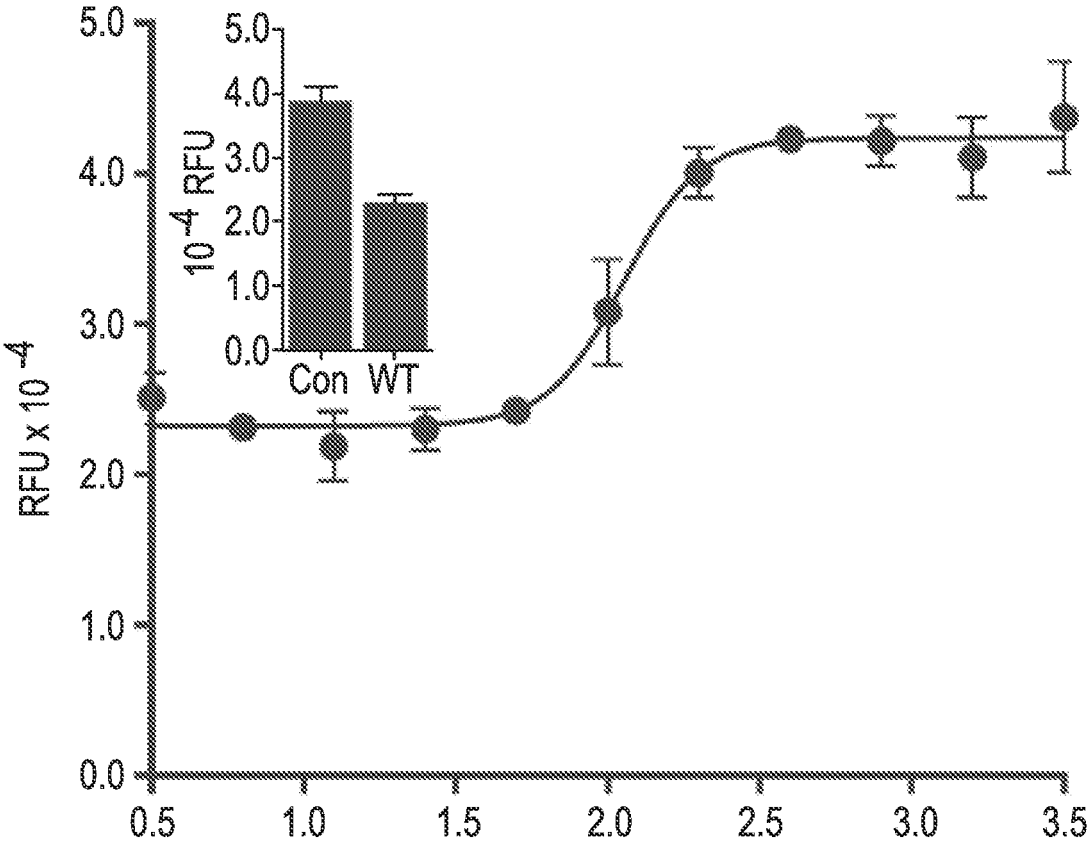

RFU x 10 -4
5.0
4.0
3.0
2.0
1.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
10-4 RFU
5.0
4.0
3.0
2.0
1.0
0.0
Con
WT

FIG. 36

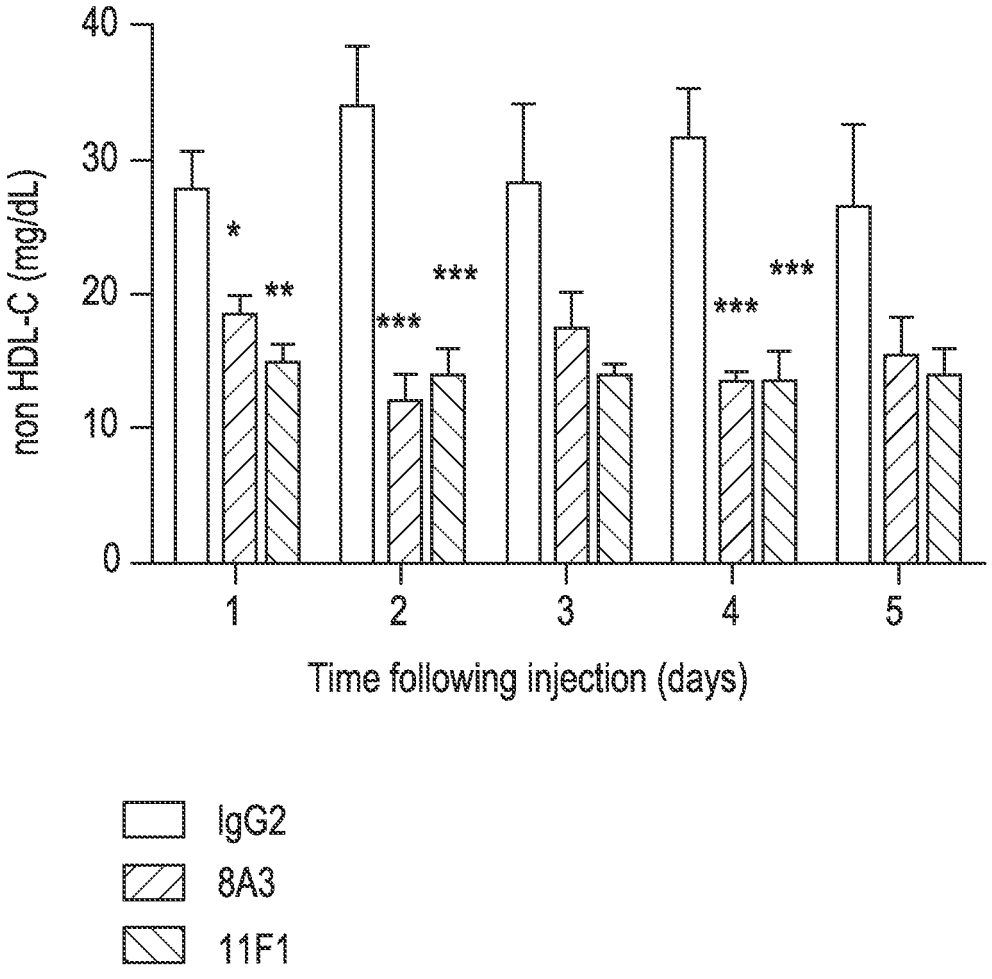

40
30
20
10
0
non HDL-C (mg/dL)
*
**
***
***
***
***
1
2
3
4
5
Time following injection (days)
IgG2
8A3
11F1

FIG. 37

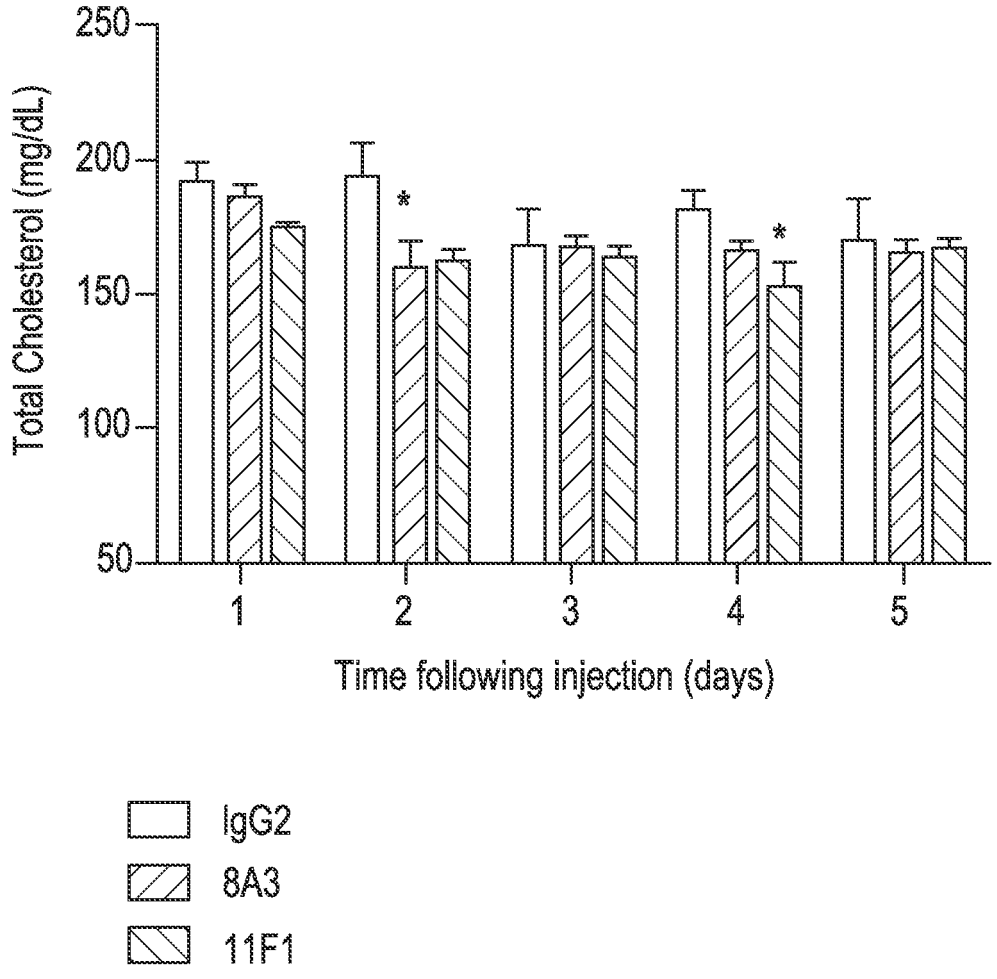

250
200
150
100
50
Total Cholesterol (mg/dL)
*
*
1
2
3
4
5
Time following injection (days)
IgG2
8A3
11F1

FIG. 38

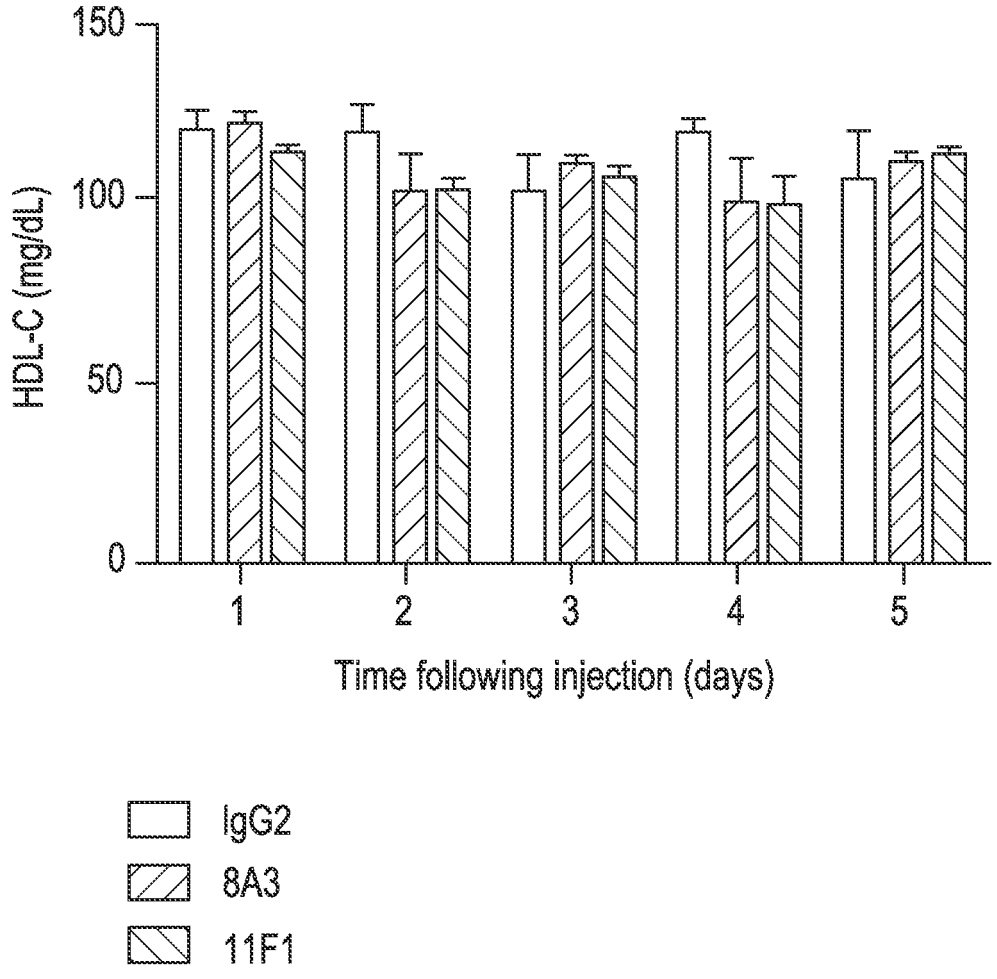

150
100
50
0
HDL-C (mg/dL)
1
2
3
4
5
Time following injection (days)
IgG2
8A3
11F1

FIG. 39

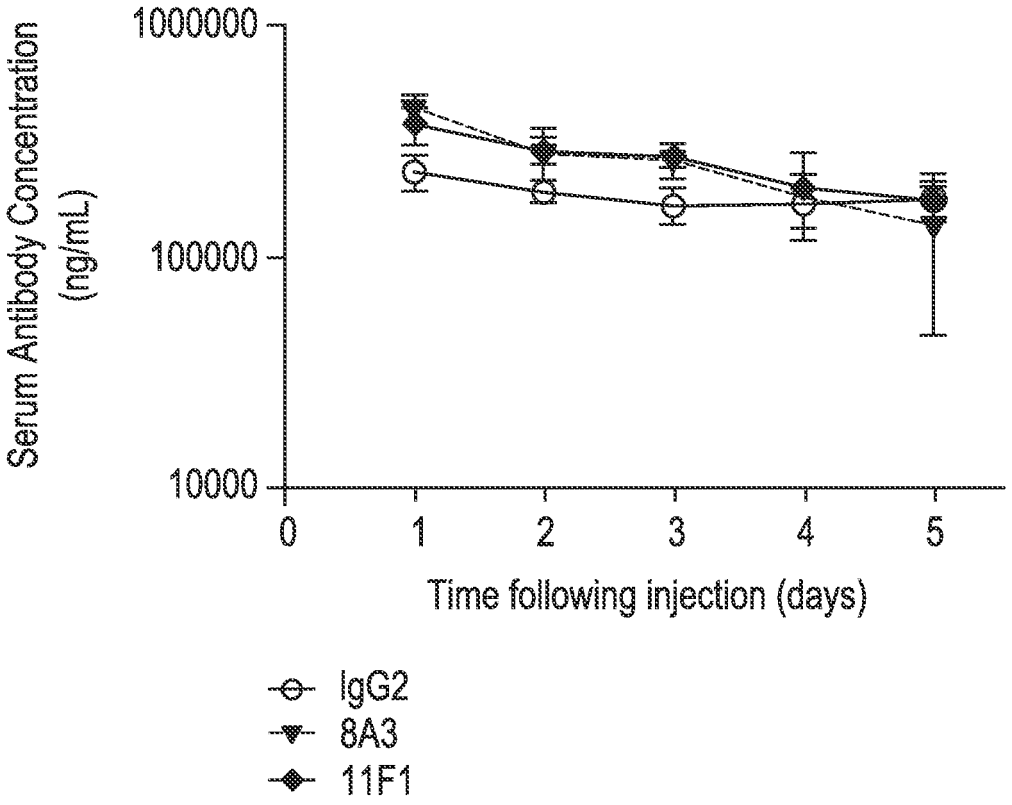

Serum Antibody Concentration (ng/mL)
1000000
100000
10000
0
1
2
3
4
5
Time following injection (days)
IgG2
8A3
11F1

FIG. 40

Antibody	AUC_{0-t} (μg·h/mL)	CL_{0-t} (mL/h/kg)	Apparent $t_{1/2}$ (h)
IgG2	23,500	0.511	>120
11F1	34,700	0.865	83
8A3	36,700	0.817	59

FIG. 41

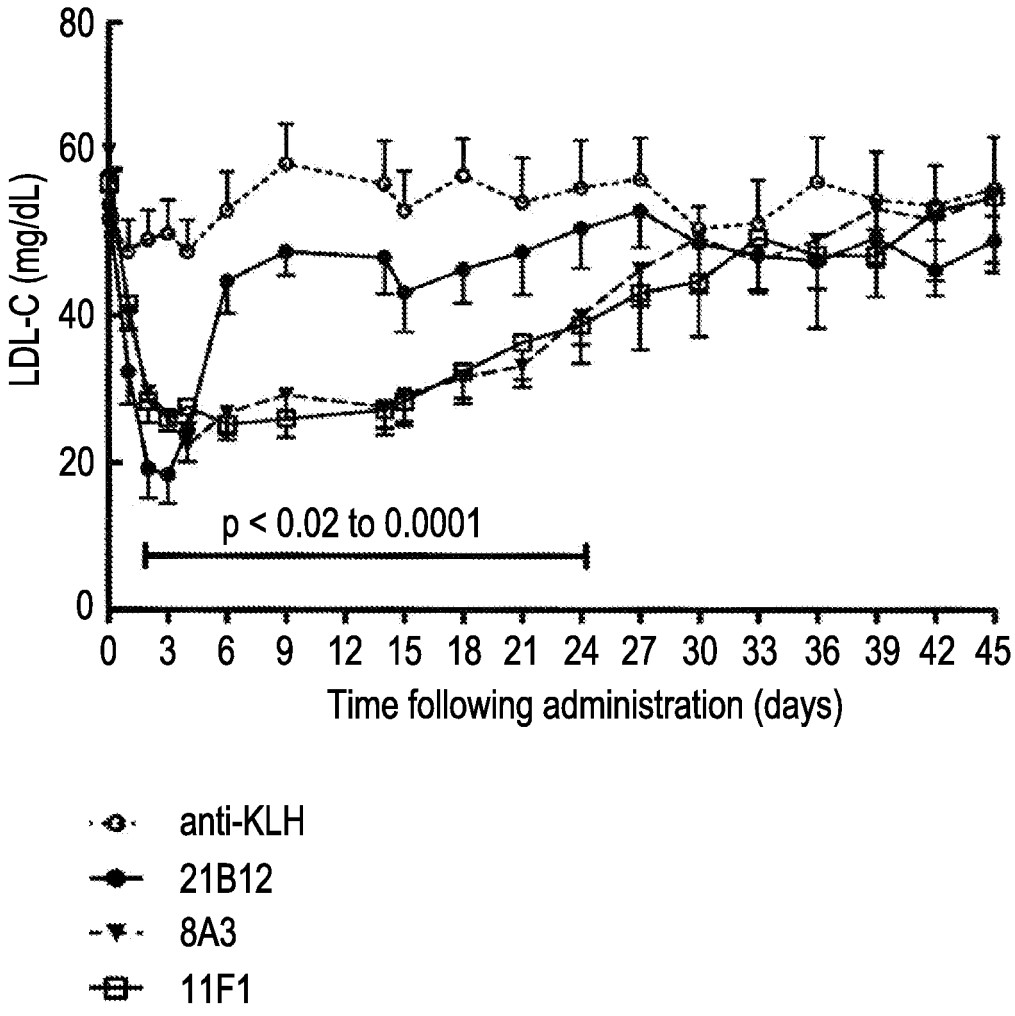

80
60
40
20
0
LDL-C (mg/dL)
p < 0.02 to 0.0001
0 3 6 9 12 15 18 21 24 27 30 33 36 39 42 45
Time following administration (days)
anti-KLH
21B12
8A3
11F1

FIG. 42

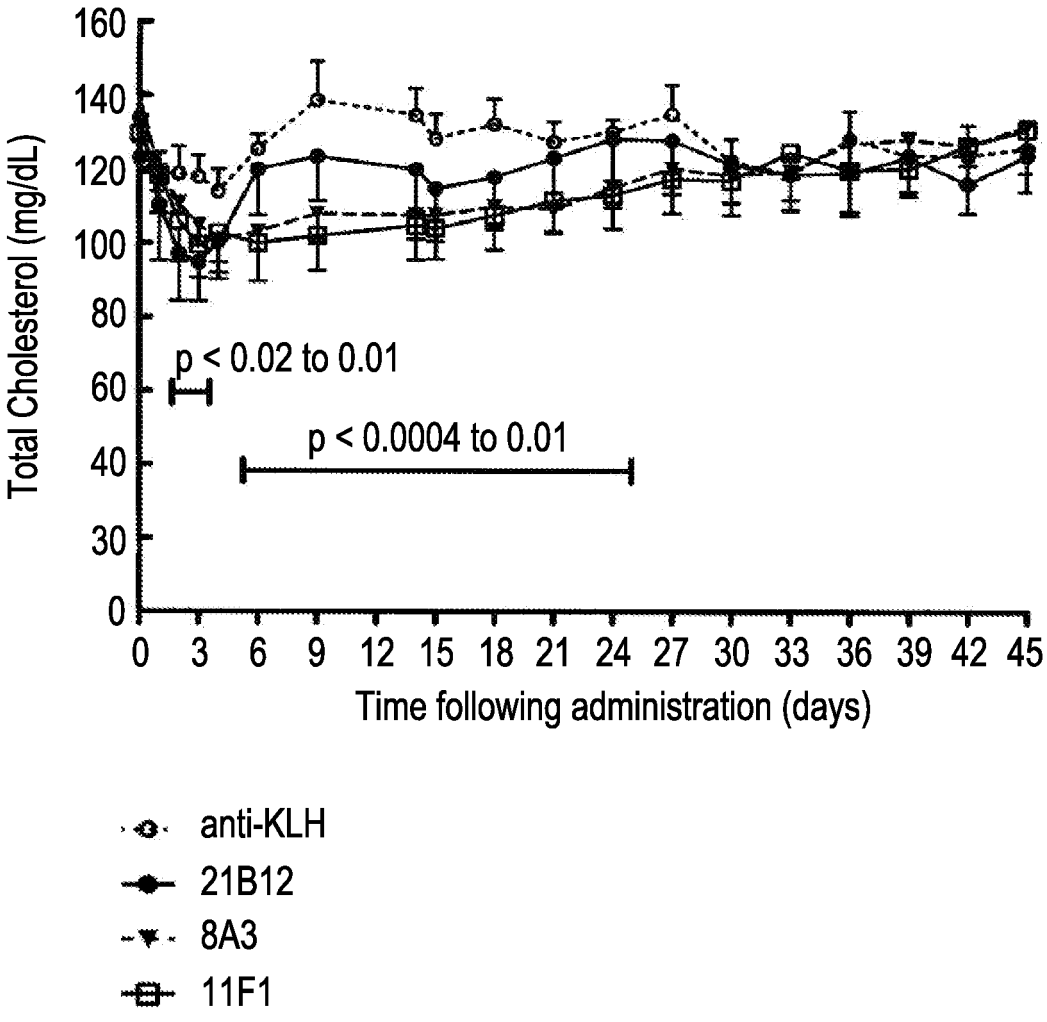

Total Cholesterol (mg/dL)
160
140
120
100
80
60
40
30
0
p < 0.02 to 0.01
p < 0.0004 to 0.01
0 3 6 9 12 15 18 21 24 27 30 33 36 39 42 45
Time following administration (days)
anti-KLH
21B12
8A3
11F1

FIG. 43

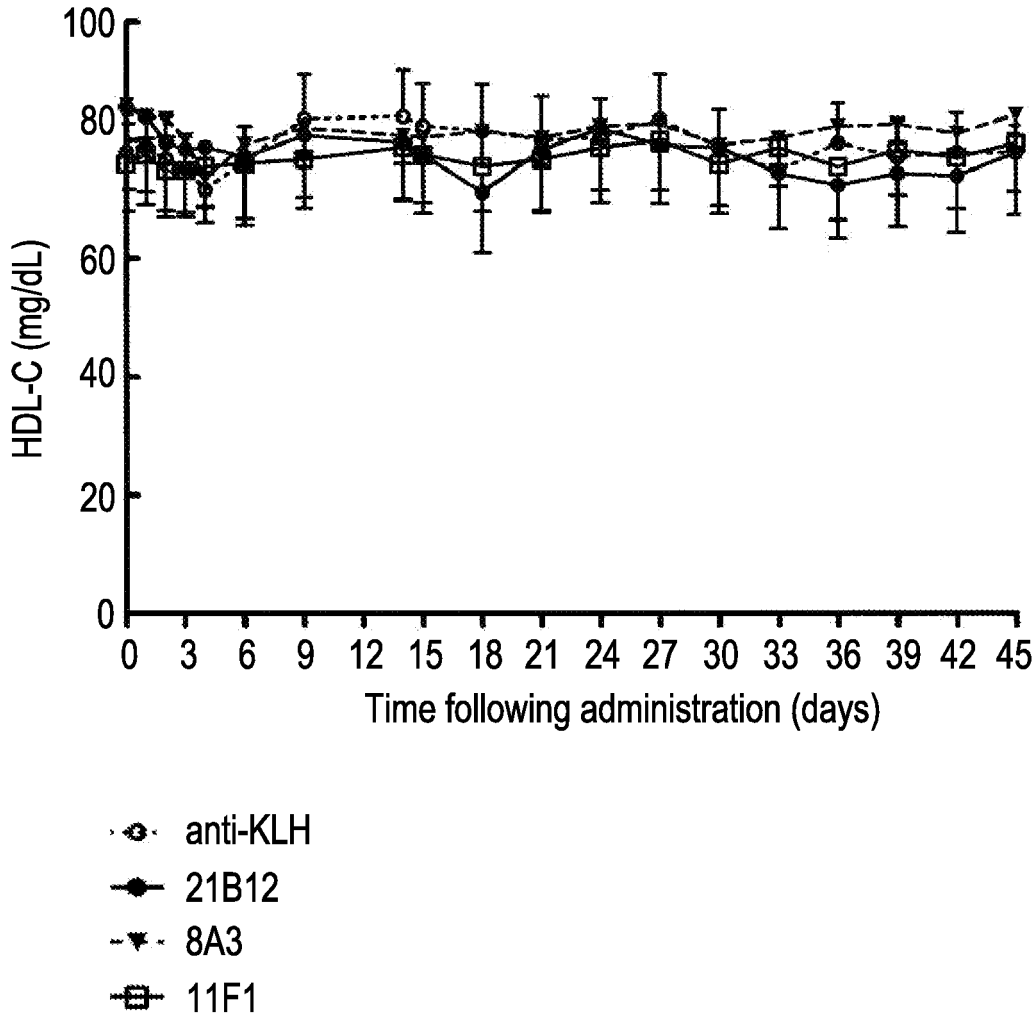

100
80
60
40
20
0
HDL-C (mg/dL)
0 3 6 9 12 15 18 21 24 27 30 33 36 39 42 45
Time following administration (days)
anti-KLH
21B12
8A3
11F1

FIG. 44

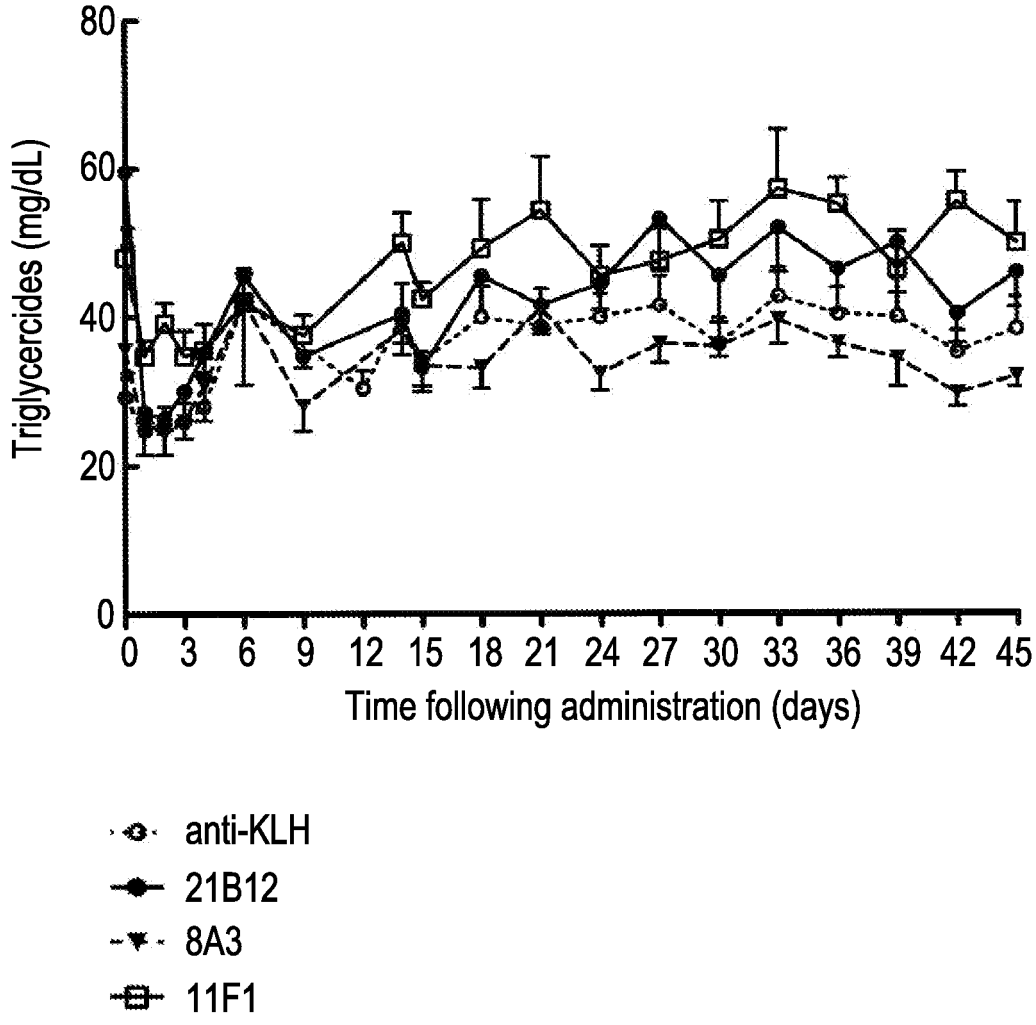

80
60
40
20
0
Triglycercides (mg/dL)
0 3 6 9 12 15 18 21 24 27 30 33 36 39 42 45
Time following administration (days)
anti-KLH
21B12
8A3
11F1

FIG. 45

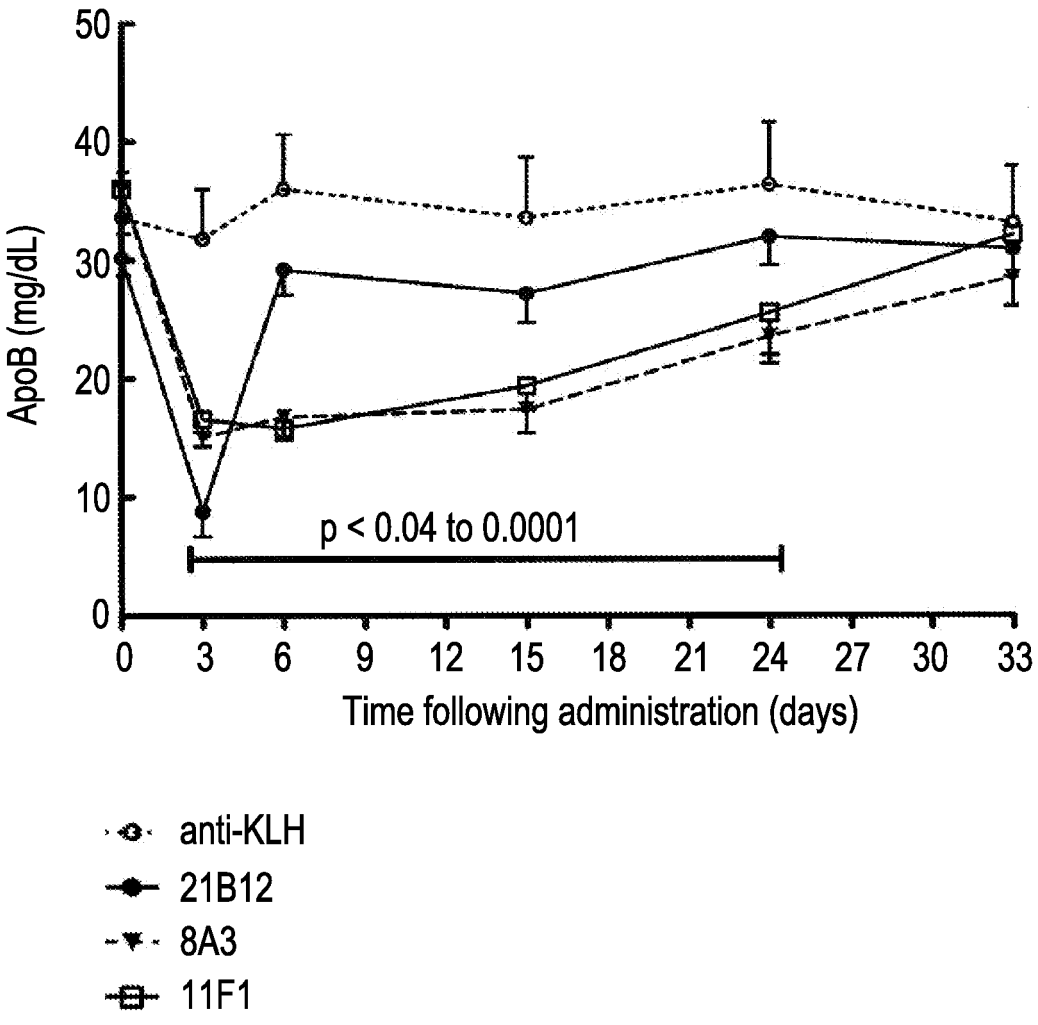

ApoB (mg/dL)
50
40
30
20
10
0
p < 0.04 to 0.0001
0
3
6
9
12
15
18
21
24
27
30
33
Time following administration (days)
anti-KLH
21B12
8A3
11F1

FIG. 46

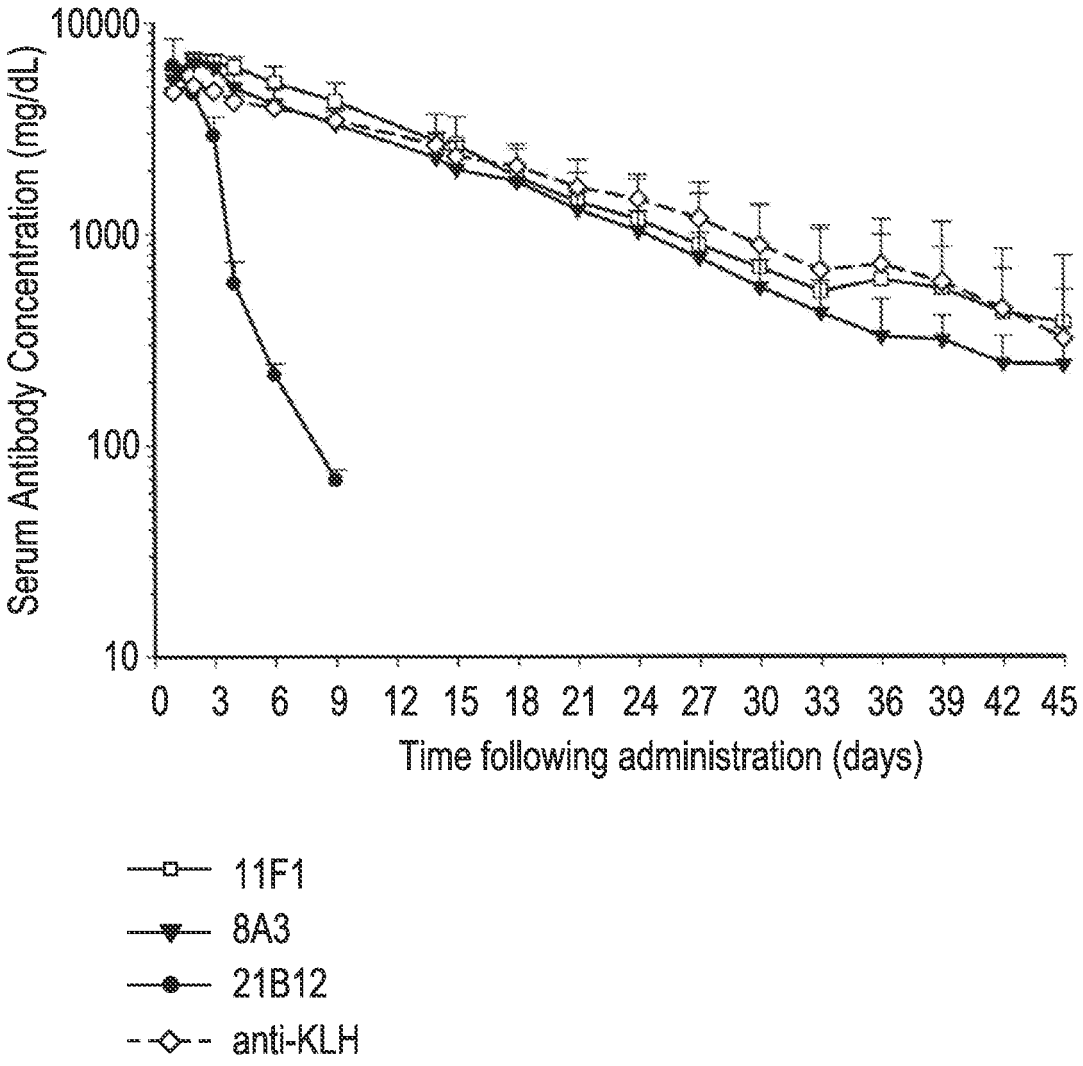

10000
1000
100
10
Serum Antibody Concentration (mg/dL)
0 3 6 9 12 15 18 21 24 27 30 33 36 39 42 45
Time following administration (days)
11F1
8A3
21B12
anti-KLH

FIG. 47

Mean (± SD) Pharmacokinetic Parameters				
Antibody	$t_{1/2,z}$ (h)	CL/F (mL/h/kg)	Cmax (μg/mL)	$AUC_{0 \rightarrow \infty}$ (μg*h/mL)
Anti-KLH	220 ± 130	0.234 ± 0.036	5.08 ± 0.15	2,170 ± 320
21B12	40 ± 6	1.57 ± 0.68	6.22 ± 2.21	355 ± 109
11F1	210 ± 110	0.228 ± 0.081	6.72 ± 0.62	2,440 ± 910
8A3	190 ± 40	0.255 ± 0.039	6.63 ± 0.66	1,990 ± 290

FIG. 48A

Light Chain Variable Sequence Comparison and Consensus Sequence
(HCDR1, HCDR2 and HCDR3 are underlined):

8A1: Light Chain Variable Sequence (SEQ ID NO:485); LCDR1 (SEQ ID NO:503); LCDR2 (SEQ ID NO:504); LCDR3 (SEQ ID NO:558)
8A3: Light Chain Variable Sequence (SEQ ID NO:461); LCDR1 (SEQ ID NO:503); LCDR2 (SEQ ID NO:4); LCDR3 (SEQ ID NO:558)
11F1: Light Chain Variable Sequence (SEQ ID NO:465); LCDR1 (SEQ ID NO:503)); LCDR2 (SEQ ID NO:504); LCDR3 (SEQ ID NO:505)
Consensus: Light Chain Variable Sequence (SEQ ID NO:582); LCDR1 (SEQ ID NO:503); LCDR2 (SEQ ID NO:504); LCDR3 (SEQ ID NO:584)

8A1: 1-DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
8A3: 1-DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
11F1: 1-DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
Consensus: 1-DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNNYLDWYLQKPGQSPQLLIYLGSNRA

8A1: SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK-112 (SEQ ID NO:485)
8A3: SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK-112 (SEQ ID NO:461)
11F1: SGVPDRFSGSGSGTHLTLKISRVEAEDVGVYYCMQTLQTPLTFGGGTKVEIK-112 (SEQ ID NO:465)
Consensus: SGVPDRFSGSGSGTX_1X_2TLKISRVEAEDVGVYYCMQX_3LQTPLTFGGGTKVEIK-112 (SEQ ID NO:582)

X_1 is H or D; X_2 is F or L; and X_3 is T or A

FIG. 48B

Heavy Chain Variable Chain Sequence Comparison And Consensus Sequence
(HCDR1, HCDR2 and HCDR3 are underlined):

8A1: Heavy Chain Variable Sequence (SEQ ID NO:459); HCDR1 (SEQ ID NO:513); HCDR2 (SEQ ID NO:528); HCDR3 (SEQ ID NO:534)
8A3: Heavy Chain Variable Sequence (SEQ ID NO:461); HCDR1 (SEQ ID NO:)); HCDR2 (SEQ ID NO:501); HCDR3 (SEQ ID NO:502)
11F1: Heavy Chain Variable Sequence (SEQ ID NO:463); HCDR1 (SEQ ID NO:)); HCDR2 (SEQ ID NO:501); HCDR3 (SEQ ID NO:502)
Consensus: Heavy Chain Variable Sequence (SEQ ID NO:583); HCDR1 (SEQ ID NO:585); HCDR2 (SEQ ID NO:586); HCDR3 (SEQ ID NO:587)

8A3: 1-EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVASIKQDGSEKYY
11F1: 1-EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMSWVRQAPGKGLEWVASIKQDGSEKYY
8A1: 1-EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMTWVRQAPGKGLEWVASIKQDGSERYY
Consensus: 1-EVQLVESGGGLVQPGGSLRLSCAASGFTFSX$_1$YWMX$_2$WVRQAPGKGLEWVASIKQDGSEX$_3$YY

8A3: 61-VDSVKGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARDLVLMVYDIDYYYYGMDVW
11F1: 61-VDSVKGRFAISRDNAKNSLFLQMNSLRAEDTAVYYCARDLVLMVYDIDYYYYGMDVW
8A1: 61-VDSVKGRFTISRDTAKNSLYLQMNSLRAEDTAVYYCARPLVLMVYALHYYYYGMDVW
Consensus: 61-VDSVKGRFX$_4$ISRDX$_5$AX$_6$NSLX$_7$LQMNSLRAEDTAVYYCARX$_8$LVLMVYX$_9$X$_{10}$X$_{11}$YYYYGMDVW

8A3: GQGTTVTVSS-127 (SEQ ID NO:459)
11F1: GQGTTVTVSS-127 (SEQ ID NO:463)
8A1: GHGTTVTVSS-127 (SEQ ID NO:483)
Consensus: GX$_{12}$GTTVTVSS-127 (SEQ ID NO:583)

X$_1$ is S or N; X$_2$ is S or T; X$_3$ is K or R; X$_4$ is A or T; X$_5$ is N or T; X$_6$ is K or R; X$_7$ is Y or F; X$_8$ is D or P; X$_9$ is D or A; X$_{10}$ is I or L; X$_{11}$ is D or H; and X$_{12}$ is Q or H