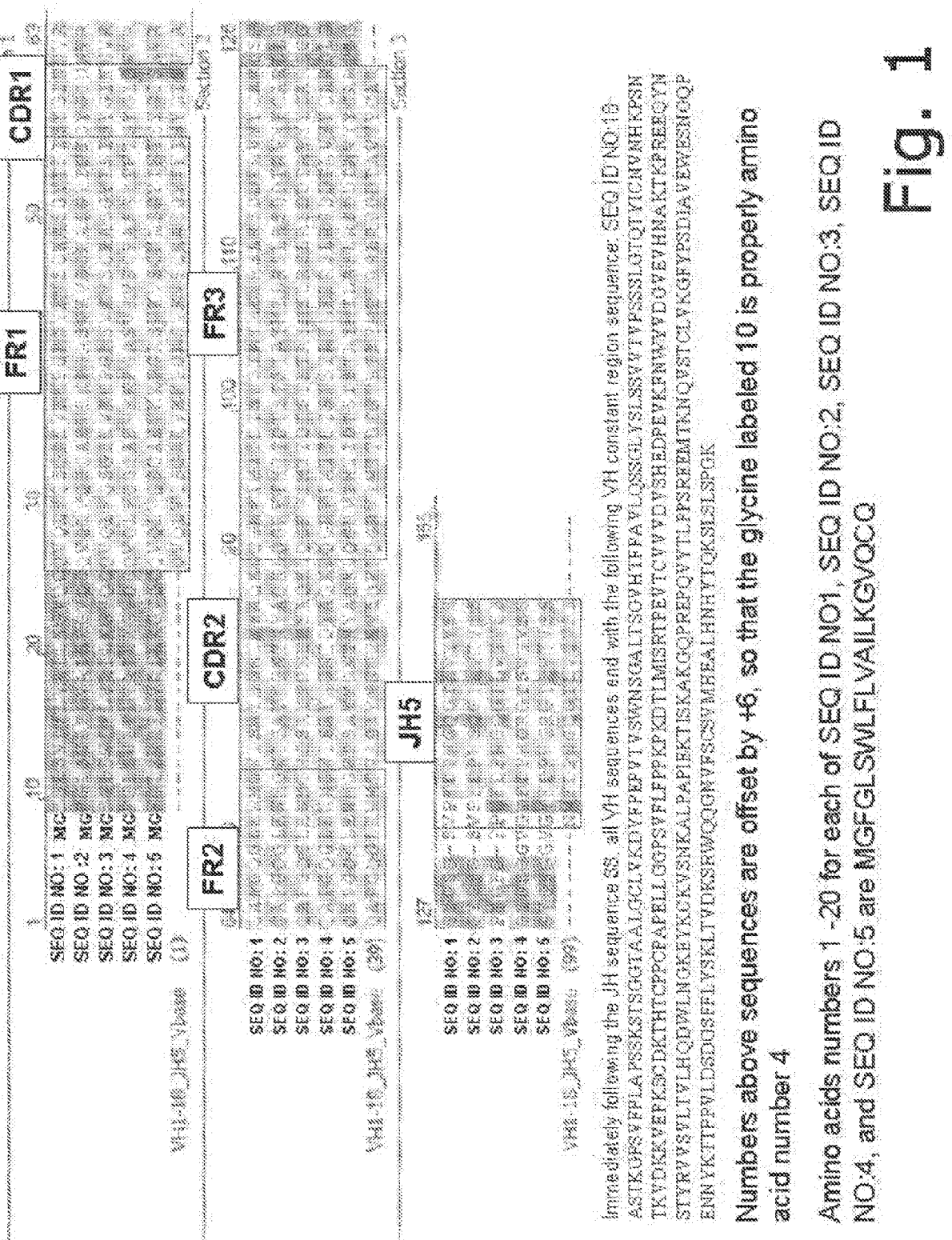

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
JH5
SEQ ID NO: 1
SEQ ID NO: 2
SEQ ID NO: 3
SEQ ID NO: 4
SEQ ID NO: 5
Immediately following the JH sequence SS, all VH sequences end with the following VH constant region sequence, SEQ ID NO:18
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5 are MGFGLSWLFLVAILKGVQCQ

Fig. 1

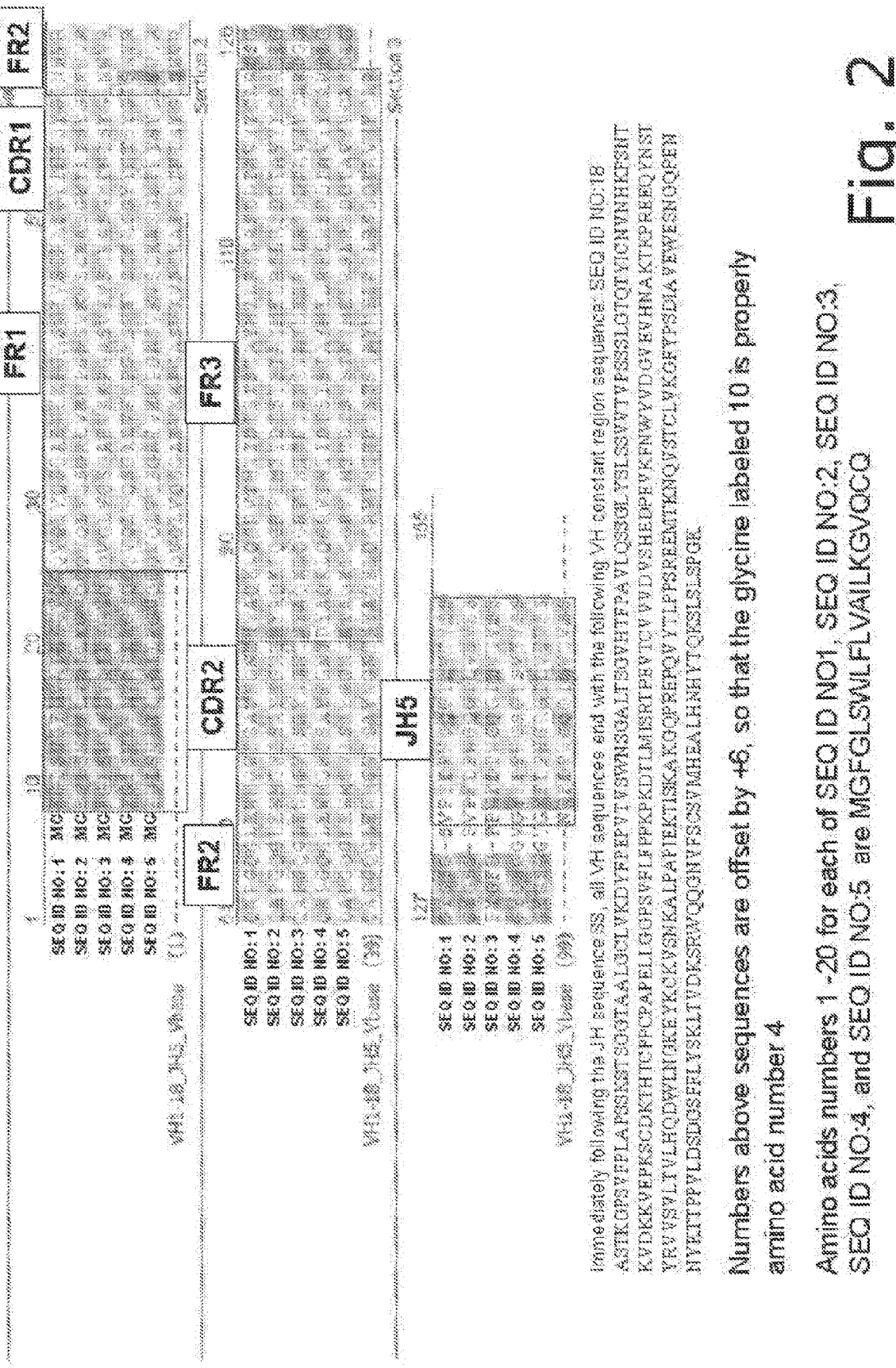

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
FR2
CDR2
FR3
JH5
SEQ ID NO: 1
SEQ ID NO: 2
SEQ ID NO: 3
SEQ ID NO: 4
SEQ ID NO: 5
Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:5 are MGFGLSWLFLVAILKGVQCQ

Fig. 2

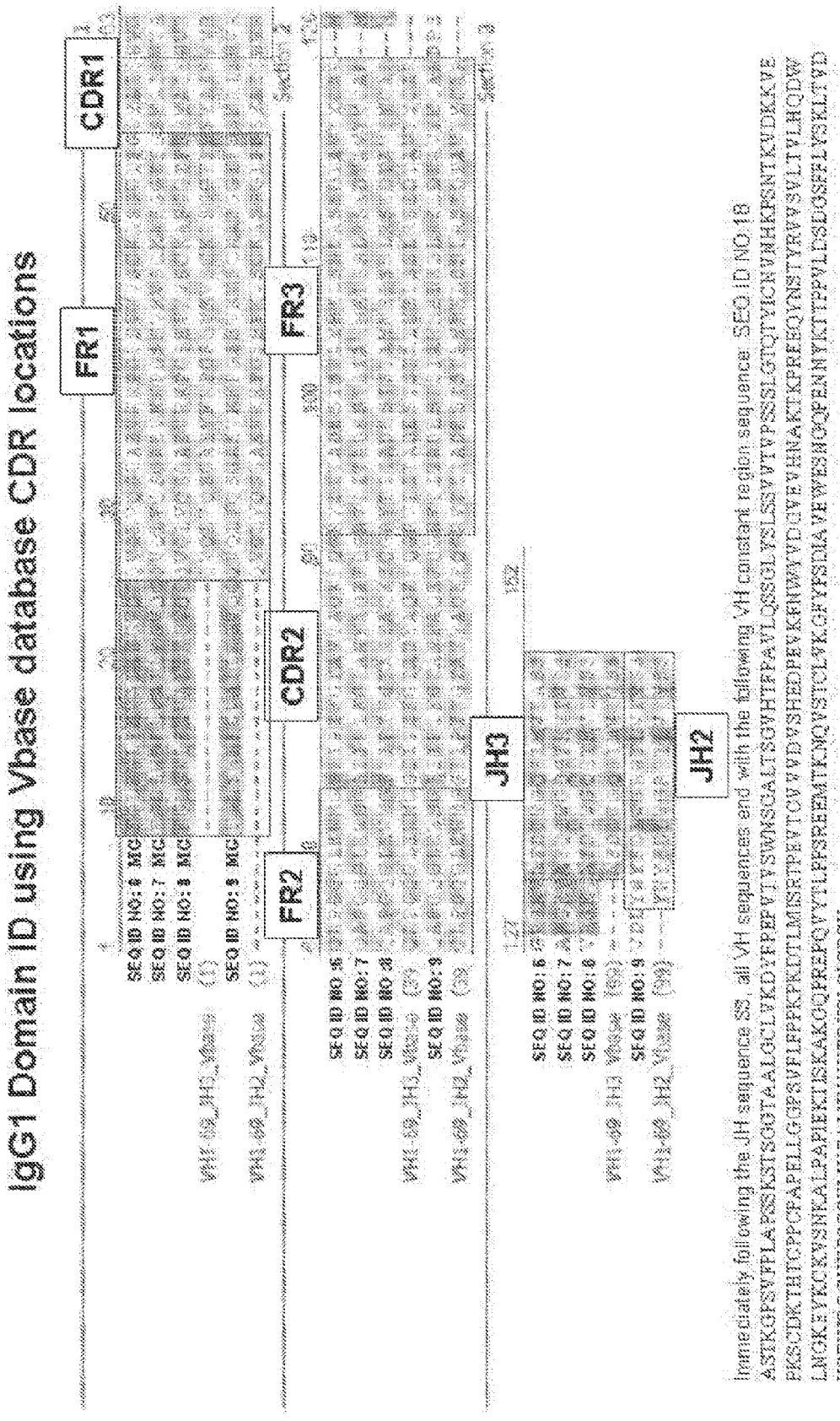

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
JH3
JH2
SEQ ID NO: 6 MG
SEQ ID NO: 7 MG
SEQ ID NO: 8 MG
SEQ ID NO: 5 MG
SEQ ID NO: 6
SEQ ID NO: 7
SEQ ID NO: 8
SEQ ID NO: 5
Immediately following the JH sequence SS, all VH sequences end with the following VH constant region sequence: SEQ ID NO:18
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE
PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO6, SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:9 are MGFGLSWLFLVAILKGVQCQ

Fig. 3

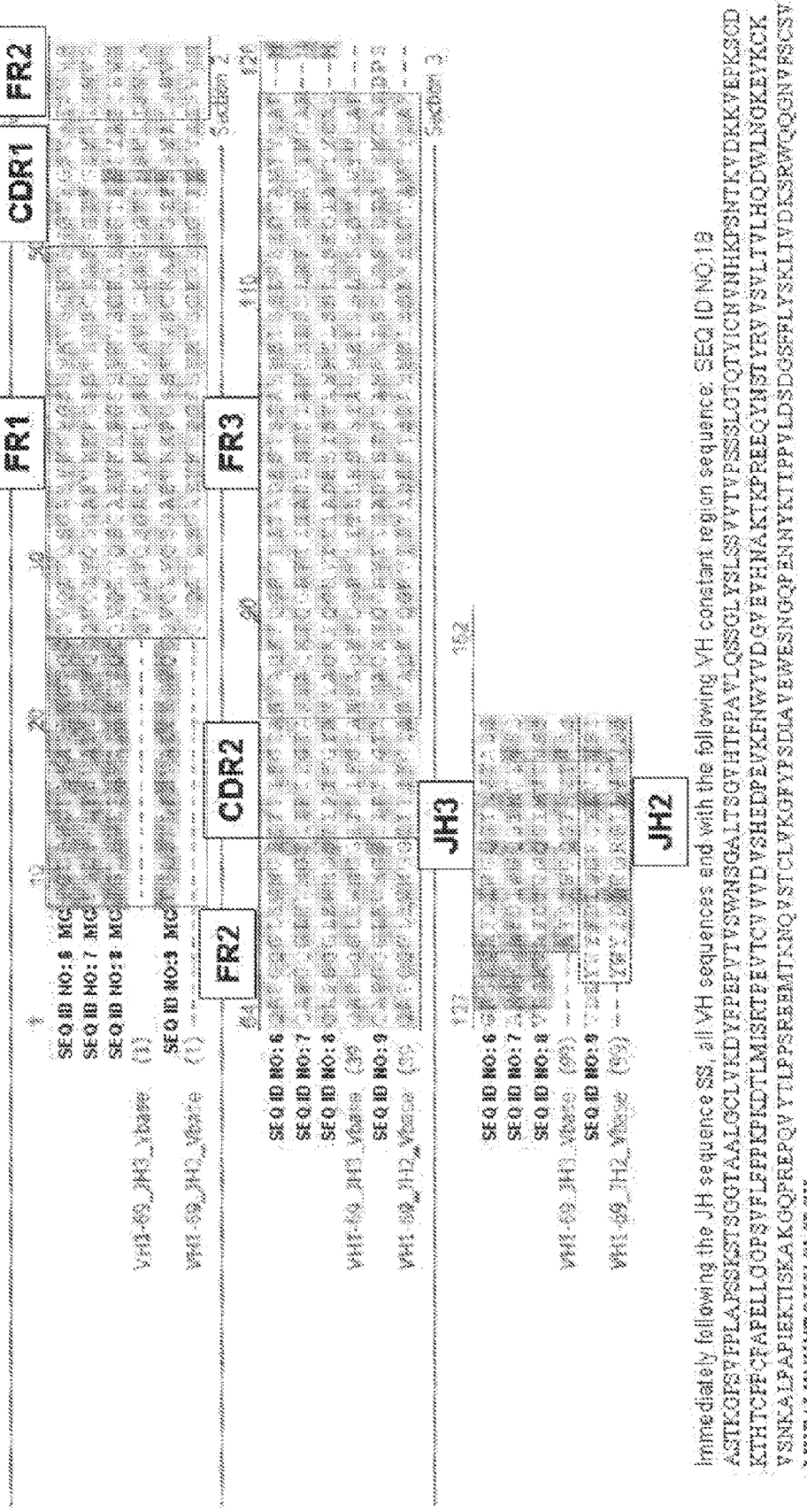

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
JH3
JH2
SEQ ID NO: 6
SEQ ID NO: 7
SEQ ID NO: 8
SEQ ID NO: 9
VH1-69_JH3_Vbase
VH1-69_JH2_Vbase
Immediately following the JH sequence SS, all VH sequences end with the following VH constant region sequence: SEQ ID NO:18
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD
KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK
Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO6, SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:9 are MGFGLSWLFLVAILKGVQCQ

Fig. 4

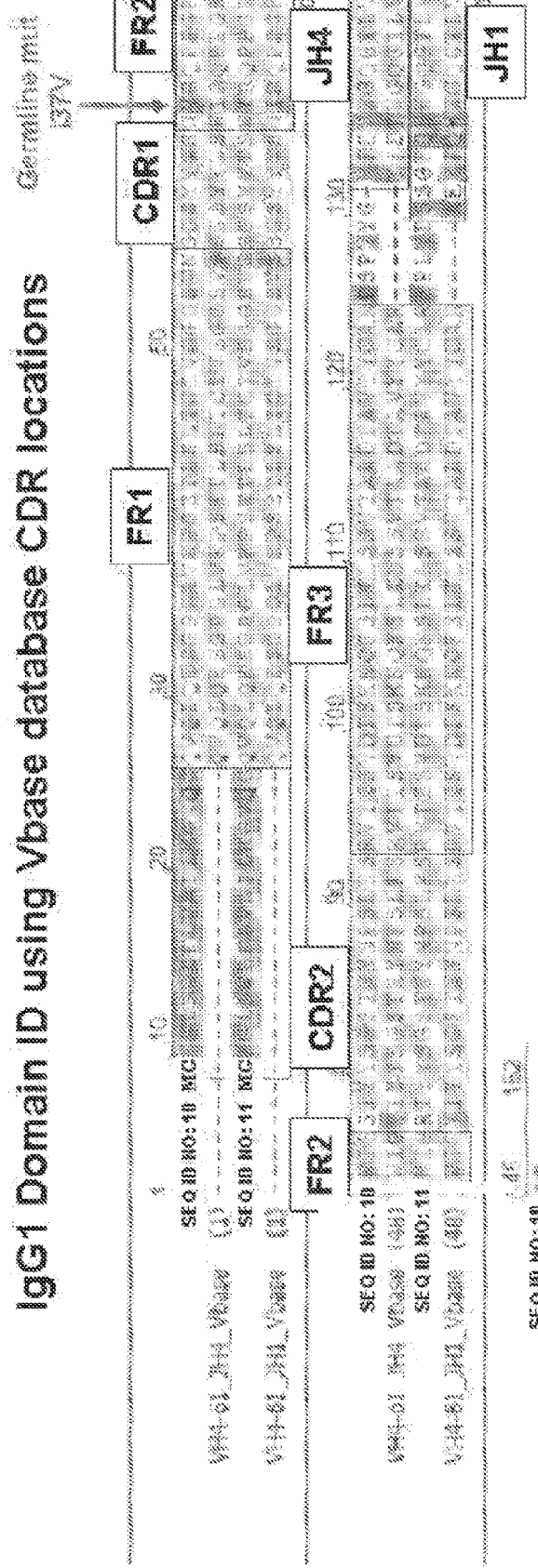
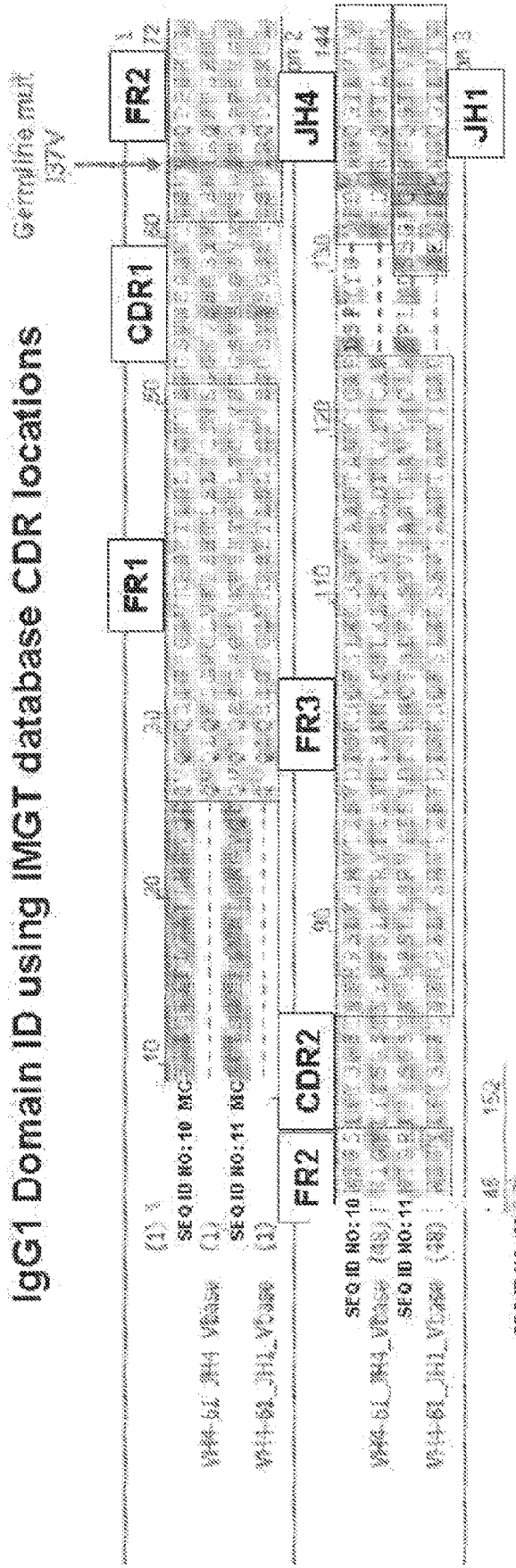

IgG1 Domain ID using Vbase database CDR locations
Germline mut
IGHV
FR1
CDR1
FR2
CDR2
FR3
JH4
JH1
SEQ ID NO: 10
SEQ ID NO: 11
SEQ ID NO: 12
SEQ ID NO: 13
SEQ ID NO: 14
SEQ ID NO: 15
SEQ ID NO: 16
SEQ ID NO: 17
SEQ ID NO: 18
Immediately following the sequence SS C-terminal to the JH region, all VH sequences end with the following VH constant region sequence:
SEQ ID NO:18
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV
EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO 11 and SEQ ID NO:12 are
MGFGLSWLFLVAILKGVQCQ

Fig. 5



Immediately following the sequence SS C-terminal to the JH region, all VH sequences end with the following VH constant region sequence:
SEQ ID NO:18
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP
KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Numbers above sequences are offset by +6, so that the glycine labeled 10 is properly amino acid number 4

Amino acids numbers 1 -20 for each of SEQ ID NO 11 and SEQ ID NO:12 are MGFGLSWLFLVAILKGVQCQ

Fig. 6

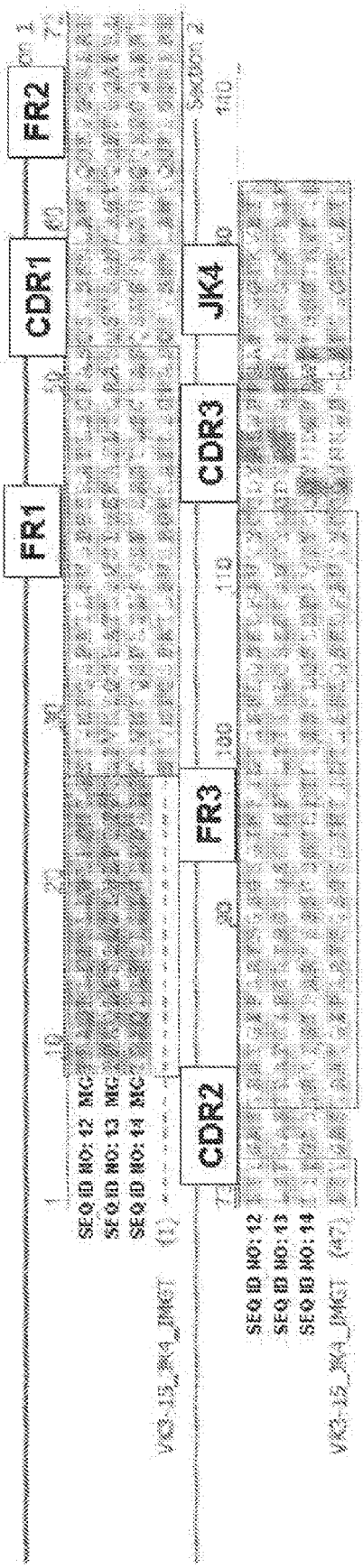

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 12
SEQ ID NO: 13
SEQ ID NO: 14
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence, SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO 12, SEQ ID NO:13, and SEQ ID NO:14 are MGTPAQLLFLLLLWLPDTTG

Fig. 7

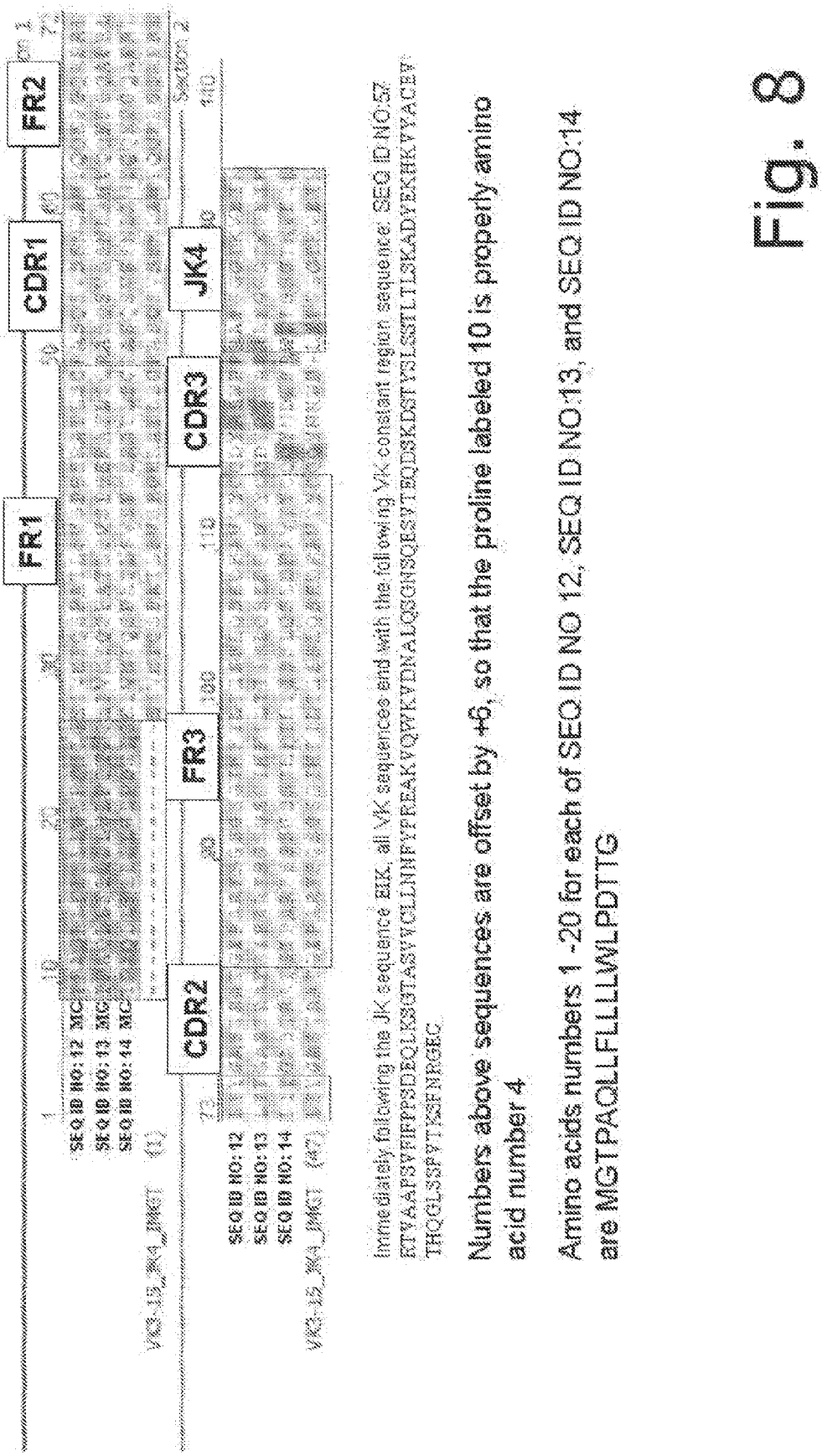

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 12
SEQ ID NO: 13
SEQ ID NO: 14
VK3-15_JK4_IMGT
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
THQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO 12, SEQ ID NO:13, and SEQ ID NO:14 are MGTPAQLLFLLLLWLPDTTG

Fig. 8

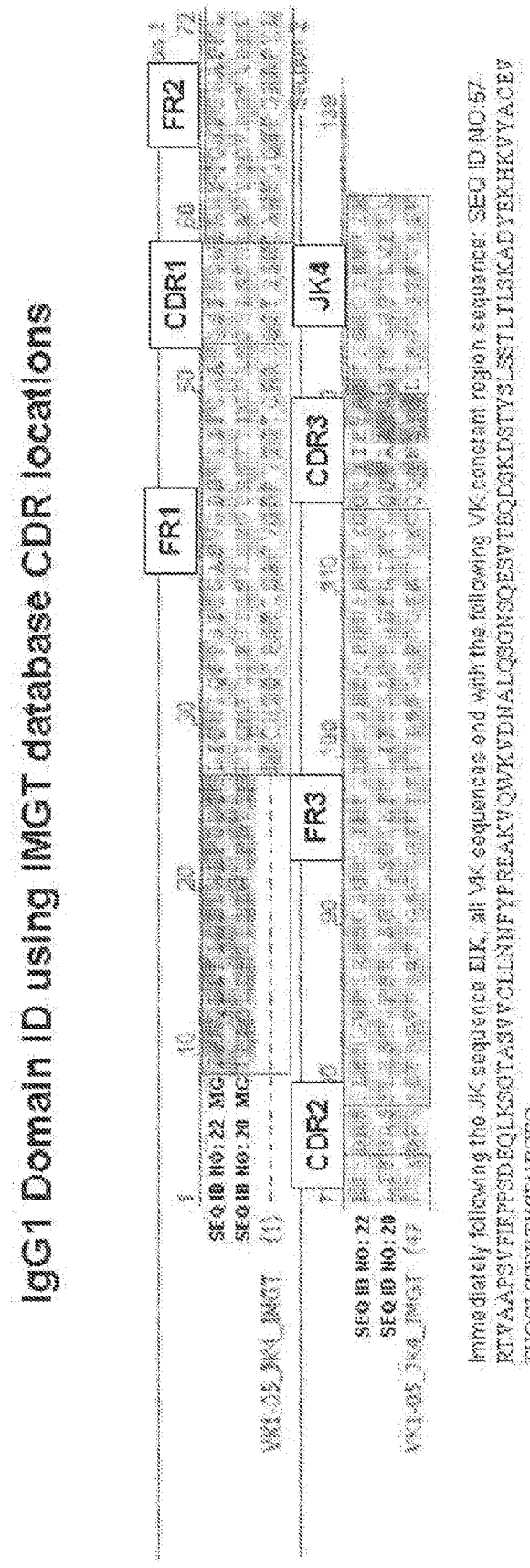

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 22
SEQ ID NO: 20
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
THQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO 20 and SEQ ID NO:22 are
MGTPAQLLFLLLLWLPDTTG

Fig. 9

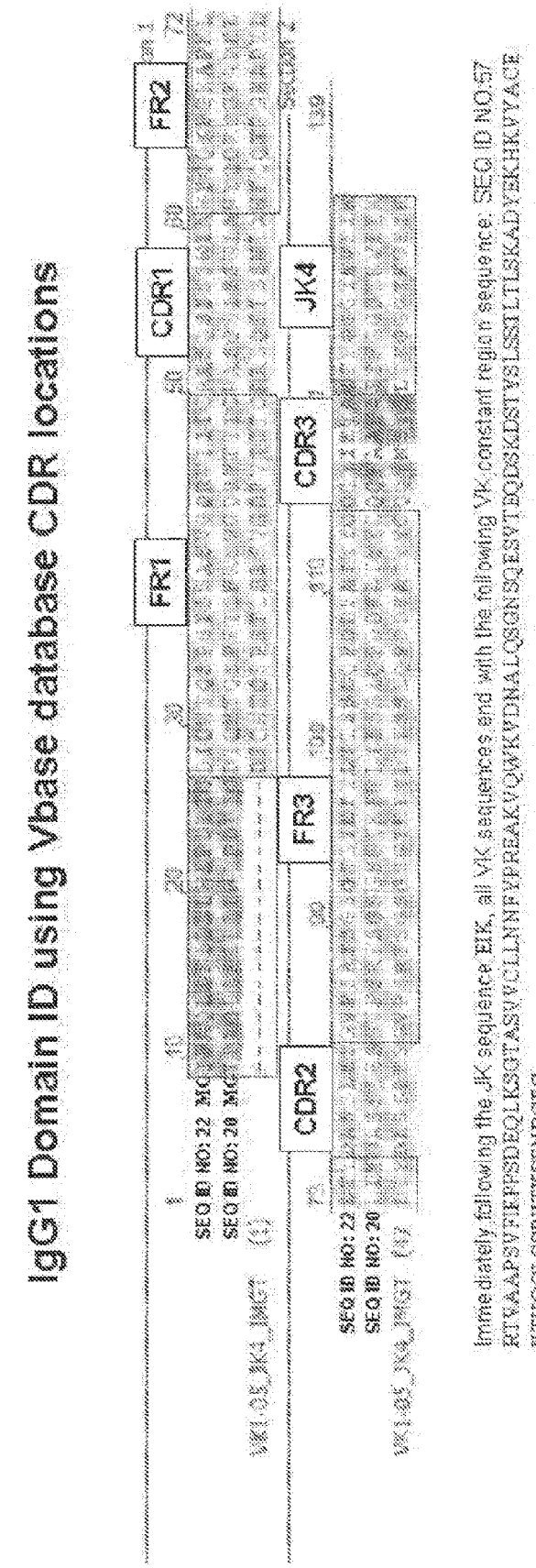

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 22
SEQ ID NO: 20
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence. SEQ ID NO:67
RTVAAPSVFIFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly amino acid number 4
Amino acids numbers 1 -20 for each of SEQ ID NO 20 and SEQ ID NO:22 are
MGTPAQLLFLLLLWLPDTTG

Fig. 10

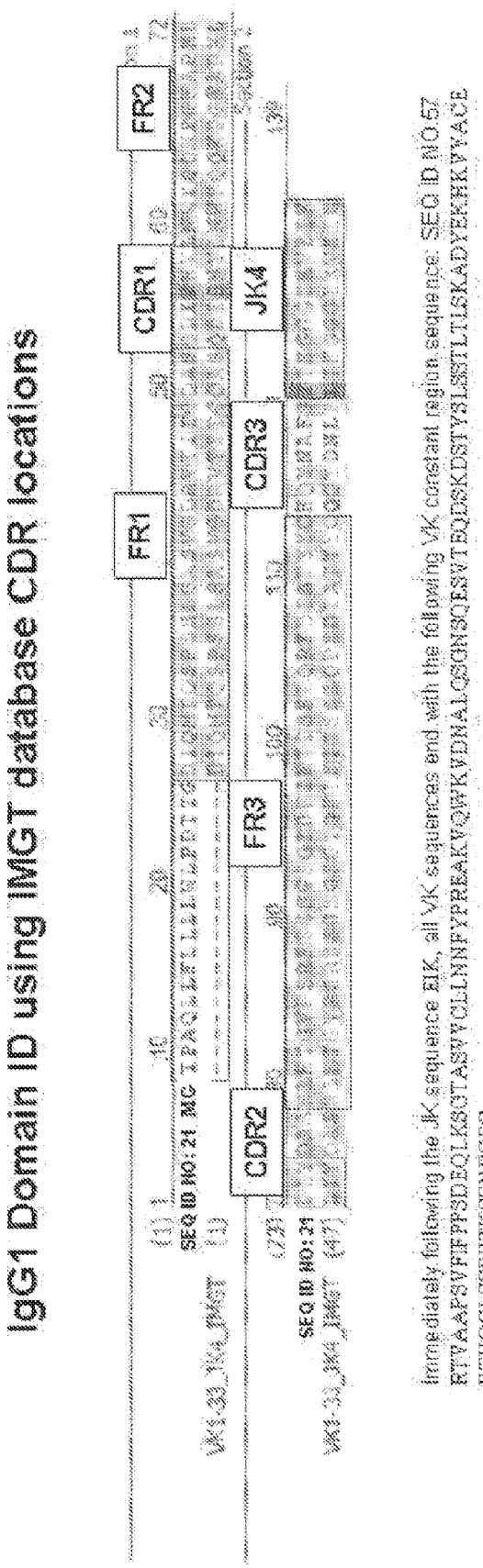

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 21
VK1-33_JK4_IMGT
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is
properly amino acid number 4
Amino acids numbers 1 -20 for SEQ ID NO: 21 are MGTPAQLLFLLLLWLPDTTG

Fig. 11

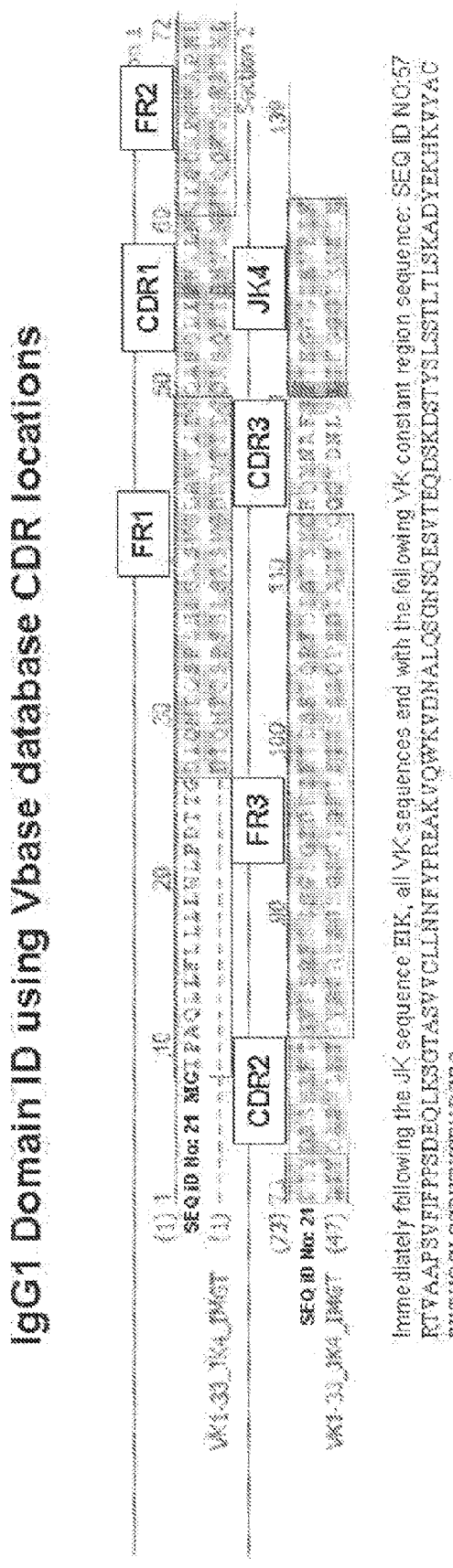

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID No: 21 MGTPAQLLFLLLLWLPDTTG
VK1-33_JK4_IMGT
SEQ ID No: 21
VK1-33_JK4_IMGT
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is
properly amino acid number 4
Amino acids numbers 1 -20 for SEQ ID NO: 21 are
MGTPAQLLFLLLLWLPDTTG

Fig. 12

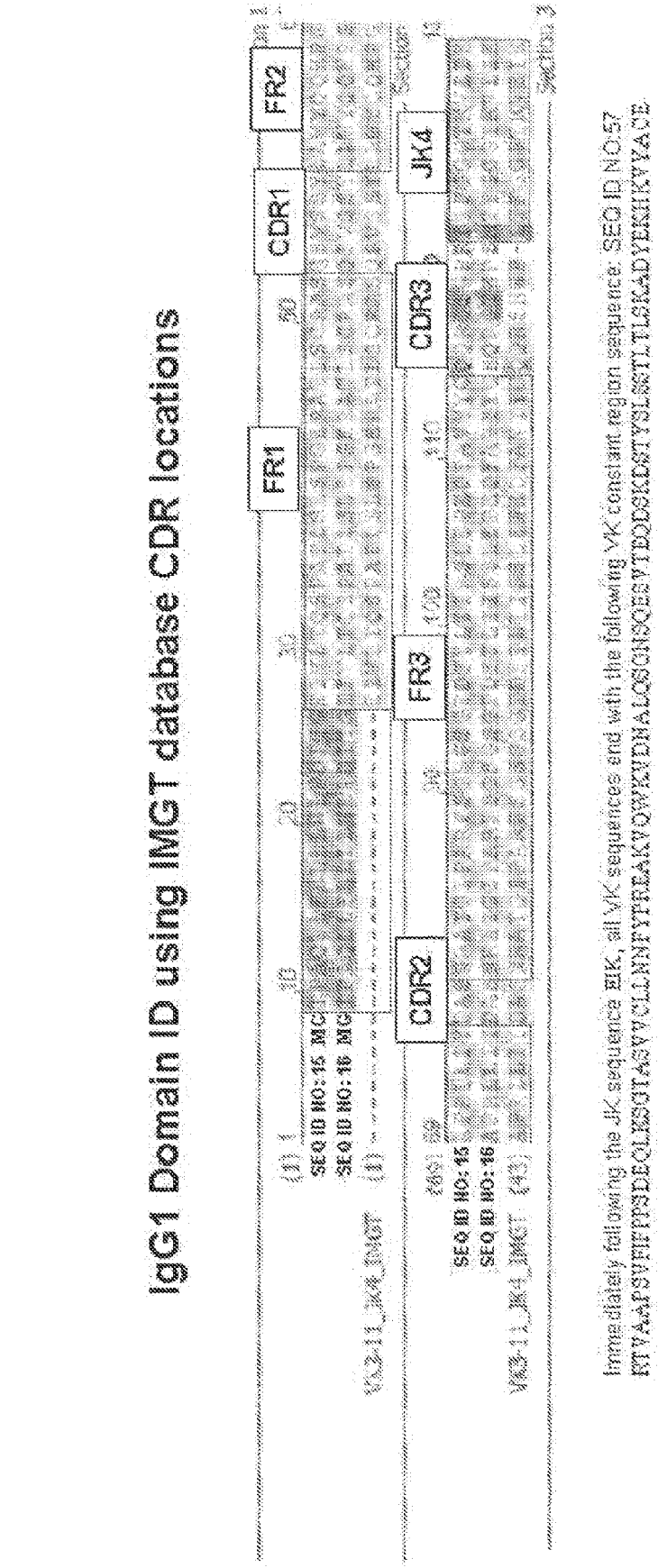

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
ETVAAPSVFIFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly
amino acid number 4
Amino acids numbers 1 -20 for EACH OF SEQ ID NO: 15 and SEQ ID NO: 16 are
MGTPAQLLFLLLLWLPDTTG

Fig. 13

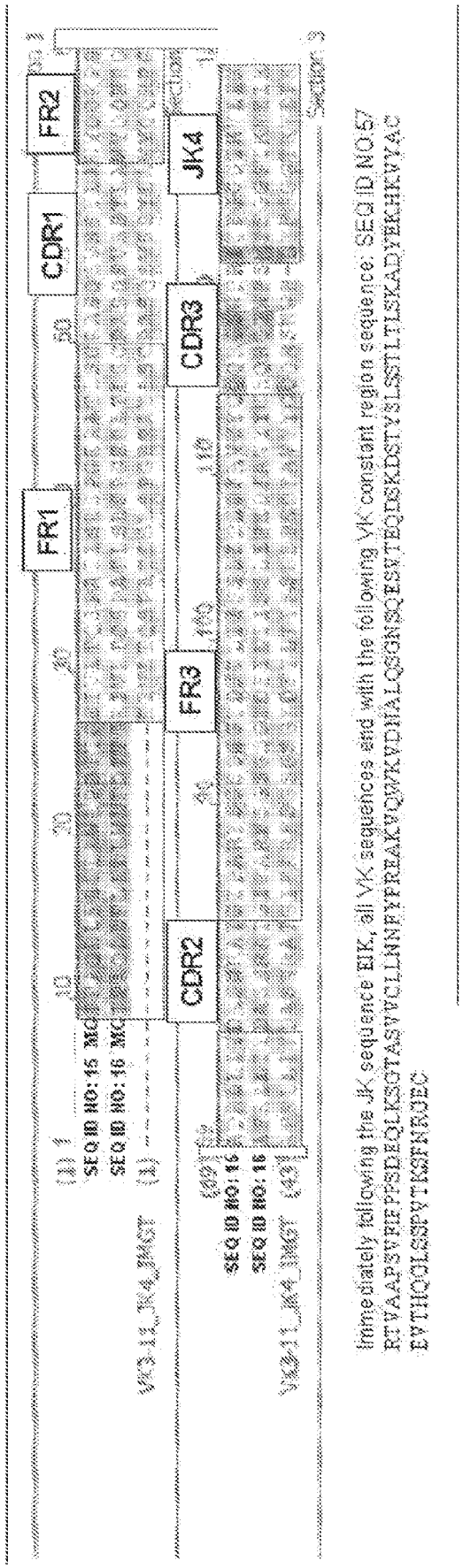

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO: 15
SEQ ID NO: 16
VK3-11_JK4_IMGT
Section 3
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is
properly amino acid number 4
Amino acids numbers 1 -20 for EACH OF SEQ ID NO: 15 and SEQ ID NO: 16
are MGTPAQLLFLLLLWLPDTTG

Fig. 14

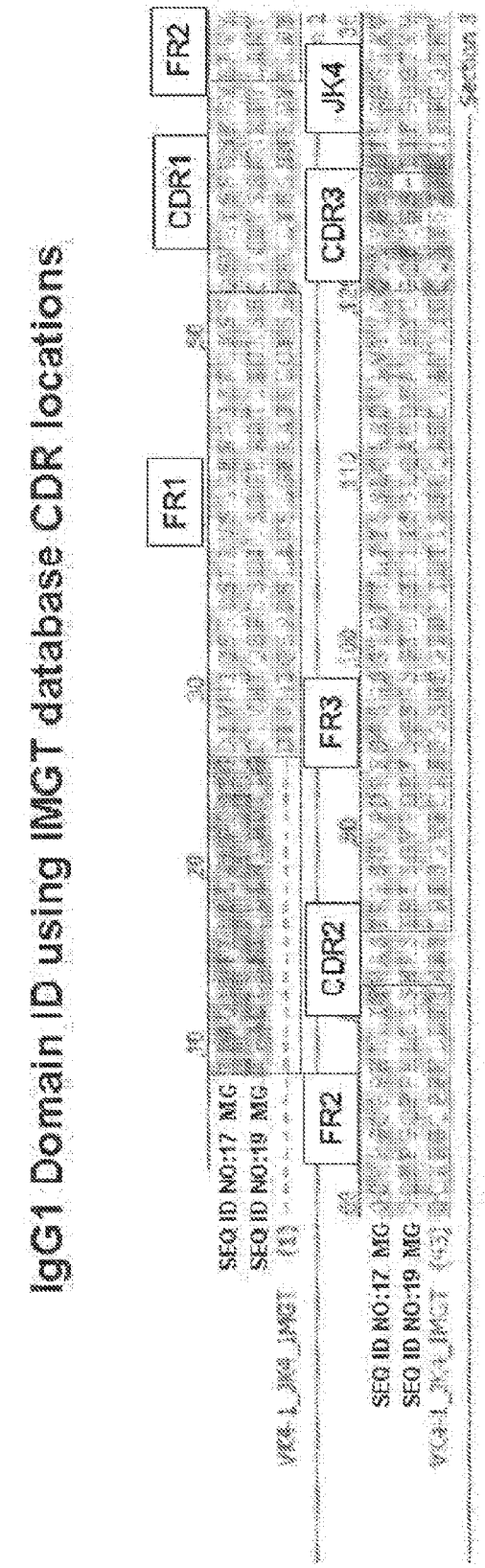

IgG1 Domain ID using IMGT database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO:17 MG
SEQ ID NO:19 MG
VK4_JK4_IMGT
SEQ ID NO:17 MG
SEQ ID NO:19 MG
VK4_JK4_IMGT
SEQ ID NO:17 MG
SEQ ID NO:19 MG
VK4_JK4_IMGT
Immediately following the JK sequence are all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is
properly amino acid number 4
Amino acids numbers 1-20 for EACH OF SEQ ID NO: 17 and SEQ ID NO: 19
are MGTPAQLLFLLLLWLPDTTG

Fig. 15

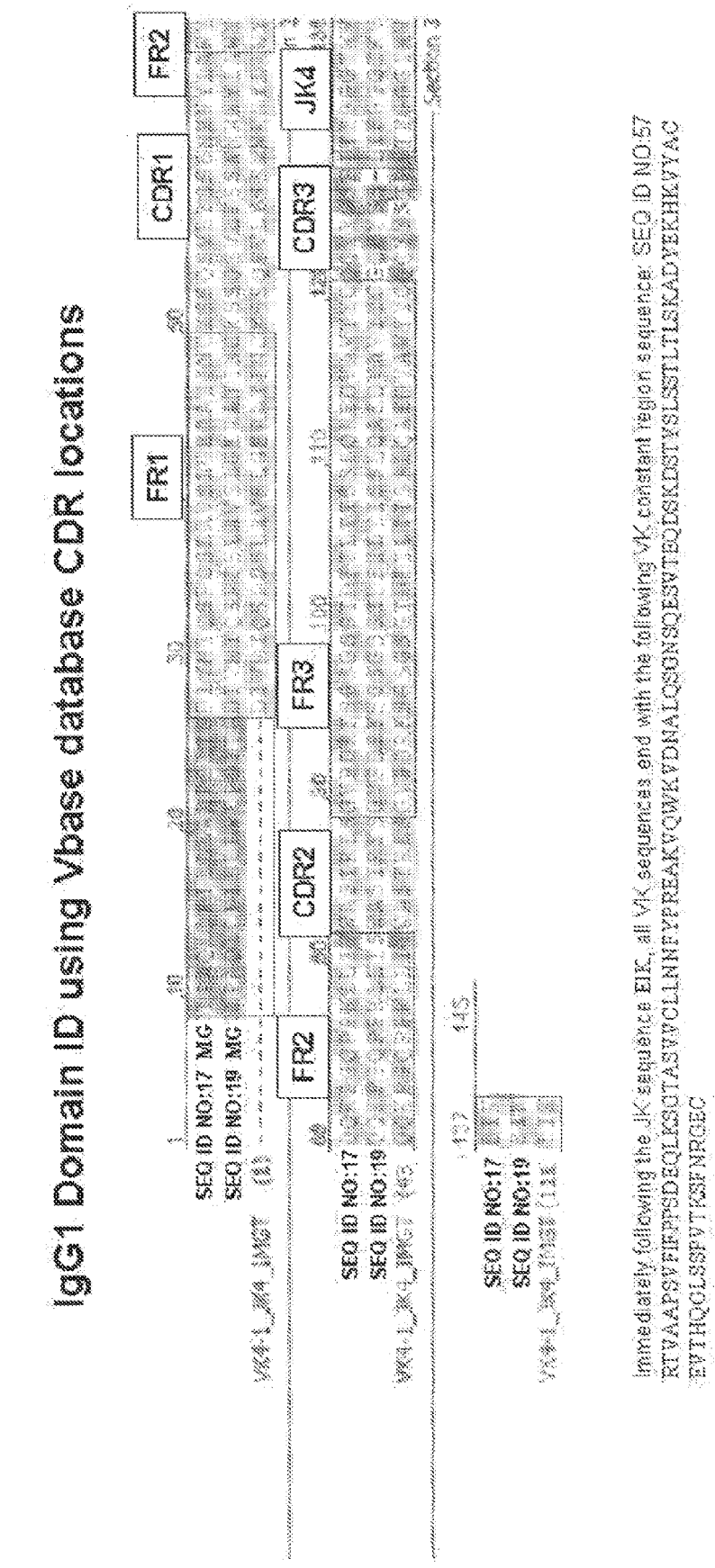

IgG1 Domain ID using Vbase database CDR locations
FR1
CDR1
FR2
CDR2
FR3
CDR3
JK4
SEQ ID NO:17
SEQ ID NO:19
Immediately following the JK sequence EIK, all VK sequences end with the following VK constant region sequence: SEQ ID NO:57
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC
EVTHQGLSSPVTKSFNRGEC
Numbers above sequences are offset by +6, so that the proline labeled 10 is properly amino acid number 4
Amino acids numbers 1-20 for EACH OF SEQ ID NO: 17 and SEQ ID NO: 19 are MGTPAQLLFLLLLWLPDTTG

Fig. 16

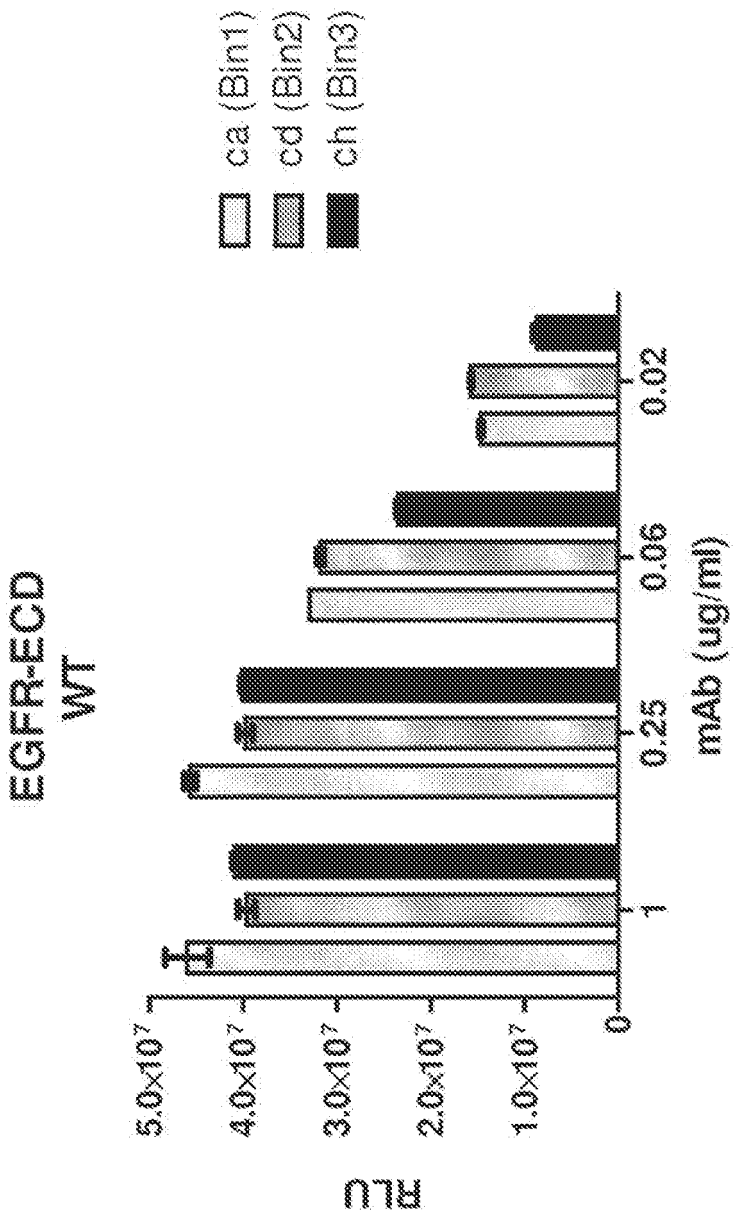

ca (Bin1)
cd (Bin2)
ch (Bin3)
EGFR-ECD
WT
RLU
5.0x10^7
4.0x10^7
3.0x10^7
2.0x10^7
1.0x10^7
0
1
0.25
0.06
0.02
mAb (ug/ml)

Figure 17A

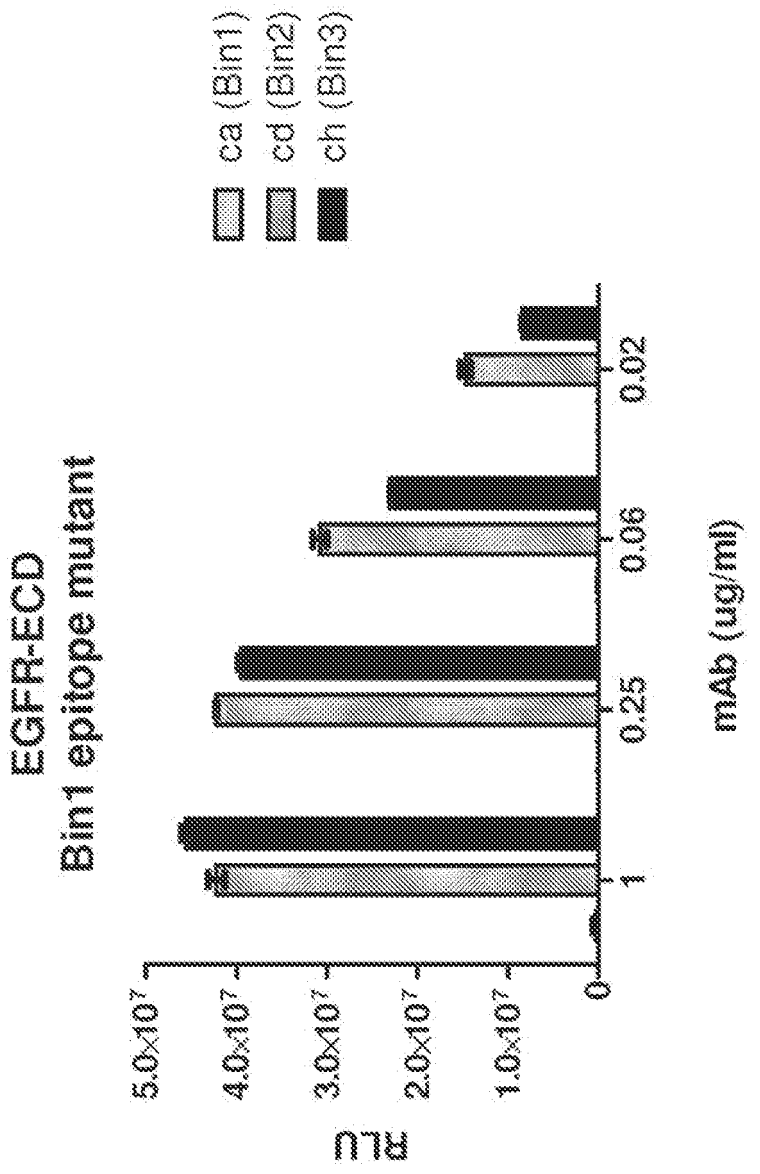

EGFR-ECD
Bin1 epitope mutant
ca (Bin1)
cd (Bin2)
ch (Bin3)
RLU
5.0x10⁷
4.0x10⁷
3.0x10⁷
2.0x10⁷
1.0x10⁷
0
1
0.25
0.06
0.02
mAb (ug/ml)

Figure 17B

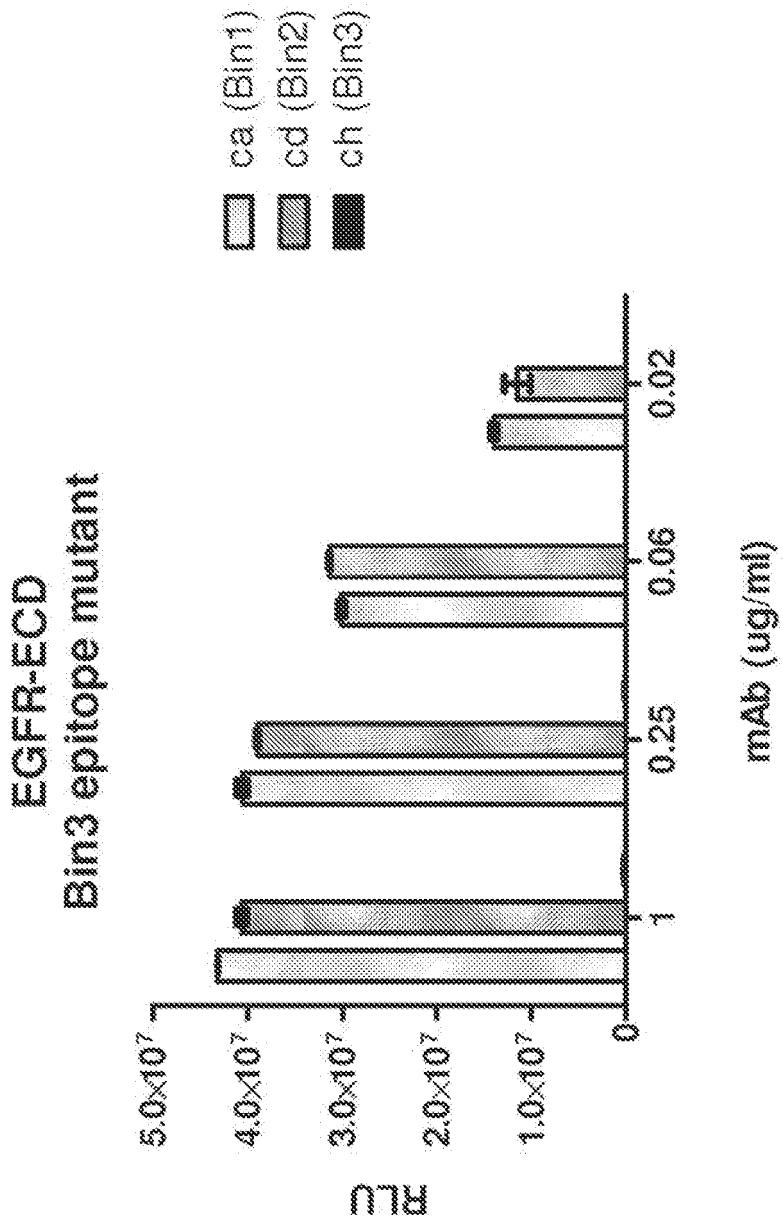

ca (Bin1)
cd (Bin2)
ch (Bin3)
EGFR-ECD
Bin3 epitope mutant
RLU
5.0x10^7
4.0x10^7
3.0x10^7
2.0x10^7
1.0x10^7
0
1
0.25
0.06
0.02
mAb (ug/ml)

Figure 17C

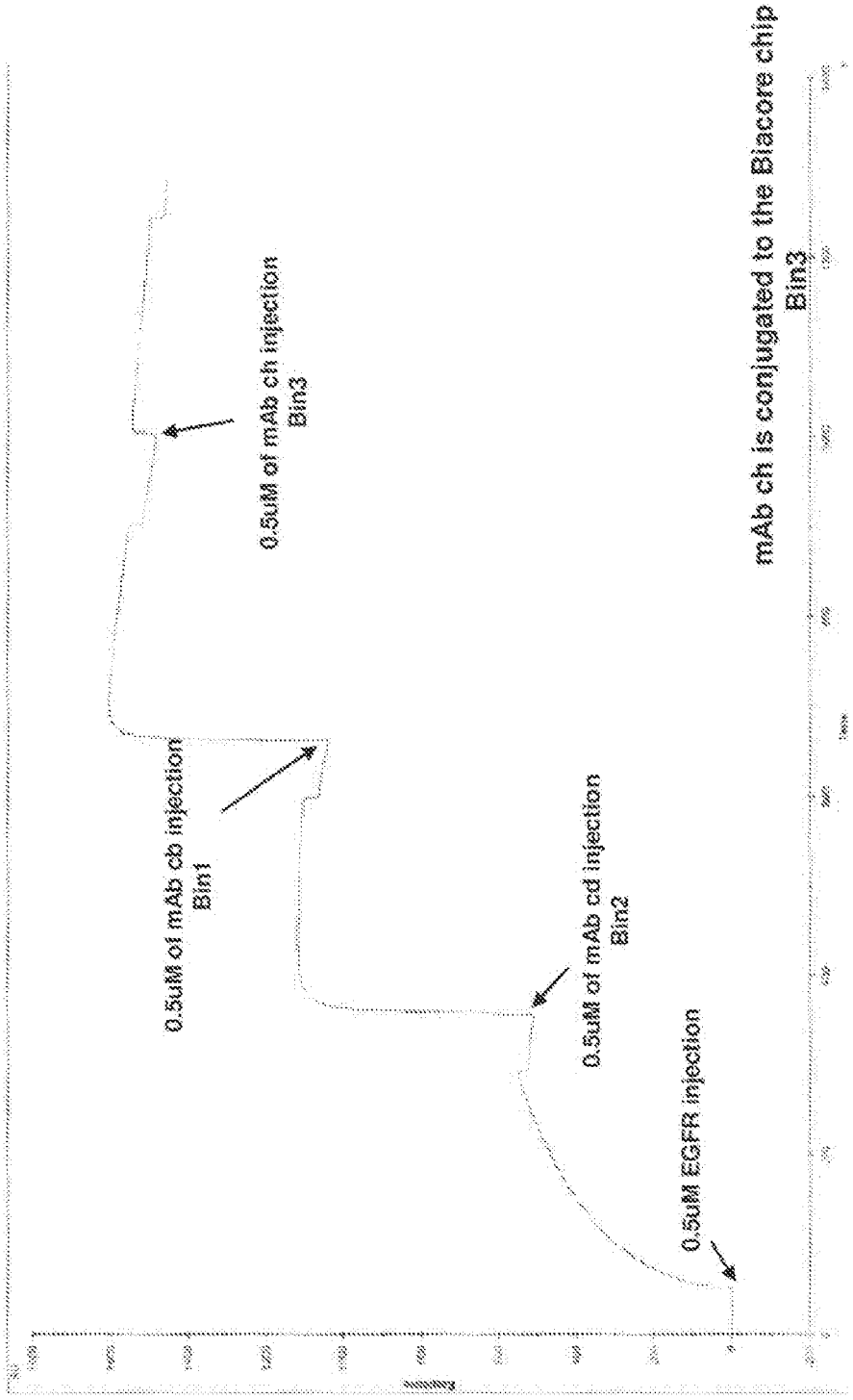
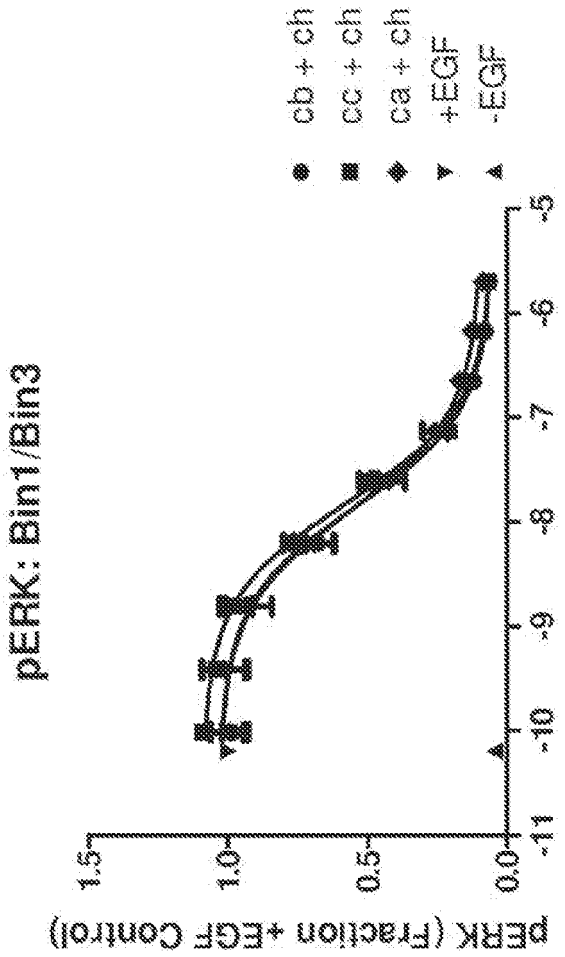
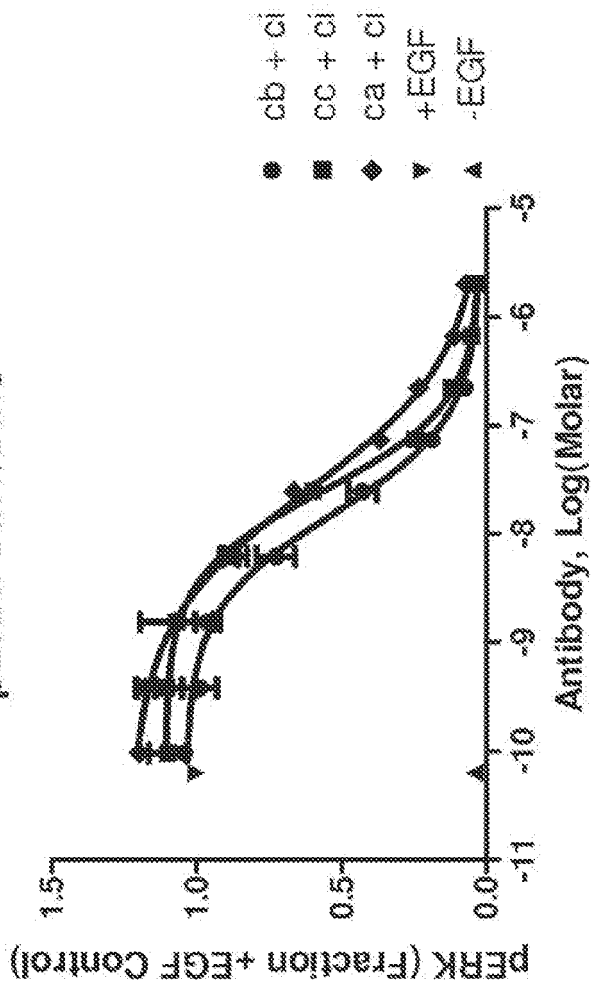

mAb ch is conjugated to the Biacore chip
Bin3
0.5uM of mAb ch injection
Bin3
0.5uM of mAb cb injection
Bin1
0.5uM of mAb cd injection
Bin2
0.5uM EGFR injection

Figure 17D



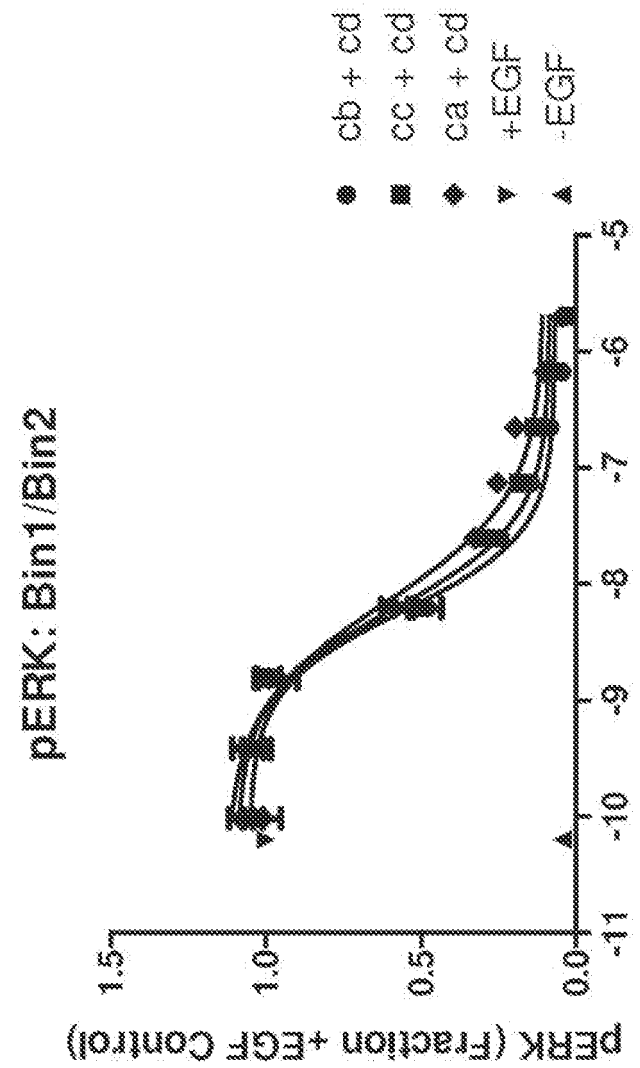
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cb + ch	0.057	1.405e-008	1.426e-007
cc + ch	0.057	1.531e-008	1.591e-007
ca + ch	0.097	1.268e-008	1.429e-007

Figure 18A



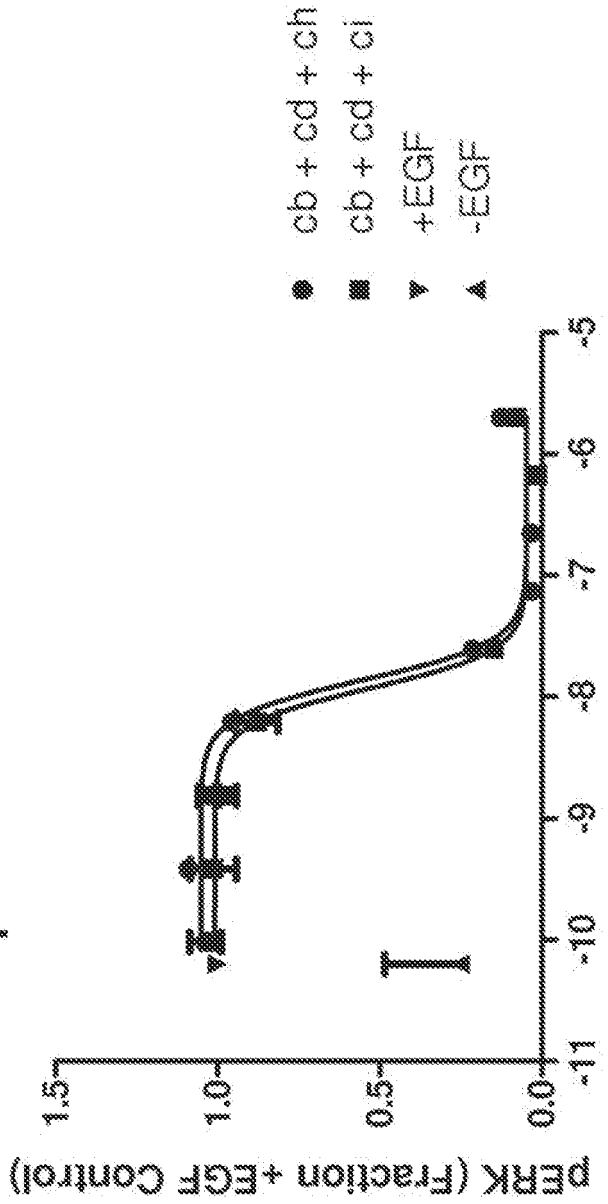
	Bottom	IC50	IC90
cb + ci	0.021	1.528e-008	1.416e-007
cc + ci	0.023	2.487e-008	1.841e-007
ca + ci	0.006	2.504e-008	5.916e-007

Figure 18B



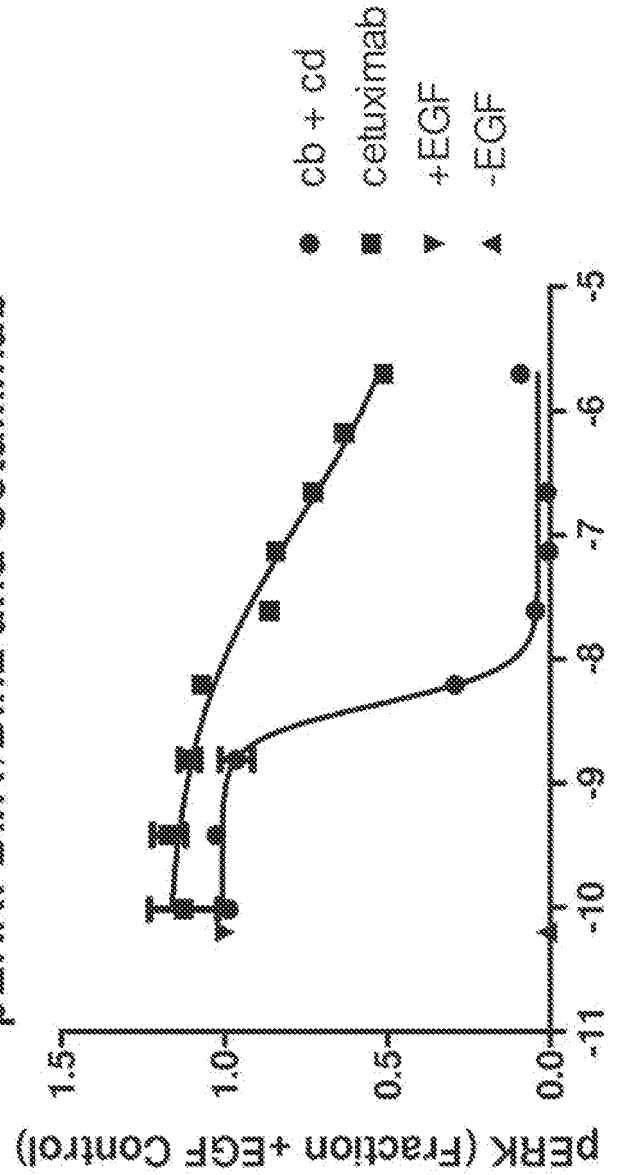
	Bottom	IC50	IC90
cb + cd	0.070	5.765e-009	3.089e-008
cc + cd	0.086	6.047e-009	4.077e-008
ca + cd	0.105	6.825e-009	7.013e-008

Figure 18C



	Bottom	IC50	IC90
cb + cd + ch	0.048	1.379e-008	3.020e-008
cb + cd + ci	0.048	1.179e-008	2.543e-008

Figure 19A



	Bottom	IC50	IC90
cb + cd	0.039	4.358e-009	9.165e-009
Cetuximab	0.351	1.337e-007	1.296e-005

Figure 19B

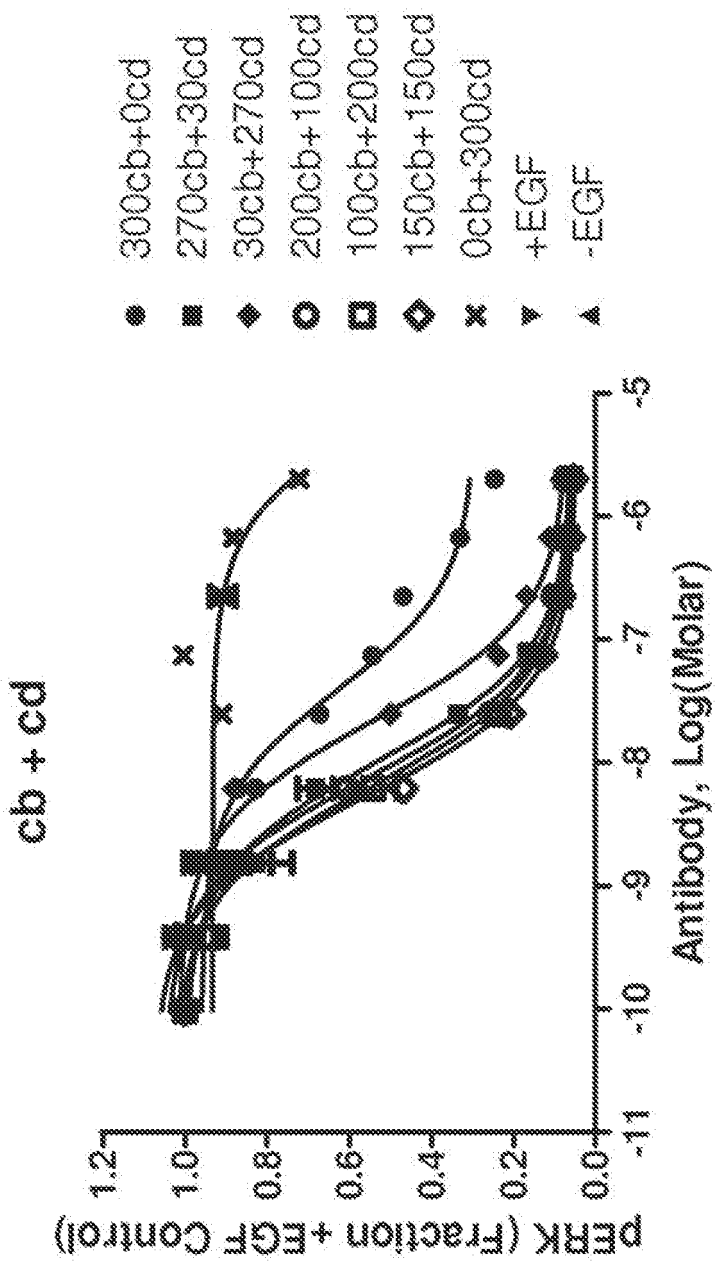

cb + cd
300cb+0cd
270cb+30cd
30cb+270cd
200cb+100cd
100cb+200cd
150cb+150cd
0cb+300cd
+EGF
-EGF
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)

Figure 20A

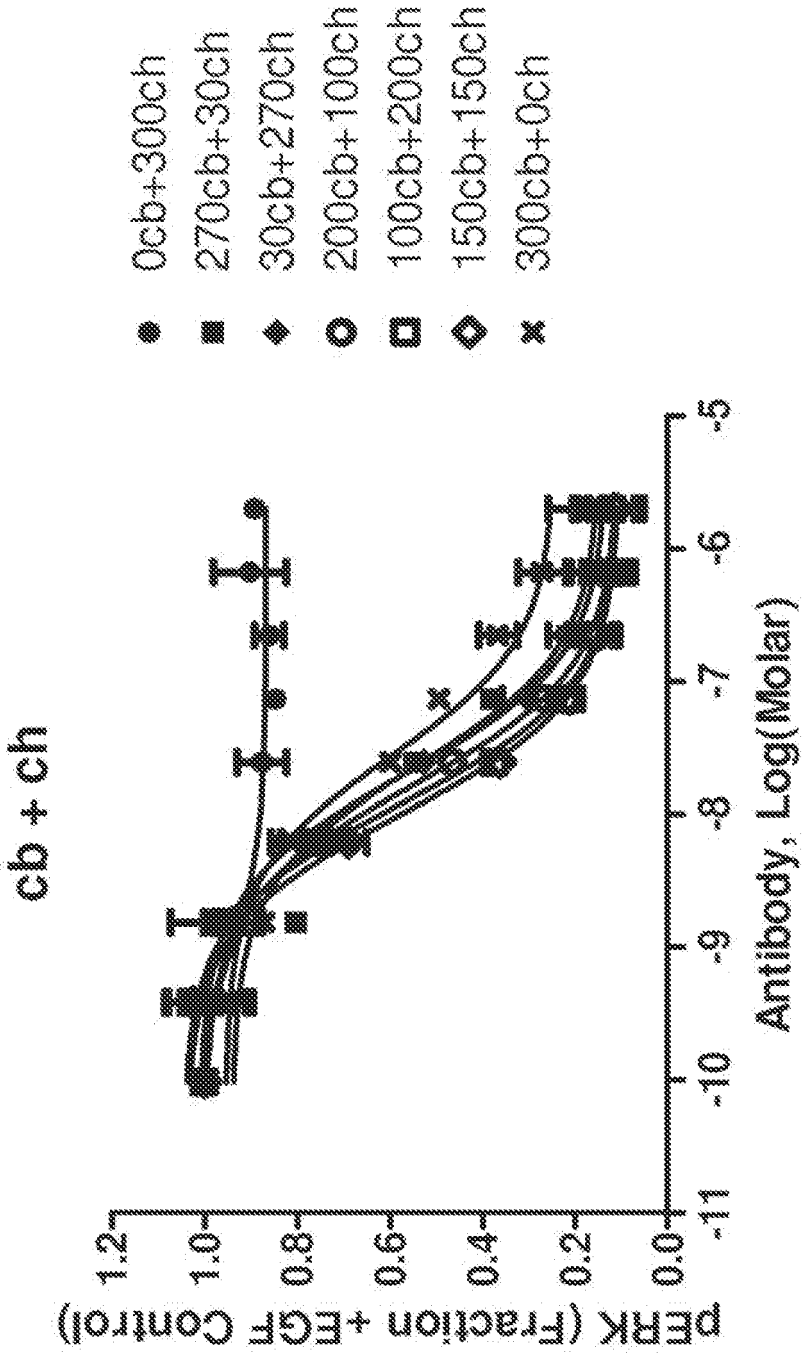

0cb+300ch
270cb+30ch
30cb+270ch
200cb+100ch
100cb+200ch
150cb+150ch
300cb+0ch
cb + ch
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)

Figure 20B

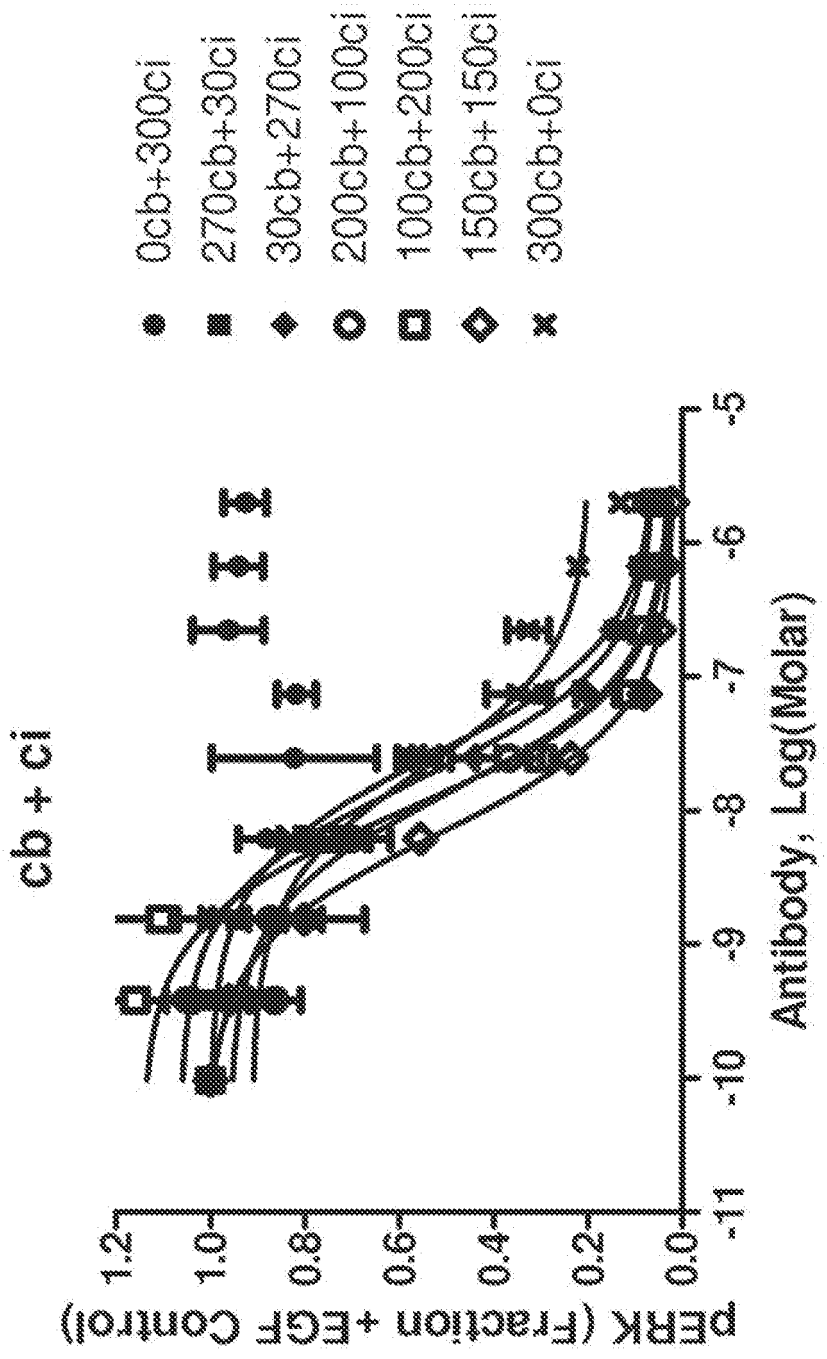

0cb+300ci
270cb+30ci
30cb+270ci
200cb+100ci
100cb+200ci
150cb+150ci
300cb+0ci
cb + ci
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)

Figure 20C

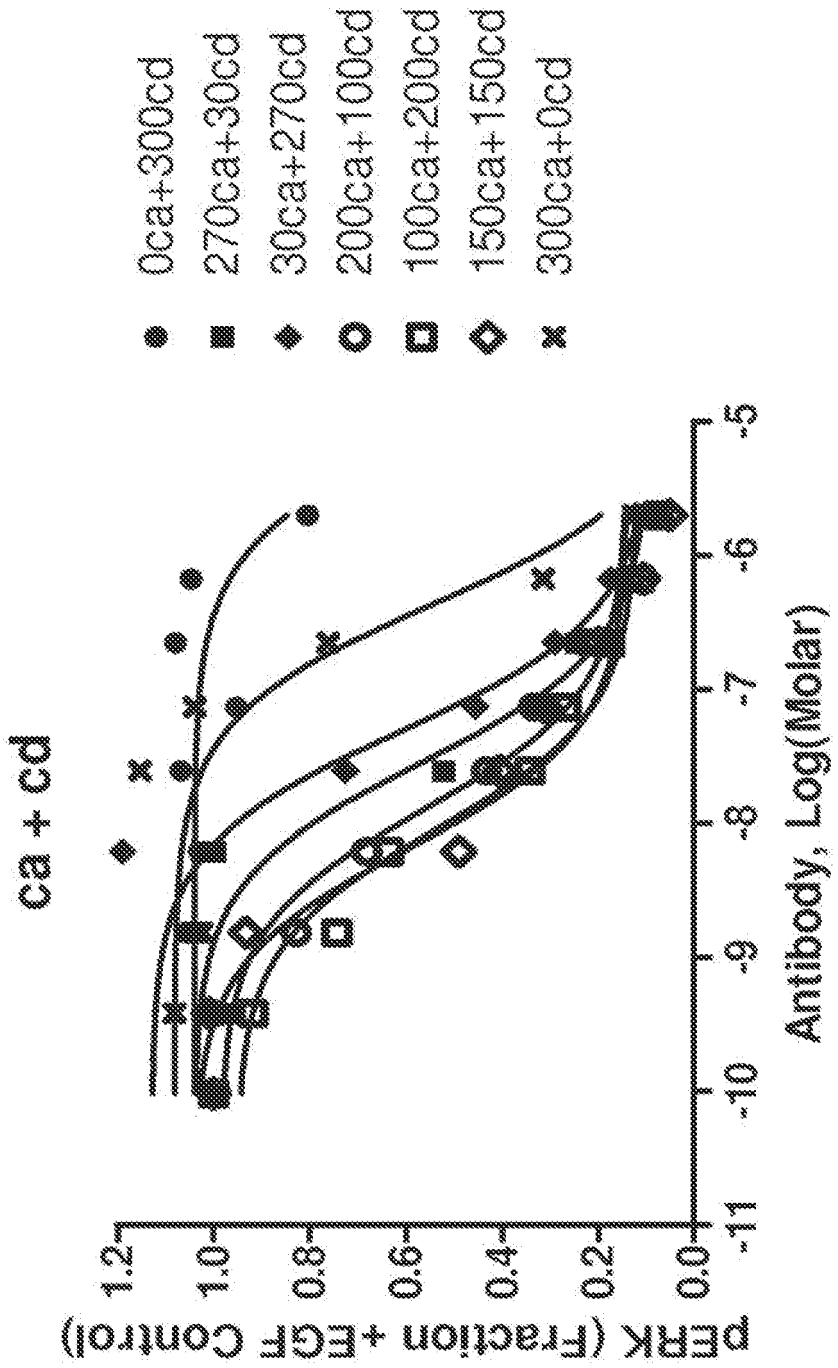

0ca+300cd
270ca+30cd
30ca+270cd
200ca+100cd
100ca+200cd
150ca+150cd
300ca+0cd
ca + cd
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)

Figure 20D

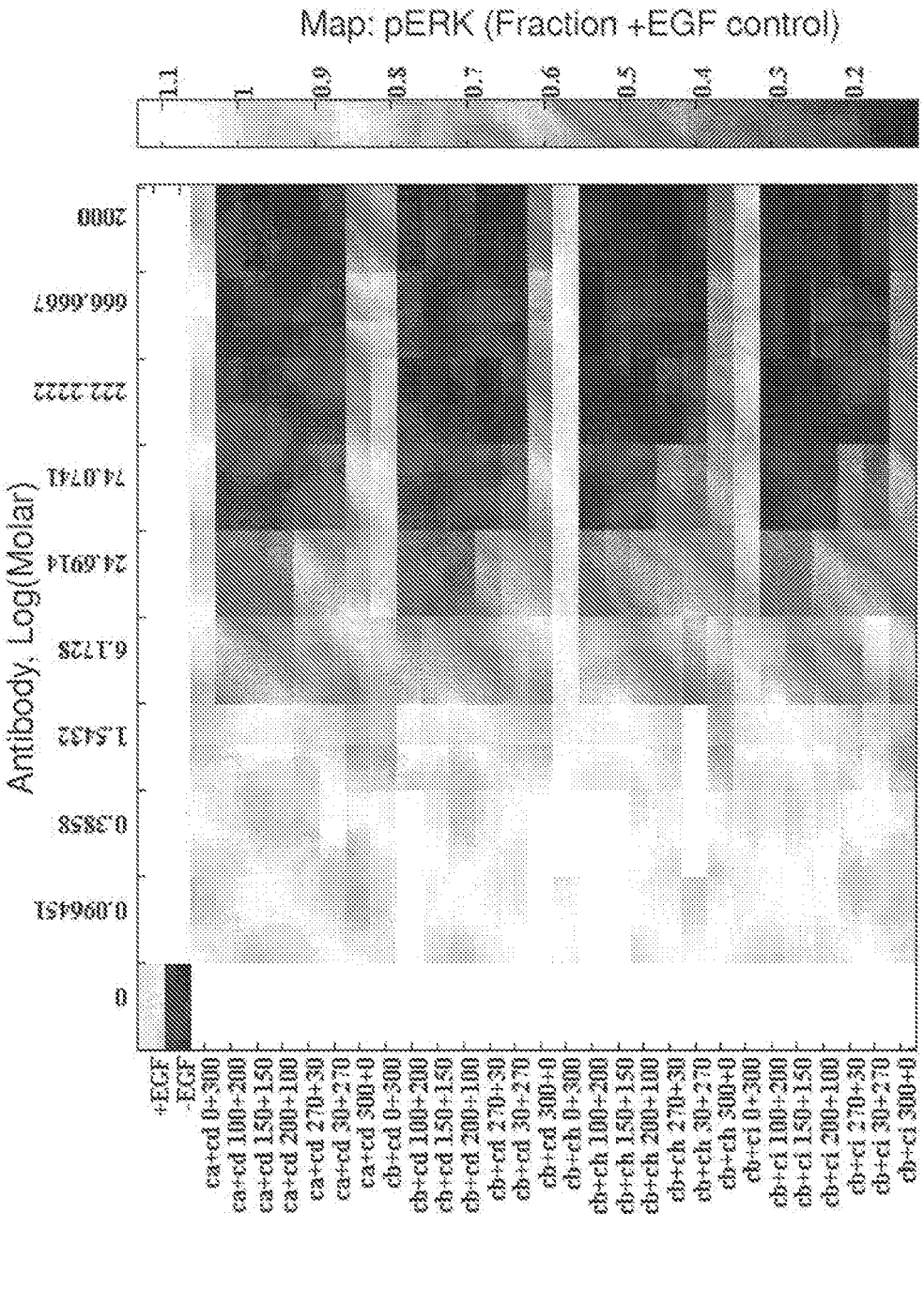

Map: pERK (Fraction +EGF control)
1.1
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
Antibody, Log(Molar)
2000
666.6667
222.2222
74.0741
24.6914
8.2305
2.7435
0.9145
0.3048
0
+EGF
-EGF
ca+cd 0+300
ca+cd 100+200
ca+cd 150+150
ca+cd 200+100
ca+cd 270+30
ca+cd 30+270
ca+cd 300+0
cb+cd 0+300
cb+cd 100+200
cb+cd 150+150
cb+cd 200+100
cb+cd 270+30
cb+cd 30+270
cb+cd 300+0
cb+ch 0+300
cb+ch 100+200
cb+ch 150+150
cb+ch 200+100
cb+ch 270+30
cb+ch 30+270
cb+ch 300+0
cb+ci 0+300
cb+ci 100+200
cb+ci 150+150
cb+ci 200+100
cb+ci 270+30
cb+ci 30+270
cb+ci 300+0

Figure 21

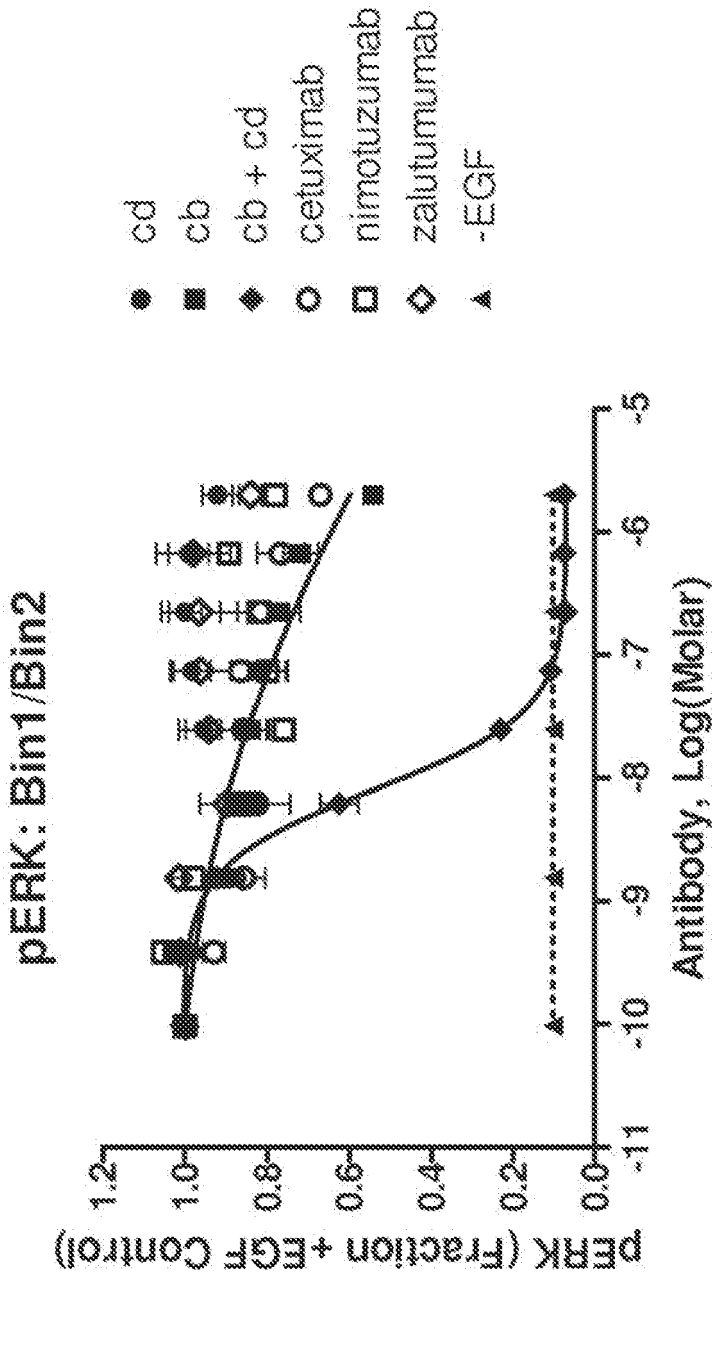

cd
cb
cb + cd
cetuximab
nimotuzumab
zalutumumab
-EGF
pERK: Bin1/Bin2
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)

Figure 22A

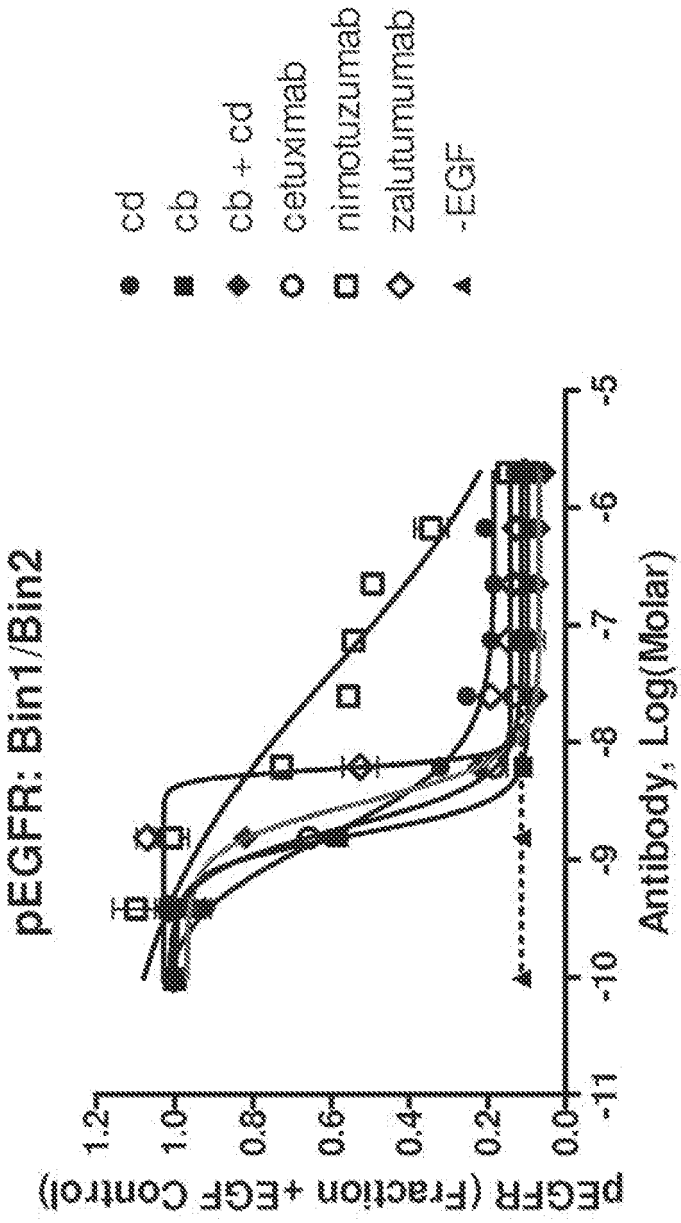

pEGFR: Bin1/Bin2
pEGFR (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-11
-10
-9
-8
-7
-6
-5
Antibody, Log(Molar)
cd
cb
cb + cd
cetuximab
nimotuzumab
zalutumumab
-EGF

Figure 22B

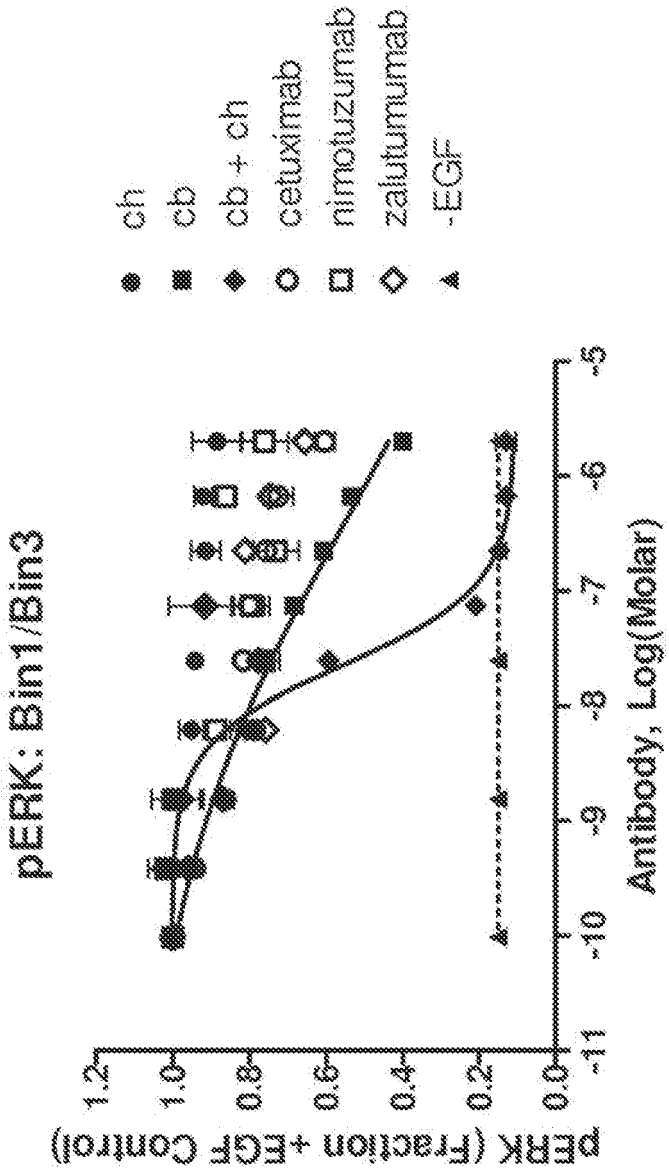

pERK: Bin1/Bin3
ch
cb
cb + ch
cetuximab
nimotuzumab
zalutumumab
-EGF
pERK (Fraction +EGF Control)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
-5
-6
-7
-8
-9
-10
-11
Antibody, Log(Molar)

Figure 22C

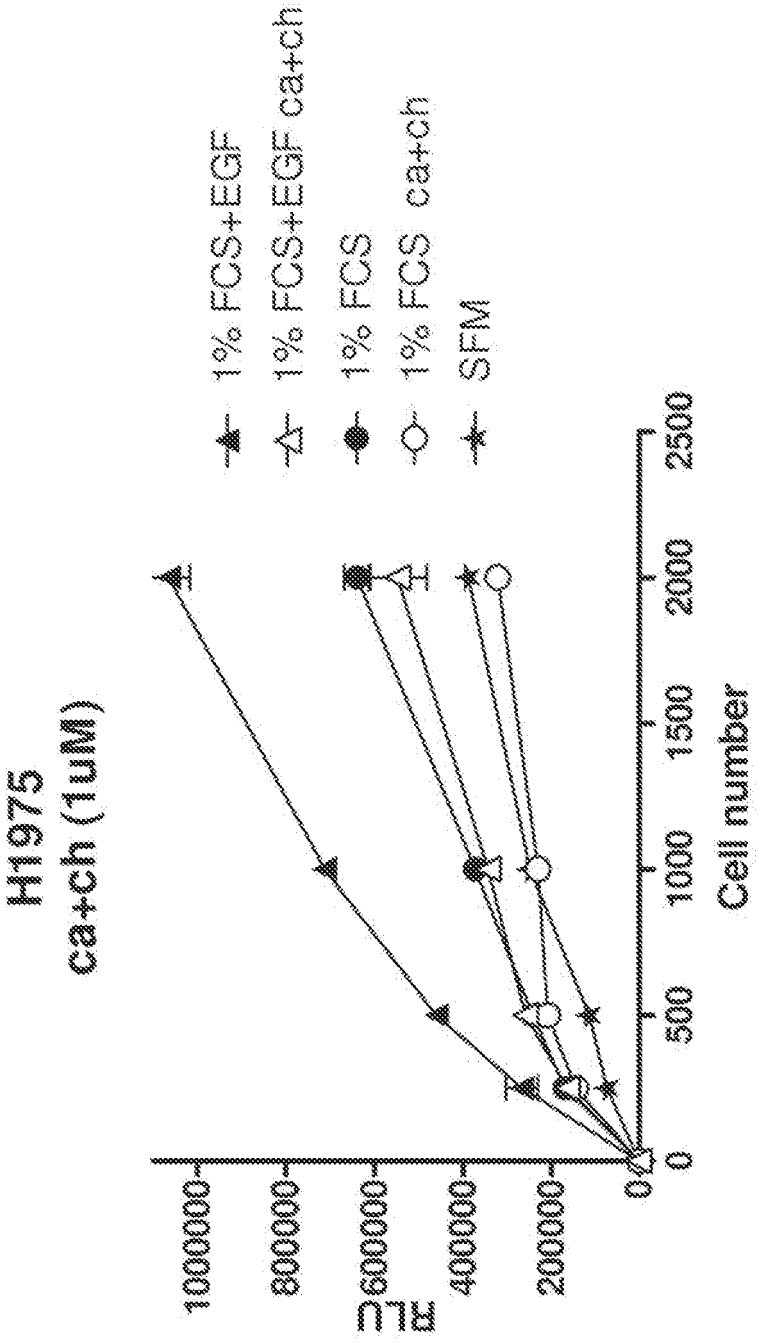

H1975
ca+ch (1uM)
1% FCS+EGF
1% FCS+EGF ca+ch
1% FCS
1% FCS ca+ch
SFM
RLU
1000000
800000
600000
400000
200000
0
0
500
1000
1500
2000
2500
Cell number

Figure 23A

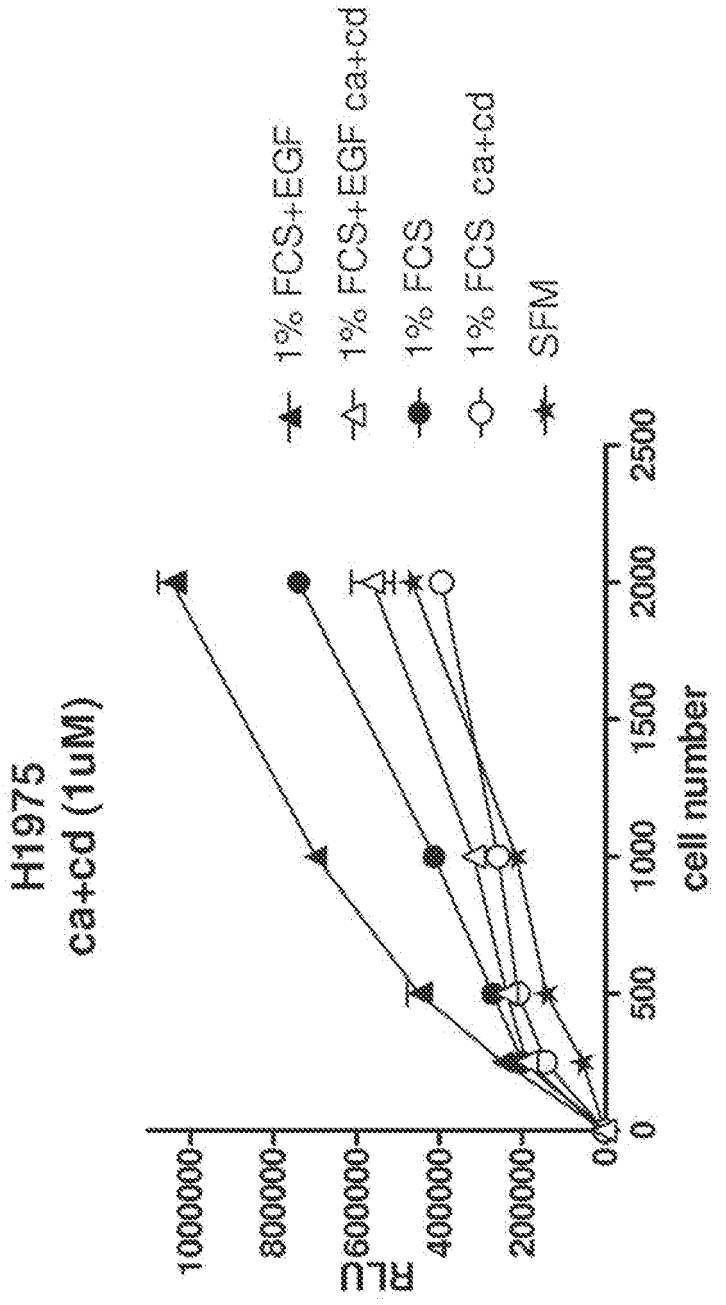

H1975
ca+cd (1uM)
1% FCS+EGF
1% FCS+EGF ca+cd
1% FCS
1% FCS ca+cd
SFM
RLU
1000000
800000
600000
400000
200000
0
0
500
1000
1500
2000
2500
cell number

Figure 23B

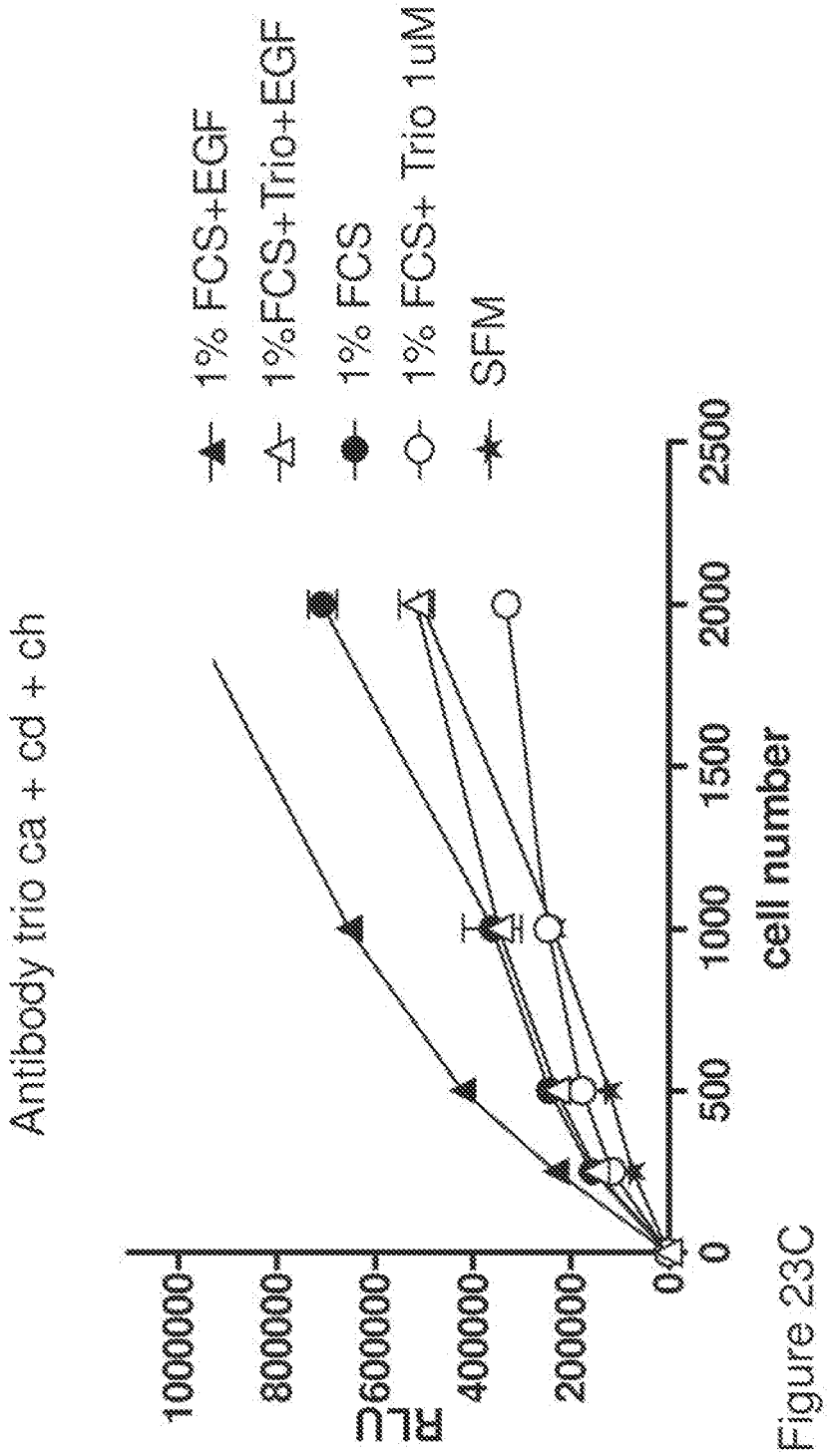

Antibody trio ca + cd + ch
1% FCS+EGF
1%FCS+Trio+EGF
1% FCS
1% FCS+ Trio 1uM
SFM
RLU
1000000
800000
600000
400000
200000
0
0
500
1000
1500
2000
2500
cell number

Figure 23C

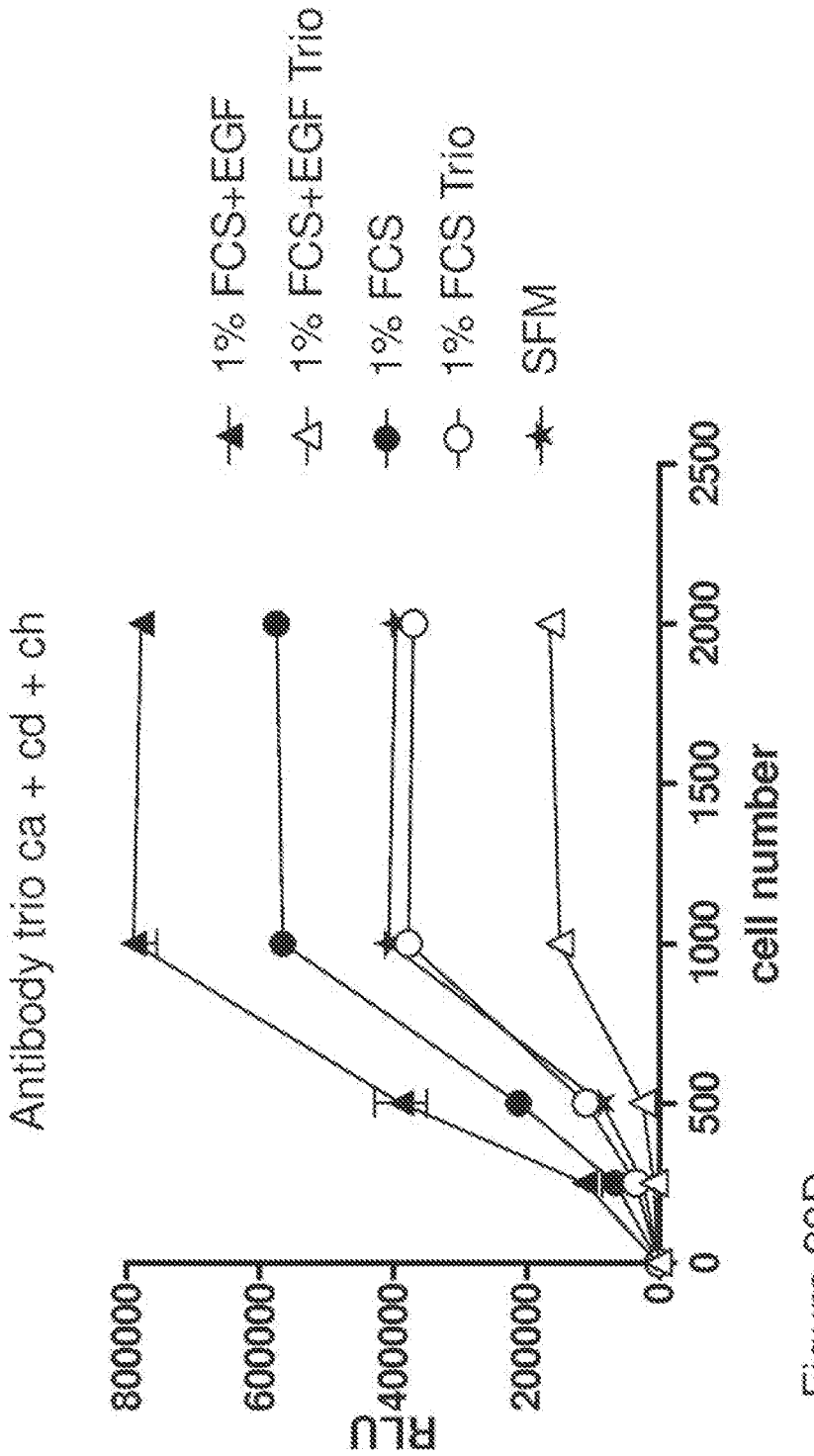

Antibody trio ca + cd + ch
1% FCS+EGF
1% FCS+EGF Trio
1% FCS
1% FCS Trio
SFM
RLU
800000
600000
400000
200000
0
0
500
1000
1500
2000
2500
cell number

Figure 23D

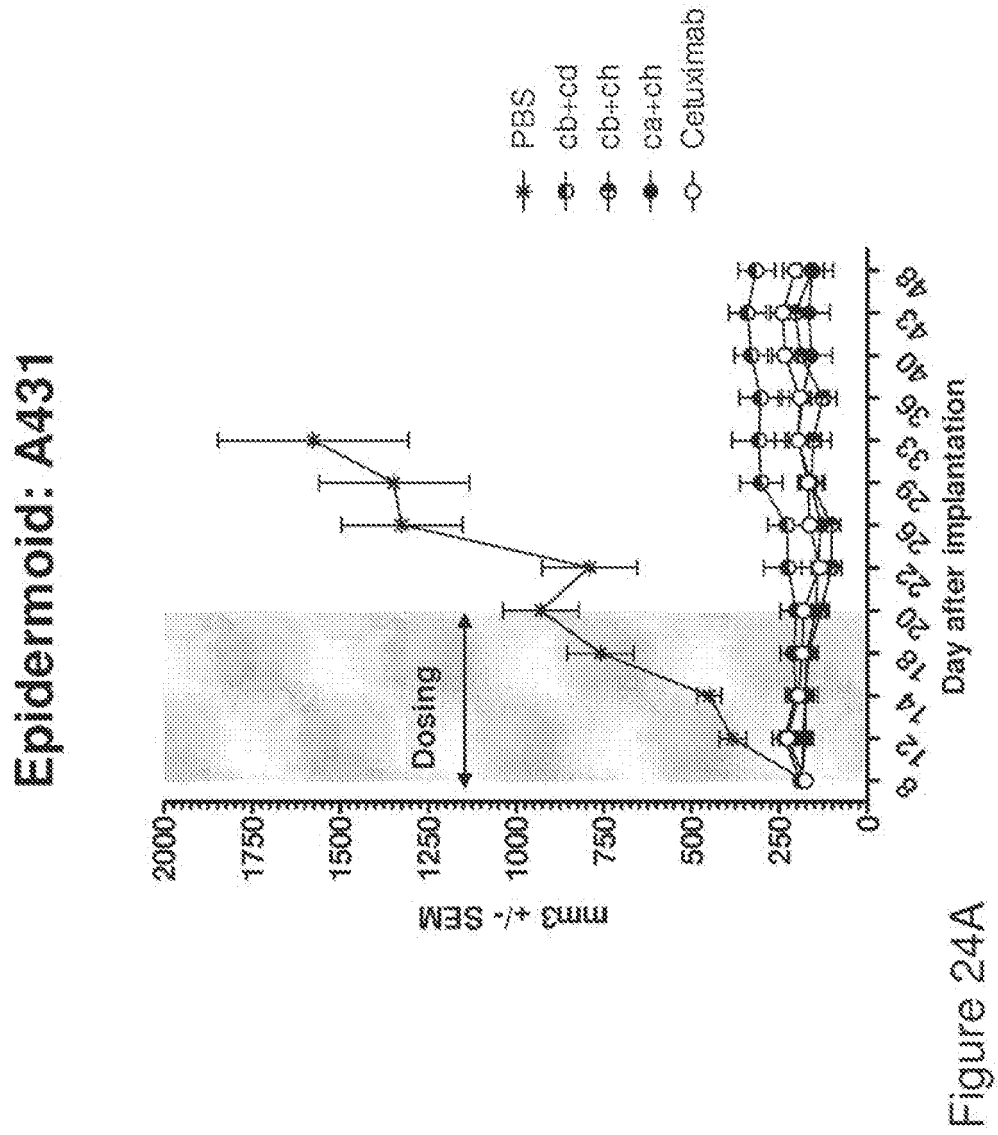

Epidermoid: A431
PBS
cb+cd
cb+ch
ca+ch
Cetuximab
Dosing
mm3 +/- SEM
2000
1750
1500
1250
1000
750
500
250
0
6 10 14 18 22 26 30 33 36 40 43 48
Day after implantation

Figure 24A

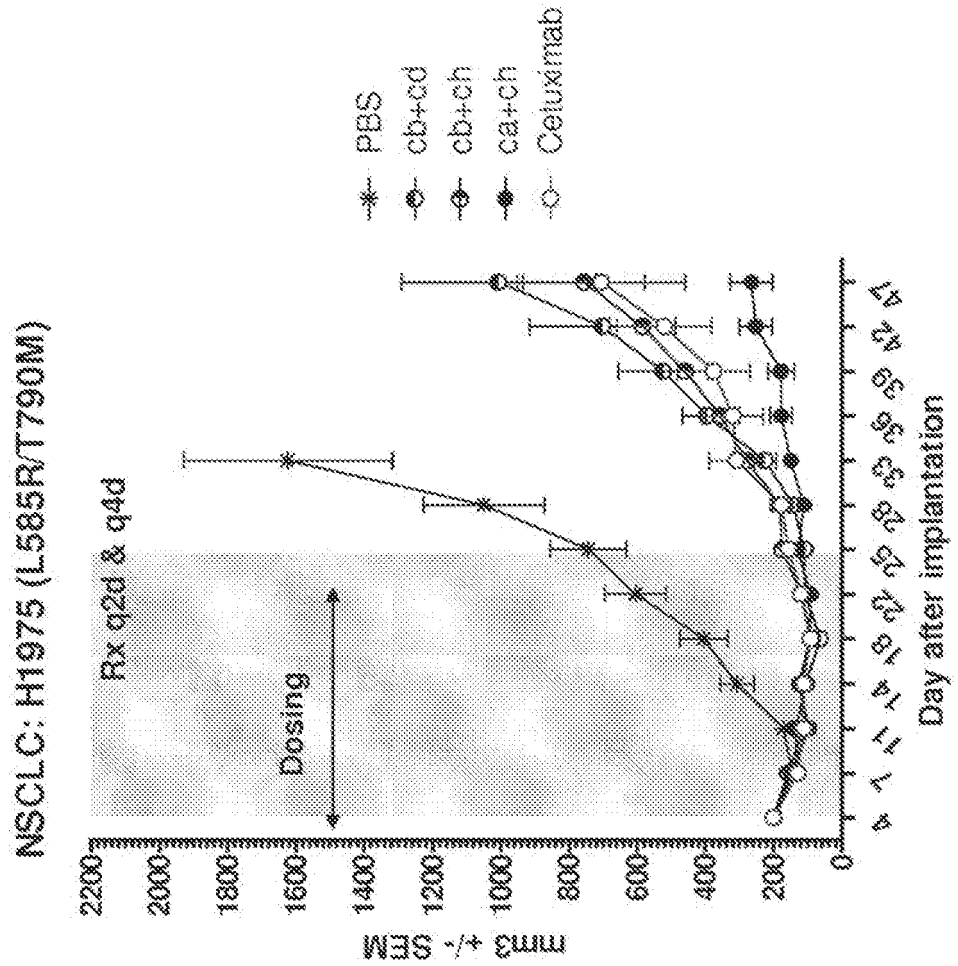

NSCLC; H1975 (L585R/T790M)
Rx q2d & q4d
Dosing
PBS
cb+cd
cb+ch
ca+ch
Cetuximab
mm3 +/- SEM
Day after implantation

Figure 24B

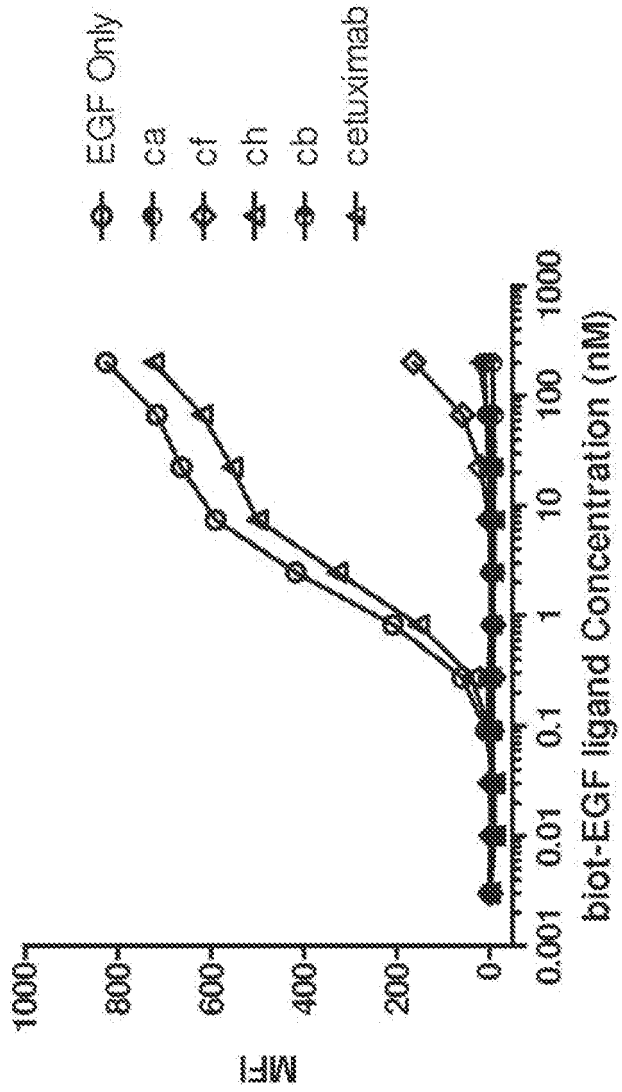

EGF Only
ca
cf
ch
cb
cetuximab
MFI
1000
800
600
400
200
0
0.001
0.01
0.1
1
10
100
1000
biot-EGF ligand Concentration (nM)

Figure 25