Figure 1

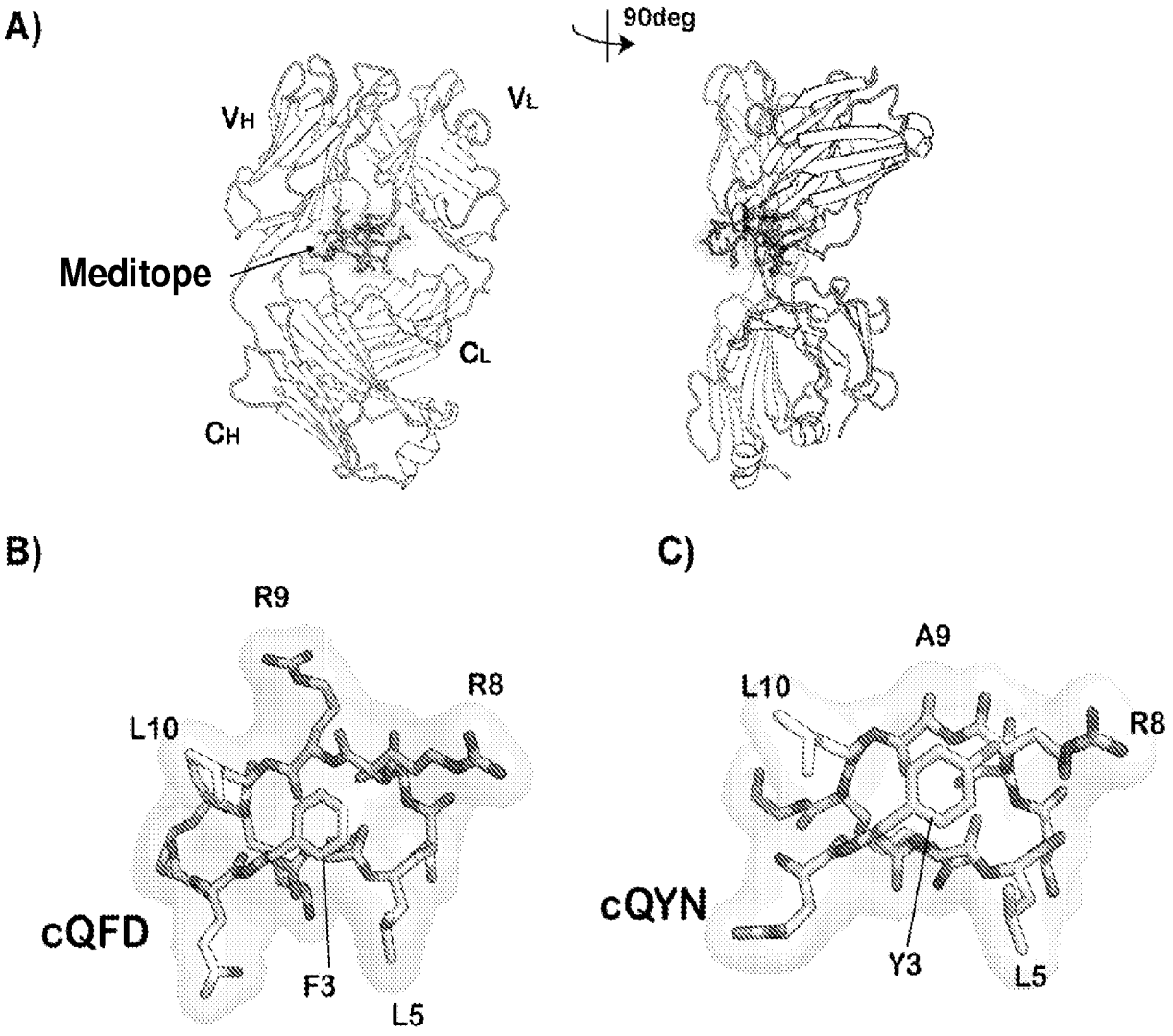

A)
90deg
VH
VL
Meditope
CL
CH
B)
R9
R8
L10
cQFD
F3
L5
C)
A9
L10
R8
cQYN
Y3
L5

Figure 2 2/34

A)

Light Chain

Kabat Number	10	38-------43	83-----87	100----105	165
cetuximab	I	QRTNGS	IADYY	AGTKLE	E
ch 14.18	S	QKPGQS	LGVYF	AGTKLE	E
trastuzumab	S	QKPGKA	FATYY	QGTKVE	E

Heavy Chain

Kabat Number	39--------44	87-89	105-108	149	168-169
cetuximab	QSPGKG	TAI	QGTL	E	PA
ch 14.18	QNIGKS	SAV	QGTS	E	PA
trastuzumab	QAPGKG	TAV	QGTL	E	PA

B)

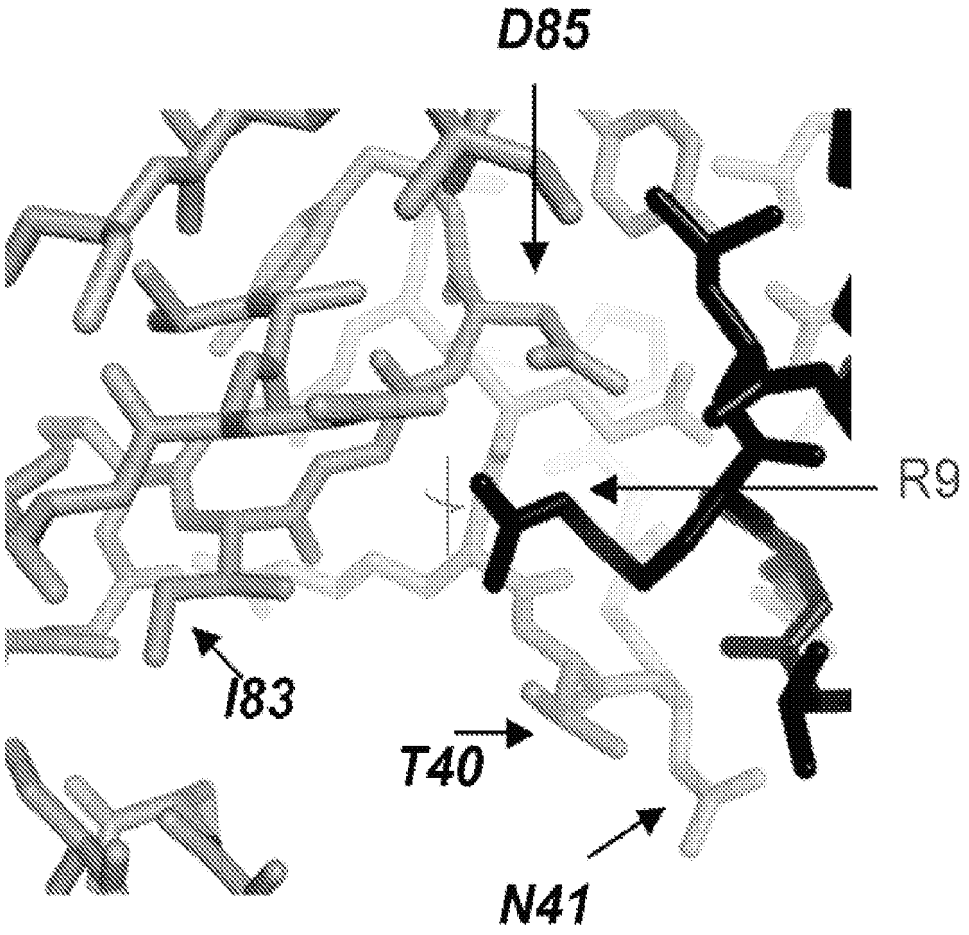


Figure 3A

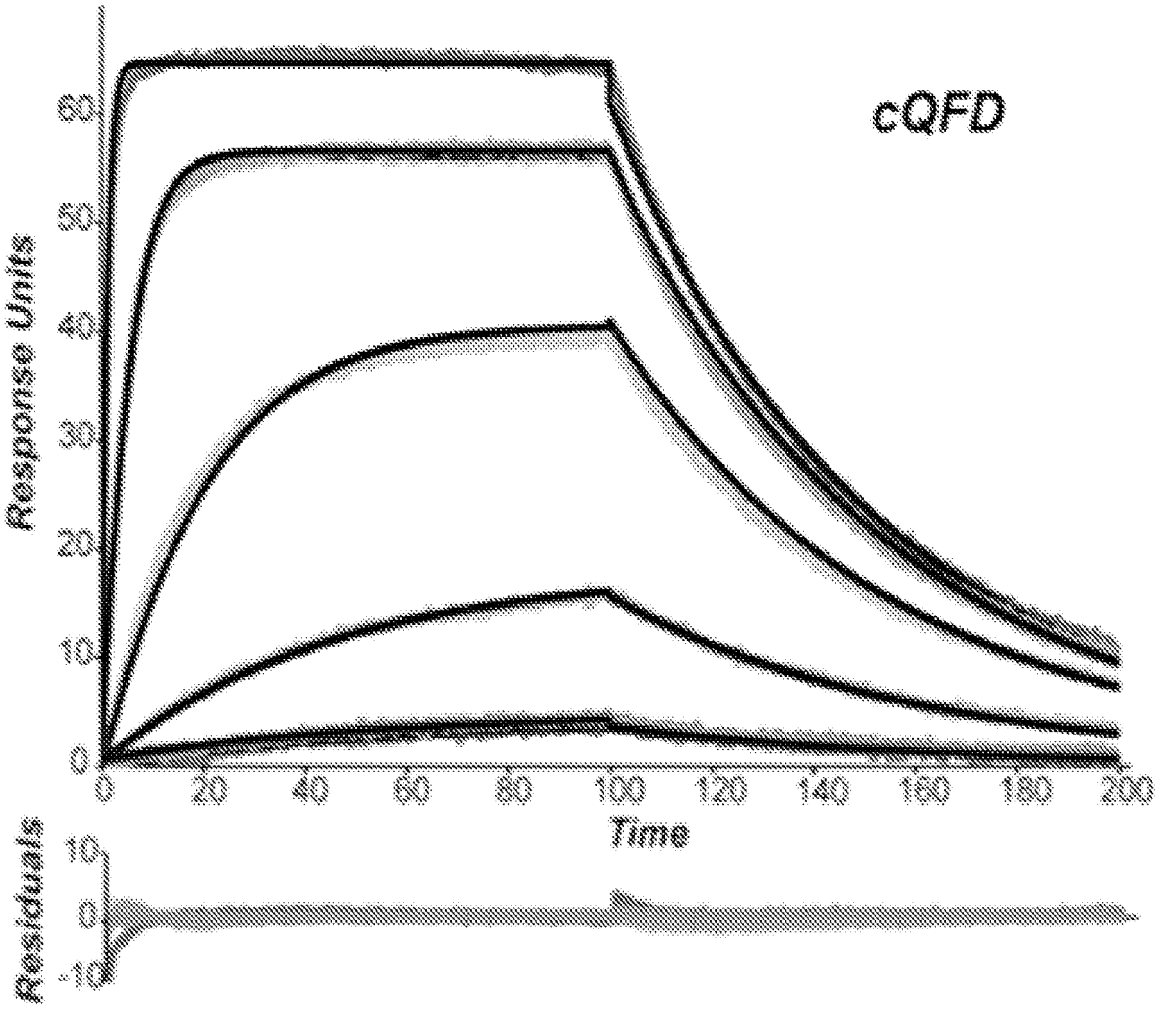

cQFD
Response Units
0
10
20
30
40
50
60
0
20
40
60
80
100
120
140
160
180
200
Time
Residuals
10
0
-10

Figure 3B

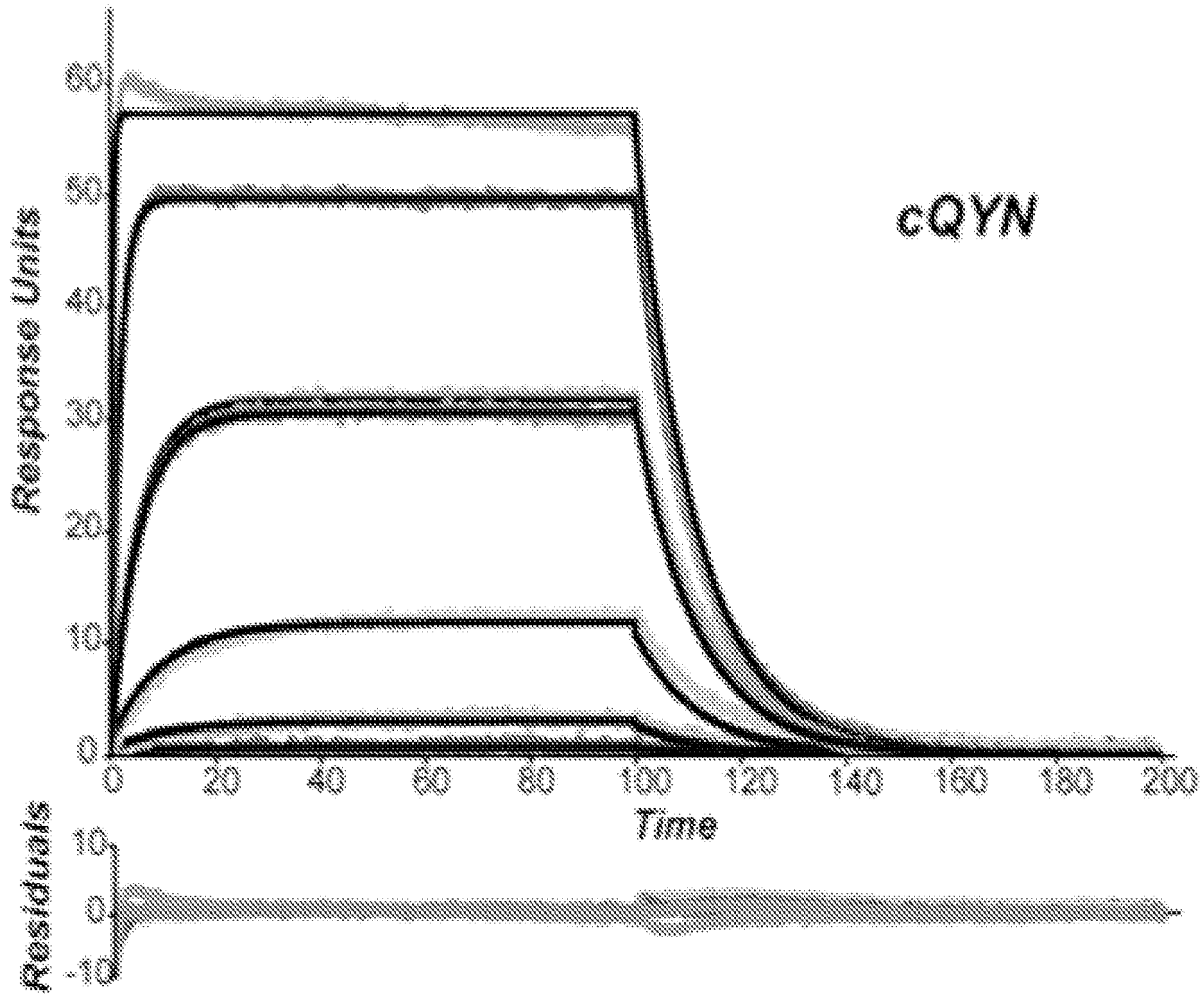

cQYN
Response Units
60
50
40
30
20
10
0
0
20
40
60
80
100
120
140
160
180
200
Time
Residuals
10
0
-10

Figure 4 A-B

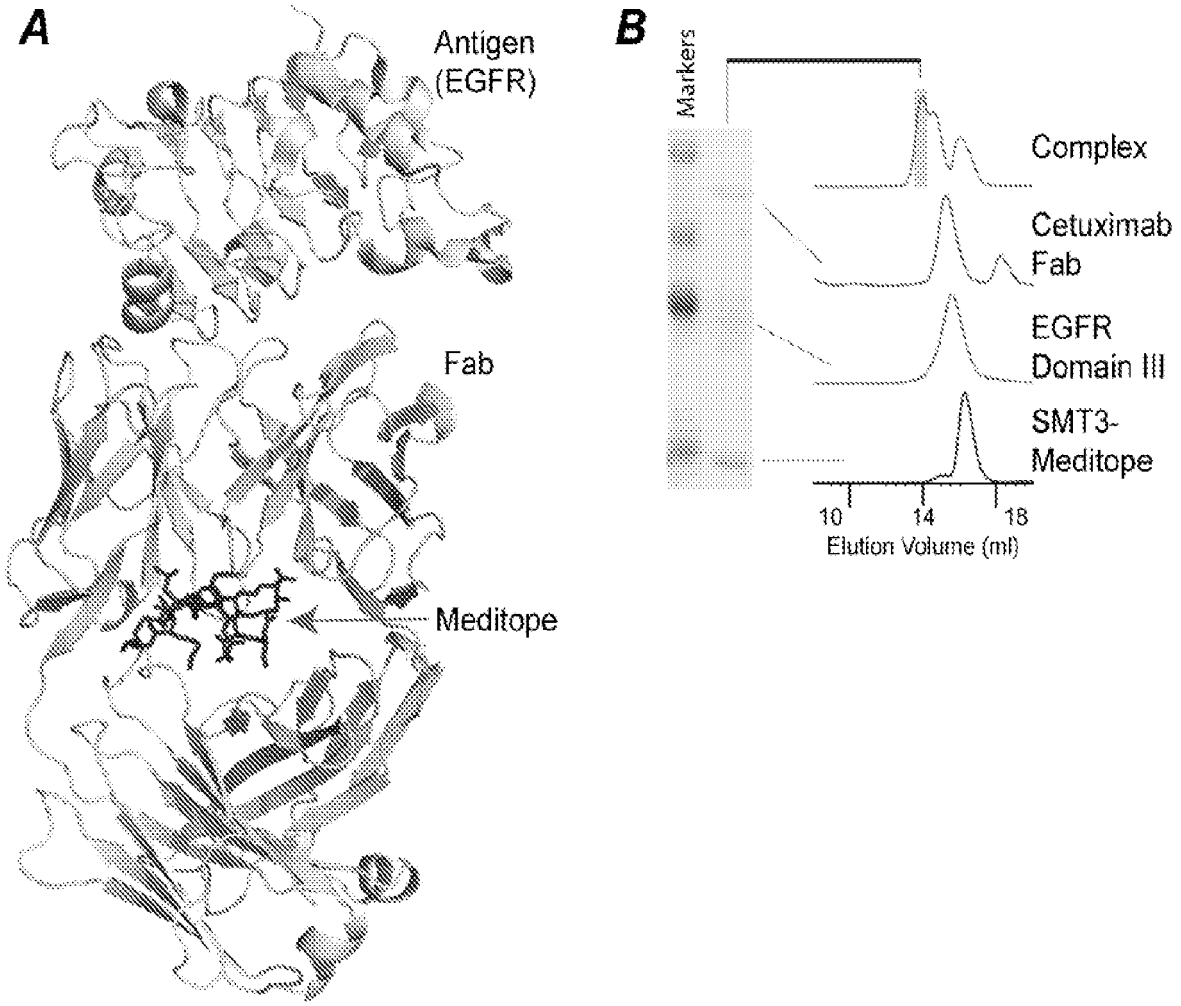

A
Antigen
(EGFR)
Fab
Meditope
B
Markers
Complex
Cetuximab
Fab
EGFR
Domain III
SMT3-
Meditope
10
14
18
Elution Volume (ml)

Figure 4C

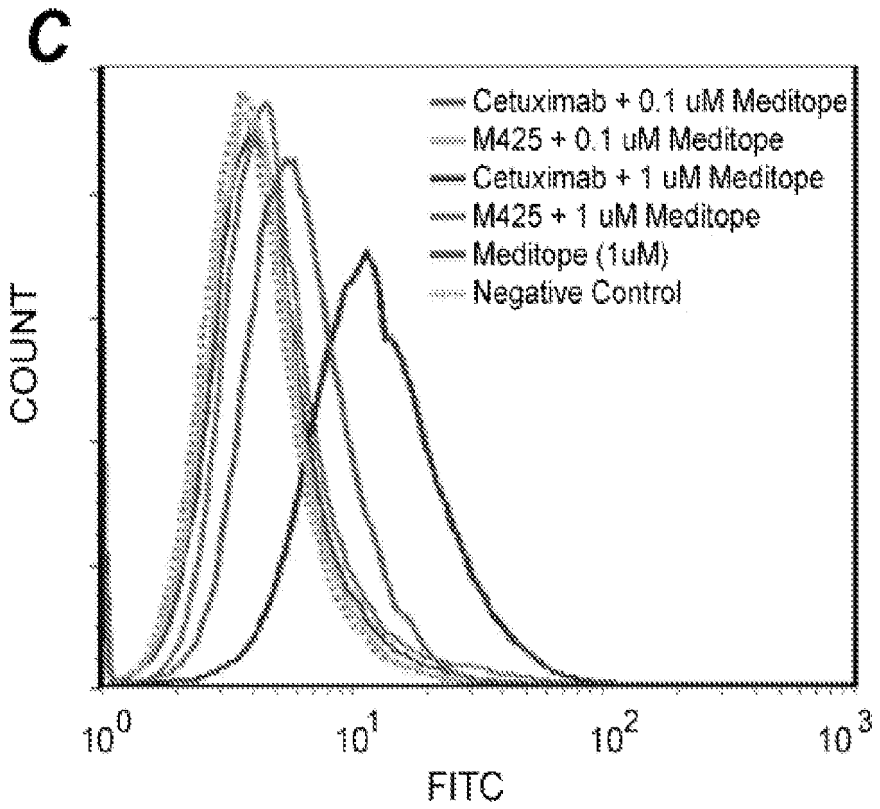

C
Cetuximab + 0.1 uM Meditope
M425 + 0.1 uM Meditope
Cetuximab + 1 uM Meditope
M425 + 1 uM Meditope
Meditope (1uM)
Negative Control
COUNT
10^0
10^1
10^2
10^3
FITC

Figure 4D

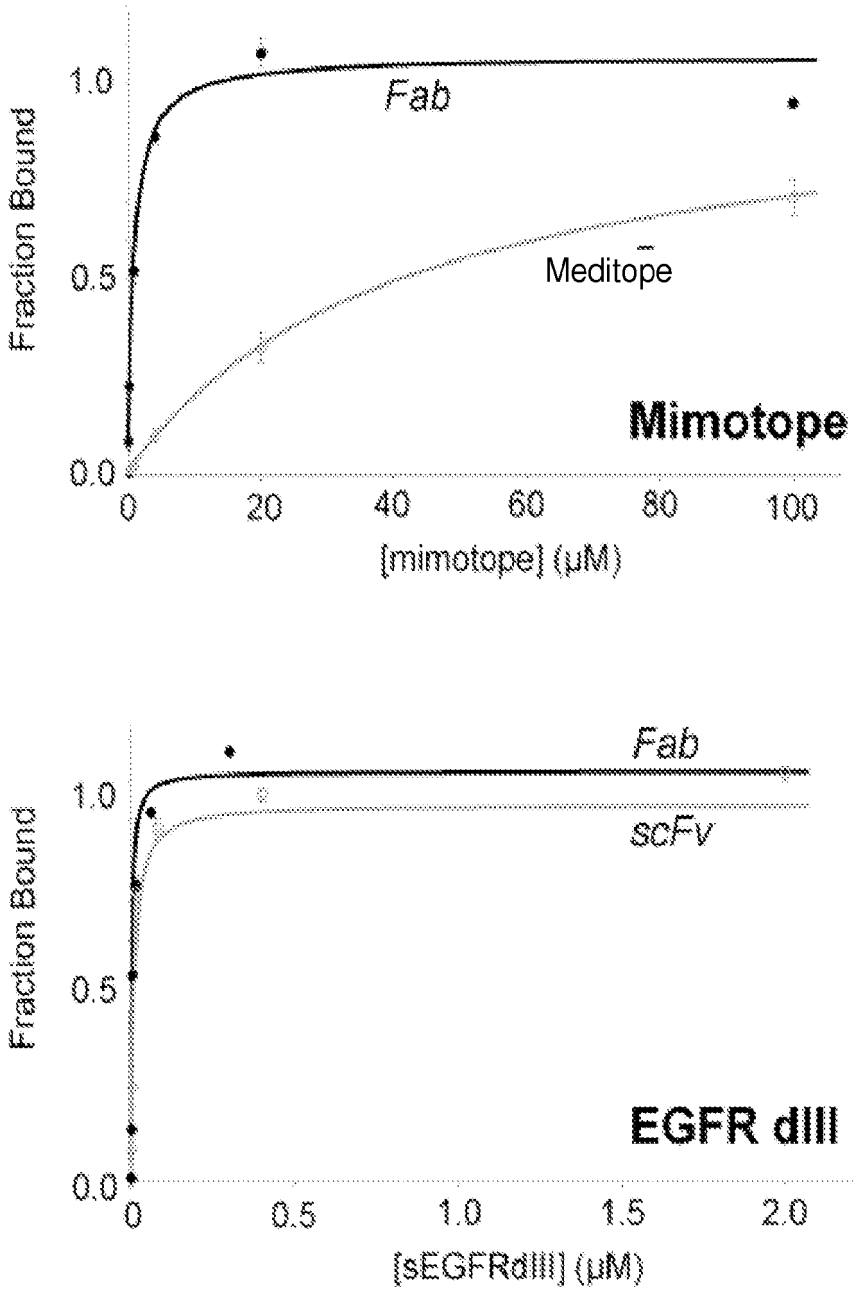

Fraction Bound
1.0
0.5
0.0
Fab
Meditope
Mimotope
0
20
40
60
80
100
[mimotope] (μM)
Fraction Bound
1.0
0.5
0.0
Fab
scFv
EGFR dIII
0
0.5
1.0
1.5
2.0
[sEGFRdIII] (μM)

Figure 5

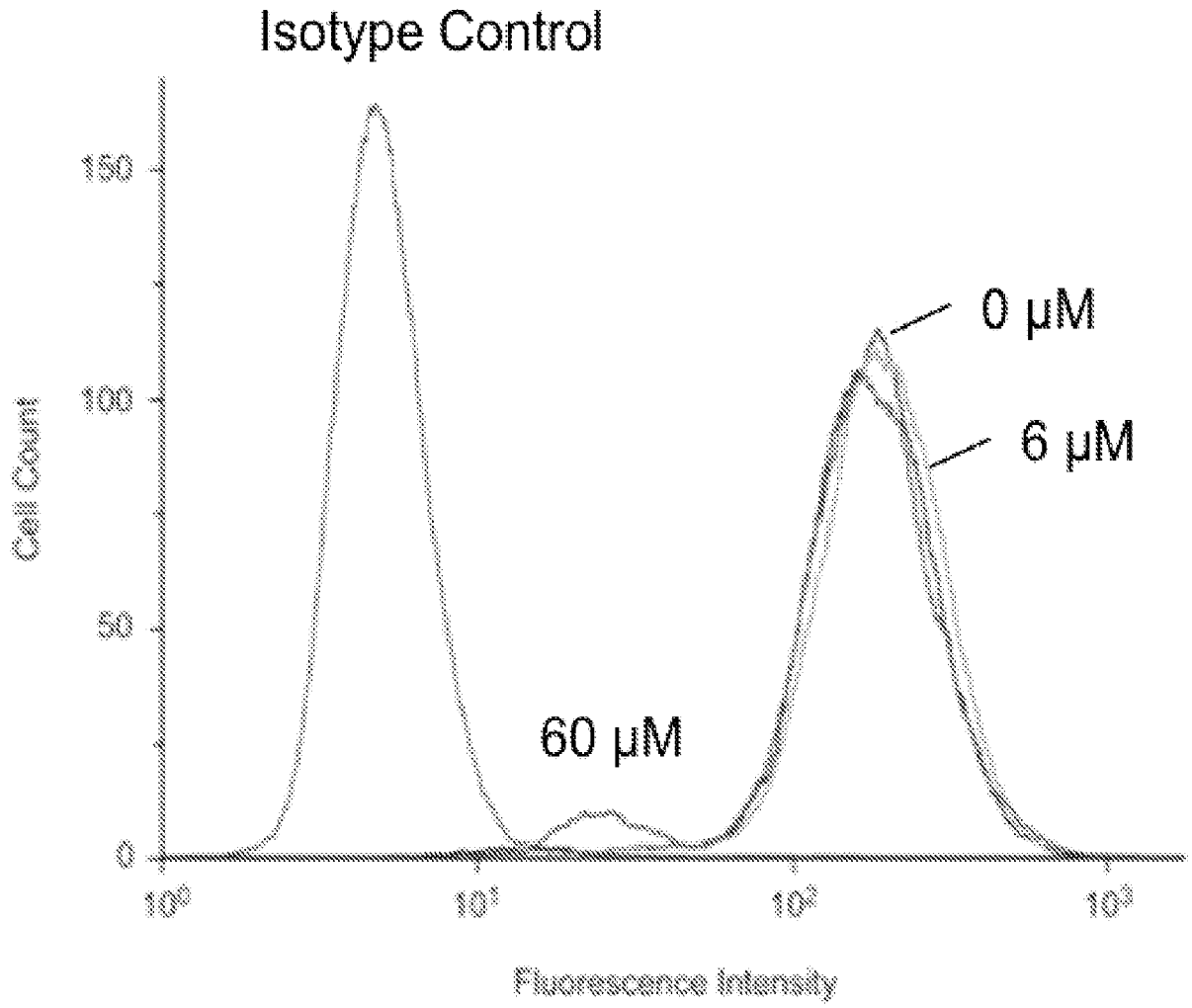

Isotype Control
150
100
50
0
Cell Count
0 µM
6 µM
60 µM
10^0
10^1
10^2
10^3
Fluorescence Intensity

Figure 6

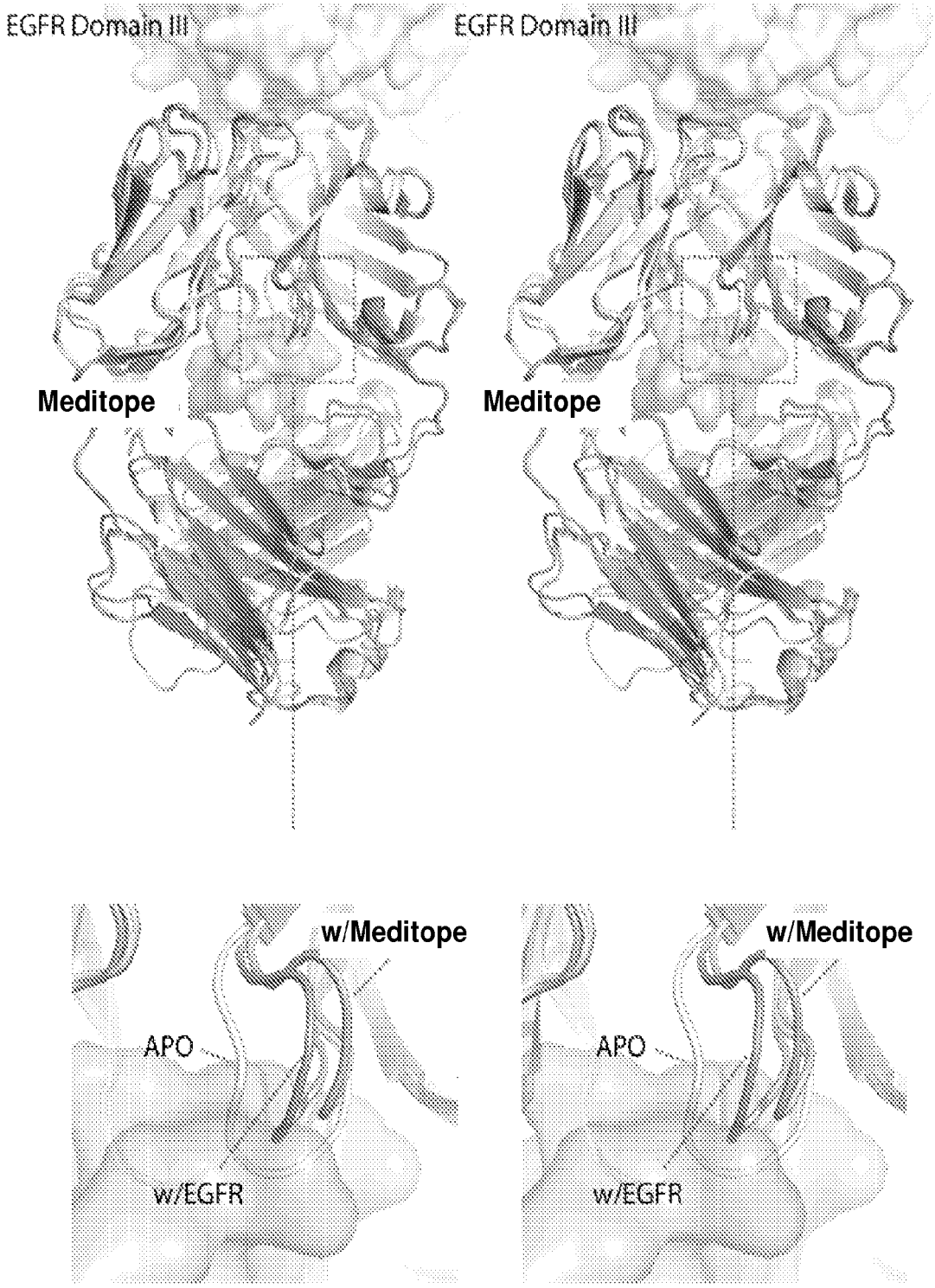

EGFR Domain III
EGFR Domain III
Meditope
Meditope
w/Meditope
APO
w/EGFR
w/Meditope
APO
w/EGFR

Figure 7

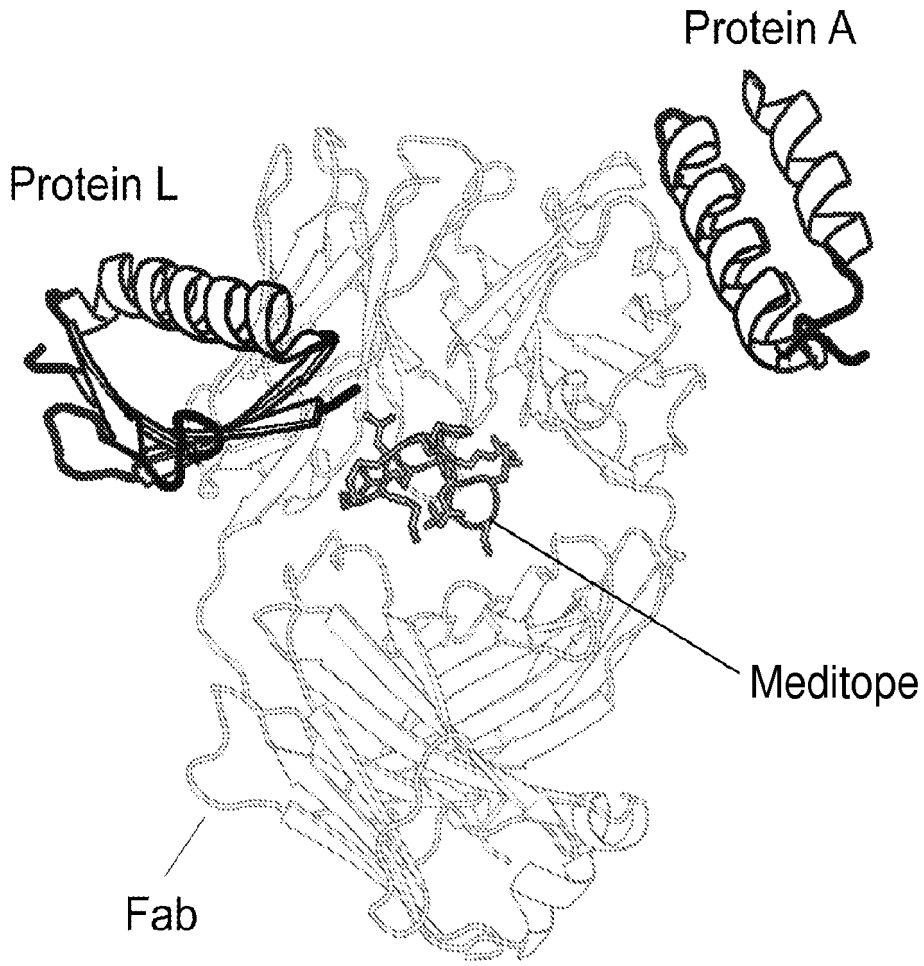


Figure 8

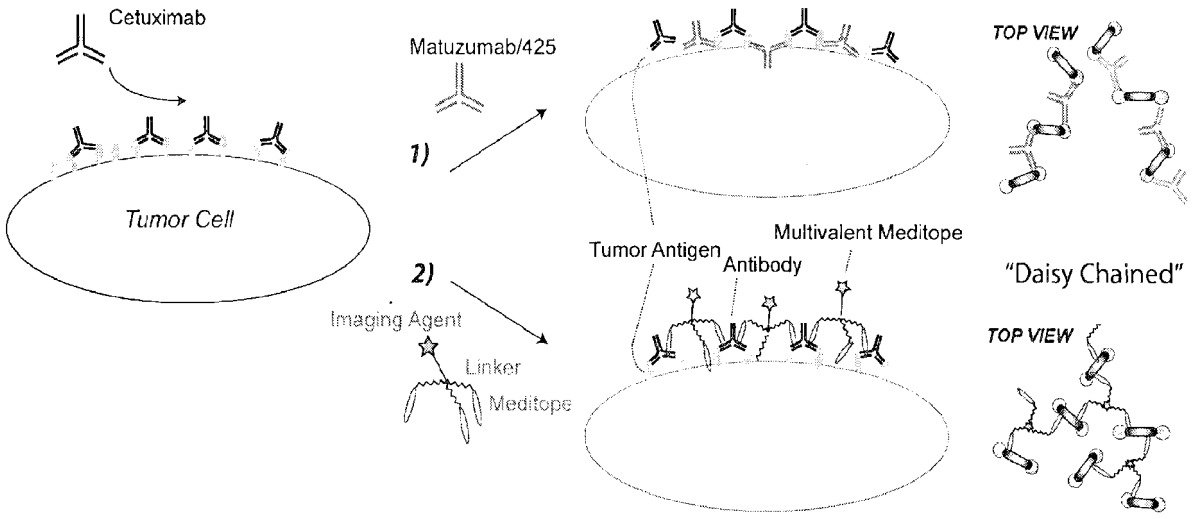

Cetuximab
Tumor Cell
Matuzumab/425
1)
2)
Imaging Agent
Linker
Meditope
Tumor Antigen
Antibody
Multivalent Meditope
TOP VIEW
"Daisy Chained"
TOP VIEW

Figure 9

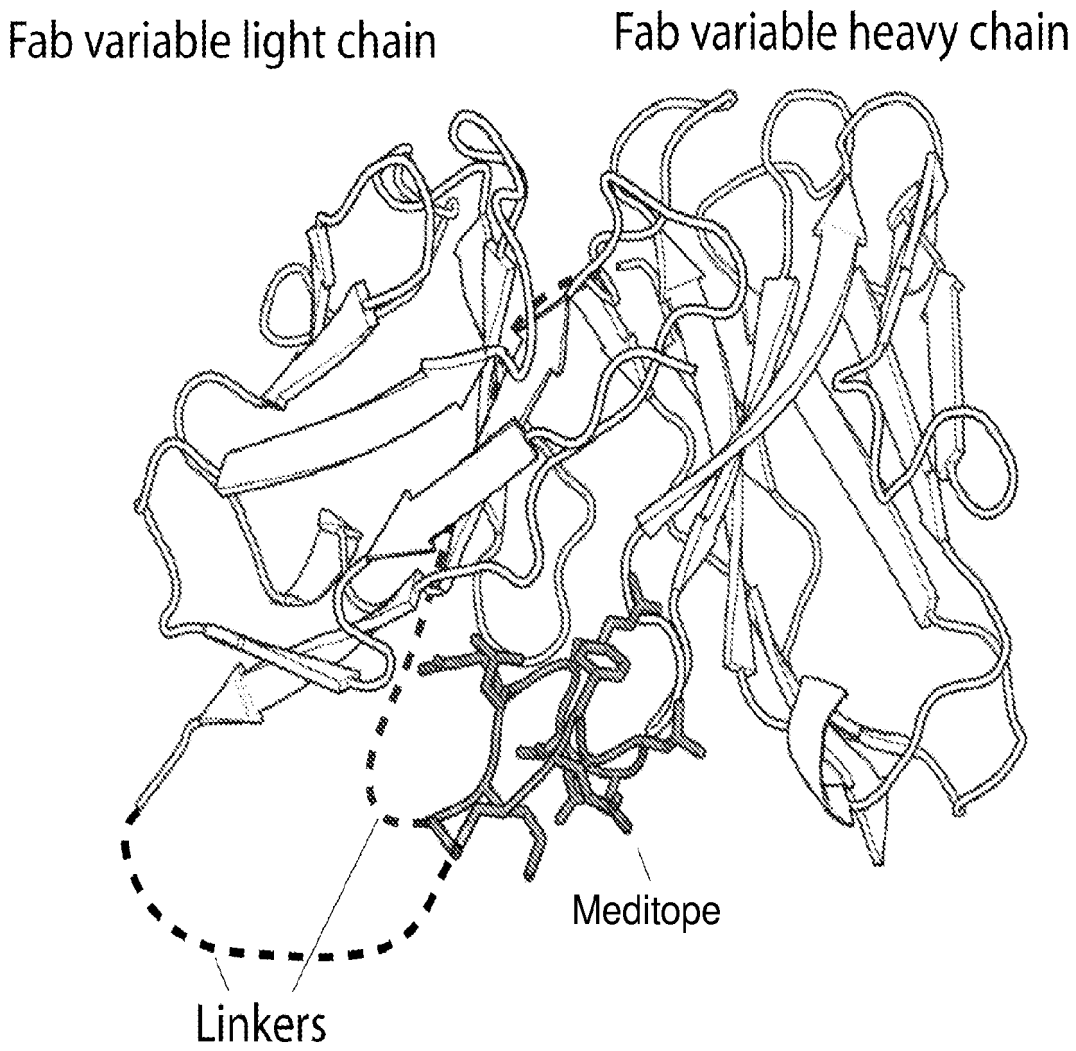

Fab variable light chain
Fab variable heavy chain
Meditope
Linkers

Figure 10

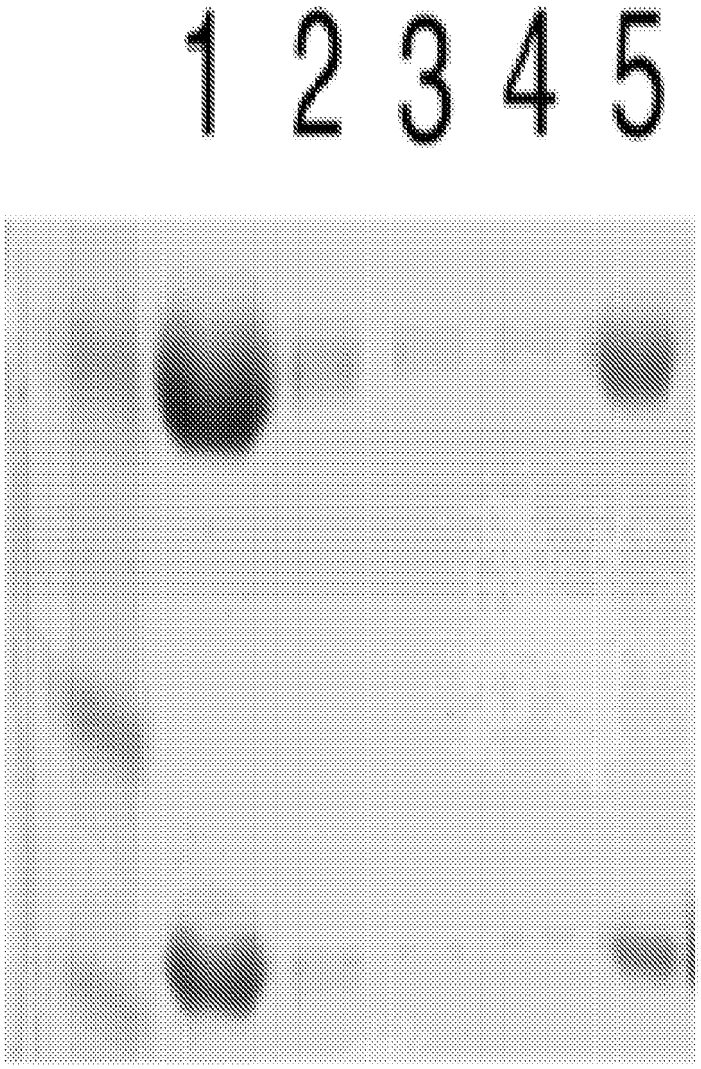


Figure 11

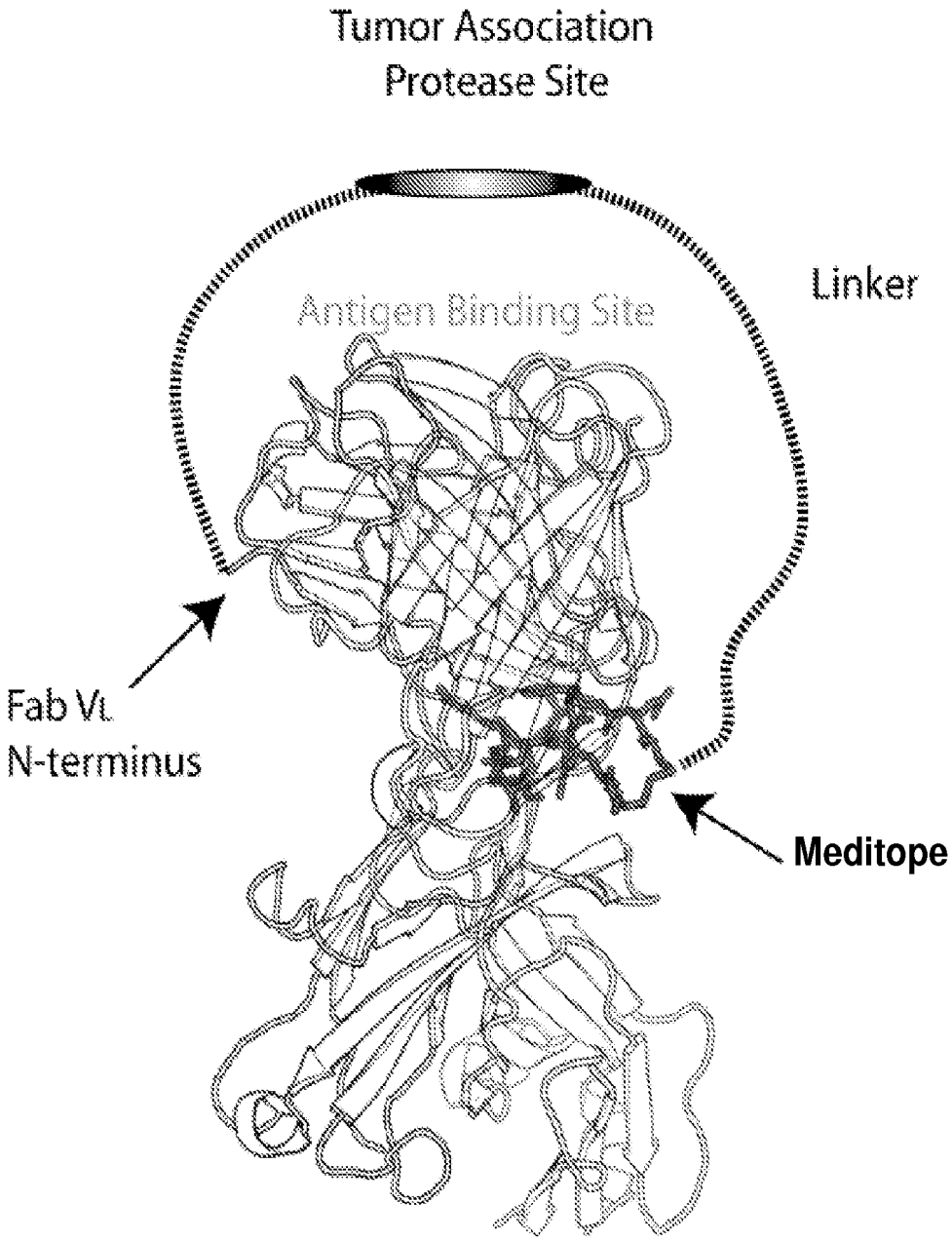

Tumor Association
Protease Site
Linker
Antigen Binding Site
Fab VL
N-terminus
Meditope

Figure 12

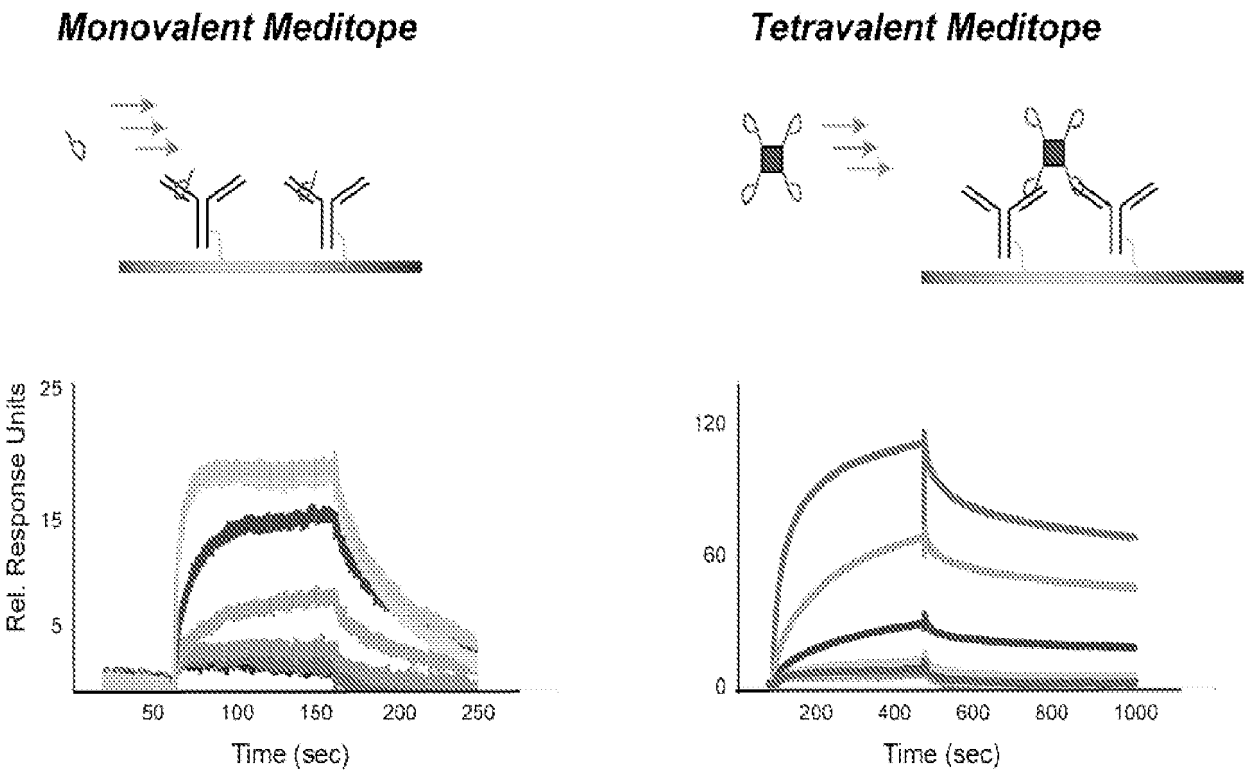

Monovalent Meditope
Tetravalent Meditope
Rel. Response Units
25
15
5
50
100
150
200
250
Time (sec)
120
60
0
200
400
600
800
1000
Time (sec)

Figure 13

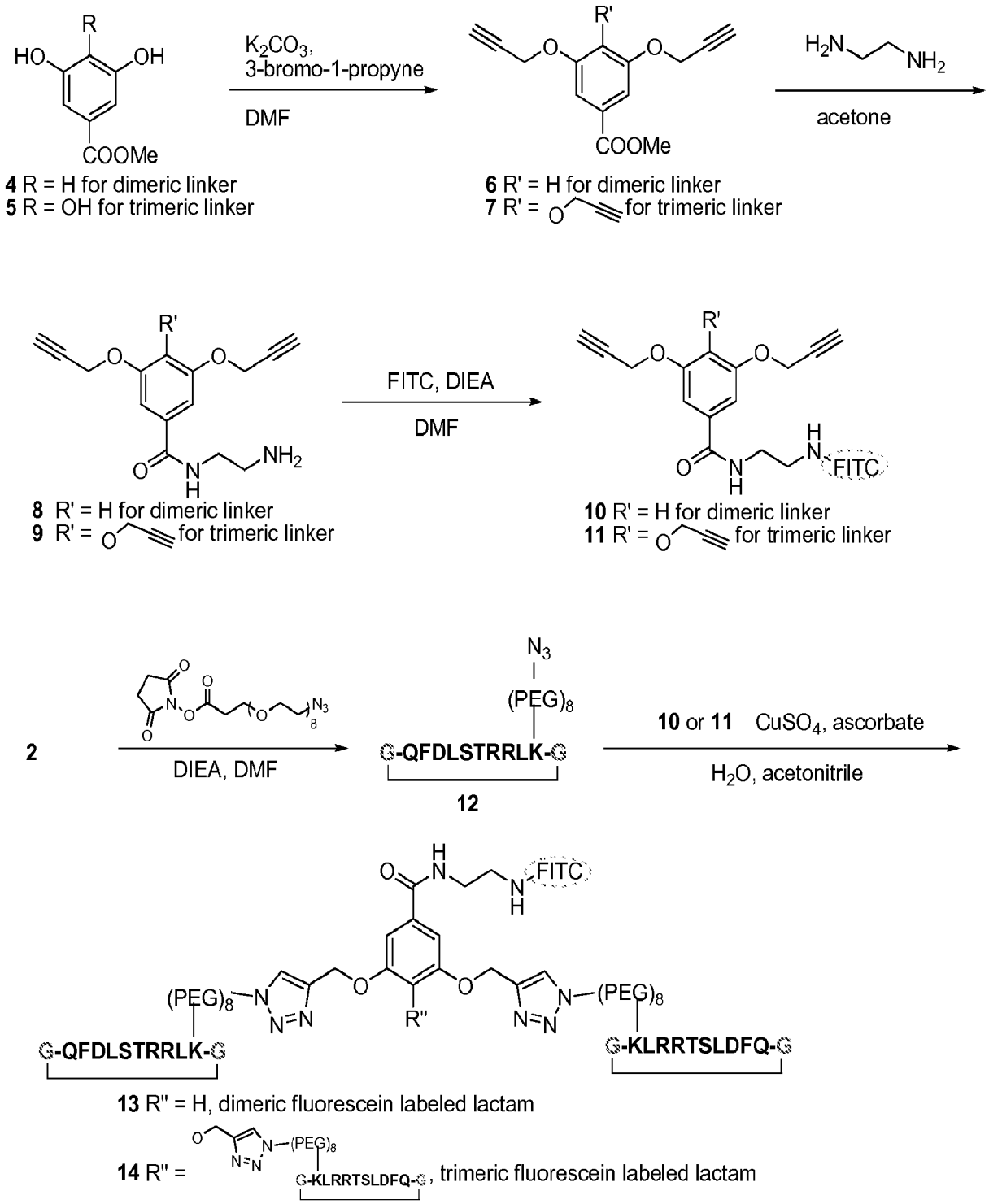
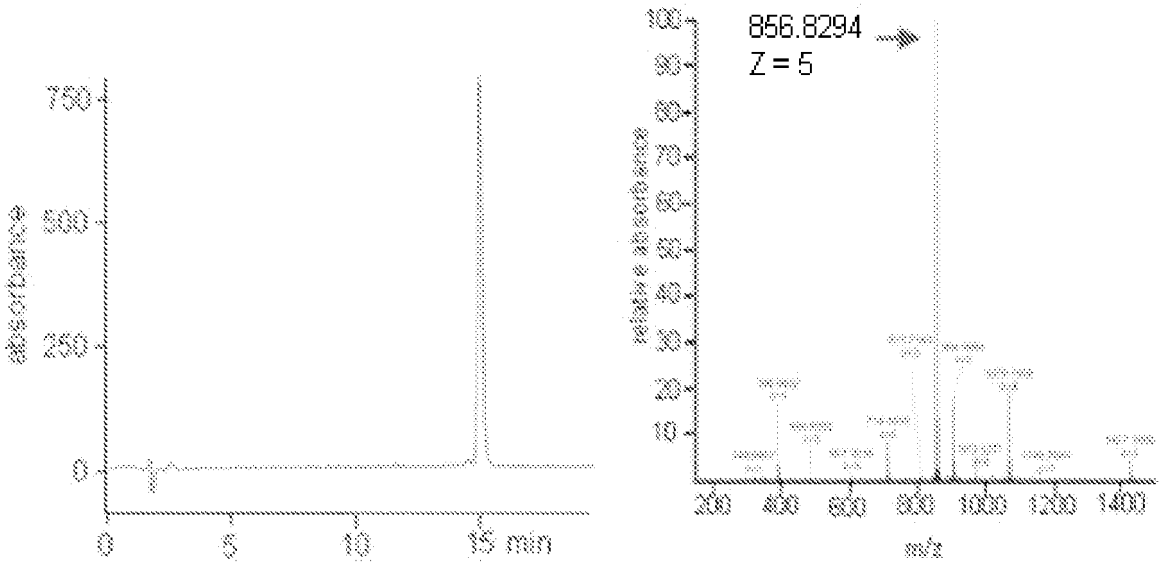
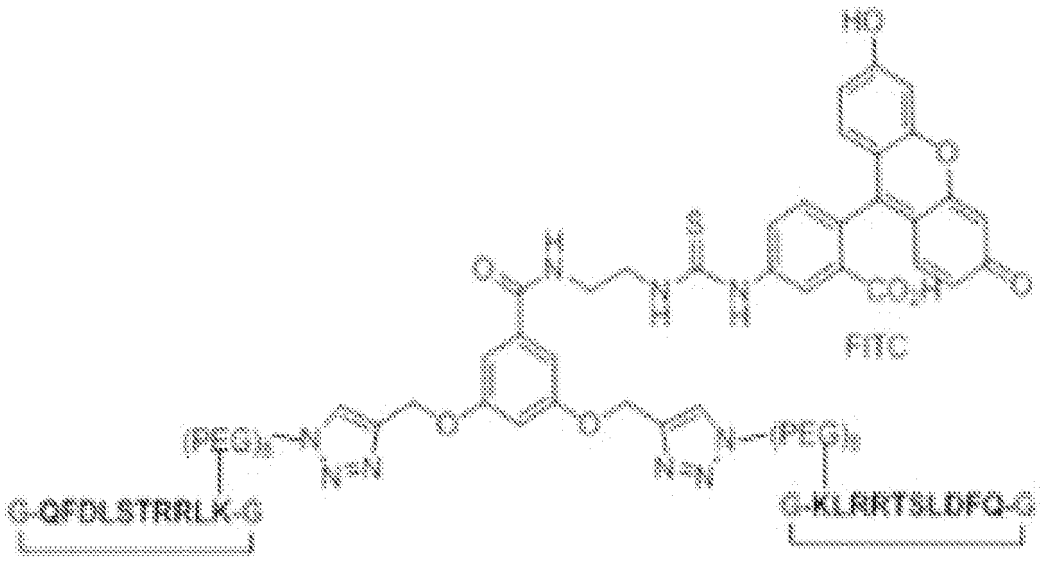

R
HO
OH
COOMe
K2CO3,
3-bromo-1-propyne
DMF
R'
O
O
COOMe
H2N
NH2
acetone
4 R = H for dimeric linker
5 R = OH for trimeric linker
6 R' = H for dimeric linker
7 R' = for trimeric linker
R'
O
O
O
N
H
NH2
FITC, DIEA
DMF
FITC
8 R' = H for dimeric linker
9 R' = for trimeric linker
10 R' = H for dimeric linker
11 R' = for trimeric linker
2
DIEA, DMF
N3
(PEG)8
G-QFDLSTRRLK-G
12
10 or 11 CuSO4, ascorbate
H2O, acetonitrile
(PEG)8
R''
G-KLRRTSLDFQ-G
13 R'' = H, dimeric fluorescein labeled lactam
14 R'' =
trimeric fluorescein labeled lactam

Figure 14





for Z = 5
Expected MW: 856.8328
Found MW: 856.8294

Figure 15

Meditope-Fc (SEQ ID NO:3 nucleic acid and SEQ ID NO: 4 amino acid)

```
acacccaagctggctagcgacaccatgaagtgtagctgggtcatcttctttctgatggca
 T  P  K  L  A  S  D  T  M  K  C  S  W  V  I  F  F  L  M  A
gtcgtgacaggagtgaattcgtgccagtttgacctgtcaactcggcgactgaaatgcggt
 V  V  T  G  V  N  S  C  Q  F  D  L  S  T  R  R  L  K  C  G
ggggggctccggttcaggctcgggcggttcatcgggaggaggggggaggggaacctaagtca
 G  G  S  G  S  G  S  G  G  S  S  G  G  G  G  G  E  P  K  S
tgcgataagacgcacacctgtcctccatgcccagcccccgagttgcttggtgggccctca
 C  D  K  T  H  T  C  P  P  C  P  A  P  E  L  L  G  G  P  S
gtattcctcttccctccaaaacccaaagacaccttgatgatttcccgcacgccggaagtc
 V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V
acgtgtgtggtcgtggatgtgagccatgaggatcccgaggtgaagttcaattggtacgtg
 T  C  V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V
gatggagtagaggtacacaacgcgaaaacgaagcccagggaggaacagtacaattccaca
 D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q  Y  N  S  T
tatcgcgtggtgtccgtgcttactgtgttgcatcaagactggctgaatgggaaggagtat
 Y  R  V  V  S  V  L  T  V  L  H  Q  D  W  L  N  G  K  E  Y
aagtgcaaagtatcaaacaaggcgctgcctgctccaatcgaaaagaccatctcgaaggcg
 K  C  K  V  S  N  K  A  L  P  A  P  I  E  K  T  I  S  K  A
aaaggacaacccagagaaccccaagtctacacgcttccgcccctcgcgggatgagctcacc
 K  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  T
aaaaaccaggtatccctcacttgtttggtaaaaggattctacccgtcggacattgcagtc
 K  N  Q  V  S  L  T  C  L  V  K  G  F  Y  P  S  D  I  A  V
gagtgggagtcgaatgggcagccggaaaacaactacaaaacaacaccgcccgtcttggac
 E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P  V  L  D
tccgatggttcgttctttctctattcgaagctcaccgtagacaagtcgaggtggcagcag
 S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R  W  Q  Q
ggcaacgtcttttcgtgctcagtgatgcatgaggcccttcacaatcactatacgcagaaa
 G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y  T  Q  K
agcctgagcctgtcaccggggaagtaa
 S  L  S  L  S  P  G  K  -
```

Figure 16

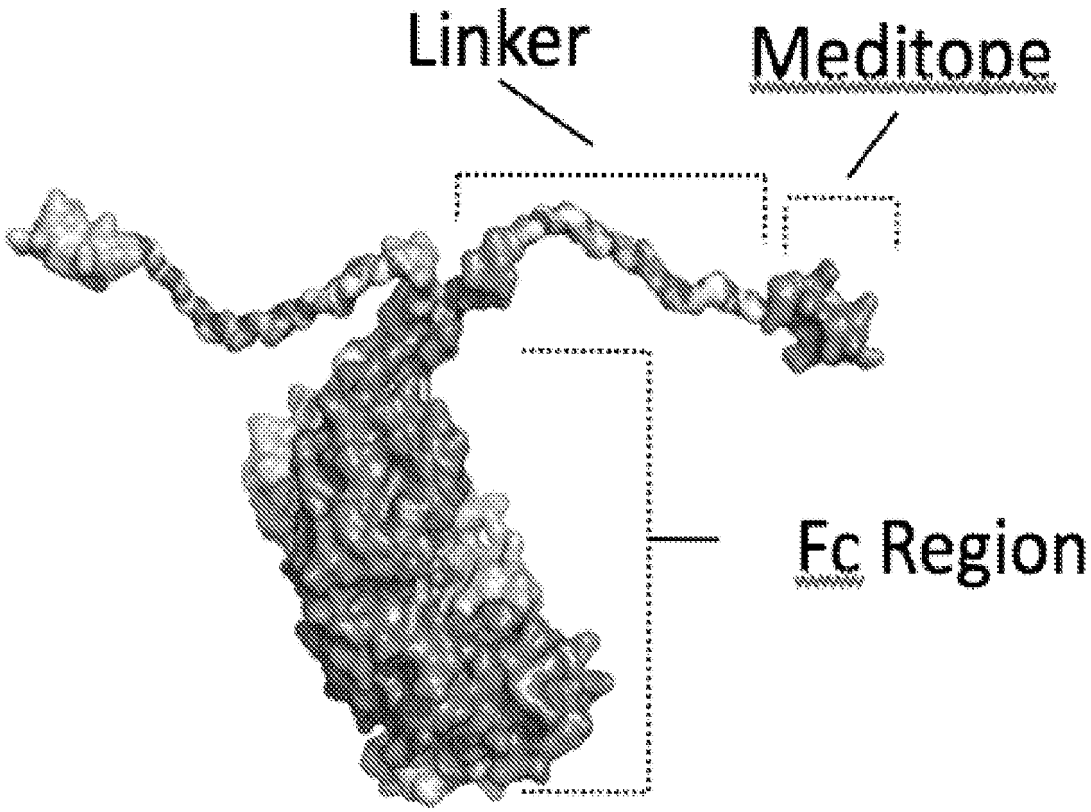


Figure 17

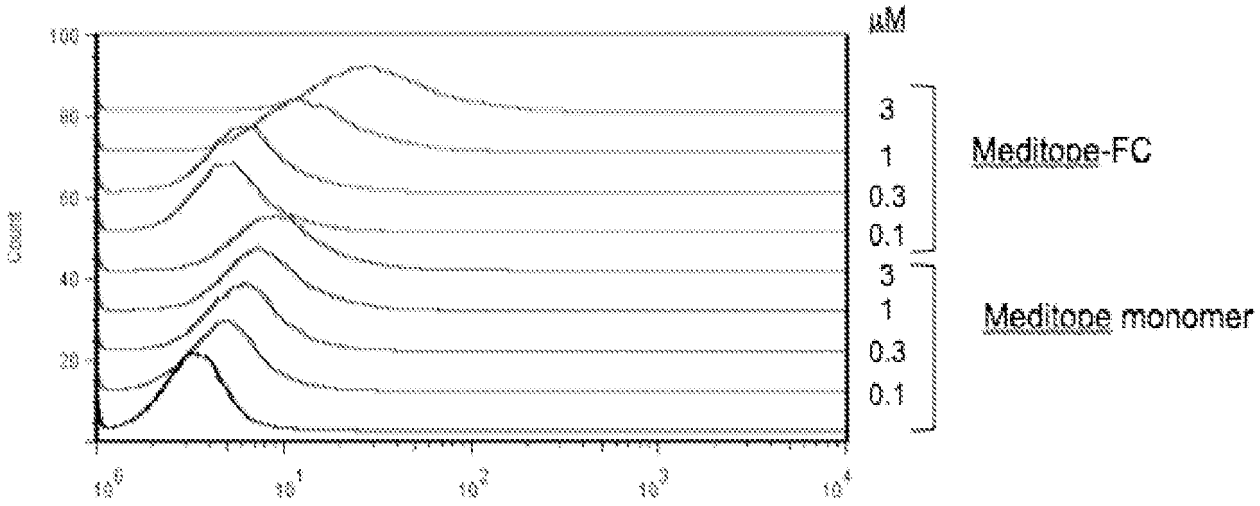


Figure 18

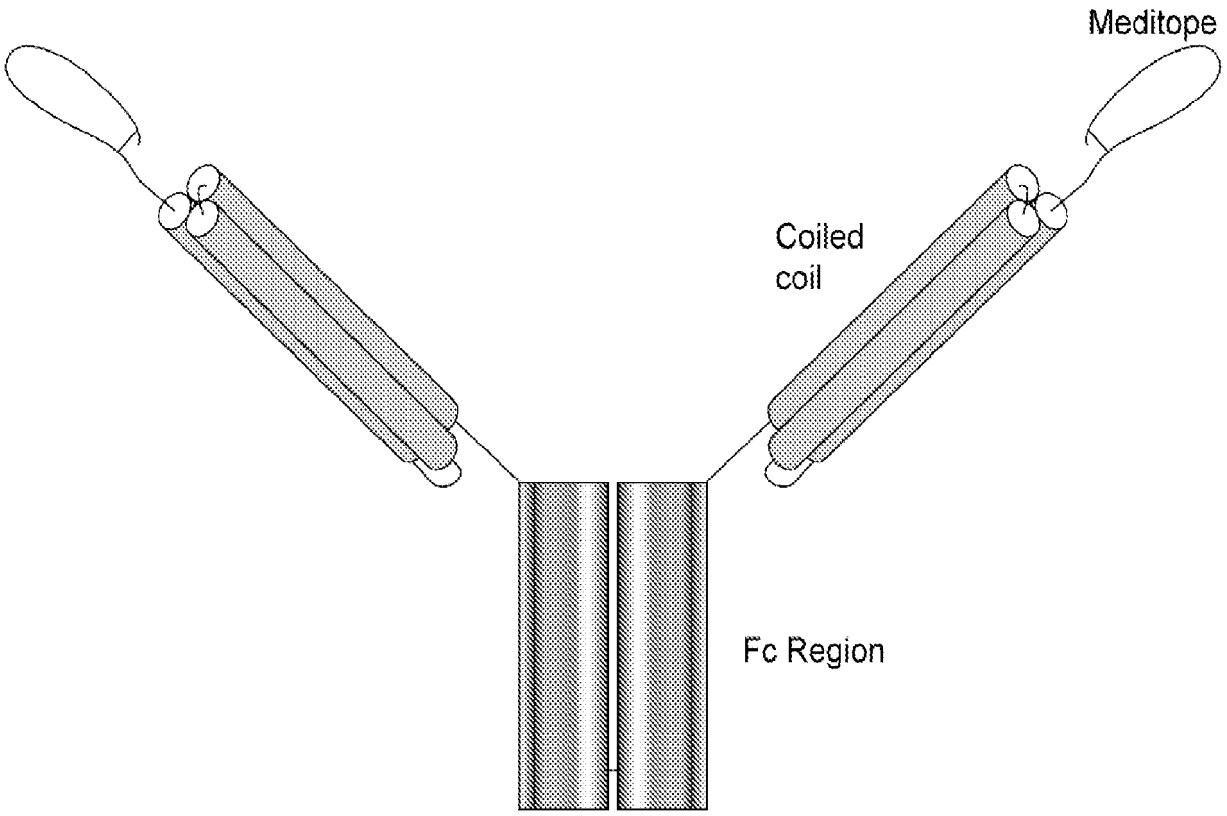
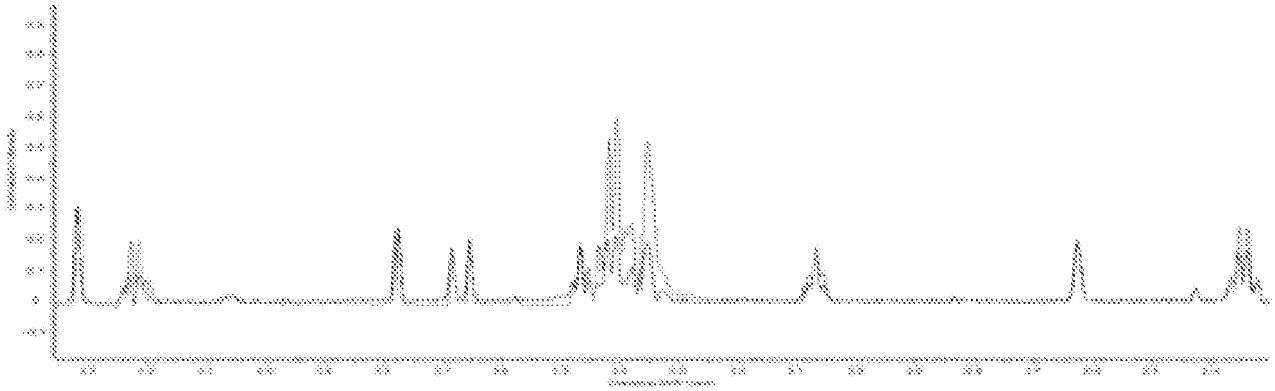
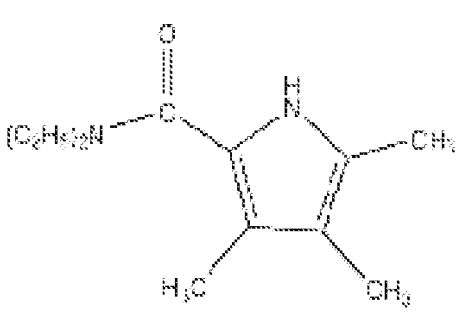
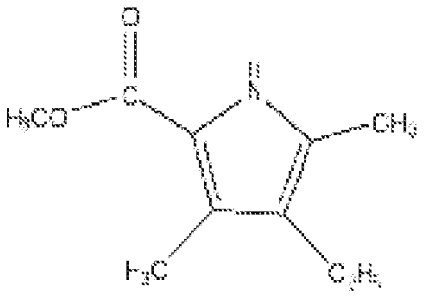


Figure 19







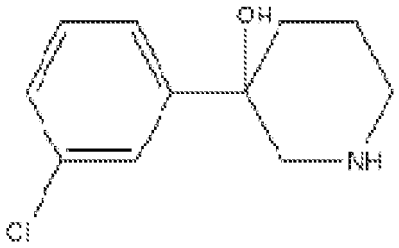


Figure 20

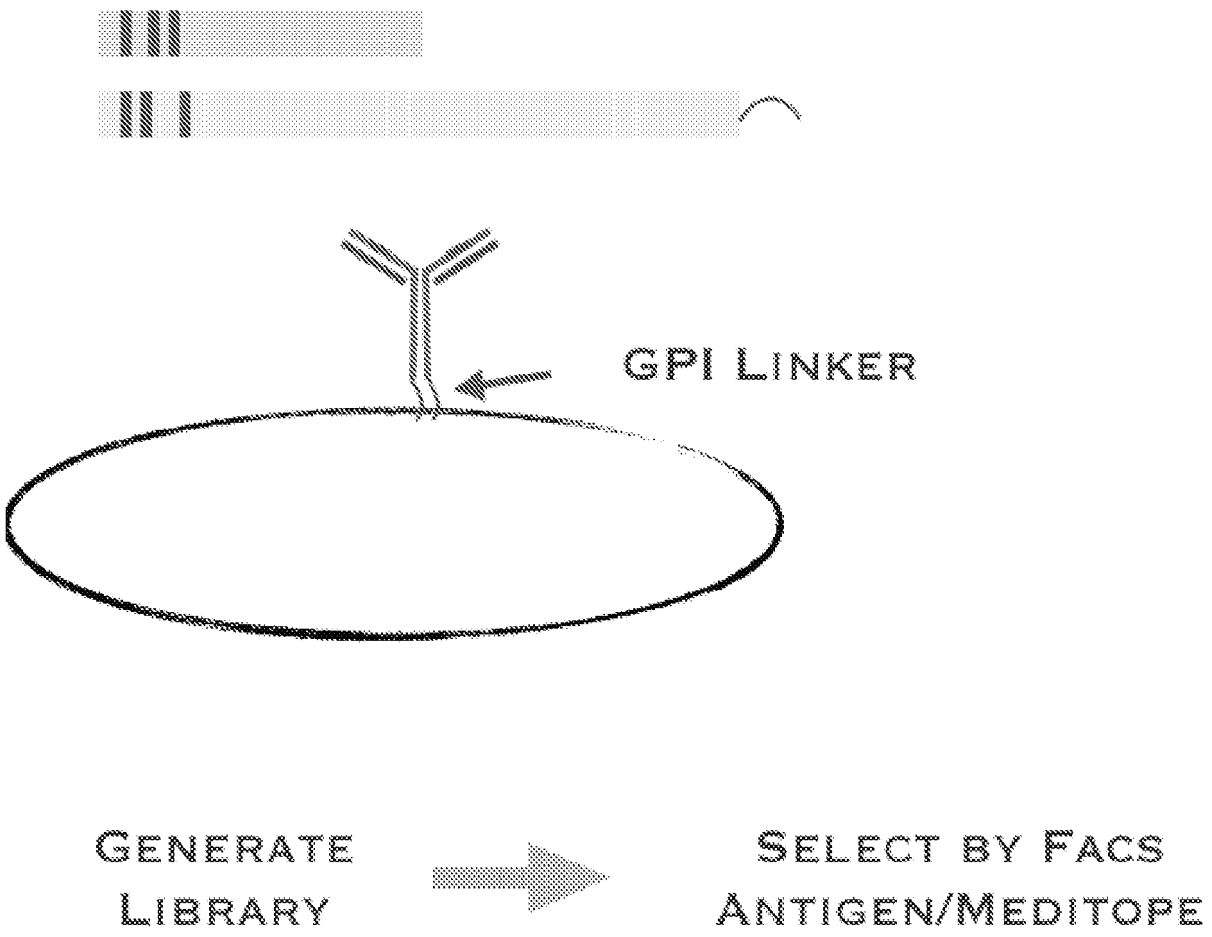

GPI LINKER
GENERATE LIBRARY
SELECT BY FACS ANTIGEN/MEDITOPE

Figure 21

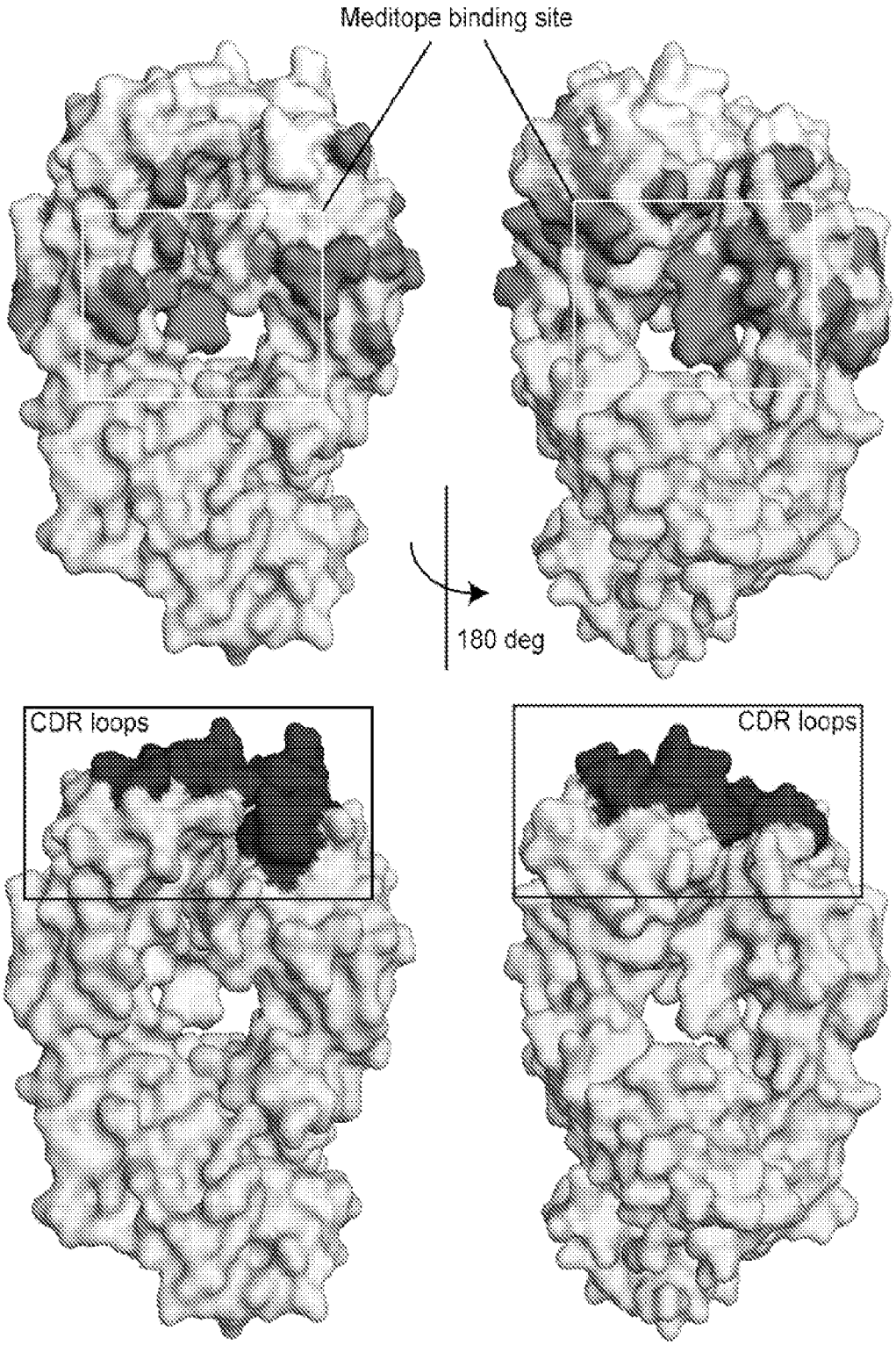


Figure 22

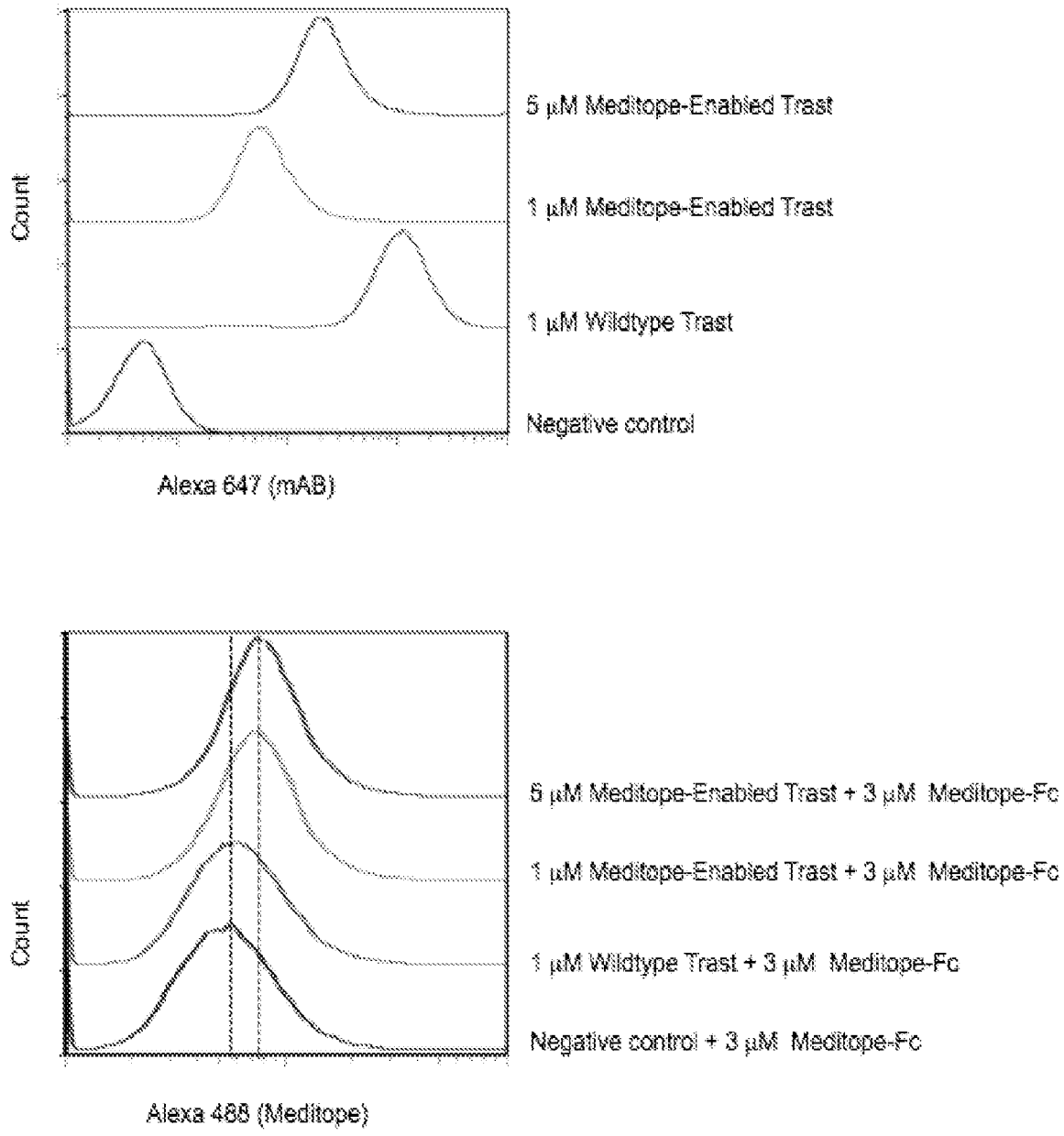

Count
5 μM Meditope-Enabled Trast
1 μM Meditope-Enabled Trast
1 μM Wildtype Trast
Negative control
Alexa 647 (mAB)
Count
5 μM Meditope-Enabled Trast + 3 μM Meditope-Fc
1 μM Meditope-Enabled Trast + 3 μM Meditope-Fc
1 μM Wildtype Trast + 3 μM Meditope-Fc
Negative control + 3 μM Meditope-Fc
Alexa 488 (Meditope)

Figure 23A

```
ATGAAATGCT CGTGGGTGAT CTTTTTCCTT ATGGCGGTAG TAACCGGAGT AAACTCCGAG GTCCAGCTCG
TCGAATCCGG TGGCGGCTTG GTGCAGCCGG GTGGGTCGTT GCGACTGTCG TGCGCAGCGT CGGGGTTTAA
CATCAAAGAC ACCTATATCC ACTGGGTGAG GCAATCGCCC GGAAAGGGGC TCGAATGGGT AGCCAGAATC
TACCCTACGA ATGGTTATAC TCGATATGCG GACTCCGTGA AAGGAAGATT CACCATCAGC GCAGATACGT
CCAAAAACAC TGCATACCTC CAGATGAATA GCCTTCGGGC GGAGGACACG GCGATCTACT ACTGTAGCCG
GTGGGGTGGG GACGGGTTCT ATGCGATGGA CTACTGGGGA CAGGGGACGC TTGTAACGGT CAGCTCGGCG
TCAACAAAGG GACCTAGCGT GTTTCCCTTG GCTCCCTCAT CGAAATCAAC GTCCGGTGGG ACGGCGGCAT
TGGGGTGTCT TGTCAAGGAC TATTTCCCCG AGCCCGTGAC AGTCTCGTGG AACTCGGGTG CCCTTACAAG
CGGCGTACAT ACGTTTCCCG CCGTGCTCCA ATCATCCGGA CTGTATTCCC TTTCATCCGT CGTGACTGTG
CCGTCCTCGT CACTCGGAAC GCAAACTTAC ATTTGCAATG TCAACCACAA ACCGTCAAAT ACAAAGGTCG
ATAAGAAGGT CGAGCCAAAG TCGTGTGATA AGACCCACAC ATGCCCTCCC TGTCCAGCGC CGGAGCTGTT
GGGAGGGCCT TCAGTGTTCC TCTTCCCGCC CAAACCCAAG GACACCCTGA TGATTAGCCG CACACCCGAG
GTGACGTGTG TCGTCGTCGA TGTCTCACAT GAGGACCCGG AGGTAAAGTT CAACTGGTAC GTGGATGGAG
TCGAAGTGCA CAACGCAAAA ACAAAACCTC GGGAAGAGCA GTACAATAGC ACGTACAGAG TAGTCAGCGT
GCTCACCGTG CTGCACCAGG ATTGGCTCAA TGGAAAGGAG TACAAGTGTA AAGTGTCGAA TAAGGCGCTG
CCTGCCCCCA TCGAAAAGAC AATTTCCAAA GCTAAAGGGC AACCCCGCGA GCCGCAAGTA TACACCCTCC
CACCCTCGCG CGATGAACTG ACCAAGAACC AGGTGTCATT GACGTGTCTC GTCAAGGGCT TCTATCCGAG
CGACATTGCA GTAGAATGGG AAAGCAACGG ACAGCCGGAA AACAACTACA AGACTACACC GCCTGTCCTT
GATTCGGATG GTTCCTTCTT TCTTTACTCA AAACTTACAG TCGACAAATC GAGGTGGCAG CAGGGAAATG
TGTTTTCGTG CAGCGTGATG CACGAGGCCT TGCATAATCA CTATACACAG AAGTCGTTGT CACTGTCGCC
GGGAAAGTAA
```

Figure 23B

```
                10        20        30        40        50        60
Medi   VESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQSPGKGLEWVARIYPTNGYTRYADSV
       ::::::::::::::::::::::::::::::::::::.::::::::::::::::::::::
WT     VESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSV
                10        20        30        40        50        60

                70        80        90       100       110       120
Medi   KGRFTISADTSKNTAYLQMNSLRAEDTAIYYCSRWGGDGFYAMDYWGQGTLVTVSSASTK
       ::::::::::::::::::::::::::::::.:::::::::::::::::::::::::::::
WT     KGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTK
                70        80        90       100       110       120

               130       140       150       160       170       180
Medi   GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
WT     GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
               130       140       150       160       170       180
```

Figure 23C

```
ATGGAGACAC ACACGCTTTT GCTTTGGGTG TTGTTGTTGT GGGTCCCCGG TTCGACGGGG GATATTCAGA
TGACCCAGTC ACCGATCCTT CTCTCGGCGA GCGTGGGGGA TAGAGTAACG ATCACGTGTA GAGCGTCCCA
AGACGTCAAC ACAGCTGTCG CGTGGTATCA GCAGCGGACA AATGGATCGC CGAGGCTCCT GATCTACAGC
GCATCATTTC TCTATTCGGG AGTCCCCTCC CGATTTTCCG GATCGCGCAG CGGTACTGAC TTCACCCTCA
CGATTTCCTC CCTTCAACCG GAAGATATCG CTGATTACTA CTGTCAGCAG CACTATACAA CACCTCCCAC
TTTCGGAGCA GGGACAAAAG TGGAGATTAA GCGCACTGTA GCAGCCCCCT CGGTCTTTAT CTTCCCTCCT
AGCGACGAAC AATTGAAGTC AGGGACCGCC TCGGTGGTAT GCCTGCTTAA CAACTTTTAC CCACGGGAAG
CCAAAGTACA GTGGAAGGTG GATAATGCGC TCCAGAGCGG AAACTCCCAA GAGAGCGTGA CAGAACAGGA
CTCGAAGGAT TCGACGTACT CACTCAGCTC AACGCTGACC CTGTCGAAAG CGGACTATGA GAAACACAAG
GTCTACGCGT GCGAGGTGAC CCATCAGGGC CTGAGCTCCC CCGTAACTAA GTCATTCAAC CGGGGTGAAT
GCTAA
```

Figure 23D

```
            10        20        30        40        50        60
medi    DIQMTQSPTTLSASVGDRVTITCRASQDVNTAVAWYQQRTNGSPRLLIYSASFLYSGVPS
        :::::::: ::::::::::::::::::::::::::::: . . :.:::::::::::::::
WT      DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPS
                10        20        30        40        50        60

                70        80        90       100       110       120
medi    RFSGSRSGTDFTLTISSLQPEDIADYYCQQHYTTPPTFGAGTKVEIKRTVAAPSVFIFPP
        :::::::::::::::::::::: :::::::::::::::: ::::::::::::::::::::
WT      RFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPP
                70        80        90       100       110       120

               130       140       150       160       170       180
medi    SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
WT      SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
               130       140       150       160       170       180

               190       200       210
medi    LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
        ::::::::::::::::::::::::::::::::
WT      LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
               190       200       210
```

Figure 24

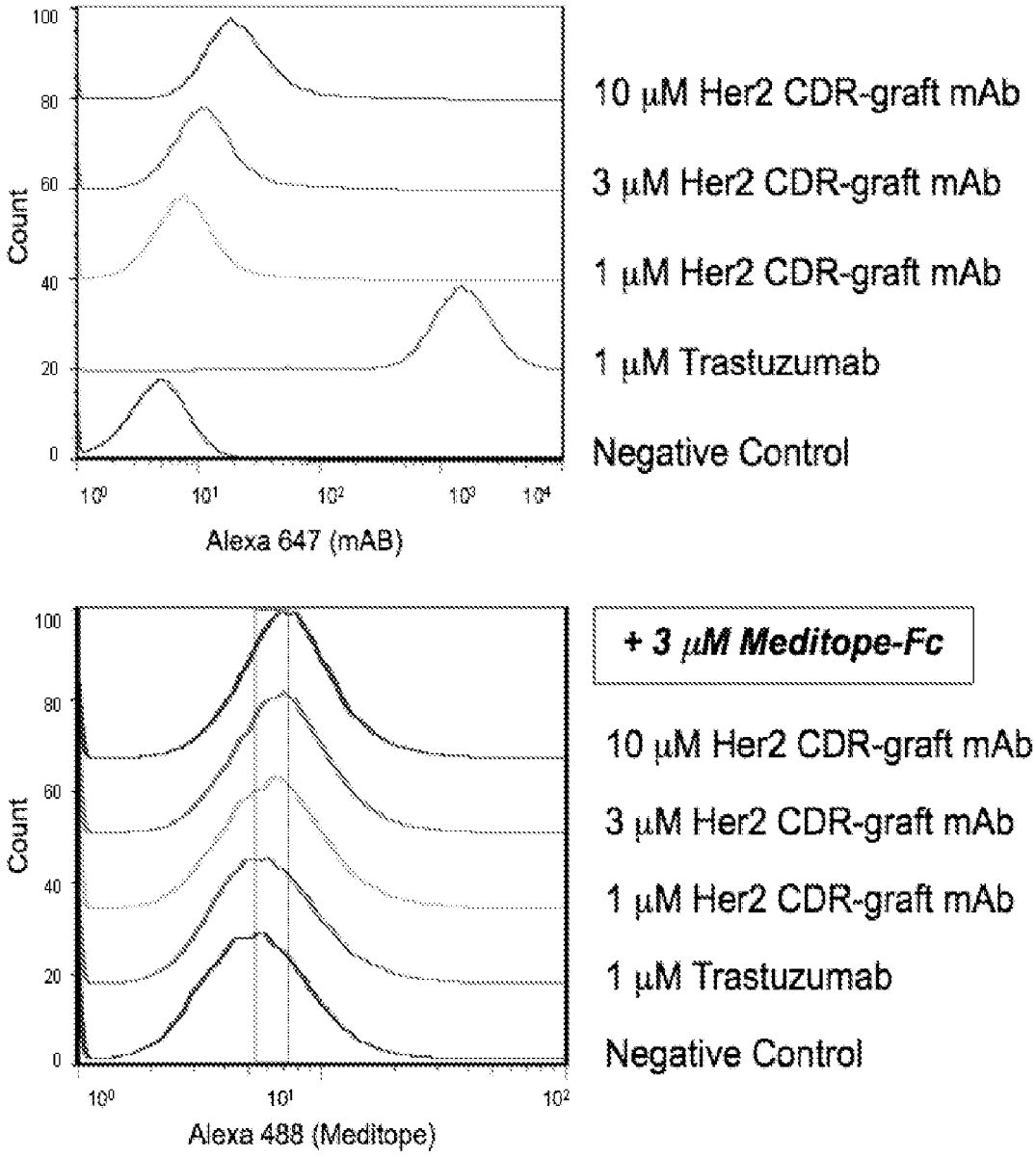

Count
Alexa 647 (mAB)
10 μM Her2 CDR-graft mAb
3 μM Her2 CDR-graft mAb
1 μM Her2 CDR-graft mAb
1 μM Trastuzumab
Negative Control
+ 3 μM Meditope-Fc
Count
Alexa 488 (Meditope)
10 μM Her2 CDR-graft mAb
3 μM Her2 CDR-graft mAb
1 μM Her2 CDR-graft mAb
1 μM Trastuzumab
Negative Control

Figure 25A

```
tcactatagggaagcttgccgccaccatgaaatgctcgtgggtgatctttttccttatg
 S  L  -  G  K  L  A  A  T  M  K  C  S  W  V  I  F  F  L  M
gcggtagtaaccggagttaactccgaggtccagctcgtcgaatccggtggcggcttggtg
 A  V  V  T  G  V  N  S  E  V  Q  L  V  E  S  G  G  G  L  V
cagccgggtgggtcgttgcgactgtcgtgcgcagcgtcggggtttaacatcaaagacacc
 Q  P  G  G  S  L  R  L  S  C  A  A  S  G  F  N  I  K  D  T
tatatccactgggtgaggcaagcgcccggaaaggggctcgaatgggtagccagaatctac
 Y  I  H  W  V  R  Q  A  P  G  K  G  L  E  W  V  A  R  I  Y
cctacgaatggttatactcgatatgcggactccgtgaaaggaagattcaccatcagcgca
 P  T  N  G  Y  T  R  Y  A  D  S  V  K  G  R  F  T  I  S  A
gatacgtccaaaaacactgcatacctccagatgaatagccttcgggcggaggacacggcg
 D  T  S  K  N  T  A  Y  L  Q  M  N  S  L  R  A  E  D  T  A
gtctactactgtagccggtggggtggggacgggttctatgcgatggactactggggacag
 V  Y  Y  C  S  R  W  G  G  D  G  F  Y  A  M  D  Y  W  G  Q
gggacgcttgtaacggtcagctcggctagcacaaagggacctagcgtgtttcccttggct
 G  T  L  V  T  V  S  S  A  S  T  K  G  P  S  V  F  P  L  A
ccctcatcgaaatcaacgtccggtgggacggcggcattggggtgtcttgtcaaggactat
 P  S  S  K  S  T  S  G  G  T  A  A  L  G  C  L  V  K  D  Y
ttccccgagcccgtgacagtctcgtggaactcgggtgcccttacaagcggcgtacatacg
 F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S  G  V  H  T
tttcccgccgtgctccaatcatccggactgtattccctttcatccgtcgtgactgtgccg
 F  P  A  V  L  Q  S  S  G  L  Y  S  L  S  S  V  V  T  V  P
tcctcgtcactcggaacgcaaacttacatttgcaatgtcaaccacaaaccgtcaaataca
 S  S  S  L  G  T  Q  T  Y  I  C  N  V  N  H  K  P  S  N  T
aaggtcgataagaaggtcgagccaaagtcgtgtgataagacccacacatgccctccctgt
 K  V  D  K  K  V  E  P  K  S  C  D  K  T  H  T  C  P  P  C
ccagcgccggagctgttgggagggccttcagtgttcctcttcccgcccaaacccaaggac
 P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D
accctgatgattagccgcacacccgaggtgacgtgtgtcgtcgtcgatgtctcacatgag
 T  L  M  I  S  R  T  P  E  V  T  C  V  V  V  D  V  S  H  E
gacccggaggtaaagttcaactggtacgtggatggagtcgaagtgcacaacgcaaaaaca
 D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T
aaacctcgggaagagcagtacaatagcacgtacagagtagtcagcgtgctcaccgtgctg
 K  P  R  E  E  Q  Y  N  S  T  Y  R  V  V  S  V  L  T  V  L
caccaggattggctcaatggaaaggagtacaagtgtaaagtgtcgaataaggcgctgcct
 H  Q  D  W  L  N  G  K  E  Y  K  C  K  V  S  N  K  A  L  P
gcccccatcgaaaagacaatttccaaagctaaagggcaaccccgcgagccgcaagtatac
 A  P  I  E  K  T  I  S  K  A  K  G  Q  P  R  E  P  Q  V  Y
accctcccaccctcgcgcgatgaactgaccaagaaccaggtgtcattgacgtgtctcgtc
 T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T  C  L  V
aagggcttctatccgagcgacattgcagtagaatgggaaagcaacggacagccggaaaac
 K  G  F  Y  P  S  D  I  A  V  E  W  E  S  N  G  Q  P  E  N
aactacaagactacaccgcctgtccttgattcggatggttccttctttctttactcaaaa
 N  Y  K  T  T  P  P  V  L  D  S  D  G  S  F  F  L  Y  S  K
cttacagtcgacaaatcgaggtggcagcagggaaatgtgttttcgtgcagcgtgatgcac
 L  T  V  D  K  S  R  W  Q  Q  G  N  V  F  S  C  S  V  M  H
gaggccttgcataatcactatacacagaagtcgttgtcactgtcgccgggaaagtaatga
 E  A  L  H  N  H  Y  T  Q  K  S  L  S  L  S  P  G  K  -  -
```

Figure 25B

```
ataggggaagcttgccgccaccatggagacagacacgcttttgctttgggtgttgttgttg
  -  G  K  L  A  A  T  M  E  T  D  T  L  L  L  W  V  L  L  L
tgggtccccggttcgaccggtgatattcagatgacccagtcaccgtcatccctttcggcg
 W  V  P  G  S  T  G  D  I  Q  M  T  Q  S  P  S  S  L  S  A
agcgtgggggatagagtaacgatcacgtgtagagcgtcccaagacgtcaacacagctgtc
 S  V  G  D  R  V  T  I  T  C  R  A  S  Q  D  V  N  T  A  V
gcgtggtatcagcagaagccaggaaaagcgccgaagctcctgatctacagcgcatcattt
 A  W  Y  Q  Q  K  P  G  K  A  P  K  L  L  I  Y  S  A  S  F
ctctattcgggagtcccctcccgattttccggatcgcgcagcggtactgacttcaccctc
 L  Y  S  G  V  P  S  R  F  S  G  S  R  S  G  T  D  F  T  L
acgatttcctcccttcaaccggaagattttgctacttactactgtcagcagcactataca
 T  I  S  S  L  Q  P  E  D  F  A  T  Y  Y  C  Q  Q  H  Y  T
acacctcccactttcggacaggggacaaaagtggagattaagcggaccgtagcagccccc
 T  P  P  T  F  G  Q  G  T  K  V  E  I  K  R  T  V  A  A  P
tcggtctttatcttccctcctagcgacgaacaattgaagtcagggaccgcctcggtggta
 S  V  F  I  F  P  P  S  D  E  Q  L  K  S  G  T  A  S  V  V
tgcctgcttaacaacttttacccacgggaagccaaagtacagtggaaggtggataatgcg
 C  L  L  N  N  F  Y  P  R  E  A  K  V  Q  W  K  V  D  N  A
ctccagagcggaaactcccaagagagcgtgacagaacaggactcgaaggattcgacgtac
 L  Q  S  G  N  S  Q  E  S  V  T  E  Q  D  S  K  D  S  T  Y
tcactcagctcaacgctgaccctgtcgaaagcggactatgagaaacacaaggtctacgcg
 S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K  V  Y  A
tgcgaggtgacccatcagggcctgagctcccccgtaactaagtcattcaaccggggtgaa
 C  E  V  T  H  Q  G  L  S  S  P  V  T  K  S  F  N  R  G  E
tgctaatga
 C  -  -
```

Figure 26

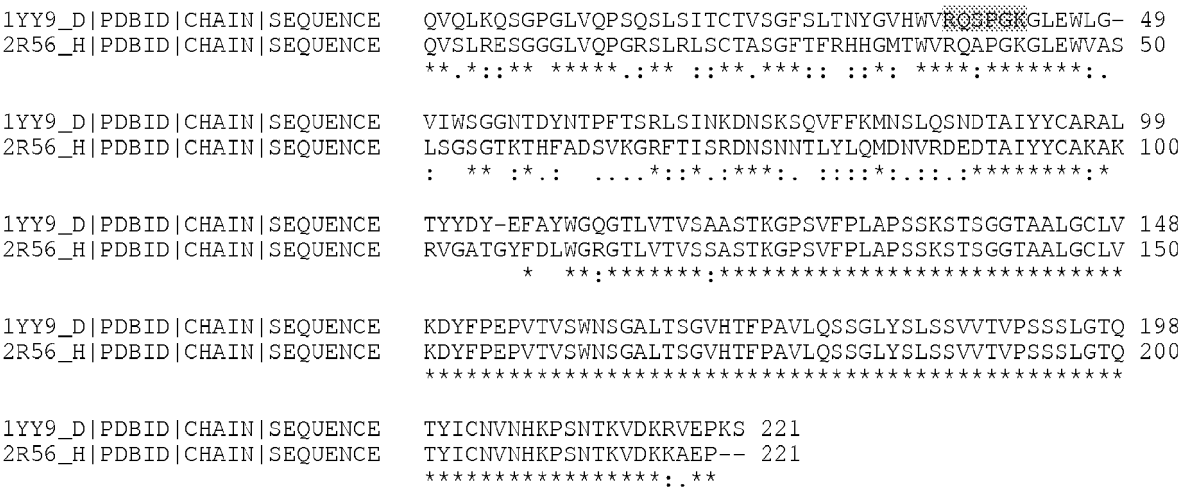

1YY9_D|PDBID|CHAIN|SEQUENCE QVQLKQSGPGLVQPSQSLSITCTVSGFSLTNYGVHWVRQSPGKGLEWLG- 49
2R56_H|PDBID|CHAIN|SEQUENCE QVSLRESGGGLVQPGRSLRLSCTASGFTFRHHGMTWVRQAPGKGLEWVAS 50
1YY9_D|PDBID|CHAIN|SEQUENCE VIWSGGNTDYNTPFTSRLSINKDNSKSQVFFKMNSLQSNDTAIYYCARAL 99
2R56_H|PDBID|CHAIN|SEQUENCE LSGSGTKTHFADSVKGRFTISRDNSNNTLYLQMDNVRDEDTAIYYCAKAK 100
1YY9_D|PDBID|CHAIN|SEQUENCE TYYDY-EFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLV 148
2R56_H|PDBID|CHAIN|SEQUENCE RVGATGYFDLWGRGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV 150
1YY9_D|PDBID|CHAIN|SEQUENCE KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ 198
2R56_H|PDBID|CHAIN|SEQUENCE KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ 200
1YY9_D|PDBID|CHAIN|SEQUENCE TYICNVNHKPSNTKVDKRVEPKS 221
2R56_H|PDBID|CHAIN|SEQUENCE TYICNVNHKPSNTKVDKKAEP-- 221

Figure 27

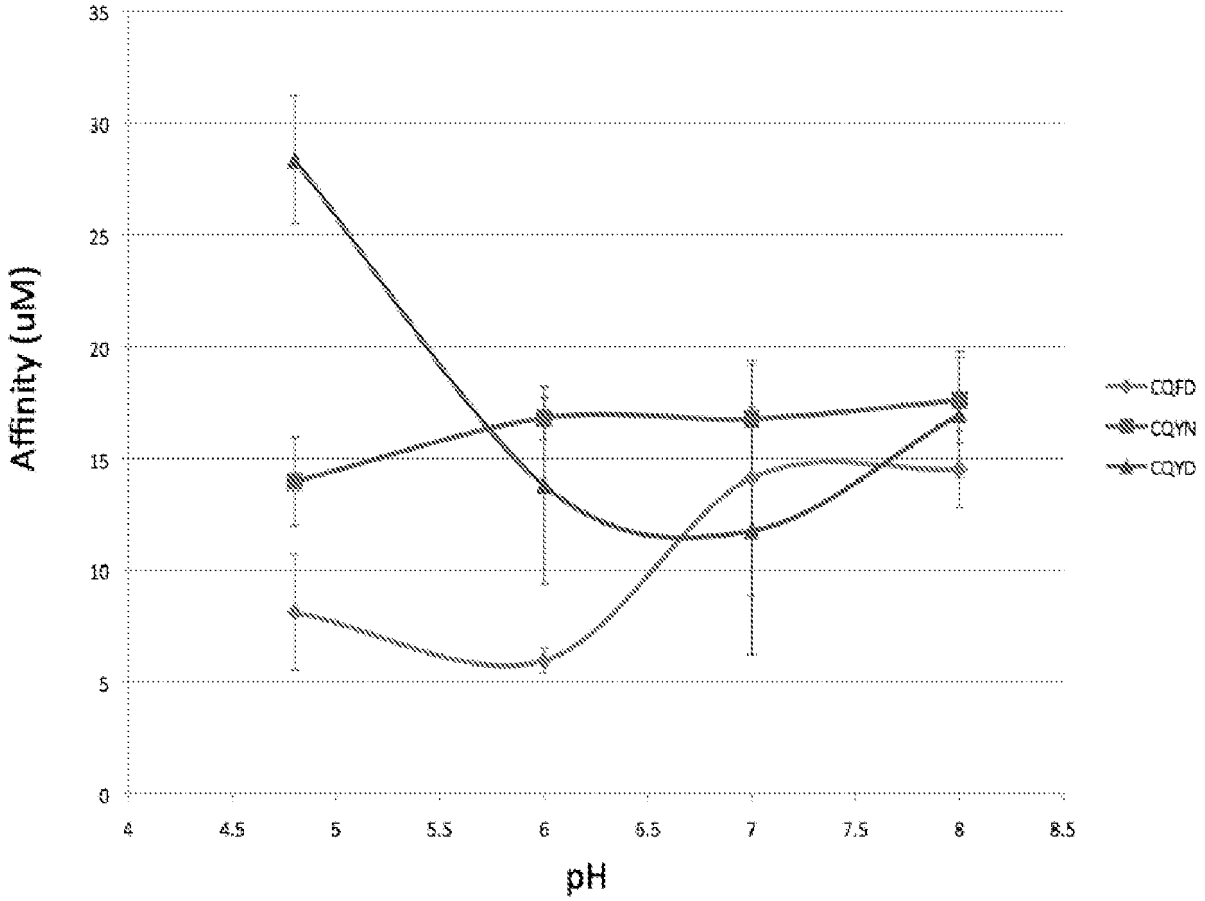
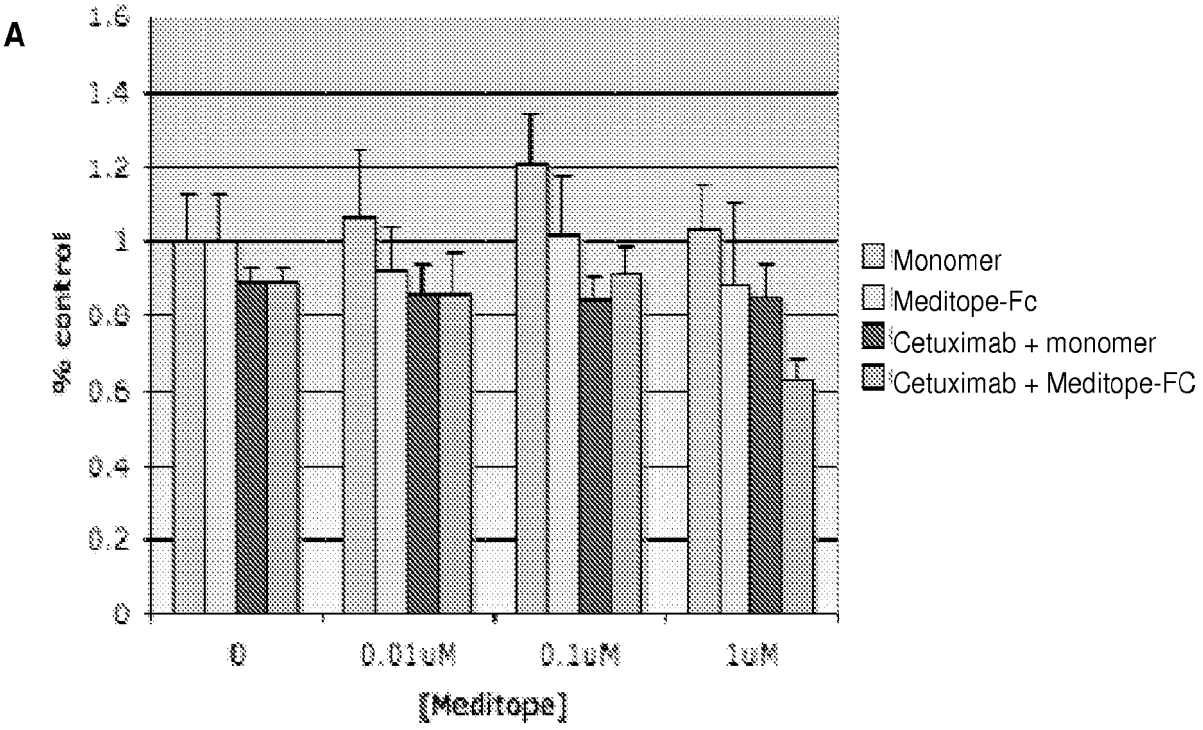

35
30
25
20
15
10
5
0
Affinity (uM)
4
4.5
5
5.5
6
6.5
7
7.5
8
8.5
pH
CQFD
CQYN
CQYD

Figure 28


A
% control
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
0.01uM
0.1uM
1uM
[Meditope]
Monomer
Meditope-Fc
Cetuximab + monomer
Cetuximab + Meditope-FC

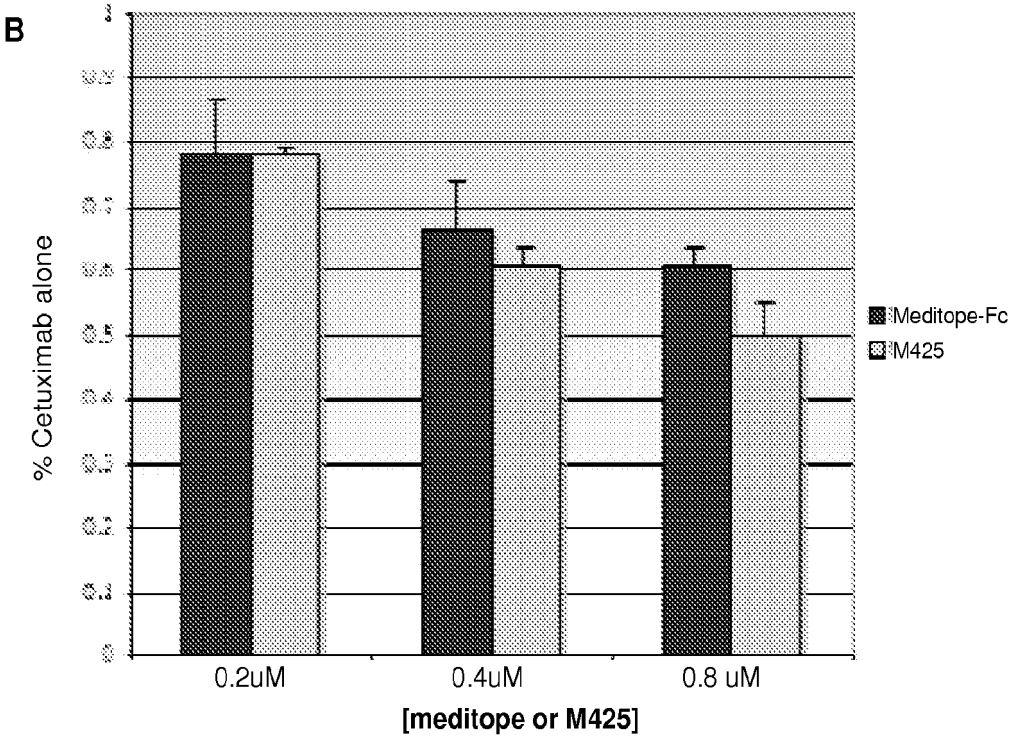
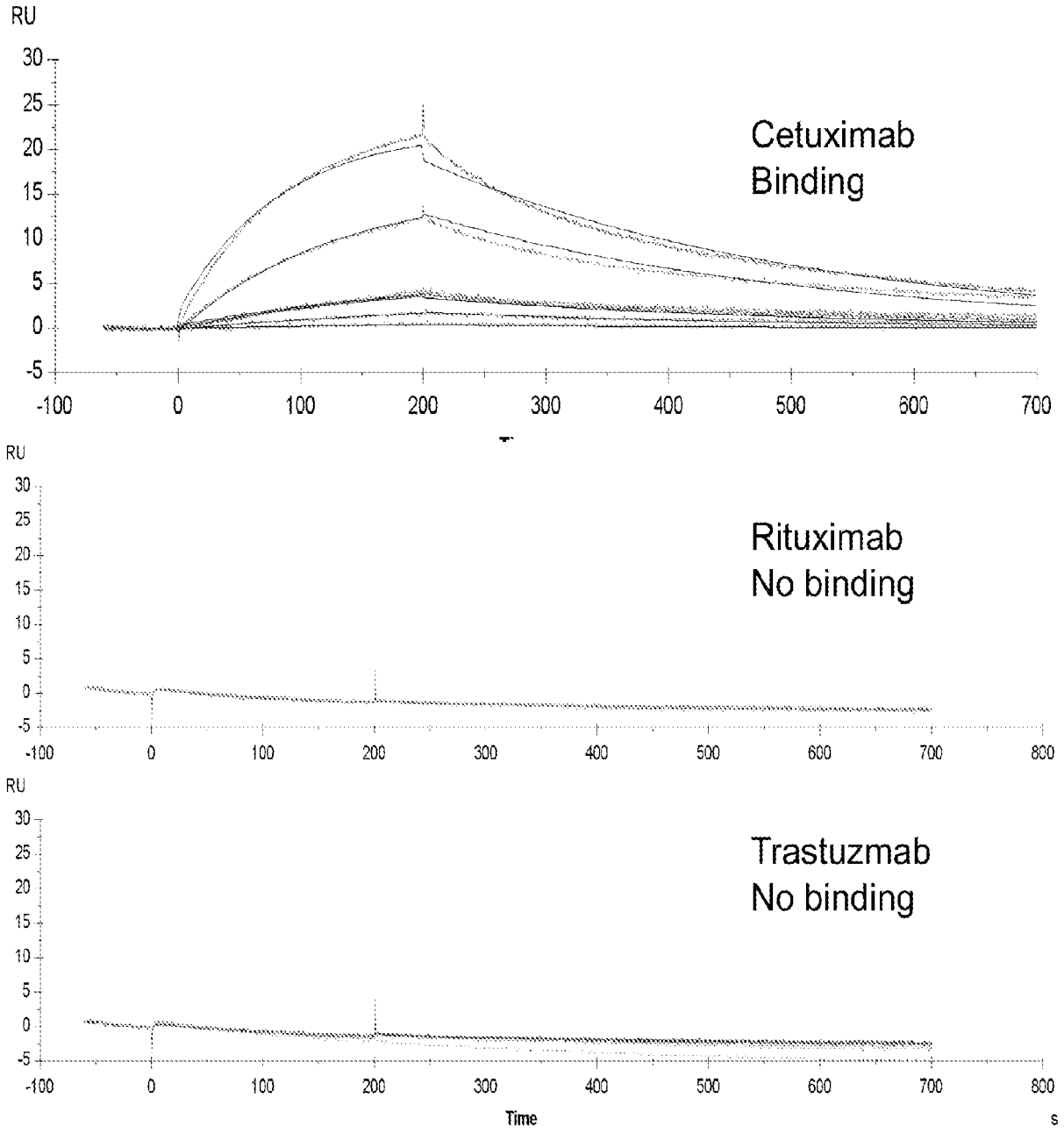

B
% Cetuximab alone
0.2uM
0.4uM
0.8 uM
[meditope or M425]
Meditope-Fc
M425

Figure 29


RU
30
25
20
15
10
5
0
-5
-100
0
100
200
300
400
500
600
700
Cetuximab
Binding
RU
Rituximab
No binding
800
RU
Trastuzmab
No binding
Time
s