

1/34

Figure 1

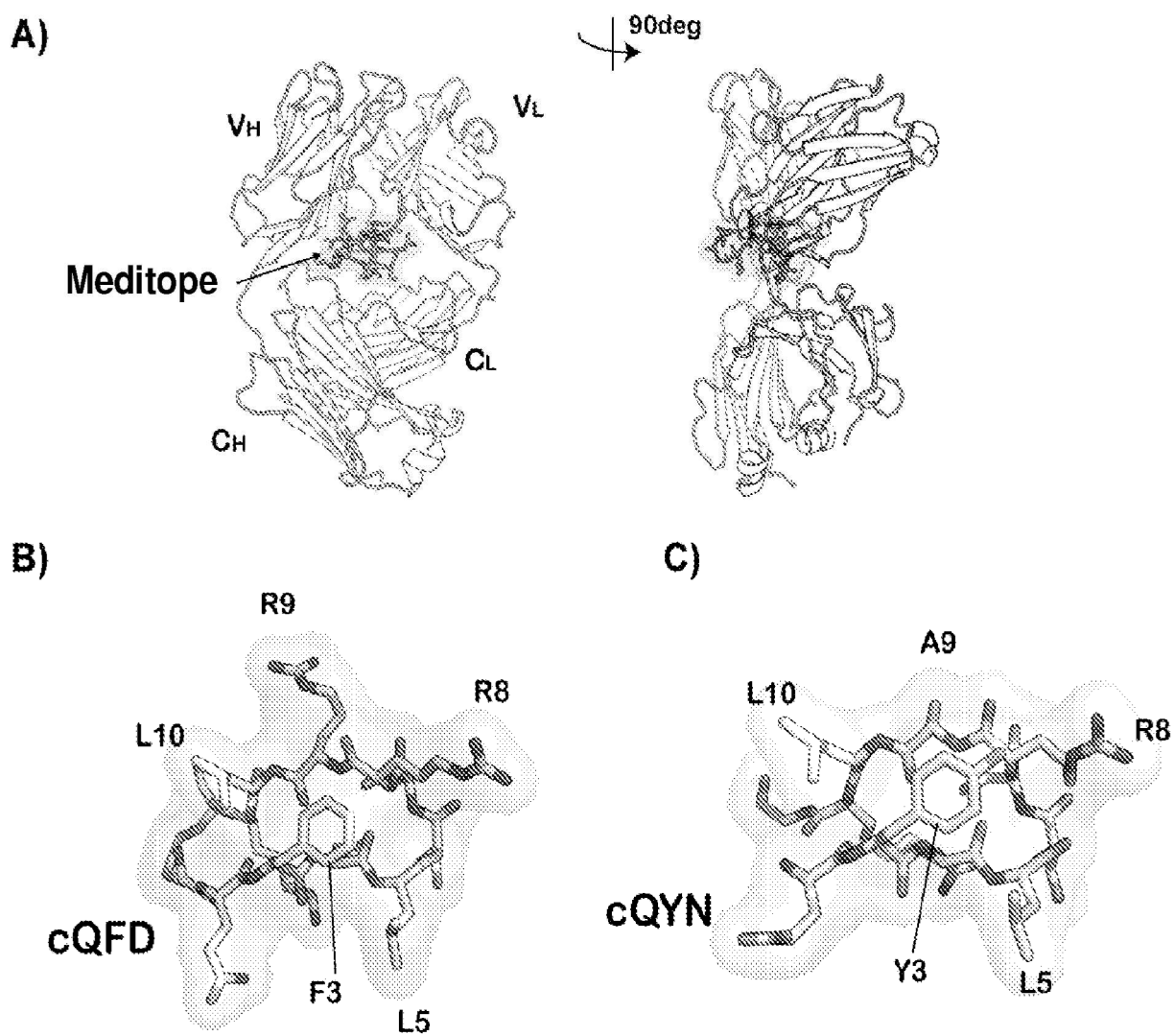


Figure 2

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A)

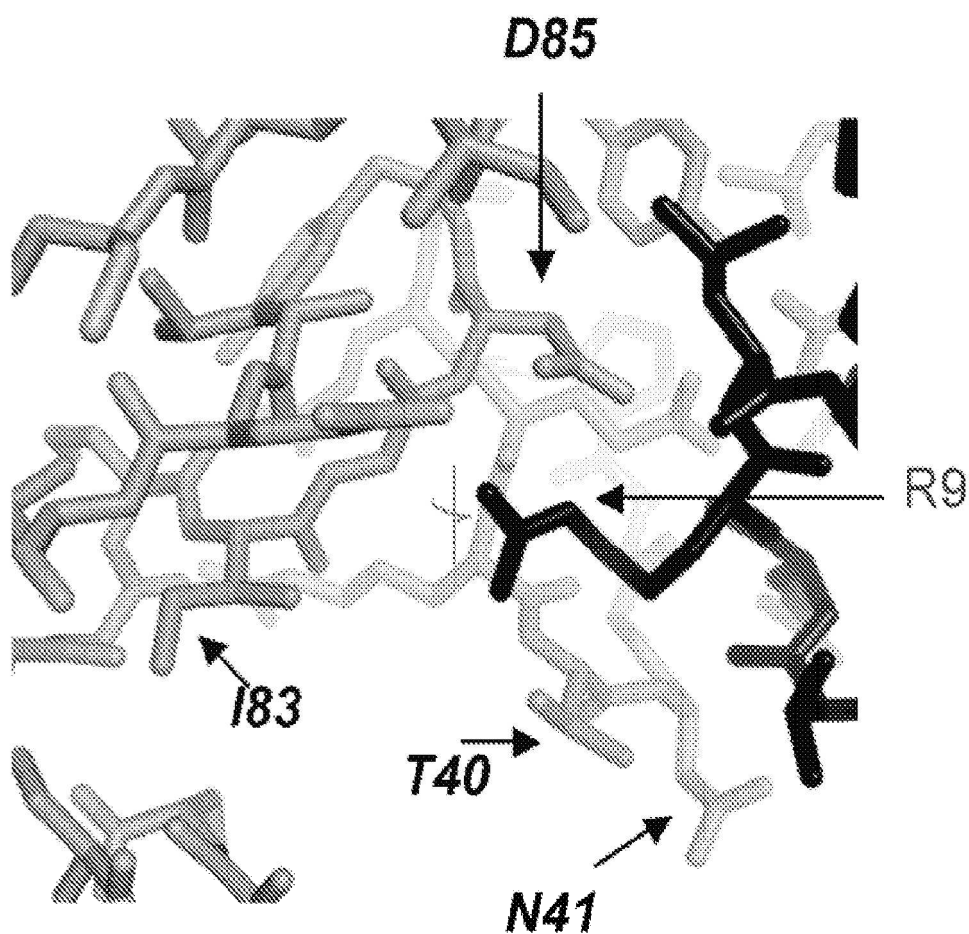
Light Chain

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

Heavy Chain

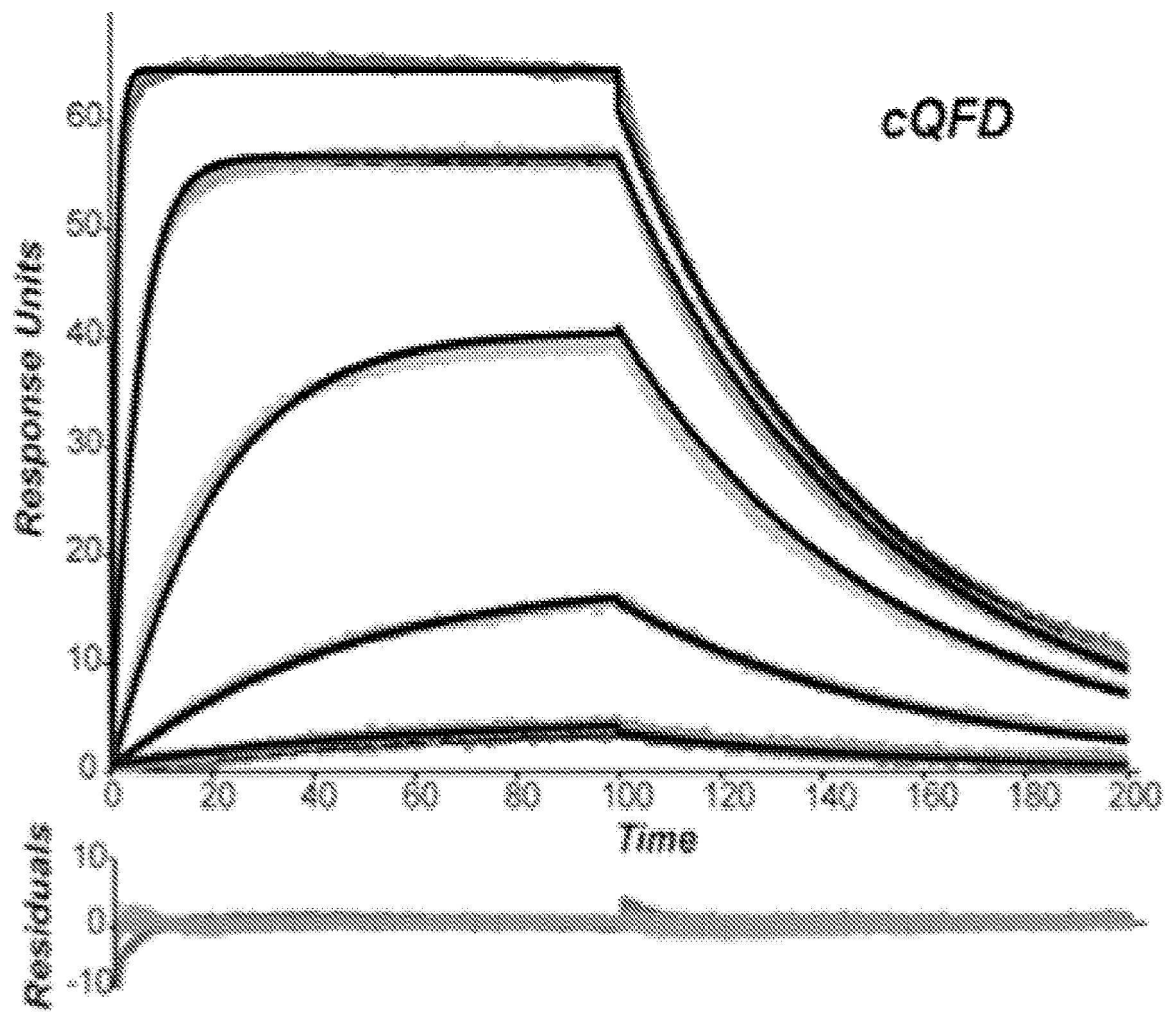
Kabat Number	39-----44	87-89	105-108	149	168-169
<i>cetuximab</i>	QSPGKG	TAI	QGTL	E	PA
<i>ch 14.18</i>	QNIGKS	SAV	QGTS	E	PA
<i>trastuzumab</i>	QAPGKG	TAV	QGTL	E	PA

B)



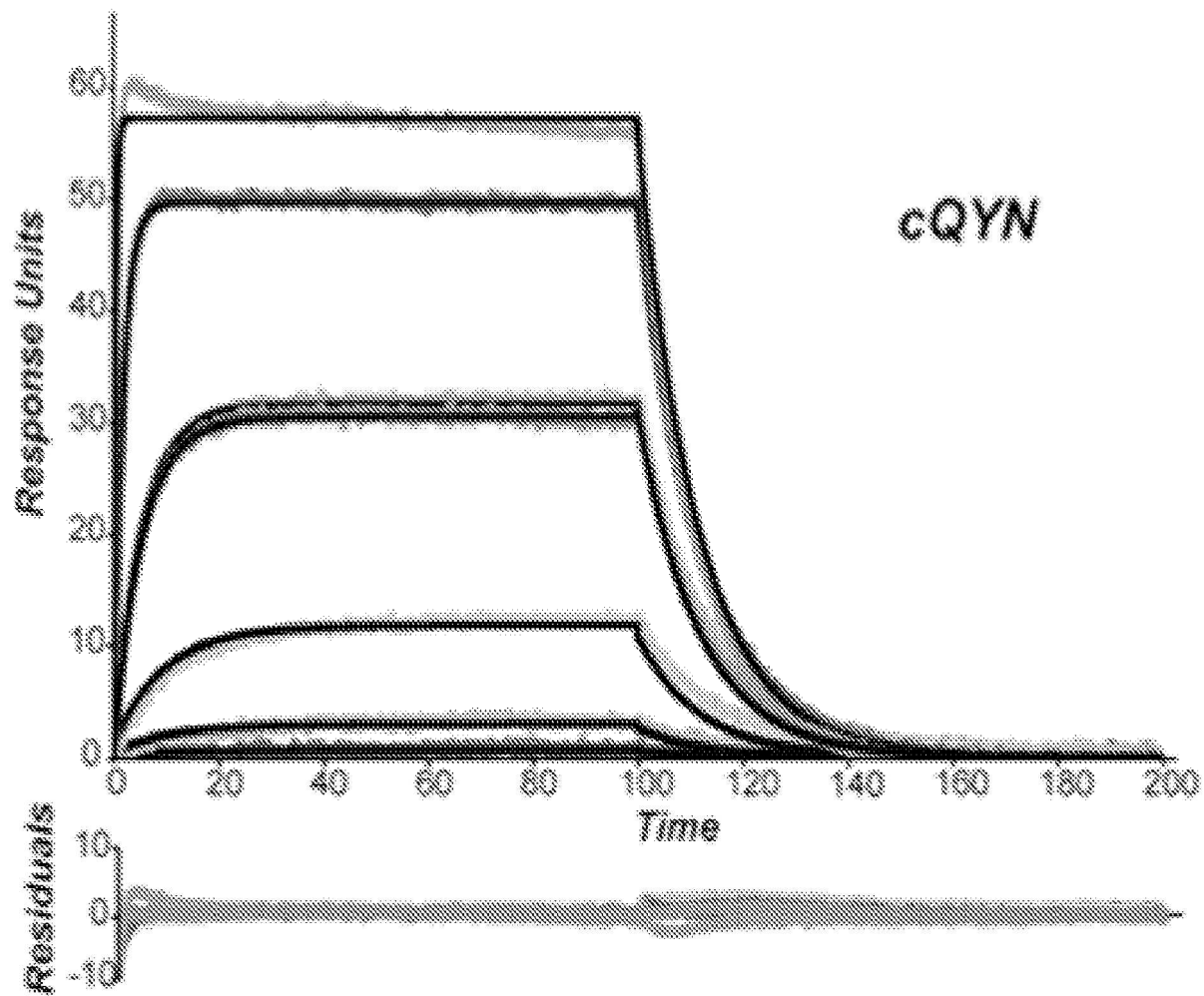
3/34

Figure 3A



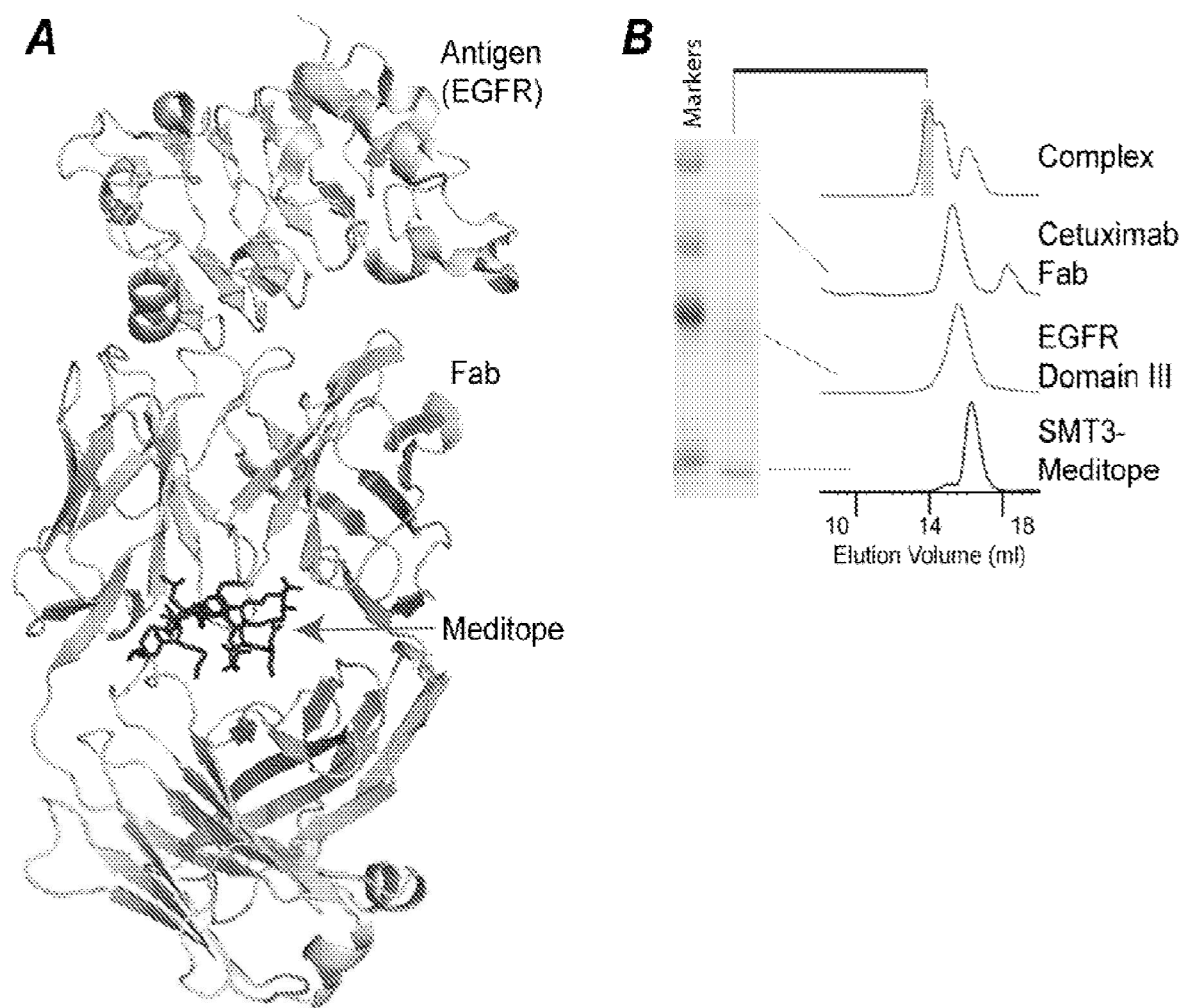
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Figure 3B



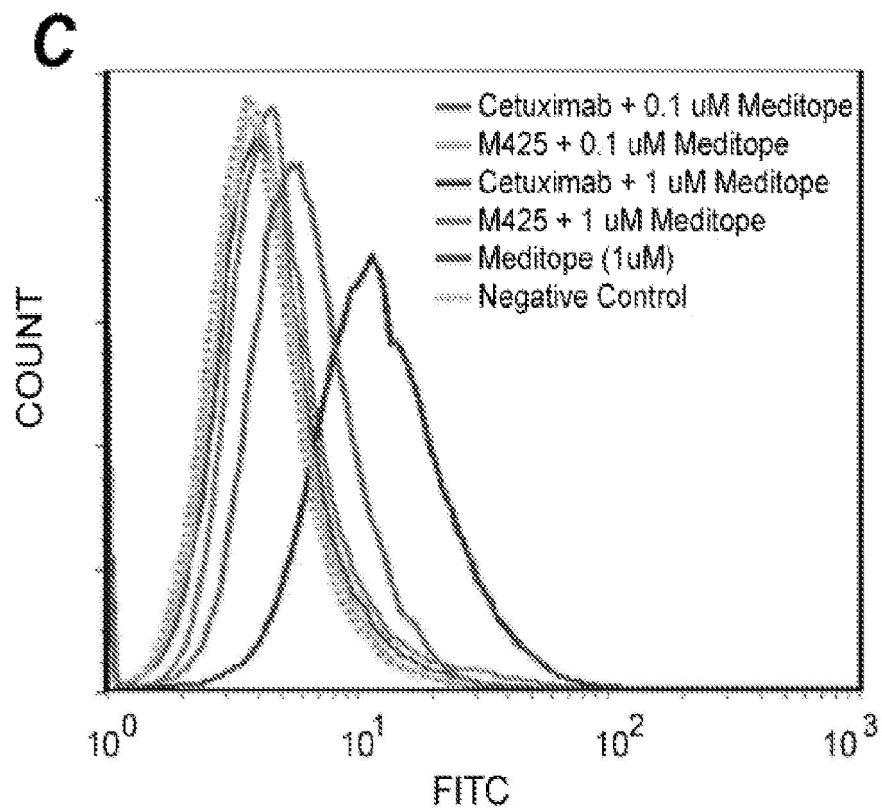
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Figure 4 A-B



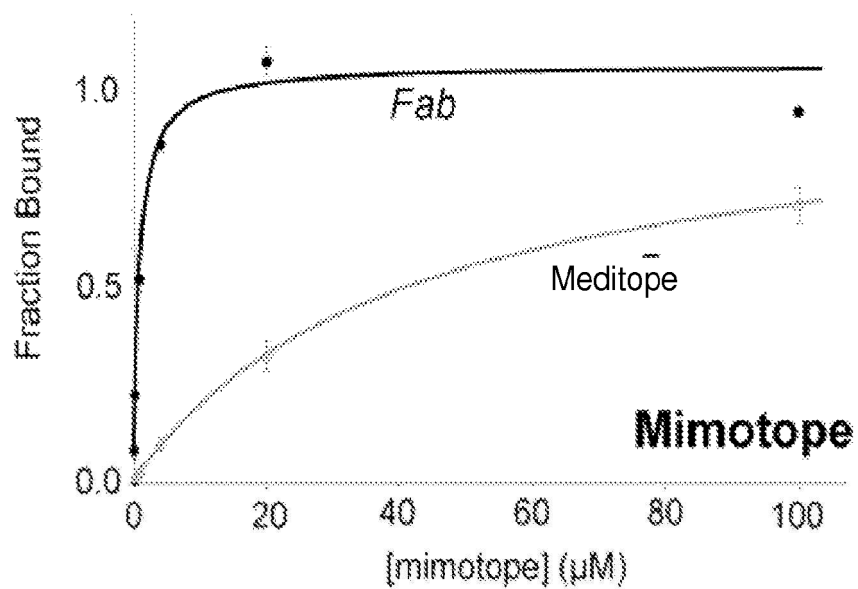
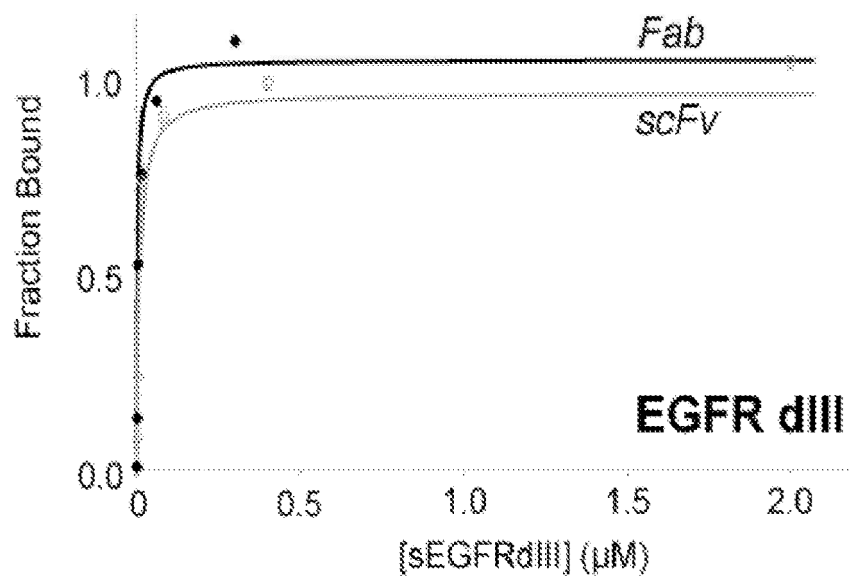
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Figure 4C



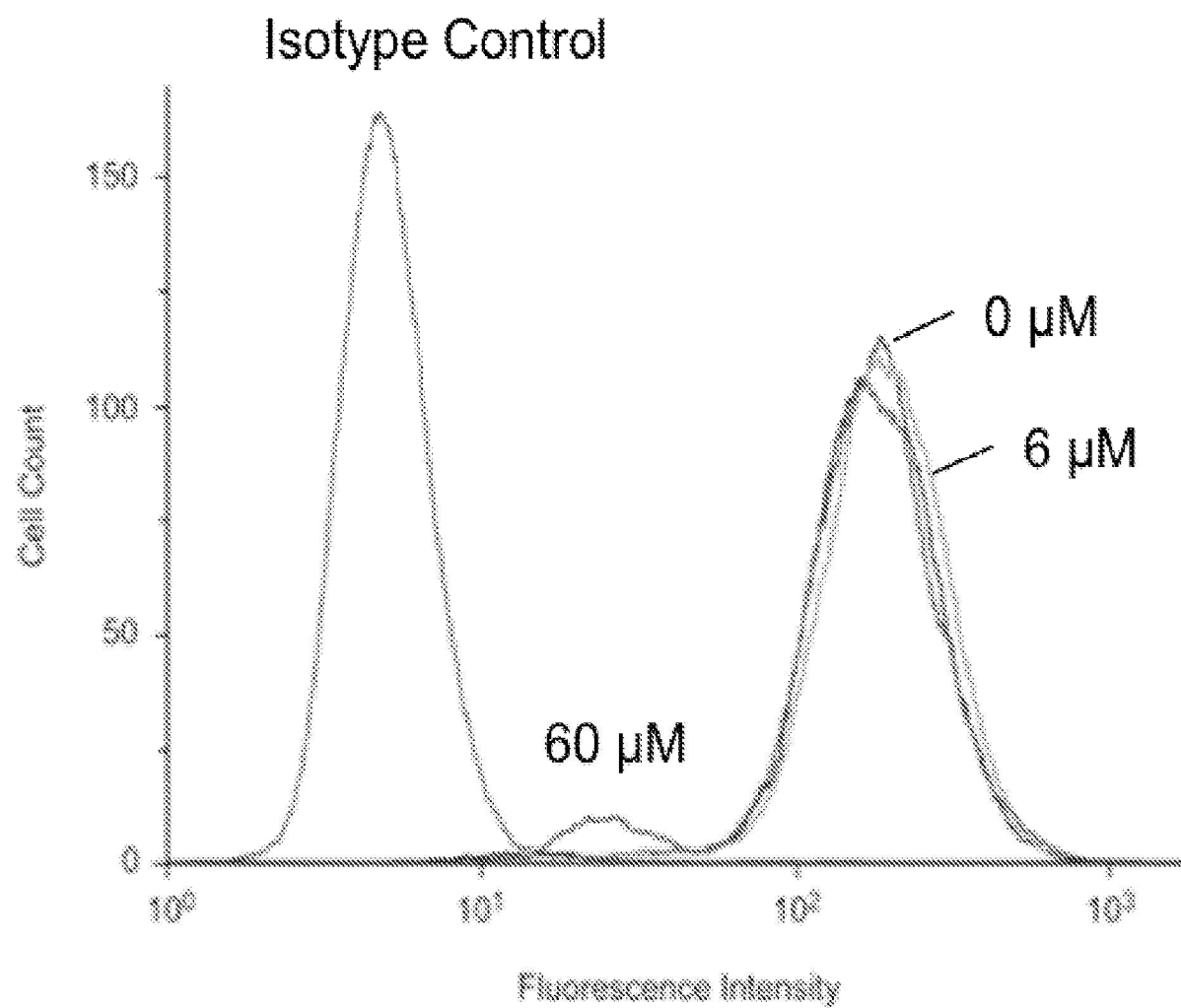
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Figure 4D



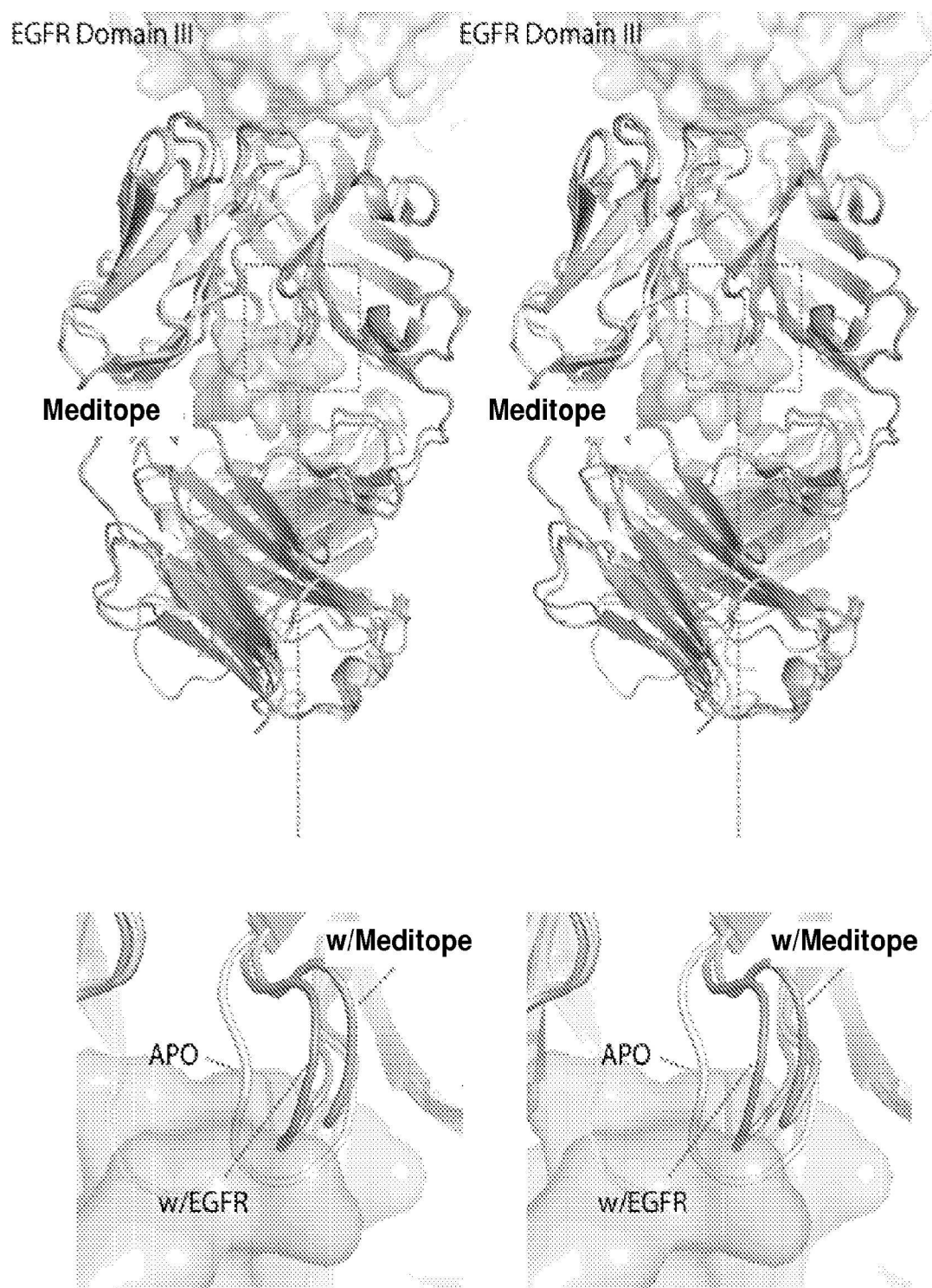
8/34

Figure 5



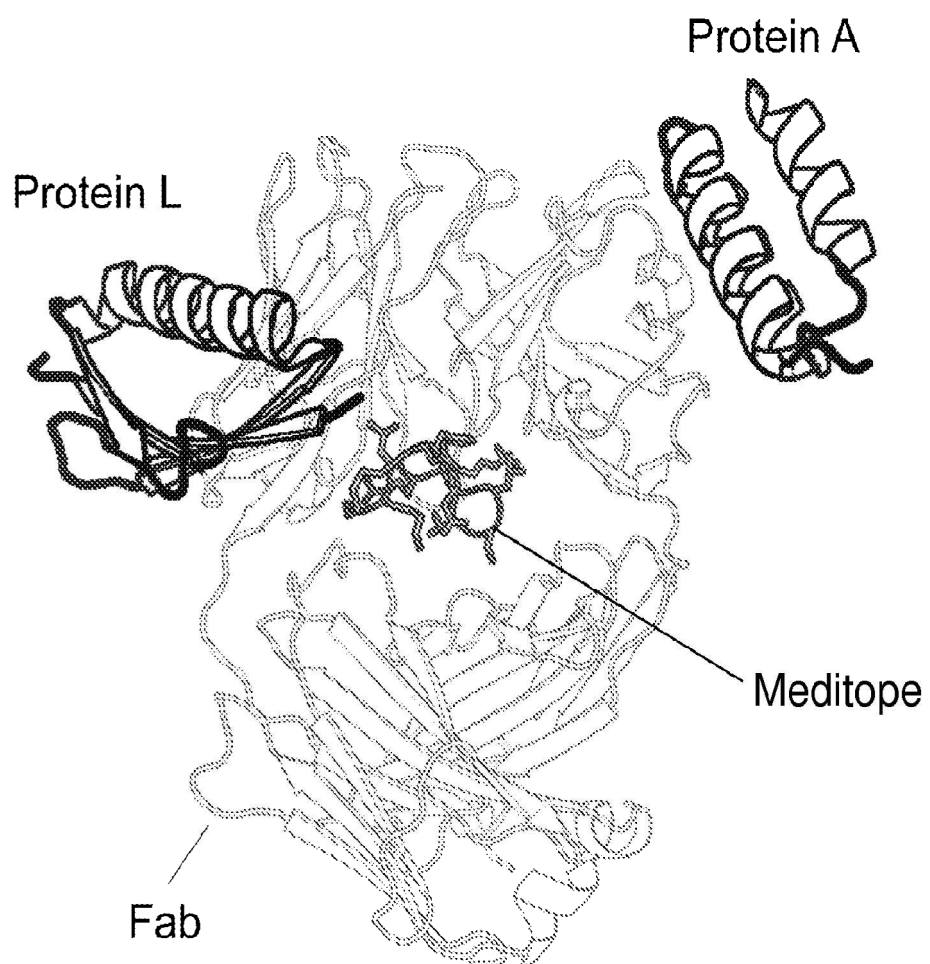
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Figure 6



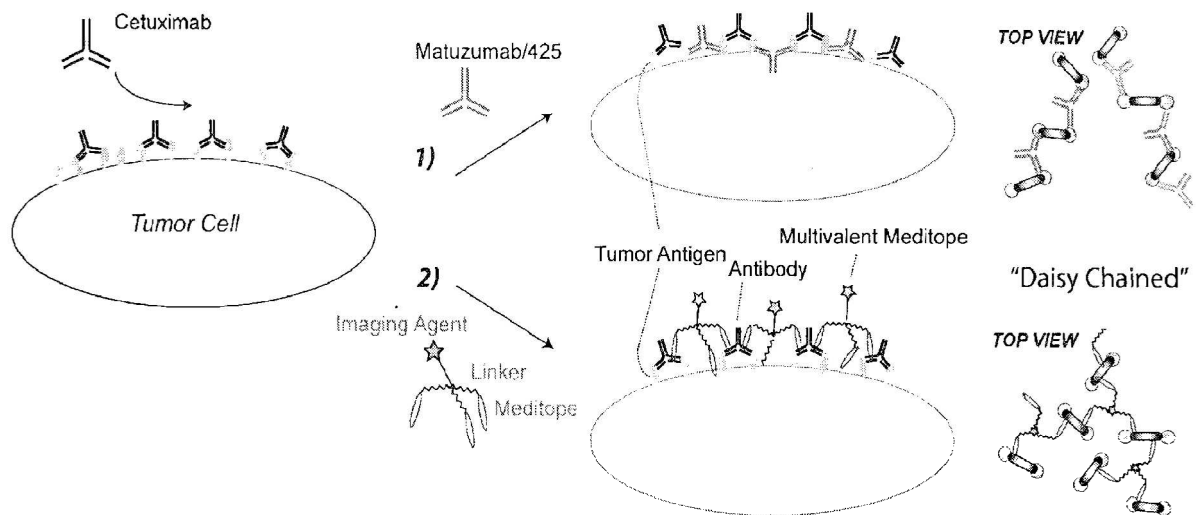
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Figure 7



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Figure 8

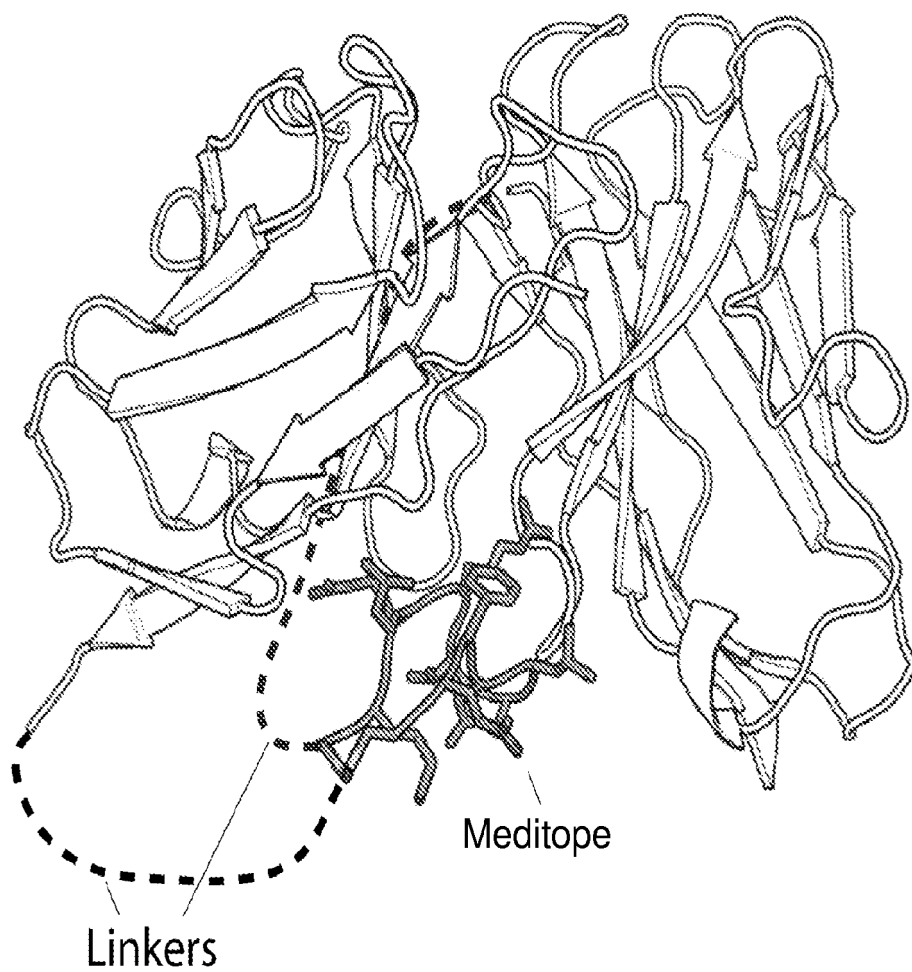


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Figure 9

Fab variable light chain

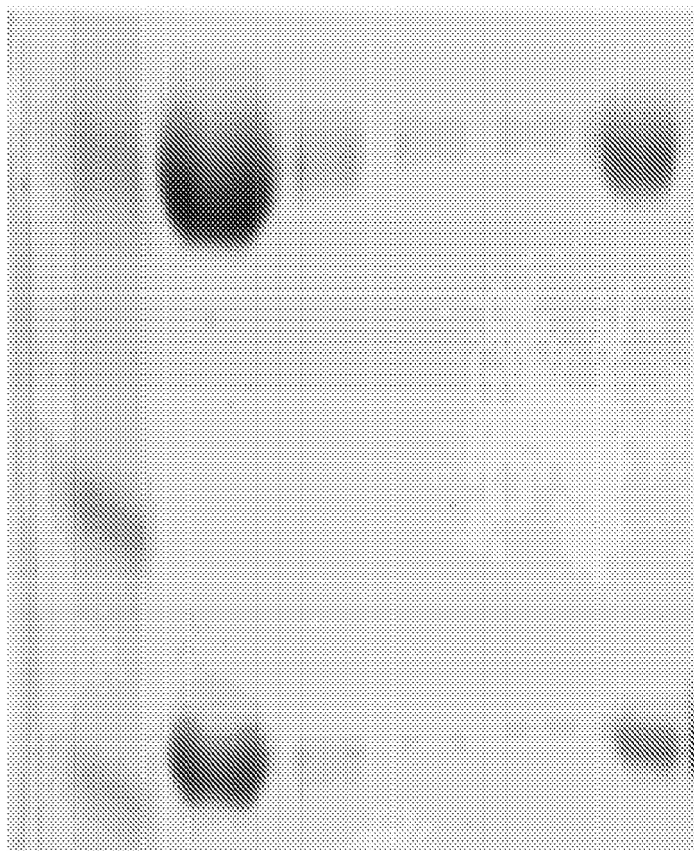
Fab variable heavy chain



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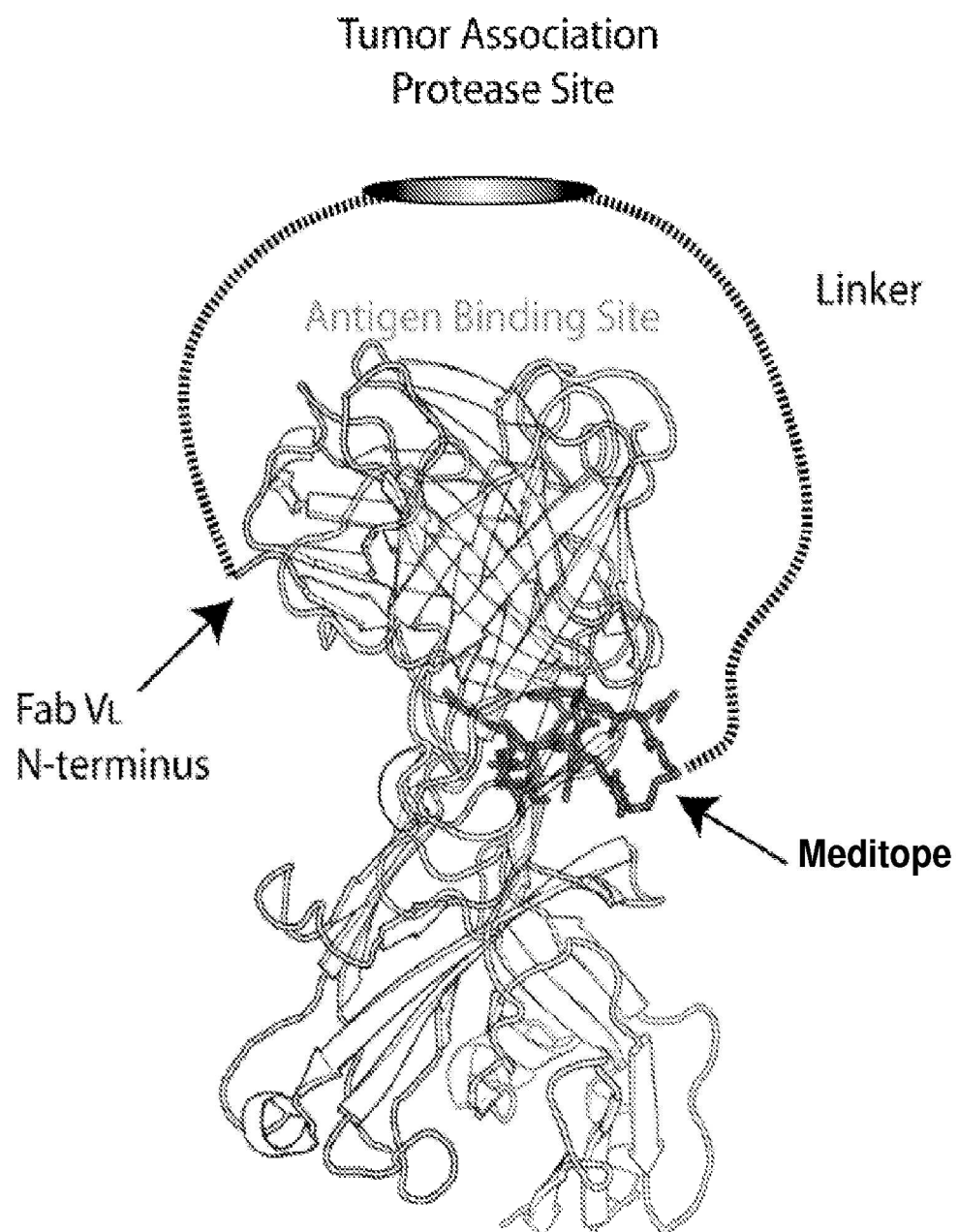
Figure 10

1 2 3 4 5



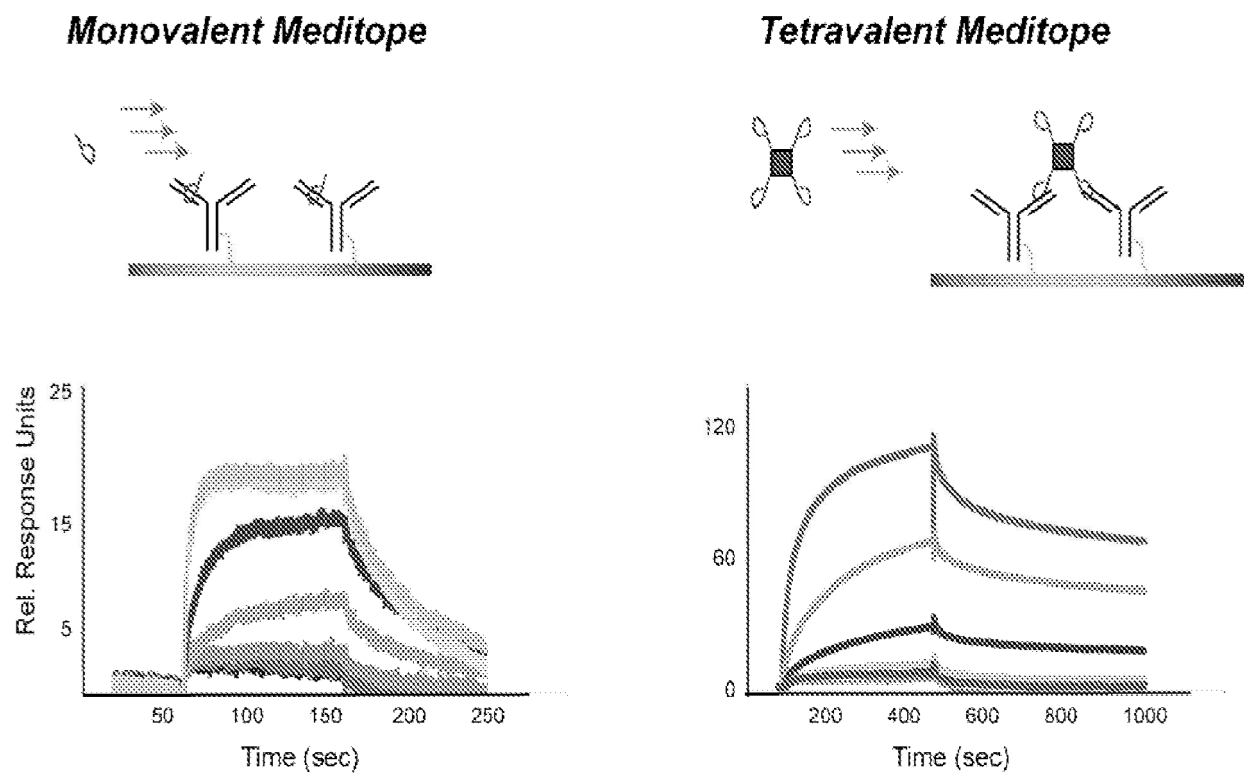
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Figure 11



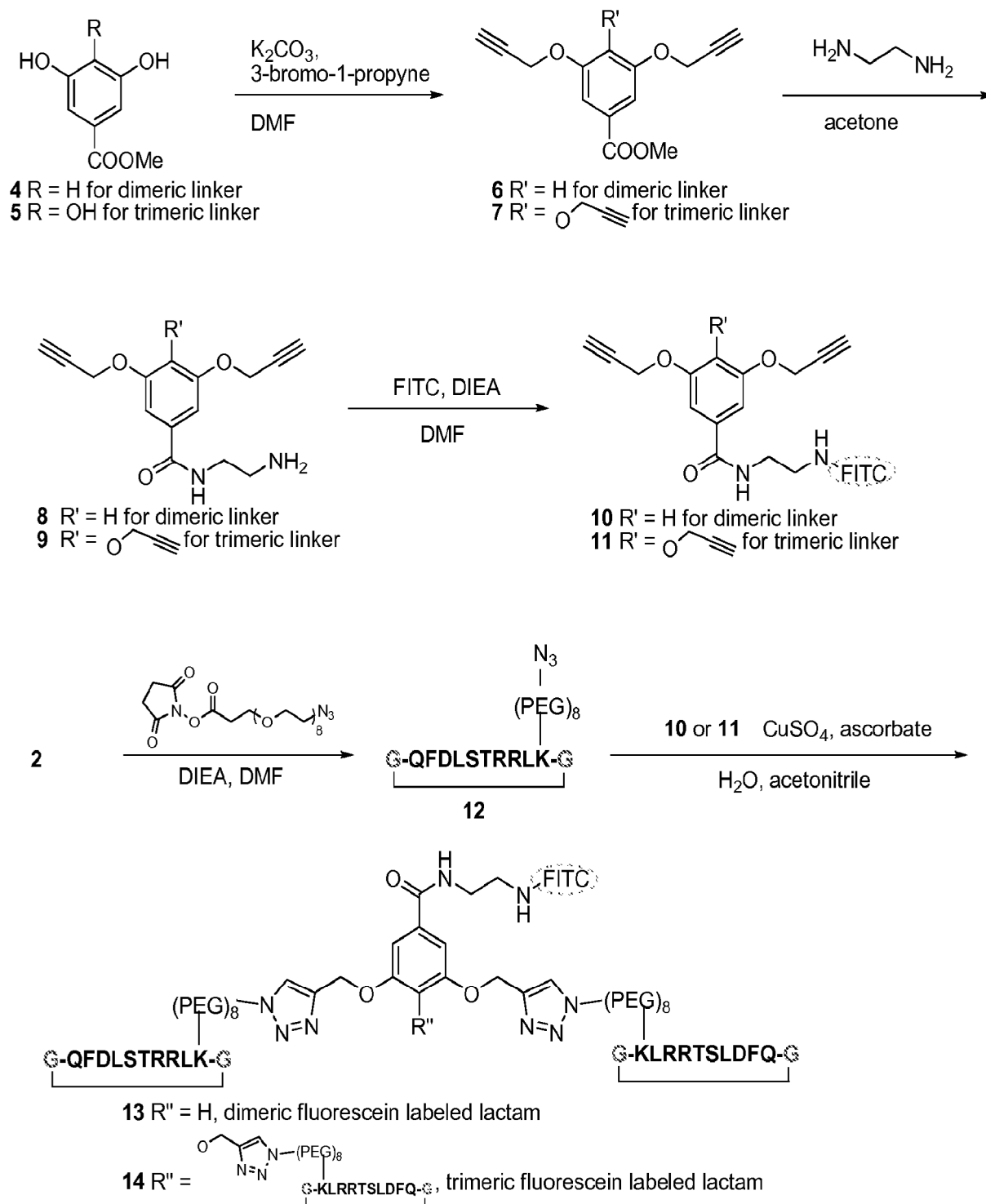
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Figure 12



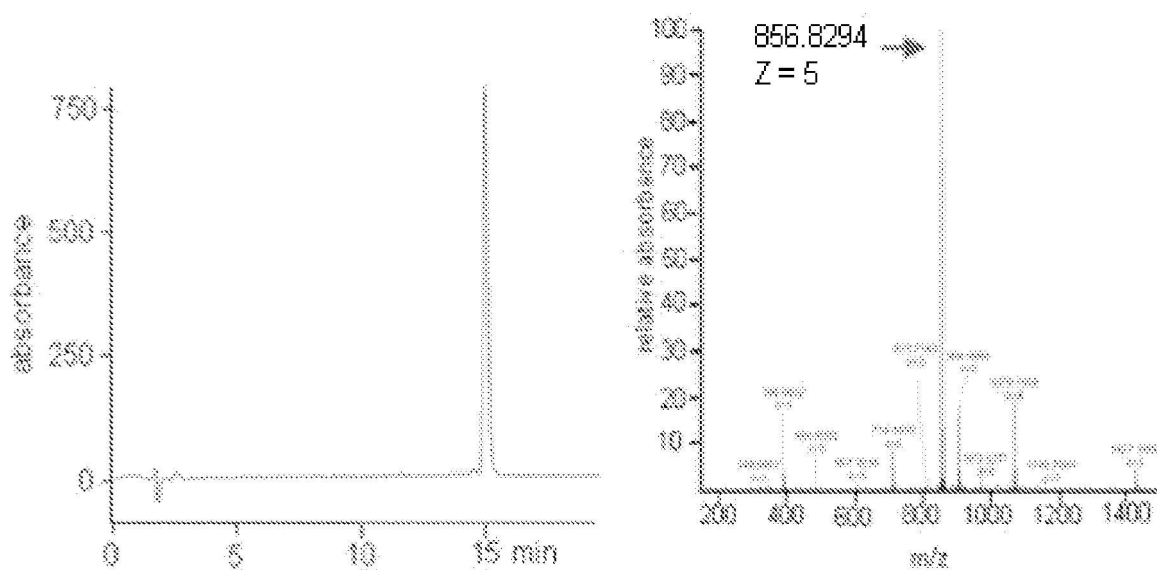
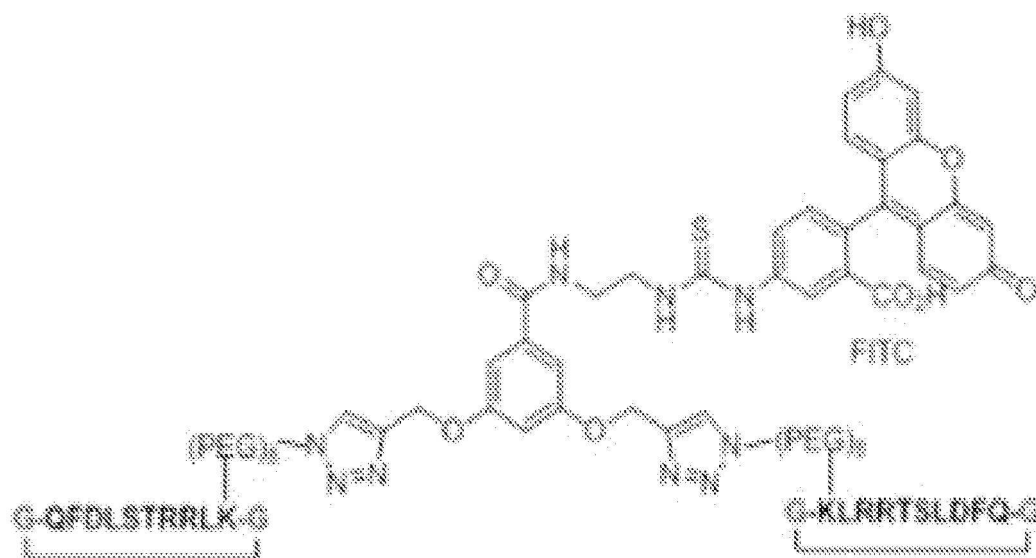
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Figure 13



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Figure 14

for $Z = 5$

Expected MW: 856.8328

Found MW: 856.8294

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Figure 15

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

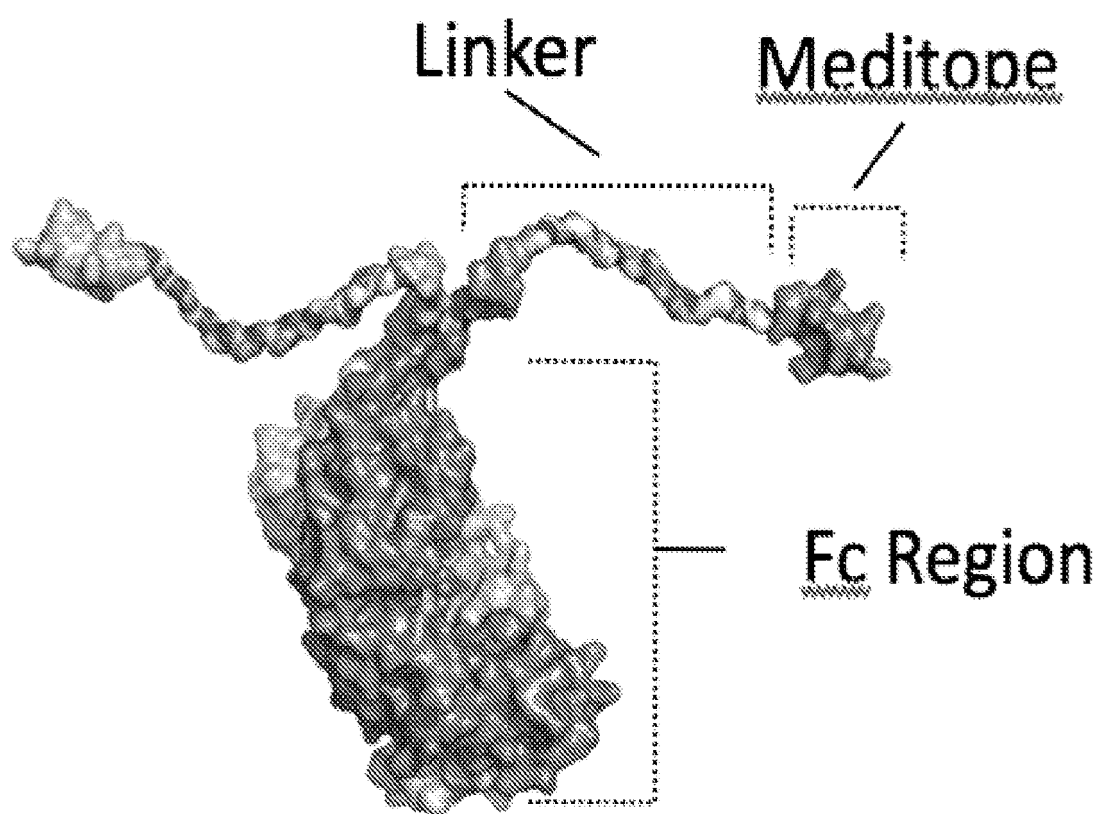
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V V T G V N S C Q F D L S T R R L K C G
gggggctcgggttcaggctcgggoggttcacgggaggagggggaggggaacctaagtca
G G S G S G S G S S G G G G G E P K S
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C D K T H T C P P C P A P E L L G G P S
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V F L F P P K P K D T L M I S R T P E V
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T C V V V D V S H E D P E V K F N W Y V
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D G V E V H N A K T K P R E E Q Y N S T
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K C K V S N K A L P A P I E K T I S K A
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S L S L S P G K -

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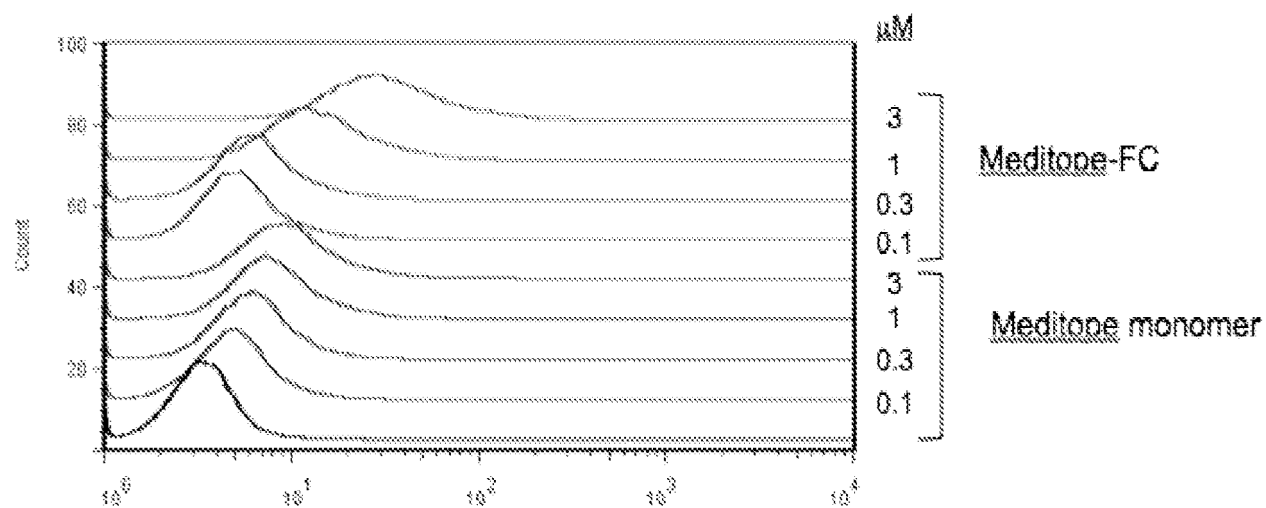
19/34

Figure 16



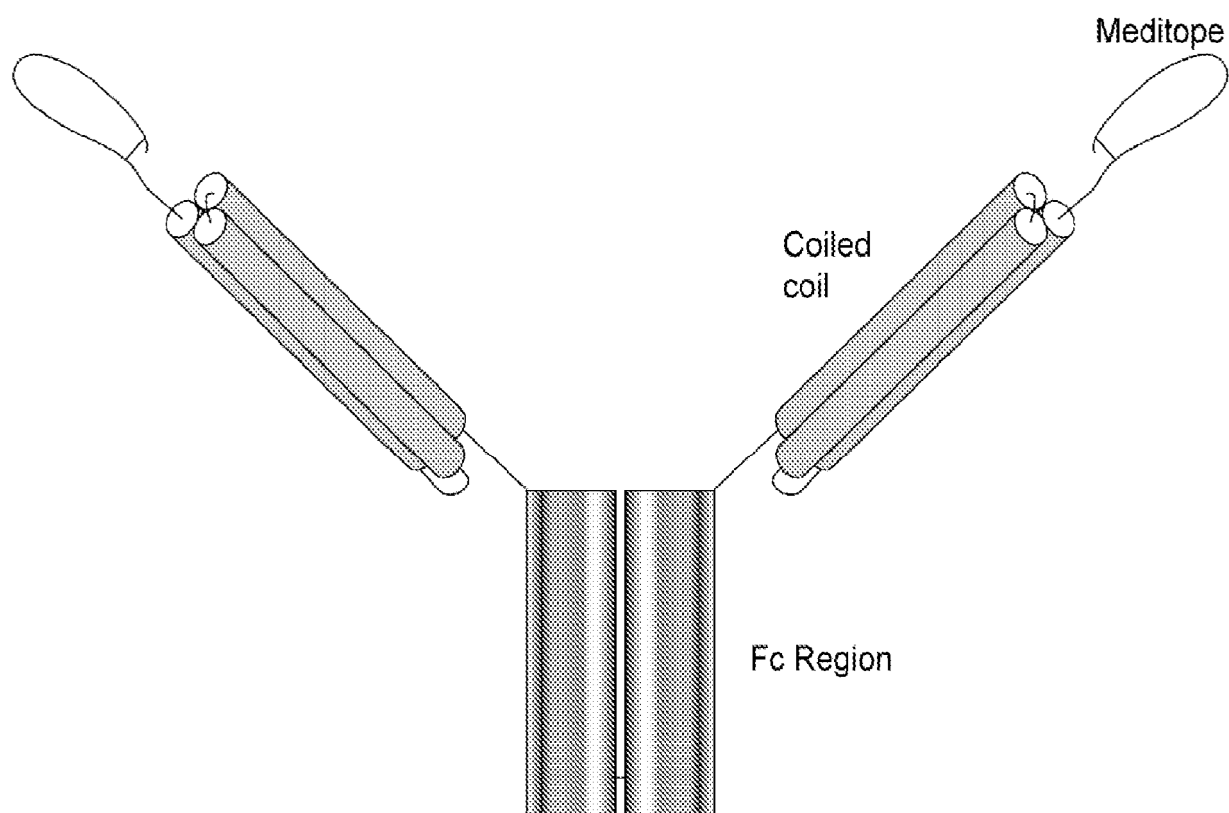
20/34

Figure 17



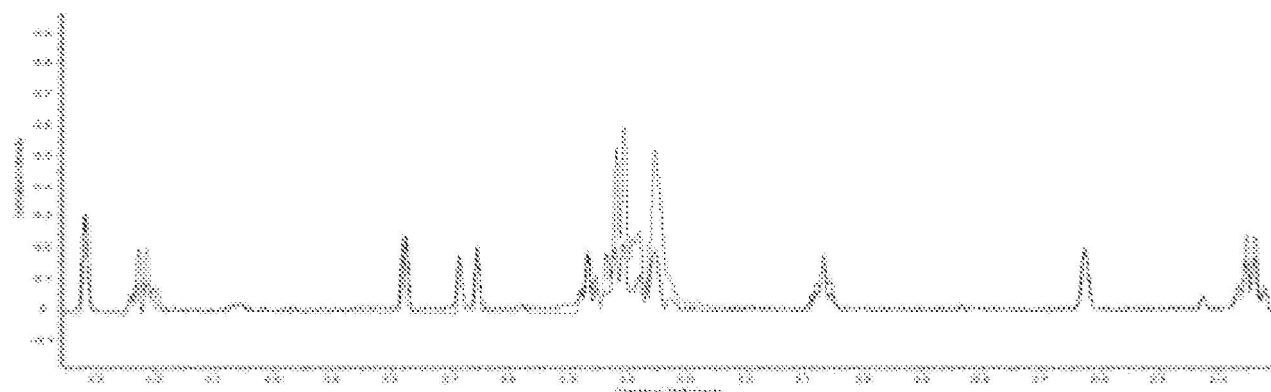
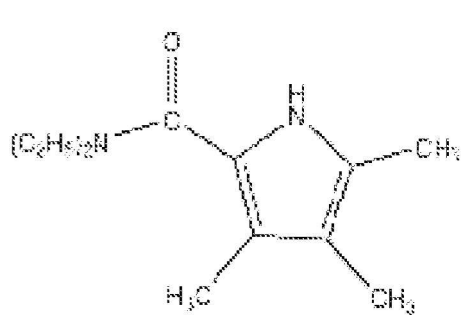
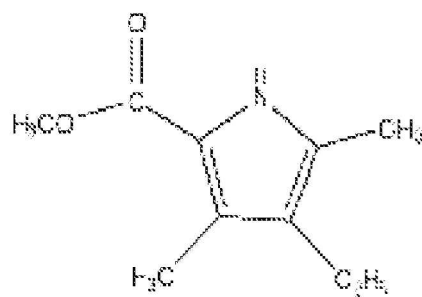
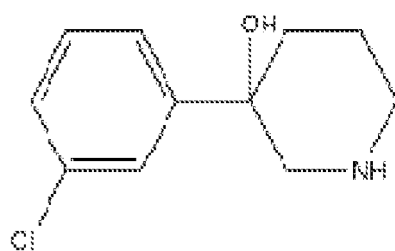
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Figure 18



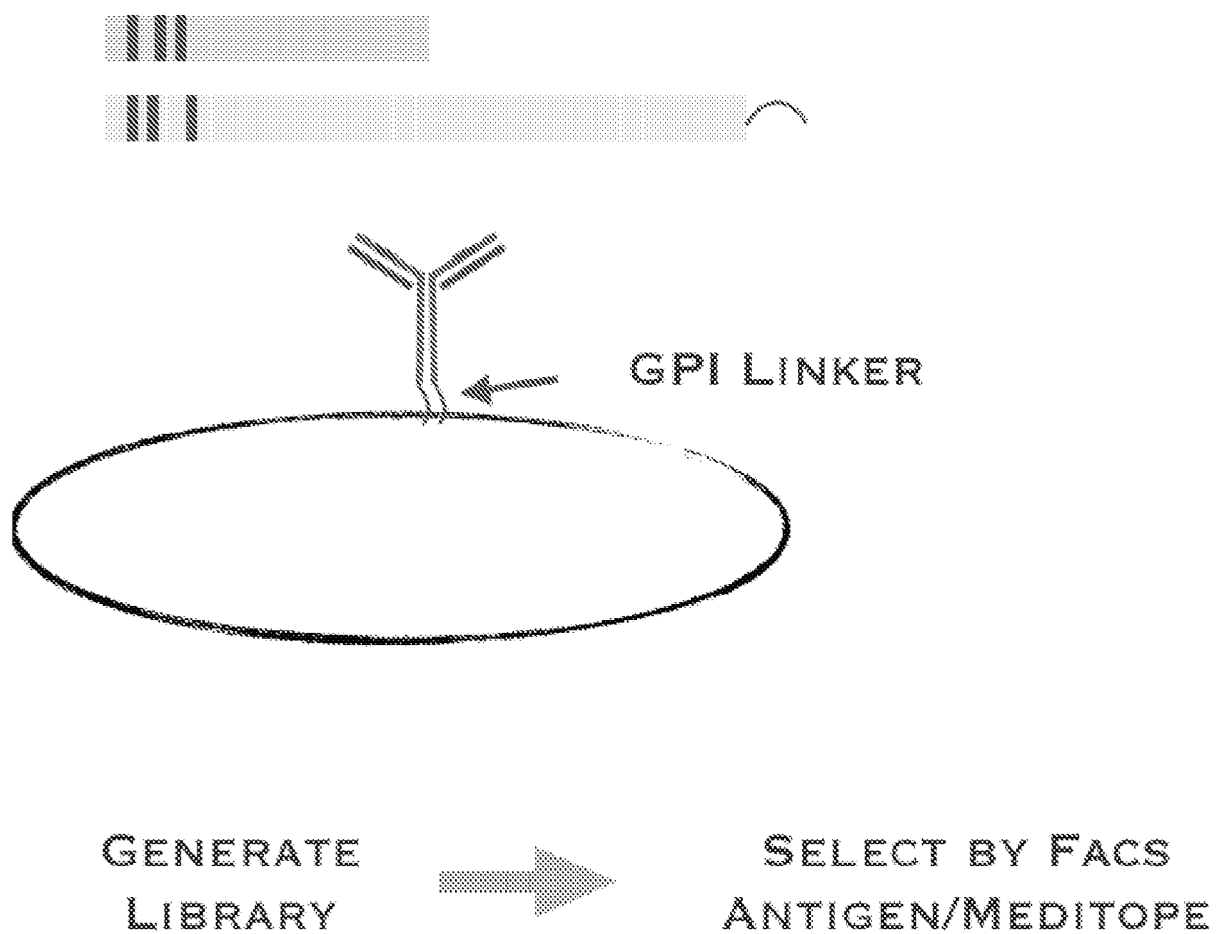
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Figure 19



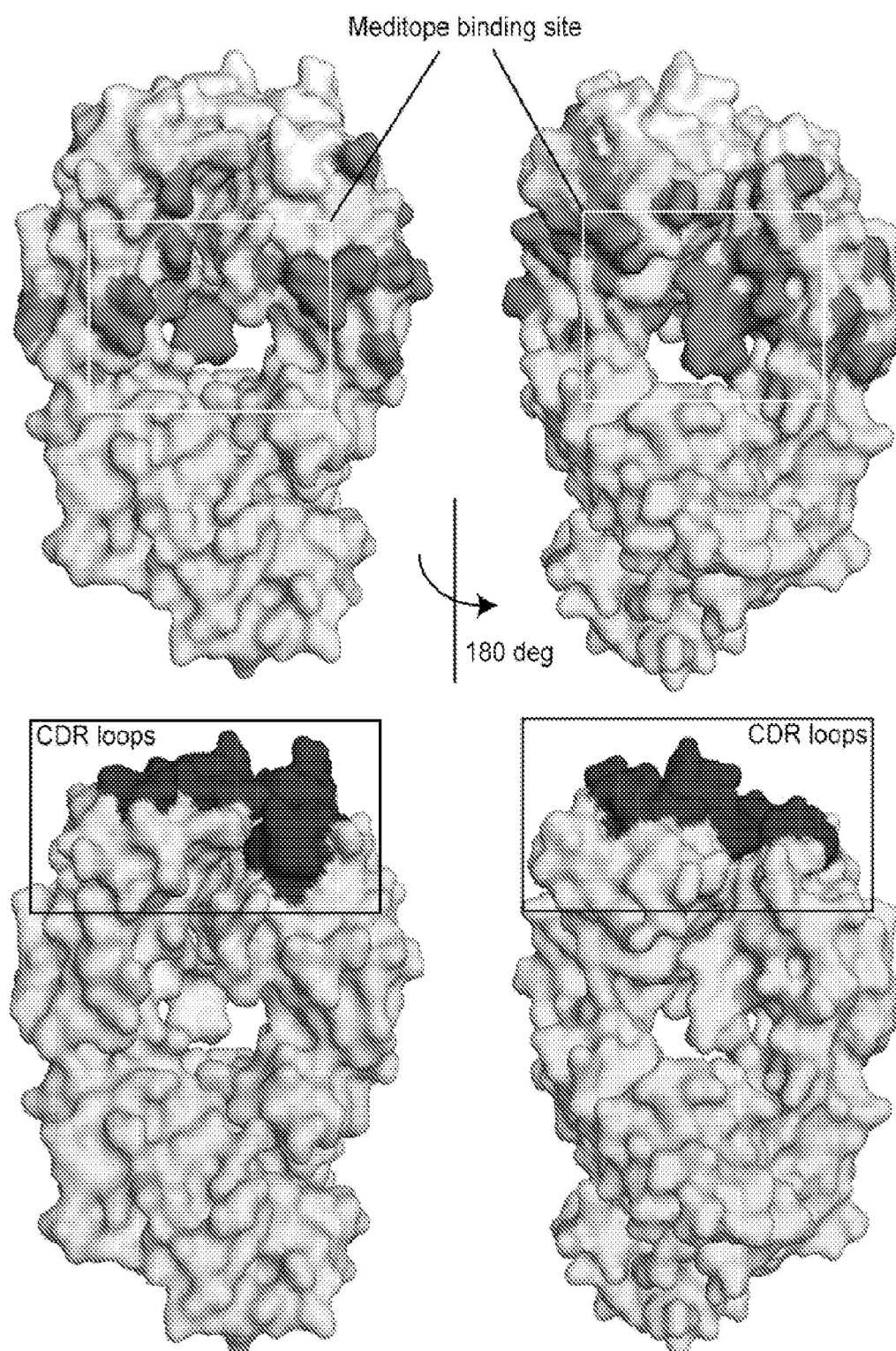
23/34

Figure 20



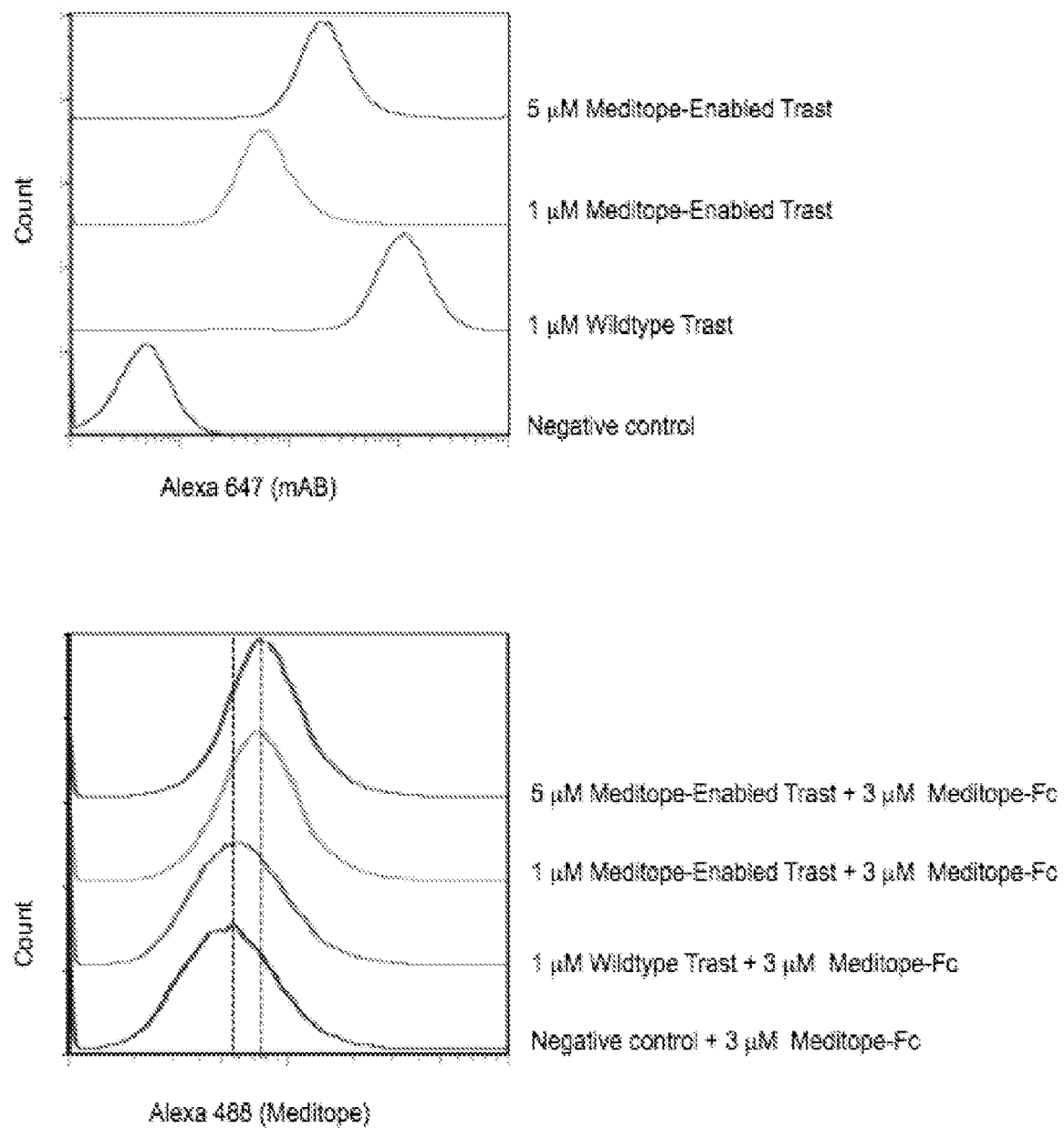
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Figure 21



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Figure 22



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Figure 23A

```

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TCGAATCCGG TGGCGGCTTG GTGCAGCCGG GTGGGTCTGT GCGACTGTCT TGCGCAGCGT CGGGGTTTAA
CATCAAAGAC ACCTATATCC ACTGGGTGAG GCAATCGCCC GGAAAGGGGC TCGAATGGGT AGCCAGAATC
TACCCTACGA ATGGTTATAC TCGATAATCG GACTCCGTGA AAGGAAGATT CACCATCAGC GCAGATACGT
CCAAAAACAC TGCATACCTC CAGATGAATA GCCTTCGGGC GGAGGACACG GCGATCTACT ACTGTAGCCG
GTGGGGTGGG GACGGGTTCT ATGCGATGGA CTACTGGGGA CAGGGGACGC TTGTAACGGT CAGCTCGGCG
TCAACAAAGG GACCTAGCGT GTTTCCTTG GCTCCCTCAT CGAAATCAAC GTCCGGTGGG ACGGCGGCAT
TGGGGTGTCT TGCAAGGAC TATTTCCCG AGCCCGTGAC AGTCTCGTGG AACTCGGGTG CCCTTACAAG
CGGCGTACAT ACGTTTCCCG CCGTGCTCCA ATCATCCGGA CTGTATTCCC TTTCAICCGT CGTGACTGTG
CCGTCTCTGT CACTCGGAAC GCAAACCTAC ATTTGCAATG TCAACCACAA ACCGTCAAAT ACAAAGGTCG
ATAAGAAGGT CGAGCCAAAG TCGTGTGATA AGACCCACAC ATGCCCTCCC TGTCCAGCGC CGGAGCTGTT
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GTGACGTGTG TCGTCGTCGA TGTCTCACAT GAGGACCCGG AGGTAAAGTT CAACTGGTAC GTGGATGGAG
TCGAAGTGCA CAACGCAAAA ACAAAACCTC GGAAGAGCA GTACAATAGC ACGTACAGAG TAGTCAGCGT
GCTCACCCTG CTGCACCAGG ATTGGCTCAA TGGAAAGGAG TACAAGTGTA AAGTGTGCGA TAAGGCGCTG
CCTGCCCCCA TCGAAAAGAC AATTTCCAAA GCTAAAGGGC AACCCCGCGA GCCGCAAGTA TACACCCTCC
CACCTCGCG CGATGAACTG ACCAAGAACC AGGTGTGATT GACGTGTCTC GTCAAGGGCT TCTATCCGAG
CGACATTGCA GTAGAAATGG AAAGCAACGG ACAGCCGGAA AACAACCTACA AGACTACACC GCCTGTCCCTT
GATTCGGATG GTTCTTCTT TCTTTACTCA AAACCTACAG TCGACAAATC GAGGTGGCAG CAGGGAAAATG
TGTTTTCTGT 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  KGRFTISADTSKNTAYLQMNSLRAEDTAYYCSRWGGDGFYAMDYWGQGLTVTVSSASTK
      .....
WT    KGRFTISADTSKNTAYLQMNSLRAEDTAYYCSRWGGDGFYAMDYWGQGLTVTVSSASTK
          70      80      90      100     110     120

          130     140     150     160     170     180
Medi  GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
      .....
WT    GPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
          130     140     150     160     170     180

```

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Figure 23C

```

ATGGAGACAG ACACGCTTTT GCTTTGGGIG TTGTTGTTGT GGGTCCCCGG TTCGACGGGG GATATTCAGA
TGACCCAGTC ACCGATCCTT CTCTCGGCGA GCGTGGGGGA TAGAGTAACG ATCACGTGTA GAGCGTCCCA
AGACGTCAAC ACAGCTGTCG CGTGGTATCA GCAGCGGACA AATGGATCGC CGAGGCTCCT GATCTACAGC
GCATCATTTT TCTATTCGGG AGTCCCCTCC CGATTTTCCG GATCGCGCAG CGGTACTGAC TTCACCCTCA
CGATTTCTTC CCTTCAACCG GAAGATATCG CTGATTACTA CTGTCAGCAG CACTATACAA CACCTCCCAC
TTTCGGAGCA GGGACAAAAG TGGAGATTAA GCGCACTGTA GCAGCCCCCT CGGTCITTAT CTTCCTCCT
AGCGACGAAC AATTGAAGTC AGGGACCGCC TCGGTGGTAT GCCTGCTTAA CAACTTTTAC CCACGGGAAG
CCAAAGTACA GTGGAAGGTG GATAATGCGC TCCAGAGCGG AAACGCCCAA 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  DIQMTQSPELLSASVGDRVITICRASQDVNTAVAWYQQRINGSPRLLIYSASFLYSGVPS
      .....
WT    DIQMTQSPELLSASVGDRVITICRASQDVNTAVAWYQQRINGSPRLLIYSASFLYSGVPS
      10      20      30      40      50      60

      70      80      90      100     110     120
medi  RFSGSRSGTDFLTISSLQPEDIAYYCQOHYTTPTFGAGTKVEIKRTVAAPSVFIFPP
      .....
WT    RFSGSRSGTDFLTISSLQPEDIAYYCQOHYTTPTFGAGTKVEIKRTVAAPSVFIFPP
      70      80      90      100     110     120

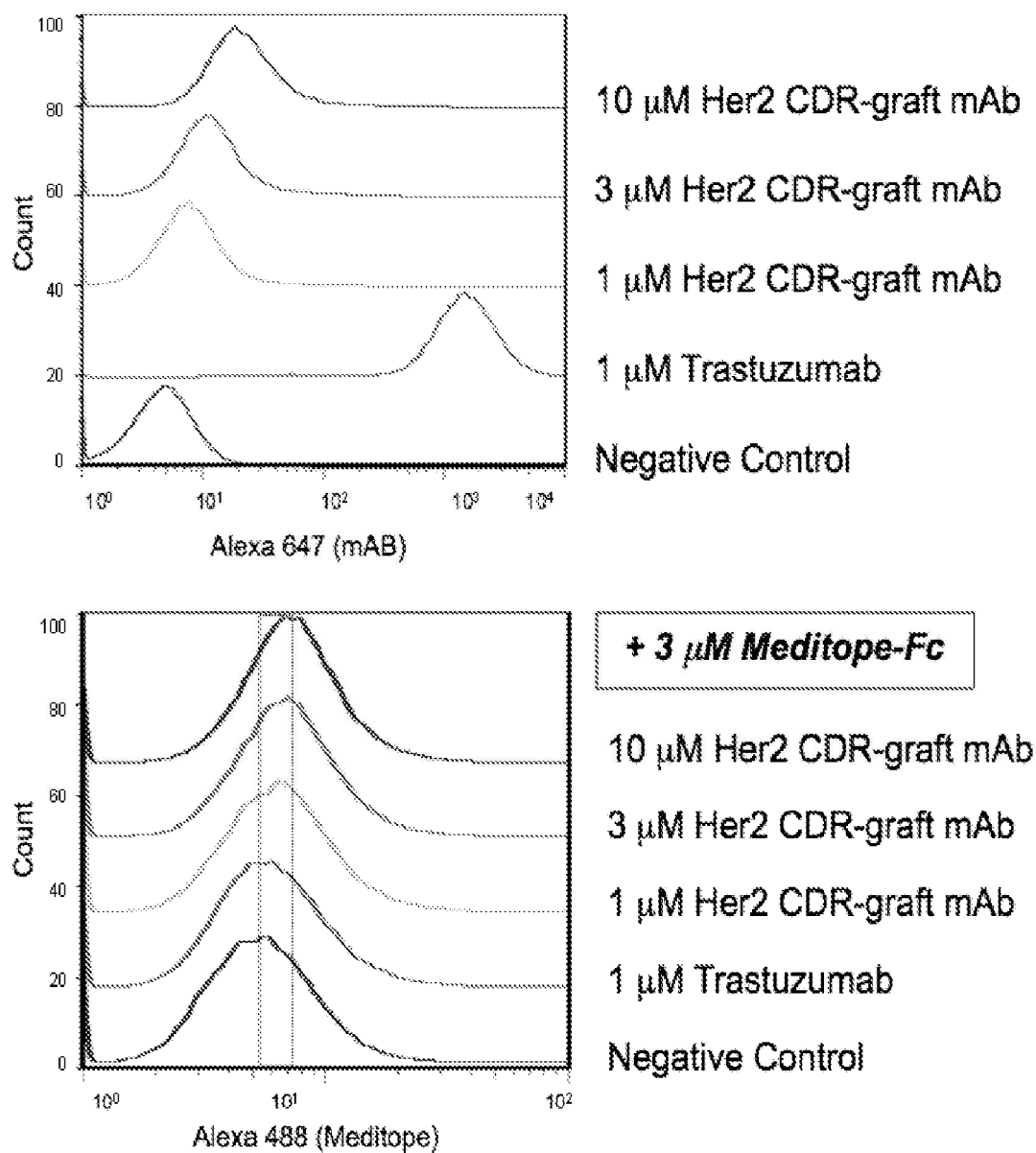
      130     140     150     160     170     180
medi  SDEQLKSGTASVVCLLNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
      .....
WT    SDEQLKSGTASVVCLLNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLT
      130     140     150     160     170     180

      190     200     210
medi  LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
      .....
WT    LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
      190     200     210

```

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Figure 24



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Figure 25A

T C A T A T A G G G G A A G C T T G C G C C C C A C C A T G A A A T G C T G T G G G T G A T C T T T T C C T T T G
S L - G K L A A T M K C S W V I F F L M
G C G G T A G T A A C C G G A G T T A A C T C C G A G G T C C A G C T C G T C G A A T C C G G T G G C G G C T T G G T
A V V T G V N S E V Q L V E S G G G L V
C A G C G G G T G G G T C G T T G C G A C T G T C G T G C G C A G C G T C G G G G T T T A A C A T C A A A G A C A C C
Q P G G S L R L S C A A S G F N I K D T
T A T A T C C A C T G G G T G A G G C A A G C G C C C G G A A A G G G G C T C G A A T G G G T A G C C A G A A T C T A C
Y I H W V R Q A P G K G L E W V A R I Y
C C T A C G A A T G G T T A T A C T C G A T A T G C G G A C T C C G T G A A A G G A A G A T T C A C C A T C A G C G C A
P T N G Y T R Y A D S V K G R F T I S A
G A T A C G T C C A A A A C A C T G C A T A C C T C C A G A T G A A T A G C T T C G G G C G G A G G A C A C G G C G
D T S K N T A Y L Q M N S L R A E D T A
G T C T A C T A C T G T A G C C G G T G G G G T G G G G A C G G G T T C T A T G C G A T G G A C T A C T G G G G A C A G
V Y Y C S R W G G D G F Y A M D Y W G Q
G G G A C G C T T G T A A C G G T C A G C T C G G C T A G C A A A G G G A C C T A G C G T G T T C C C T T G G C T
G T L V T V S S A S T K G P S V F P L A
C C C T C A T C G A A A T C A A C G T C C G G T G G G A C G G C G G C A T T G G G G T G T C T T G T C A A G G A C T A T
P S S K S T S G G T A A L G C L V K D Y
T T C C C C G A G C C C G T G A C A G T C T C G T G G A A C T C G G G T G C C C T T A C A A G C G G C G T A C A T A C G
F P E P V T V S W N S G A L T S G V H T
T T C C C G C G C G T G C T C C A A T C A T C C G G A C T G T A T T C C C T T T C A T C C G T C G T G A C T G T G C C G
F P A V L Q S S G L Y S L S S V V T V P
T C C T C G T C A C T C G G A A C G A A A C T T A C A T T T G C A A T G T C A A C C A C A A A C C G T C A A A T A C A
S S S L G T Q T Y I C N V N H K P S N T
A A G G T C G A T A A G A A G G T C G A G C C A A A G T C G T G T G A T A A G A C C C A C A C A T G C C C T C C C T G T
K V D K K V E P K S C D K T H T C P P C
C C A G C G C C G G A G C T G T T G G G A G G G C C T T C A G T G T T C C T C T T C C C G C C C A A A C C C A A G G A C
P A P E L L G G P S V F L F P P K P K D
A C C C T G A T G A T T A G C C G C A C A C C C G A G G T G A C G T G T G T C G T C G T C G A T G T C T C A C A T G A G
T L M I S R T P E V T C V V V D V S H E
G A C C C G G A G G T A A A G T T C A A C T G G T A C G T G G A T G G A G T C G A A G T G C A C A A C G C A A A A A C A
D P E V K F N W Y V D G V E V H N A K T
A A A C C T C G G G A A G A G C A G T A C A A T A G C A C G T A C A G A G T A G T C A G C G T G C T C A C C G T G C T G
K P R E E Q Y N S T Y R V V S V L T V L
C A C C A G G A T T G G C T C A A T G G A A A G G A G T A C A A G T G T A A A G T G T C G A A T A A G G C G T G C C T
H Q D W L N G K E Y K C K V S N K A L P
G C C C C C A T C G A A A A G A C A A T T T C C A A A G C T A A A G G G C A A C C C C G C G A G C C G C A A G T A T A C
A P I E K T I S K A K G Q P R E P Q V Y
A C C C T C C C A C C C T C G C G C A T G A A C T G A C C A A G A A C C A G G T G T C A T T G A C G T G T C T C G T C
T L P P S R D E L T K N Q V S L T C L V
A A G G G C T T C T A T C C G A G C G A C A T T G C A G T A G A A T G G G A A G C A A C G G A C A G C C G G A A A A C
K G F Y P S D I A V E W E S N G Q P E N
A A C T A C A A G A C T A C A C C G C C T G T C C T T G A T T C G G A T G G T T C C T T C T T T C T T T A C T C A A A A
N Y K T T P P V L D S D G S F F L Y S K
C T T A C A G T C G A C A A A T C G A G G T G G C A G C A G G G A A A T G T G T T T T C G T G C A G C G T G A T G C A C
L T V D K S R W Q Q G N V F S C S V M H
G A G G C C T T G C A T A A T C A C T A T A C A G A A G T C G T T G T C A C T G T C G C G G G A A A G T A A T G A
E A L H N H Y T Q K S L S L S P G K - -

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Figure 25B

ataggggaagcttgccgccaccatggagacagacacgcttttgctttgggtggttgttgttg
- G K L A A T M E T D T L L L W V L L L
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W V P G S T G D I Q M T Q S P S S L S A
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S V G D R V T I T C R A S Q D V N T A V
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A W Y Q Q K P G K A P K L L I Y S A S F
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L Y S G V P S R F S G S R S G T D F T L
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T I S S L Q P E D F A T Y Y C Q Q H Y T
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L Q S G N S Q E S V T E Q D S K D S T Y
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tgctaataga
C - -

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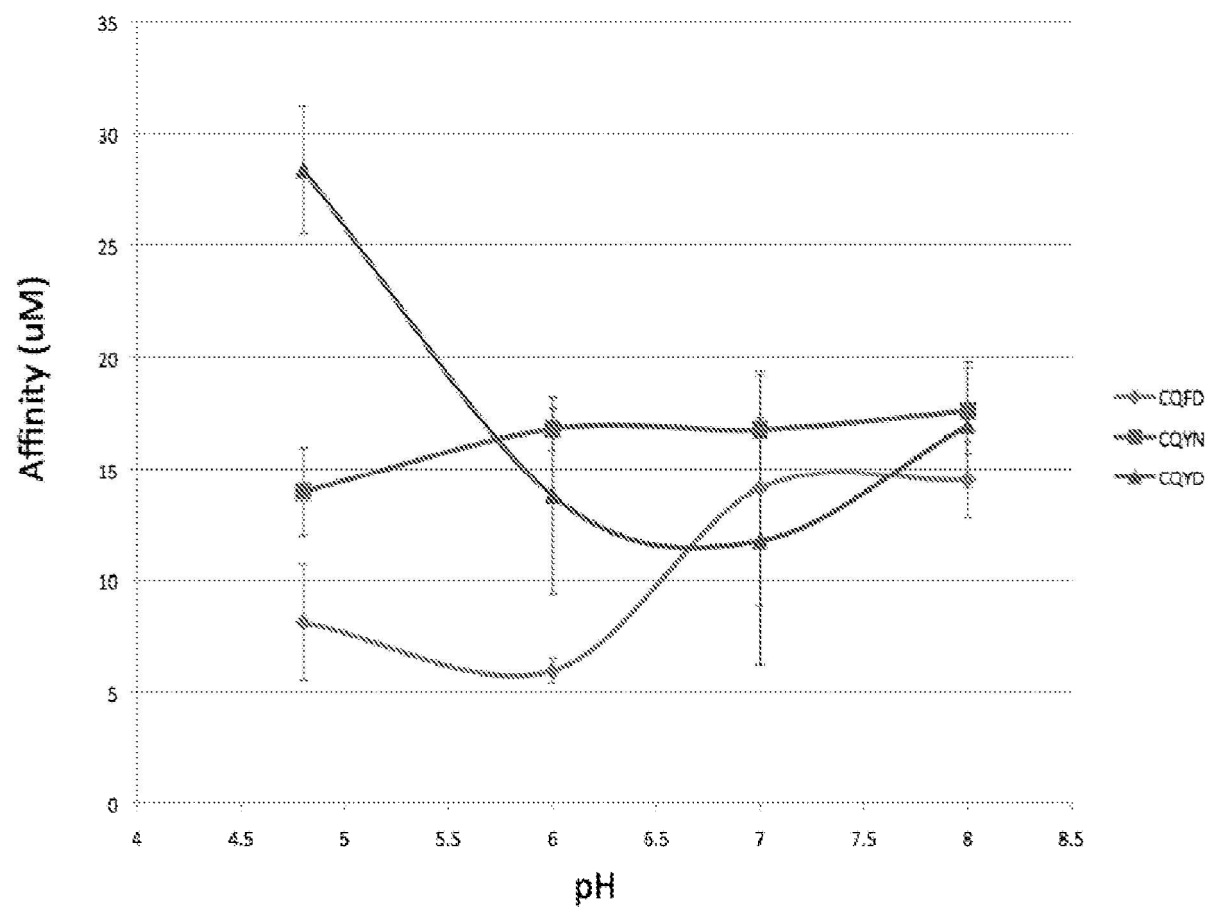
Figure 26

1YY9_D PDBID CHAIN SEQUENCE	QVQLKQSGPGLVQPQSLSITCTVSGFSLTNYGVHWVRQSPGK	49
2R56_H PDBID CHAIN SEQUENCE	QVSLRESGGGLVQPGRSLRLSCTASGFTFRHHGMTWVRQAPGKGLEWVAS	50
	.*:.* *.*:.* :.*.**:.* :.*: ***.*****:.*	
1YY9_D PDBID CHAIN SEQUENCE	VIWGGNTDYNTPTFTSRLSINKDNSKSQVFFKMNSLQSNDAIYYCARAL	99
2R56_H PDBID CHAIN SEQUENCE	LSGSGTKTHFADSVKGRFTISRDNSENNTLYLQMDNVRDEDAIYYCAKAK	100
	: ** :*.:*:*:*:*:. :*:.*:.*:.*:.*:.*:.*:.*	
1YY9_D PDBID CHAIN SEQUENCE	TYIDY-EFAYWGQGLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLV	148
2R56_H PDBID CHAIN SEQUENCE	RVGATGYFDLWGRGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV	150
	* **:*	
1YY9_D PDBID CHAIN SEQUENCE	KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ	198
2R56_H PDBID CHAIN SEQUENCE	KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ	200

1YY9_D PDBID CHAIN SEQUENCE	TYICNVNHKPSNTKVDKRVPEPKS	221
2R56_H PDBID CHAIN SEQUENCE	TYICNVNHKPSNTKVDKKAEP--	221
	*****:.*	

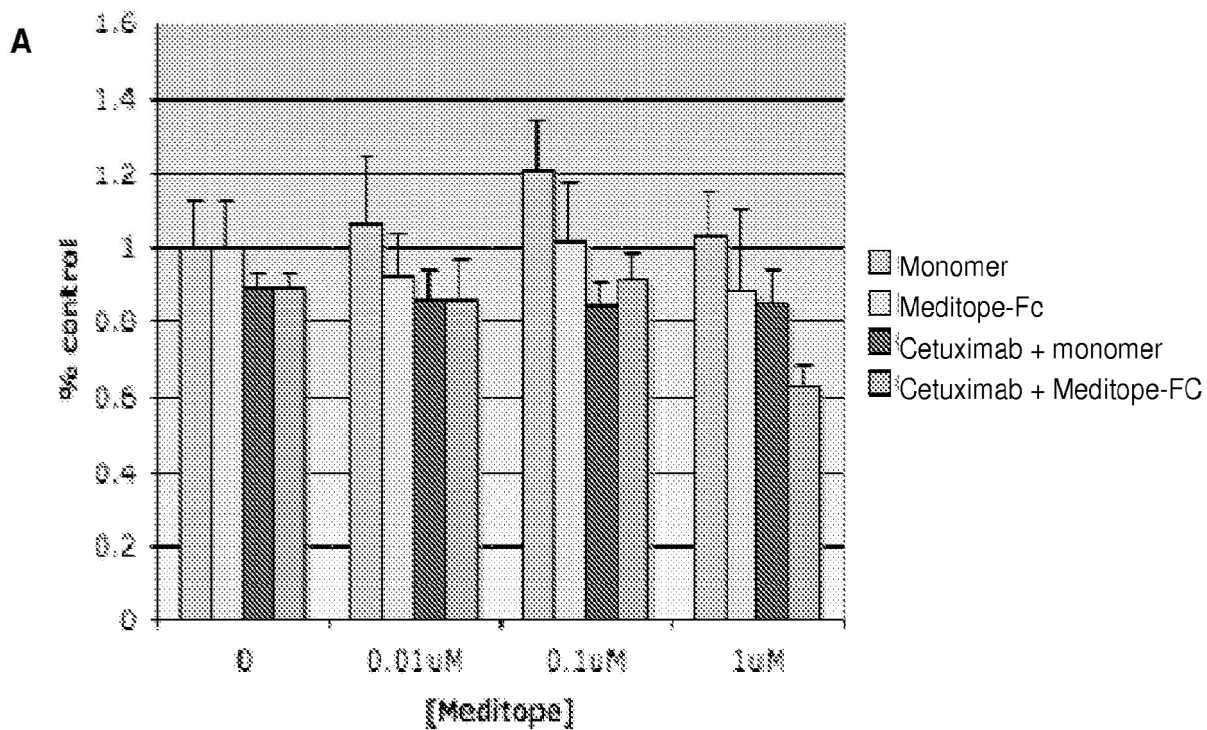
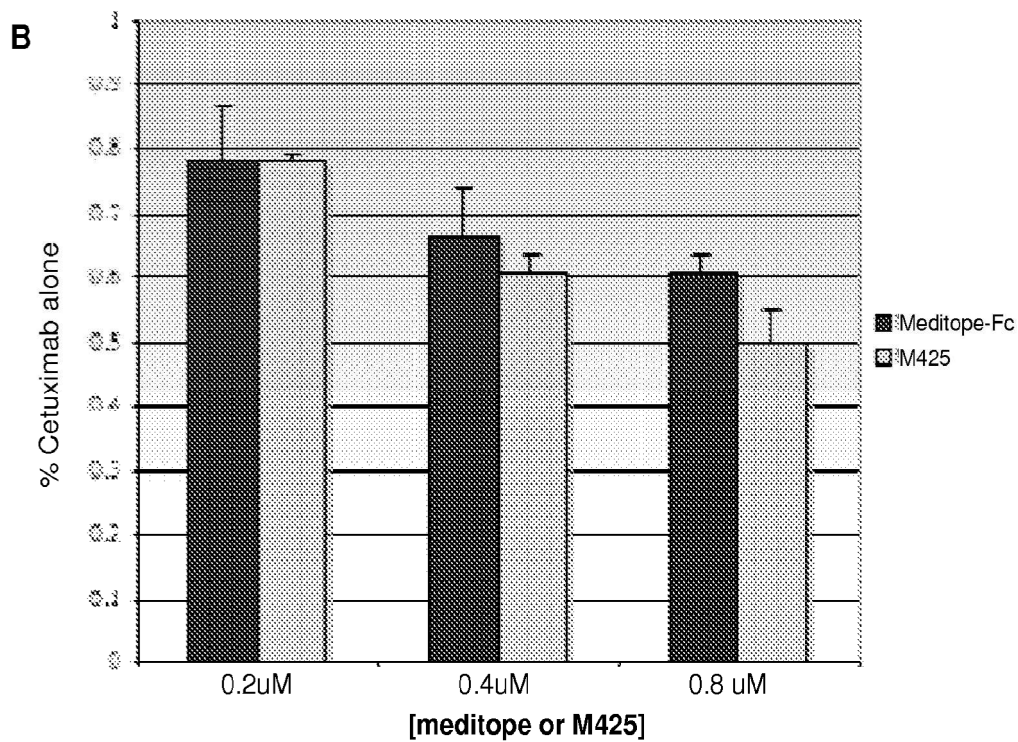
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Figure 27



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Figure 28



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Figure 29

