

FIG. 1A

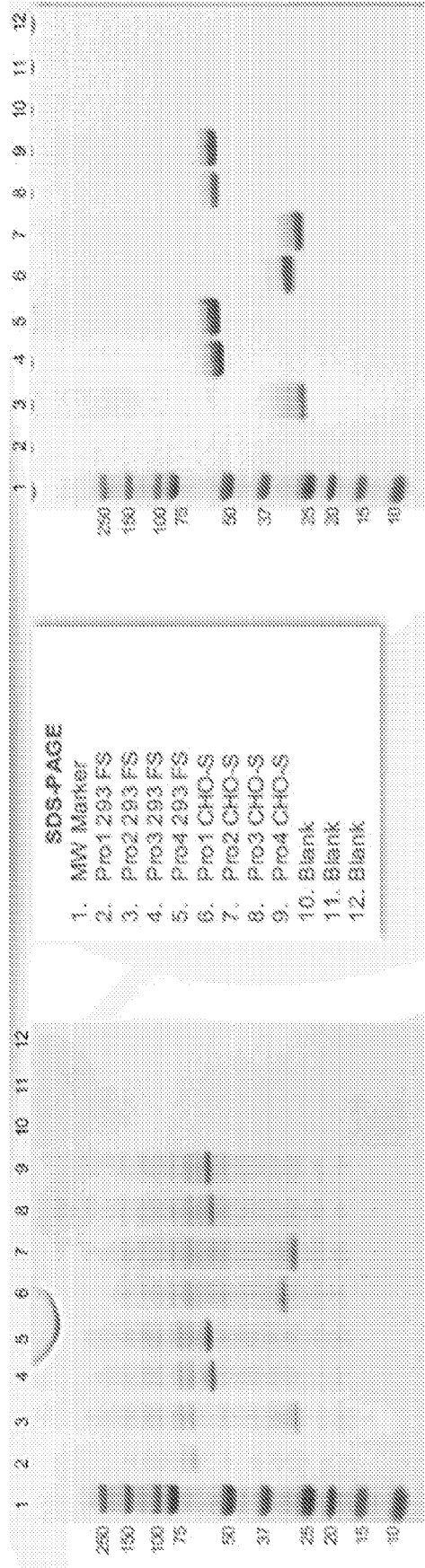


FIG. 1B

Lot No.	Sample Description	Extinction Coefficient	Concentration (mg/mL)	Volume (mL)	Total (mg)	Harvest Volume (mL)	Back-Calculated Titer (mg/L)
BP-016-016-1	Pro1 293 FS	2.26	0.00	5	0.00	24.4	00.0
BP-016-016-2	Pro2 293 FS	2.09	0.33	5	1.67	23	72.4
BP-016-016-3	Pro3 293 FS	2.21	0.39	5	1.93	23.9	80.8
BP-016-016-4	Pro4 293 FS	2.23	0.42	5	2.12	22.7	93.4
BP-016-016-5	Pro1 CHO-S	2.28	0.32	5	1.62	21	77.3
BP-016-016-6	Pro2 CHO-S	2.09	0.39	5	1.93	20.8	92.9
BP-016-016-7	Pro3 CHO-S	2.21	0.31	5	1.55	20.8	74.4
BP-016-016-8	Pro4 CHO-S	2.23	0.39	5	1.97	20.6	95.6

FIG. 2A

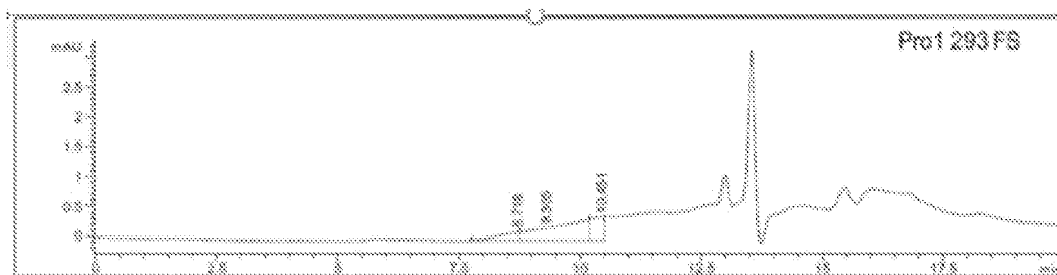


FIG. 2B

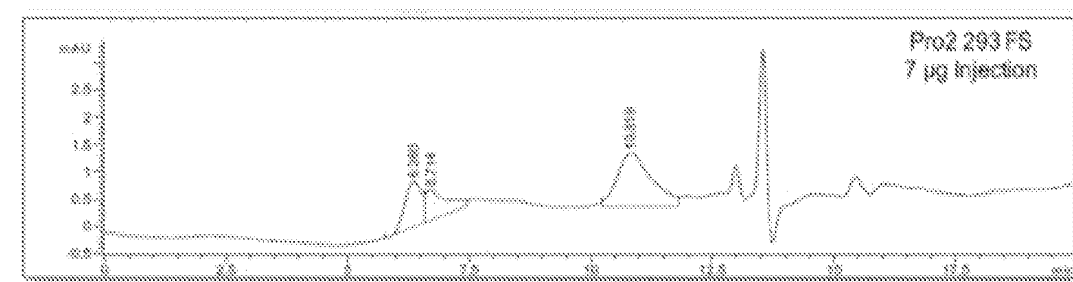


FIG. 2C

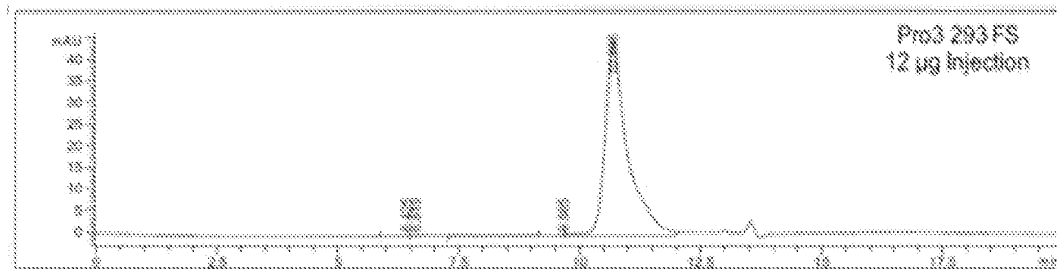


FIG. 2D

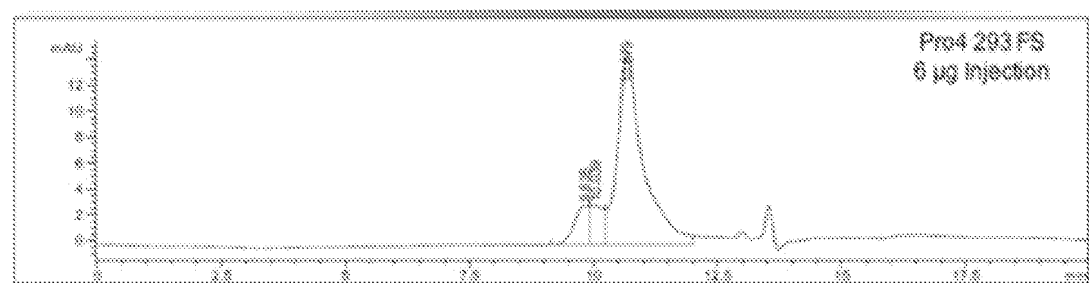


FIG. 3

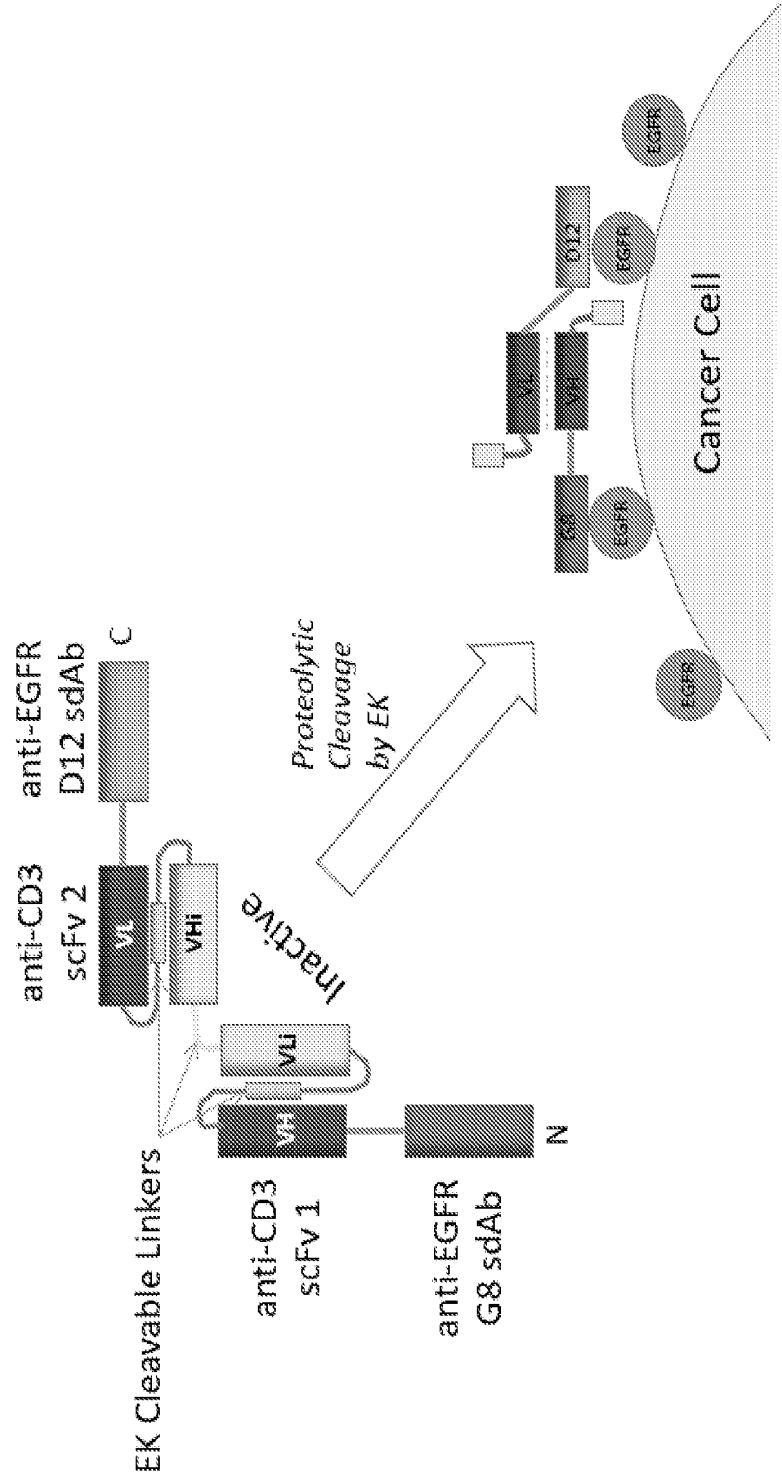


FIG. 4

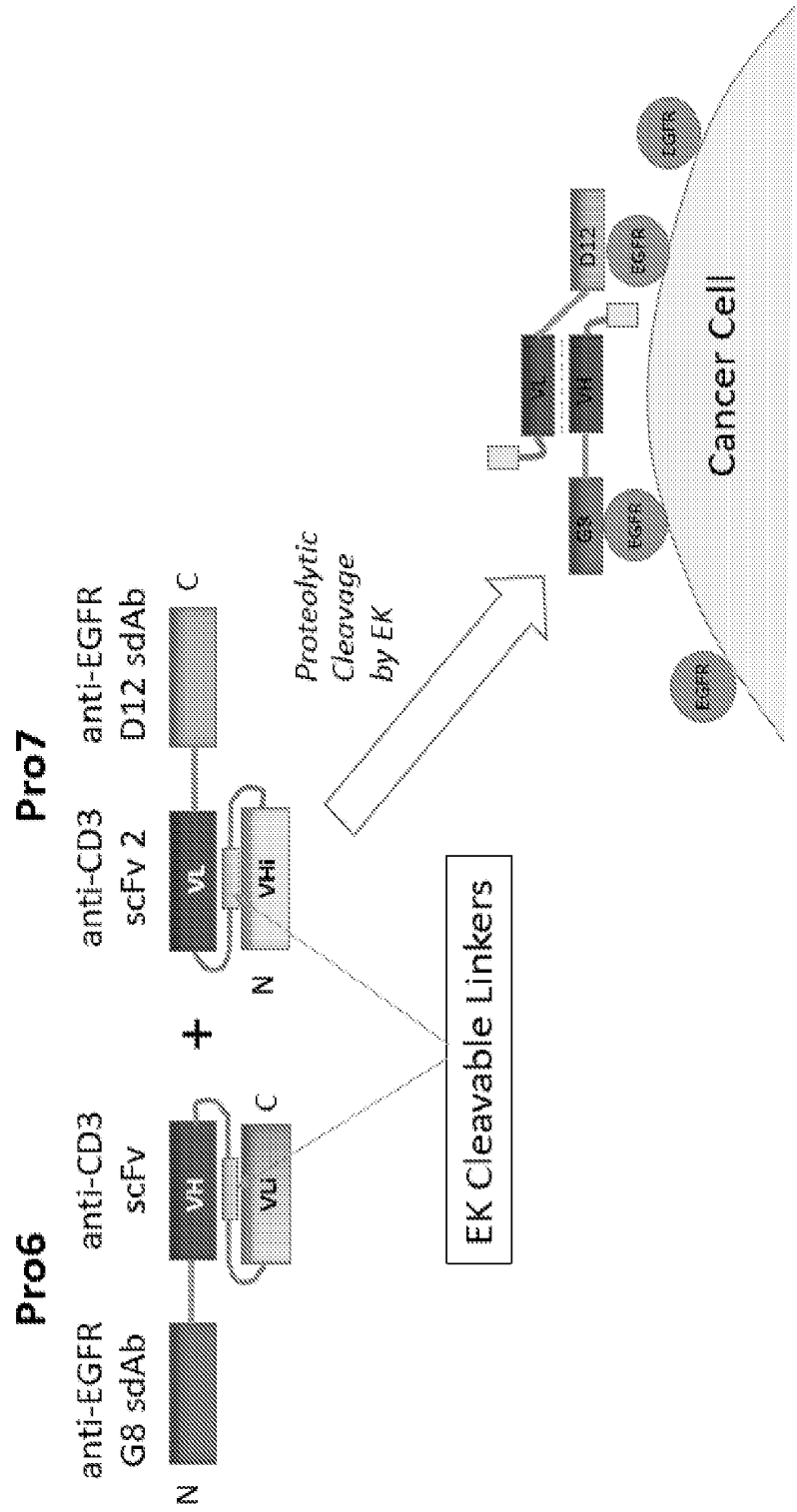


FIG. 5

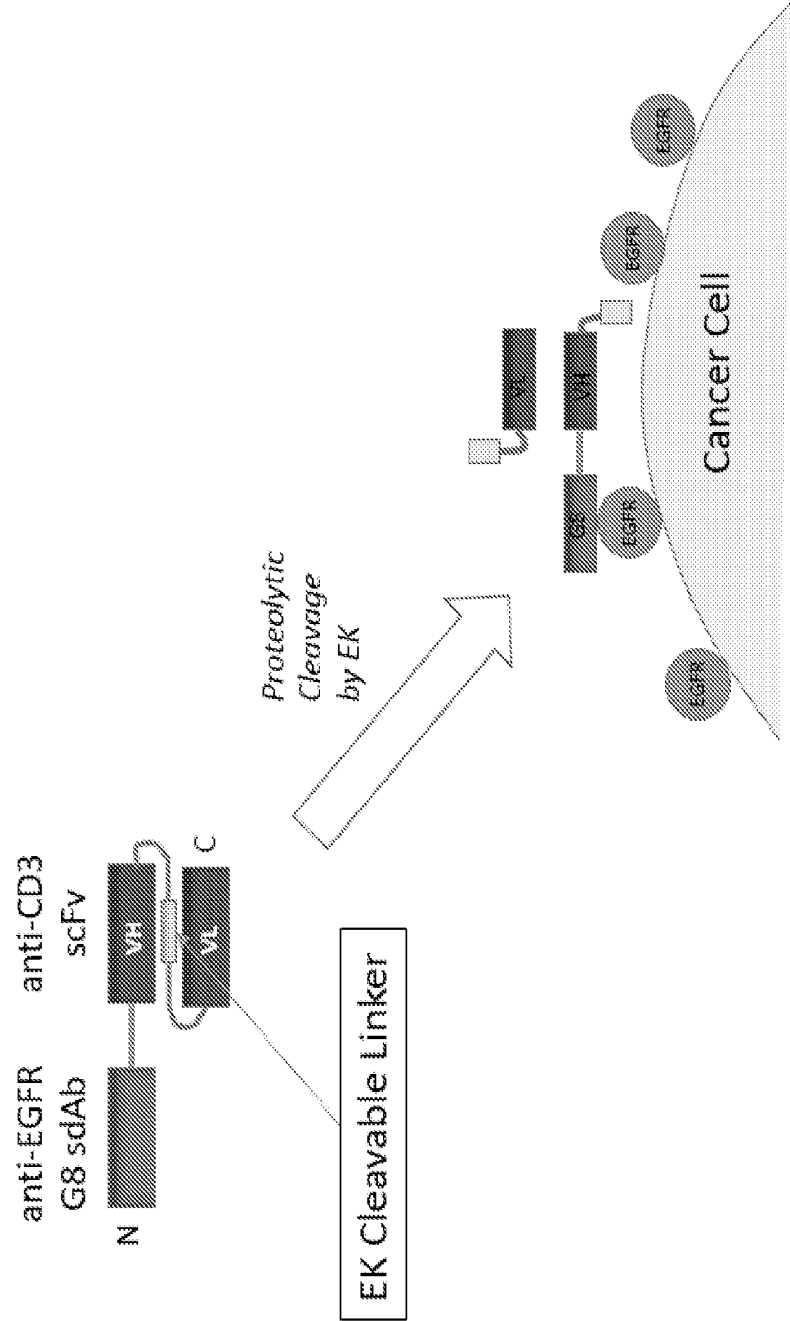


FIG. 6

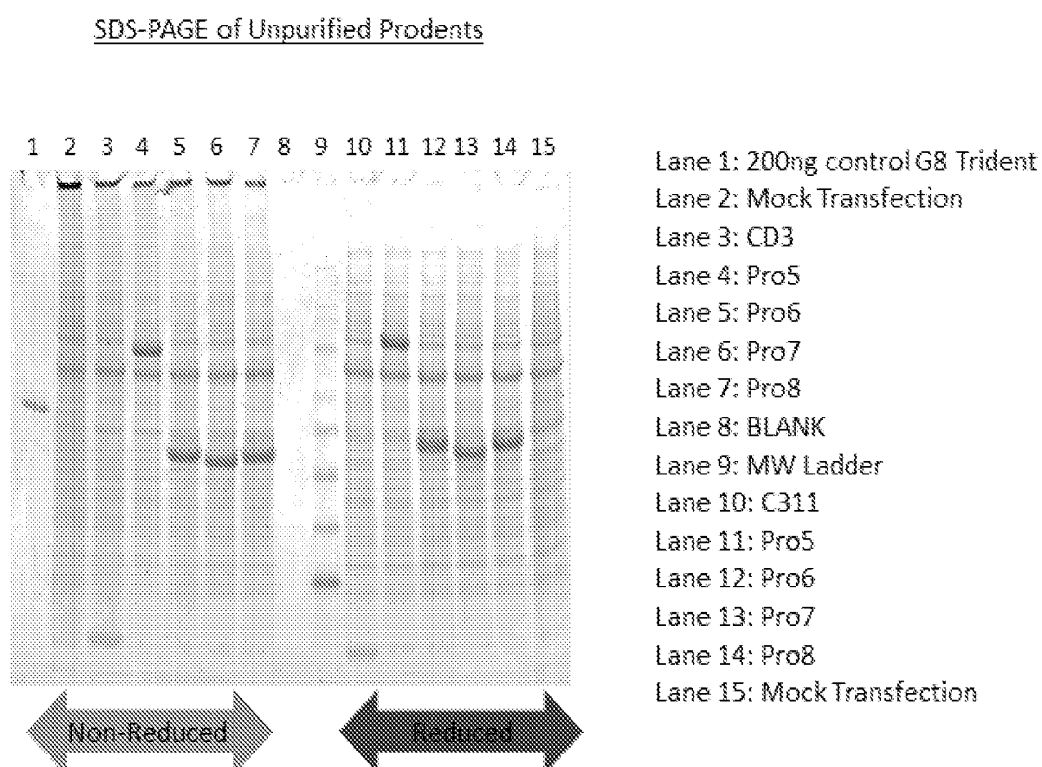
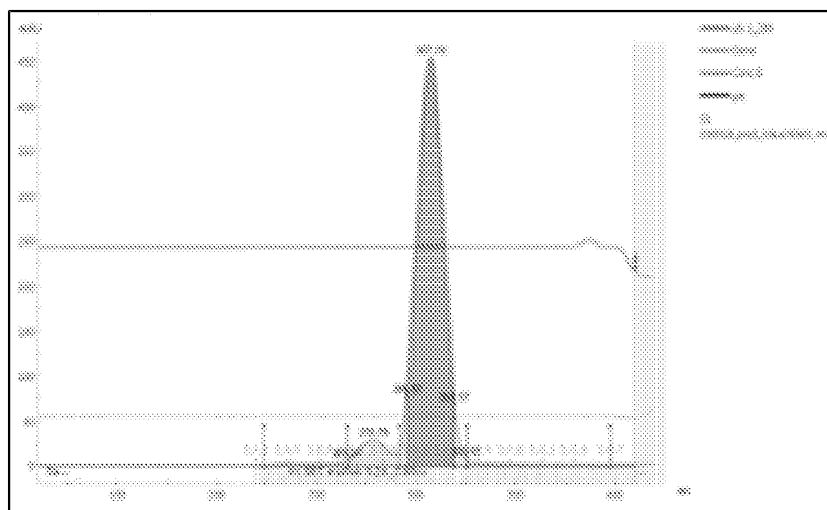
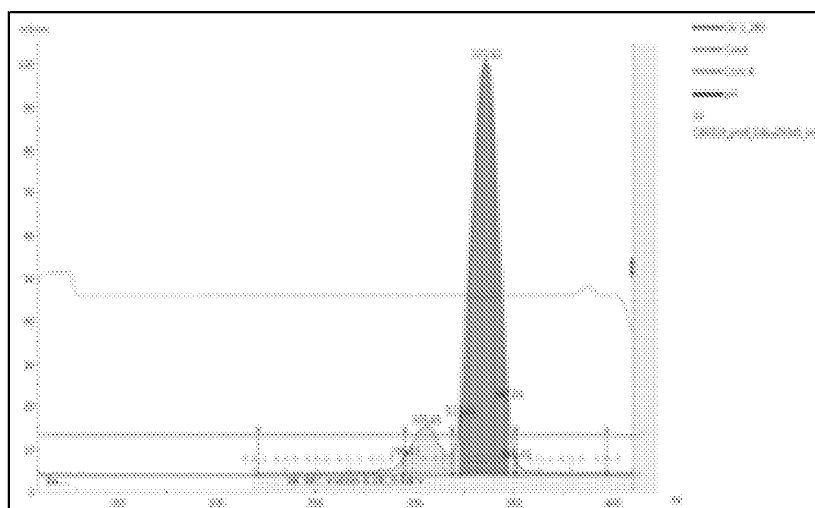


FIG. 7A



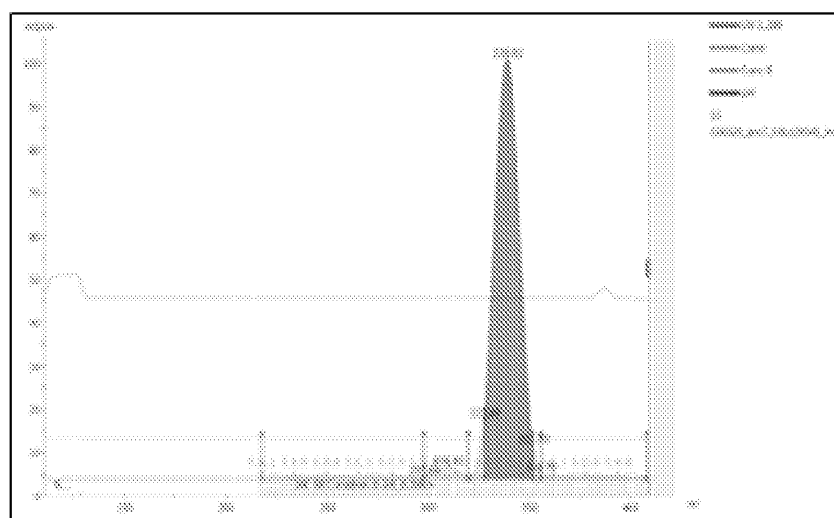
Pro 5
G8:(I2ci)x2:D12::His6

FIG. 7B



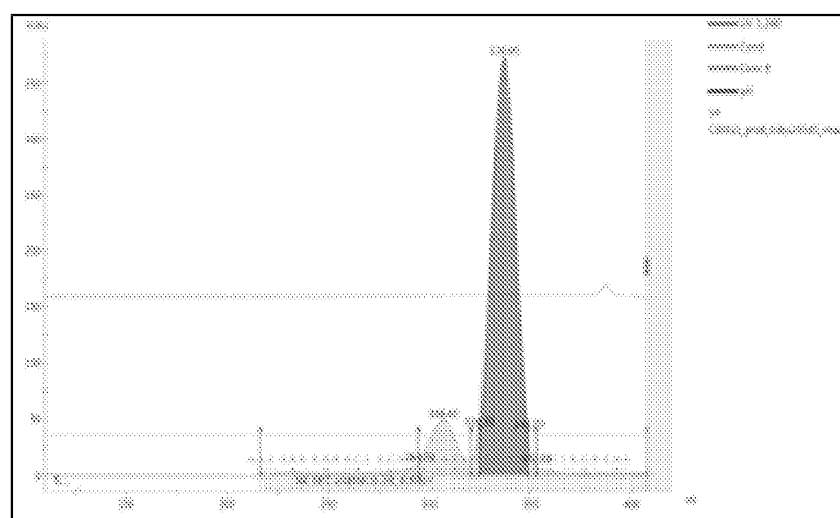
Pro 6
G8(sdAb):I2Ci::His6

FIG. 7C



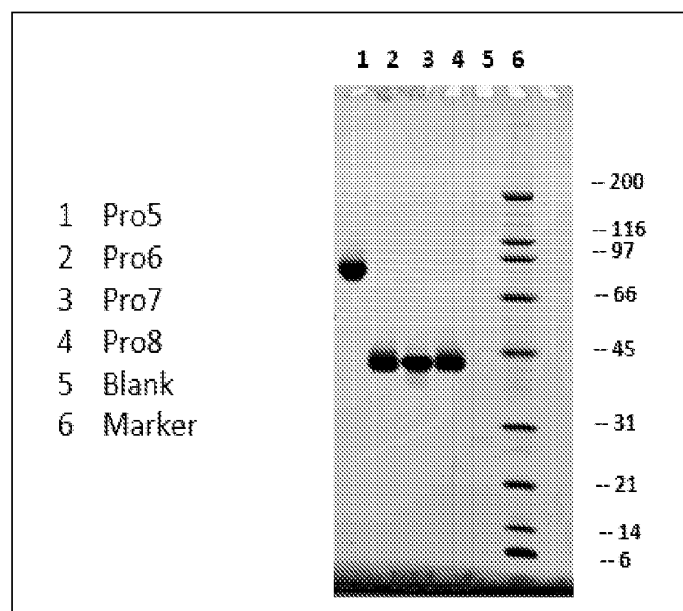
Pro 7
I2Ci:D12(sdAb)::His6

FIG. 7D



Pro 8
G8(sdAb):I2Cflag::His6

FIG. 8



Protein	MW	lot mg/ml	lot mg	lot mls	lot yield mg / L	Expr days	CM L
Prodent 5 G8(sdAb):i2Ci x2:D12(sdAb)::His6	83889	0.473	14.7	31	18.3	5	0.8
Prodent 6 G8(sdAb):i2Ci::His6	42471	0.205	6.4	31	8.0	5	0.8
Prodent 7 i2Ci:D12(sdAb)::His6	41686	0.983	30.5	31	38.1	5	0.8
Prodent 8 G8(sdAb):i2CFlag::His6	42191	0.348	10.8	31	13.5	5	0.8

FIG. 9

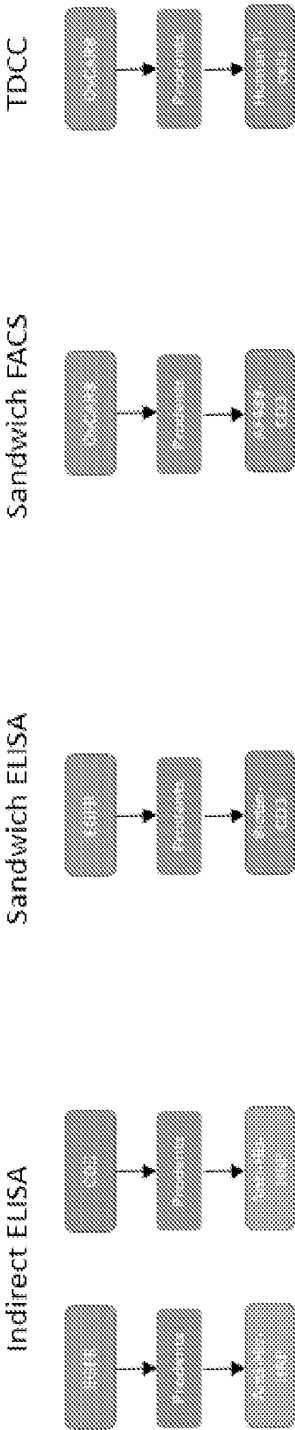


FIG. 10A

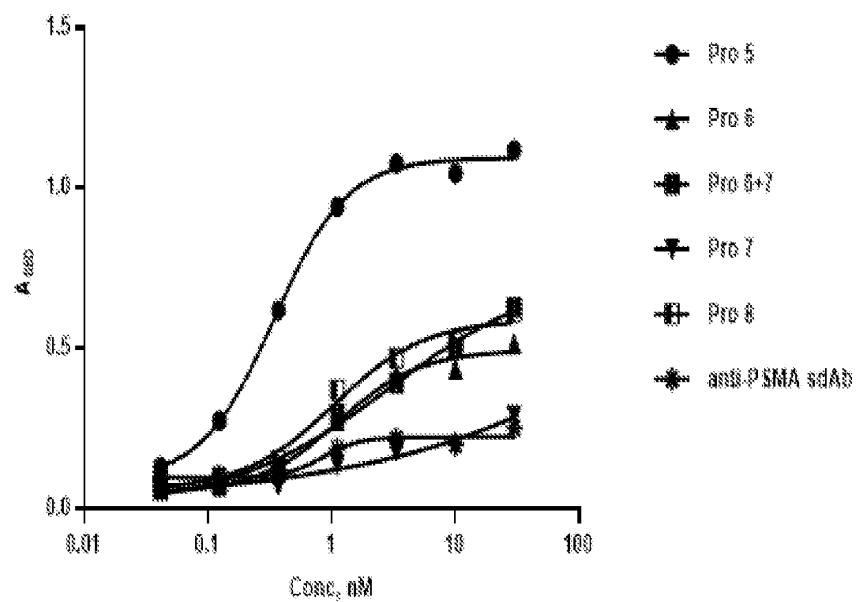


FIG. 10B

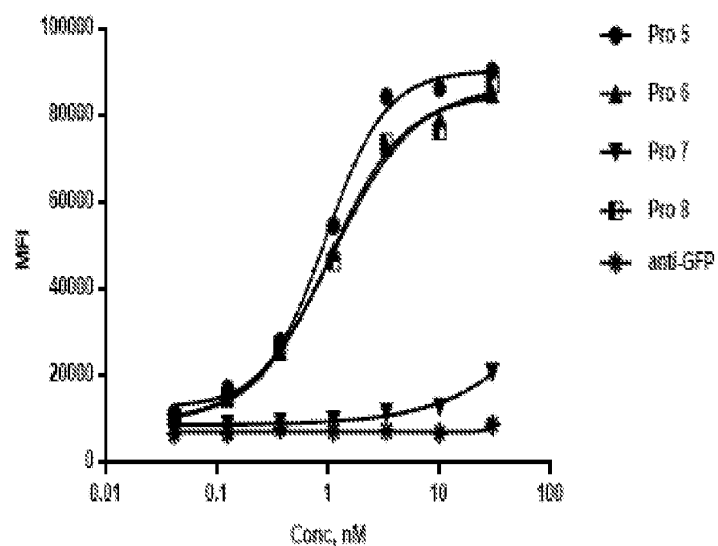


FIG. 11A

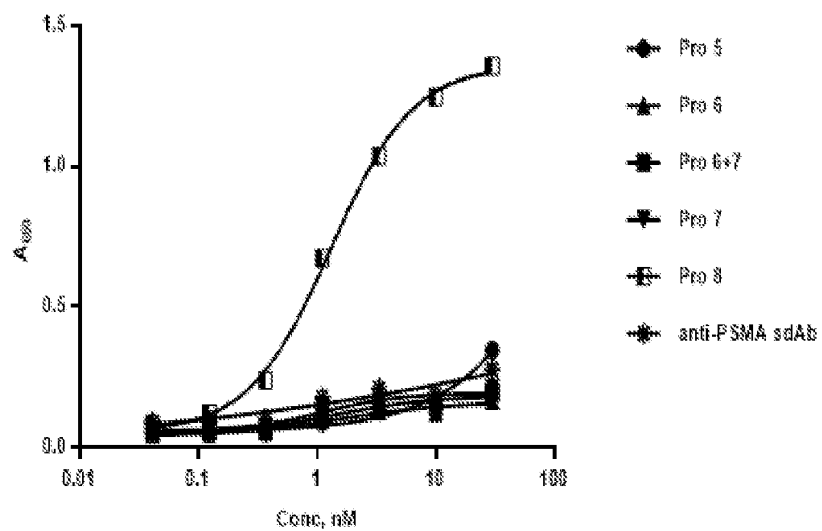


FIG. 11B

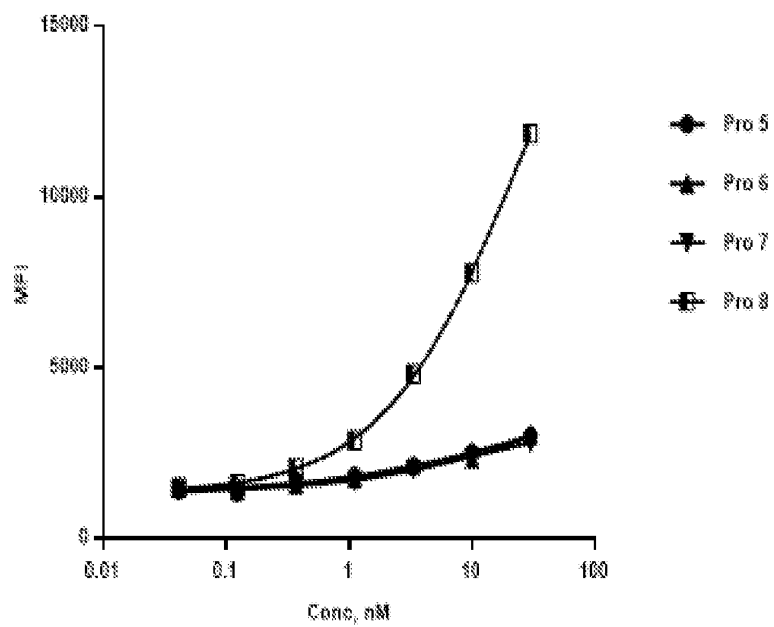


FIG. 12

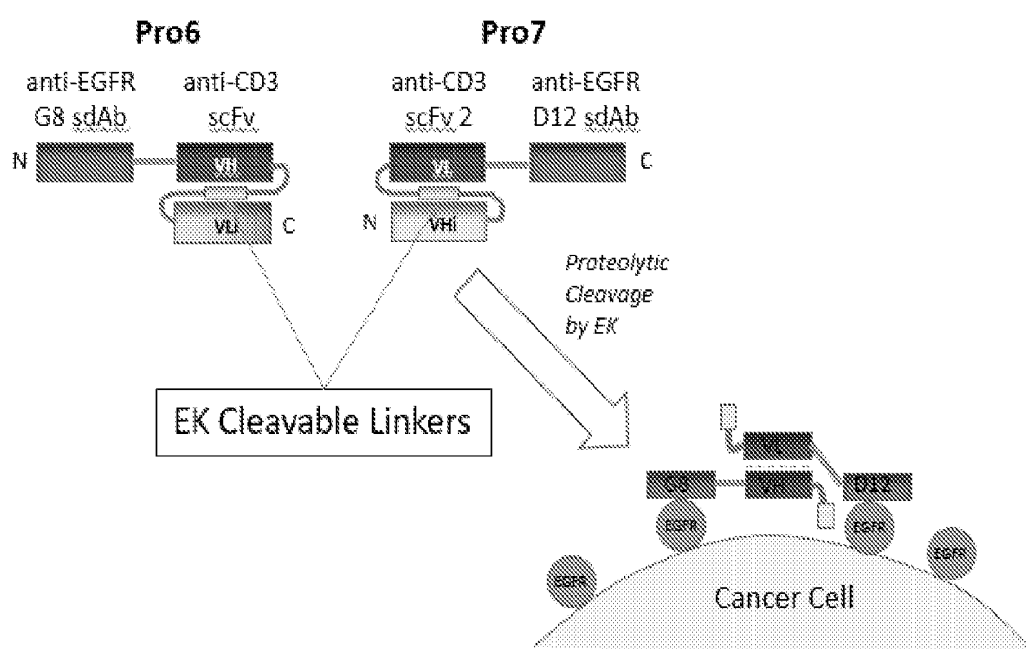


FIG. 13

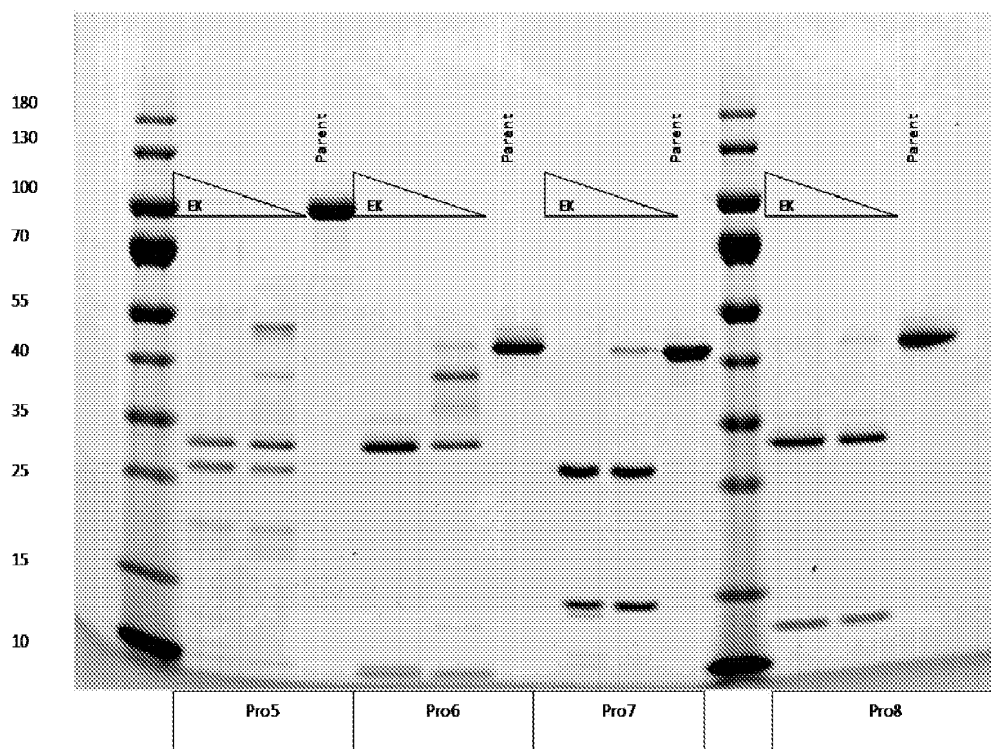


FIG. 14A

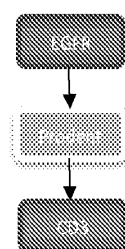


FIG. 14B

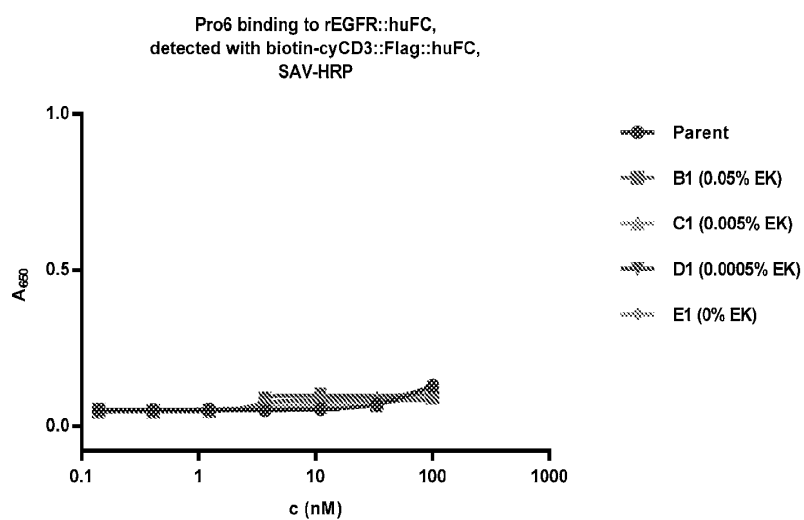


FIG. 14C

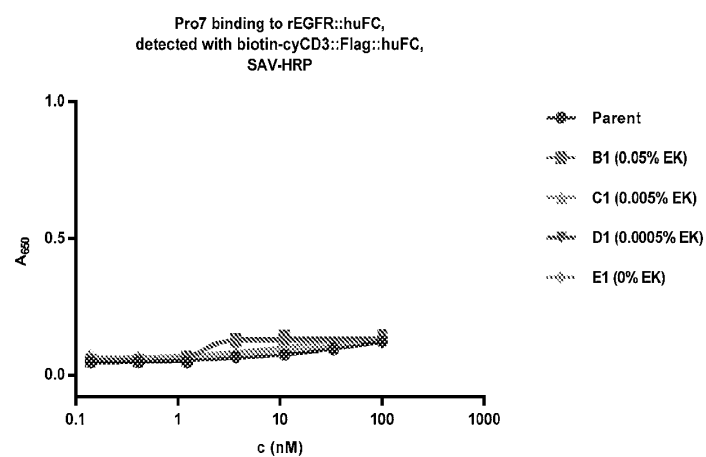


FIG. 14D

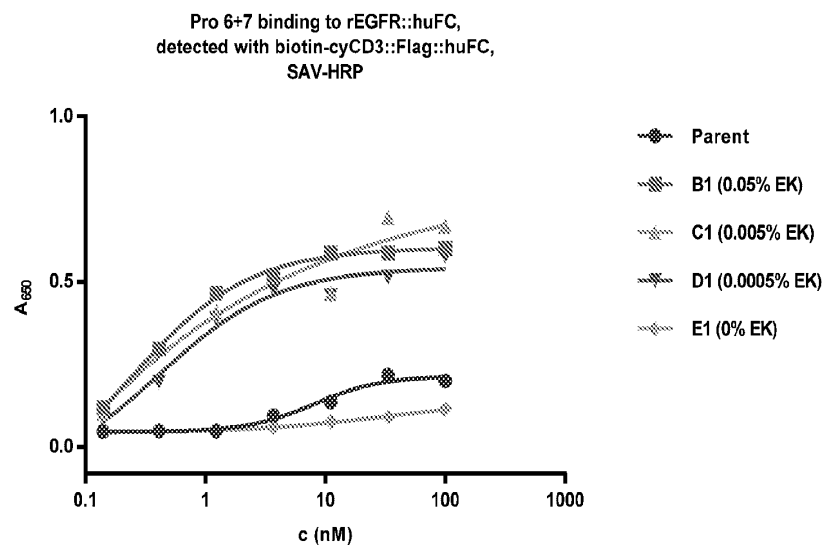


FIG. 14E

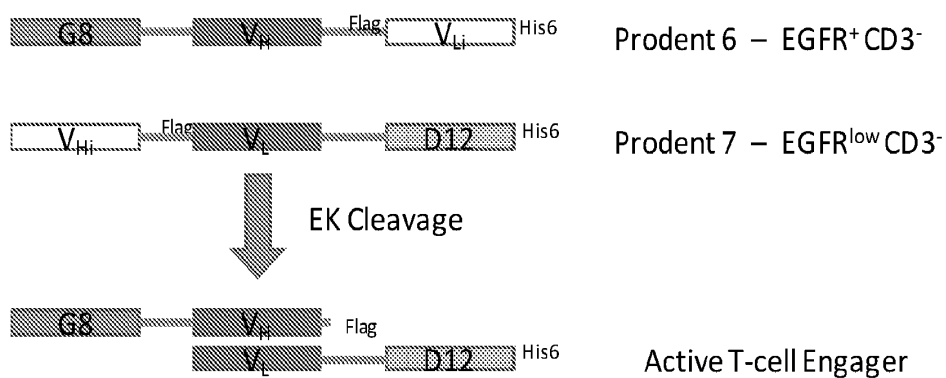


FIG. 15A

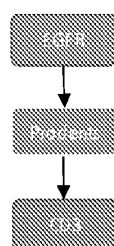


FIG. 15B

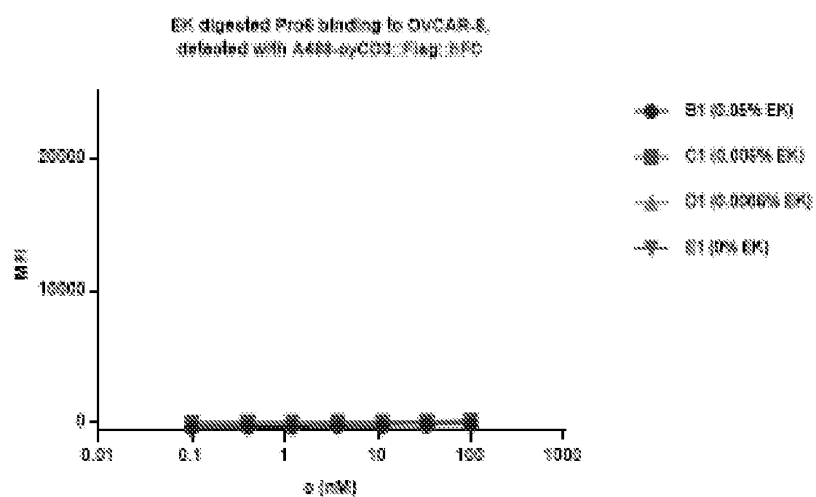


FIG. 15C

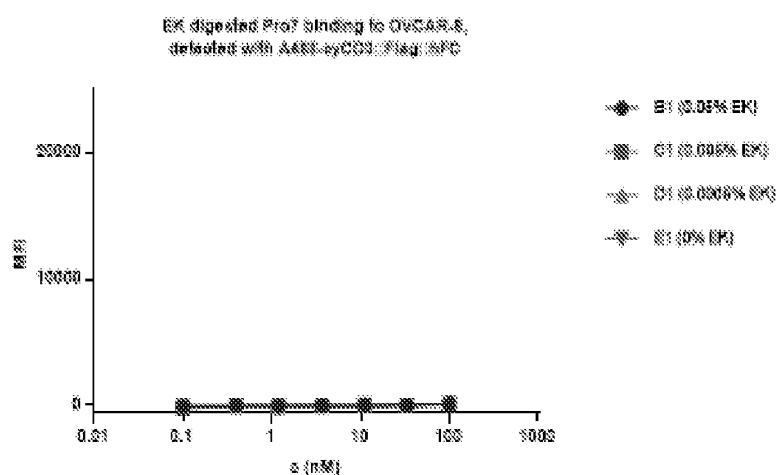


FIG. 15D

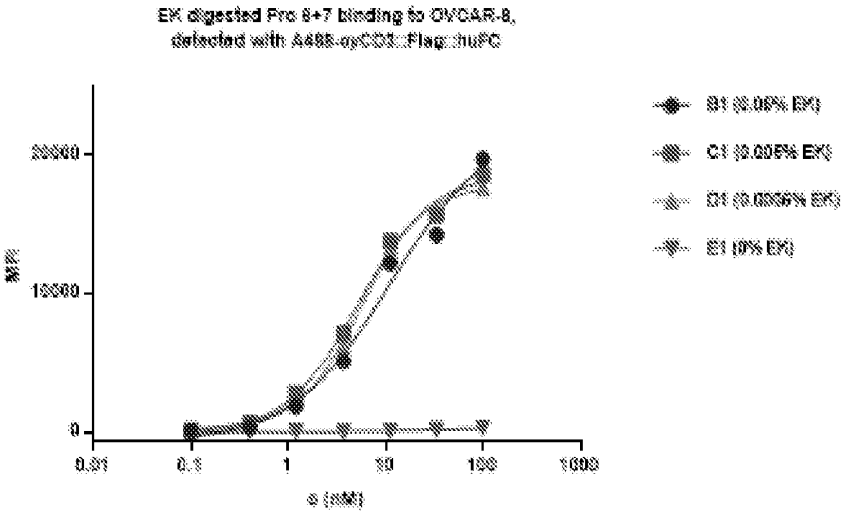


FIG. 15E

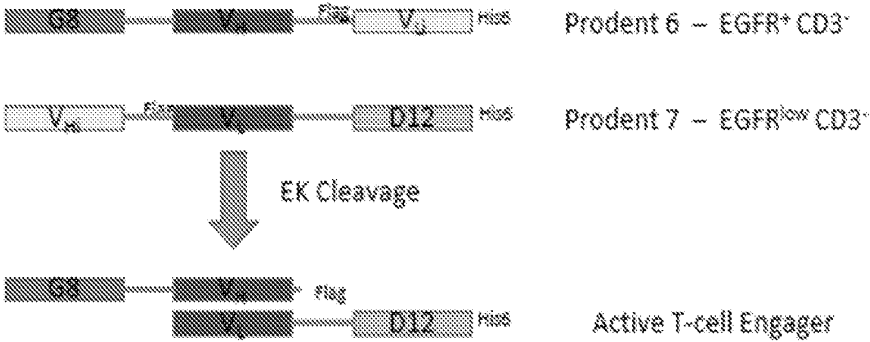


FIG. 16

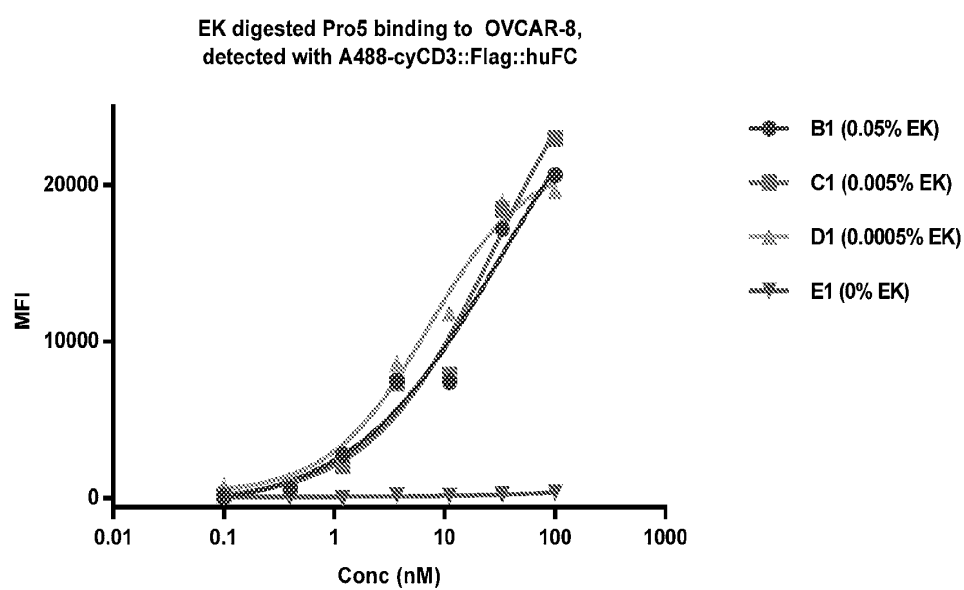


FIG. 17

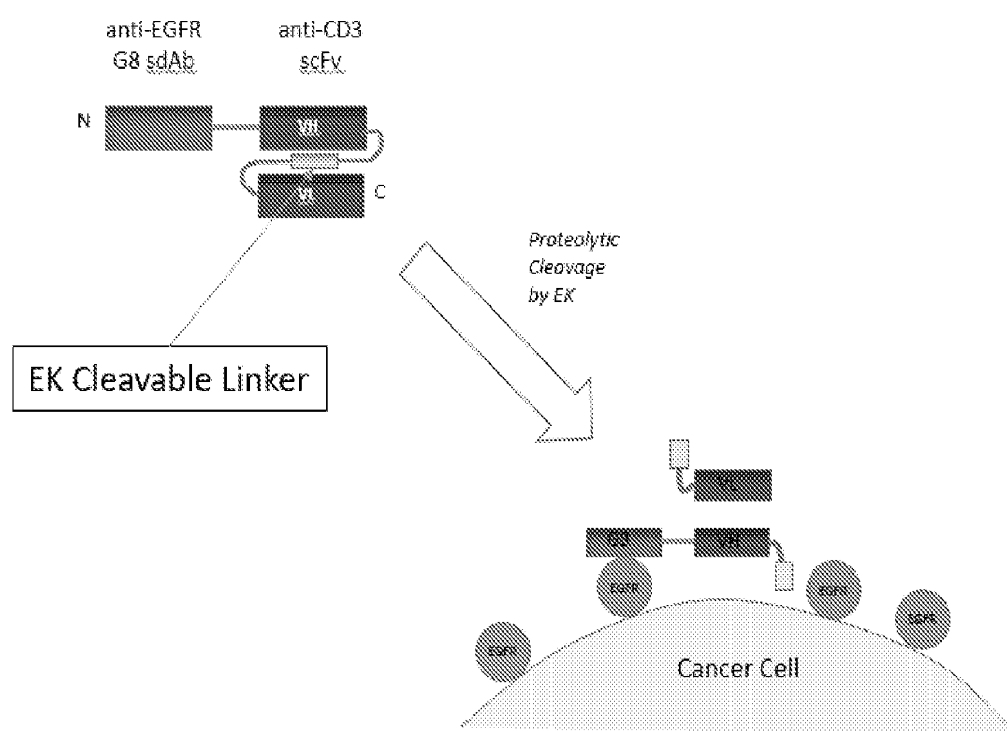


FIG. 18A

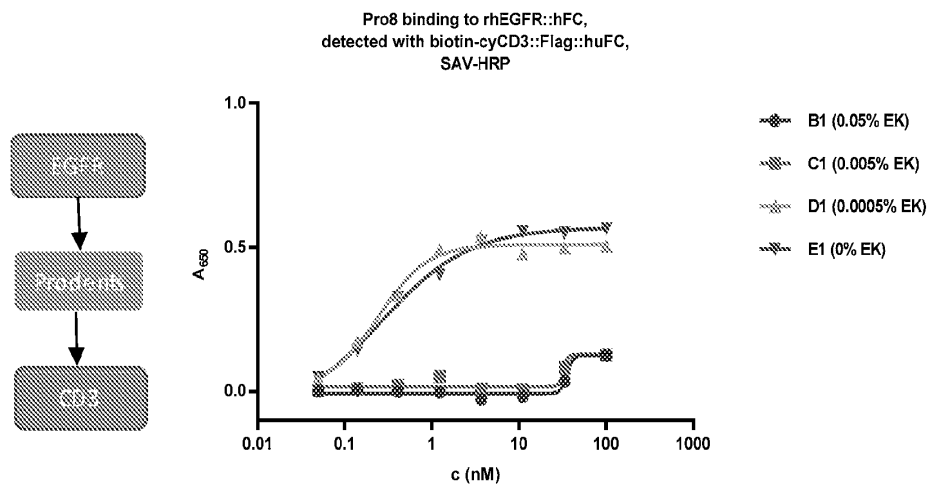


FIG. 18B

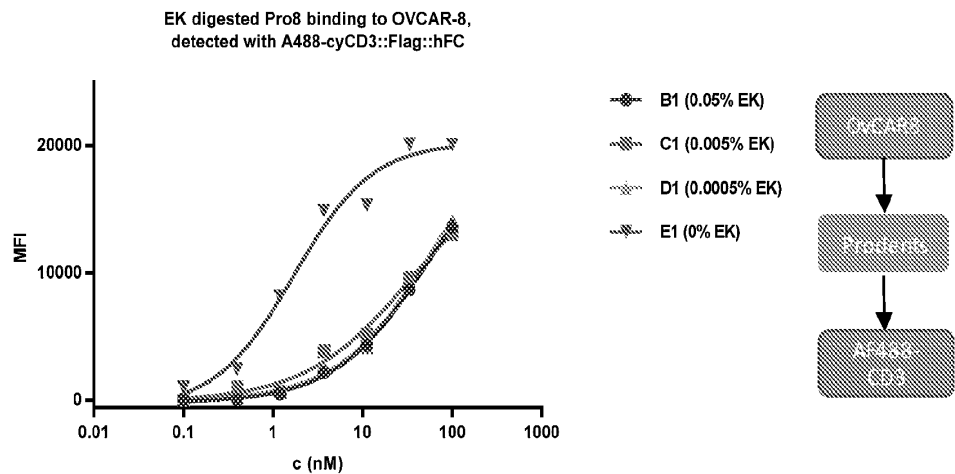


FIG. 18C

FIG. 19A

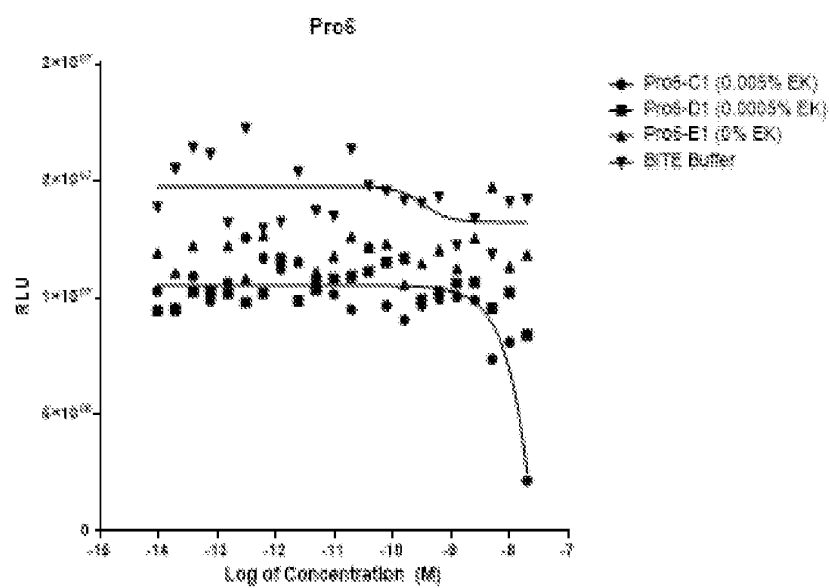


FIG. 19B

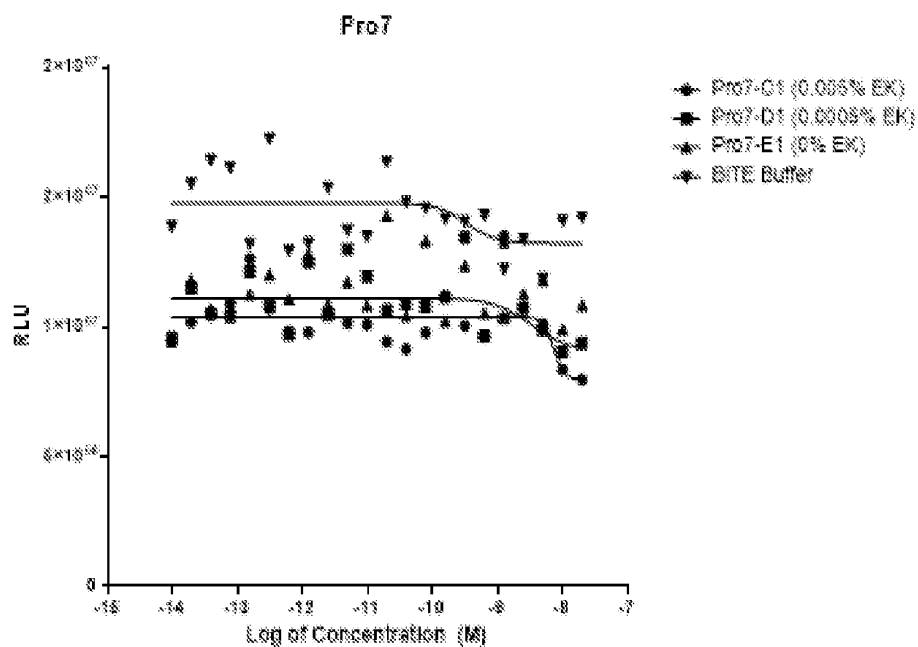
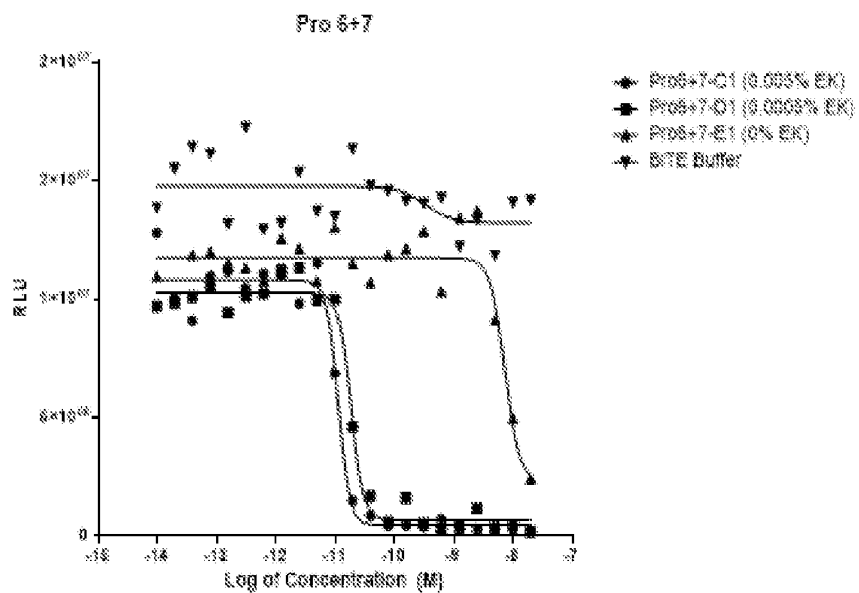


FIG. 19C



19D

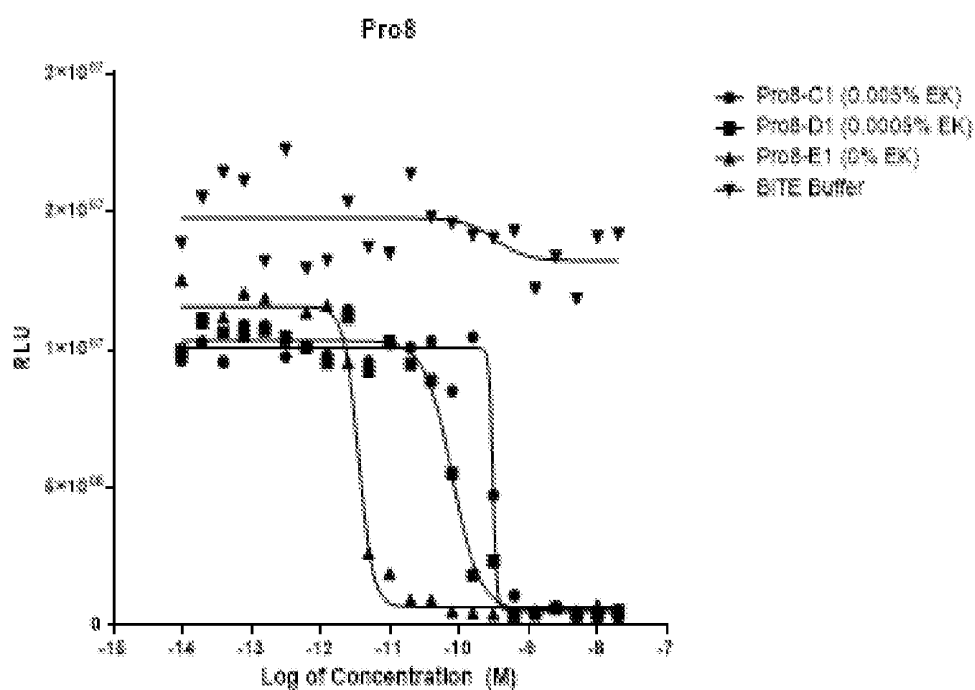


FIG. 20A



FIG. 20B



FIG. 20C



FIG. 21A

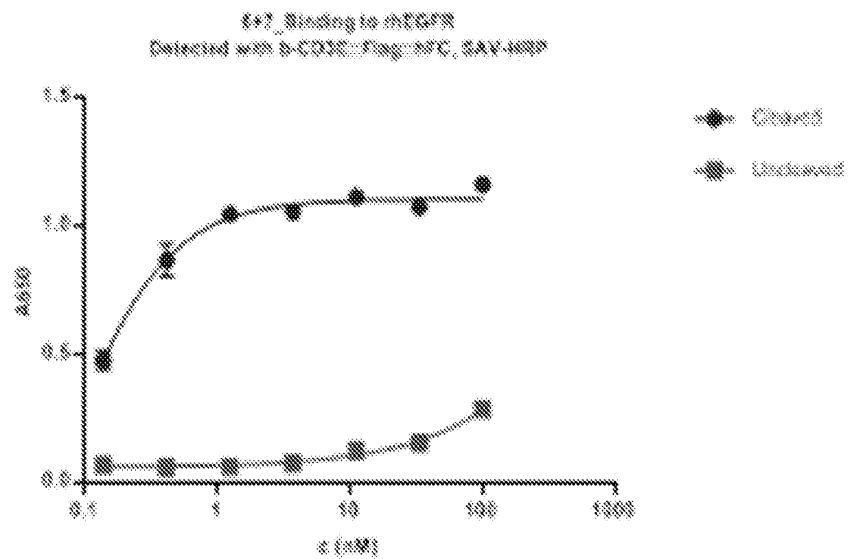


FIG. 21B

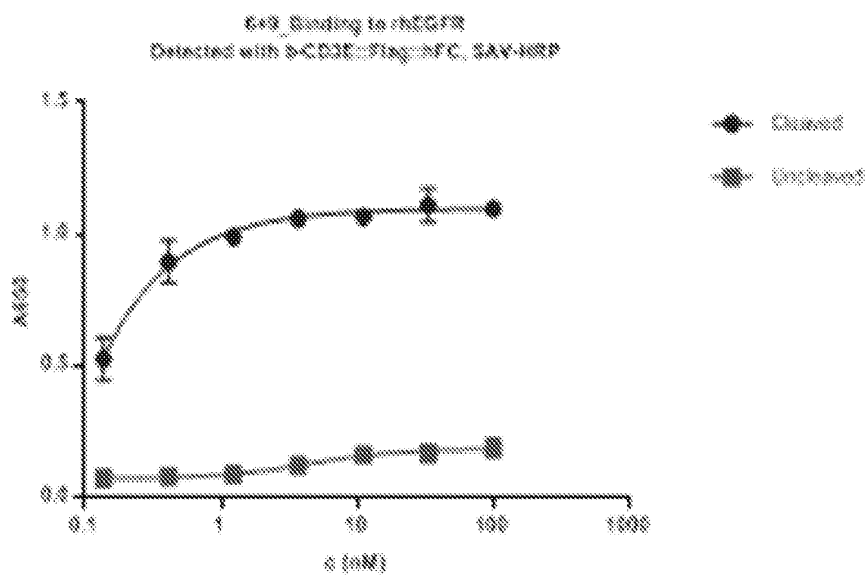


FIG. 21C

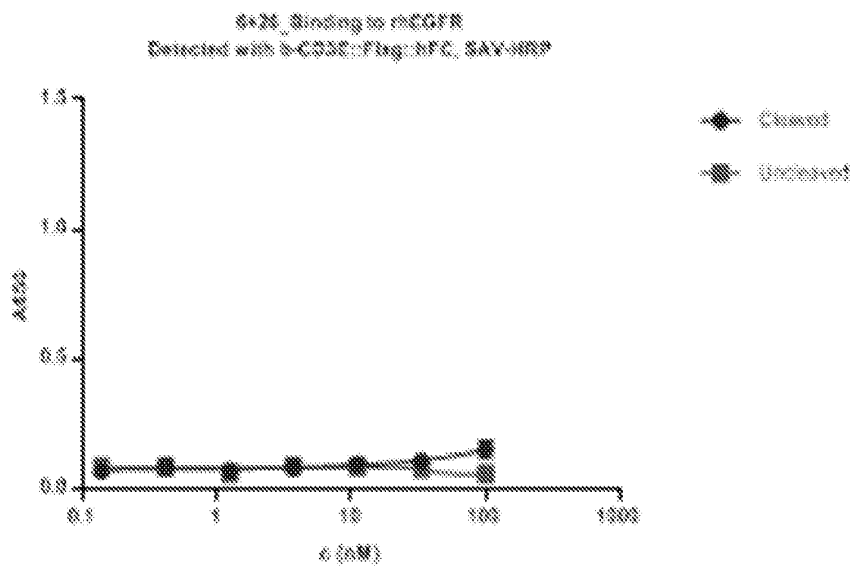


FIG. 21D

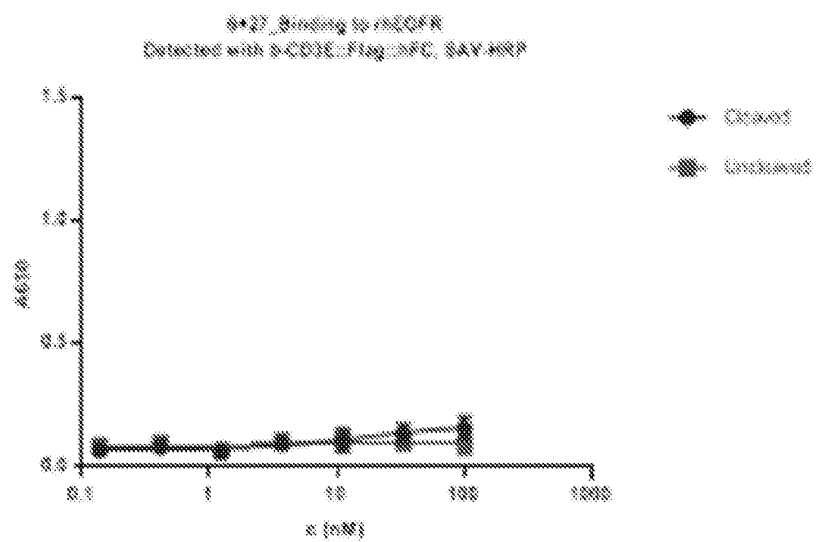


FIG. 21E

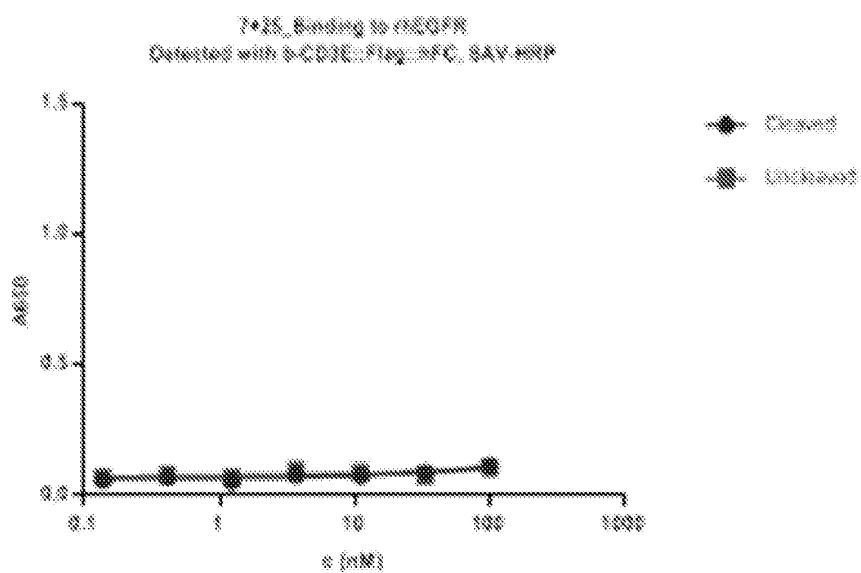


FIG. 21F

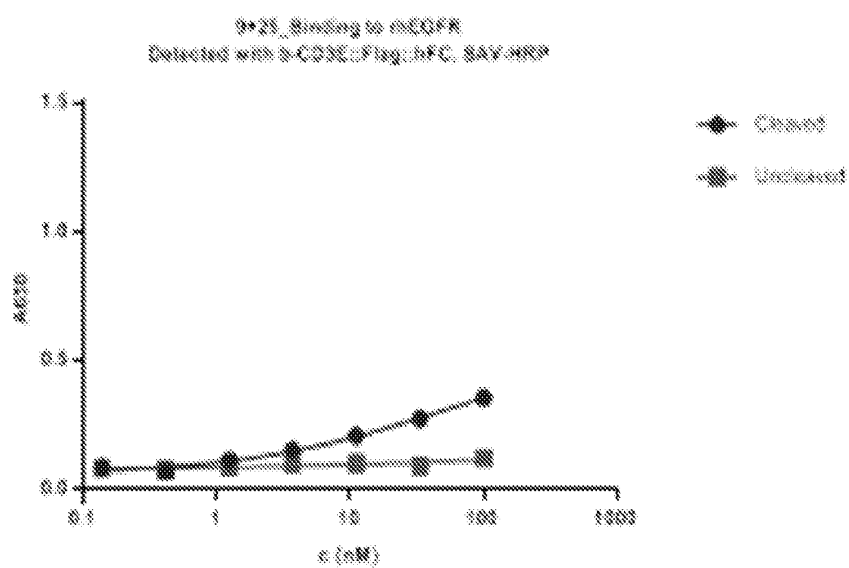


FIG. 22

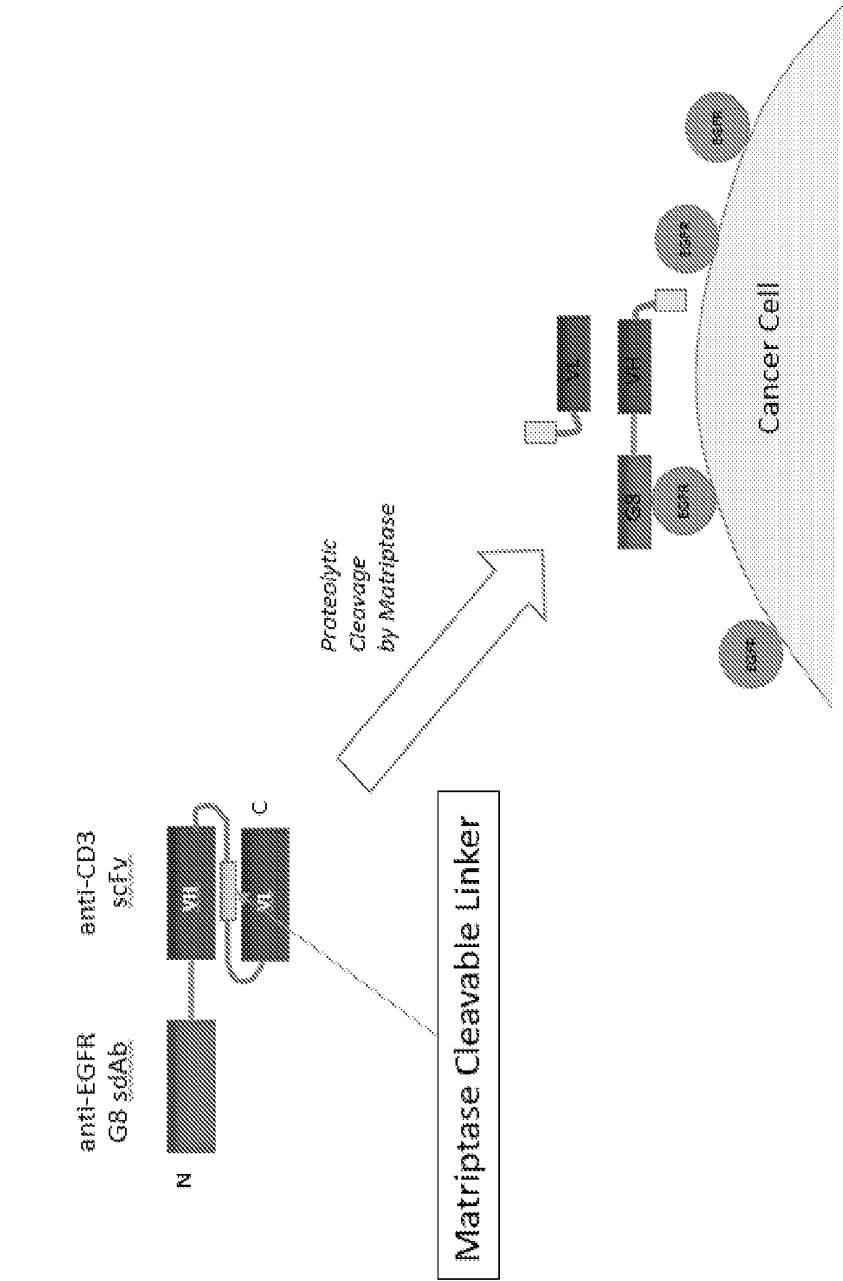


FIG. 23A

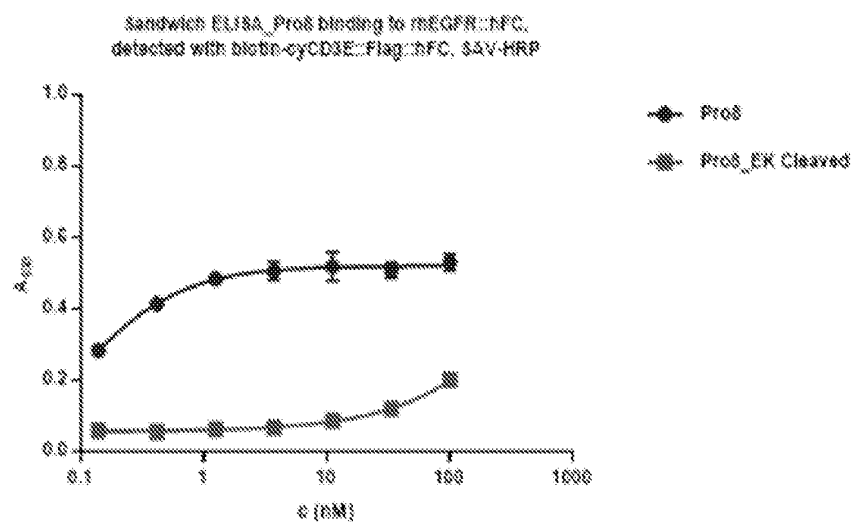


FIG. 23B

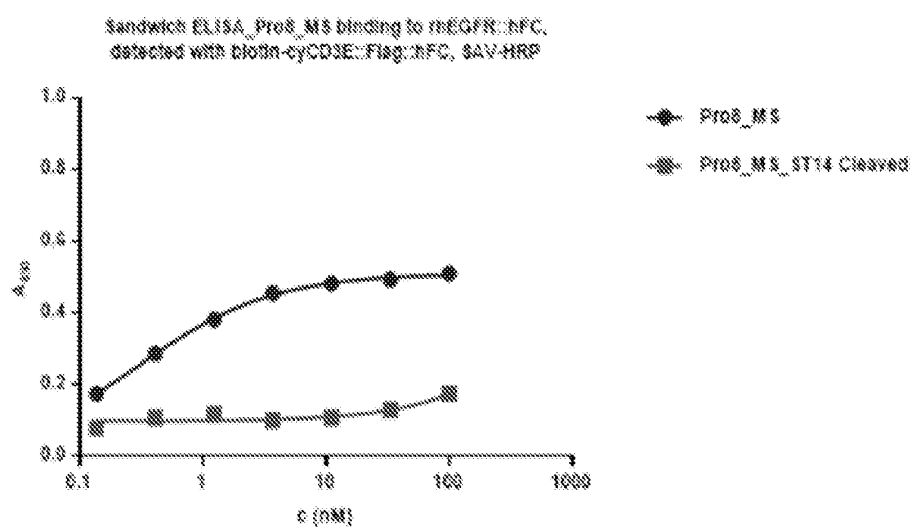


FIG. 23C

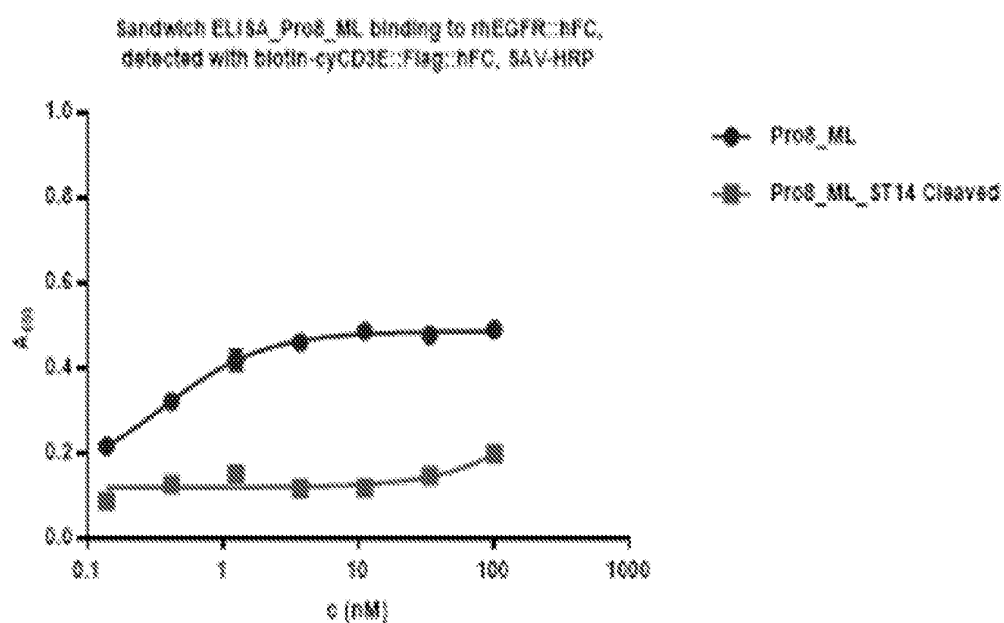


FIG. 24A

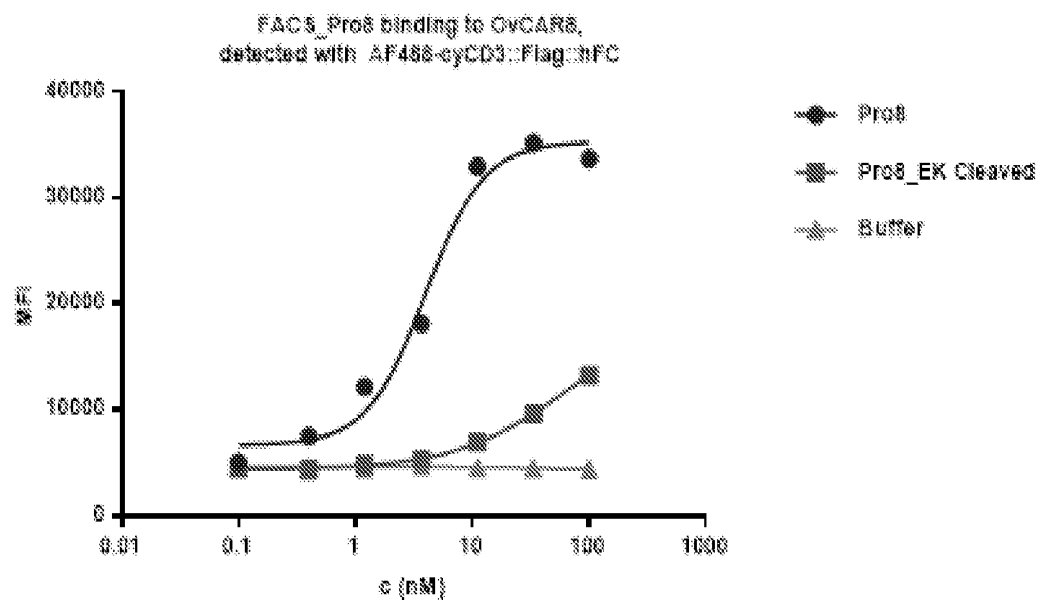


FIG. 24B

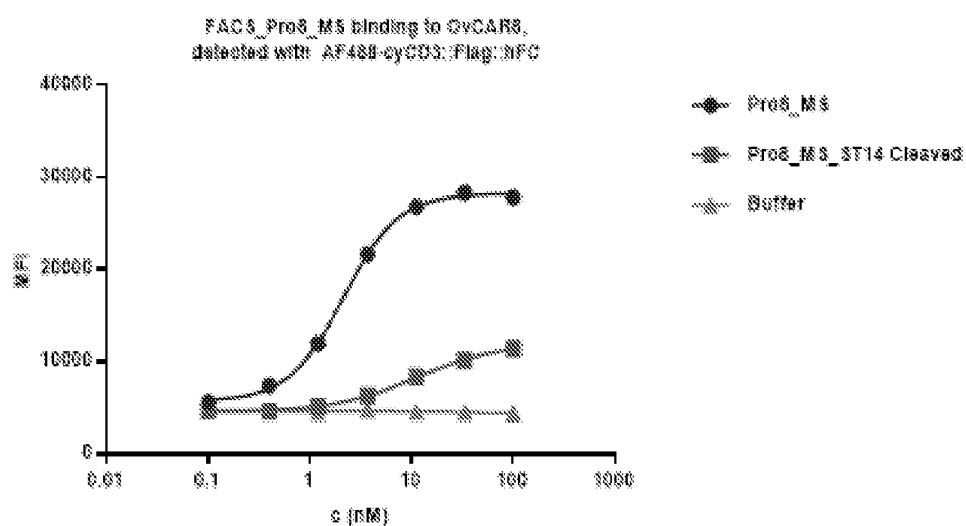


FIG. 24C

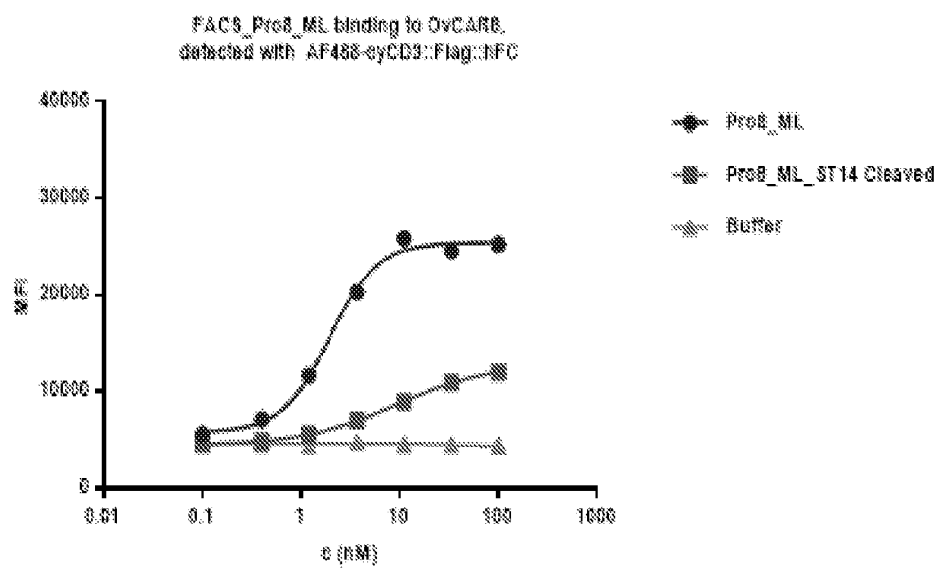


FIG. 25

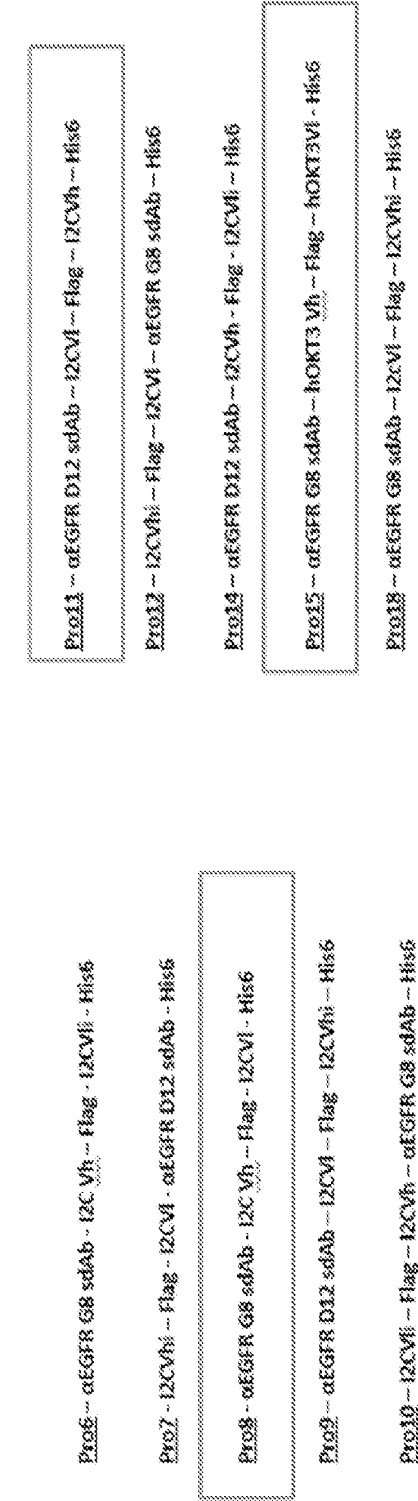


FIG. 26

Proteins	tgFR	CD3
6+10	+	-
6+14	+	-
7+9	+	-
7+12	+	-
9+12	+	-
10+14	+	-

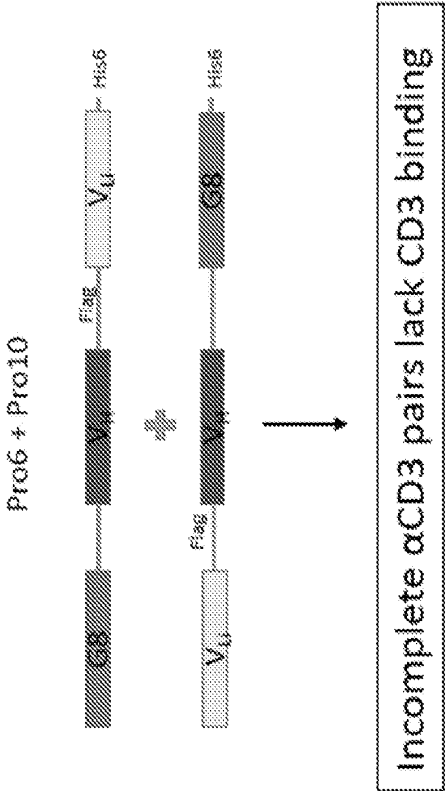


FIG. 27A

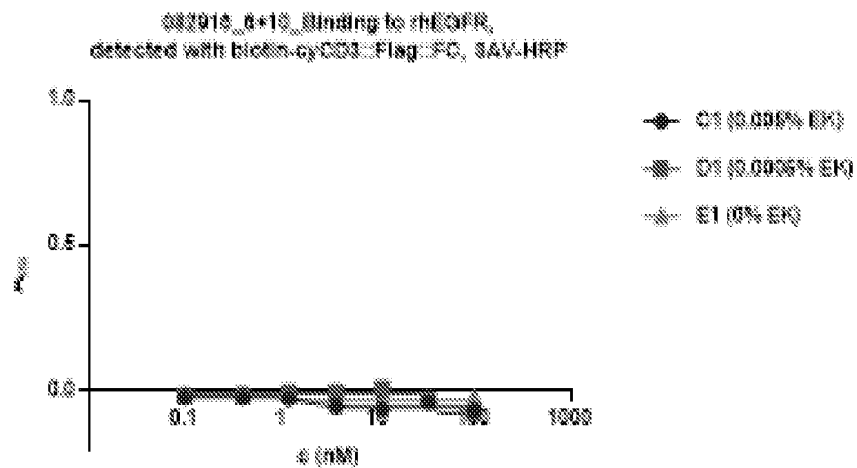


FIG. 27B

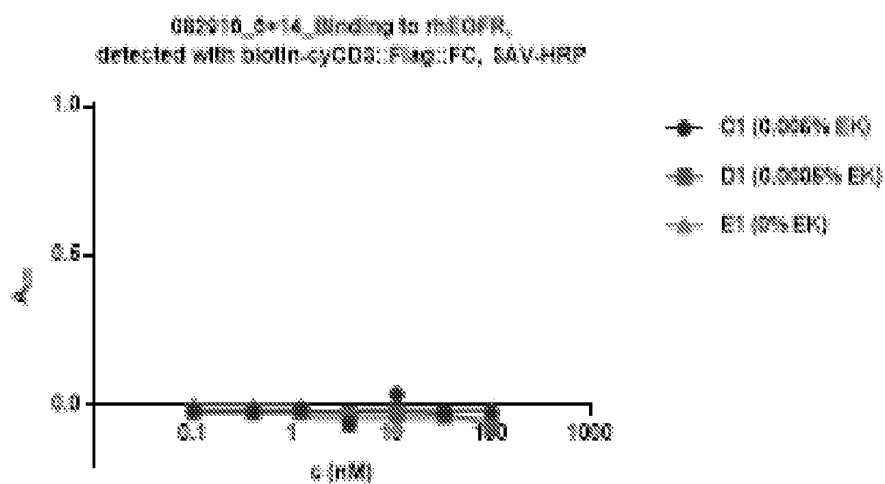


FIG. 27C

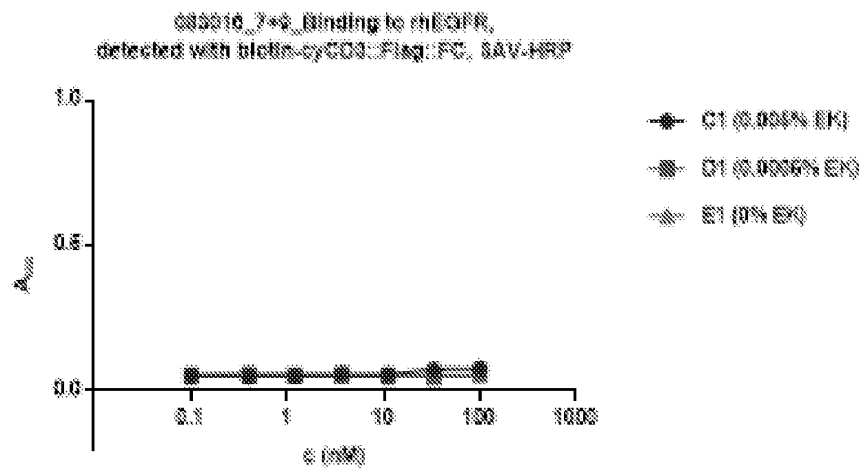


FIG. 27D

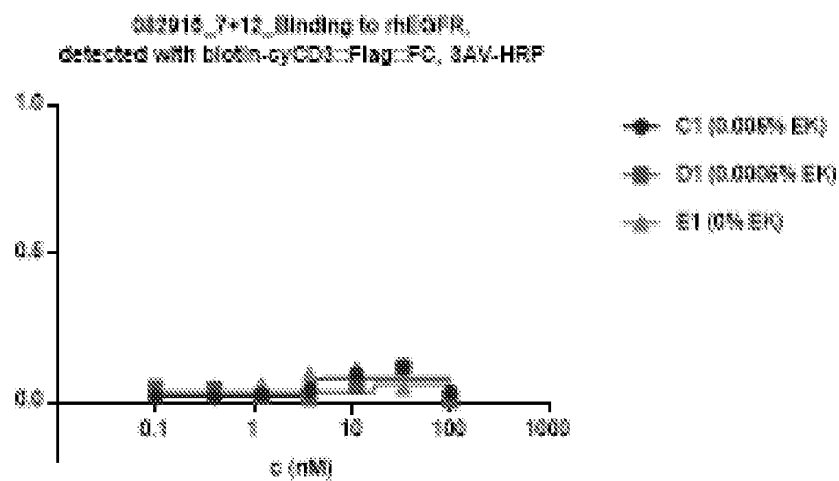


FIG. 27E

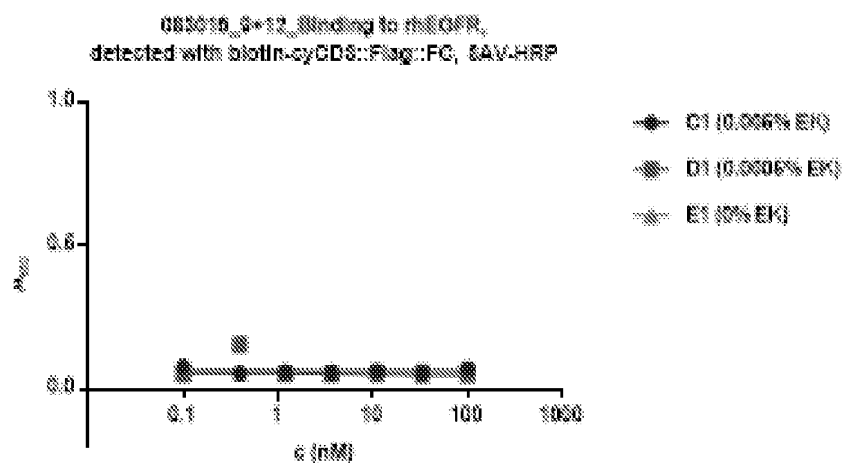


FIG. 27F

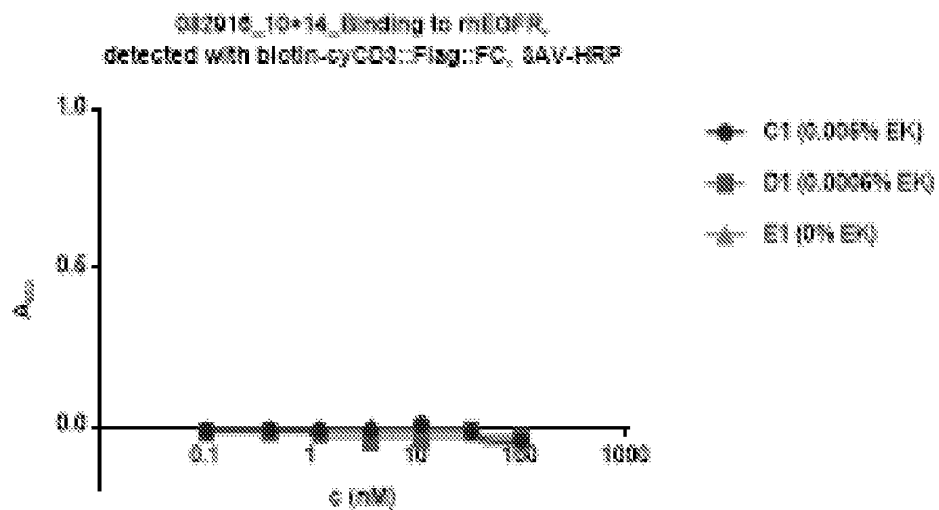


FIG. 28

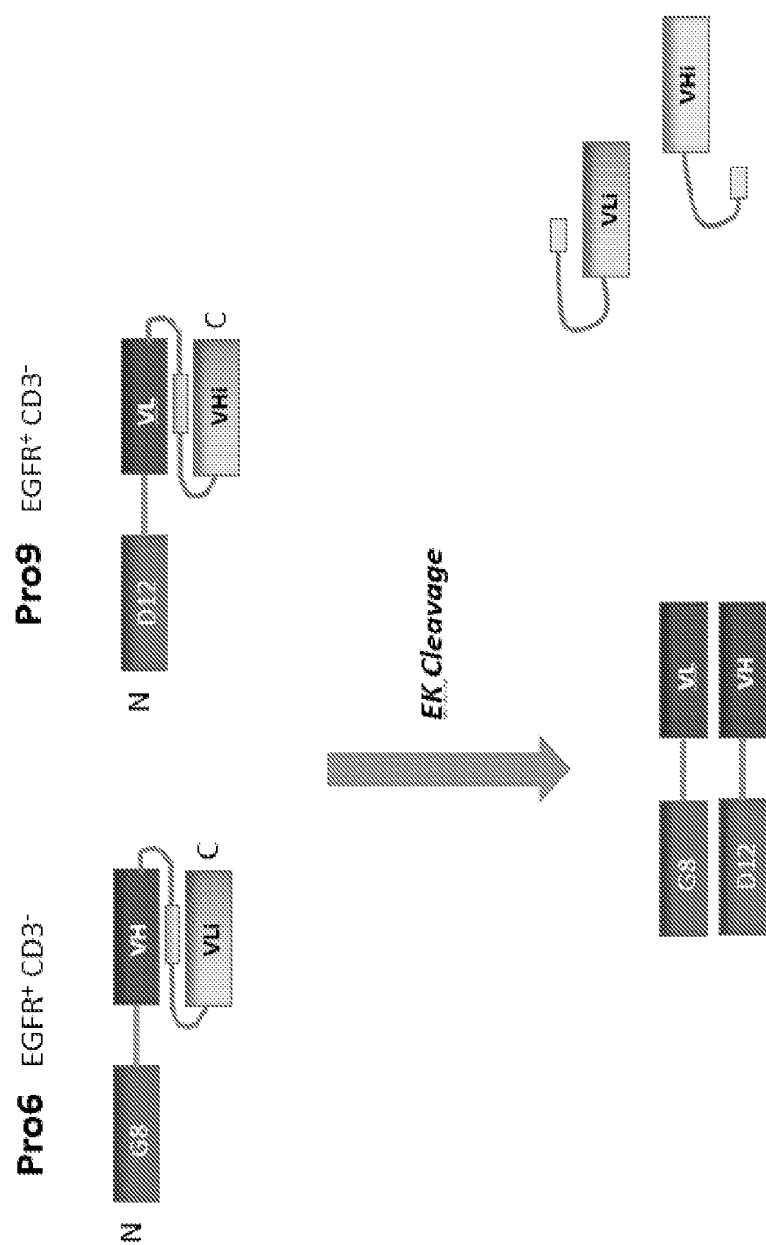


FIG. 29A

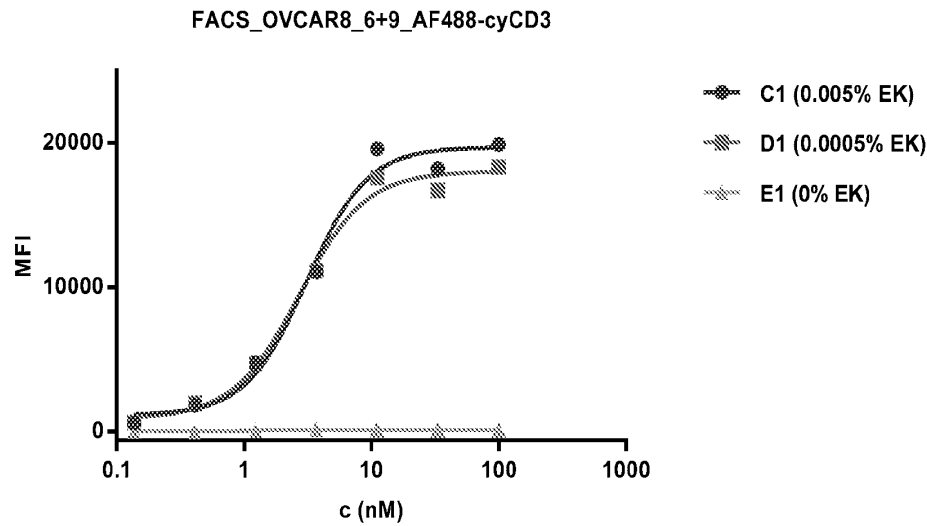


FIG. 29B

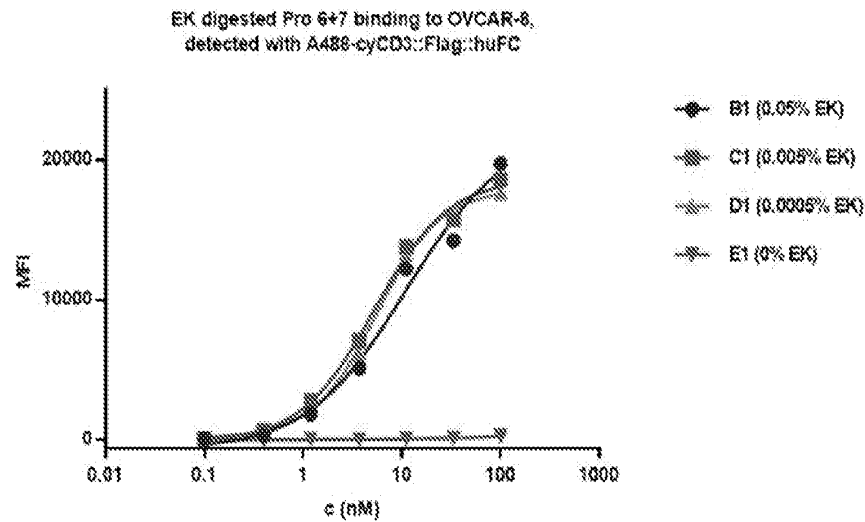


FIG. 30

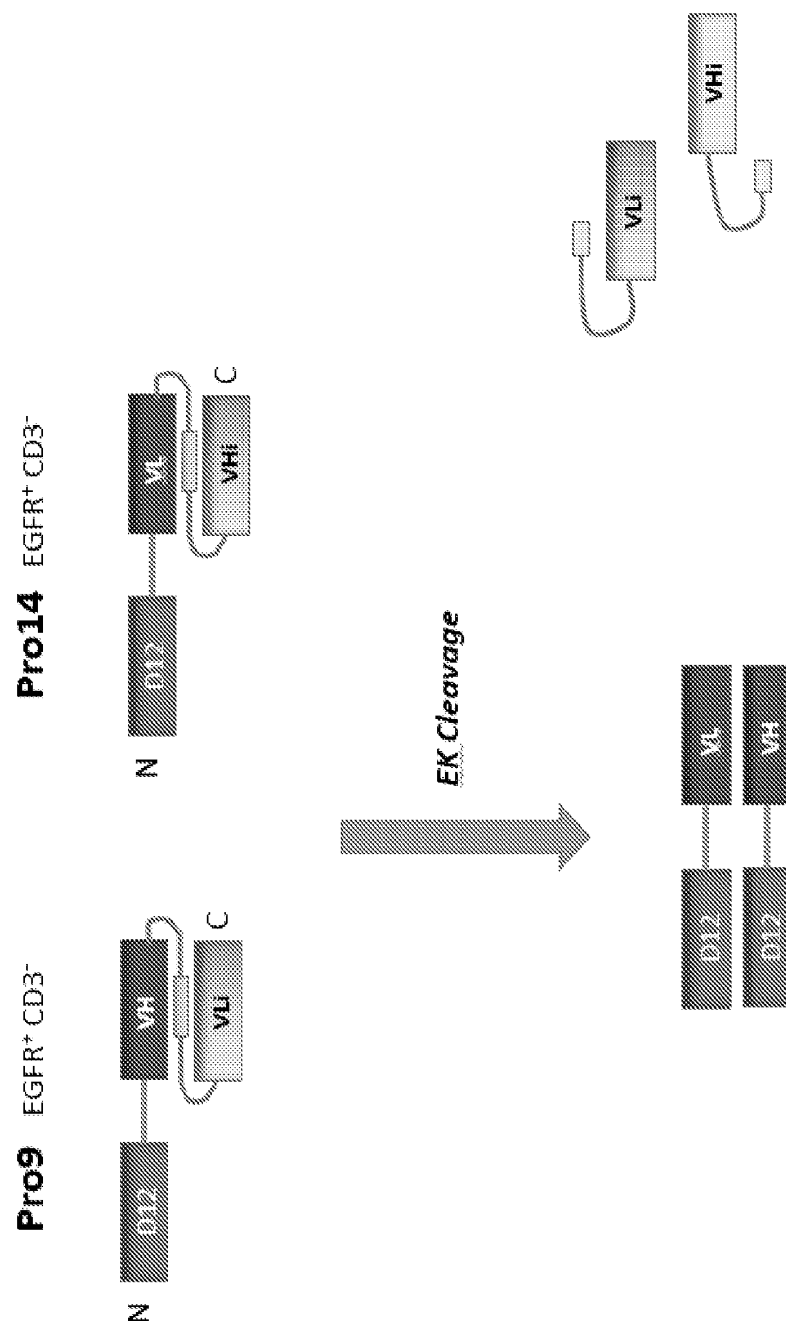


FIG. 31A

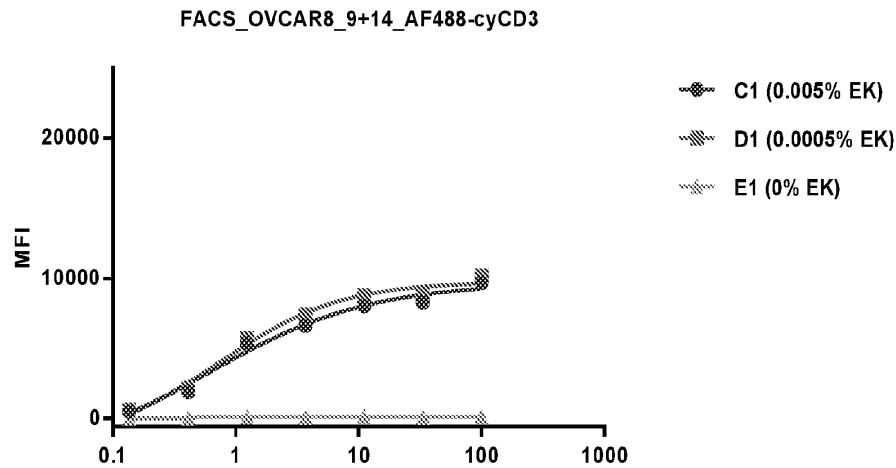


FIG. 31B

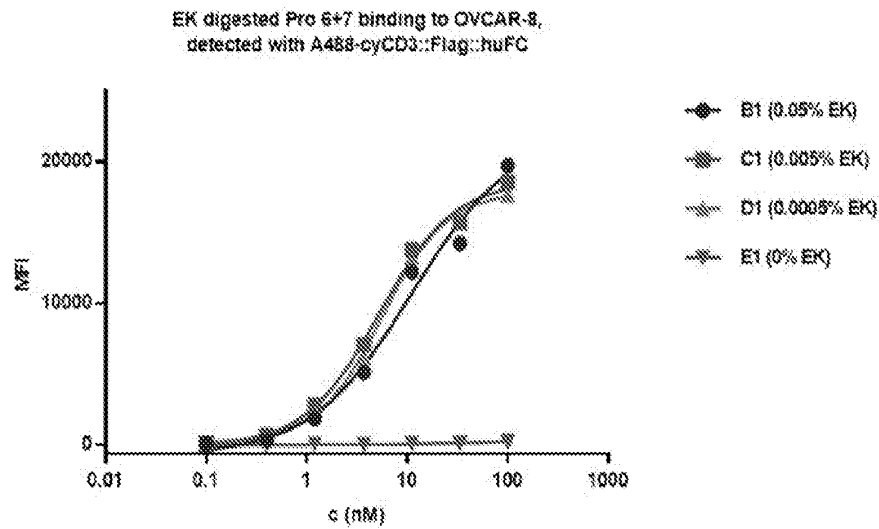


FIG. 32A

Prodents	EGFR	CD3	Cis/Trans
6+7	+	+	Cis+ Trans
6+9	+	+	Cis+ Trans
7+10	+	+	Cis+ Trans
9+10	+	+	Cis+ Trans
12+14	+	+	Cis+ Trans
6+12	+	+	Trans Only
7+14	+	+	Trans Only
9+14	+	+	Trans Only
10+12	+	+	Trans Only

FIG. 32B

Cis + Trans

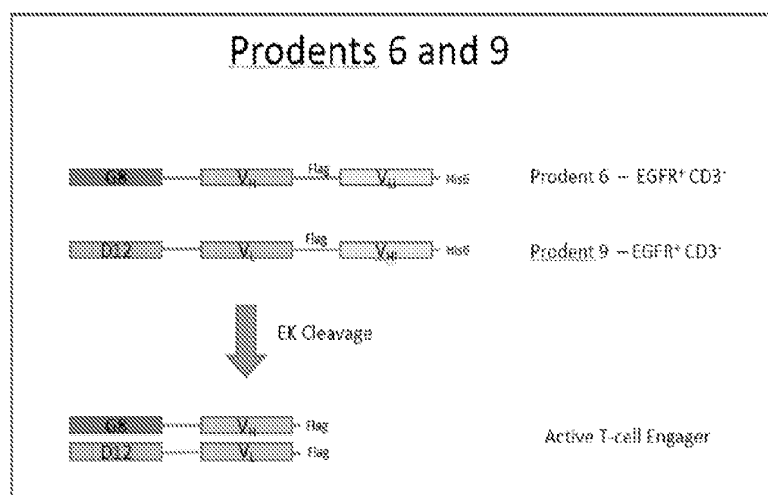


FIG. 32C

Trans Only

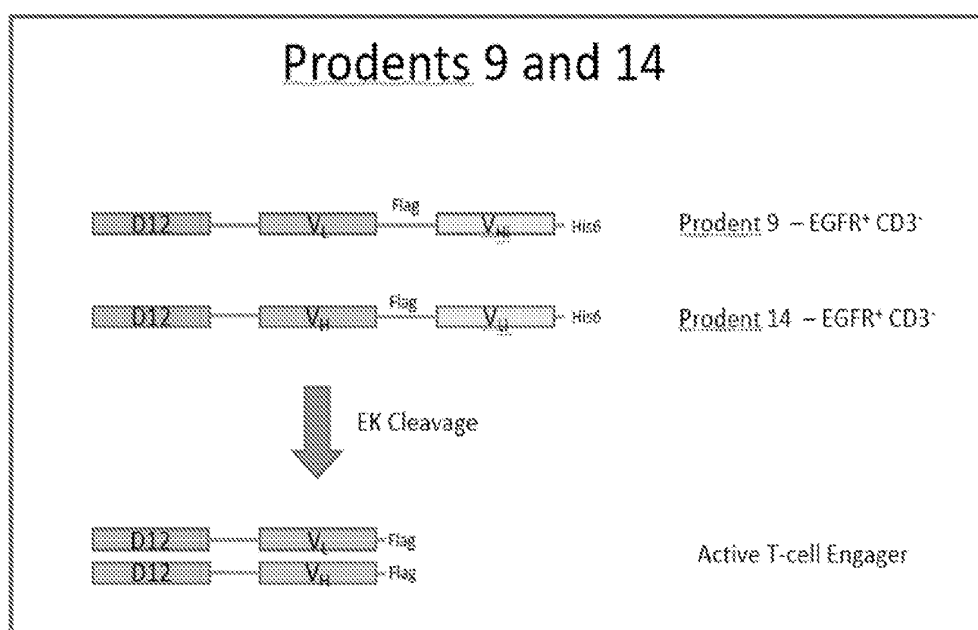


FIG. 33A

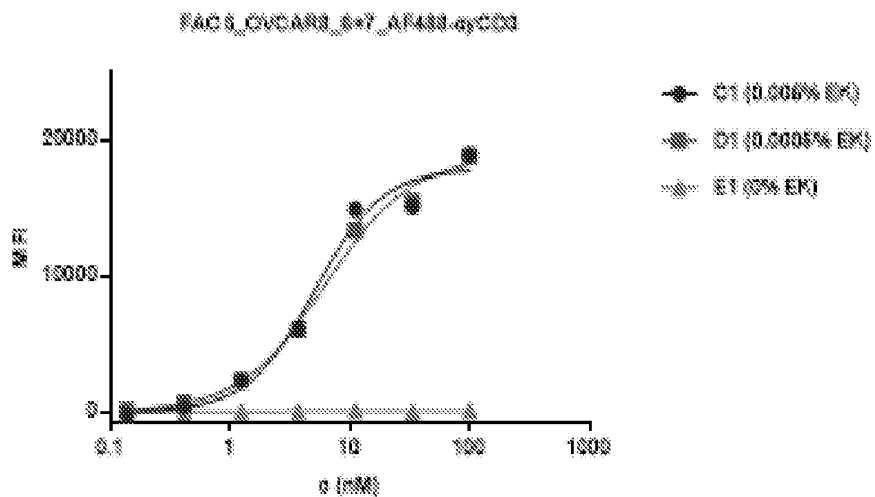


FIG. 33B

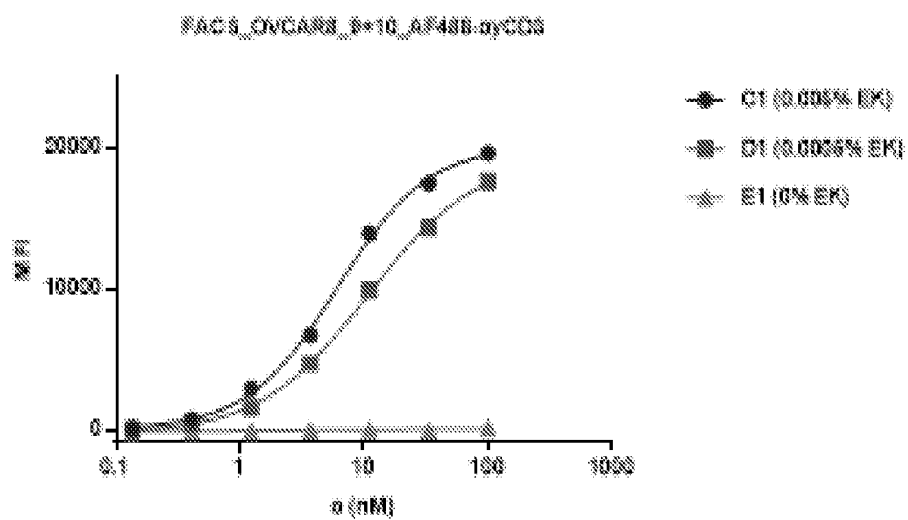


FIG. 33C

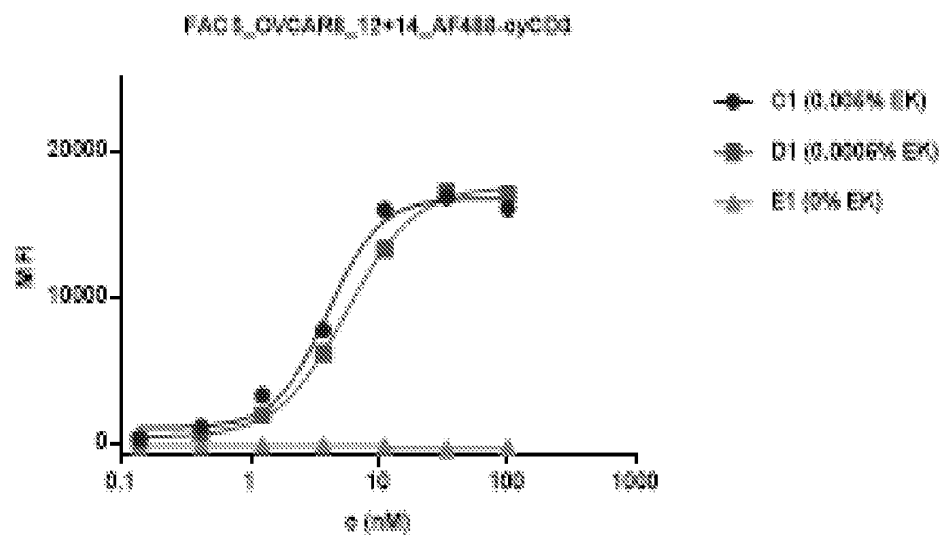


FIG. 33D

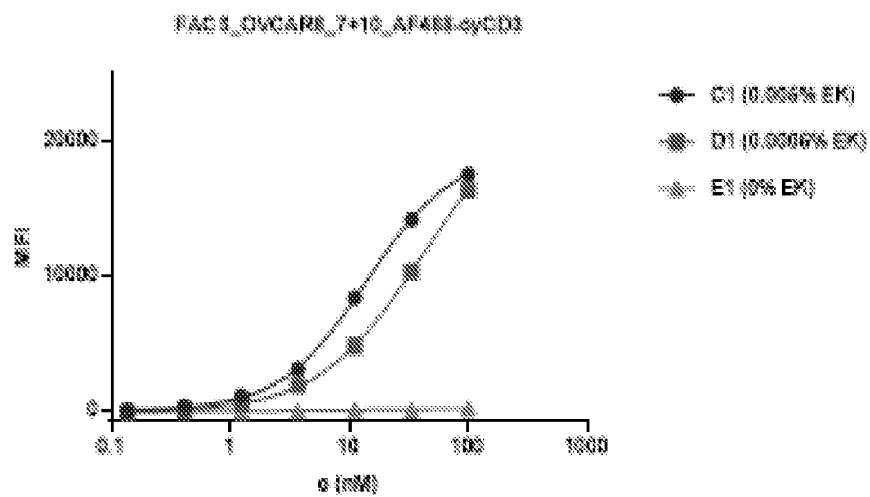


FIG. 33E

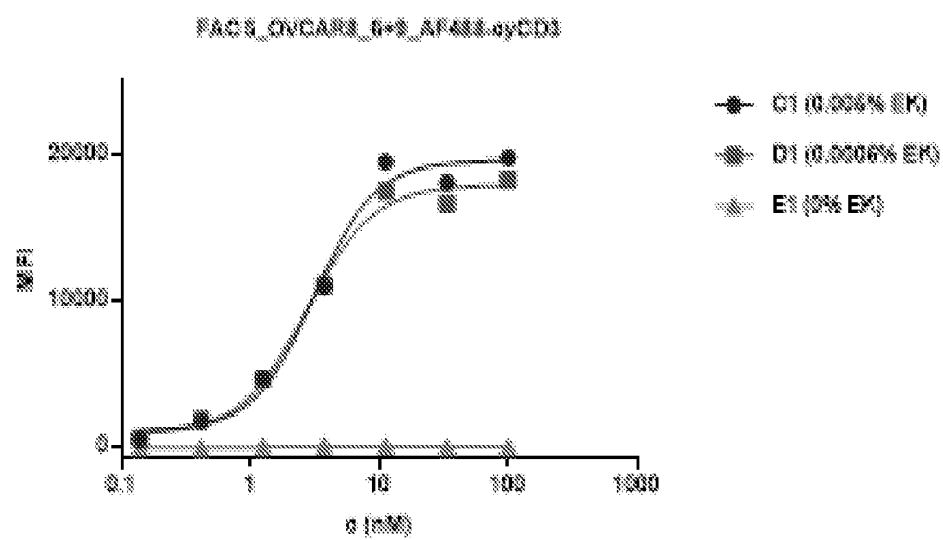


FIG. 34A

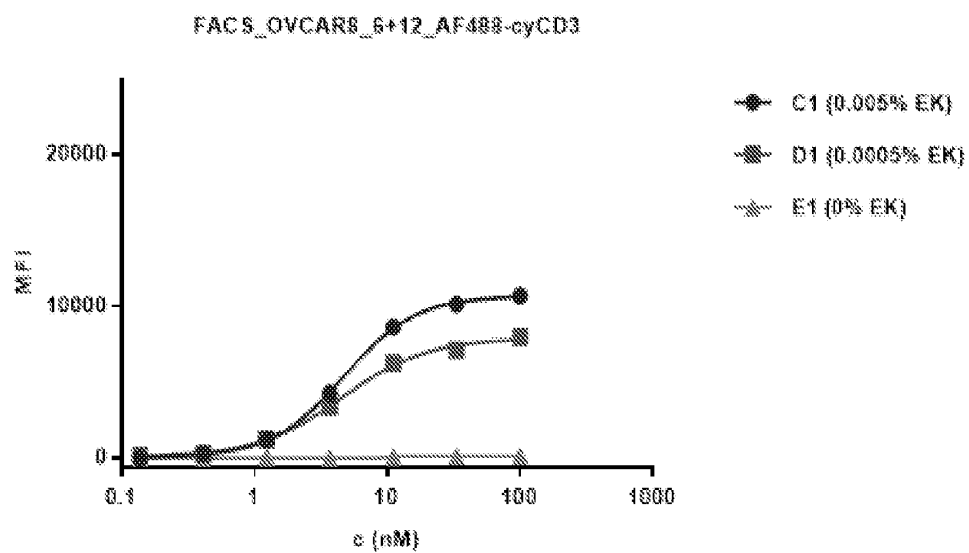


FIG. 34B

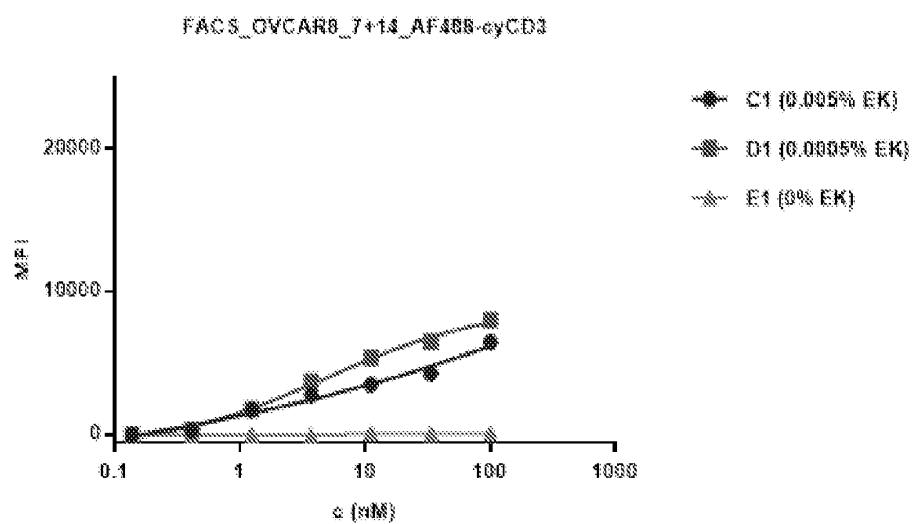


FIG. 34C

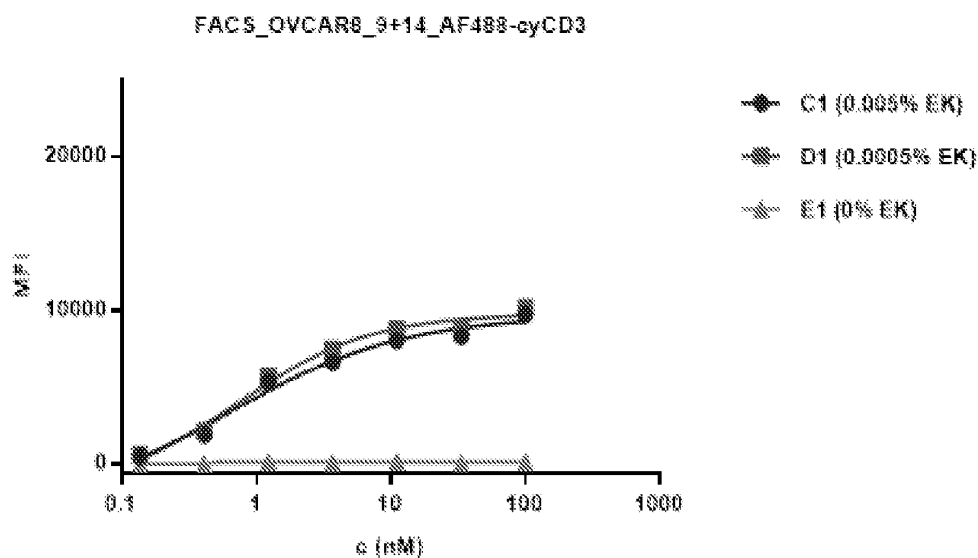


FIG. 34D

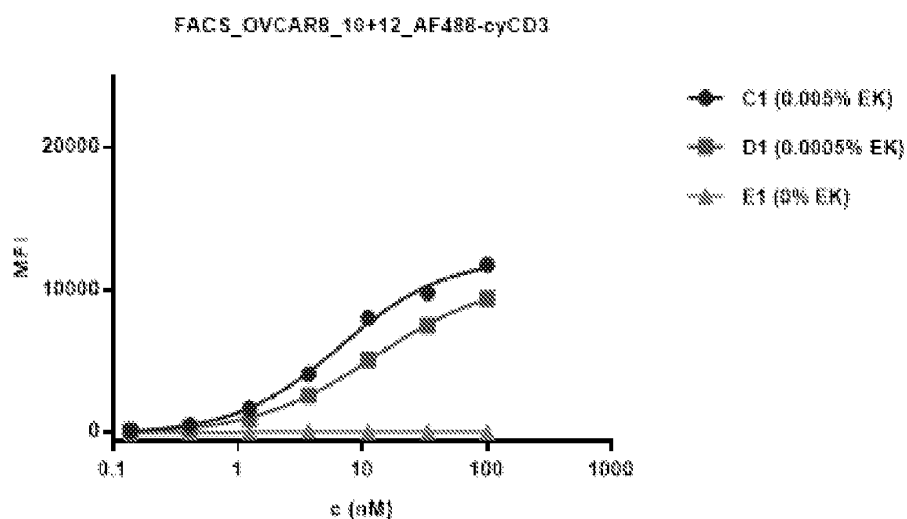


FIG. 35A

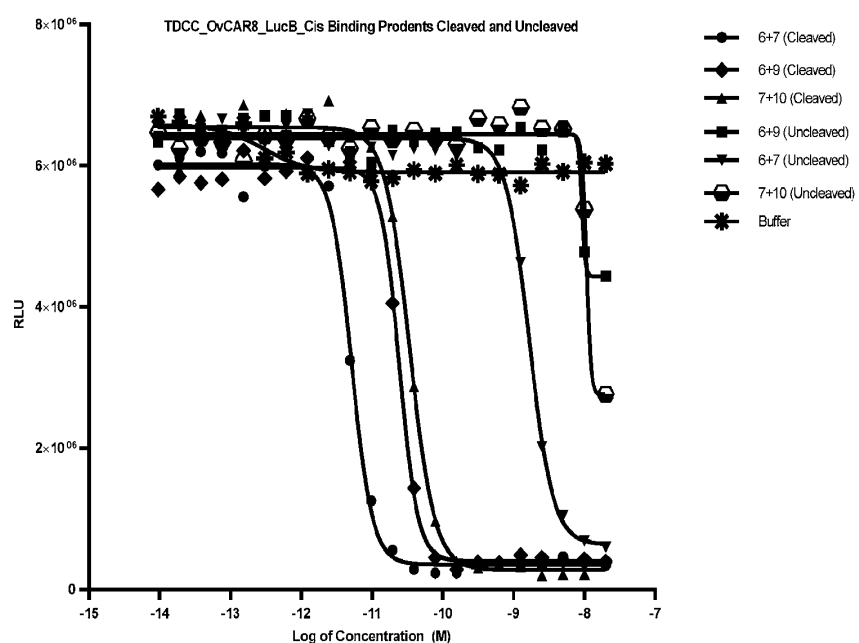


FIG. 35B

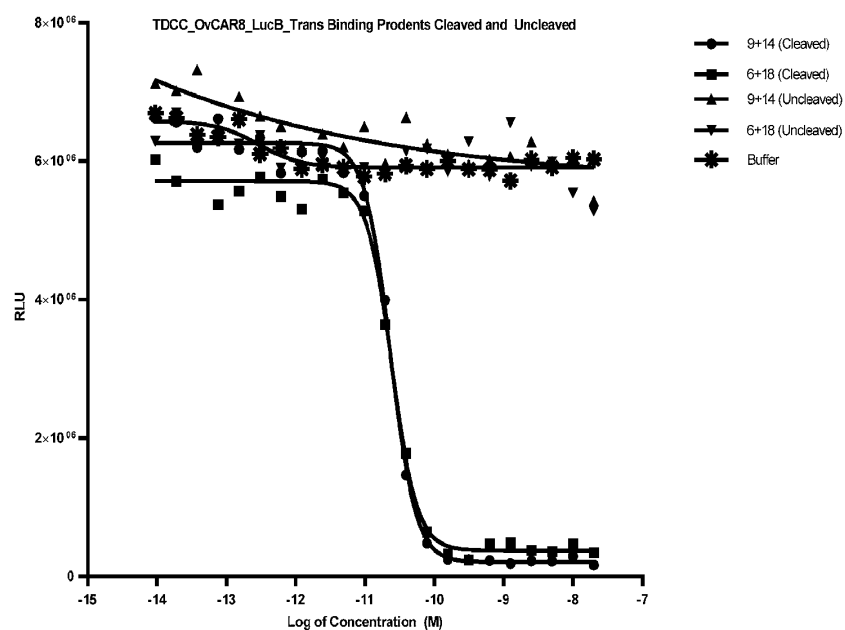


FIG. 36

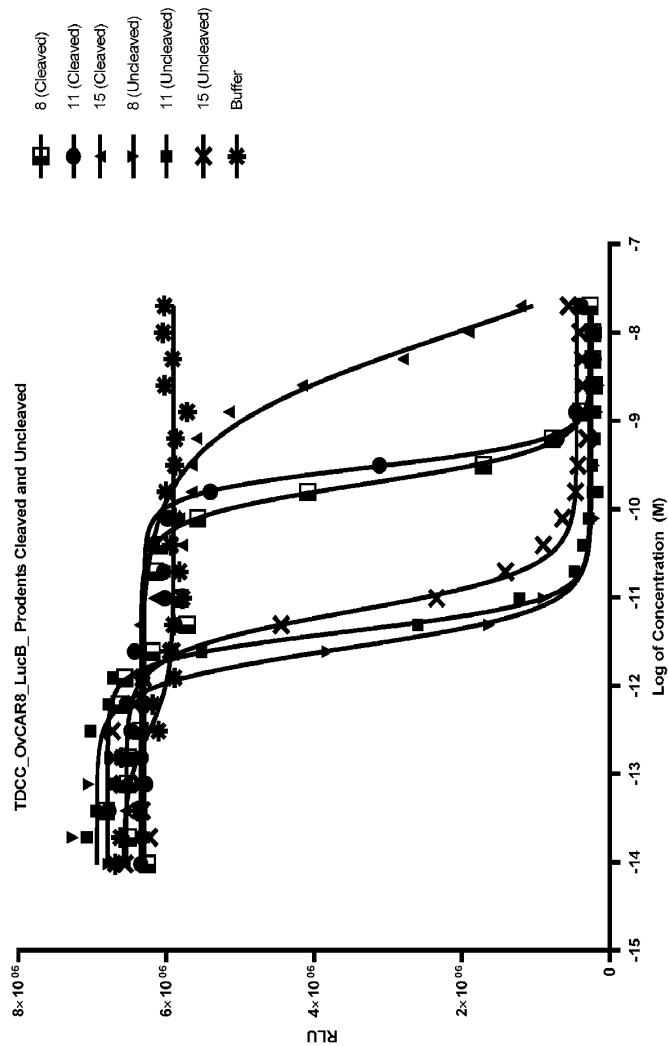


FIG. 37

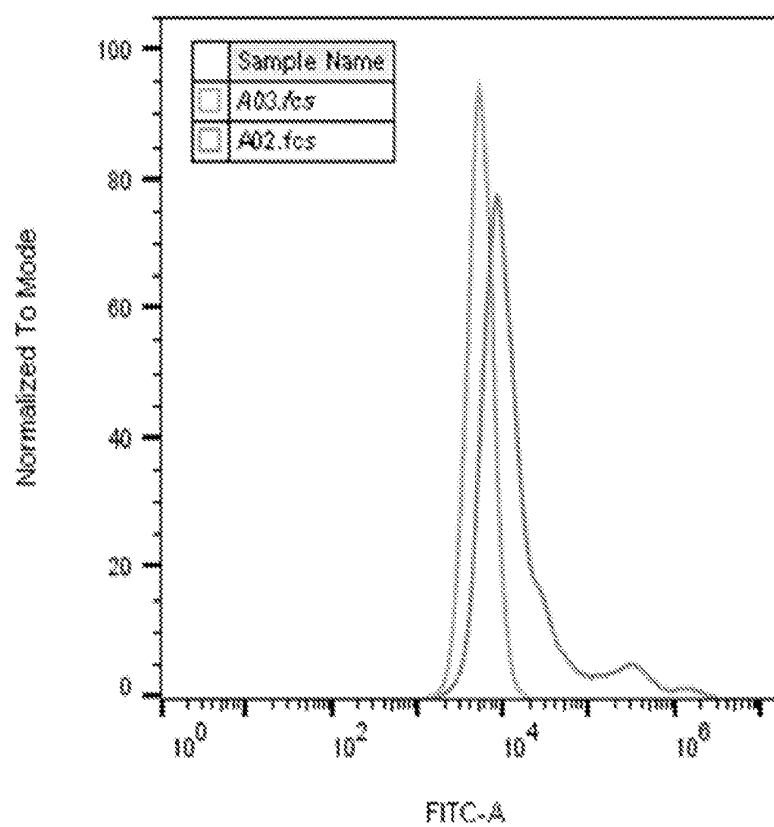


FIG. 38

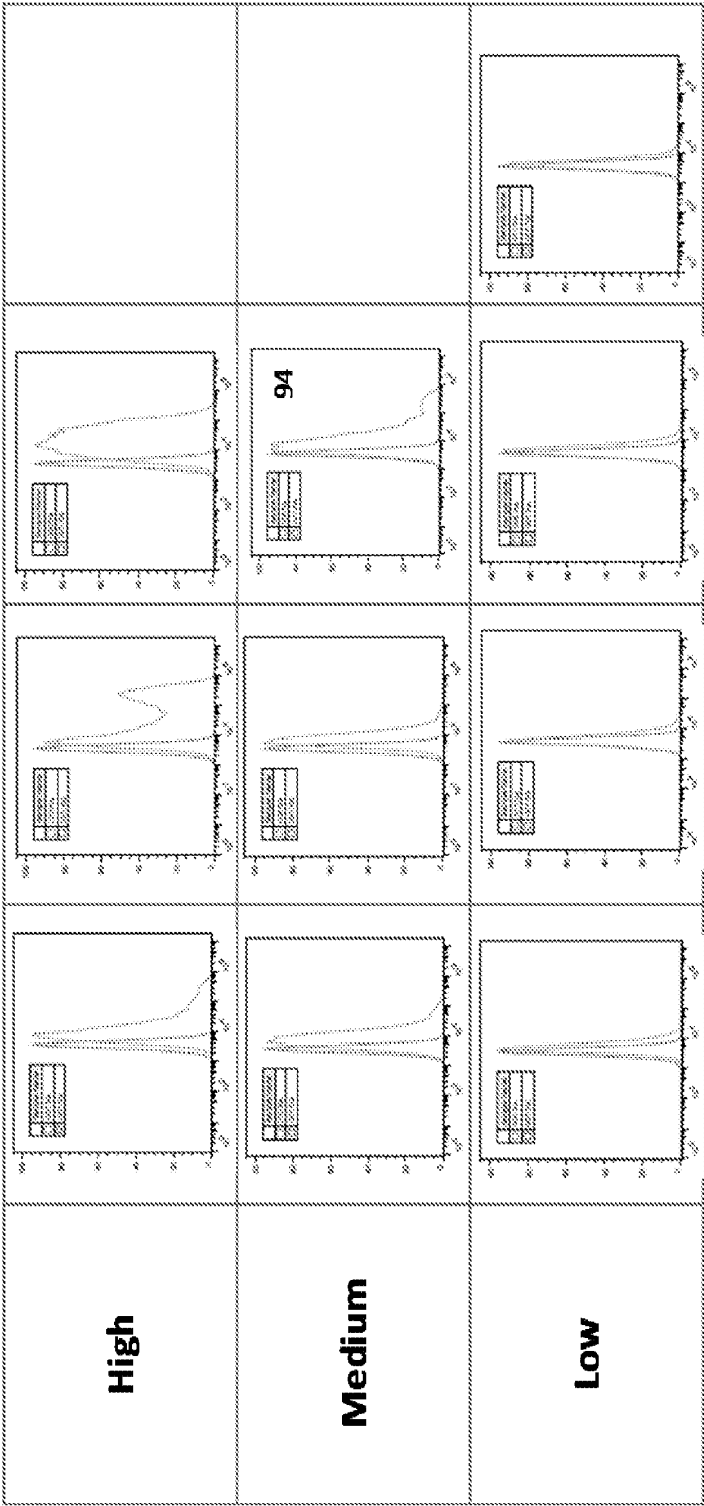


FIG. 39A

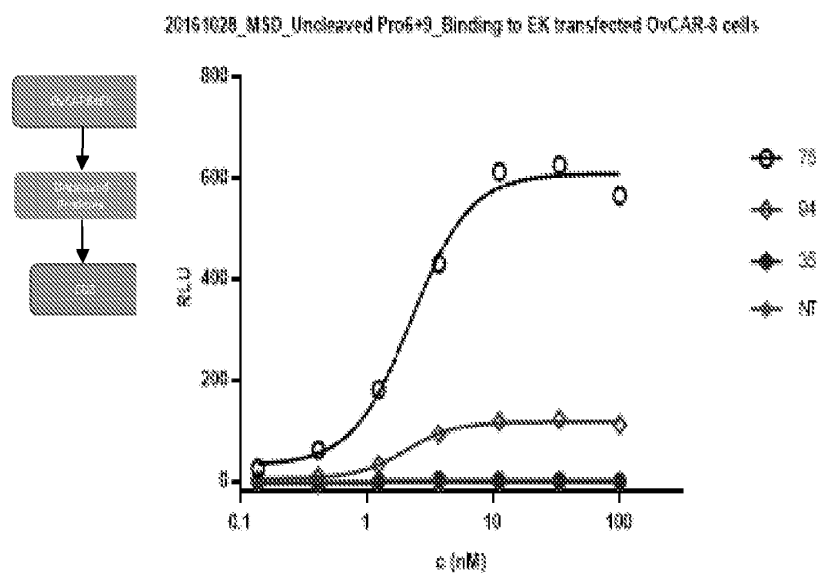


FIG. 39B

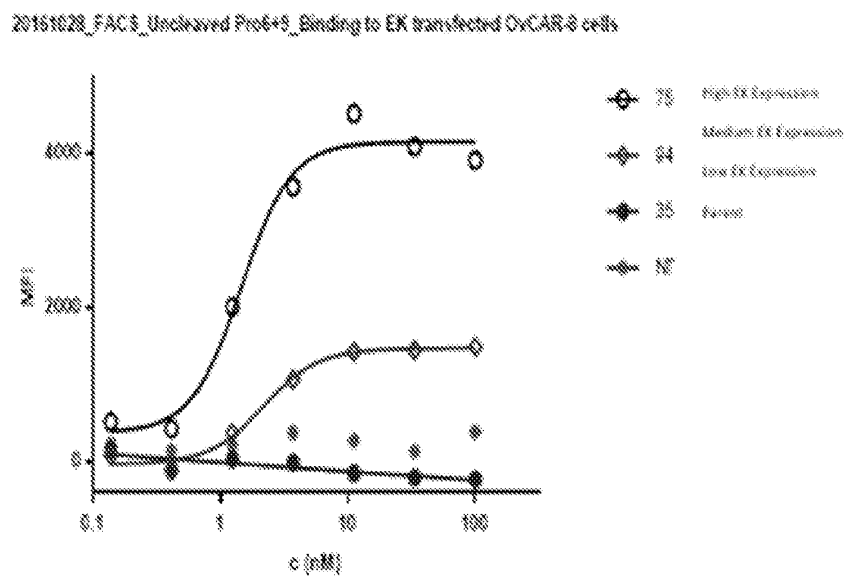


FIG. 40A

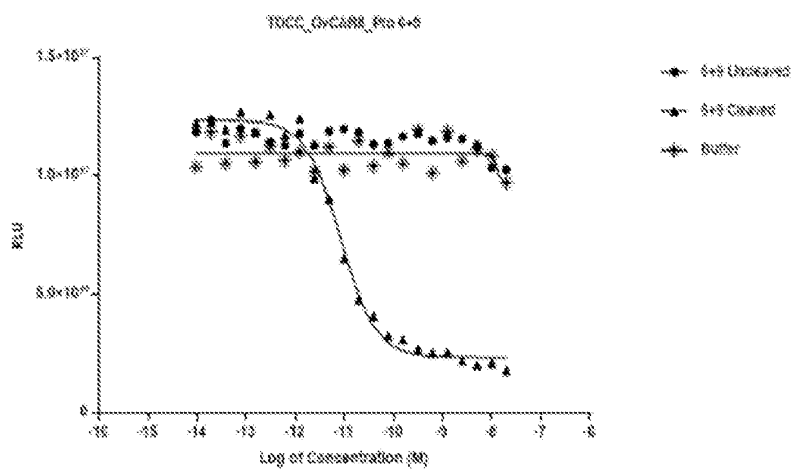


FIG. 40B

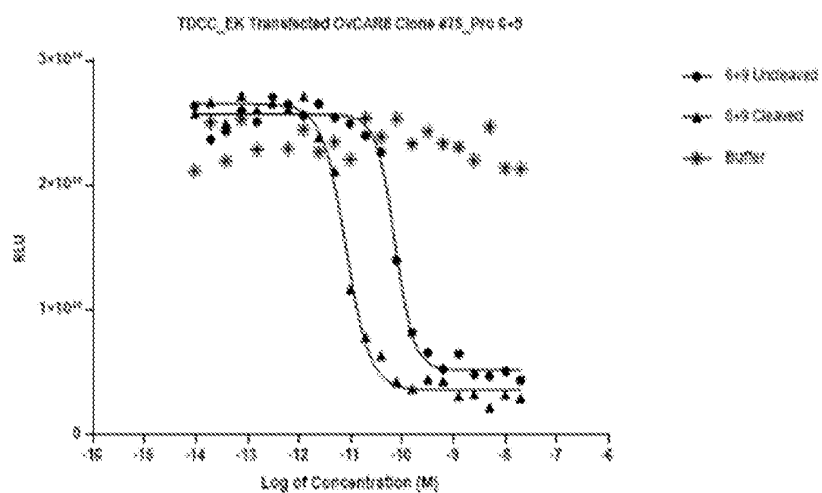


FIG. 41A

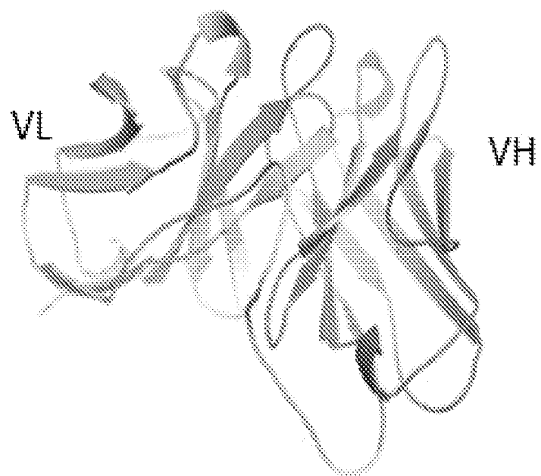


FIG. 41B

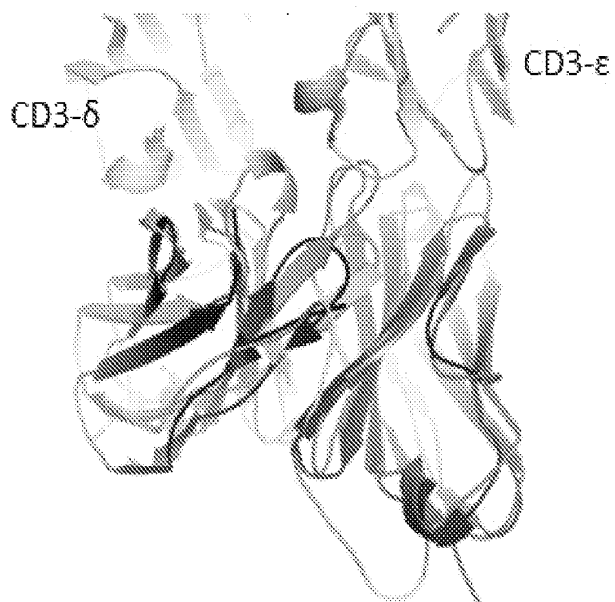


FIG. 42A

[illegible]

FIG. 42B

<u>Pro21</u> EVQLVESGGGLVQPGGSLKLSCAASGFTFSSAMNHWVRQAPGKGLEWVARRISKNNQSYATATATTA*SVKDRFTISRDDSKNTAYLQMNILKT EDTAVVYCVRRHGRFGNSYIAETFWAYWGQGLTVTVSS	Does not express well
<u>Pro29</u> [Y32S Y61A D64A S110A Y111F] EVQLVESGGGLVQPGGSLKLSCAASGFTFNKSSAMNHWVRQAPGKGLEWVARRISKYNNYATATATTA*SVKDRFTISRDDSKNTAYLQMNILKT EDTAVVYCVRRHGRFGNSYIAETFWAYWGQGLTVTVSS	Expressed, inactive
<u>Pro30</u> [Y32S Y61A S110T Y111F] EVQLVESGGGLVQPGGSLKLSCAASGFTFNKSSAMNHWVRQAPGKGLEWVARRISKYNNYATATATTA*SVKDRFTISRDDSKNTAYLQMNILKT EDTAVVYCVRRHGRFGNSYIAETFWAYWGQGLTVTVSS	Expressed, inactive
<u>Pro31</u> [N30S, K31G, Y55A, N57S, Y61E, D64A, F104A, Y108A] EVQLVESGGGLVQPGGSLKLSCAASGFTFSSAMNHWVRQAPGKGLEWVARRISKNNQSYATATTA*SVKDRFTISRDDSKNTAYLQMNILKT AVVYCVRRHGRFGNSYIAETFWAYWGQGLTVTVSS	Expressed, inactive
<u>Pro32</u> [N30S, K31G, Y32H, Y55A, N57S, N103A, F104N] EVQLVESGGGLVQPGGSLKLSCAASGFTFSSAMNHWVRQAPGKGLEWVARRISKNNQSYATATTA*SVKDRFTISRDDSKNTAYLQMNILKT AVVYCVRRHGRFGNSYIAETFWAYWGQGLTVTVSS	Expressed, inactive

FIG. 43

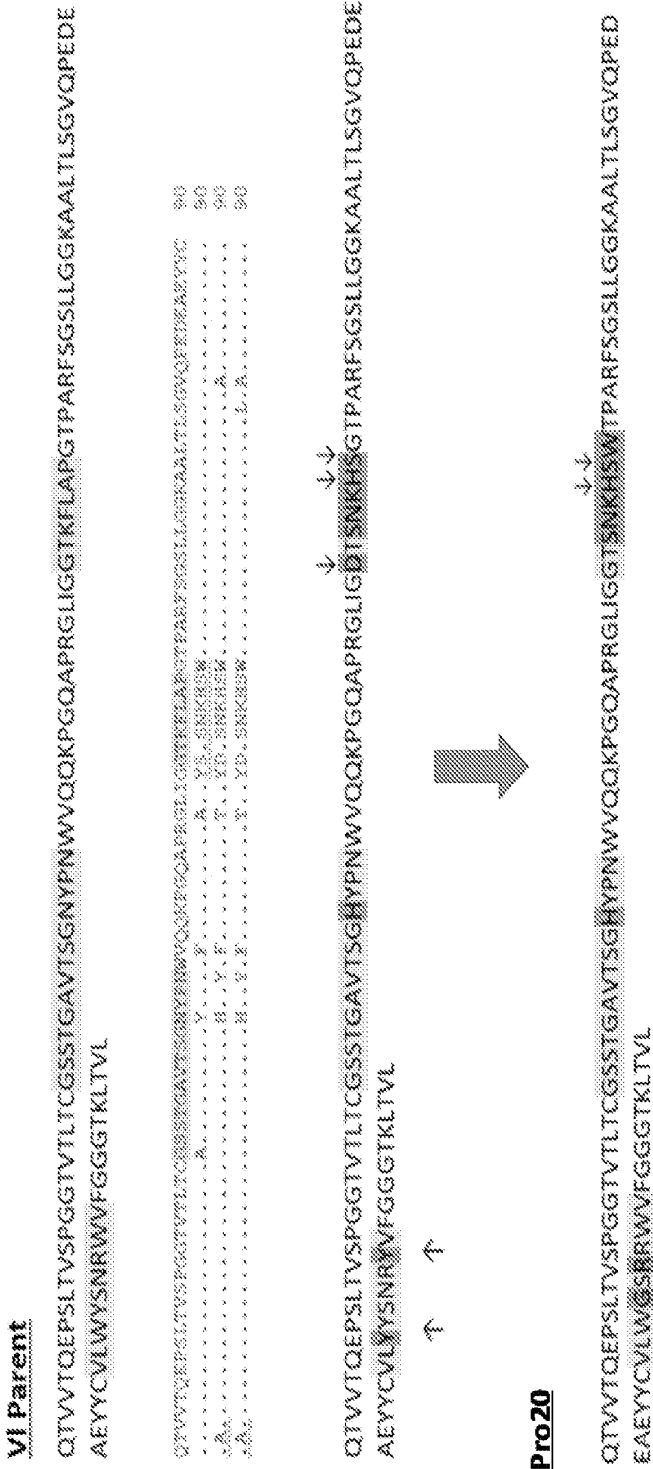


FIG. 44A

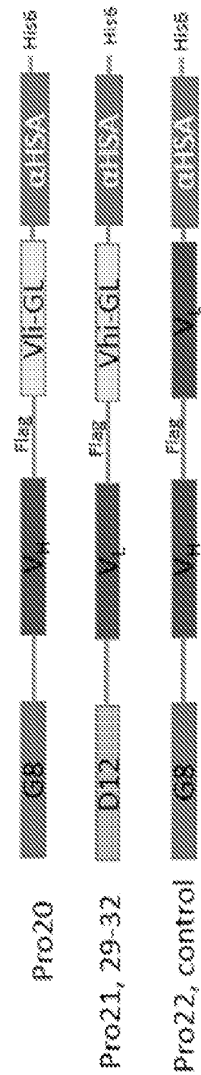


FIG. 44B

Protein samples	hEGFR.hFc	hCD3ε.flag.hFc	anti-EGFR.hFc KD value nM	anti-hCD3ε.flag.hFc KD nM	conc in supe uM
Pro19 (αCD3 Vhl)	+	-	1.49 nM	0	3.25
Pro20 (VhGL)	+	-	0.39% nM	0	1.88
Pro21 (VhGL1)	+/-	-	0.11% nM	0	0.23
Pro22 (WT αCD3)	+	+	0.652 nM	11.9 nM	3.99
Pro29 (VhGL2)	+	-	1.12 nM	0	4.08
Pro30 (VhGL3)	+	-	1.21 nM	0	6.88
Pro31 (VhGL4)	+	-	1.17 nM	0	6.12
Pro32 (VhGL5)	+	-	1.29 nM	0	2.91

FIG. 45A

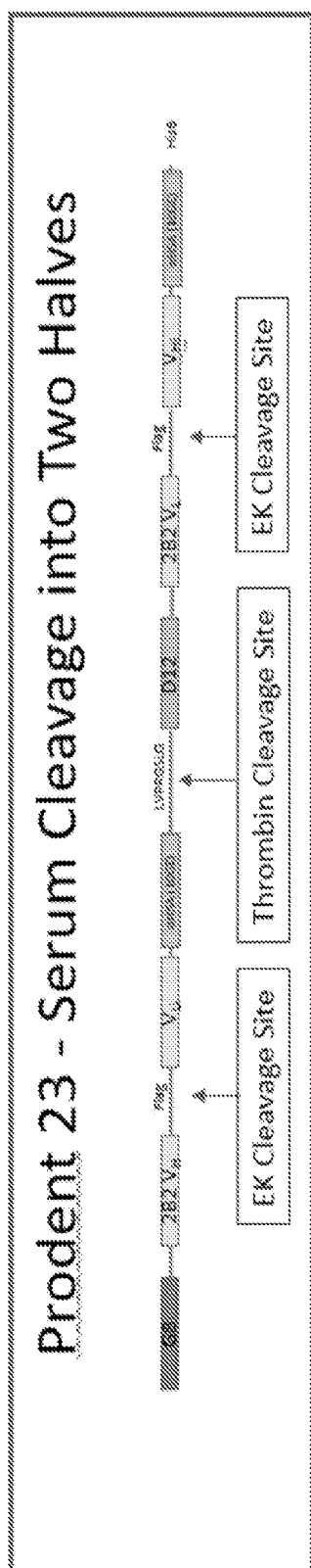


FIG. 45B

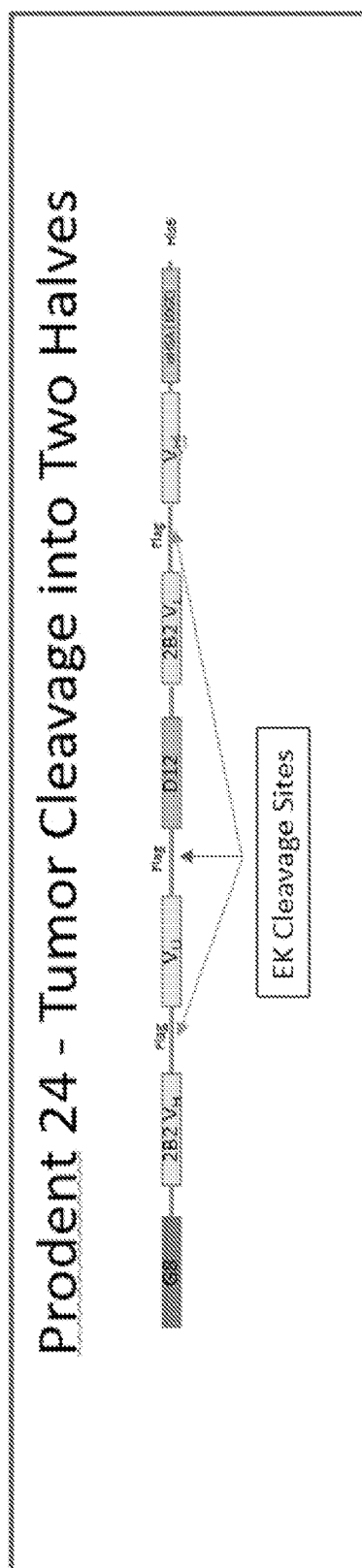


FIG. 46

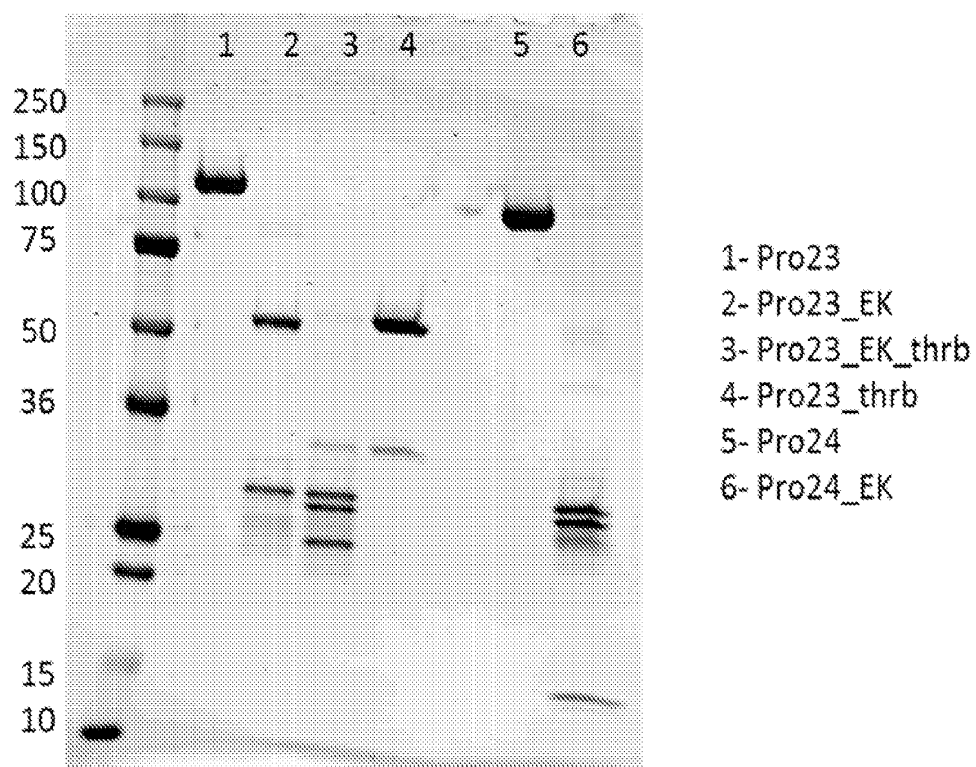


FIG. 47A

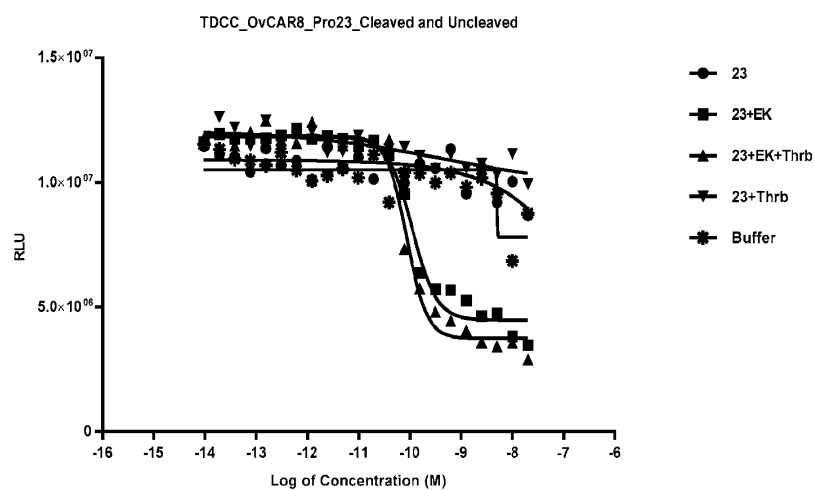


FIG. 47B

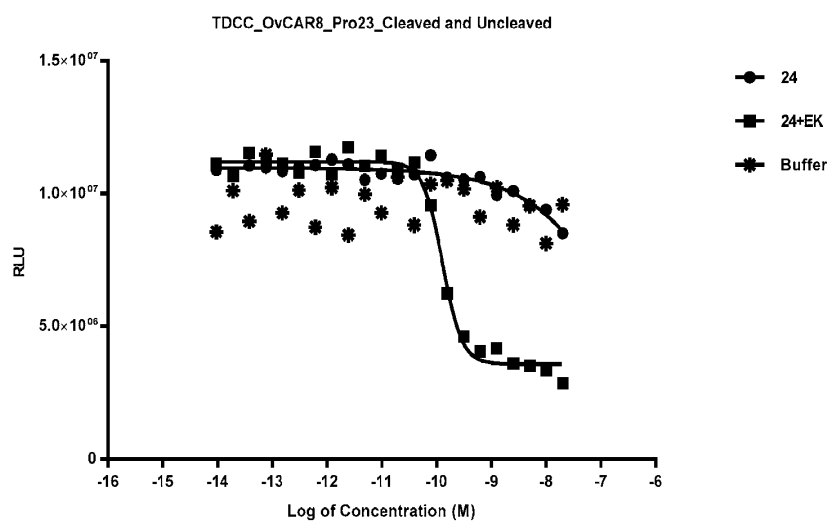


FIG. 48A

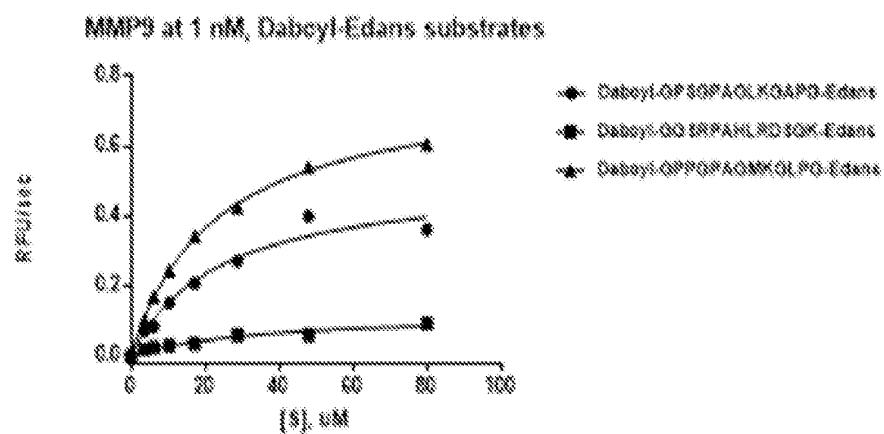


FIG. 48B

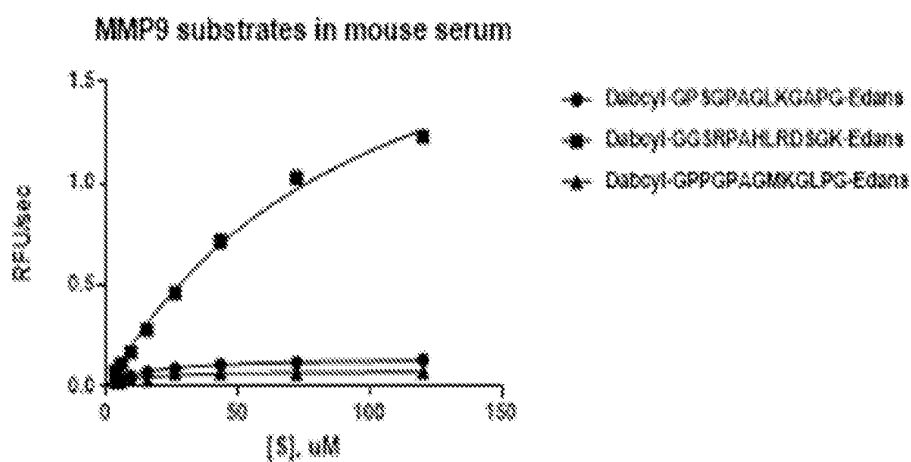


FIG. 48C

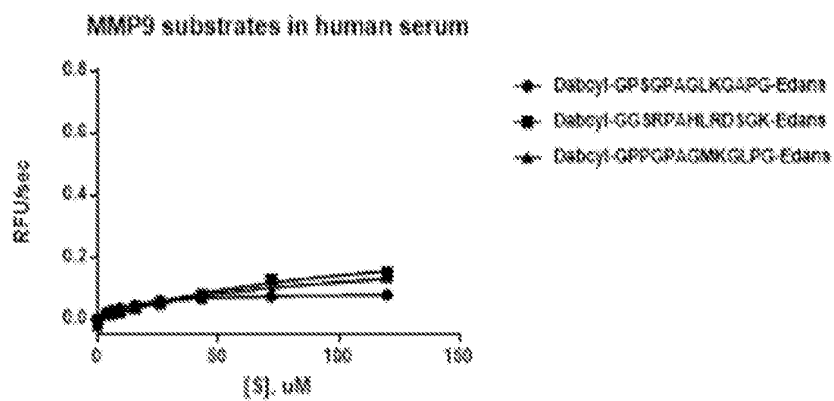


FIG. 48D

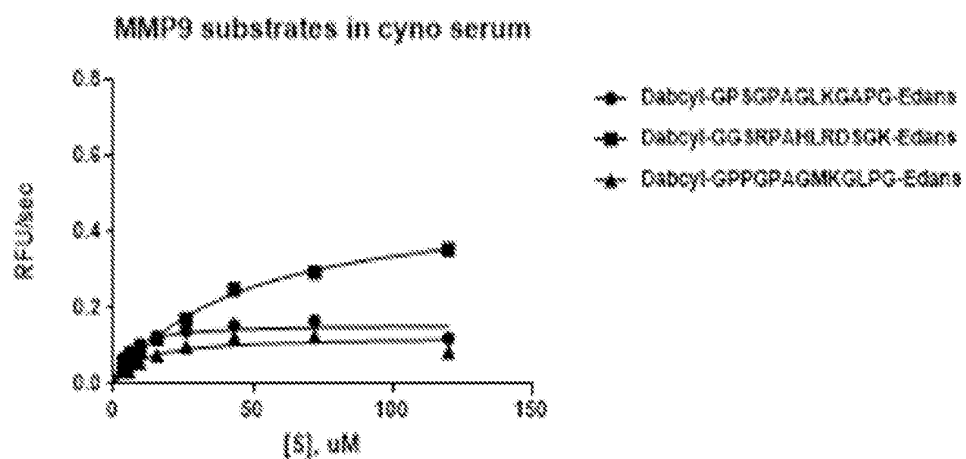


FIG. 49A

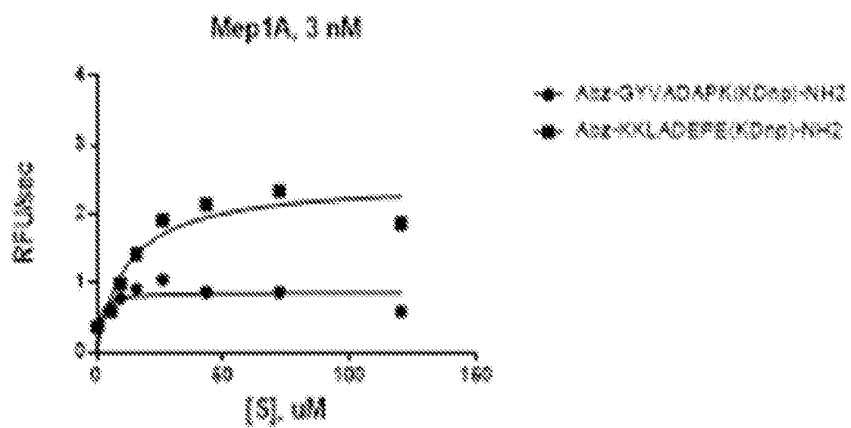


FIG. 49B

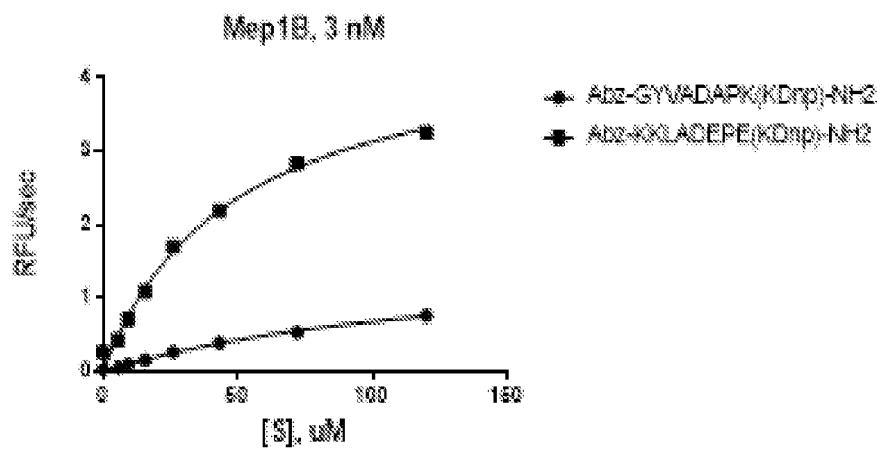


FIG. 49C

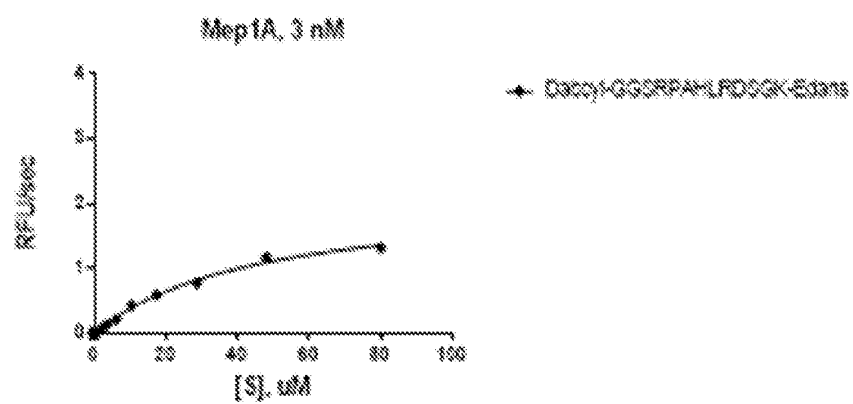


FIG. 49D

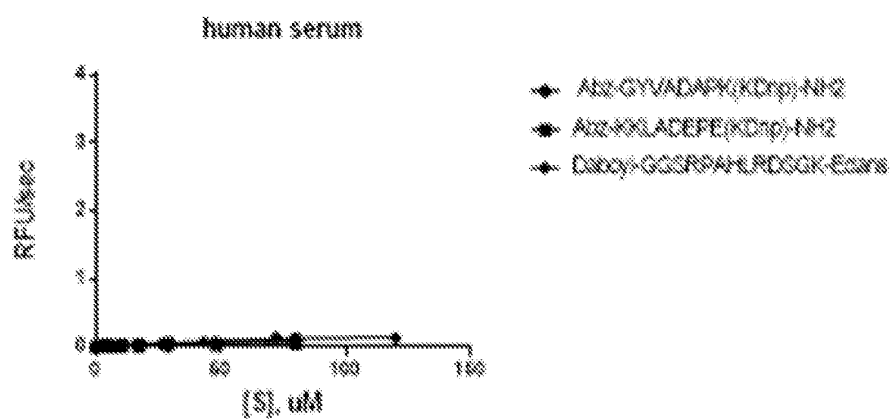


FIG. 49E

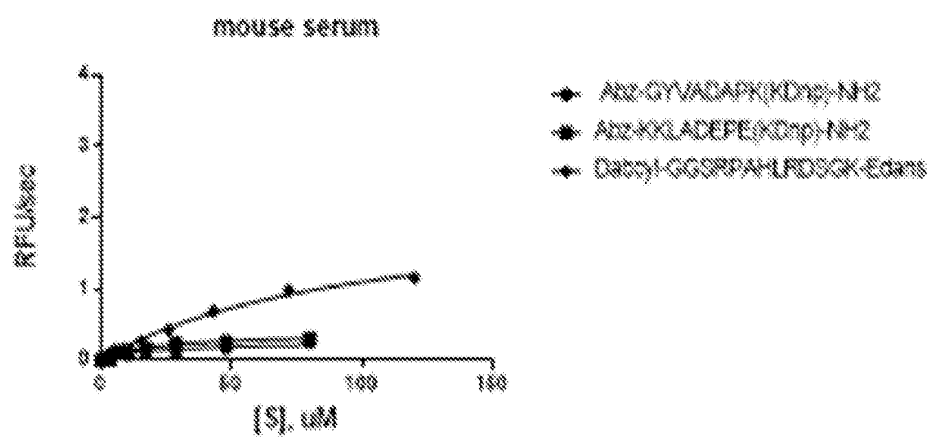


FIG. 49F

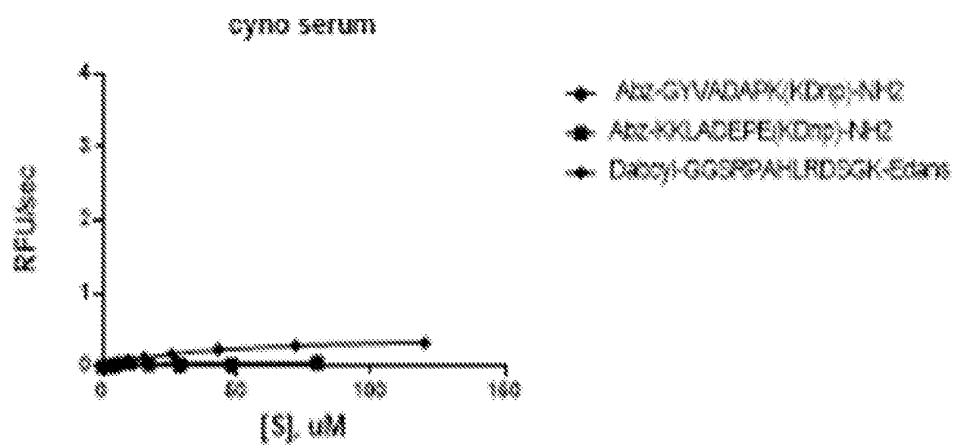


FIG. 50A

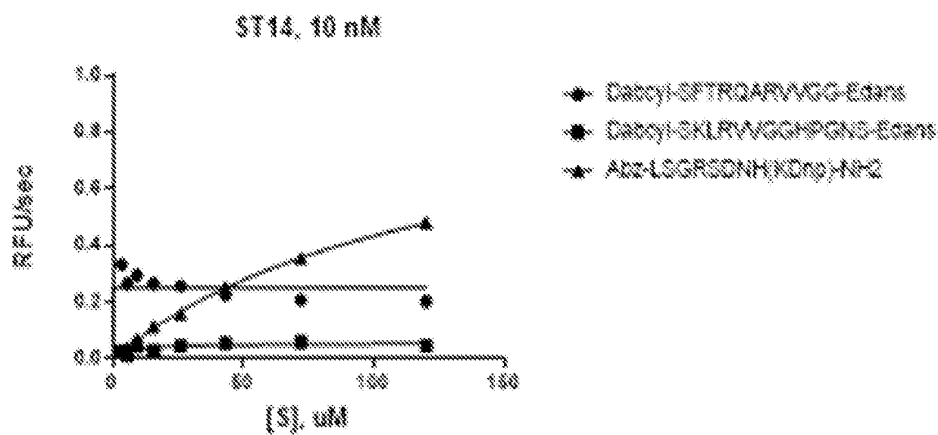


FIG. 50B

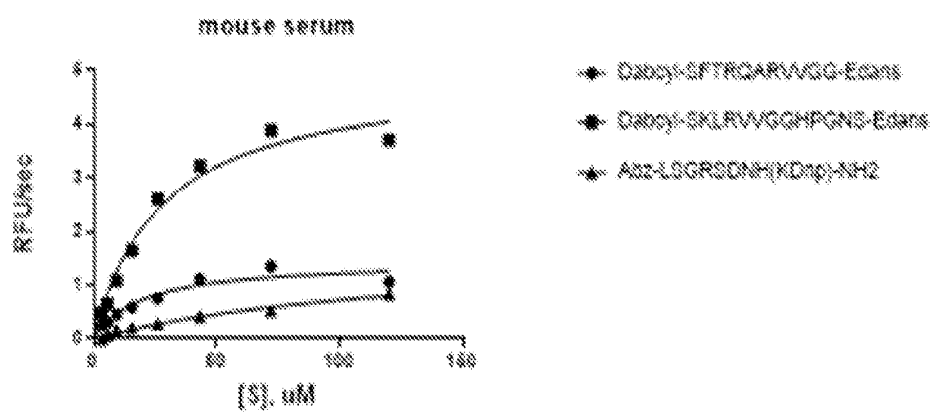


FIG. 50C

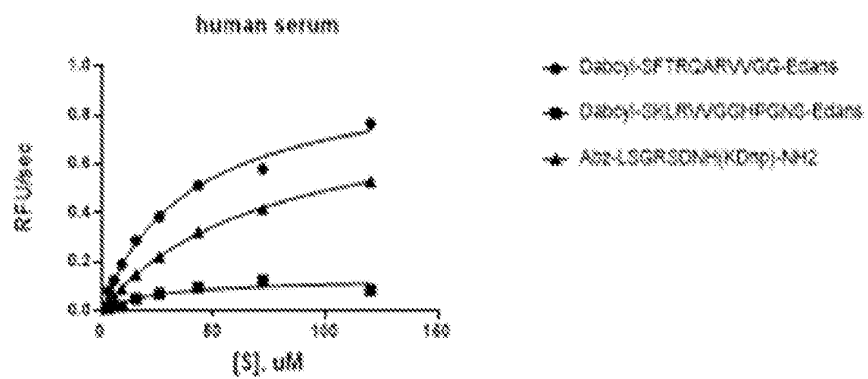


FIG. 50D

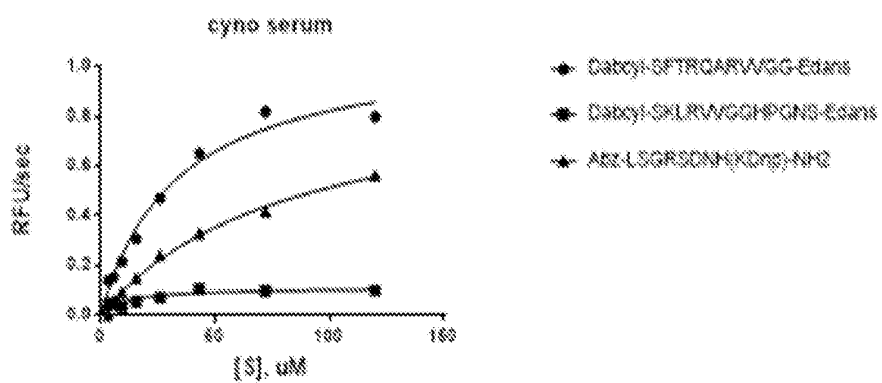


FIG. 51A

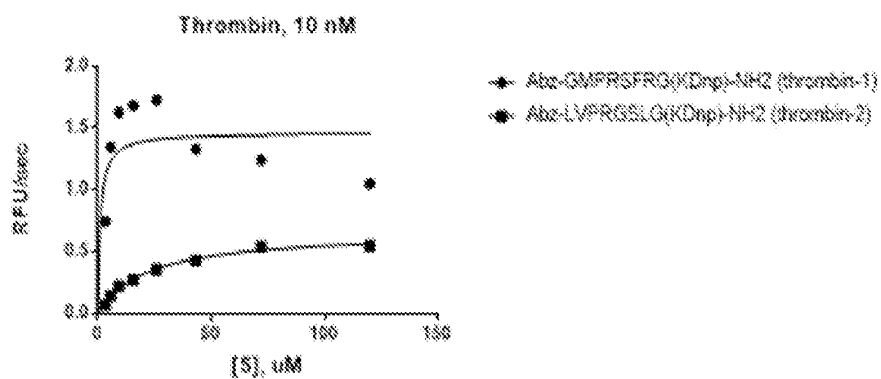


FIG. 51B

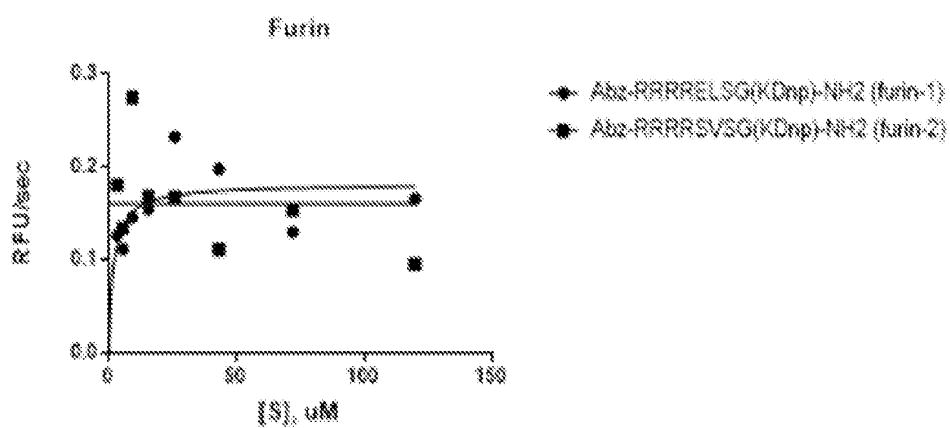


FIG. 51C

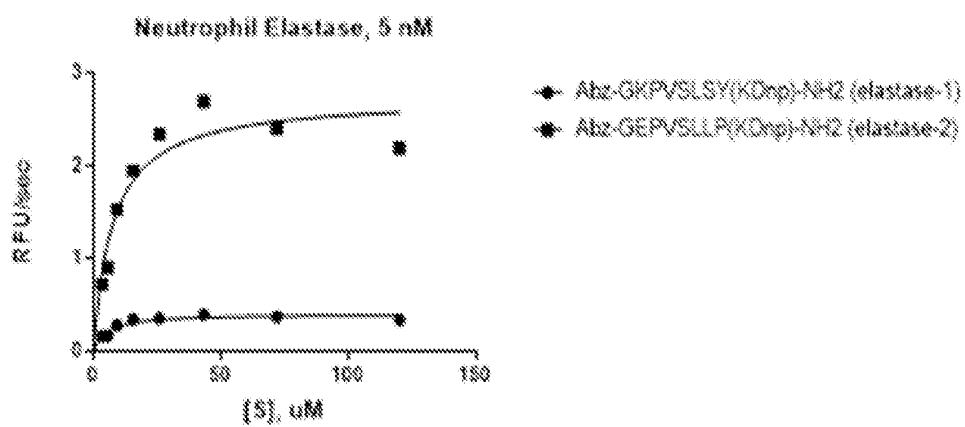


FIG. 52A

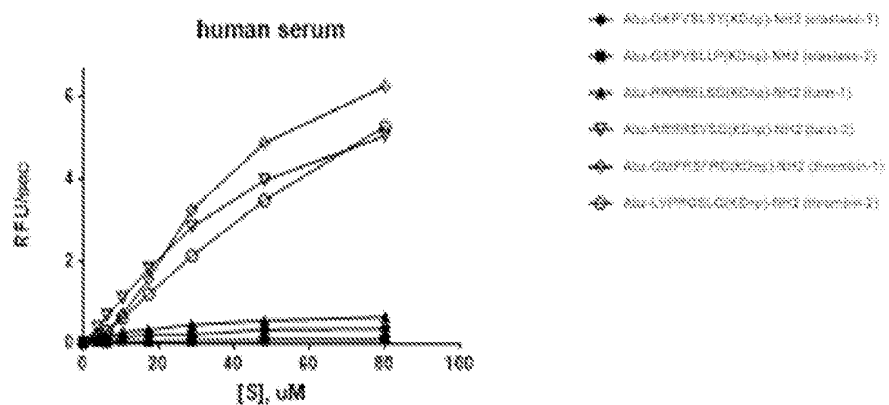


FIG. 52B

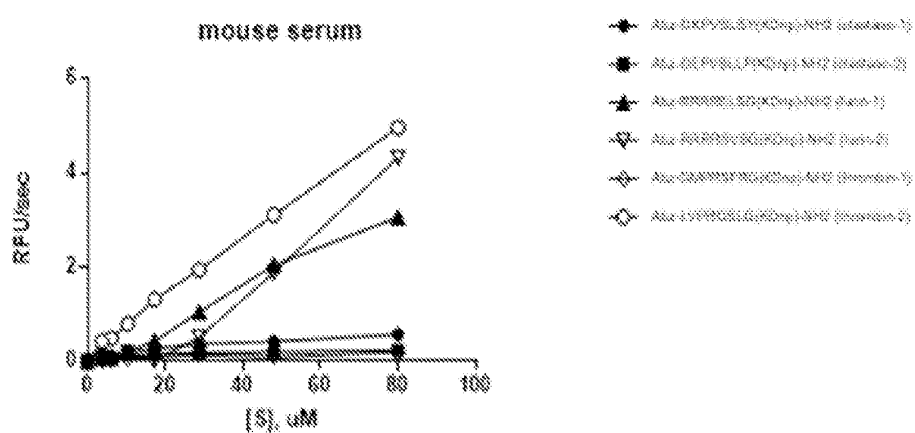


FIG. 52C

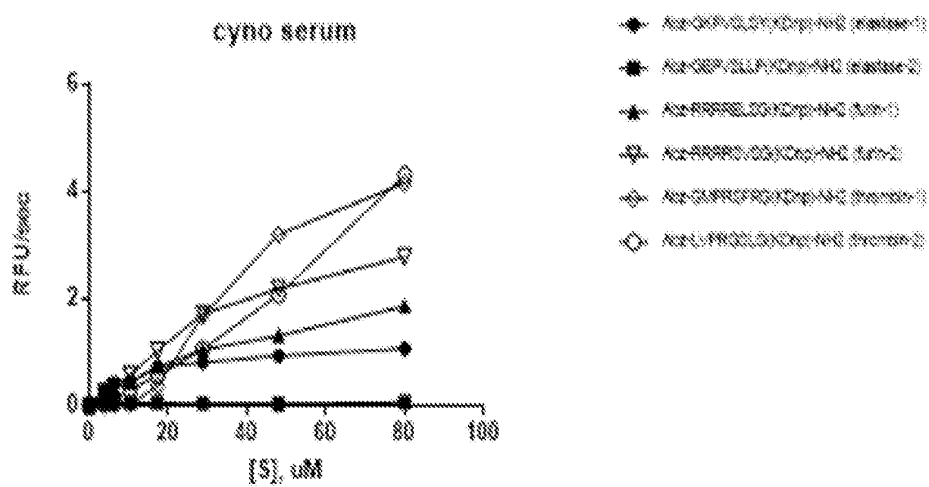


FIG. 53A

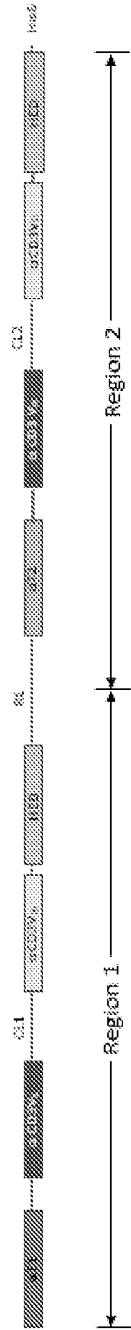


FIG. 53B

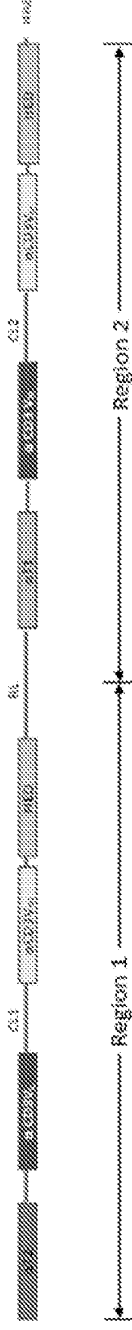


FIG. 53C

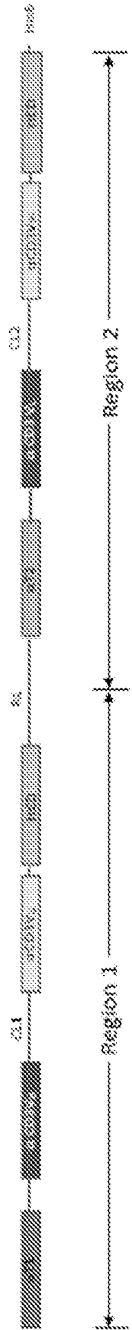


FIG. 53G

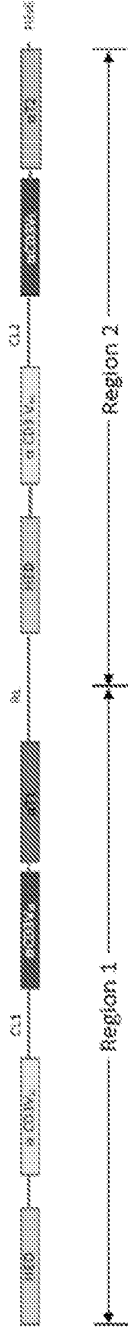


FIG. 53H

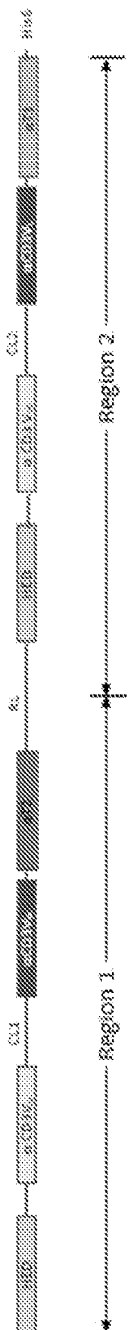


FIG. 53I



FIG. 53J



FIG. 53K

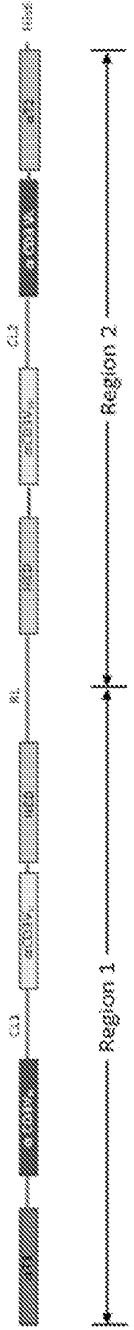


FIG. 53L

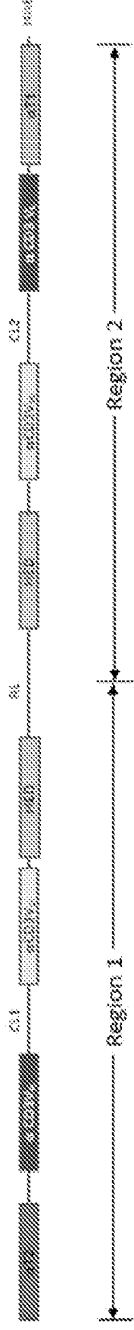


FIG. 53M

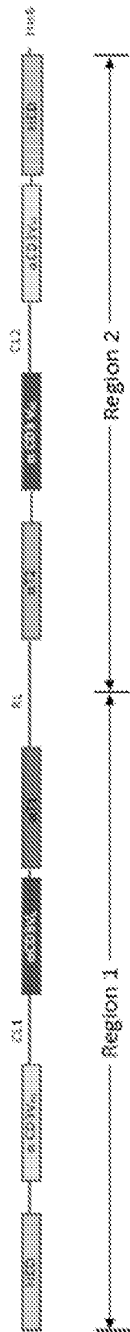


FIG. 53N



FIG. 53O

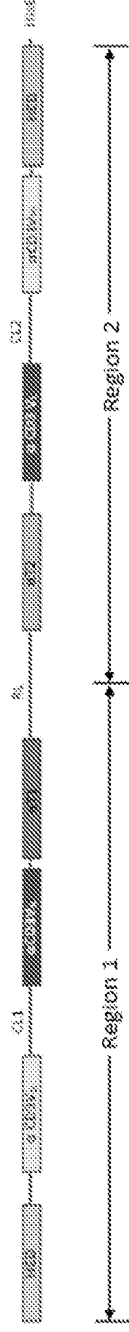


FIG. 53P



FIG. 54A

Prodeints 1 - 38

Pro1 - aEGFR G8 sdAb – aCD3 Vh – His10

EVQLVESGGGLVQAGSLRLSCAASGRITFSSYAMGWFRQAPGKEREFVAINWSSGSITYYADSVKGRFTISRDNAKNTIMYLQMNSL
KPEDTAVYYCAAGYQINSNGYNFKDYEYDYWGQGTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAWWGQGT
VTVSSHHHHHHHHHH SEQ ID NO: 44

GAAGTCCAACTGGTGGAATCGGGCGGTGACTCGTGCAAGGCCGGAGGTTCCCTGCGCCCTTTCTGTGCGGCTTCGGGAAGAACCT
TCTCCTCGTATGCCATGGGATGGTTCGCCAAGCCCCCTGGAAAGAGCGGGAATTCGTCTGGCGATCAATTGGAGCTCCGGTTC
GACTTACTACGCCGACTCCGTGAAGGGCCGTTCAACATTAGCCGGGACAAATGCTAAGAACACCATGTATCTGCAGATGAACCTC
ACTGAAACCTGAGGACACGGCGGTGTAATACTGCGCCGCTGGGTACCGATCAATTCGGAACTCAACTTCAAGGACTACGA
GTACGACTACTGGGTCAGGCAACCCAGTCAACCGTGTCCAGCGAGGAGGTGGAAGCGGAGCGGTTCCGAAAGTGCAGTCTCGT
CGAGTCCGGGGTGGACTGTCTCAACCGGGCGGATCACTGAAGCTGAGCTGCGCAGCTCCGGATTCACTTCAACAAAGTACGC
CATGAAGTGGTCAAGACAGGCAACCGGGAAGGACTGGAATGGGTGGCCCGGATCAGGTCCAAAGTACAACAACACTACGCCACCT
ACTACGGGACAGCGTGAAGGATAGGTTCACCATCTCCGGGACGACAGCAAGAACACTGCTACCTCCAAATGAACAACCTCA
AGACCGAAGATACTGCGGTGTATTACTGCGTGGCCACGGGAACCTTCGGAACACAGCTACATCAGTCTGCGGCTACTGGGCTACTGGGGCC
AGGGCACTCTGGTGACCGGTGTCATCCACCATCACCACCATCATCACCATCAC SEQ ID NO: 45

FIG. 54B

Pro2 – aCD3 V1 – aEGFR D12 sdAb – His10
QTVVTQEPSLTVSPGGTVTLTCGSTGAVTSGNYPNWVQQKPGQAPRGLIGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCVLWYSNRWVFGGGTKLTVLGGGSGGSQVKLEESGGSVQTGGSRLTCAASGRTSRSYGMWFRQAPGKEREFVSGISWRGD
STGYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSSHHHHHHHHHH
SEQ ID NO: 46

CAGACCGTGGTGACCCAGGAACCCCTCACTGACCGTGTCCCCAGGAGGAACCGTGACCCCTTACCTGTGGCTCCTCGACCGGTGCCG
TGACGTCCGGGAAC TACCCC AACTGGGTCCAGCAAAGCCGGGACAAGCCCCCTCGGGGACTGATCGGGGGGACTAAGTTCCCTGG
CCCCTGGCACTCCTGCCGCTTACGCGGACGCTCCTGGGAGGAAAGCGGCCCTGACACTCTCGGGGTGCAGCCTGAAGATG
AGGCCGAATACTACTGCGTGTGTACTCCAATCGCTGGTGTGAGGGGGCACCAAGCTGACCGTGTGGGAGGAGGAG
GAAGCGCGGAGGTTCCAGGTCAAGCTGGAGGAATCGGTGGAGGCTCAGTGCAGACAGGAGGTAGCCTCCGGCTCACTTGCG
CCGCTTCCGGAAGGACTTCCCGGAGCTACGGGATGGCTGGTTTCGGCAAGCCCCCGAAAGGAGAGAGAAATTCGTGTCCGGAA
TTAGCTGGAGGGGCGACTCAACTGGATACGCGGACTCCGTCAAGGGCAGATTCACTATCTCTCGGGACAACGCCAAGAACACCG
TGGACTTGCAATGAAATTCCTGAAGCCGGAGGACACTGCCATCTACTGTGTGCTGGGCAAGCAGGATCTGCTGTGACGGCAC
CCTTTATGAATACGATTACTGGGGACAGGGAACCCAGGTACCGGTGTGTCGTCGCCACCATCACCAACCATCATCACCATCAC
SEQ ID NO: 47

FIG. 54C

Pro3 - aEGFR G8 sdAb - aCD3 scFv - aEGFR D12 sdAb - His10

EVQLVESGGGLVQAGGSLRLSCAASGRTFSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNINFKDYEDYWGGQTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
 WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAWYWGQGT
 LTVSSGGSGGGSGGGSQTVVTEPSLTVSPGGITVLTGSSSTGAVTSGNYPNWVQKPKQAPRGLIGGTFKFLAPGTPARFSGSL
 LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGSGGGSVQKLEESGGSVQGTGSLRLTCAASGRTSRSYGMG
 WFRQAPGKEREFVSGISWRGDSSTGYADSVKGRFTISRDNAKNTVLDQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQV
 VSSHHHHHHHHHH SEQ ID NO: 48

GAAGTCCAACTGGTGAATCGGGCGGTGACTCGTGCAAGGCCGGAGGTTCCCTGCGCCTTTCTGTGCGGCTTCGGGAAGAACCT
 TCTCCTCGTATGCCATGGGATGGTTCGCCAAGCCCTGGAAAAGAGCGGGAATTCGTCTGGCGATCAATTGGAGCTCCGGTTC
 GACTTACTACGCCGACTCCGTGAAGGGCCGTTCAACATTAGCCGGGACAAATGCTAAGAACACCATGTATCTGCAGATGAACCTC
 ACTGAACCTGAGGACACGGCGGTACTACTGCGCCGTGGTACCAGATCAATCCGGAACCTACAACCTCAAGGACTACGA
 GTACGACTACTGGGTCAGGCAACCCAGTCAACCGTGTCCAGCGAGGAGGTGGAAGCGGAGGCGGTTCCGAAAGTGCAGCTCGT
 CGAGTCCGGGTGACTGTCTCAACCGGCGGATCACTGAAGCTGAGCTGCGCAGCTCCGGATTCACTTCAACAAGTACGC
 CATGAAGTGGTCAAGAGCAACCGGAAGGACTGGAATGGTGGCCCGGATCAGGTCCAAAGTACAACAACACTACGCCACCT
 ACTACGGGACAGCTGAAGGATAGGTTCAACCTCCCGGACGACAGCAAGAACACTGCTACCTCCAAATGAACAACCTCA
 AGACCGAAGATACTGCGGTGTATTACTGCTGCGCCACGGGAACCTTCGGAACACAGCTACATCAGCTACTGGGCTACTGGGGCC
 AGGCACTCTGTTGACCGTGAGCTCAGGAGGAGCGGCTCCGAGGCGGAGGCTCAGGGGAGGAGGTTCCGACAGCCGTGGTG
 ACCCAGGAACCTCACTGACCGTGTCCCCAGGAGAACCGTACCTGCTGCTCCGACCGGTGCTGACCTGCGGCTGCGGCTCGGCACTC
 ACTACCCCAACTGGGTCCAGCAAAGCCCGGACAAAGCCCTCGGGGACTGATCGGGGGAATAAGTTCTCGCCCTGGCACTC
 CTGCCCGCTTCAGCGCAGCTCTGGGAGGAAAAGCGGCCCTGACACTCTCGGGGTGACGCTGAAGATGAGGCCGAATACT
 ACTGCGTGTGTGTAATCCAAATCGCTGGGTGTTTGGAGGGGCAACCAAGCTGACCGTGTGCTGGGAGGAGGAGGAGCGCGGAG
 GTTCCCAGGTCAAGCTGGAAGAAATCGGGTGGAGGCTCAGTCAGACAGGAGTAGCTCCGGCTCACTTGGCCGCTTCCGGAA
 GGACTTCCCGGAGCTACGGGATGGGTGGTTTCGGCAAGCCCCGGAAAGGAGAGAGAAATTCGTGTCCGGAATTAGCTGGAGGG
 GCGACTCAACTGGATACCGGACTCCGTCAAGGCGAGATTCACTATCTCTGGGACACGCCAAGAACACCGTGGACTTGCAAA
 TGAATCCCTGAAGCCGAGGACACTGCCATCTACTGTGTGCGGACAGGATCTGCTGTACGGCACCTTTATGAATA
 CGATTACTGGGACAGGGAAACCCAGGTACGGTGTGCTGCCACCATCACCAACCATCATCACCATCAC SEQ ID NO: 49

FIG. 54D

Pro4 - aEGFR G8 sdAb -- aCD3 Vh -- ^{Flag} -- aCD3 VI -- aEGFR D12 sdAb -- His10

EVQLVESGGGLVQAGGSLRLSCAASGTRFSSYAMGWFRQAPKEREFFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
KKPEDTAVYYCAAGYQINSGNYNFKDYEYDWGQGTQVTVSSGGSGSGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAWWGQGT
LVTVSSDYKDDDKGGQTVVTQEPSLTVSPGGTVTLTCSGSTGAVTSGNYPNWVQKPKGQAPRGLIGGTKFLAPGTPARFSGSLGKGK
AALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGSGSGGSQVKLEESGGSVQTGGSLRLTC AASGRTSRSYGMGWFRQ
APGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSH
HHHHHHHHH SEQ ID NO: 50

GAAGTCCAACTGGTGGAATCGGGCGGTGACTCTGTGCAGGCCGGAGGTTCCCTGCGCCTTCTCTGTGCGGCTTCGGGAAGAACAACCT
TCTCTCGTATGCCATGGATGTTCCGCCAAGCCCTGGAAAAGACGGGAATTCGTCTGGCGATCAATTGGAGCTCCGGTTC
GACTTACTACGCCACTCCGTGAAGGCCGTTCAACATTAGCCGGGACAATGCTAAGAACACCATGATATCTGCAGATGAACCTC
ACTGAAACCTGAGGACACGGCGGTGTACTACTGCGCGTGGTACAGATCAATTCCGGAACACTACAATTC AAGGACTACGA
GTACGACTACTGGGTCAGGACACCAAGTCAACCGTGTCCAGCGGAGGTGGAAGCGGCGGTTCCTCC AAGTGCAGCTCGT
CGAGTCCGGGGTGACTGTCTCAACCGGCGGATCACTGAAGCTGAGCTGCGCAGCCTCCGGATTCACCTTCAACAAGTACGC
CATGAAC TGGGTGACAGAGCACCCGGAAAGGACTGGAATGGTGCCCGGATCAGGTCCAAGTACAACAAC TACGCCACCT
ACTACCGGCACACGCTGAAGGATAGGTTCACCATCTCCCGGACGACAGCAACACTGCCTACCTCCAATGAAACAACCTCA
AGACCGAAGATACTCGGTGTAATTACTGCTGCGCCACGGGAACCTTCGGAACACAGTACATCAGTACTGGGCTACTGGGGCC
AAGGCAC TCTGTTGACCGTCTCCGACTACAAGACGATGACGATAAGGCGGCCAGACCGTGGTGACCAAGCAACCTCAC
TGACCGTGTCCCCAGGAGAACCGTGACCTTACCTGTGCTCTCGACCGGTCCGTGACGTCCGGGAAC TACCCCAACTGGGT
CAGGCAAAAGCCGGACAAGCCCTCGGGACTGATCGGGGGACTAAAGTTCTTGGCCCTGGCACTCTGCCGCTTCAAGCGG
CCAGCTCTCTGGAGGAAAAGCGCCCTGACACTCTCGGGGTGCAGCTGAGTAGGCCGCAATACTACTGCTGCTGTGGTA
CTCCAATCTGCTGGTGTITGGAGGGGCACCAAGCTGACCTGTGGAGGAGGAGCAAGCGCGGAGGTTCCTCCAGGTCAAGCT
GGAGGAATCGGGTGAGGCTCAGTGACAGAGGAGTACCTCCGGCTCACTTGCGCCCTTCGGAAGGACTTCCCGGAGCTA
CGGGATGGCTGTTTCGCAAGCCCCCGAAAGGAGAGAAATTCGTGTCGGAATTAGCTGAGGCGGCACTCAACTGGATA
CGCGGACTCCGTC AAGGCAGATTCACTATCTCTGGGACAACGCCAAGAACACCGTGGACTTGC AATGAAATCCCTGAAGCC
GGAGGACACTGCCATCTACTGTGCTCGGCAGCAGGATCTGCCTGTACGCGACCCCTTTATGAATACGATTACTGGGACAG
GGAAACCAAGTACCGTGTGCTCCACCATCACCAACCATCATCACCATTAC SEQ ID NO: 51

FIG. 54E

Pro5 – aEGFR G8 sdAb – aCD3 Vh – ~~ggggg~~^{ggggg} – aCD3 Vi – ~~ggggg~~^{ggggg} – aCD3Vh_i – ~~ggggg~~^{ggggg} – aCD3Vl – aEGFR D12 sdAb – His6
 EVQLVESGGGLVQAGSLRLSCAASGRTFSYAMGWFRQAPGKEREFVAINWSSGTYYSADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGQGTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
 WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNGSYISYWAYW
 VTVSSGGGGDYKDDDKGGGSQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDKGTPARF
 SGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
 AMNWVRQAPGKGLEWVARIRSKYDYKDDDKADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFNGSYISYWAYW
 GQGTLVTVSSGGGGDYKDDDKGGGSQTVVTQEPSTLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGTKFLAPGTP
 ARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGSGGGSVQKLESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNAKNTVDLQMNLSLKPEDTAIYYCAAAAGSAWYGTLYEYDYW
 GQGTQVTVSSHHHHHH SEQ ID NO: 52

GAAGTGCAGCTCGTTGAGTCAGCGGGGGTCTGTTACAGCGGGTGGTAGTCTCCGCTTGAGCTGCGCAGCTAGCGGCCGAACC
 TTCTCATCTTACGCAATGGGTGGTTAGACAGGCCCTTGAAAGGAAGAGAAATTCGTGGTTGCAATTAACTGGAGCAGCGGCT
 CAACTTACTATGCCGATTACGTGAAGGCGAGTTACCATAGCCGAGACAAATGCCAAAAACACCATGTACCTTCAAATGAATA
 GCCTCAACCTGAGATACCCCGTTTACTACTGTGCAGTGGCTATCAATAACTCAGGGAATTAATTTTAAGGACTATGA
 GTACGATTACTGGGTCAAGGCACCCAAAGTAAGTTCGGTGGGGAGGCAGTGGTGGAGGAGCGAAGTACAGTTGGT
 CGAGTCTGGCGGGGTGGTTCAACCAAGTGTCTCTTAACTTAGTTGCGCGCATCCGGTTTCACTTCAACAAATATGCA
 ATGAATTGGTTAGGCAAGCCCCGGGAAGGGCCTCGAATGGTAGCTAGGATTAAGATCAAAATACAACTATGCTACTTAT
 TACCGGACAGTGTAAGGACAGGTTTACCATCTCCCGGATGACTCTAAAAACACTGCTATCTGCAAAATGAATAACCTTAAG
 ACCGAAGATACGGCGTCTACTATTGTGTCGGCATGGTAATTTTGGCAACTCATACATAAGCTATTGGCATATTGGGCCAAG
 GTACTCTGGTTACCGTAAGCAGCGGAGGCGGCGACTACAAGACGATGACGATAAAGAGGTGGAAGTCAGACGGTGGTG
 ACACAGGAGCCTTCCGTACCGGTATCCCGGAGGTACTGTACTTACTTGTGATCAAGCACAGGGCAGTAACCTCTGGCA
 ACTACCAAACTGGGTACAACAGAGCCAGGTACCGCAGGCTTAGAGATTACAAAGACGACGACGACAAAGGC
 ACTCCAGCAAGATTTTCAGGAGCCTGCTCGCGGTAAAGCAGCGCTGACCCGTAGCGGAGTCCAAACCGAAGATGAAGCGGAA
 TATTACTGTCTTGTGTTATCTAATCGGTGGTATTCGGTGGTGAACCAAGCTTACCGTGTGGTGGCGGTGGTAGCGGTG
 GCGGAGTGAGGTTGAGTGTGATCAGGGGAGGTCTGTACAGCAGCGGAAAGTTGAACCTGAGTTGTGTCAGCTTCTG
 GATTACGTTCAACAAATACGCCATGAATTGGTGAGACAGGCACCGGCAAGGGCTTGAATGGTTCGCAAGGATCCGGTCCA
 AGTACGACTACAAGGACGATGACGATAAGGCTGACTCTGTAAAGACCGATTACAAATATCCAGAGACGATTCAAAACACATG
 CGTATCTCCAGATGAACAATTGAAAACAGAGGATACTCGGGTTTACTATTGTGTGAGACACGGCAACTTCGGCAACAGCTACAT

FIG. 54F

CAGCTATTGGGCCTATTGGGGACAGGGCACTCTCGTAACGGTTTTCATCCGGGGGAGGAGACTACAAGGACGATGACGATAA
GGCGGAGGCTCTCAGACGGTCGTAACTCAGGAGCCATCTCTCACTGTTAGCCCGGGCGGAACGTGTTACTCTCACCTGTGGGAGC
AGTACTGGGGCGGTACTTCCGGCAACTACCTAACTGGGTTCACAGAACCCAGGTCAAGCACCAAGAGGTCTGATAGGCGGA
ACTAAATTCCCTCGCCCCCTGGTACCCCTGCACGATTACAGCGATCCCTTTTGGCGGCAAGCGGCTCTTACACTTTCTGGAGTCCA
ACCGGAAGATGAGGCGGAATACTATTGTGTACTTTGTATAGTAAATCGCTGGGTATTCGGCGGCGCACCAAACTCACTGTTCCTT
GGAGGAGGAGGAAGCGCGGAGGTTCCAGGTCAAGCTGGAGGAATCGGGTGGAGGCTCAGTGCAGACAGGAGGTAGCCTCCG
GCTCACTTGCCTTCCGGAAGGACTTCCCGGAGCTACGGGATGGGCTGGTTTCGGCAAGCCCCCGGAAGGAGAGAGAATT
CGTGTCGGGAATTAGCTGGAGGGGCGACTCAACTGGATACGCGGACTCCGTCAAGGGCAGATTCACTCTCGGGACAAACGC
CAAGAACACCGTGACTTGCAATGAATTCCCTGAAGCCGGAGGACACTGCCATCTACTGTGCTGCGGCAGCAGGATCTGC
CTGGTACGGCACCCCTTATGAATACGATTACTGGGGACAGGGAACCCAGGTACGGTCTCGAGTCAACCAACCAATCACCAC
SEQ ID NO: 53

FIG. 54G

Pro6 – aEGFR G8 sdAb – aCD3 Vh – ~~ggggg~~ – aCD3Vh₁ - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRTFSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGGQTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
 WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAWWGGQTL
 VTVSSGGGGYKDDDKGGGSQIVVTQEPSTVSPGGTVTLTCSGSTGAVTSGNYPNWWVQKPKQAPRGLIGDYKDDDKGTPARF
 SGLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH SEQ ID NO: 54

GAAGTTCAACTGGTTGAATCCGGTGGTGGCCCTTGTCACAGCGGGAGGGCTCCCTTCGACTGCTTGTGCCGCCAGCGGTGCACAT
 TCAGCAGTTATGCCATGGGATGGTTCCGGCAGGCCCTGGTAAGAGCGGGAGTTCGTCGTTGCCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATTCGTAAAGGCGAGTTCACTATCTACCGGATATGCAGAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGTTACAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTACAGGCACCCAGGTAAACCGTCAGCAGCGGGAGGGGATCAGGAGCGGTTCAGAGGTTCAGCTCGTTG
 AGAGTGGTGAGGGCTGGTTCAGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTTTCACTTTAAACAAATACGCTAT
 GAACTGGGTACGACAAAGCCCCCGTAAAGGGCTTGCAAGTAAACAGTAAATACAATAATATGCGACTTATTA
 TGCCGATAGTGTAAGGACCGCTTACTATCAGTAGAGATGACAGTAAGAACAACAGGCTTATTGCAATGAACAACCTGAAGAC
 AGAAGATACGGCGTCTATTATTGTGACGACACGGTAATTTGGGAATTCATATATAGCTATTGGGCATCTGGGGTCAAGGA
 ACCCTTGTTACGGTGAGCAGCGGGCGGTGGTACTATAAGGACGACGATGACAAAGCGGGGCTCCAGACTGTGGTAACA
 CAGGAACCATCTTTGACAGTAAGTCTGGAGGTACGGTCAACGCTCACTGTGGTCTCAACCGGGGTGTAAACGTCAGGCAATT
 ACCCTAACTGGGTCCACAGAAAGCCTGGACAAGCTCCAGGGTCTGATAGGCGATTACAAAGATGATGATGAAGGGCACTC
 CAGCGCGCTTAGCGGTCTCTCTGGGTGGAAAGCAGCCCTCACTGAGTGGAGTACAACCCGAGGATGAGCGGGAATATT
 ATTGCGTCTCTGGTATTCAAACCGCTGGGTCTTCGGTGCGGTACGAAACTTACTGTACTGCATCATCATCACCCAC
 SEQ ID NO: 55

FIG. 54H

Pro7 – aCD3Vh_i – ~~ggggg~~_{112gggs} – aCD3V1 – aEGFR D12 sdAb – His6
 EVQLVESGGGLVQPGLSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYNKDDDKADSVKDRFTISRDDSKNTAYLQ
 MNNLKTEDTAVYYCVRHGNFNSYISYWAYWGQGLTVTVSSGGGGDYKDDDKGGGSQTVVTQEPSTVSPGGTVTLTCGSSTGA
 VTSGNYPNWVQKPGQAPRLIGGTFKFLAAGTPARFSGSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGS
 GGSQVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMWFRQAPGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNNAKNTVDLQM
 NSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSHHHHH SEQ ID NO: 56

GAGGTTCAAGCTTGTGAAATCAGGGGGAGGTCTGGTACAGCCAGGCGGAAGTTTGAAACTGAGTTGTGCAGCTTCTGGATTACGT
 TCAACAATAACGCCATGAATTGGGTGAGACAGCACCGGCAAGGGCTTGAATGGGTCCGAAGGATCCGGTCCAAAGTACGACT
 ACAAGGACGATGACGATAAGGCTGACTCTGTAAAGACCGATTACAATATCCAGAGACGATTCAAAAACACTGCGTATCTCC
 AGATGAACAATTGAAAAACAGAGGATACTGCGGTTTACTATTGTGAGACACGGCAACTTCGGCAACAGCTACATCAGCTATT
 GGGCTATTGGGACAGGCACTCTCGTAACGGTTTCATCCGGGAGGAGGAGACTACAAGGACGATGACGATAAGGGCGGA
 GGCCTCAGACGGTCGTAACTCAGGAGCCATCTCACTGTTAGCCCGGGCGAACTGTTACTCTCACCCTGTGGGAGCAGTACTG
 GGGCGGTTACTTCCGGCAACTACCCTAACCTGGGTTCAACAGAACCCAGGTCAGGCACCAAGAGGTCTGTATAGGCGGAACATAAT
 TCCTCGCCCTGTACCCCTGCACGATTACGCGGATCCCTTTTGGCGGC AAAGCGGCTCTTACACTTTCTGGAGTCCAACCGGA
 AGATGAGGCGGAATACTATTGTGTAATTTGGTATAGTAAATCGCTGGGTATTCGGCGGCGGCACCAACTCACTGTCTTGGAGGA
 GGAGGAAGCGGCGGAGGTTCCCAGGTC AAGCTGGAGGAATC GGGTGGAGGCTCAGTGCAGACAGGAGGTAGCCTCCGGCTCAC
 TTGCGCCGCTTCCGGAAGGACTTCCCGGAGCTACGGGATGGGCTGGTTTCGGCAAGCCCCCGGAAAGGAGAGAGAAATTCGTGTC
 CGGAATTAGCTGGAGGGCGACTCAACTGGATACGCGGACTCCGTCAAGGGCAGATTCACTATCTCTCGGGACAACGCCAAGAA
 CACCGTGGACTTGCAAAATGAATTCCCTGAAGCCGGAGGACACTGCCATCTACTGTGCTGCGGCAAGCAGGATCTGCCTGGTAC
 GGCACCCCTTTATGAATACGATTACTGGGACAGGGAACCCAGGTCACGGTCTCGAGTCAACCAACCATCACAC
 SEQ ID NO: 57

FIG. 54I

Pro8 - aEGFR G8 sdAb - aCD3 Vh - gggg₁₂₃₄₅₆₇₈₉gggs - aCD3Vl - His6

SLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTLHHHHH SEQ ID NO: 58

GAAGTCCAACCTGGTGGAATCGGGCGGTGACTCTGTGACAGGCCGGAGGTTCCCTGCGCCTTCTCTGTGCGGCTTCGGGAAGAACAACCTTCTCTCTCGTATGCCATGGGATGTTCCGCCAAGCCCTTGAAAGAGCGGAATTCGTCTGTGCGGATCAATTGGAGTTCGGGTTCGACTTACTACGCCGACTCCGTGAAGGCCGGTTCAACCATTAGCCGGGACAATGCTAAGAACACCATGTATCTGCAGATGAACACTCACTGAAACCTGAGGACACGGCGGTGTACTCTGCGCCCTGGTACCAGATCAATTCGGAAACTACAATTCAAAGGACTACGAGTACGACTACTGGGTACGGCACCCAGTCAACCGTGTCTCAGCGGAGAGGTGGAAGCGGAGCGGTTCCGAAGTGCAAGCTCGTCCGATCCGGGTGGACTGTCCAACCGGCCGACTCATGAGCTGCGTAGCCTCCGGATTCACCTTCAACAAGTACCGCATGAACCTGGGTGACAGAGCACCCGGAAAGGACTGGAATGGTGGCCCGGATCAGTCCAGTACAACAACACTACGCCACCTCACTACCGCGGACACGGTGAAGGATAGGTTCACCATCTCCGGGACGACAGCAAGACATGCTACCTCCAAATGAAACAACCTCAAGACCGAAGATACTGCGGTATTA

ACTGCTGCGCCACGGGA

ACTTCGGAACACAGTACATAGTACTGGGCTACTGGGGCCAGGGCACTCTGTTGACCTGAGTTCAAGGAGAGCGCGACTACAAGGACGATGACGATAAGGGAGGAGGTTCGCAGACCGGTGAGACCCAGGAACCTCACTGACCTCCAGGAGAACCTGACCTTACCTGTGCTCTCGACCGGTGCCGTGACGTCCGGAACTACCCCAACTGGGTCCAGCAAAAGCCGGGACAAGCCCTCGGGGACTGATCGGGGAACATAATTCCTCGCCCTGGCACTCTGCCCCCTCAGCGCAGCTCTCGGAGGA

AAAGCGGCCCTGACACTCTCGGGGTGCAGCCTGAAGATGAGGCCGAAT

ACTACTGCGTGTGTACTCCAATCGCTGGGTGTTTGAGGGGGCACCAAGCTTACCGTGTGCACCAACCATCAC

SEQ ID NO: 59

FIG. 54J

Pro8 MS - aEGFR G8 sdAb - aCD3 Vh - GGLSGRSDNHGGG - aCD3V1 - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRTFSYAMGWFRQAPGKEREFVVAINSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGGQTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN
 WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGGQTL
 VTVSSGGGLSGRSDNHGGGQIVVTQEPSLIVSPGGIVTLTCGSSTGAVTSGNYPNWWVQQKPGQAPRGLIGITKFLAPGTPARFSGSLL
 GSKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH SEQ ID NO: 60

GAGGTTCAACTGGTGGAATCAGGAGGCGGTTTGGTTCAGGCAGGAGGTCATTGCGATTGTCAATGTGCGGCGTCCGGCGGACT
 TTCAGTTCCTTACCGCATGGGTGGTTTAGGCAAGCGCCGGCAAGAGAGGAGTTTGTAGTGGCAATTAAGTGGAGTTCCTGGAT
 CAACTTATTACGCTGATCCGTCAGGACGCTTACGATTAGCCGGGATATGCAAAACACTATGTACCTTCAATGAATCACTC
 TCTGAAACCGGAGACACCGCGCTCTACTATTGCGCGCTGTTATCAGATCAACTCTGGGAATTATAATTTCAAAGACTATGAA
 TATGATTATTGGGTCAGGCACGCAGTTACAGTTAGCAGCGGAGCGGGGTCAGGTGGGAGTGAAGTCAATTGGTC
 GAATCTGGAGGCGCTGTCCAAACCGGGGCTCATTGAAGTTGTCTGTGCCGAAGTGGATTACGTTCAATAAAGTACGCTA
 TGAAC TGGGTGAGACAAGCCCTGGAAGGGACTGGAATGGTGGCGCGCATAAAGTCAAAATACAATACTACGCAACCTACT
 ATGCCGATAGTGTAAAGACAGATTACCAATTTCTCGAGACGATTCTAAAATACCGCGTATCTTCAATGATATAATTTGAAGAC
 CGAGGATACAGCAGTGTATTACTGTGTAGACATGGCAACTTGGGAACCTTACATATCTTATTGGCGGTATTGGGGACAAGGG
 ACCCTGGTGACAGTAAGTAGCGGAGGCGGACTGTCCGGGCAAGCGACAACCATGGGGCAGTCAGACAGTGGTAACGCAAGA
 ACCGAGTCTCACTGTATCACAGGAGGTACAGTGACCCCTCACATGCGGATCTCCACGGGGCAGTCACATCTGGTAATTATCCA
 AATTGGGTTACAGCAGAAGCCAGGACAAGCTCCACGAGGATTGATTGGCGGGACAATAATTTCTGGCCCCAGGAACCGCGCCAGG
 TTTAGTGGTAGCCTGCTTGGAGGTAAAGCGGCGCTGACGCTTTCGGCGGTACAACTGAAGACGAGGCAGAGTACTACTGTGTAC
 TCTGGTACTCTAACAGGTGGGTGTTTCGGAGGTGGAACCAAACTCACGGTTTTGCATCACCATCATCAT SEQ ID NO: 61

FIG. 54K

[illegible]

CGAGGTTCAACTGGTGAATCAGGAGCGGTTTGGTTCAGCAGGAGGGTCAATTGCGATTGTCAATGTGCGGCTCCGGCGGAGCTTTCAGTTCTTACGCCATGGGTGGTTTAGCAAGCCCGGCAAGAGAGGGAGTTGTAGTGGCAATTAACTGGAGTTCTGGATCCAACCTTATACGCTGATTCCGTAAGGACCGTTTACGATTAGCCGGGATATGCAAAAACACTATGTACCTTCAAATGAACATCTGTGAAAACCGGAGGACACCGCCGCTACTATTGCCGGCTGGTTATCAGATCAACTCTGGGAATTATAATTTCAAAGACTATGAAATATGATTATTGGGTCAAGGCACGCAAGTTACAGTTAGCAGCGGAGCGGGGTCAAGTGGTGGAGTGAAGTGCAATTGGTCGAATCTGGAGCGGCTGTCCAACCCGGGGCTCATTGAAGTTGCTGTGCCGCAAGTGGATTACGTTCAATAAGTACGCTATGAATCTGGTGAGACAAGCCCTGGAAAGGACTGGAATGGTGGCGGCATAAGGTCAAAATACATAAATACGCAACCTACTACCGCATAGTGTAAAAGACAGATTCACCAATTTCTGAGAGATTCTAAAATAACCCGCTATCTTCAATGAATAATTTGAAGACCGAGGATACAGCATGTATTACTGTGTAGACATCGCAACTTTGGAACTCTTACATATCTTATTGGCGGTATTGGGGACAAGGGACCTGTGACAGTAAGTAGCGGAGCGGGAGCGGGACTCTGGACTTAGTGGCCGGTACATATCATGGAAGACCGCGGATCACGGGGCAGTCAGACAGTGGTAACGCAAGAACCGAGTCTCACTGTATCACCGAGGTCACAGTACCCCTACATGCGGATCTCACCGGGGCAGTCACATCTGTAATTATCCAAATTGGGTTACAGCAAGCCAGGACAAGCTCCACAGGATTGATTGGCGGGACAATAAATTCTGGCCCCAGGAACGCCAGGTTTAGTGTAGCCTGCTTGGAGGTAAAGCGGCGCTGACGCTTTTCCGGCGTACACACTGAAGACGAGGCAGAGTACTGTGTACTCTGTAACAGGTGGTGTCTCGAGGTGGAACCAAACTACCGTTTTGATCACCATCATCATCAT SEQ ID NO: 63

FIG. 54L

Pro9 – aEGFR D12 sdAb – aCD3V1 – ~~ggggg~~¹¹²²²²ggs – aCD3Vh_i – His6
 QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRRQAPGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQ
 KPGQAPRGLGGTKFLAPGTPARFSGSLLGKKAALTLSSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDYKDDDDKGGGSE
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQM
 NNLKTEDTAVYYCVVRHGNFGNSYISYWAYWGQGLVTVSSHHHHHH SEQ ID NO: 64

CAAGTCAAACTTGAAAGAAAGTGGTGGTGATCCGTGCAACAGCGGGATCCCTGCGCCTGACGTGTGCGGGCTCAGGAAGGACT
 TCTAGGTCATACGGTATGGGTGGTTCAGGCAAGCCCTGGGAAGAGAGAGGAGTTCGTTTCAGGCATCAGCTGGAGGGGAGAC
 TCTACTGGCTACGCAGACAGCGTCAAGGCAGATTACATCAGCAGAGACAATGCAGACAACACTGTTGACCTGCAATGAAC
 AGCTTGAAACCAAGAGATACAGCTATCTACTATTGCGTCCGCGAGCCGGATCAGCTGTGACGGCACGCTGTATGAGTATGATT
 ATTGGGAC AAGGCACGAGTAACAGTCACTCTGGCGTGGGGAGCGGGGTGGAAGTCAAAACCCTGTTACTCAGGAA
 CCATCACTGACTGTCTCCTGGGGCACTGTAACTCTTACGTGTGGTTCATCTACAGGCGCTGTCAACCAGTGGCAACTATCCTAA
 CTGGTCCAGCAGAACCTGGTCAAGCTCCTCGGGGGCTTATTGGAGGTACAAAGTTCCTCGGGCACACCCGCAAGGTTT
 AGCGGGTCAATTGCTTGGAGGCAAGCTGCCCTCACTTTCCGGCGTGCAACAGAGATGAAGCCGAATATTATTCGTGTGTGT
 GGTACTCCAATCGATGGGTCTTTGGTGGGACTAAGCTACAGTCTTGGGGGCGGGGACTATAAGATGATGATGATA
 AGGGGGTGGGTCCGAGTGCAGCTTGTGAATCTGGCGGGGCCCTTGTGCAACCTGGGGGTCCCTGAAGCTCAGCTGTGCCG
 CTTTCAGGTTTCACATTCAATAAGTACGCCATGAACCTGGGTGGGCAAGCCCCAGGTAAAGGGTCTTGAATGGGTGCTAGAATACG
 CAGTAAGTACGACTACAAAGACGATGACGACAAAGCGGACTCAGTAAAAGACCCGCTTACGATAAGTTCGCGACGATTCCCAAGA
 ACACGGCGTATCTCCAAATGAACAATCTTAAACGGAGGACACAGCAGTCTACTGTGTCCGCCACGGCAATTTCGGTAATA
 GTTACATCAGTTATTGGGCCTACTGGGGCCAGGGTACTCTCGTACTGTCTCATCATCACCACCACCATCAC SEQ ID NO: 65

FIG. 54M

Pro10 – aCD3Vh – gggg¹¹²² – aCD3Vh – aEGFR G8 sdAb – His6
 QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNVWVQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLGKAAALTLSGVQPEDEA
 EYYCVLWYSNRWVFGGKLTVLGGGGDYKDDDDKGGSEVQLVESGGGLVQPGGSLKLSAASGFTENKYAMNWVRQAPGKGL
 EWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYCVRHGNFNSYISYAWYWGQGLVTVSSGGGS
 GGGSEVQLVESGGGLVQAGGSLRLSCAASGRITFSYAMGWFRQAPGKEREFVVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQ
 MNSLKPEDTAVYYCAAGYQINSNGYNFVKDYEDYWGQGTQVTVSSHHHHHH SEQ ID NO: 66

CAGACGGTGTCACTCAAGAACCTTCCTTGACTGTATCTCCGGCGGGACAGTCACCTTACGTGTGGATCAAGCACTGGCGCGG
 TTAAGTGGCAACTACCTAAATTGGGTACAGCAGAAACCGGGCCAAAGCCCGAGAGTCTGATTGGGGATTATAAGGATGACG
 ACGACAAGGTACGCCAGCACGCTTTCTGGGTCTTGCTCGGTGGAAGGCAGCCCTGACTCTCAGTGGCTTCAGCCGAGG
 ACGAGGCTGAATATTATTGCTGTGTACTCCAACAGGTGGTCTTCGGGGCGGTACAAGTTGACCTCCTCGGGGCGG
 AGCGACTATAAAGACGATGATGACAAAGGTGGTGTTCAGAAAGTCAAGTGTGAGAGCGGGGTGGTCTGGTCAACCGG
 GAGGCTCTCAAGCTCAGTTGCGCAGCATCTGGGTTTACTTCAACAAATACCGGATGAACCTGGGTAGGCAGGCTCCGGGTAA
 GGGCTCGAATGGTTGCCAGAAATCCGGTCTAAGTATAAACAATATGCTACTTATACGCTGACAGTGAAGGATCGCTTTACT
 ATCTCCCGAGATGATTCAGAAACACGGCGTATTGAGATGAACAATTGAAGACGGAGGATACCGCTGTTTACTATTGTGTTT
 GGCATGGGAATTCGGAAACTCTATATAAGTTACTGGGCATCTGGGGTCAAGGCACACTCGTACTGTAAGTTCTGGGGCGG
 GTGGAAGCGGAGGGGATCAGAGGTGCAACTCGTTGAGAGCGGGGGCTTGGTACAGGCAGGGGGGTCACTCAGGCTCTCTT
 GTCGGCTCAGGGAGAACTTTCAGTTTATATCGGATGGTTGGTTAGGCAGGCTCCTGGTAAAGAAAGAAATTTGTCTGTGGC
 AATCAATTGGAGTCCCGTTCCACGTATTATGCGGATAGCGTTAAGGCGAGATTACGATAAGTAGGATAACGCGAAACAC
 CATGTACCTGCAAAATGAATCTCTTAAACCGGAGGACACAGCGGTTTATTACTGTGCGCGGATACCAATCAACAGCGGTAAT
 TATAACTTCAAGACTACGAATATGATTACTGGGGCAGGGGACTCAGGTAACCTGTTAGTTACACCATCACCATCATCAT
 SEQ ID NO: 67

FIG. 54N

Pro11 – aEGFR D12 sdAb – aCD3V1 – gggg¹¹²gggs – aCD3Vh – His6
 QVKLEESGGGSVQTGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDS¹¹²TGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCGSSTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGTFKFLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDYKDDDDKGGGSE
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN
 NLKTEDTAVYYCVRHGNFGNSYISYWAWYWGQGTLVTVSSHHHHH SEQ ID NO: 68

CAGGTCAAACTCGAAGAGTCTGGAGGAAAGTGTGCAGACGGCGGTAGCCTGCGCCTTACTTGCGCGGCTTCAGGCCGAACA
 TCCAGATCATACGGAATGGGATGGTTTAGACAAGCCCTGGTAAAGACGGGAGTTCGTTTCAGGAATATCATGCGCGGAGAT
 TCAACAGGGTATGCCACAGCGTCAAGGACGTTCACTATTAGCAGAGACAATGCAAAAATAC¹¹²TGTAGACCTTCAGATGAAT
 TCCCTGAAGCCGAGGATACGGCTATTTACTATTGCGCGGTGCTGCGGGTCAGCCTGGTACGGGACATTGTATGAATATGATT
 ATTGGGGCAAGGAACCCAAAGTTACAGTTAGCAGTGGGGTGGGGCAGTGGAGTGGTTCCCAAACGGTGGTGA¹¹²CTCAAGAA
 CCATCCCTGACTGTTAGTCCGGAGGACCCTAACCTCTCACTTGTGTTATCCACAGGAGCCGTGACGTCCGGTAACCTATCCGA
 ACTGGGTACAACAAAGCCGGGCCAAGCACCCGAGGTCTGATTGGTGGGACAAAGTTTCTGGCCCCCTGGGACACCCGCTCGGT
 TCTCAGGGTCCCTCCTGGCGGAAAGGCCGCTTACGTTGTCGGGTGCAAGCCTGAAGATGAGCAGAAATACTATTGTGTGCT
 TTGGTACTCTAATAGGTGGGTTTGTGGGGGTACCAAGTTGACTGCTGGGTGGAGGGGAGACTATAAAGACGATGACGA
 CAAAGGTGGAGGAAGTGGGTGCAACTCGTAGAAAGTGGGGCGGACTTGTTCACCCAGGGGGCAGCCTGAAGCTGTCTGTGC
 AGCAAGTGGGTTCACTTTAATAATACGCAATGAATTGGGTGAGACAGGCCCCAGGCAAGGGCCTT¹¹²GAGTGGTCCGCCGAAT
 ACGAAGCAAGTACAATAACTATGCTACATACTATGCGGACTCTGTAAAGGACCGATTCAACATCAGTCGAGATGACTCTAAAAAT
 ACGGCGTACCTCCAAATGAATAACCTCAAAACGGAAGACACGGCGGTGATTACTGTGTAGGCATGGCAACTTTGGTAATAGC
 TACATTAGCTACTGGGCTTACTGGGGCCAAAGGCACCTTGGTTACTGTAGTTCCCATCACCATCATCATCAC SEQ ID NO: 69

FIG. 54O

Pro12 – aCD3Vh_i – gggg₁₁₂₂gggs – aCD3V1 – aEGFR G8 sdAb – His6

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDKADSVKDRFTISRDDSKNTAYLQ
 MNLKTEDTAVYYCVRHGNFNSYISYWYWGQGLVTVSSGGGDKDDDKGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGA
 VTSNYPNWVQKPGQAPRGLIGTKFLAFTGPARFSGSLGGKAALTLSGVQPEDEAEYCYCVLWYSNRWVFGGGLTVLGGGGS
 GGGSEVQLVESGGGLVQAGGSLRLSCAASGRITFSYAMGWFRQAPGKREFVVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQ
 MNSLKPEDTAVYYCAAGYQINSNGYNFKDYEYDYWGQGTQVTVSSHHHHHH SEQ ID NO: 70

GAAGTGCAGCTGGTAGAGAGCGGTGGTGGTGGTGCAGCCTGGTGGTAGCTTGAAATTGTCAATGTGCGGCATCTGGGTTTACTT
 TTAATAAGTACGCCATGAACCTGGGTGCGCCAAGCGCTGGTAAAGGCTTTGAGTGGTGCAGAAATACGGTCTAAATATGATT
 ACAAGATGACGACGAC AAGCCGACAGCGTGAAAGACCGCTTACAATAGTAGGATGACAGTAAACACCGCTTATTTC
 AAATGAATAACCTTAAGACGGAGGACACTGCTGTATATTATTGTGAAGGCATGGCACTTCGGGAATTCATACATTTCATATTG
 GGCATACTGGGTCAAGGACGCTCGTAACGGTCAAGTCCGGCGGGGAGACTATAAGGATGATGACGACAAGGGCGGAG
 GTTCCAGACAGTCGTACGCAAGAACCCAGCCTTACAGTTTCTCTGGCGGTACAGTAACATTGACCTGTGGCAGCAGCACTGG
 TCGGTGACATCTGGTAATTACCCAACTGGGTTCAGCAAAAGCCTGGCCAAAGCCAGGACTGATTGGTGGAACCAAGTT
 CCTGGCCCTGGCACACCGCGAGATTTCCGGGTCAATTGTTGGGGGTAAAGCTGCGTGAATTTGTCTGGTGTCAACCTGAA
 GATGAAGCCGAATAATTATTGTGCTTTGGTACAGTAATAGATGGGTGTTGGTGGGGGACTAAGCTAACGGTCTTGGCGGAG
 GGGATCTGGTGGAGGATCTGAGTGCAACTTGTGAGAGCGCGGAGGACTTGTTCAGGCCGGAGGCTCACTTCGCCCTTAGCT
 GTGCTGCTAGTGAAGAACGTTCACTTACGCTATGGGATGGTTAGACAAAGCTCCAGGAAAAGAAAGGAGTTCGTCGTGG
 CTATAAATTGGTCTTCCGGGAGTACATATTACGCCGACAGCGTCAAAAGGAGATTACGATCTCTCGGACACCGCTAAAACA
 CGATGTACCTGCAATGAATAGCTTGAAACCCGAGGATACCGCTGTGTACTACTGCGCCCGGGTATCAGATCAACAGTGGTA
 ACTATAACTTCAAGGACTACGAGTACGACTACTGGGGCCAGGGAACCTCAGGTCACTGAGTTCTCATCACCAATCACCAC
 SEQ ID NO: 71

FIG. 54P

Pro14 – aEGFR D12 sdAb – aCD3Vh – ~~ggggg~~gggs – aCD3Vh1 – His6
QVKLEESGGGVQTGSLRLTCAASGRTSRSYGMGWFRAQPKEREFVSGISWRGDS~~TGY~~ADSVKGRFTISRDNAKNTVDLQMNSLK
PEDTAIYYCAAAGSAWYGTLYEYDWGQGTQTVSSGGSGSGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ
APGKGLEWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHNFGNSYISYWAYWGQGTLVTVS
SSGGGGD~~YKDDDDK~~GGGSQIVVTQEPSLTVSPGGITVLTTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG~~YDKDDDK~~GTGPARFSGSL
LGKKAALTLGSVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH SEQ ID NO: 72

CAAGTCAAGTTGGAAGAGTCCGGTGGTTCAGTACAGACCGGGGTCTCTCCGACTTACGTGTGCCGCAAGCGGACGAACA
TCCAGGTCCTATGGCATGGTGTGTTCCGACGGCTCCAGGAAGAAACGCGAGTTCGTACGTGGGATTAGTTGGCGAGGTGACT
CCACTGGGTACGCAGATTACGTTAAAGGCGCTTCAACCATCTCACGAGACAATGCTAAGAATACAGTTGATCTCCAAATGAATAG
TCTCTAAACCGAAGATACAGCTATCTATTATTGTGCGGTGCCGAGGGTCAGCTGGTATGGAACCTTTGTATGAATACGACTAT
TGGGGCAGGGACGCAAGTCACAGTTTCTCCGTGGAGGTGATCAGGGGAGGCTCCGAGGTGCAACTCGTAGAGTCGCGGT
GGCGGACTCGTCCAGCTGGCGGATCACTGAAGTTGTATCGCGGCTAGTGTTCACCTTCAATAATAACGCCATGAATTGGG
TACGCCAAGCGCTGGGAAGGCACTTGAATGGTGGCGAGAATCCGCTCCAAATAATAAATACTACGTACGTATTATGCAGACT
CTGTCAAGGATCGGTTCACAAATATCCAGGACGACAGTAAAAACACCGCTTACCTTCAGATGAACAATTGAAGACGGAAGATA
CCCGCGGTGATTAATTGTACGCCATGTGTAATTTGGTAACCTCTATAATTTCTACTGGCCTACTGGGGACAAGGAACCTCTGGTC
ACTGTGTCATCTGTGGGGAGGCGACTACAAAGATGATGACAAAGGAGGAGCAAGCCAAACAGTAGTAACCCAGGAACC
TAGTCTTACTGTCAGTCTGGTGTACGTTAACCTTGACGTGTGTTCCAGCACGGGAGCAGTCACTTCAGGCACTATCTCAAC
TTGGGTACAACAGAAACCCGGACAAGCACCAAGGATTGATTGGTGACTACAAAGACGACGACGATAAAGGCACCCCCGCTAG
GTTCTCTGTAGTCTTTGGGAGGCAAGCAGCGTTGACACTCTCAGGGGTGCAACCCGAGGATGAGGCAGAAATAATTACTGTGTA
CTGTGGTACTCAATAGATGGGTGTTTGGCGGGGCACAAAACCTTACTGTATTGCATCACCACCAAC SEQ ID NO: 73

FIG. 54Q

Pro15 – aEGFR G8 sdAb – hOKT3 Vh – ~~ggggg~~¹²³⁴⁵⁶⁷⁸⁹gggs – hOKT3V1 - His6
 EVQLVESGGGLVQAGSLRLSCAASGRFTFSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGGQTQVTVSSGGSGGGSQVQLVQSGGGVVPQGRSLRLSCKASGYTFTRYTMH
 WVRQAPGKGLEWIGYNPSRGYTNYNQKVKDRFTISRDNKNTAFLQMDSLRPEDTGVYFCARYYYDDHYCLDYWGQGTPVTVSSGG
 GGDYKDDDKGGGSDIQMTQSPSSLSASVGDRTVITCSASSSVSYMNWYQQTPGKAPKRWIYDTSKLASGVPSRFSGSGSGTDYTFI
 SSLQPEDIAITYYCQQWSSNPFTFGQGTKLQITRHHHHH SEQ ID NO: 74

GAGGTTCAAGTGGGGGCTTGGTTCAAGCAGGTGGAAGTCTGCGGCTTCTCTGTGCGGCTAGTGTCGGACCT
 TCAGTTCATATGCTATGGGATGTTCCGGCAAGCCCCGGCAAGGAGCGGAGTTTGTCTGTAGCGATTAAATTGGTCATCAGGGTC
 TACGTATTACGCGGATCCGTTAAGGCGAGGTTCAAAATATCCCGGACACGCCAAGAAATACCATGTATCTTCAAATGAATCC
 CTTAAACCAGAGGATACTGCTGTTTATTACTGCGCGGTGGGTATCAAAATAAACAGCGGAACACAACTTCAAAGACTATGAGT
 ACGACTACTGGGTCAGGAAACCAAGTCACTGTGAGTTCAGGTGGAGCGGAAGCGGAGGCGGTTCCCAAGTGCAACTGGTTC
 AGTCCGGAGGCGGTGTTACGCCGGCGAAGCCTCAGGCTGCTTGTAAAGCATCCGGATATACATTACCAAGGTACACCA
 TGCAC TGGGTGAGAC AAGCACC TGTAAAGGCGCTT GAGTGGATCGGATACATAAACCC AAGTCGAGGATACACCAATTACAATC
 AAAAGGTCAAAGACAGGTTACGATCTCACGAGATAATTCAA AAAACACTGCTTCTGCAAATGGATAGCCTGCGGCTGAGG
 ATACGGGTGTACTTCTGTGCACGCTACTATGATGACCACTACTGTCTTGATTACTGGGGACAAGGACCCCGGTGACGGTATC
 CTCCGGGGAGGCGGCACTACAAGATGACGACGATAAAGGGGAGGCTCCGACATCAATGACCCCAATCTCCAGTAGTCT
 GAGTGCTCCGTCGGTGACCGGTTACAATAACGTGCTCAGCGTCTCTGCTCTTACATGAATTGTTACCAAGCAACCCCG
 GCAAAGCCCCTAAGAGATGGATCTATGATACCTCCAATTGGCGTCTGGCGTCCCCGATTGAGTGGGTCTGGATCAGGTAC
 GGACTACACCTTCACAATTTCTCATTTGCAGCCAGAAAGATATAGCAACCTACTACTGTCAACAATGGTCTCCTCAAATCCCTTTACCT
 TCGGGCAAGGAACCAAGCTCCAATACGCGGCACCAACCATCACAC SEQ ID NO: 75

FIG. 54R

Pro16 – aEGFR G8 sdAb – aCD3 Vh (2B2) – ~~ggggg~~ – aCD3Vh – aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWERQAPGKEREFVAINWSSGTYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGQGTQVTVSSGGGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKLTEDTAVYYCVRHANFGNSYISYWAYWGQGT
 TVSSGGGG~~YKDDDDK~~GGGSQTVVTVQEPSLTVSPGGITVLTCSSTGAVTSGNYPNWVQKPGQAPRGLIG~~YKDDDDK~~GT
 PAFS
 GSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGGGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFG
 MSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
 LVTVSSHHHHHH
 SEQ ID NO: 76

GAAGTTCAACTGGTTGAATCCGGTGGTGGCCTTGTCACGGGGGAGGCTCCCTTCGACTGTCTGTGTGCCCGCAGCGGTGCACAT
 TCAGCAGTTATGCCATGGATGGTTCGGCAGGCCCTGGTAAAGAGCGGGAGTTCGTCTGTCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGATTCTGTAAGGCGAGTTCACATATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTATTACTGTGCTGCCGGTTACAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTACGGCACCCAGGTAAACCGTCAAGCAGCGGGAGCGGATCAGGAGCGGTTCAGAGGTTCAGCTCGTTG
 AGAGTGGTGGAGGCTGGTTCAGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTGTTTCACTTTAAACAATACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTTCAGAAAGTAAACAGTAATAACAATAATTATGCGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTACTATCAGTAGAGATGACAGTAAGAACACGGCTTATTGCAAAATGAACAACACTTGAAGAC
 AGAAGATACGGCGGTCTATTATTGTGTCGACACGCAATTTGGGAATTCATATATAAGCTATTGGGCATACTGGGTCAAGGA
 ACCCTTGTACGGTGAGCAGCGGGCGGTGTGACTATAAGGACGACGATGACAAAGCGCGGCTCCAGACTGTGTTAACA
 CAGGAACCATCTTTGACAGTAAGTCCTGAGGTACGGTCAACGCTCACTTGTGGTCTCAACCGGGCTGTAAACGTCAGGCAATT
 ACCCTAACTGGGTCCACAGAAAGCTGGACAAGCTCCAGGGTCTGATAGGCGATTACAAGATGATGATAAGGGCACTC
 CAGCGCTTTAGCGGATCCCTTCTGGTGGAAGAACAGCCCTCACTGTAGTGGAGTACAACCCAGGATGAGCGGAATATT
 ATTGCGTCTCTGGTATTCAACCGCTGGGTCTTCGGTGGCGGTACGAAACTTACTGTACTGGGGGAGGCGGTCAAGCGCGG
 ATCAGAAGTGCACTTGTGTAATCTGGCGGAGGTCTGGTCCAGCCAGGTACAGCTTGAGACTGTCTGTGCTAGCGGCTTT
 ACCTTCTCTAAATTCGGTATGAGTTGGTTCGGCAAGCCCTGGAAAGGGTTGGATGGGTATCAAGCATTAGTGGTCTGGGC
 GAGATACACTCTATGCCGAATCAGTGAAGGGCGCTTACCATTAGTAGGATAACGCTAAACTACTCTGTATCTGCAAAATGAA
 TAGTCTGAGACCAAGATACCTGCGTTTACTACTGACACAATAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTGTGACT
 GTTAGCAGTCATCATCATCATCACACCAC SEQ ID NO: 77

FIG. 54S

Pro17 – aHSA (10GE) – aCD3Vhi – ggggg – aCD3V1 (2B2) – aEGFR D12 sdAb – His6
 EVQLVESGGGLVQPNSLRSLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRP
 EDTAVYYCTIGGSLVSSQGLVTIVSSGGSGGGSEVQLVESGGGLVQPGLSKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARI
 RSKYDYKDDDKADSVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSIYSYWAYWQGGLTVTVSSGGGGDYKDD
DDKGGGSQIVVTQEPSLTVSPGGTIVLTLCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLGKAAALTLSGVQ
 PEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGSQVKLEESGGSVQTGSLRLTCAASGRTSRSYGMGWFRQAPGKREFVS
 GISWRGDSSTGYADSVKGRFTISRDNAKNTVDLQMNLSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSSHHHHHH
 SEQ ID NO: 78

GAAGTGCAGCTTGTTGAATCTGGCGGAGGTCTGGTCCAGCCAGGTAAACAGCTTGAGACTGTCTGTGCTGCTAGCGGCTTTACCT
 TCTCTAAATTCGGTATGAGTTGGGTTCGGCAAGCCCTGGAAAGGTTTGGAATGGGTATCAAGCATTAGTGGTTCTGGCGGAGA
 TACACTCTATGCCGAATCAGTGAAGGGCGCTTACCATTAGTAGGATAACGCTAAACTACTCTGTATCTGCAATGAATAGT
 CTGAGACCAAGATACTGCCGTTACTACTGCACAAATAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTTGTGACTGTTA
 GCAGTGGGGAGCGGCTCAGCGCGGATCAGAGTTTCAGCTTGTGAATCAGGGGAGGTCTGTACAGCCAGCGGAAAGT
 TTGAAACTGAGTTGTGCAAGCTTCTGGAATTAAGTTCAACAAATACGCCATGAATTGGGTGAGACAGCACCGGGCAAGGGGCTT
 GAATGGGTGCAAGGATCCGGTCCAAAGTACGACTACAAGGACGATGACGATAGGCTGACTCTGTAAAGACCGATTACATA
 TCCAGAGACGATTCAAAAACACTGCGTATCTCCAGATGAACAATTTGAAACAGAGGATACATGCGGTTTACTATTGTGTGAGA
 CACGGCAACTTCGGCAACAGCTACATCAGCTATTGGGCTATTGGGACAGGGCACTCTGTACGGTTTCACTCCGGGGAGGA
 GGAGACTACAAGGACGATGACGATAAGGGCGGAGGCTCTCAGACGGTCTGTAACCTCAGGAGCCATCTCCTGTTAGCCCCGGC
 GGAACTGTTACTCTCACTGTGCTAGCAGTACTGGGGCGGTTACTTCCGGCAACTACCTAAGTGGGTTCAACAGAAAGCCAGGTC
 AGGCACCAAGAGTCTGATAGCGGAACTAAATTCCTCGTCCCTGGTACCCCTGCACGATTCAGCGGTTCCCTTTTGGCGGCA
 AGCGGCTCTTACACTTCTGGAGTCCAAACCGGAAGATGAGCGGAATACTATTGTACCTTTGGTATAGTAATCGCTGGGTATTC
 GGCGCGGCACCAAACTCACTGTCTTGGAGGAGGAGGAGCGGCGGAGGTTCCAGGTCAAGCTGGAGGAATCGGGTGGAGG
 CTCAGTGCAGACAGGAGGTAGCTCCGGCTCACTTGGCGGCTTCCGGAAGGACTTCCCGGAGCTACGGGATGGGTGGTTTCGG
 CAAGCCCCGGAAAGGAGAGAGAAATTCGTGTCCGGAATTAGCTGGAGGGGCGACTCAACTGGATACCGGACTCCGTCAGGG
 CAGATTCACTATCTCTGGGACACGCCAAGAACACCGTGGACTTGCAATGAATCCCTGAAGCCGGAGGACACTGCCATCTA
 CTACTGTGCTGCGGCAGCAGGATCTGCCTGGTACGGCACCCCTTATGAATACGATTACTGGGACAGGGAACCCAGGTACGGTC
 TCGAGTCACCAACCATCACAC SEQ ID NO: 79

FIG. 54T

Pro18 – aEGFR G8 sdAb – aCD3V1 – ~~ggggg~~²¹²²²²ggs – aCD3Vhi – His6
 EVQLVESGGGLVQAGSLRLSCAASGRFTSSYAMGWFRQAPGKERFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGQGTQVTVSSGGGGGGGSGTQVTVQEPSTLVSPGGTVTLTCGSTGAVTSGNYPN
 WVQQKPGQAPRLIGGKFLAPGTPARFSGSLLGKAAALTLSGVQPEDEAEYCYLVWYSNRWVFGGGTKLTVLGGGGDYKDDDDK
 GGGSEVQLVESGGGLVQPGSLKLSCAASGFITENKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTA
 YLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYWGQGLVTVSSHHHHH SEQ ID NO: 80

GAGGTCCAACTTGTTGAGAGCGGTGGGGACTTGTACAGGCCGGAGGGTCCTTGAGGCTGAGTTGTGCTGCGTCCGGACGCACC
 TTCAGTAGTTATGCGATGGGATGTTCCGGCAAGCCCGGGGAAAGAGAGAGAAATTTGTGTCGTATCAATTGTCAGTGGG
 AGCACTTATTACGCTGACTCTGTAAAGGAAGATTTACTATATCTCGAGATAATGCTAAGAACACCATTGTATCTTCAGATGAAC
 CTCTGAACCCAGAGGATACTGCTGTGTTACTGTGCTGCGGATATCAGATAAATTCAGGTAATTATACTTTAAAGACTATGA
 GTATGACTACTGGGACAGGGGACTCAAGTTACGGTGAATTCAGCGCGGGGTTCTGGGGTGGAGCCAGACCGTCGTGAC
 CCAGGAACCATCTTACAGTCTCCCGGAGGCACTGTAAACCTTACCTGCGGTCAATCACTGGCGTGTAAACGTCCGGCAAC
 TACCCCAACTGGGTGCAAGCAAAACCGGACAGCGCCACGAGGCTGATAGGTGGGACTAAGTTTCTTGCTCCAGGAACCTCT
 GCTCGATTTTCTGGCAGTCTGTTGGCGGCAAGCAGCCCTGACACTTTCTGGTGTGCAACCGGAGGACGAGGCTGAGTACTACT
 GCGTACTCTGTTATCAATCGATGGGTTTTTGGGGGTGGAACGAAATTGACCGTTCTCGGAGGTGGTGGTACTATAAGATGA
 TGACGACAAAGGTGGTGGATCCGAAGTCCAACTCGTCGAGTCCGGGGGAGGACTTGTCCAACTGGAGGATCATTGAAACTCAG
 TTGTGACGCTCCGGGTTACATTTAATAATACGCCATGAATTGGGTCCGGCAAGCCCCAGGCAAGGGGCTTGAAGTGGTGGC
 CGGATCCGATCAAGTACGACTATAAAGACGATGACGATAAAGGCTGATTCAGTCAAAAGACAGGTTTACCATAAGTCGCGATGAC
 AGCAAGAACACCGCTTACCTTCAATGAACATCTGAAACAGAAAGACACCGCAGTATACTACTGCGTGGCCACGGCAATTT
 GGTAACAGTTACATTTCTATTGGGCGTATTGGGGGCAAGGGAAC'TCTCGTACGGTAAGTTCCCATCATCACCATCATCAT
 SEQ ID NO: 81

FIG. 54U

Pro19 – **aEGFR D12 sdAb** – **aCD3V1 (2B2)** – **gggg¹¹¹¹²²²gs** – **aCD3Vhi** – **aHSA (10GE)** – **His6**
 QVKLESGGGSVQTGSLRLTCAASGRTSRSYGMGWFQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWWVQQ
 KPGQAPRGLIGGTFKFLVPGTPARFSGSLLGKKAALTLGVSQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGDYKDDDDKGGGSE
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIISKYDYKDDDKADSVKDRFTISRDDSKNTAYLQM
 >NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVTVSSGGGSGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWV
 RQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTLLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSSHHHHHH
 SEQ ID NO: 82

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAAACGGTCAAGTTCGGTGGTGGGTCCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGGAAGAGCCGCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGTCTTCGGAGGAGGACGAAACTTACTGTACTTGGAGCGCGGTGACTACAAGACGACGATGACA
 AAGCGCGGCAGCAGGTCCAGTTGGTGAATCCGAGGTGATTGTTCAACCGGGAGGAAGCCTTAAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCAATAAGTACGCAATGAATTGGGTAGACAGGCACCAAGTAAAGGGTTGGAATGGGTGGCACGCATTA
 GGTCTAATAACGATTACAAGGACGACGACAAAGCTGACAGCGTAAAGACCGGATTACGATAAGCCGGGATGATCTAAGA
 ACACCTGCTTATTGTCAGATGAATAATTGAAGACCGAGGATACCTGTCTATTATTGCTCCGCCACGGTAATTTTGGTAACCTCT
 TACATTAGCTATTGGGCGTATTGGGGCAGGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCAAGTGGCGGGGTCAGAG
 GTTCAACTTGTGAGTCTGGAGCGGTCTCGTACAACCGGGGAATAGTCTCCGACTCTCTTGGCTGCTCCGGGTTACAGTTCTC
 AAAGTTGGGATGCTTTGGGTAGGCAAGCCCAAGTAAGGACTCGAATGGTCAAGCATCTCAGGCTCCGGCAGAGACAC
 GTTGTATGCCGAAAGTGTCAAAGGGAGGTTCAATCTCTCGGGACAATGCAAAACCACTTGTATCTCCAATGAACCTCCTC
 CGGCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCCTTAGCGTATCTTCTCAGGGAACCTTGTGTAACGGTCAGCT
 CCCACACCATCATCATCAC SEQ ID NO: 83

FIG. 54V

Pro19 CD3+ - aEGFR D12 sdAb - aCD3V1 (2B2) - gggg¹¹²¹³³gggs - aCD3Vh - aHSA (10GE) - His6
 QVKLESGGGSVQTGGSRLTCAASGRTSRSYGMGWFRRQAPKEREFSVGSWVRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGSGGGGSGTQVTVQEPSLTVSPGTVTLTCASTGAVTSGNYPNWWVQQ
 KPGQAPRGLIGGTFKFLVPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGDYKDDDDKGGGSE
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMN
 NLKTEDTAVYYCVRHGNFGNSYISYWAYWQGQTLTVSSGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR
 QAPGKGLEWVSSISGSRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLLTVSSHHHHHH
 SEQ ID NO: 84

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAGCCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCCGGTGGGGGTCTGGTGGTGGATCCCAAACAGTTGTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCAACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGGAAGAGCCCTTGACCTTGTCAGGCTTCAAGCCGAAAGATGAGGCCGAATATTATGACCGCTGT
 GGTAATCTAACCGTGGGTCTTCGGAGGAGGACGAAACTTACTGTACTTGGAGCGCGGTGACTACAAGGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTAGAATCCGAGGTGATTGTTCAACCGGAGGAAGCCTTAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCATAAAGTACGCAATGAATTGGGTAGACAGGCACCAAGTAAAGGGTTGGAATGGGTGGCACGCATTA
 GGTCCAAGTACAACACTACGCCACCTACTACGCGACAGCGTAAAGACCGGATTACGATAAGCCGGGATGATTCTAAGAACA
 CTGCTTATTGTCAGATGAATAATTGAAGACCGAGGATACTGTGTCTATTATTGCTCCGCCACGGTAATTTGGTAACTCTTAC
 ATTAGCTATTGGCGTATTGGGGCAGGGCACTCTGTCAACCGTCTCATCTGCGGAGGGGCGAGTGGCGCGGTTCAGAGGTT
 CAACTGTCTGAGTCTGAGCGGTCTCGTACAACCGGGGAATAGTCTCCGACTCTTGGCGTGGCTCCGGTTCACGTCTCTCAA
 AGTTTGGGATGTCTTGGTTAGGCAAGCCCCAGGTAAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGT
 TGTATGCCGAAGTGTCAAAGGGAGGTTCAATCTCTCGGGACAATGCAAAAACCACTTGTATCTCCAATGAACACTCACTCCG
 GCCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCCTTAGCGTATCTTCTCAGGGAACCTTGGTAACGGTCAGCTCC
 CACCACCATCATCATCAC SEQ ID NO: 85

FIG. 54W

Pro20 - aEGFR G8 sdAb - aCD3 Vh (2B2) - gggg¹¹ggggs - aCD3Vh¹⁰² - aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKEREFVAINWSSGTYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGQGTQVTVSSGGGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLV
 TVSSGGGG¹¹KKDD¹¹GGGSQTVVTVQEPSTVSPGGITVLTCSSTGAVTSGHYPNWVQQKPGQAPRGLIGGTSNKHWSWTPARFSGS
 LLGGKAALTLSGVQPEDEAEYVCVLWGSRRWVFGGKLTVLGGGGGGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMS
 WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 86

GAAGTTCAACTGGTTGAATCCGGTGGTGGCCTTGTCAGGGGGAGGCTCCCTTCGACTGCTTGTCGCCAGCGGTGCGACAT
 TCAGCAGTTATGCCATGGATGGTTCCGGCAGGCCCTGGTAAAGAGCGGGAGTTCGTCGTTGCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATTCTGTAAGGCGAGGTTCACTATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGGTTACAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTACGGCACCCAGGTAAACCGTCAAGCAGCGGGAGCGGATCAGGAGCGGTTCAGAGGTTACAGCTCGTTG
 AGAGTGGTGGAGGCTGGTTACGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTTTCACTTTAAACAATAACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTTGCAAGAATACGCAAGTAAATACAATAATTATCGGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTACTATCTCTCGAGATGACAGTAAAGACACGGCTTATTTGCAAAATGAACAACCTTGAAGAC
 AGAAGATACGGCGGTCTATTATTGTACGACACGCAAAATTTGGGAATTCATATAAGCTATTGGGCATCTGGGTCAAGGA
 ACCCTTGTTACGGTGAGCAGCGGGGCGGTGTGACTATAAGGACGACGATGACAAAGGCGCGGATCCCAGACTGTGTTAACA
 CAGGAACCATCTTTGACAGTAAGTCCGGAGGTACGGTCAACGCTCACTTGTGGTCTCAACCGGGCTGTAAACGTCAGGCCATT
 ACCCTAACTGGGTCCACAGAAGCCTGGACAAGCTCCAGGGTCTGATAGCGGAACCTTCAACAACGACTCTTGGACTCCAG
 CGCGCTTTAGCGGTTCCCTTCTGGGTGGAATAAGCAGCCCTCACTCTGAGTGGAGTACAACCCGAGGATGAGCGGAATATTATTG
 CGTGCTCTGGGTTACGCCGCTGGTCTTCGGTGGCGGTACGAAACTTACTGTACTGGGGGAGCGGCTCAGCGCGGATC
 AGAAGTGCAGCTTGTGAACTCTGGCGGAGTCTGGTCCAGCCAGGTAAACAGCTTGAGACTGTCTGTGCTGCAAGCGGCTTACC
 TTCTCTAAATTCGGTATGAGTTGGGTCGGCAAGCCCCCTGGAAAGGTTTGGAAATGGGTATCAAGCATTAGTGGTCTGGGCGAG
 ATACACTCTATGCCGAATCAGTGAAGGGCCGCTTACCATTAGTAGGATACCGCTAAACTACTCTGTATCTGCAATGAATAG
 TCTGAGACCAAGAAATACGCCGTTTACTACTGCACAATAGGGGATCTCTGAGCGTTTCATCTCAAGGTACACTTGTGACTGT
 AGCAGTCATCATCATCATCACAC SEQ ID NO: 87

FIG. 54X

Pro21 - aEGFR D12 sdAb - aCD3V1 (2B2) - gggg¹³²ggs - aCD3Vh¹³² - aHSA (10GE) - His6
 QVKLEESGGGSVQTGSLRLTCAASGRTSRYGMGWFQAPGKEREFVSGISWRGDSLTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGTFKFLVPGTPARFSGSLLGKKAALTLSSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGYKDDDDKGGGSE
 VQLVESGGGLVQPGSLKLSCAASGFTFSAMNWNVRQAPGKGLEWVGRIRSKANSYATAYAAASVKDRFTISRDDSKNTAYLQMNIN
 LKTEDTAIYYCVRHGFKFSYIAFWAYWGQGTLVTVSSGGGSGGSVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWVRQ
 APGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 88

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGGTACGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCGGTGGGTCTGGTGGTATCCCAACAGTTGTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGTGTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCCGCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGTCTTCGGAGGAGGAGCAAACTTACTGTACTTGGAGCGGGGTGACTACAAGGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTGAATCCGAGGTGATTGTTCAACCGGAGGAAGCCTTAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCTCTGGTCCGCAATGAATTGGGTAGACAGGCACCAAGGTAAAGGTTGGAATGGTGGGAAGAATAC
 GCAGTAAAGCCCAATCTTATGCGACTGCTTATGCCGCTAGTGTAAAGGACCGGATTACGATAAGCCGGGATGATTCTAAGAACAC
 TGCTTATTTCAGATGAATAATTGAAGACCGAGGATACTGTGTCTATTATTGCTCCGCCACGTAATTTGGTAAGTCTTACA
 TTGCCTTTTGGCGTATTGGGGCAGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCAAGTGGCGCGGGTCAAGAGTTCA
 ACTTGTCGAGTCTGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTCTTGGCTGCTCCGGGTACCGTTCTCAAAG
 TTTGGGATGCTTGGGTAGGCAAGCCCAAGTAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGTTG
 TATGCCGAAAGTGTCAAAGGGAGGTTCAATCTCTCGGGACAATGCAAAAACCACTTGTATCTCCAATGAATCACTCCTCGGC
 CTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGGTCCCTTAGCGTATCTTCTCAGGGAACCTTGTGAACGGTCAGCTCCCA
 CCACCATCATCATCAC SEQ ID NO: 89

Pro22 - aEGFR G8 sdAb – aCD3 Vh (2B2) – gggg~~g~~gggs – aCD3Vl (2B2) – aHSA (10GE) - His6
 PVESGGGLVQAGGSLRSCAASGRFTSSYAMGWFRQAPGKEREFVVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEYDWGGGTQVTVSSGGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VVRQAPGKGLEWVARISKYNNYATYADQVKDRFTISRDSDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLV
 TVSSGGGGGGYKDDDKGGGSQTVVTQEPSLTVSPGGITVLTCASTGAVTSGNYPNWVQQKPGQAPRGLIGTKFLVPGTPARFSGS
 LLGLGKAALTLGSVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGGGGGSEVQLVESGGGLVQPGNSLRSCAASGFTFSKFGMS
 WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLVSSSQGTLVTVSSHHHHH
 SEQ ID NO: 90

GAAGTTCAACTGGTTGAATCCGGTGTGGCTTGTCCAGCGGGAGGCTCCCTTCGACTGTCTTGTGCCGCCAGCGGTGCGCACAT
TTCAGCAGTTATGCCATGGGATGTTCCGGCAGGCCCTGGTAAAGAGCGGAGTTCTGCTGTTGCGATCAATTGGAGTAGCGGTTT
CACAGTATTATGCGATTCTGTAAAGGCGAGTTCACTATCTCACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
CTGAAGCCCGAGGACACGGCAGTTTATTACTGTCTGCCGTTACAGATCAATTCGGAAATTACAATTTCAAGGACTACGAGT
ACAGATTATTGGGTACGGCACCCAGGTAAACCGTCAGCAGCGGGGAGCGGATCAGGAGCGGTTTCAGAGTTTCAGCTCGTTG
AGAGTGTGGAGGCTGTTTCAGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTTTACCTTTAAACAAATACGCTAT
CAACTGGTACGACAAGCCCCCGTAAAGGGCTTGAATGGTTCAGAAATACGAGTAATAACAATAATTATGCGACTTATTATTA
TGCCGATCAAGTAAAGGACCGCTTACTATCTCTGAGATGACAGTAAGAACAACGGCTTATTGCAATGAACAACCTTGAAGAC
AGAAGATACGGCGTCTATTATTGTGTACGACACGCAATTTTGGGAATTCATATATAAGCTATTGGGCATACTGGGGTCAAGGA
AACCTTGTACGGTGAGCAGCGGGCGGTGTGACTATAAGGACGACGATGACAAGCGCGGATCCCAACACAGTTGTTACT
CAGGAGCCATCTTGACAGTATCCCCCGGTGAAACGGTGACCTTGACATCGCTTCAAGTACAGGTGCTGTACCTCAGGTAACCT
ACCCGAATTGGTGACGAATAACCTGGACAAGCACCCCGGCTTTATCGGGGGACGAAGTTCTTGTACCGGGTACCCCTG
CGCGTTACCGGAAGCTTCTGGTGGAATAAGCCGCTTGACCTTGTCAGCGTTACGCCGAAGATGAGGCCGAATATTATTG
CACGCTGGTATTCTAACCCGTTGGTCTTCGAGGAGGACAACTTACTGTACTTGGGGAGCGGCTCAGCGCGGGATC
AGAAGTGCAGCTTGTGAATCTGGCGGAGTCTGTCCAGCCAGGTAAACAGCTTGAGACTGTCTGTCTGCAAGCGGCTTACC
TTTCTCTAAATTCGTTAGTTGGTTCGGCAAGCCCCCTGAAAGGGTTTGGAAATGGGTATCAAGCATTAGTGTTCTGGCGGAG
ATACACTCTATGCCGAATCAGTGAAGGGCGCTTACCATTAGTAGGGATAACGCTAAAACTACTCTGTATCTGCAAAATGAATAG
TCTGAGACCAAGATACTGCCGTTTACTACTGCACATAAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTTGTGACTGTT
AGCAGTCATCATCATCACCAC SEQ ID NO: 91

FIG. 54Z

Prodent 23 – Serum Cleavage into two halves

aEGFR G8 sdAb – aCD3 Vh (2B2) – ~~ggggg~~¹¹¹¹¹~~ggggs~~ – aCD3Vh_i – aHSA (10GE) – ~~gggg~~¹¹¹¹¹~~L~~**PRGSLG**~~gggs~~–

aEGFR D12 sdAb – aCD3Vh (2B2) – ~~ggggg~~¹¹¹¹¹~~ggggs~~ – aCD3Vh_i – aHSA (10GE) – His6

EVQLVESGGGLVQAGGSLRLSCAASGRTFSYAMGWFRQAPGKEREFVAINWSSGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 KPEDTAVYYCAAGYQINSNGYNFKDYEYDWGQGTQVTVSSGGSGGGSEVQLVPMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTILV
 VRQAPGKLEWVARIKSKYNNYATYADQVKDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTILV
 TVSSGGGGDYKDDDDKGGGSQTVVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGGTPARFS
 GLLGGKAALTLVSGVQPEDEAEYCYVWYSNRWVFGGGTKLTVLGGGSGGGSEVQLVESGGGLVQPGNLSRLSCAASGFTFSKFG
 MSWVRQAPGKLEWVSSISGGRDLYAESVKGRFTISRDNKATTLYLQMNLSRPEDTAVYYCTIGGSLVSSQGTILVTVSSGGGGGLV
~~PRGSLG~~GGGSQVKLEESGGSVQTGGSLRLTCAASGRTSRSYGMWFRQAPGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNKAKN
 TVDLQMNLSLKPEDTAIYYCAAAGSAWYGTLYEYDWGQGTQVTVSSGGSGGGSQTVVTQEPSTVSPGGTVTLTCAASSTGAVT
 SGNYPNWVQQKPGQAPRGLIGTKFLVPGTPARFSGSLGGKAALTLVSGVQPEDEAEYCYVWYSNRWVFGGGTKLTVLGGGGDYK
~~DDDDK~~GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKLEWVARIKSKYDYKDDDDKADSVKDRFTISR
 DSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTILVTVSSGGSGGGSEVQLVESGGGLVQPGNLSRLSCAASGF
 TFSKFGMSWVRQAPGKLEWVSSISGGRDLYAESVKGRFTISRDNKATTLYLQMNLSRPEDTAVYYCTIGGSLVSSQGTILVTVSSH
 HHHH SEQ ID NO: 92

GAAGTTCAACTGGTTGAATCCGGTGGTGGCTTGTCAGCGGGAGGGCTCCCTCGACTGCTTGTCGCCAGCGGTCGCACAT
 TCAGCAGTTATGCCATGGATGTTCCGGCAGGCCCTGGTAAAGAGCGGGAGTTCGTGCGATCAATTGGAGTAGCGGTTTC
 CACGTATTATGCGATTCTGTAAGGCGAGGTTCACATATCACGCGATAATGCAAAAATACCATGTATCTTACATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGTTACAGATCAATTCGGAAATTACATTTCAAGGACTACGAGT
 ACGATTATTGGGTACAGGCACCCAGGTACCGTCAAGCAGCGGGAGCGGATCAGGAGCGGTTTCAGAGTTTCAGCTCGTTG
 AGAGTGGTGAGGGCTGTTACGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTTTCACTTTAACAAATACGCTAT
 CACTGGGTACGACAGCCCCGGTAAAGGGCTTGAATGGGTGCAAGAATACGCAATAATACAAATATGCGACTTATTA
 TGCCGATCAAGTAAGGACCGCTTACTATCAGTAGAGATGACAGTAAGAACACCGCTTATTGCAAAATGAACAACCTGAAGAC
 AGAAGTACGGCGGTCTATTATTGTGACGACACGCAATTTGGGAATTCATATAAGCTATTGGGCATCTGGGTCAAGGA
 ACCCTTGTACGGTGAGACGGGGCGGTGTTGACTATAAGGACGACGATGACAAAGCGGGCTCCAGACTGTGTTAACA
 CAGGAACCATCTTTGACAGTAAGTCCTGGAGGTACGGTCAACGCTCACTTGTGGTCTCAACCGGGCTGTAACTGCAAGCAATT
 ACCCTAACTGGGTCCAACAGAGCGCTGGACAAGCTCCAGGGTCTGATAGGCGATTACAAAGATGATGATAAGGGCACTC
 CAGCGCGCTTACGGGATCCCTTCTGGGTGGAAGAGCAGCCCTCACTCTGAGTGGAGTACACCCGAGGATGAGCGGGAATATT

FIG. 54AA

ATTGCGTGCTCTGGTATTCAAAACCGCTGGGTCTTCGGTGGCGGTACGAAACTTACTGTACTGGGGGAGGCGGCTCAGGCGGCGG
 ATCAGAAGTGCAGCTTGTGTAATCTGGCGGAGGTCTGGTCCAGCCAGGTAACAGCTTGAAGACTGTCTGTCTGTCTAGCGGCTTT
 ACCTTCTCTAAATTCGGTATGAGTTGGTTCCGCAAGCCCTGGAAAGGTTTGGAAATGGGTATCAAGCATTAGTGGTTCTGGGC
 GAGATACACTCTATGCCAATCAGTGAAGGCGGCTTACCATAGTAGGGATAACGCTAAACTACTCTGTATCTGCAAAATGAA
 TAGTCTGAGACCAGAAGATACTGCCGTTTACTACTGCAATAAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTTGTGACT
 GTTAGCAGTGTGGGAGGACTTGTACCTCGAGTAGCTTGGGTGGAGGGGATCCCAGTCAAACTTGAGGAAAAGCGGGG
 AGGTAGCGTACAGACTGGTGGATCTCTGAGTTGACTTGCGCCAGTGGCCGACATCCAGAGTTACGGGATGGGTGGTTT
 CGACAGGCTCCGGGAAAAGAGCGGAGTTTGTATCTGGCATAAGCTGGAGGGGCGACTCCACTGGTTACGCAGATTCCGTCAA
 GGGCGGTTTACGATCTCTCGGATACCGGAAGATAACCGTTGATCTCCAAATGAACCTCTTAAACCCGAGGATACAGCAATAT
 ACTATTGCCGCCCGCTGCGGGGTCAGCCTGGTATGGCACATTGTACGAATATGACTATTGGGTCAAGGTACCCCAAGTAACGGT
 CAGTTCGGTGGTGGGGTCTGGTGGATCCCAACAGTTGTACTCAGGAGCCATCCTTGACAGTATCCCCCGGTGGAACG
 GTGACCTGACATGCGCTTCAAGTACAGGTCTGAACCTCAGGTAACTACCCGAATTGGGTGCAGCAAAACCTGGACAAGCA
 CCCCAGGGTCTTATCGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCTTACGCGAAGTCTTCTGGGTGAAAAGCCG
 CCTTGACCTTGTACGGGTTTCAGCCCGAAGATGAGCCGAATATTATGACGCTGTGTATTCTAACCGGTGGGTCTTCGGAGG
 AGGGACGAAACTTACTGTACTTGGAGGCGCGGTGACTACAAGGACGACGATGACAAAGCGGGCGGCAAGCGAGGTCCAGTTGG
 TAGAATCCGAGGTGGATTGGTTCAACCGGAGGAAGCCTTAAGCTTTCATGCGCCGATCCGGATTCACTTCAATAGTACGC
 AATGAATTGGTTAGACAGGCACCAGGTAAAGGTTGGAATGGGTGGCACGCAATAGGTCTAAATACGATTACAGGACGACGA
 CGACAAAGCTGACAGCGTAAAAGACCGATTACGATAAGCCGGGATGATTCTAAGAACACTGCTTATTGACAGATGAATAATT
 GAAGACCGAGGATACTGCTGTCTATTATTGCTCCGCAACGGTAATTGTGTAACCTTACATTAGCTATTGGCGTATTGGGG
 CAGGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCAAGTGGCGGGGTACAGAGTTCAACTTGTGAGTCTGGAGGCGGT
 CTCGTACAACCGGGGAATAGTCTCCGACTCTCTTTCGCTGCTCCGGTTACGTTCTCAAAGTTTGGGATGTCTTGGTTAGGCA
 AGCCCCAGGTAAAGGACTCGAATGGGTACAGCATCTCAGGCTCCGGCAGAGACACGTTGTATGCCGAAAAGTGTCAAAGGAG
 GTTCACAATCTCTCGGGACAATGCAAAACCACTTGTATCTCAAATGAACCTCACTCCGGCTGAGGACACAGCAGTTTACTAC
 TGTACGATAGGAGGTCCCTTAGCGTATCTTCTCAGGGAACTTTGGTAACGGTCAAGTCCCAACCATCATCATCAC

SEQ ID NO: 93

FIG. 54AB

Prodent 24 – Tumor Cleavage into two halves

aEGFR G8 sdAb – aCD3 Vh (2B2) – ~~ggggf12gggs~~ – aCD3Vi – ~~ggggf12gggs~~ –
aEGFR D12 sdAb – aCD3Vi (2B2) – ~~ggggf12gggs~~ – aCD3Vhi – aHSA (10GE) - His6
 EVQLVESGGGLVQAGSLRLSCAASGRTFSYAMGWFRQAPKEREFVAINWSSGGTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSNGYNFKDYEDYWGGQTQVTVSSGGGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGITLV
 TVSSGGGGDYKDDDDKGGGSQTVVTQEPSLTVSPGGITVTLTCSSTGAVTSNGYNPNWVQKPGQAPRGLIGDYKDDDDKGGTARFS
 GSLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTLVGGGGDYKDDDDKGGGSQVKLEESGGSVQTGSLRLTCAAS
 GRTSRSYGMWFRQAPKEREFVSGISWRGDSGTGYADSVKGRFTISRDNAKNTVLDQMNSLKPEDTAIYYCAAAAGSAWYGTLYEY
 DYWGQGTQVTVSSGGGGGGSGQTVVTQEPSLTVSPGGITVTLTCASTGAVTSNGYNPNWVQKPGQAPRGLIGGTGKFLVPGTPARFS
 GSLGGKAALTLSGVQPEDEAEYYCTLVWYSNRWVFGGGLTLVGGGGDYKDDDDKGGSEVQLVESGGGLVQPGGSLKLSCAAS
 GFTFNKYAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI
 SYWAYWGQGITLVTVSSGGGGGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA
 ESVKGRFTISRDNAKTLLYLQMNSLRPEDTAVYYCTIGGSLVSSQGITLVTVSSHHHHH SEQ ID NO: 94

GAAGTTCAACTGGTTGAATCCGGTGGTGGCTTGTCACAGCGGGAGGCTCCCTTCGACTGTCTTGTCGCCAGCGGTGCACAT
 TCAGCAGTTATGCCATGGATGGTTCGGCAGGCCCTGGTAAGAGCGGGAGTTCGTGTCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATCTGTAAAGGCGAGTTCACTATCTACCGGATATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGTTACAGATCAATCCGGAATTACATTTCAAGGACTACGAGT
 ACGATTATTGGGTACAGGCACCCAGGTAAACCGTCAGCAGCGGGAGGCGGATCAGGAGCGGTTCAGAGGTTCAGCTCGTTG
 AGAGTGGTGAGGGCTGGTTACGCCAGGGGAAGTTGAAGCTTCTGTGCGGCCTCTGTTTACCTTTAAACAAATACGCTAT
 CAACCTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTGCAAGAAATACGAGTAAATACAATAATTATGCGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTTACTATCAGTAGAGATGACAGTAAGAACACGGCTTATTGCAATGAACAACTTGAAGAC
 AGAAGATACGGCGGTCTATTATTGTGACGACACGCAAAATTTGGGAATTCATATATAAGCTATTGGGCATACCTGGGTCAAAGGA
 ACCCTTGTACGGTGAGCAGCGGGGGGTGGTACTATAAGGACGATGACAAGCGGGGCTCCAGACTGTGGTAACA
 CAGGAACCATCTTTGACAGTAAGTCCTGGAGGTACGGTCACTGTGGGTCTCAACCGGGGTGTAACGTCAGGCAATT
 ACCCTAACTGGGTCCACAGAAGCCTGGACAAGCTCCAGGGTCTGATAGGCGATTACAAAGATGATGATATAGGGCACTC
 CAGCGCGCTTACGGGATCCCTTCTGGGTGGAAGACGCCCTCACTCTGAGTGGAGTACAACCCGAGGATGAGCGGAATATT
 ATTGCGTCTCTGGTATTCAAAACCGCTGGGTCTTCGGTGCGGTACGAAACTTACTGTACTGGGTGGAGGTGGTACTACAAGGA
 TGACGACGACAAGGGGGCGGAGTCAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGT
 TGACTTGCGCCCGCAGTGGCCGAACATCCAGAAATTACGGGATGGGTGGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTG

FIG. 54AC

TATCTGGCATAAGCTGGAGGGCGACTCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTTACGATCTCTCGGGATAACGCGA
AGAATACCGTTGATCTCCAAATGAACCTCTTAAACCCGAGGATACAGCAATATACTATTGCCGCCGCTGCGGGGTCAAGCCTG
GTATGGCACATTGTACGAATATGACTATTGGGGTCAAGGTACCCAAAGTAACGGTCAAGTCCGGTGGTGGGGGTCTGGTGGTGG
ATCCCAAACAGTTGTTACTCAGGAGCCATCCTTGACAGTATCCCCCGGTGGAACGGTGACCCCTGACATGCGCTTCAAGTACAGGT
GCTGAACCTCAGGTAACTACCCGAAATTGGGTGCAGCAAAACCTGGACAAGCAACCCGGGCTCTTATCGGGGGACGAAGTTC
TTGGTACCGGGTACCCCTGCGCTTCAGCGGAAGTCTTCTGGTGGAAGCCGCTTGACCTTGTCAGGCGTTTCAGCCCGAAG
ATGAGGCCGAATATATTGACGCTGTGGTATTCTAACCGGTGGTCTTTCGGAGGAGGACGAAACTTACTGTACTTGGAGGCGG
CGGTGACTACAAGGACGACGATGACAAAGCGCGGCGACGAGGTCCAGTTGGTAGAATCCGGAGGTGGATTGGTTCAACCGG
GAGGAAGCCTTAAGCTTTCATGCGCCGATCCGGATTCACTTCAATAGTACGCAATGAATTGGGTAGACAGGCACCAAGGT
AAGGTTGGAATGGGTGGCACGCAATTAGGTCTAAATACGATTACAAGGACGACGACAAAGCTGACAGCGTAAAGACCCGA
TTTACGATAAGCCGGGATGATTCTAAGAACAAGTCTTATTGTCAGATGAATAATTTGAAGACCGAGGATCTGCTGTCTATTAT
GCGTCCGCCACGGTAATTTTGGTAACTCTTACATTAGCTATTGGGCGTATTGGGGCAGGGCACTCTGGTCAACCGTCTCATCTGGC
GGAGGGGCGAGTGGCGGGTCAGAGGTTCAACTTGTCGAGTCTGAGGCGGTCTCGTACAACCGGGGAATAGTCTCCGACTC
TCTTGCGCTGCTCCGGTTCACGTTCTCAAAGTTTGGGATGTCAGGCAAGCCCAAGGTAAAGGACTCGAATGGGTCA
GCAGCATCTCAGGCTCCGGCAGAGACACGTTGTATGCCGAAAGTGTCAAAGGAGGTTTCAATCTCTCGGGACAATGCAGAA
CCACCTTGATCTCCAAATGAACCTCACTCCGGCTGAGGACACAGCAGTTTACTGTACGATAGGAGGGTCCCTTAGCGTATC
TTCTCAGGGAACTTTGGTAACGGTCAGCTCCCAACCATCATCATCAC SEQ ID NO: 95

FIG. 54AD

Pro25 – aGFP sdAb – aCD3 Vh – gggg¹³²gggs – aCD3 Vl₁ – H6 (aGFP Pro6)
 QVQLVESGGALVQPGGSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYEDSVKGRFTISRDDARNITVYLQMNSL
 KPEDTAVYYCNVNVGFEYWGQGTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEW
 VARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSIYWAYWGQGTLVTVSSGGGGDYK
 DDDDKGGGSQIVVTQEPSLIVSPGGTVLITCGSSTGAVTSGNYPNWVQQKPQAPRGLIGDYKDDDDDKGTPARFSGSLLGGKAALTL
 SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHHH SEQ ID NO: 96

CAGGTACAGTTGGTAGAAAGCGCGGTGCATTGGTACAACCCGGCGGCTCCTTGAGGCTCAGCTGCGCGGCGTCCGGCTTTCCG
 GTTAACCGCTATTCTATGATGGTACAGGCAAGCACCGGCAAGAACGCGAGTGGTCCGAGGTATGACAGCGCGGAGAG
 CCGATCCTCTATGAAGACTCCGTTAAAGTAGGTTACCATTAGTCGAGACGATGCTAGAAACACGGGTACCTTCAGATGAAT
 AGTTGAAACCAGAAATACGGCCGTGTTATTGTAATGTGAACGTAGGTTTCGAGTACTGGGGCAAGGAACACAGGTTACC
 GTGAGCAGCGGAGCGGATCTGGCGCGGTTCTGAGGTTCAACTTGTGAAGTGAGGAGGTCCTCGTTCAACCCGGTGTCTC
 TTAACCTGAGCTGCGCAGCCAGTGGGTTCACTCAATAAATATGCGATGAACCTGGTGGCAGGCTCCAGGCAAGGCGCTTG
 AATGGGTCGCCCGGATCAGGTCTAATACATAAATATGCGACCTATTATGCCGATAGTGTCAAAGATCGCTTCACGATATCTAG
 AGATGACTCAAGAACACACAGCGTACCTGCAATGAATAACCTGAAACAGAAAGACACAGCTGTATATTATTGTTCAGACATGG
 TAATTTTGGGACAGTTACATCAGTACTGGGCTTATTGGGGACAAAGAACCTCTGTGACTGTCTCTGGAGGAGCGGAGAT
 TACAAAGACGACGATGACAAGGCGCGGCTCACAACTGTGCTCACACAGGAACCTTCCCTCACTGTAGCCCGGGGGGACA
 GTCACACTTACTTGTGGAGTAGCACCGGAGCCGTAACTCCGGAACCTATCCTAATTGGGTACAGCAGAAACCCGGGCCAGGCT
 CCTAGAGGCTTGATTGGCGATTATAAGGATGATGATGATAAGGGCACGCGGCTAGGTTCTCTGGGTCCTTGTGGCGGGGAAG
 GCCGCTCTTACGTTGCTGGGGTGCAGCCTGAGGACGAAGCAGATATTACTGTGCTCTGGTATTCAAAATCGATGGGTGTTG
 GTGGAGGAACAAAGTTGACTGTACTGCACCAACCATCACCAT SEQ ID NO: 97

FIG. 54AE

Pro26 – aCD3 Vh₁ – ~~ggggg~~₁₃₃gggs – aCD3 V1 – aGFP sdAb – H6 (aGFP Pro7)
 EVQLVESGGGLVQP~~GGSL~~KLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYD~~YKDDDDK~~ADSVKDRFTISRDDSKNTAYLQ
 MNNLKTEDTAVYYCVRHGNFNSYISYWYWGQGT~~LVTVSSGGGGDYKDDDDK~~GGGSQTVVTQEP~~SL~~TVSPGGTVTLTCGSSTGA
 VTS~~GNYP~~NWVQKPGQAPRGLIGTKFLA~~PTGPAR~~FGSLLGGKAAL~~TL~~SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGS
 GGSQVQLVESGGALVQP~~GGSL~~RLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYEDSVKGRFTISRDDARNITVYLQ
 MNSLKPEDTAVYYCNVNVGFEYWGQGTQVTVSSHHHHH SEQ ID NO: 98

GAAGTACAGCTCGTTGAGTCCGGAGGGCGCCTCGTTCAGCCTGGAGGTTCTCTTAAGCTTTCTTGTGCAGCATCTGGATTACGTT
 TAATAATATGCGATGAAC~~TGGTG~~CGCCAGCACCCGGAAAGGGCTCGAATGGGTAGCACGAATCAGGAGCAAGTATGACT
 ACAAGATGACGACGACAAAGCTGACTCCGTTAAGACAGATTTCAGATTTCACGAGACGACAGCAAGAATACGGCGTACCTTC
 AAATGAATAATCTTAAACGGAGGATACCGCAGTTTATTATTCGTGAGGCATGGTAAC~~TTCGG~~AAC~~TCTT~~ACATTAGCTACTG
 GGCTTATTGGGTCAAAGGACATTGGTGACGGTCTCTCCGGTGGCGCGGAGACTATAAAGATGACGACGACAAGGGGGCGG
 GTCTCAGACAGTAGTTACACAGGAGCCTAGTCTTACCGTATCACCCGGTGGACCGTAAC~~TCTT~~ACCTGCGGTTCTTCTACGGGC
 GCAGTAACGTCGGGAATTACCCGAAC~~TGGTT~~CAAGCAAAACCGGACAACTCCGAGGGCCTCAATTGGTGGTACTAAATTC
 CTCGACCTGGCACACTGCGCGGTTTTCAGGAGCTTGCTCGAGGCAAGCGGCCCTGACATTGTCGGCGTTCAACCGGAGG
 ACGAAGCTGAGTACTATTGCGTACTGTGGTATAGCAATAGTGGGTATTTGGTGGTACGAAGCTCACGGTCTTGGGGGAG
 GCGGCTCTGGGGAGGAGCCAGGTGCAGCTTGTGAATCTGGTGGTGCCTTGTCCAGCCCGAGGAAGTCTTCGACTCAGTTG
 CGCAGCATCTGGCTTTCGGTGAATCGATATTCATGCGGTGGTACCGACAGCGCCTGGAAAGAACGCGAGTGGGTGCGAGG
 TATGAGTTCTGCTGGCATCGGAGTTCTACGAGGATAGTGTGAAGGCGAGATTACTATTAGTCGAGATGATCGCGGAATACG
 GTGTA~~CTT~~GCA~~GAT~~GAACAGCCTGAAGCCGGAGGATACAGCAGTTTATTATTGTAATGTCAACGTCGGATTGGAATACTGGGGC
 AGGGGACACAAGTTACTGTAAAGCTCACATCATCATCACCAC SEQ ID NO: 99

Pro27 - aGFP sdAb - aCD3 VI - aCD3 Vh1 - H6 (aGFP Pro9)

Pro27 – aGFP sdAb – aCD3 VI – ^{ggggg}₁₂₃₄₅₆₇₈₉gggs – aCD3 Vh₁ – H6 (aGFP Pro9)

QVQLVESGGALVQPGGSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYEDSVKGRFTISRDDARNTVYLQMNSL
KPEDTAVYYCNVNVGFEYWQGQTQVTVSSGGGSGGGSQTAVTQEPSLTVSPGTVTLTCSGSTGAVTSGNYPNVWVQKPGQAPRG
LLIGGTFKLAPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGYKDDDKGGGSEVQLVESGG
GLVLPQGGSLKLSCAASGFTFNKYAMNWNVRQAPGKLEWVARIRSKYDYKDDDKADSVKDRFTISRDDSKNTAYLQMNNLKLTEDT
AVYYCVRHRGNFNSYISYWAWYWGQGLVTVSSHHHHHH SEQ ID NO: 100

CAAGGTACAACTGGTCGAGTCAAGCGGGGCAC TTGTACAGCCTGGTGGCTCTCTTCGGCTTCTTCGCCCGCTTCGGGATTCGCCAGT
GAACCGGTACTCTATGCGTGTGACAGGCAGGCCCGGGGAAGGAGCGCGAATGGTTGCGGGAATGTCCAGTGCGGGGGATC
GAAGCAGTTATGAAGACAGCGTCAAGGTCGGTTCACTATTAGTAGAGATGACGCGCAACACGGTTTACTTGCATAATGAATA
GTCTGAAGCCAGAGGATACTGCCGTTTACTGTAATGTAACGTAGGATTGTAATATTGGGACAAAGGACGC AAGTAAACCG
TCTCTCCGGCGGAGGAGGACGGGGTGGTTCTCAAAC TGTGTTACGACGAGCCCTCACTTACCGTGATCCCGCGGGA
CTGTCAACGTCACCTGTGTTCCAGTACAGGGCCGTCACTCCGAAATACCCAAATTGGGTACAACAAAGCCAGGACAAG
CCCCCAGAGGCCTTATAGGAGAACCAAGTTCTCGCGCTGGTACTCCAGCCCGCTTCTTGTTCTGTTGGGGGTAAAGC
AGCGCTTACTCTGTCGGCGTTCAGCCTGAGGATGAAGCGAGTACTATTGCTACTCTGTACAGCAACCGCTGGGTGTTCCGT
AGGGGGACTAACTTACTGTGTCGGGGCGGGGACTACAAGACGACGACGATGAAGGTGGGGGTCTCAGAAGTCCAAC T
TGTTGAATCTGGGTGGTGGTTGTTACGCCAGGGGATCCCTGAAGCTAGCTAGTCGCCCGCAAGTGGATTACATTC AATGAATAC
GCAATGAAC TGGTGAGGCAAGCGCCAGGAAGGGACTTGAATGGTTGCTAGAA TCCGATCCAAATATGACTACAAGATGA
CCGACGACAAAGCGGATTCCGTGAAGACAGATTCACTCTCGGATGATCAAAAACACTGCGTACCTCCAATGAATAA
TCTGAAAACAGAGGACACAGCAGTCTATTATTGTGTCGGCACGGAAACTTTGGCAATAGTTACATCTCATATTGGGCATATTGG
GCCAGGGTACACTCGTCACAGTCAGTAGCCATCATCATCAC ACCATCAC SEQ ID NO: 101

FIG. 54AG

Pro28 – aCD3 V_H – gggg₁₂₃gggs – aCD3 V_H – aGFP sdAb – H6 (aGFP Pro10)
 QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNVVQQKPGQAPRGLIGDYKDDDDKGT₁₂₃PARFSGSLGGKAALTL₁₂₃SGVQPEDEA
 EYYCVLWYSNRWVFGGKLT₁₂₃VLGGGGDYKDDDDKGGSEVQLVESGGGLVQP₁₂₃GSLKLSAASGFTENKYAMN₁₂₃WVRQAPGKGL
 EWVARIRSKYNNYATYADSVKDRFTISRDDSKNTAYLQMN₁₂₃NLTEDTAVYCVRHGNFNGNSYISYWAYWGQGLVTVSSGGGGS
 GGSQVQLVESGGALVQP₁₂₃GSLRLSCAASGFPVNRYSMRWYRQAPGKEREWVAGMSSAGDRSSYEDSVKGRFTISRDDARNTVYLQ
 MNSLKPEDTAVYYCNVNVNGFEYWGGGTQVTVSSHHHHH SEQ ID NO: 102

CAAAACGGTTGTTACCCAAAGAGCCTAGTTTGACAGTTTCTCCCGGTGGGACAGTCAC₁₂₃TTTGACTTGTGGATCATCCACGGGAGCTG
 TGACCTCAGGGAAC₁₂₃TACCCGAATTGGGTTCAGCAGAAGCTGGACAAGCACCAGAGTTTGATAGGAGATTACAAAGATGACG
 ATGATAAAGGCACCCCGCTCGATTTCAGTGGTCTCTCC₁₂₃TGGCGGAAGGCTGCTCTCACC₁₂₃TGAGCGGGTGCAGCCAGAGG
 ATGAAGCTGAGTACTACTGCTTCTGTGGTATAGCAACCGGTGGTTTTCGAGGGGTACGAAATTGACTGTCTCGCGGTGG
 GGGTACTATAAGGATGACGACGATAAGGGCGGTGGTCTGAGGTCCAACTCGTGGAAAGTGGAGGAGGTCTTGTACAAACCGG
 GCGGTCACTTAAGCTCAGTTGCGCGGCTCAAGGCTTCACTTTCATAAGTATGCCATGAAC₁₂₃TGGTGAGACAGGCTCCCGGAAA
 GGGA₁₂₃CTTGAATGGGTCGCCGAATTAGGTCTAAGTATAACAATTAACGCAACCTATTACGCTGATTCAAGTAAAGACCGGTTTACA
 ATTTACGCGCAGATAGTAAGAACACCGCATATCTCCAGATGAATAACTGAAGACCGAGGATACTGCCGTATAATTATTGTGTTT
 GACATGGCAATTTTCGGAAACTCATATATAAGCTACTGGGCGTACTGGGGCAGGTACTCTTGTACCGTATCTTCTGGGGGTGG
 AGGTTACGGGGCGGTTC₁₂₃CCAGGTTCAACTGGTAGAAAGCGGGGTGCTTTGGTGCAACCCGGTGGCTCACTGCGATTGCTCTGT
 GCCGCTTCAGGTTTCCCCGTAAACCGGTACTCCATGAGATGGTATCGACAGCGCGCGGCAAGGAACGCGAGTGGGTTCAGGG
 ATGTCTAGCGCGGTGATCGGTCTTCTTACGAAGATTCAAGTCAAGGACGATTCACTCCCGCGATGACGCGAGGAACACTG
 TATACCTGCAAAATGAACTCTTAAGCCCGAAGACACCGCTGTCTACTACTGTAAACGTAATATGTCGGGTTCGAGTACTGGGGCCA
 AGGCACCCAAAGTGACGGTTTCCAGTCAACCAACCATCATCAC SEQ ID NO: 103

FIG. 54AH

Pro29 - aEGR D12 sdAb - aCD3V1 (2B2) - ~~ggggg~~₁₂₂gggs - aCD3Vh₁₂₂ - aHSA (10GE) - His6
 QVKLESGGGSVQTGSLRLTCAASGRTSYGMGWFQAPGKEREFVSGISWRGDS¹²²TGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGTKFLVPGTPARFSGSLGKKAALTLSSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGYKDDDDKGGGSE
 VQLVESGGGLVQPGSLKLSCAASGFTFNKSAMNWNVRQAPGKGLEWVARIRSKYN¹²²NYATAYAAASVKDRFTISRDDSKNTAYLQMNN
 LKTEDTAVYYCVRHGNFGNSYIAFWAYWGQGTLVTVSSGGGSGGSVEQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQ
 APGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSH¹²²HHHH
 SEQ ID NO: 104

CAAGTCAAACTTGAGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCAGAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGTACCCAAAGTAACGGTCAAGTCCCGTGGTGGGCTCTGGTGGTGGATCCCAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCCGCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATCTAACCGTGGTCTTCGGAGGAGGAGCAAACTTACTGTACTTGGAGCGGGGTGACTACAAGGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTAGAATCCGAGGTGATTGTTCAACCGGAGGAAGCCTTAAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCAATAAGTCCGCAATGAATTGGTTAGACAGGCACACAGTAAAGGGTGGAAATGGGTGGCACGCATTA
 GGTCCAAGTACAACACTACGCCACCGCTACCGGCCAGCGTAAAGACCGGATTTACGATAAGCCGGGATGATTCTAAGAACA
 CTGCTTATTGTCAGATGAATAATTGAAGACCGAGGATAGTGTCTATTATTGCTCCGCCACGGTAATTTGGTAACCTTTAC
 ATTGCCTTTGGCGTATTGGGGCAGGGCACTCTGGTACCGTCTCATCTGGCGGAGGGGCGAGTGGCGGGTTCAGAGGTTTC
 AACTTGTCAGTCTGGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTTGGCTGCGTCCGGGTTCACGTTCTCAAA
 GTTTGGGATGCTTTGGGTTAGGCAAGCCCCAGGTAAGGGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGTT
 GTATGCCGAAGTGTCAAAGGAGGTTCAATCTCTCGGGACATGCAAAACCACTTGTATCTCCAATGAACCTCACTCCG
 GCCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCTTACGCTATCTCTCAGGGAACCTTGGTAACGGTCAGCTCC
 CACCACCATCATCATCAC SEQ ID NO: 105

FIG. 54AI

Pro30 - aEGR D12 sdAb - aCD3V1 (2B2) - gggg¹²³gggs - aCD3Vh¹²³ - aHSA (10GE) - His6
 QVKLESGGGSVQTGSLRLTCAASGRTSYGMGWFQAPGKEREFVSGISWRGDS¹²³TGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGTKFLVPGTPARFSGSLGKKAALTLGQVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGYKDDDDKGGGSE
 VQLVESGGGLVQPGSLKLSCAASGFTFNKSAMNWVRQAPGKGLEWVARIRSKYN¹²³NYATAYADSVKDRFTISRDDSKNTAYLQMNN
 LKTEDTAVYYCVRHGNFGNSYITFWAYWGQGLVTVSSGGGSGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWVRQ
 APGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSH¹²³HHHH
 SEQ ID NO: 106

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGTACCCAAAGTAACGGTCAAGTTCGGTGGGGTCTGGTGGTGGATCCCAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGTGTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCCGCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATCTAACCGTGGTCTTCGGAGGAGGAGCAAACTTACTGTACTTGGAGCGGGGTGACTACAAGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTAGAATCCGAGGTGATTGGTTCAACCGGAGGAAGCCTTAAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCAATAAGTCCGCAATGAATTGGTTAGACAGGCACACAGTAAAGGGTTGGAATGGGTGGCACGCATTA
 GGTCCAAGTACAACAACTACGCCACCGCTACCGGACAGCGTAAAGACCGGATTTACGATAAGCCGGGATGATTCTAAGAACA
 CTGCTTATTGCAATGAATAATTGAAGACCGAGGATACGTGTCTATTATTGCTCCGCCACGGTAATTTGGTAACCTTTAC
 ATTACCTTTTGGCGTATTGGGGCAGGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCGAGTGGCGGGTTCAGAGGTTT
 AACTTGCAGTCTGGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTTGGCTGCGTCCGGGTTCACGTTCTCAAA
 GTTTGGGATGTCTTGGGTAGGCAAGCCCCAGGTAAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGTT
 GTATGCCGAAGTGTCAAAGGAGGTTCAATCTCTCGGGACATGCAAAACCACTTGTATCTCCAATGAACCTCACTCCG
 GCCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCTTACGCTATCTTCTCAGGGAACCTTGGTAACGGTCAGCTCC
 CACCACCATCATCATCAC SEQ ID NO: 107

FIG. 54AJ

Pro31 - aEGR D12 sdAb - aCD3V1 (2B2) - ~~ggggg~~₁₂₃gggs - aCD3Vh~~123~~₁₂₃ - aHSA (10GE) - His6
 QVKLEESGGSVQTGSLRLTCAASGRTSYGMGWFQAPKEREFSVGSWVRGDS~~T~~GYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGTFKFLVPGTPARFSGSLGKKAALTLGVPQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGYKDDDDKGGGSE
 VQLVESGGGLVQPGSLKLSCAASGFTFSYAMNWVRQAPGKGLEWVARIRSKANSYATEYAAASVKDRFTISRDDSKNTAYLQMNIN
 LKTEDTAVYYCVRHGNAGNSAISYWAYWGQGTLVTVSSGGGSGGSEVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQ
 APGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 108

CAAGTCAAACTTGAGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCGGTGGGGTCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTACCTGACATGCGCTTCAAGTACAGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCGCCCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGACCGCTGT
 GGTATTCTAACCGTGGTCTTCGGAGGAGGACGAAACTTACTGTACTTGGAGCGGGGTGACTACAAGGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTGAATCCGAGGTGGATTGTTCAACCGGGAGGAAGCCTTAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCAGTGGTACGCAATGAATTGGGTAGACAGGCACCAAGTAAAGGGTTGGAATGGGTGGCACGCATTA
 GGTCCAAGGCCAACAGTACGCCACCGAGTACCGGCCAGCGTAAAGACCGATTACGATAAGCCGGGATGATTCTAAGAACA
 CTGCTTATTGTCAGATGAATAATTGAAGACCGAGGATACTGTGTCTATTATTGCTCCGCCACGGTAATGCTGGTAACTCTGCC
 ATTAGCTATTGGCGTATTGGGGCAGGGCCTCTGTCACTGTCACTGTGCGGAGGGGCGAGTGGCGGGTTCAGAGGTT
 CAATTGTCGAGTCTGAGCGGTCTCGTACAACCGGGGAATAGTCTCCGACTCTTGGCGTGGCTCCGGTTCACGTTCTCAA
 AGTTGGGATGTCTTGGGTAGGCAAGCCCCAGGTAAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGT
 TGTATGCCGAAGTGTCAAAGGGAGGTTACAACTCTCGGGACAATGCAAAAACCACTTGTATCTCCAATGAACACTCCTCCG
 GCCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCCTTAGCGTATCTTCTCAGGGAACCTTGGTAACGGTCAGCTCC
 CACCACCATCATCATCAC SEQ ID NO: 109

FIG. 54AK

Pro32 - aEGR D12 sdAb - aCD3V1 (2B2) - ~~ggggg~~^{132gggs} - aCD3Vh^{142.5} - aHSA (10GE) - His6
 QVKLEESGGSVQTGSLRLTCAASGRTSYGMGWFQAPKEREFSVGSWVRGDS¹³²TGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGSGGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWWVQQ
 KPGQAPRGLIGTKFLVPGTPARFSGSLGKKAALTLGVSQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGG¹³²YK^{142.5}DDDKGGGSE
 VQLVESGGGLVQPGSLKLSCAASGFTFSGHAMNWRQAPGKGLEWVARIRSKANSYATYADSVKDRFTISRDDSKNTAYLQMNN
 LKTEDTAVYYCVRHGANNSYISYWAYWGQGT¹³²LVTVSSGGSGGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWWVQQ
 APGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSVSSQGT¹³²LVTVSSHHHHHH
 SEQ ID NO: 110

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGTTACGATCTCTCGGATAACGCGAAGATACCGTTGATCTCCAATGAAC
 CTCCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGTACCCAAAGTAACGGTCAAGTTCGGTGGGTCTGGTGGTATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCGCCCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGTCTTCGGAGGAGGACGAAACTTACTGTACTTGGAGCGGGGTGACTACAAGGACGACGATGACA
 AAGCGCGGCAGCGAGTCCAGTTGGTAGAATCCGAGGTGATTGTTCAACCGGAGGAAGCCTTAAAGCTTTCATGCGCCG
 CATCCGGATTCACTTCAGTGGCACGCAATGAATTGGGTAGACAGGCACCAAGGTTGGAATGGGTGGCACGCATTA
 GGTCCAAGGCCAACAGCTACGCCACCTACTACGGGACAGCGTAAAGACCGATTACGATAAGCCGGGATGATTCTAAGAACA
 CTGCTTATTGCAATGATAATTGAAGACCGAGGATACTGCTGTCTATTATTGCTCCGCCACGGTGTCTAATGGTAACTCTTAC
 ATTAGCTATTGGCGTATTGGGGCAGGGCCTCTGTCACTGTCACTGTGCGGAGGGGCGAGTGGCGGGTTCAGAGGTT
 CAATTGTCGAGTCTGGAGCGGTCTCGTACAACCGGGGAATAGTCTCCGACTCTTGGCGTGGCTCCGGTTCACGTTCTCAA
 AGTTTGGGATGCTTGGGTAGGCAAGCCCCAGGTAAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGAGACACGT
 TGTATGCCGAAGTGTCAAAGGGAGGTTCAATCTCTCGGGACAATGCAAAACCACTTGTATCTCCAATGAACACTCACTCCG
 GCCTGAGGACACAGCAGTTTACTACTGTACGATAGGAGGTCCCTTAGCGTATCTCTCAGGGAACCTTGGTAACGGTCAGCTCC
 CACCACCATCATCATCAC SEQ ID NO: 111

FIG. 54AL

Pro39 (MMP9) - aEGFR G8 sdAb - aCD3 Vh (2B2) - ~~SCGPQAPQMKQLPQS~~ - aCD3Vh¹⁰² - aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWERQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYWGGQTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLV
 TVSSGGPQAPQMKQLPQSQTIVVTQEPSLTVSPGGTIVLTGSSSTGAVTSGHYPNWVQQKPGQAPRGLIGGTSNKHSWTPARFSGSLL
 GGKAAALTLSGVQPEDEAEYCYVLWGSRRWVFGGKLTIVLGGSGGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWV
 RQAPGKGLEWVSSISGSGRDTILYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLLVTVSSHHHHHH
 SEQ ID NO: 112

GAA GTTCAA ACTGGTTGAATCCGGTGGTGGCCCTTGTC CAGCGGGAGGCTCCCTTCGACTGTCTTGTGCCGCCAGCGGTGCACAT
 TCAGCAGTTATGCCATGGGATGGTTCGGCAGGCCCTGGTAAAGAGCGGGAGTTCGTCTGTCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATTCGTAAAGGCGAGGTTCACTATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGGTTAC CAGATCAATTCGGAAATTACAATTTCAAGGACTACGAGT
 ACGATTATTGGGTCAAGGCAACCCAGGTAAACCGTCAAGCAGCGGGAGGCGGATCAGGAGCGGTTTCAGAGGTTTCAGCTCGTTG
 AGAGTGGTGGAGGCTGGTTCAGCCAGGGGAAGTTTGAAGCTTTCCTGTGCGGCTCTGTGTTTCACTTTAAACAATACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTGCAAGAATACGCAAGTAAATACAATAATTATGCGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTACTATCTCTCGAGATGACTCTAAGAACACTGCCTATTTGCAGATGAACAATCTTAAAAACA
 GAGGACACAGCGGTGTAATTGTGTAAGACATGCCAACTTTGGAAACAGCTATATTAGCTATTGGGCTTACTGGGGCAGGGC
 ACTCTGTCAACCGTCAGTTCTCTGGGGGCCAGGGCCAGCGGCTGAAAGGCTTCCGGGATCCAGACTGTGTTAAACACAG
 GAACCATCTTTGACAGTAAGTCCTGGAGTACGGTCACTGTGGGTCTCAACCGGGCTGTAAACAGCACTCTTGACTCCAGCGC
 CTAAC TGGGTCCAACAGAACCTTGACAAAGCTCCAGGGTCTGATAGCGGAACTTCAAAACAGCACTCTTGACTCCAGCGC
 GCTTAGCGGTTCCTCTGGGTGAA AAGCAGCCCTCACTCTGAGTGGAGTACAACCGAGGATGAGCGGAAATATTATTGCGT
 GCTCTGGGTTTACGCCGCTGGGTCTTCGGTGGCGGTACGAAACTTACTGTACTGGGGGAGCGGCTCAGCGCGGATCAGA
 AGTGACGCTTGTGAAATCTGGCGGAGGTCTGGTCCAGCCAGGTAACAGCTTGAGACTGTCTGTGTGCAAGCGGCTTACCTTC
 TCTAAATTCGGTATGAGTTGGGTCGGCAAGCCCCCTGGAAAGGGTTTGGAAATGGGTATCAAGCATTAGTGGTCTGGCGGAGATA
 CACTCTATGCCGAATCAGTGAAGGGCCGCTTACCATTAGTAGGGATAACGCTAAACTACTCTGTATCTGCAATGAATAGTCT
 GAGACCAAGAGATACTGCCGTTTACTACTGCACAATAGGGGATCTCTGAGCGTTTCATCTCAAGGTACACTTGTGACTGTTAGC
 AGTCATCATCATCATCACCCAC SEQ ID NO: 113

FIG. 54AM

Pro40 (MMP9) - aEGFR D12 sdAb - aCD3V1 (2B2) - ~~SGGPGAGMKQLPGS~~ - aCD3Vh¹⁰⁰¹ - aHSA (10GE) - His6
 QVKLEESGGSVQTGSLRLTCAASGRTSRSGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGSGGGSQTVVTQEPSLTVSPGTVTLTCAASGTGAVTSGNYPNWWVQQ
 KPGQAPRGLGGTKFLVPGTPARFSGSLLGKKAALTLGQVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL~~SGGPGAGMKQLPGSEVQ~~
 LVESGGGLVQPGGSLKLSCAASGFTFSGYAMNWWVRQAPGKLEWVARIRSKANSYATEYAAASVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHGNAGNSAISYWAYWGQGTLVTVSSGGSGGGSEVQLVESGGGLVQPQNSLRSLSCAASGFTFSKFGMSWVVRQAP
 GKLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 114

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGGTACGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCCGGTGGGGTCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGGAAGAGCCGCTTGACCTTGTCAGGCTTCAAGCCGGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGTCTTTGGGGTGGTACGAAGTTGACCGTTCTCAGCGGTGGCCAGGACAGCATGTAAGGGGT
 TGCCCGGCTCAGAAAGTCCAGTTGGTAGAATCCGGGGGGGACTGGTTCAACCAAGGAGGTAGTTTGAAGCTTTCATGCGCCGCAT
 CCGGATTCACCTTCAGTGGTACGCAATGAATTGGTTAGACAGGCACCAAGGTAAAGGTTGGAATGGTGGCACGCAATTAGGT
 CCAAGGCCAACAGTACGCCACCGAGTACGCGCCAGCGTAAAGACCGGATTTACGATAAGCCGGGATGATTTCTAAGAAACACTG
 CTTATTTGCAGATGAATAATTGAAGACCGAGGATACTGCTGTCTATTATTGCGTCCGCCACGGTAATGCTGGTAACTCTGCCATT
 AGCTATTGGGCGTATTGGGGCAGGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGGCAGTGGCGGGGTCAGAGGTTCAA
 CTTGTGAGTCTGGAGCGGTCGTACAAACCGGGAATAGTCTCCGACTCTTTCGCTGCTCGGTTCCAGTTCTCAAGTT
 TGGGATGCTTTGGGTAGGCAAGCCAGGTAAAGGACTCGAATGGGTACGACATCTCAGGCTCCGGCAGACACGTTGTA
 TGCCGAAAGTGTCAAAGGAGGTTCAATCTCTGGGACATGCAAAACCACTTGTATCTCCAATGAACCTACTCCGGCT
 GAGGACACAGCAGTTTACTACTGTACGATAGGAGGGTCCCTTAGCGTATCTTCTCAGGGAACCTTTGGTAACGGTCAGCTCCCACC
 ACCATCATCATCAC SEQ ID NO: 115

FIG. 54AN

Pro41 (Mep) - aEGFR G8 sdAb - aCD3 Vh (2B2) - ~~SCGGKKLADPEEGGS~~ - aCD3Vh~~102~~ - aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGFRQAPGKEREFVVAINWSSGSTYYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYDWGQGTQVTVSSGGGSGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLV
 TVSS~~SCGGKKLADPEEGGS~~QIVVTVQEPSLTVSPGGTVILTCGSSTGAVTSGHYPNWVQQKPGQAPRGLIGGTSNKHSWTPARFSGSL
 GGKAAALTLSGVQPEDEAEYCYVLWGSRRWVFGGGLKLVLGSGGSGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWV
 RQAPGKGLEWVSSISGSGRDILYAESVKGRFTISRDNAKTLLYLQMNSLRPDTAVYYCTIGGSLSVSSQGTLLVTVSSHHHHHH
 SEQ ID NO: 116

GAA GTTCAA ACTGGTTGAATCCGGTGGTGGCCCTTGTCAGGGGGAGGCTCCCTTCGACTGTCTTGTGCCGCCAGCGGTGCGACAT
 TCAGCAGTTATGCCATGGATGGTTCCGGCAGGCCCTGTGTAAGAGCGGGAGTTCGTGTTGCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATCTGTAAAGGCGAGTTCACTATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGGTTACCAAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTCAAGGCAACCAAGGTAAACCGTCAAGCAGCGGGAGCGGATCAAGGAGCGGTTTCAGAGTTTCAGCTCGTTG
 AGAGTGGTGGAGGCTGGTTCAAGCAGGGGAAGTTTGAAGTTTCTGTGCGGCTCTGTGTTTCACTTTAAACAATAACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTGCAAGAATACGCAATAACAATAATATGCGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTACTATCTCTCGAGATGATTCTAAACACCCGATATTGCGAGATGAACAATCTTAAACT
 GAGGACACCGCAGTGATTACTGCTGCGACATGCGAACTTCGGTAACTTACATTCTCTACTGGCGTATTGGGGCCAGGGCA
 CGCTTGTGACGGTTAGTTCTAGCGGAGGTGTTAAAGCTCGCTGACGAGCGAGGAGGATCCCACTGTGTTAACACAGG
 AACCATCTTTGACAGTAAGTCTGGAGGTACGGTCACTGTGGGTCTCAACCGGGCTGTAACTGTCAGGCCATTACCC
 TAACTGGGTCCAAACAGAACCTGGACAAGCTCCAGGGGTCTGATAGCGGAACCTCAACAAGCACTCTTGACTCCAGCGCG
 CTTTAGCGGTTCCCTTCTGGGTGAAAAGCAGCCCTCACTCTGAGTGGAGTAAACCCGAGGATGAGCGGAATAATTATTCGTG
 CTCCTGGGTTCAACGCCGCTGGTCTTCGGTGGGTACGAACTTACTGTACTGGGGGAGCGGCTCAGCGGGGATCAGAA
 GTGCAGCTTGTGAACTCTGGCGGAGTCTGGTCCAGCCAGGTAAACAGTTGAGACTGTCTGTGTGCAAGCGGCTTACCTTCT
 CTAATTCGGTATGAGTTGGTTCGGCAAGCCCCGAAAGGGTTGGAAATGGGTATCAAGCATTAAGTGGTCTGGCGGAGATAC
 ACTCTATGCCGAATCAGTGAAGGGCCGCTTACCATTAGTAGGATAACGCTAAACTACTCTGTATCTGCAATGAATAGTCTG
 AGACCAAGAGATACTGCCGTTTACTACTGCAATAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTGTGACTGTTAGCA
 GTCATCATCATCATCACCCAC SEQ ID NO: 117

FIG. 54AO

Pro42 (Mep) - aEGFR D12 sdAb - aCD3V1 (2B2) - ~~SGGGKLLADEPEGG~~ - aCD3Vh¹⁰¹¹ - aHSA (10GE) - His6
 QVKLEESGGSVQTGSLRLTCAASGRTSRSGMGWFRQAPKEREFSVSGISWRGDSLTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDWGQGTQVTVSSGGSGGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWWVQQ
 KPGQAPRGLIGTKFLVPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL~~SGGGKLLADEPEGG~~SEVQ
 LVESGGGLVQPGGSLKLSCAASGFTFSGYAMNWWVRQAPGKLEWVARIRSKANSYATEYAAASVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHHNAGNSAISYWAYWGQGTLVTVSSGGSGGGSEVQLVESGGGLVQPQNSLRSLSCAASGFTFSKFGMSWVVRQAP
 GKLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 118

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGTTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGTCAAGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGTACCCAAAGTAACGGTCAAGTTCGGTGGGGTCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCAACCCGGGTCTTATCGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGGAAGAGCCCTTGACCTTGTCAGGCTTCAGCCCAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGGTGTTGGTGGGGTACAAATTTGACGGTCTTGTCAGGGGTGGAAGAAACTGGCAGATGAACCTG
 AGGCGGTCTGAGGTTCAAGCTTGTGAGAGCGGTGGCGGTCTTGTCACCCGGAGGCTCACTCAAGCTTTCATGCGCCGCATC
 CGGATTCACCTTCAGTGGGTACGCAATGAATTGGGTAGACAGGCACCAAGTAAAGGTTGGAATGGGTGGCACCGCATTAGGTC
 CAAGGCCAACAGCTACGCCACCGAGTACGCGCCAGCGTAAAGACCGATTACGATAAGCCGGGATGATCTAAGAACAACCTGC
 TTATTTCAGATGAATAATTTGAAGACCGAGGATACTGCTGCTATTATTGCGTCCGCCACGGTAATGCTGGTAACTCTGCCATTA
 GCTATTGGGCGTATTGGGGCAGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCAAGTGGCGGGGTCAGAGGTTCAAC
 TTGTCGAGTCTGGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTTTGCGCTGCGTCCGGTTCACGTTCTCAAAGTTT
 GGGATGCTTGGGTTAGGCAAGCCCAAGGTAAGGACTCGAATGGGTACAGCATCTCAGGCTCCGGCAGACACGTTGTAT
 GCCGAAAGTGTCAAAGGAGGTTTCAATCTCTCGGGACAATGCAAAACCACTTGTATCTCCAATGAACCTCACTCCGGCT
 GAGGACACAGCAGTTTACTACTGTACGATAGGAGGGTCCCTTAGCGTATCTTCTCAGGGAACCTTTGGTAACGGTCAGCTCCCACC
 ACCATCATCATCAC SEQ ID NO: 119

FIG. 54AP

Pro43 (ST14#2) - aEGFR G8 sdAb - aCD3 Vh (2B2) - ~~GGSTFIRQARVVGGGS~~ - aCD3Vh#2 - aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKEREFVVAINWSSGGTYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYDWGQGTQVTVSSGGGGGGGSEVQLVESGGGLVQPQGSLLKSLCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWVGQGTLY
 TVSS~~GGSTFIRQARVVGGGS~~QTIVVTQEPSLTVSPGTVILTCSSITGAVTSGHYPNWVQQKPGQAPRGLIGTSTNKHSWTPARFSGSL
 GSKAALTLSGVQPEDEAEYCYVLWGSRRWVFGGKLTIVLGGGGGGGSEVQLVESGGGLVQPQGSLLKSLCAASGFTFSKFGMSWV
 RQAPGKGLEWVSSISGSGRDTILYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLYTVSSHHHHHH
 SEQ ID NO: 120

GAAATTCAAACTGGTTGAATCCGGTGGTGGCCCTTGTCAGGGGGGAGGCTCCCTTCGACTGTCTTGTGCCGCCAGCGGTGCACAT
 TCAGCAGTTATGCCATGGATGGTTCCGGCAGGCCCTGTGTAAGAGCGGGAGTTCGTCTGTCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATCTGTAAAGGCGAGGTTCACTATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGGTTACCAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTACAGGCAACCCAGGTAAACCGTCAAGCAGCGGGAGCGGATCAGGAGCGGTTTCAGAGTTTCAGCTCGTTG
 AGAGTGGTGAGGCTGGTTCAAGCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTGTTTCACTTTTAAACAATACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTTGCAAGAATACGCAATAACAATAATATGCGACTTATTA
 TGCCGATCAAGTAAGGACCGCTTACTATCTCGAGATGACTCCAGAATACAGCTTACCTTCAAAATGAATAATCTGAAGACA
 GAGGATACCGCCGTGTTACTGCGTCCGACATCGAACTTTGGTAATCTTATATCTTATTGGGCTATTGGGTCAGGGCAC
 GTTGGTTACCGTTTCTCTGAGGTTTCATCACCCGCCAGCGGAGTTGTCGGTGAGGATCCAGACTGTGTTAACACAGGAA
 CCATCTTTGACAGTAAGTCCTGAGGTACGGTACGCTCACTGTGGTCTCAACCGGGGCTGTAACTGAGGCTTACCTACCTA
 ACTGGTCCAAACAGAGCTGGACAAGCTCCAGGGTCTGATAGGCGGAACCTTCAACAAGCACTCTTGGACTCCAGCGCGCT
 TTAGCGTTCCCTTCTGGGTGGAAGAAGAGCCCTCACTCTGAGTGGAGTACAACCGAGGATGAGCGGGAATATTATTGCGTGCT
 CTGGGTTCAAGCCGCTGGTCTTCGGTGGCGGTACGAACTTACTGTACTGGGGGAGCGGCTCAGCGCGGATCAGAAGT
 GCAGCTTGTGTAATCTGGCGGAGGTCTGGTCCAGCCAGGTACAGCTTGAGACTGTCTGTGCTGCAAGCGGCTTACCTTCTCT
 AAATTCGGTATGAGTTGGGTCGGCAAGCCCTGGAAGGGTTTGGATGGGTATCAAGCATTAGTGGTCTGGCGGAGATACA
 CTCTATGCCGATCAGTGAAGGGCCGCTTACCATTAGTAGGATACCGCTAAACTACTCTGTATCTGCAAAATGAATAGTCTGA
 GACCAGAAAGATACGCGGTTTACTACTGCAACAATAGGGGATCTCTGAGCGTTTCATCTCAAGGTACACTGTGACTGTAGCAG
 TCATCATCATCATCACCCAC SEQ ID NO: 121

FIG. 54AQ

Pro44 (ST14#2) - aEGFR D12 sdAb - aCD3V1 (2B2) - ~~CGSEFTRQARVVGGGS~~ - aCD3Vh⁰¹¹ - aHSA (10GE) - His6
 QVKLEESGGGVQTGGSRLRLTCAASGRTSRSYGMGWFRAQPKGEREFVSGISWRGDSLTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSSGGGSGGGSQTVVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGTFKFLVPGTPARFSGSLLGKKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL~~CGSEFTRQARVVGGGSEVQ~~
 LVESGGGLVQPGGSLKLSCAASGFTFSGYAMNWWVRQAPGKLEWVARIRSKANSYATEYAAASVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHGNAAGNSAISYWAYWGQGTLVTVSSGGGSGGGSVQLVESGGGLVQPGNSLRSLSCAASGFTFSGFMSWVVRQAP
 GKLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 122

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGGTACGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCGGTGGGGTCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCAACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGAAAGCGCCCTTGACCTTGTCAGGCTTCAAGCCGAAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGGTGTTGGTGGAGGACCAAACTGACCGTATTGGGGGATCATTTACGCGCCAAAGCTAGAGTCGTGG
 GAGGTGGATCAGAGGTCCAGTTGGTCGAGAGCGGGGGGTCTGGTCCAAACAGGGGTAGTCTCAAGCTTTCATGCGCCGCAT
 CCGGATTCACCTTCAGTGGTACGCAATGAATTGGGTAGACAGGCACCAAGGTAAAGGGTTGGAATGGTGGCACGCAATTAGGT
 CCAAGGCCAACAGCTACGCCACCGAGTACGCGCCAGCGTAAAGACCGGATTTACGATAAGCCGGGATGATTTCTAAGAAACACTG
 CTTATTTGCAGATGAATAATTGAAGACCGAGGATACTGCTGTCTATTATTGCGTCCGCCACGGTAATGCTGGTAACTCTGCCATT
 AGCTATTGGGCGTATTGGGGCAGGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGGCAGTGGCGCGGGTTCAGAGGTTCAA
 CTTGTGAGTCTGGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTTTGCGCTGCTCCGGGTTCACGTTCTCAAGTT
 TGGGATGCTTTGGGTAGGCAAGCCAGGTAAGGACTCGAATGGGTACGACGATCTCAGGCTCCGGCAGAGACACGTTGTA
 TGCCGAAAGTGTCAAAGGAGGTTCAATCTCTCGGGACAATGCAAAACCACTTGTATCTCCAATGAACCTACTCCGGCCT
 GAGGACACAGCAGTTTACTACTGTACGATAGGAGGGTCCCTTAGCGTATCTTCTCAGGGAACCTTTGGTAACGGTCAGCTCCCACC
 ACCATCATCATCAC SEQ ID NO: 123

FIG. 54AR

Pro45 (Thb) - aEGFR G8 sdAb - aCD3 Vh (2B2) - ~~SSQGMPRSRFGGS~~ - aCD3Vh¹⁰² - aHSA (10GE) - His6
 EVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKEREFVVAINWSSGTYADSVKGRFTISRDNAKNTMYLQMNSL
 KPEDTAVYYCAAGYQINSGNYNFKDYEDYDWGQGTQVTVSSGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW
 VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNILKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLV
 TVSS~~SSQGMPRSRFGGS~~QTVVTQEPSLTVSPGGTVILTCGSSTGAVTSGHYPNWVQQPKPQAPRGLIGGTSNKHSWTPARFSGSL
 GGKAAALTLSGVQPEDEAEYCYVLWGSRRWVFGGKLTVLGGSGGGSEVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWV
 RQAPGKGLEWVSSISGSGRDTILYAESVKGRFTISRDNAKTTLYLQMNSLRPDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH
 SEQ ID NO: 124

GAA GTTCAA ACTGGTTGAATCCGGTGGTGGCCCTTGTCAGGGGGAGGCTCCCTTCGACTGTCTTGTCGCCAGCGGTGCGACAT
 TCAGCAGTTATGCCATGGGATGGTTCGGCAGGCCCTGGTAAAGAGCGGGAGTTCGTCGTTGCGATCAATTGGAGTAGCGGTTC
 CACGTATTATGCGGATCTGTAAAGGCGAGGTTCACATATCTACGCGATAATGCAAAAATACCATGTATCTTCAGATGAACCTCA
 CTGAAGCCCGAGGACACGGCAGTTTATTACTGTGCTGCCGGTTACCAAGATCAATTCGGAAATTACAATTCAGGACTACGAGT
 ACGATTATTGGGTCAAGGCAACCAAGGTAAACCGTCAAGCAGCGGGAGCGGATCAAGGAGCGGTTCAGAGGTTCAGCTCGTTG
 AGAGTGGTGGAGGCTGGTTCAGCCAGGGGAAGTTTGAAGCTTCTGTGCGGCTCTGTGTTTCACTTTAAACAATAACGCTAT
 CAACTGGGTACGACAAGCCCCGGTAAAGGGCTTGAATGGGTGCAAGAATAACGAGTAAATACAATAATTATGCGACTTATTA
 TGCCGATCAAGTAAAGGACCGCTTACTATCTCTCGAGATGACTCAAAGAATACAGCATATCTGCAAAATGAACAATTGAA AAC
 AGAAGACACGGCAGTTTATTACTGCTTAGGCACGCTAATTCGGTAATTCATACATATCATATTGGCCCTACTGGGCCAAGGG
 ACTTTGGTCACAGTATCCTCCAGCTCAGGGGTGGTATGCTCTTTCAGGGGGCGGATCCAGACTGTGGTAACACAGG
 AACCATCTTTGACAGTAAGTCTGGAGGTACGGTCAAGCTCACTGTGGGTCTCAACCGGGCTGTAAACGTCAGGCCATTACCC
 TAACTGGGTCCAACAGAACCTGGACAAGCTCCAAGGGTCTGATAGCGGAACCTCAACAAGCACTCTTGACTCCAGCGCG
 CTTTAGCGGTTCCCTTCTGGGTGAAAAGCAGCCCTCACTCTGAGTGGAGTAAACCCGAGGATGAGCGGGAATAATTATTCGTG
 CTCTGGGGTTCACGCCGCTGGTCTTCTGGTGGGTACGAAACTTACTGTACTGGGGGAGCGGCTCAGCGGGGATCAGAA
 GTGCAGCTTGTGTAATCTGGCGGAGGTCTGTGTCAGCCAGGTAAACAGTTGAGACTGTCTGTGTCGCAAGCGGCTTACCTTCT
 CTAATTCGGTATGAGTTGGTTCGGCAAGCCCCCTGGAAGGGTTGGAAATGGGTATCAAGCATTAAGTGGTCTGGCGGAGATAC
 ACTCTATGCCGAATCAGTGAAGGGCCGCTTACCATTAGTAGGATAACGCTAAACTACTCTGTATCTGCAAAATGAATAGTCTG
 AGACCAGAAGATACTGCCGTTTACTACTGCAATAGGGGATCTCTGAGCGTTTCACTCAAGGTACACTTGTGACTGTTAGCA
 GTCATCATCATCATCACCCAC SEQ ID NO: 125

FIG. 54AS

Pro46 (Thb) - aEGFR D12 sdAb - aCD3V1 (2B2) - ~~SSGGCMPRSRFGGGS~~ - aCD3Vh~~1011~~ - aHSA (10GE) - His6
 QVKLEESGGGSVQTGSLRLTCAASGRTSRSGMGWFRQAPGKEREFVSGISWRGDSGTGYADSVKGRFTISRDNAKNTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDWGQGTQVTVSSGGGSGGGSQTIVTQEPSLTVSPGTVTLTCASTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGTKFLVPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL~~SSGGCMPRSRFGGGS~~EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFSGYAMNWWVRQAPGKLEWVARIRSKANSYATEYAAASVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHGNAGNSAISYWAYWQGTGLVTVSSGGGSGGGSQVQVLESQGLVQPGNSLRSLSCAASGFTFSKFGMSWVVRQAP
 GKLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTGLVTVSSH~~HHHH~~
 SEQ ID NO: 126

CAAGTCAAACTTGAGGAAAGCGGGGAGGTAGCGTACAGACTGGTGGATCTCTGAGGTTGACTTGCGCCGCCAGTGCGCCGAACA
 TCCAGAAGTTACGGGATGGTTGTTTCGACAGGCTCCGGGAAAGAGCGGGAGTTTGTATCTGGCATAAGCTGGAGGGCGGAC
 TCCACTGGTTACGCAGATTCCGTCAAAGGGCGGTTACGATCTCTCGGATAACGCGAAGATAACCGTTGATCTCCAATGAAC
 CTCTAAACCCGAGGATACAGCAATATACTATTGCCCGCGCTCGGGGTACGCTGGTATGGCACATTGTACGAATATGACTA
 TTGGGTCAAAGGTACCCAAAGTAACGGTCAAGTTCGGTGGTGGGTCTGGTGGTGGATCCCAAACAGTTGTTACTCAGGAGCC
 ATCCTTGACAGTATCCCCGGTGGAACGGTGACCTGACATGCGCTTCAAGTACAGGTGCTGTAACTCAGGTAACTACCCGAAT
 TGGGTGCAGCAAAACCTGGACAAGCACCCGGGGTCTTATCGGGGGGACGAAAGTTCTTGGTACCGGTACCCCTGCGCGCTTC
 AGCGGAAGTCTTCTGGGTGGAAGAGCCCTTGACCTTGTCAGGCTTACGCCGAAGATGAGGCCGAATATTATGCAAGCTGT
 GGTATTCTAACCGTGGGTCTTCGGAGGGGTACCAAGCTGACGGTGTGTCTATCTGGCGGAGGTATGCCAAGGAGCTTTCGCGG
 TGGAGGCTCAGAAGTACAACCTTGTAAGAAAGCGGGGGGTCTGGTCCAGCCAGGCGGAAGCCTCAAGCTTTCATGCGCCGCATC
 CGGATTCACCTTCAGTGGGTACGCAATGAATTGGGTAGACAGGCACCAAGGTAAAGGTTGGAATGGGTGGCACCGCATTAGGTC
 CAAGGCCAACAGCTACGCCACCGAGTACGCGCCAGCGTAAAGACCGGATTAACGATAAGCCGGGATGATCTAAGAACAACCTGC
 TTATTTCAGATGAATAATTTGAAGACCGAGGATACTGCTGTCTATTATTGCTCCGCCACGGTAATGCTGGTAACTCTGCCATTA
 GCTATTGGGCGTATTGGGGCAGGCACTCTGGTCAACCGTCTCATCTGGCGGAGGGGCAAGTGGCGGGGTCAGAGGTTCAAC
 TTGTCGAGTCTGGAGCGGTCTCGTACAACCGGGAATAGTCTCCGACTCTTTGCGCTGCGTCCGGTTCACGTTCTCAAAGTTT
 GGGATGCTTGGGTTAGGCAAGCCCCAGGTAAGGACTCGAATGGGTACAGCATCTCAGGCTCCGGCAGAGACACGTTGTAT
 GCCGAAAGTGTCAAAGGAGGTTTCAATCTCTCGGGACAATGCAAAACCACTTGTATCTCCAATGAACCTCACTCCGGCCT
 GAGGACACAGCAGTTTACTACTGTACGATAGGAGGGTCCCTTAGCGTATCTTCTCAGGGAACCTTTGGTAACGGTCAGCTCCCACC
 ACCATCATCATCAC SEQ ID NO: 127

FIG. 55A

SEQ ID NO. 44	Pro1 - aEGFR G8 sdAb - aCD3 Vh - His10
SEQ ID NO. 46	Pro2 - aCD3 VI - aEGFR D12 sdAb - His10
SEQ ID NO. 48	Pro3 - aEGFR G8 sdAb - aCD3 scFv - aEGFR D12 sdAb - His10
SEQ ID NO. 50	Pro4 - aEGFR G8 sdAb - aCD3 Vh - Flag - aCD3 VI - aEGFR D12 sdAb - His10
SEQ ID NO. 52	Pro5 - aEGFR G8 sdAb - aCD3 Vh - ggggFlaggggs - aCD3 Vli - aCD3Vhi - ggggFlaggggs - aCD3VI - aEGFR D12 sdAb - His6
SEQ ID NO. 54	Pro6 - aEGFR G8 sdAb - aCD3 Vh - ggggFlaggggs - aCD3Vli - His6
SEQ ID NO. 56	Pro7 - aCD3Vhi - ggggFlaggggs - aCD3VI - aEGFR D12 sdAb - His6
SEQ ID NO. 58	Pro8 - aEGFR G8 sdAb - aCD3 Vh - ggggFlaggggs - aCD3VI - His6
SEQ ID NO. 60	Pro8 MS - aEGFR G8 sdAb - aCD3 Vh - GGGLSGR/SDNHGGS - aCD3VI - His6
SEQ ID NO. 62	Pro8 ML - aEGFR G8 sdAb - aCD3 Vh - GGGSGGSLSGR/SDNHGSGSGGS - aCD3VI - His6
SEQ ID NO. 64	Pro9 - aEGFR D12 sdAb - aCD3VI - ggggFlaggggs - aCD3Vhi - His6
SEQ ID NO. 66	Pro10 - aCD3Vli - ggggFlaggggs - aCD3Vh - aEGFR G8 sdAb - His6
SEQ ID NO. 68	Pro11 - aEGFR D12 sdAb - aCD3VI - ggggFlaggggs - aCD3Vh - His6
SEQ ID NO. 70	Pro12 - aCD3Vhi - ggggFlaggggs - aCD3VI - aEGFR G8 sdAb - His6
SEQ ID NO. 72	Pro14 - aEGFR D12 sdAb - aCD3Vh - ggggFlaggggs - aCD3Vli - His6
SEQ ID NO. 74	Pro15 - aEGFR G8 sdAb - hOKT3 Vh - ggggFlaggggs - hOKT3VI - His6
SEQ ID NO. 76	Pro16 - aEGFR G8 sdAb - aCD3 Vh (2B2) - ggggFlaggggs - aCD3Vli - aHSA (10GE) - His6

FIG. 55B

SEQ ID NO. 78	Pro17 – aHSA (10GE) – aCD3Vhi – ggggFlaggggs – aCD3VI (2B2) – aEGFR D12 sdAb – His6
SEQ ID NO. 80	Pro18 – aEGFR G8 sdAb – aCD3VI – ggggFlaggggs – aCD3Vhi – His6
SEQ ID NO. 82	Pro19 – aEGFR D12 sdAb – aCD3VI (2B2) – ggggFlaggggs – aCD3Vhi – aHSA (10GE) – His6
SEQ ID NO. 84	Pro19 CD3+ - aEGFR D12 sdAb – aCD3VI (2B2) – ggggFlaggggs – aCD3Vh – aHSA (10GE) – His6
SEQ ID NO. 86	Pro20 - aEGFR G8 sdAb – aCD3 Vh (2B2) – ggggFlaggggs – aCD3VIIGL – aHSA (10GE) – His6
SEQ ID NO. 88	Pro21 - aEGFR D12 sdAb – aCD3VI (2B2) – ggggFlaggggs – aCD3VhiGL1 – aHSA (10GE) – His6
SEQ ID NO. 90	Pro22 - aEGFR G8 sdAb – aCD3 Vh (2B2) – ggggFlaggggs – aCD3VI (2B2) – aHSA (10GE) – His6
SEQ ID NO. 92	Prodent 23 – Serum Cleavage into two halves aEGFR G8 sdAb – aCD3 Vh (2B2) – ggggFlaggggs – aCD3Vli – aHSA (10GE) – ggggLVPRGSLGgggs- aEGFR D12 sdAb – aCD3VI (2B2) – ggggFlaggggs – aCD3Vhi – aHSA (10GE) – His6
SEQ ID NO. 94	Prodent 24 – Tumor Cleavage into two halves aEGFR G8 sdAb – aCD3 Vh (2B2) – ggggFlaggggs – aCD3Vli – ggggFlaggggs- aEGFR D12 sdAb – aCD3VI (2B2) – ggggFlaggggs – aCD3Vhi – aHSA (10GE) – His6
SEQ ID NO. 96	Pro25 – aGFP sdAb – aCD3 Vh – ggggFlaggggs – aCD3 Vli – H6 (aGFP Pro6)
SEQ ID NO. 98	Pro26 – aCD3 Vhi – ggggFlaggggs – aCD3 VI – aGFP sdAb – H6 (aGFP Pro7)
SEQ ID NO. 100	Pro27 – aGFP sdAb – aCD3 VI – ggggFlaggggs – aCD3 Vhi – H6 (aGFP Pro9)
SEQ ID NO. 102	Pro28 – aCD3 Vli – ggggFlaggggs – aCD3 Vh – aGFP sdAb – H6 (aGFP Pro10)

FIG. 55C

SEQ ID NO. 104	Pro29 - aEGFR D12 sdAb - aCD3VI (2B2) - ggggFlaggggs - aCD3VhiGL2 - aHSA (10GE) - His6
SEQ ID NO. 106	Pro30 - aEGFR D12 sdAb - aCD3VI (2B2) - ggggFlaggggs - aCD3VhiGL3 - aHSA (10GE) - His6
SEQ ID NO. 108	Pro31 - aEGFR D12 sdAb - aCD3VI (2B2) - ggggFlaggggs - aCD3VhiGL4 - aHSA (10GE) - His6
SEQ ID NO. 110	Pro32 - aEGFR D12 sdAb - aCD3VI (2B2) - ggggFlaggggs - aCD3VhiGL5 - aHSA (10GE) - His6
SEQ ID NO. 112	Pro39 (MMP9) - aEGFR G8 sdAb - aCD3 Vh (2B2) - SGGPGPAGMKGLPGS - aCD3VhiGL - aHSA (10GE) - His6
SEQ ID NO. 114	Pro40 (MMP9) - aEGFR D12 sdAb - aCD3VI (2B2) - SGGPGPAGMKGLPGS - aCD3VhiGL4 - aHSA (10GE) - His6
SEQ ID NO. 116	Pro41 (Mep) - aEGFR G8 sdAb - aCD3 Vh (2B2) - SGGGKKLADEPEGGS - aCD3VhiGL - aHSA (10GE) - His6
SEQ ID NO. 118	Pro42 (Mep) - aEGFR D12 sdAb - aCD3VI (2B2) - SGGGKKLADEPEGGS - aCD3VhiGL4 - aHSA (10GE) - His6
SEQ ID NO. 120	Pro43 (ST14#2) - aEGFR G8 sdAb - aCD3 Vh (2B2) - GGSFTRQARVVGGGS - aCD3VhiGL - aHSA (10GE) - His6
SEQ ID NO. 122	Pro44 (ST14#2) - aEGFR D12 sdAb - aCD3VI (2B2) - GGSFTRQARVVGGGS - aCD3VhiGL4 - aHSA (10GE) - His6
SEQ ID NO. 124	Pro45 (Thb) - aEGFR G8 sdAb - aCD3 Vh (2B2) - SSGGMPRFRGGGS - aCD3VhiGL - aHSA (10GE) - His6
SEQ ID NO. 126	Pro46 (Thb) - aEGFR D12 sdAb - aCD3VI (2B2) - SSGGMPRFRGGGS - aCD3VhiGL4 - aHSA (10GE) - His6

FIG. 56A**Positive charged scFv linkers**

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGSGGGGS	15	0	44
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	45
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	46
+B	GKGGSGKGGSGKGGS	15	+3	47
+C	GGKSGGKSGGKGS	15	+3	48
+D	GGKSGGKSGGKGS	15	+3	49
+E	GKGKSGKGKSGKGKS	15	+6	50
+F	GGKSGGKSGKGGS	15	+3	51
+G	GKPGSGKPGSGKPGS	15	+3	52
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	53
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	54

Negative charged scFv linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGSGGGSGGGGS	20	0	55
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	56
-B	GEGSGEGSGEGGS	15	-3	57
-C	GEGSGEGSGEGGS	15	-3	58
-D	GEGSGEGSGEGGS	15	-3	59
-E	GEGSGEGSGEGGS	15	-6	60
-F	GEGSGEGSGEGGS	15	-3	61
-G	GEGSGEGSGEGSGEGGS	20	-8	62

FIG. 56B**scFv Linkers**

GGGGSGGGSGGGGS	(SEQ ID NO:63)
GGGGSGGGSGGGSGGGGS	(SEQ ID NO:64)
GSTSGSGKPGSGEGSTKG	(SEQ ID NO:65)
PRGASKSGSASQTGSAPGS	(SEQ ID NO:66)
GTAAAGAGAAGGAAAGAAG	(SEQ ID NO:67)
GTSGSSGSGGGSGGGG	(SEQ ID NO:68)
GKPGSGKPGSGKPGSGKPGS	(SEQ ID NO:69)