

Figure 1

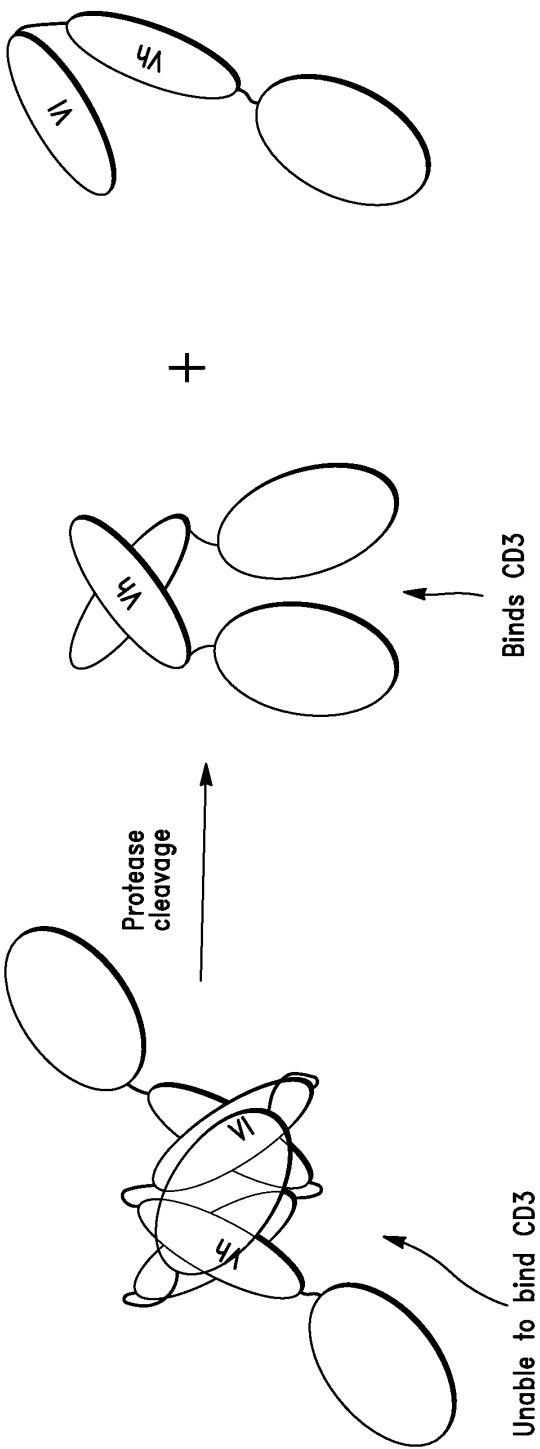
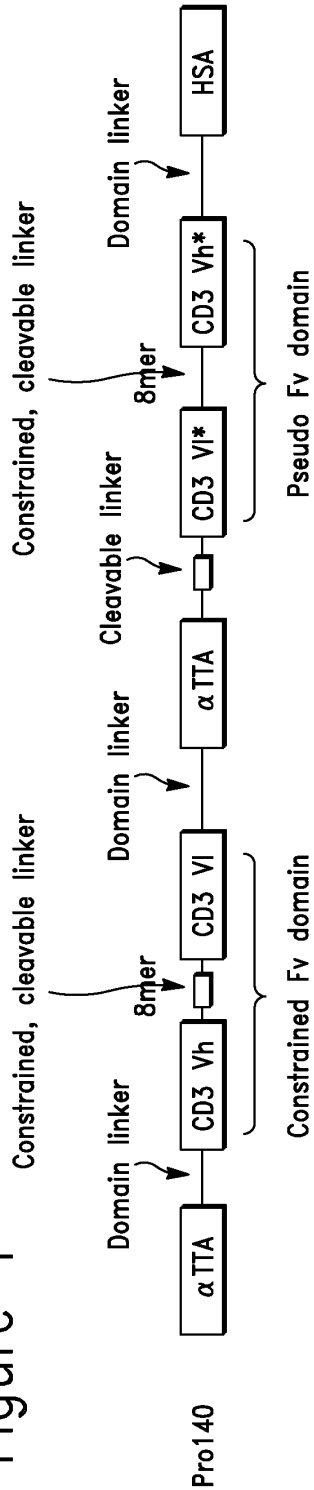


Figure 3A

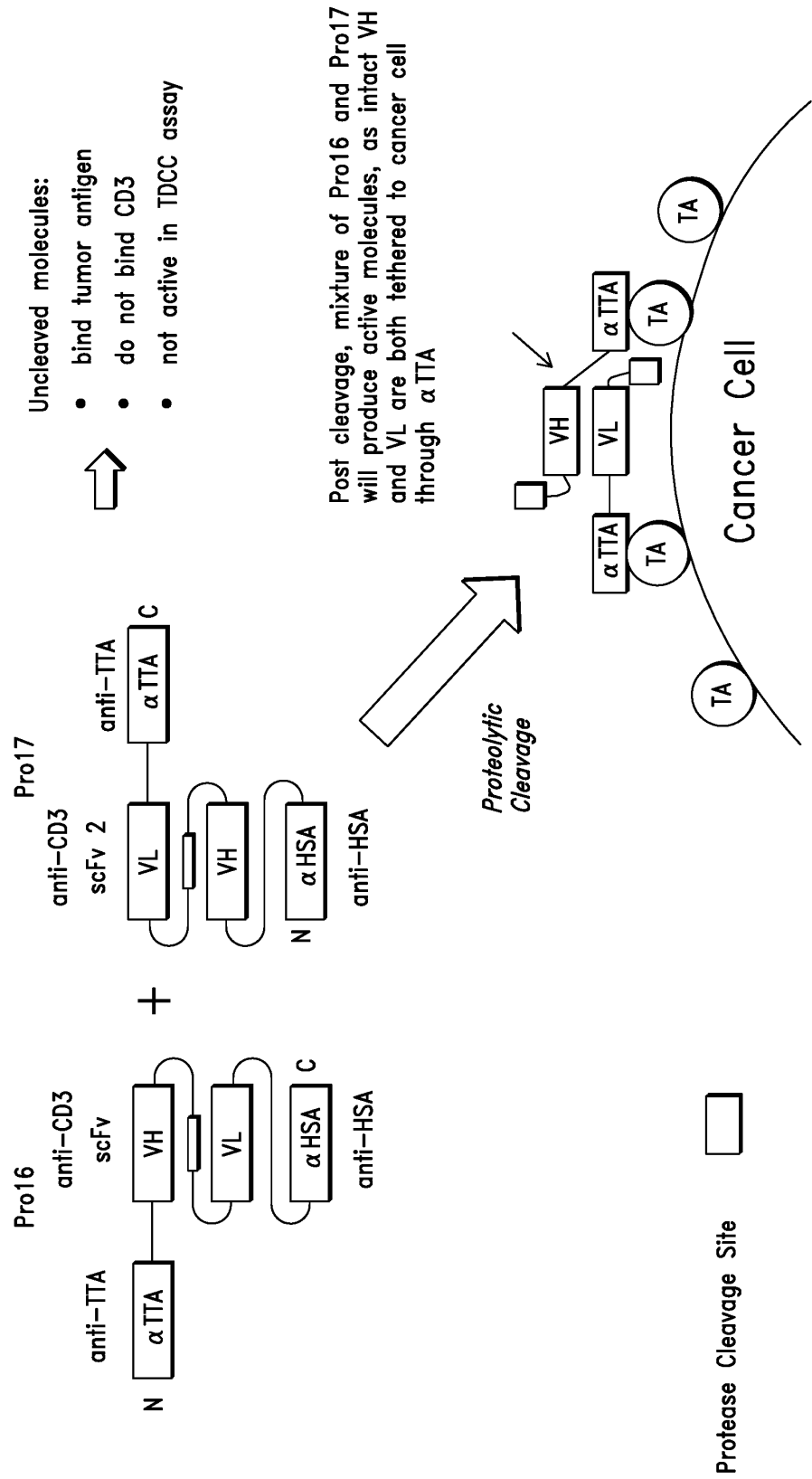


Figure 3B

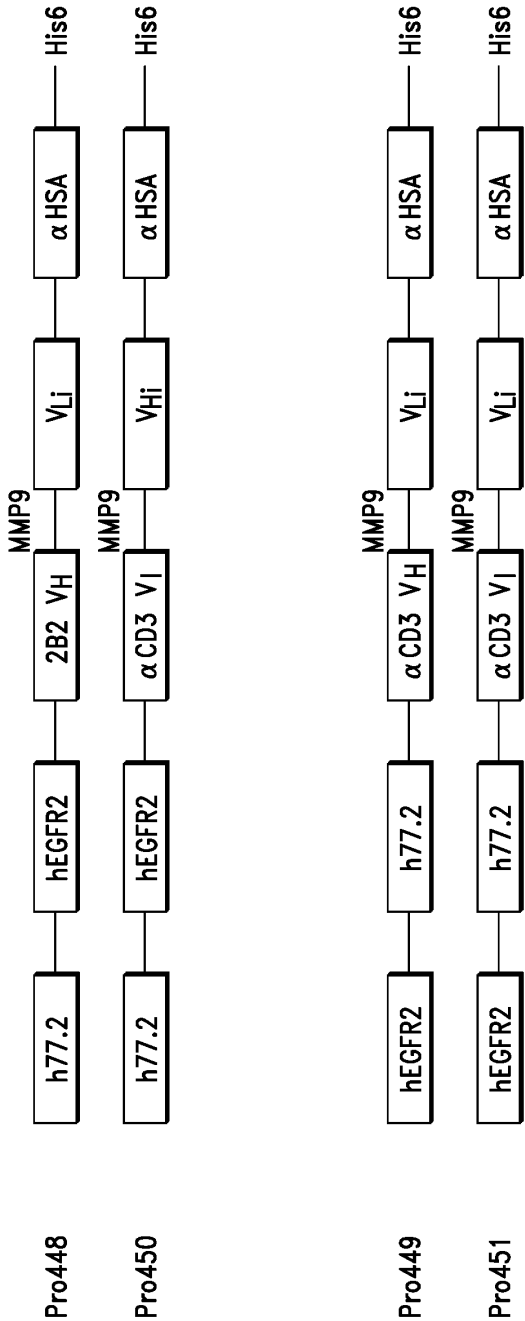


Figure 4

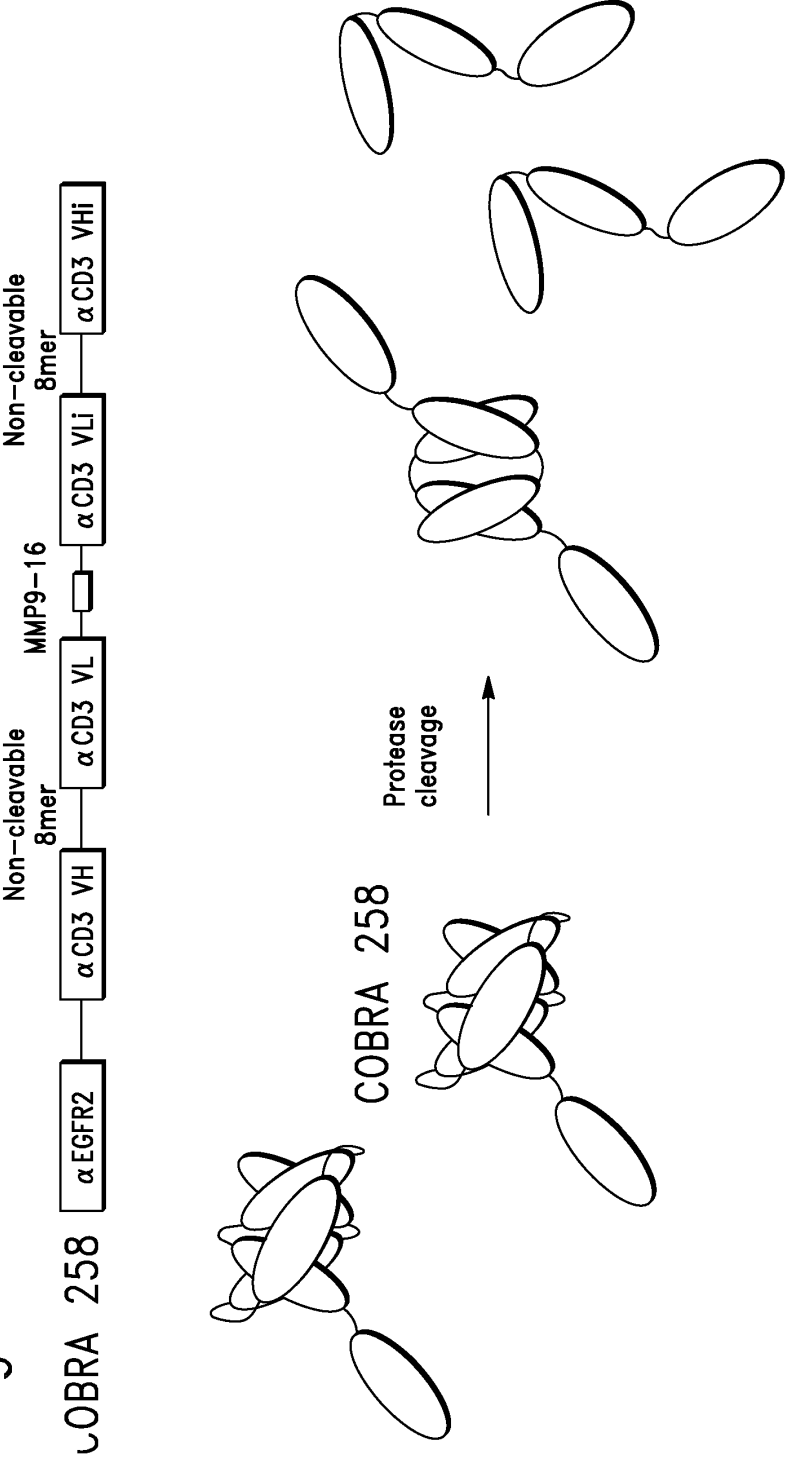


Figure 5A

Targeting sdAbs

α EGFR1

EVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAINWSSGSTYYADS
VKGRRFTISRDNKNTMYLQMNSLKPEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTQVTVS
S (SEQ ID NO:1)

sdCDR1 GRTFSSYAMG (SEQ ID NO:2)

sdCDR2 INWSSGSTYYADSVKG (SEQ ID NO:3)

sdCDR3 GYQINSGNYNFKDYEYDY (SEQ ID NO:4)

α EGFR2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYAD
SVKGRFTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS
(SEQ ID NO:5)

sdCDR1 GRTSRSYGMG (SEQ ID NO:6)

sdCDR2 GISWRGDSTGYADSVKG (SEQ ID NO:7)

sdCDR3 AAGSAWYGTLYEYDY (SEQ ID NO:8)

h α EGFR1

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAINWSSGSTYYADS
VKGRRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTQVTVSS
(SEQ ID NO:9)

sdCDR1 GRTFSSYAMG (SEQ ID NO:10)

sdCDR2 INWSSGSTYYADSVKG (SEQ ID NO:11)

sdCDR3 GYQINSGNYNFKDYEYDY (SEQ ID NO:12)

h α EGFR2

QVKLVESGGGVWRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYAD
SVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS
(SEQ ID NO:13)

sdCDR1 GRTSRSYGMG (SEQ ID NO:14)

sdCDR2 GISWRGDSTGYADSVKG (SEQ ID NO:15)

sdCDR3 AAGSAWYGTLYEYDY (SEQ ID NO:16)

Figure 5B

Targeting sdAbs - Continued

α FOLR1 h77-2

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLLTVSS (SEQ ID NO:17)

sdCDR1 GFTVSNSVMA (SEQ ID NO:18)

sdCDR2 IINSIGITNYADSVKG (SEQ ID NO:19)

sdCDR3 NFDRIY (SEQ ID NO:20)

α FOLR1 h59.3

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTNYADS
VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGTLLTVSS (SEQ ID NO:21)

sdCDR1 GNTFSISAMG (SEQ ID NO:22)

sdCDR2 VTHSDYSTNYADSVKG (SEQ ID NO:23)

sdCDR3 YGIDY (SEQ ID NO:24)

α FOLR1 h22-4

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGTLLTVSS (SEQ ID
NO:25)

sdCDR1 GTTFSRDVMG (SEQ ID NO:26)

sdCDR2 IISRGGSTNYADSVKG (SEQ ID NO:27)

sdCDR3 NTATWGRVFWGQGTLLTVSS (SEQ ID NO:28)

α B7H3 hF7

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYAD
SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGTLLTVSS
(SEQ ID NO:29)

sdCDR1 RRTFHTYHMG (SEQ ID NO:30)

sdCDR2 VINWSGGSTVYADSVKG (SEQ ID NO:31)

sdCDR3 GGATTQRATEASYDY (SEQ ID NO:32)

Figure 5C

Targeting sdAbs - Continued

α B7H3 hF12

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGT LVT VSS (SEQ ID NO:33)

sdCDR1 PRTFSTYSMA (SEQ ID NO:34)

sdCDR2 AINWSGGNTSYADSVKG (SEQ ID NO:35)

sdCDR3 GGVLAHHNYEYDY (SEQ ID NO:36)

α EpCAM h13

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARRITSGDSTVYADSVKGRRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGT LVT VSS (SEQ ID NO:37)

sdCDR1 GTGSIFSINLMG (SEQ ID NO:38)

sdCDR2 RITSGDSTVYADSVKG (SEQ ID NO:39)

sdCDR3 LLRSSPGATTPY (SEQ ID NO:40)

α EpCAM h23

QVQLVESGGGLVQPGGSLTLSCVISGSFSALWAMRWYRQAPGQQRELVASSRGGTTSYADSVKGRRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNAIDGHLAYWGQGT LVT VSS (SEQ ID NO:41)

sdCDR1 GSFSALWAMR (SEQ ID NO:42)

sdCDR2 SSRGGTTSYADSVKG (SEQ ID NO:43)

sdCDR3 IDGHLAY (SEQ ID NO:44)

α HSA half-life extension domain

EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LVT VSS (SEQ ID NO:45)

sdCDR1 GFTFSKFGMS (SEQ ID NO:46)

sdCDR2 SISGSGRDTLYAESVKG (SEQ ID NO:47)

sdCDR3 GGSLSV (SEQ ID NO:48)

EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LVT VSS/HHHHHH (SEQ ID NO:142)

Figure 5D

α CD3 scFv Domains

α CD3 V_L

QTVVTQEPSLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WWQQKPGQAPRGLIG**GTKFLVP**GTPARF
SGSLLGGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL (SEQ ID NO:49)

aVLCDR1 **ASSTGAVTSGNYPN** (SEQ ID NO:50)

aVLsdCDR2 **GTKFLVP** (SEQ ID NO:51)

aVLsdCDR3 **TLWYSNRWV** (SEQ ID NO:52)

α CD3 V_{L1}

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WWQQKPGQAPRGLIG**DYKDDDDK**GTPA
RFGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID NO:53)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:54)

iVLsdCDR2 **DYKDDDDK** (SEQ ID NO:55)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:56)

α CD3 V_{L2}

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WWQQKPGQAPRGLIG**GTKDDAP**GTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID NO:57)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:58)

iVLsdCDR2 **GTKDDAP** (SEQ ID NO:59)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:60)

α CD3 V_H

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WWRQAPGKGLEWVA**RIRSKYNNYATYYA**
DQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTLLTVSS
(SEQ ID NO:61)

aVHCDR1 **GFTFNKYAIN** (SEQ ID NO:62)

aVHsdCDR2 **RIRSKYNNYATYYADQVKD** (SEQ ID NO:63)

aVHsdCDR3 **HANFGNSYISYWAY** (SEQ ID NO:64)

Figure 5E

αCD3 scFv Domains - Continued

αCD3 V_{Hi}

EVQLVESGGGLVQPGGSLKLSKAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDDD**
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTLVTVSS
(SEQ ID NO:65)

iVHsdCDR1 **GFTFNKYAMN** (SEQ ID NO:66)

iVHsdCDR2 **RIRSKYDYKDDDDKADSVKD** (SEQ ID NO:67)

iVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:68)

αCD3 V_{Hi2}

EVQLVESGGGLVQPGGSLKLSKAAS**GFTFNKHAMN**WVRQAPGKGLEWVA**RIRSKYNNYATAY**
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTLVTVSS
(SEQ ID NO:69)

iVHsdCDR1 **GFTFNKHAMN** (SEQ ID NO:70)

iVHsdCDR2 **RIRSKYNNYATAYADSVKD** (SEQ ID NO:71)

iVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:72)

αCD3 scFv linkers

Normal/Non-cleavable

GGGSGGGSGGGGS (SEQ ID NO:73)

Constrained

GGGSGGGGS (SEQ ID NO:74)

Figure 5F

Cleavable Linkers (Recognition site in bold, cleavage site - /)

MMP 2/9

GPAG/MKGL (SEQ ID NO:75)

SGGP**GPAG/MKGL**PGS (SEQ ID NO:76)

SGGGP**GPAG/MKGL**PGGS (SEQ ID NO:77)

Meprin A/B

GGGG**KKLA/DEPE**GGGS (SEQ ID NO:78)

KKLA/DEPE (SEQ ID NO:79)

Meprin A/B (Variant, high efficiency)

GGG**KFLA/DEPE**GG (SEQ ID NO:80)

Cathepsin S, K, L

SGGG**ARLQ/SAAP**GGGS (SEQ ID NO:81)

ARLQ/SAAP (SEQ ID NO:82)

Meprin/Granzyme B

SGGGGVY**ADSLEDG**GGGS (SEQ ID NO:83)

GVYADSLEDG (SEQ ID NO:84)

Matriptase/uPA (MS)

GGGSL**SGR/SDNH**GGGS (SEQ ID NO:85)

GLSGR/SDNHG (SEQ ID NO:86)

Matriptase (MV)

SGGG**SFTR/QARVV**GGGS (SEQ ID NO:87)

SFTR/QARVV (SEQ ID NO:88)

CathepsinS/MMP9/Meprin A

ARLQ/SAAPAG/LKGA (SEQ ID NO:89)

MMP9 (Variant, high efficiency)

GGP**GPAG/MHGL**PG (SEQ ID NO:90)

MMP9 (Variant, low efficiency)

GGP**GPAG/MEGL**PG (SEQ ID NO:91)

Figure 5G

Cleavable Linkers (Recognition site in bold, cleavage site - /)-Continued

Thrombin 1

GGGGLVPR/**GSL**GGGGS (SEQ ID NO:92)

Thrombin 2

SSGG**GM**PR/**SFR**GGGS (SEQ ID NO:93)

Enterokinase/Flag

GGGG**DYKDDDDK**/GGGS (SEQ ID NO:94)

KLK7-6

SGGG**QNPY**/**SAGR**GGGS (SEQ ID NO:95)

KLK7-13

SGGG**QNPY**/**SAGG**GSGG (SEQ ID NO:96)

KLK7-11

SGGG**RNVY**/**SAGG**GSGG (SEQ ID NO:97)

KLK7-10

SGGG**QNTW**/**SAGK**GGGS (SEQ ID NO:98)

uPA

GGGS**HTGR**/**SAYF**GGGS (SEQ ID NO:99)

MMP9-2

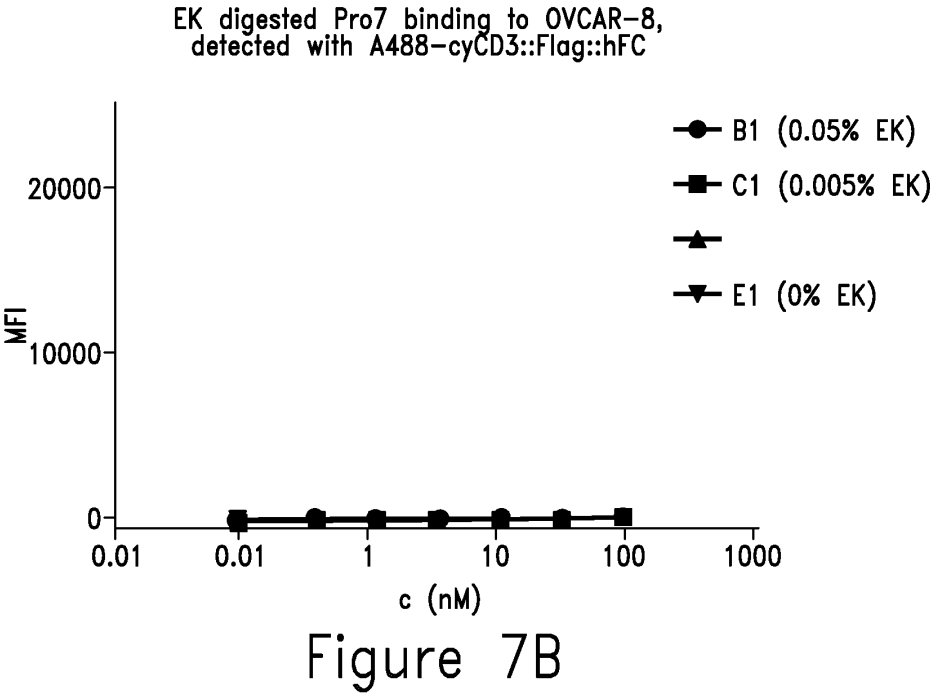
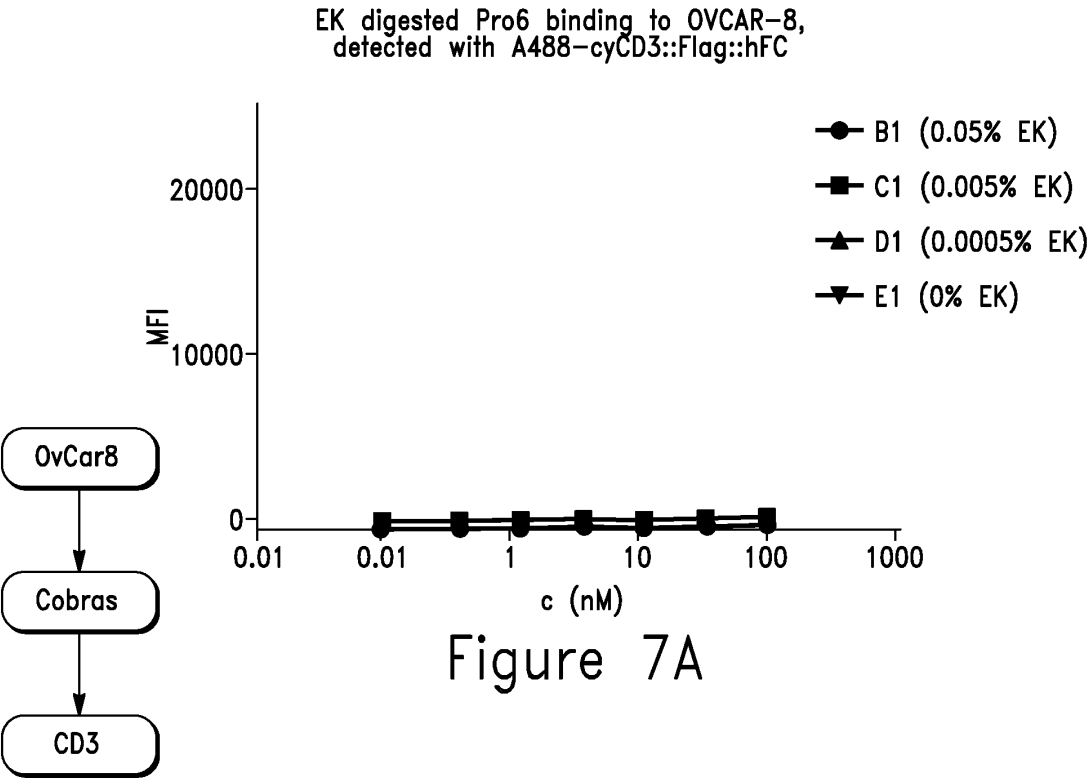
SGGPGPAG/LKGAPGS (SEQ ID NO:184)

Figure 6A

Protease	Cleavage domain sequence	Seq id no:
MMP7	KRALGLPG	100
MMP7	(DE) ₈ RPLALWRS(DR) ₈	101
MMP9	PR(S/T)(L/I)(S/T)	102
MMP9	LEATA	103
MMP11	GGAANLVRGG	104
MMP14	SGRIGFLRTA	105
MMP	PLGLAG	106
MMP	PLGLAX	107
MMP	PLGC(ME)AG	108
MMP	ESPAYYTA	109
MMP	RLQLKL	110
MMP	RLQLKAC	111
MMP2, MMP9, MMP14	EP(CIT)G(HOF)YL	112
Urokinase plasminogen activator (upa)	SGRSA	113
Urokinase plasminogen activator (upa)	DAFK	114
Urokinase plasminogen activator (upa)	GGRR	115
Lysosomal enzyme	GFLG	116
Lysosomal enzyme	ALAL	117
Lysosomal enzyme	FK	118
Cathepsin B	NLL	119
Cathepsin D	PIC(ET)FF	120
Cathepsin K	GGPRGLPG	121
Prostate specific antigen	HSSKLQ	122
Prostate specific antigen	HSSKLQL	123
Prostate specific antigen	HSSKLQEDA	124
Herpes simplex virus protease	LVLASSFGY	125
Hiv protease	GVSQNYPIVG	126
Cmv protease	GVVQASCRLA	127

Figure 6B

Protease	Cleavage domain sequence	Seq id no:
Thrombin	F(PIP)RS	128
Thrombin	DPRSFL	129
Thrombin	PPRSFL	130
Caspase-3	DEVD	131
Caspase-3	DEVDP	132
Caspase-3	KGSGDVEG	133
Interleukin 1 β converting enzyme	GWEHDG	134
Enterokinase	EDDDDKA	135
Fap	KQEQNPGST	136
Kallikrein 2	GKAFRR	137
Plasmin	DAFK	138
Plasmin	DVLK	139
Plasmin	DAFK	140
Top	ALLLALL	141



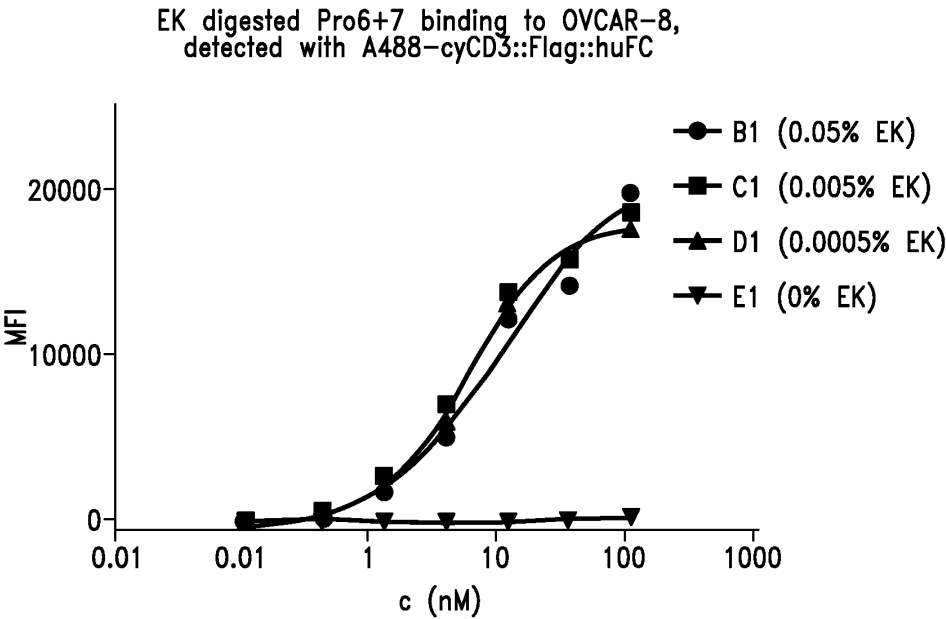


Figure 7C

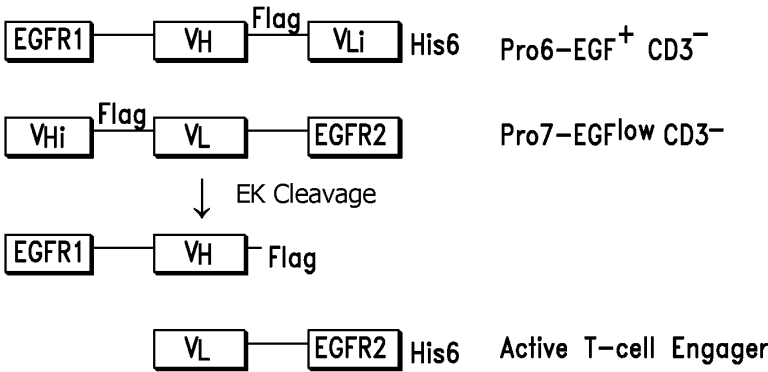


Figure 7D

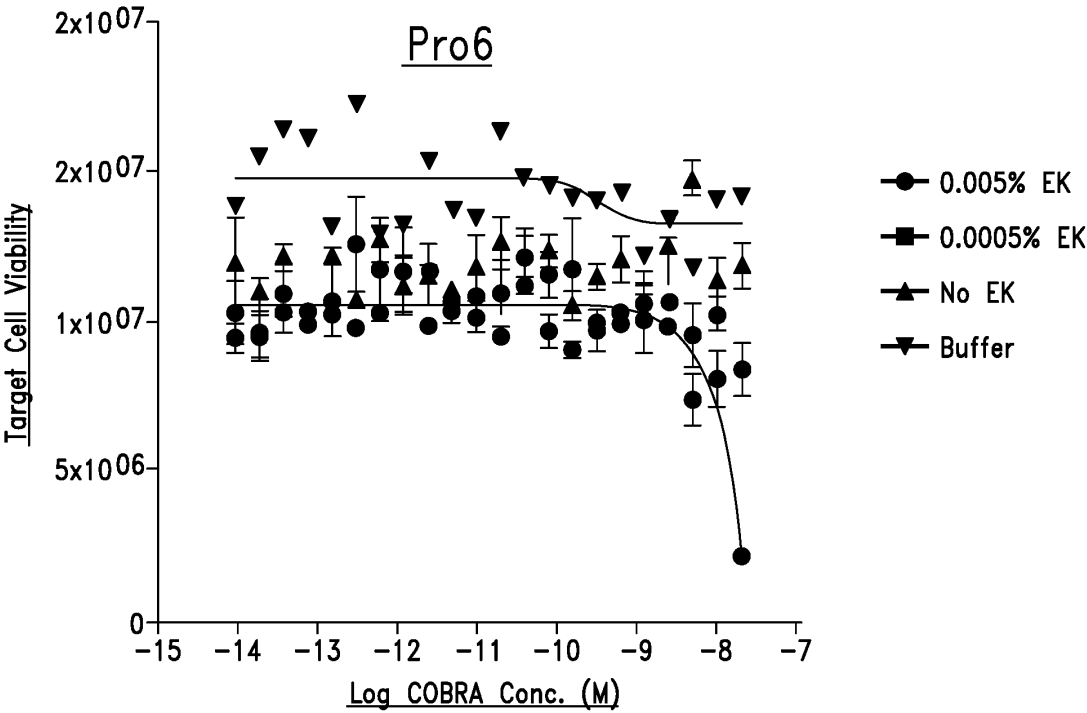


Figure 8A

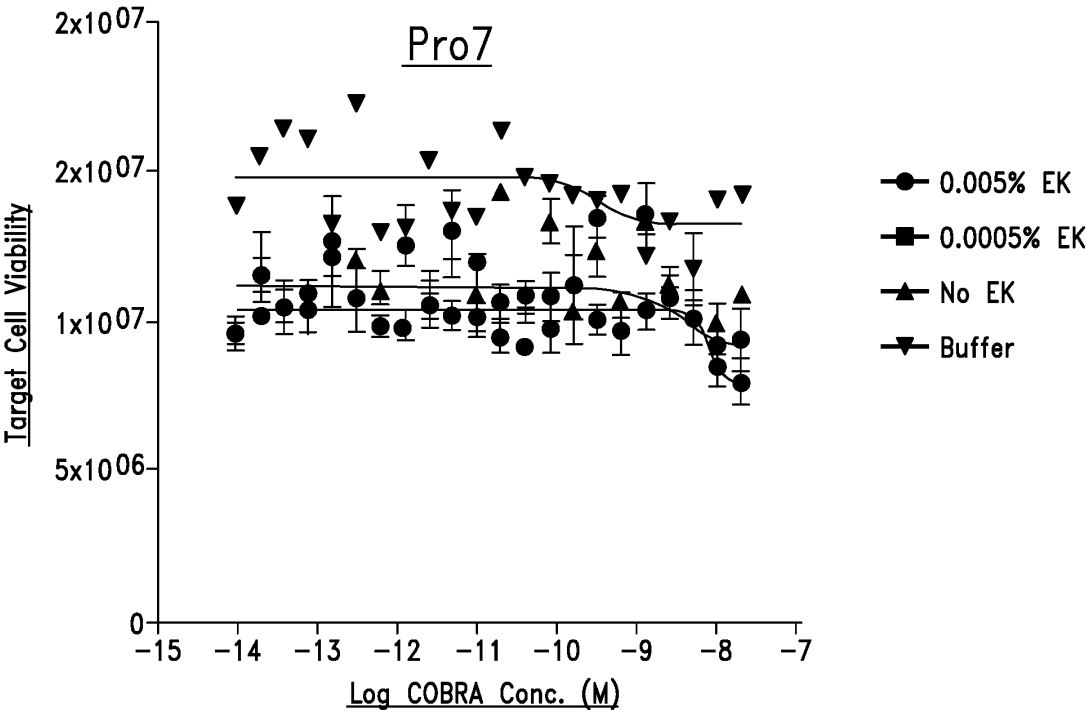


Figure 8B

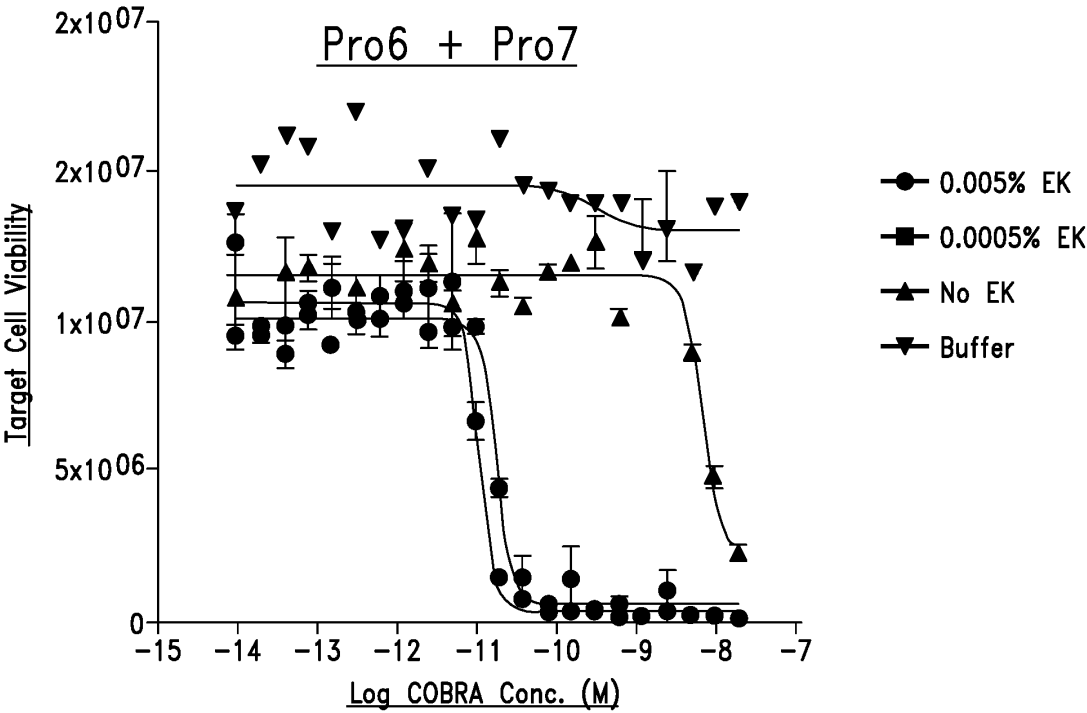


Figure 8C

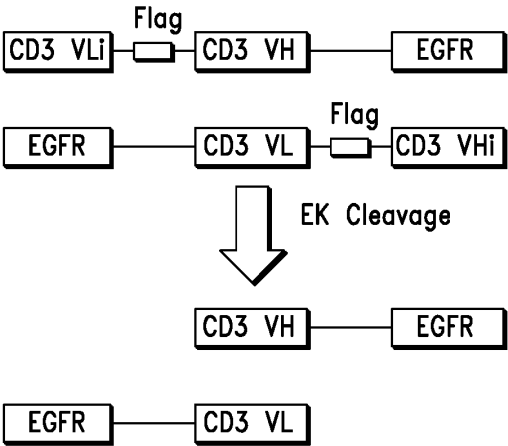
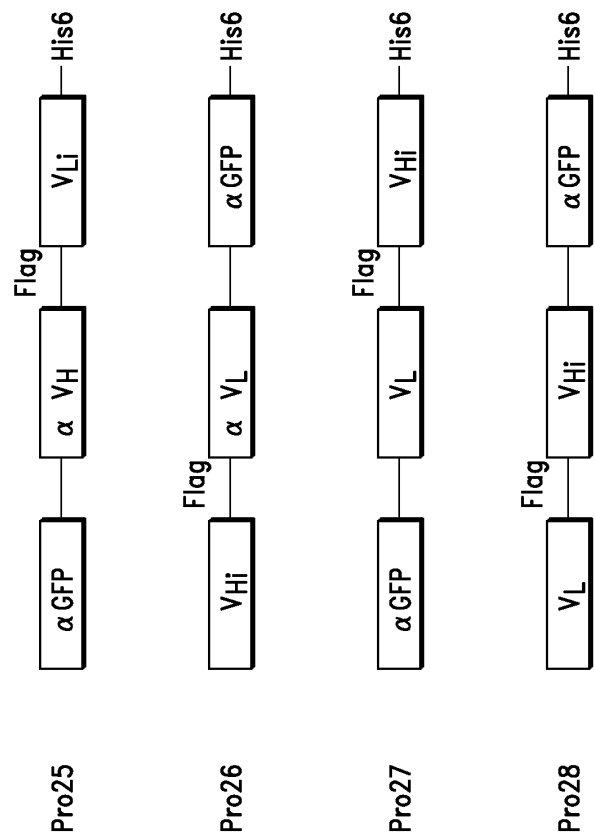


Figure 8D

Figure 9



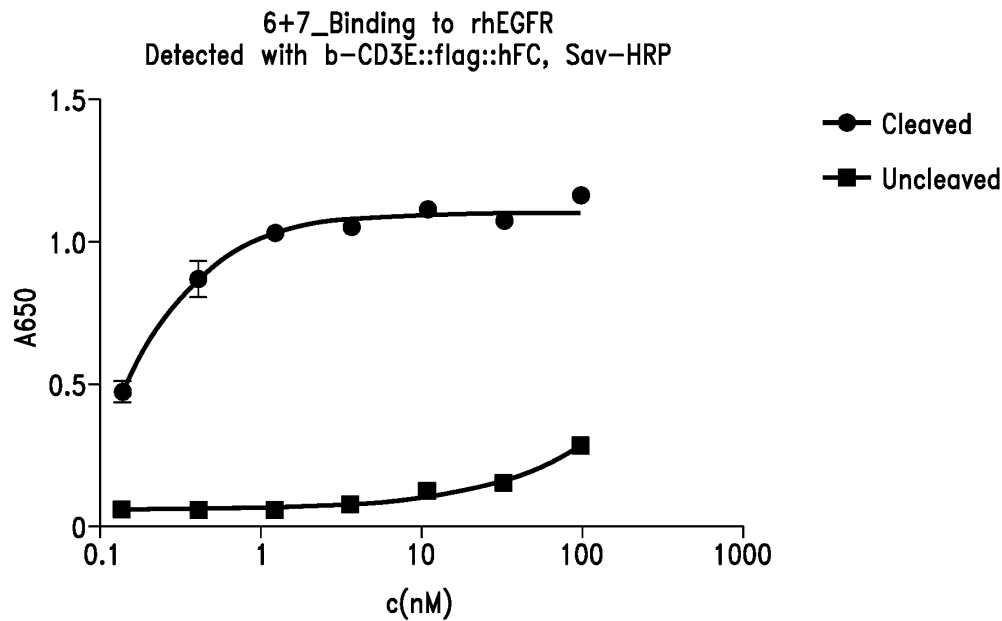


Figure 10A

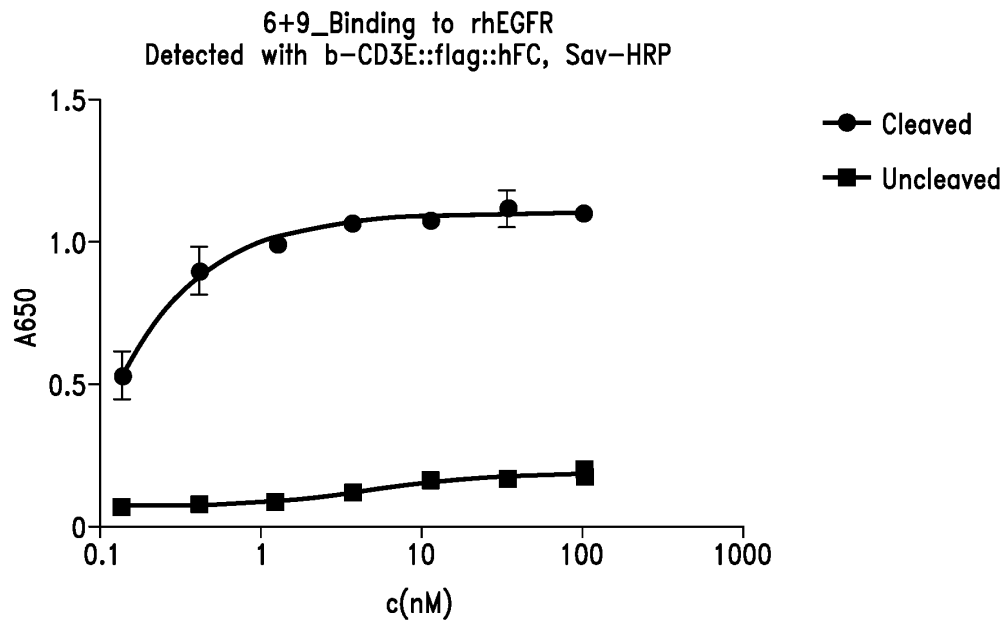


Figure 10B

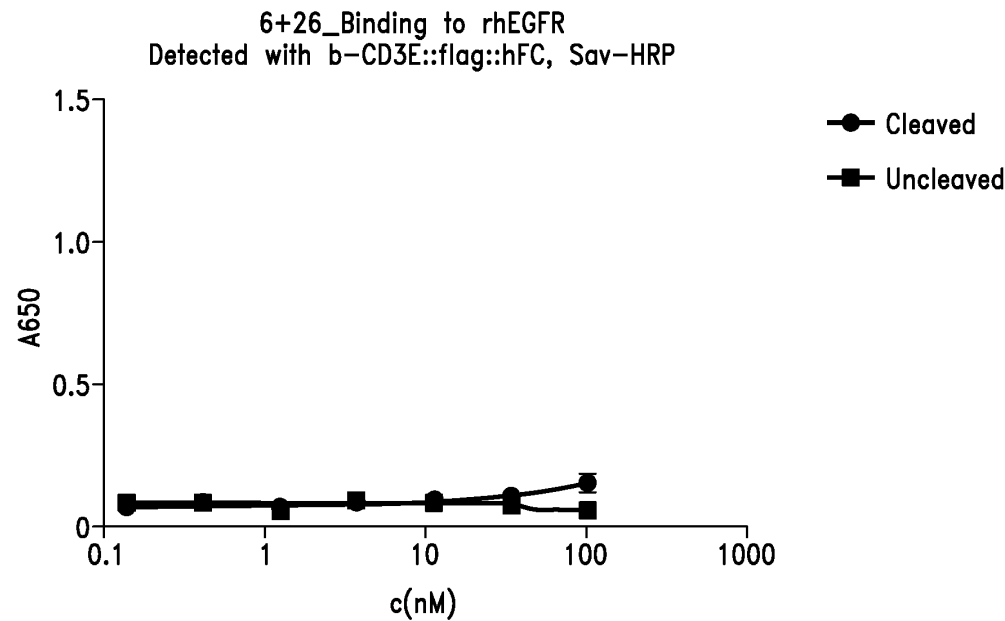


Figure 10C

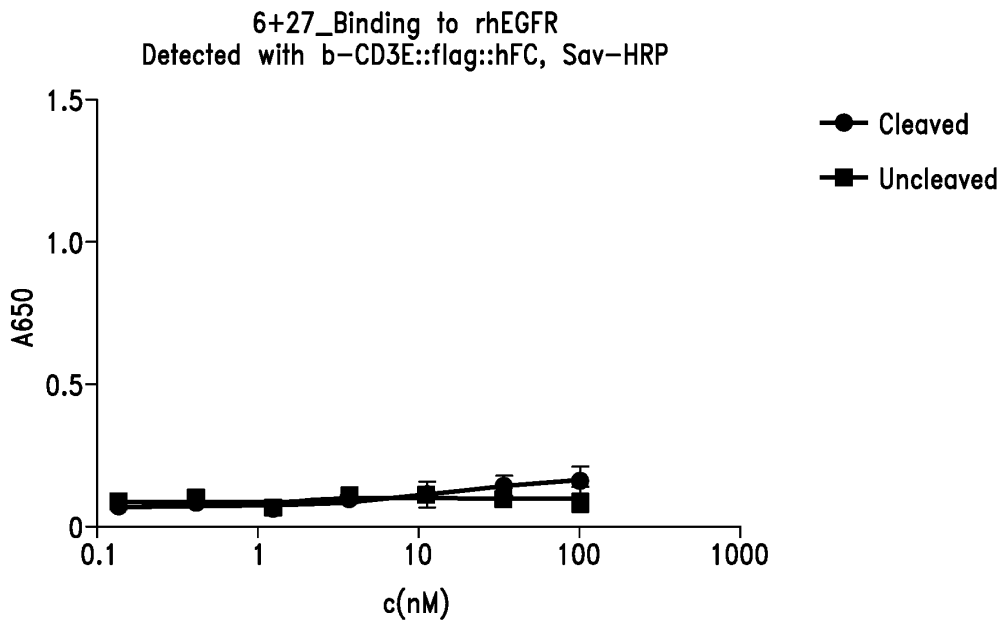


Figure 10D

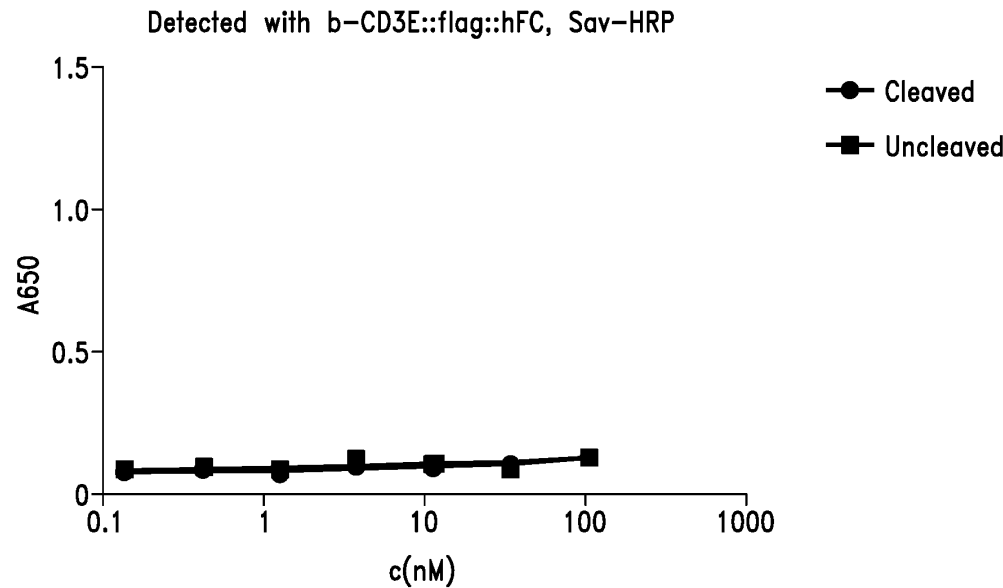


Figure 10E

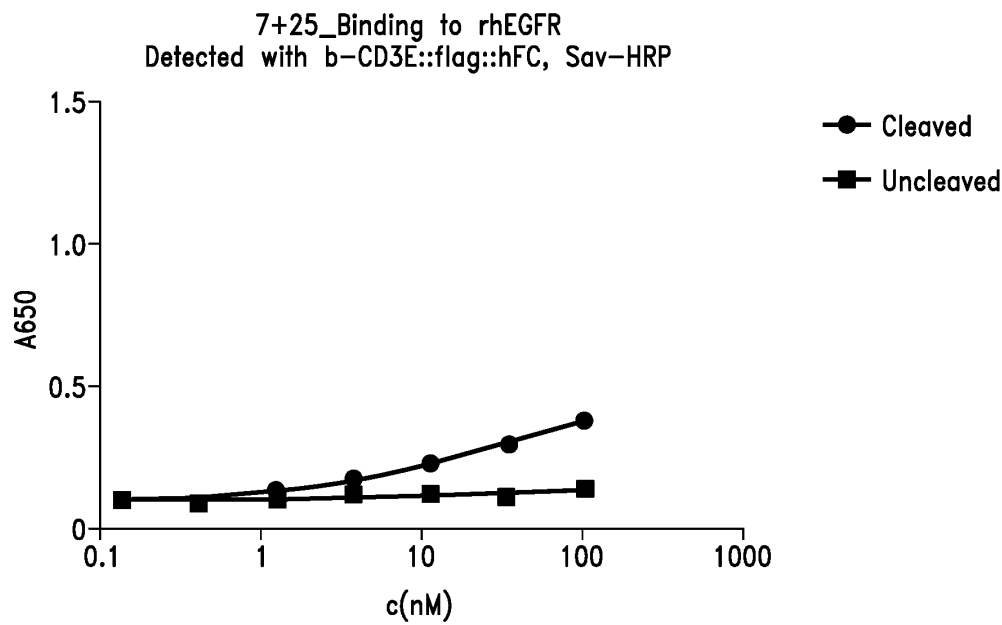
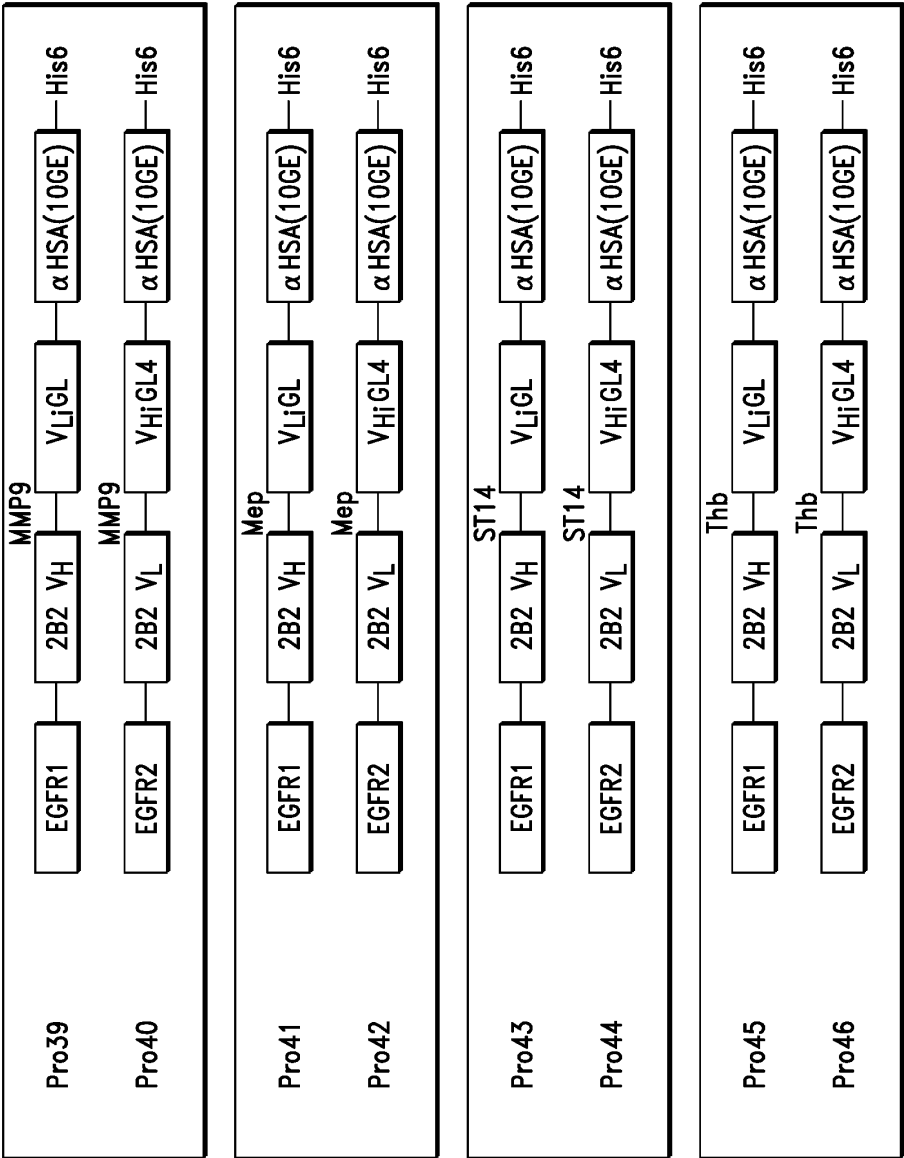


Figure 10F

Figure 11



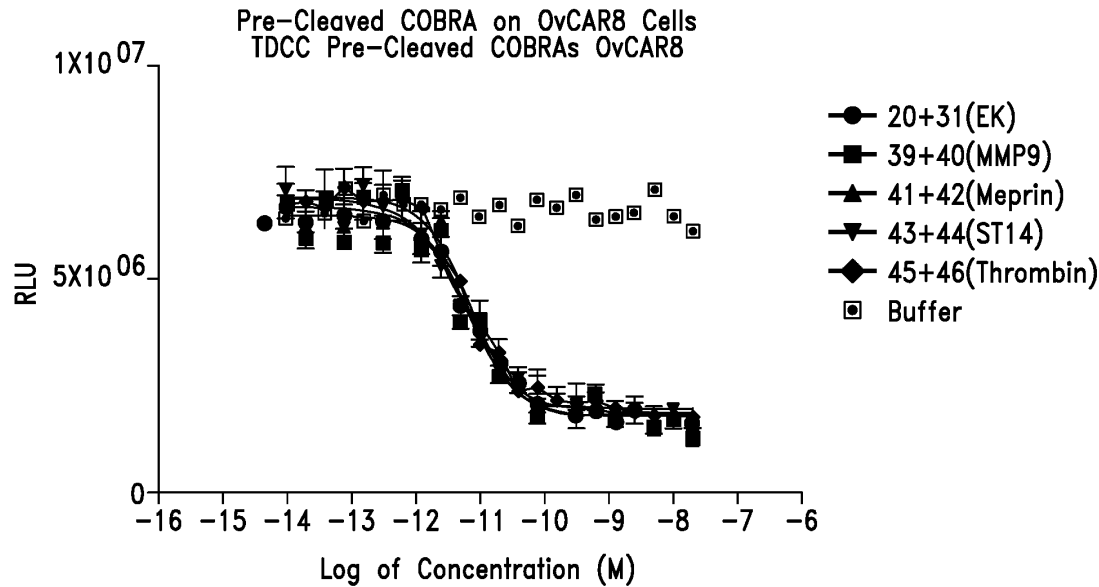


Figure 12A

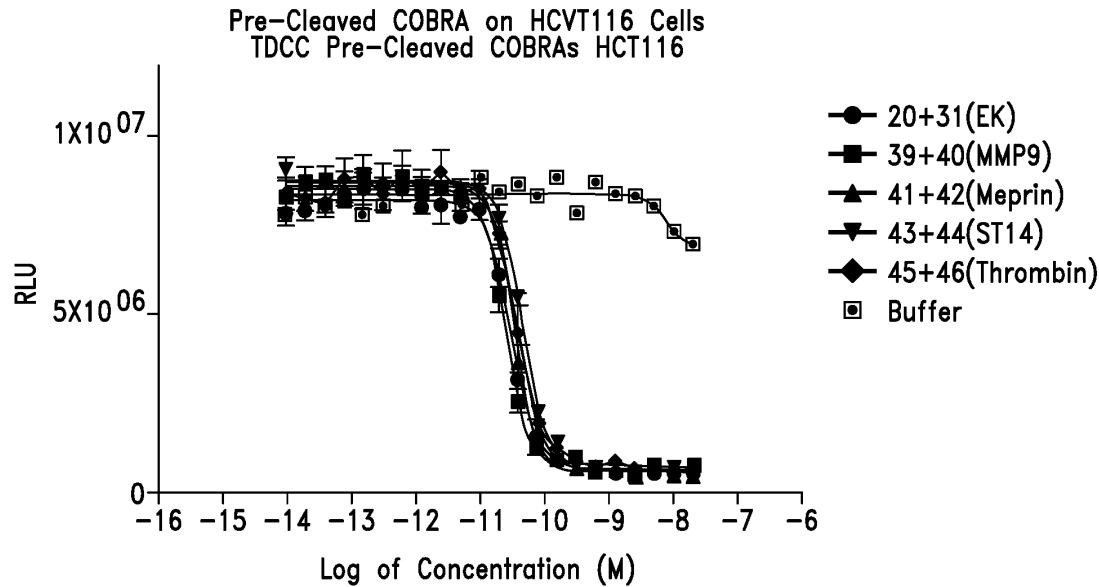


Figure 12B

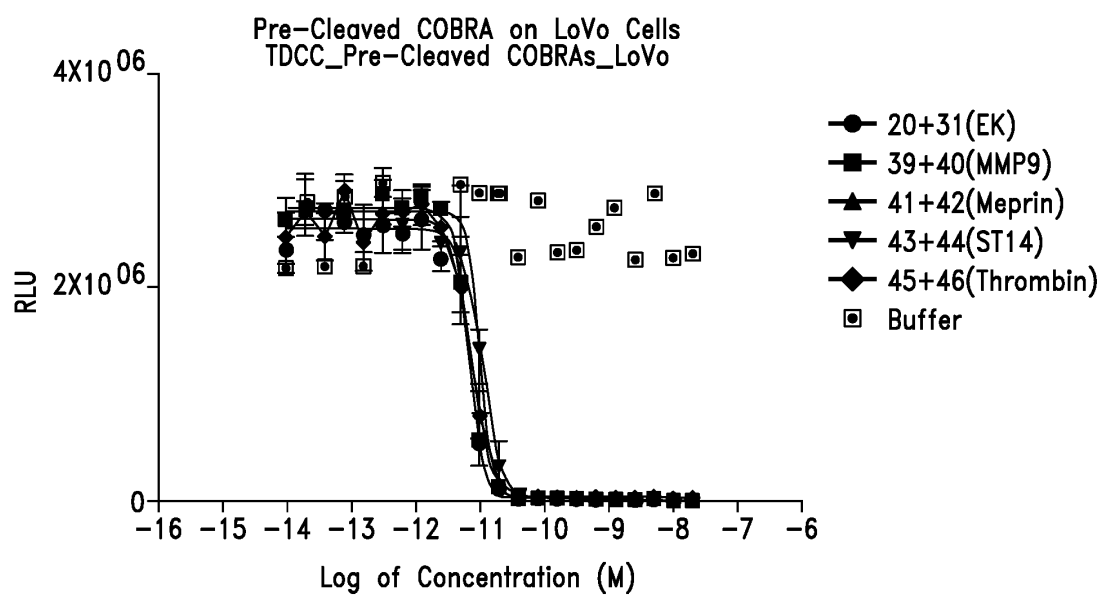


Figure 12C

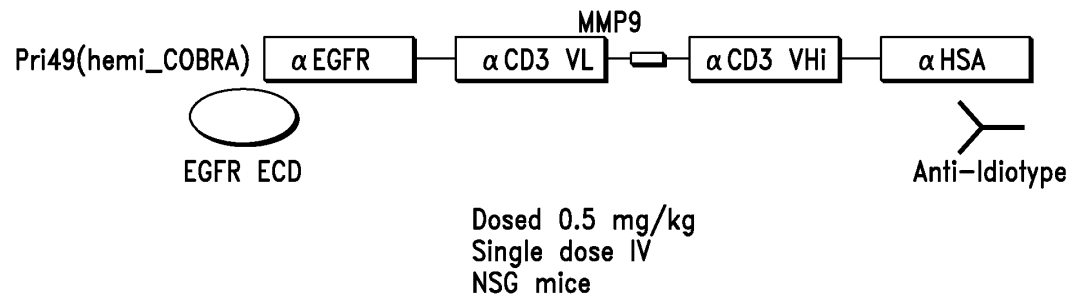


Figure 13A

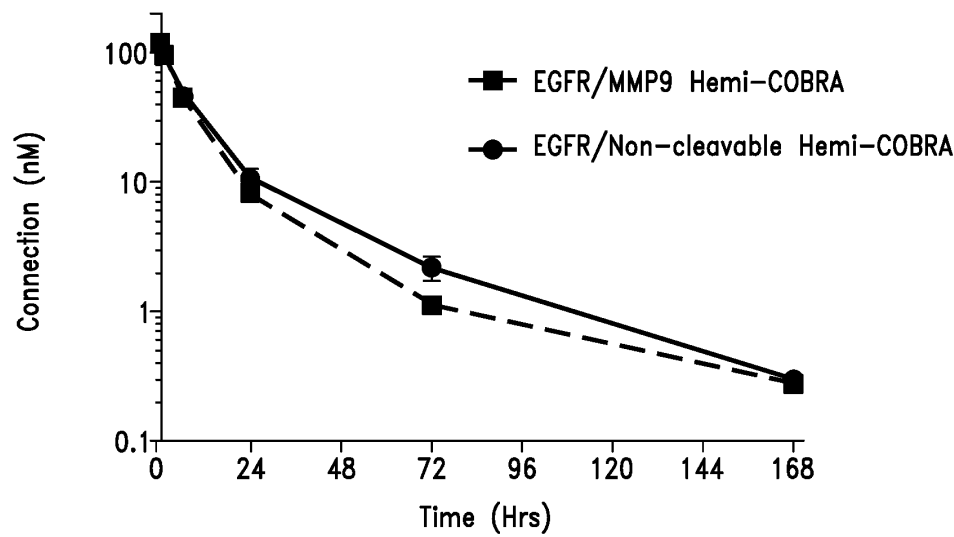


Figure 13B

Figure 14

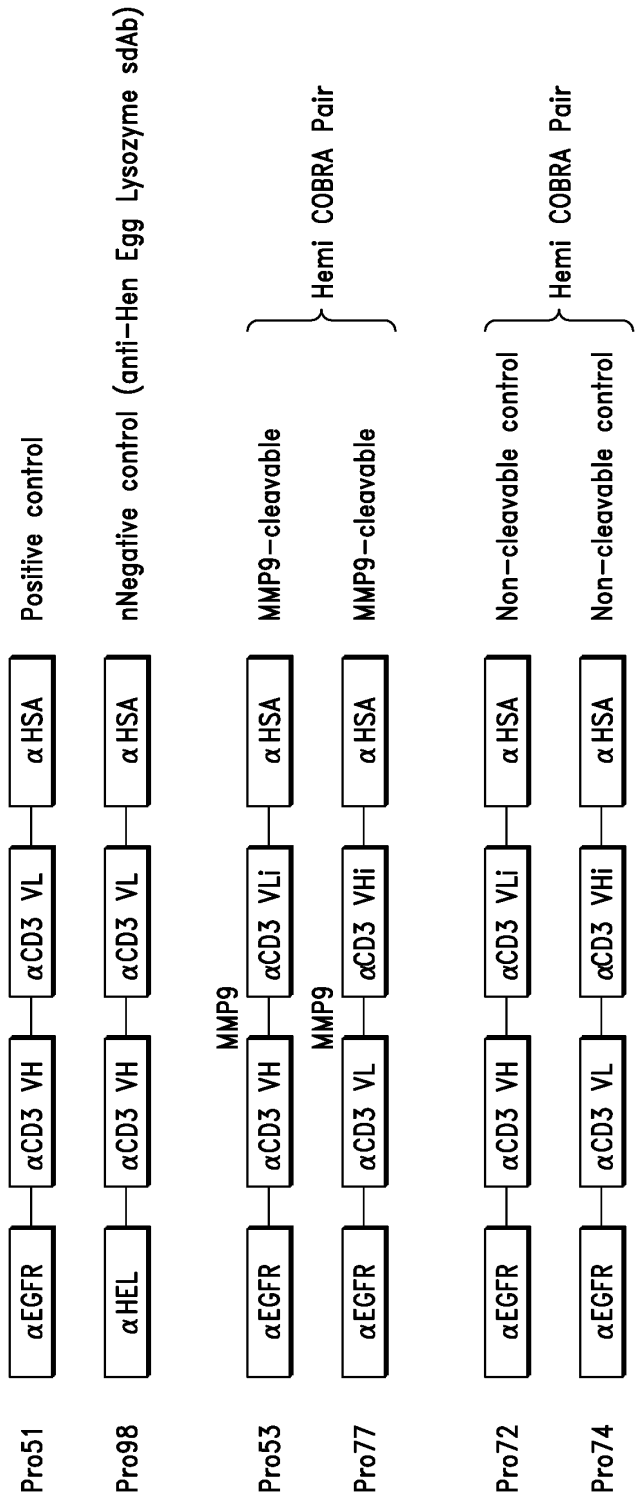


Figure 15

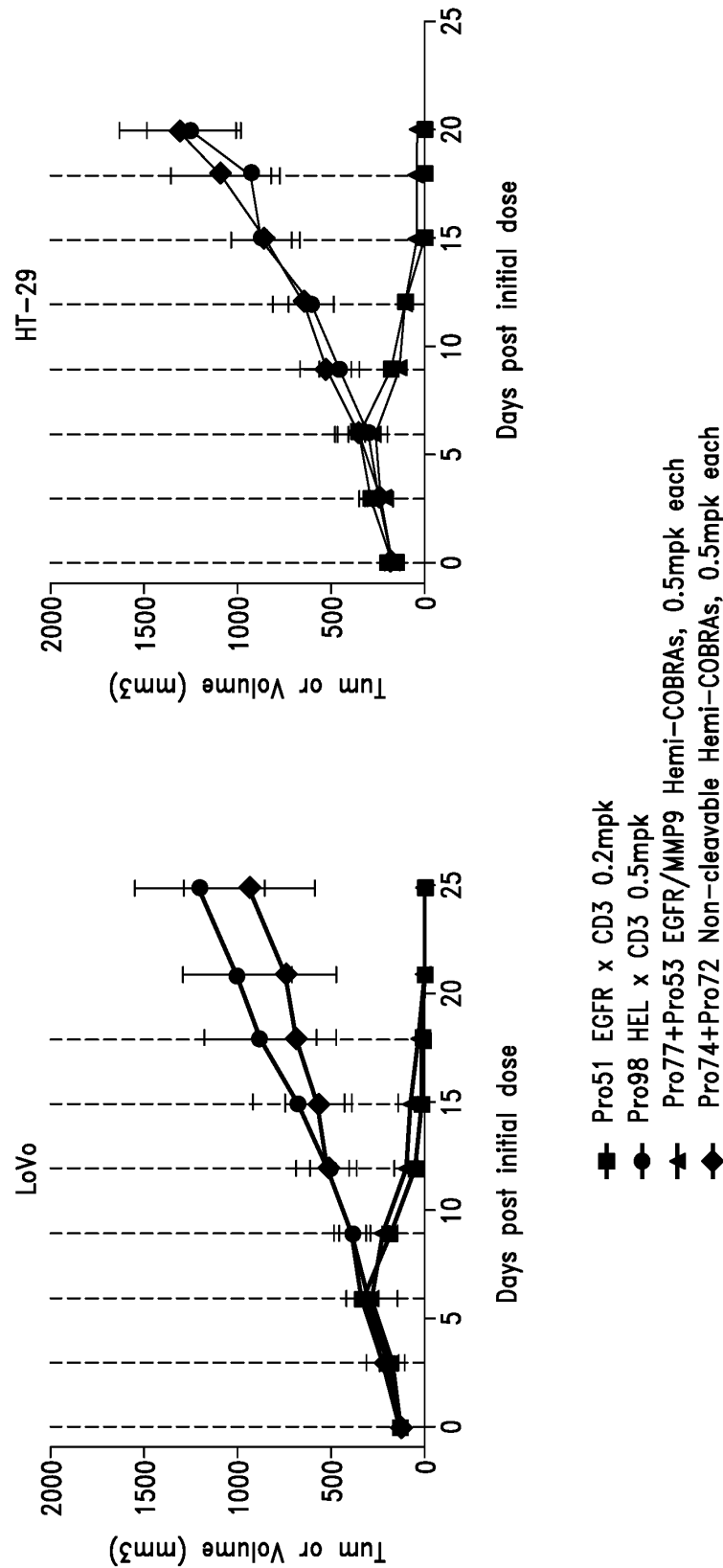


Figure 16

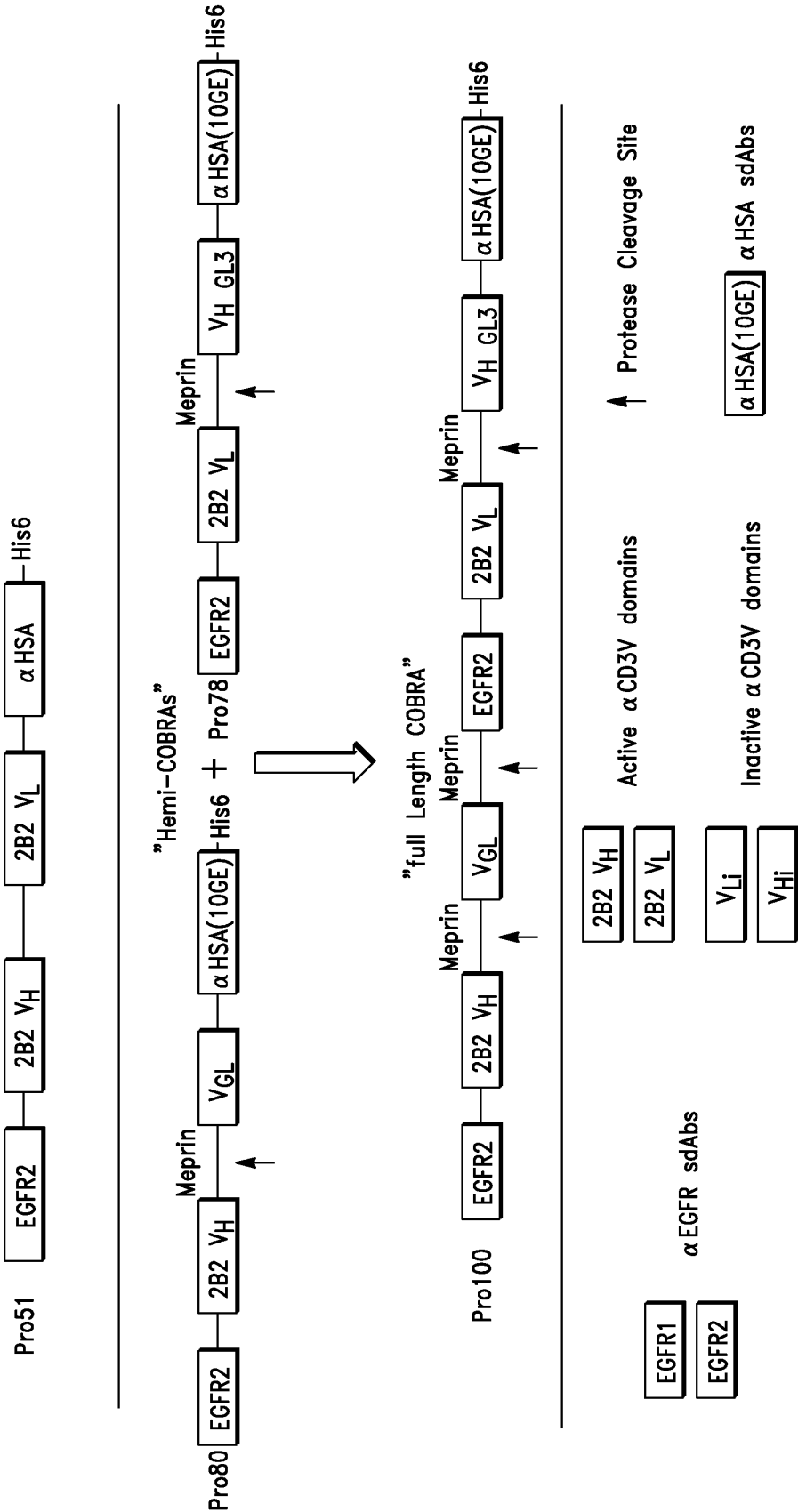


Figure 17

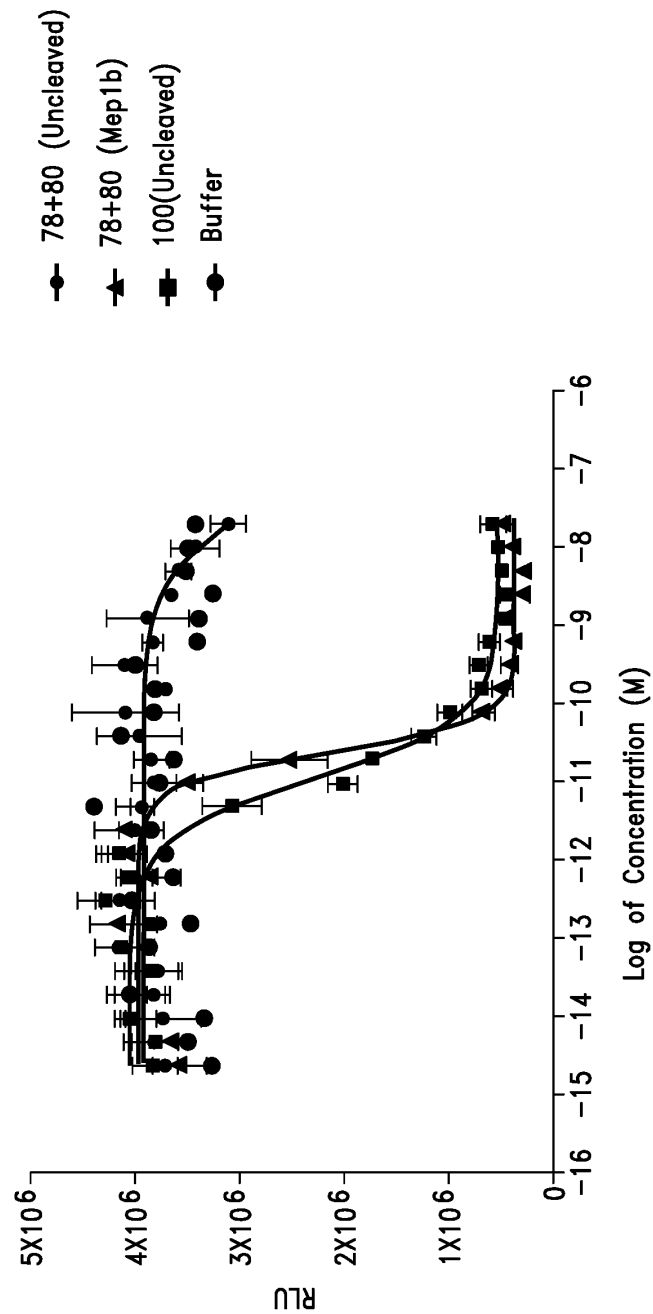


Figure 18

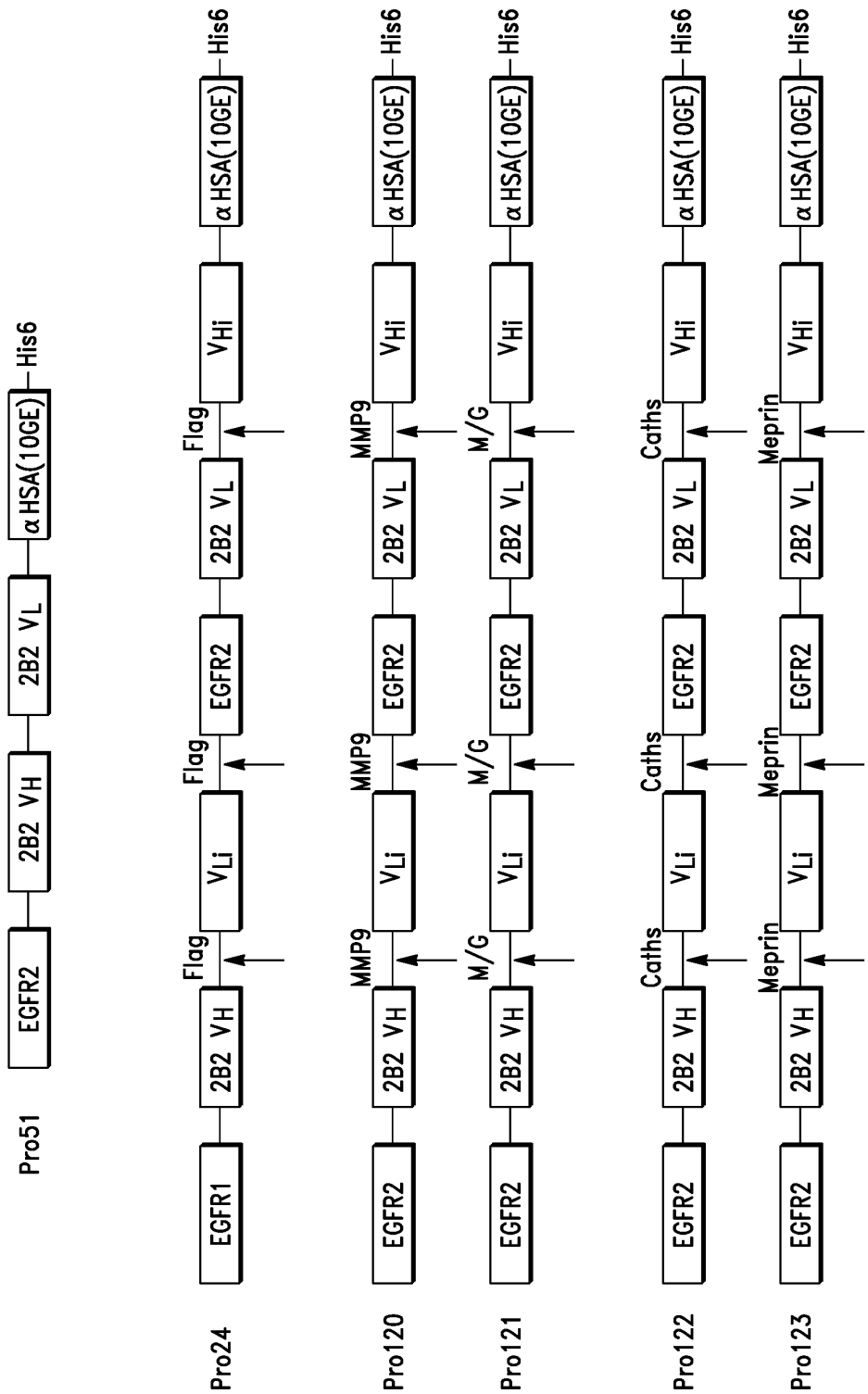
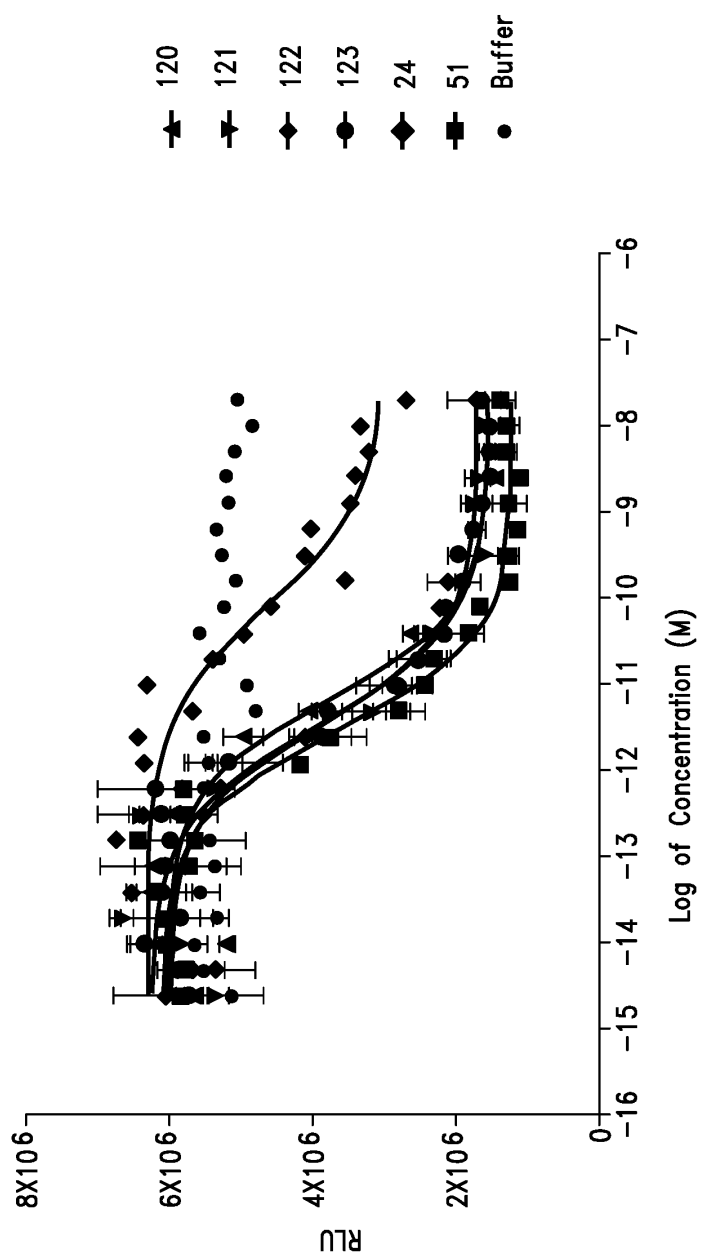


Figure 19



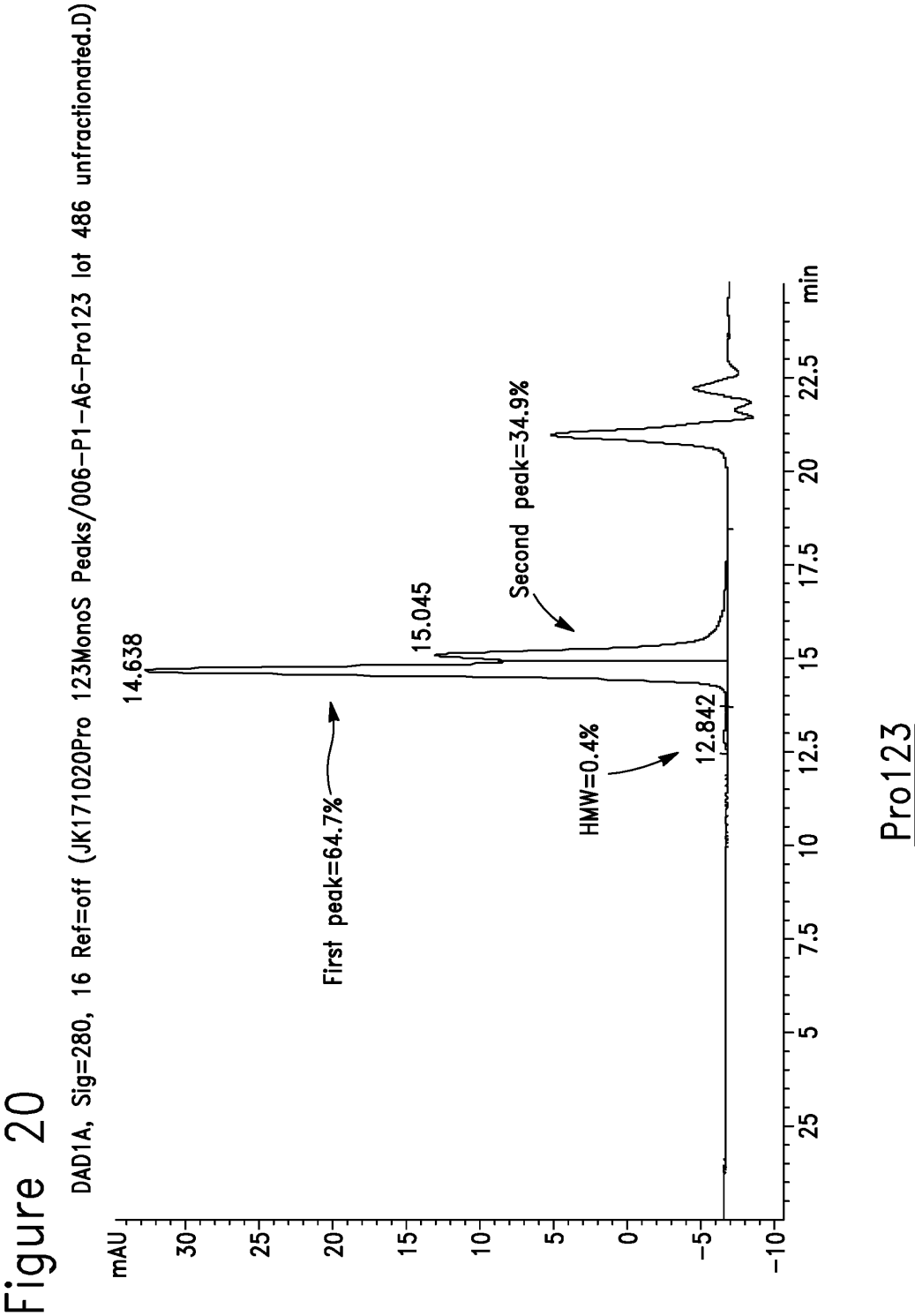


Figure 21

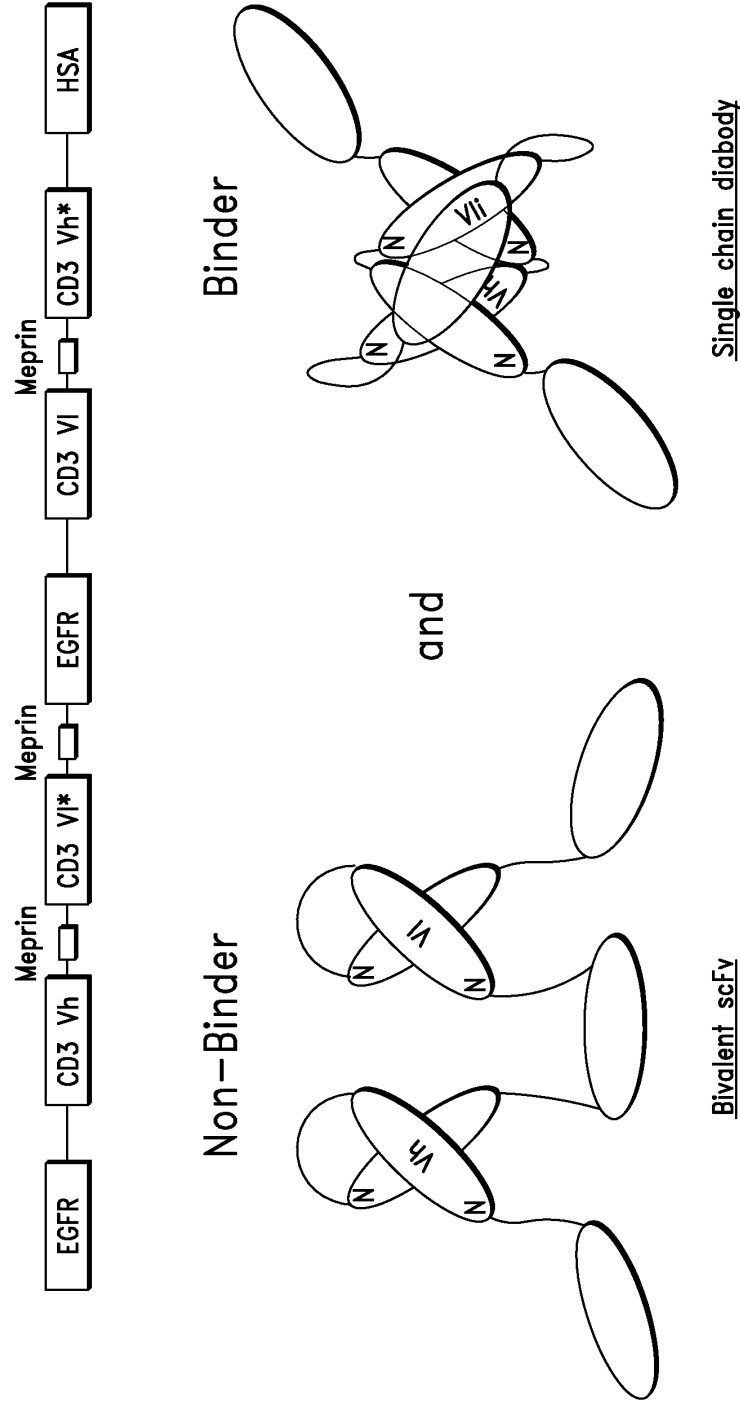


Figure 22

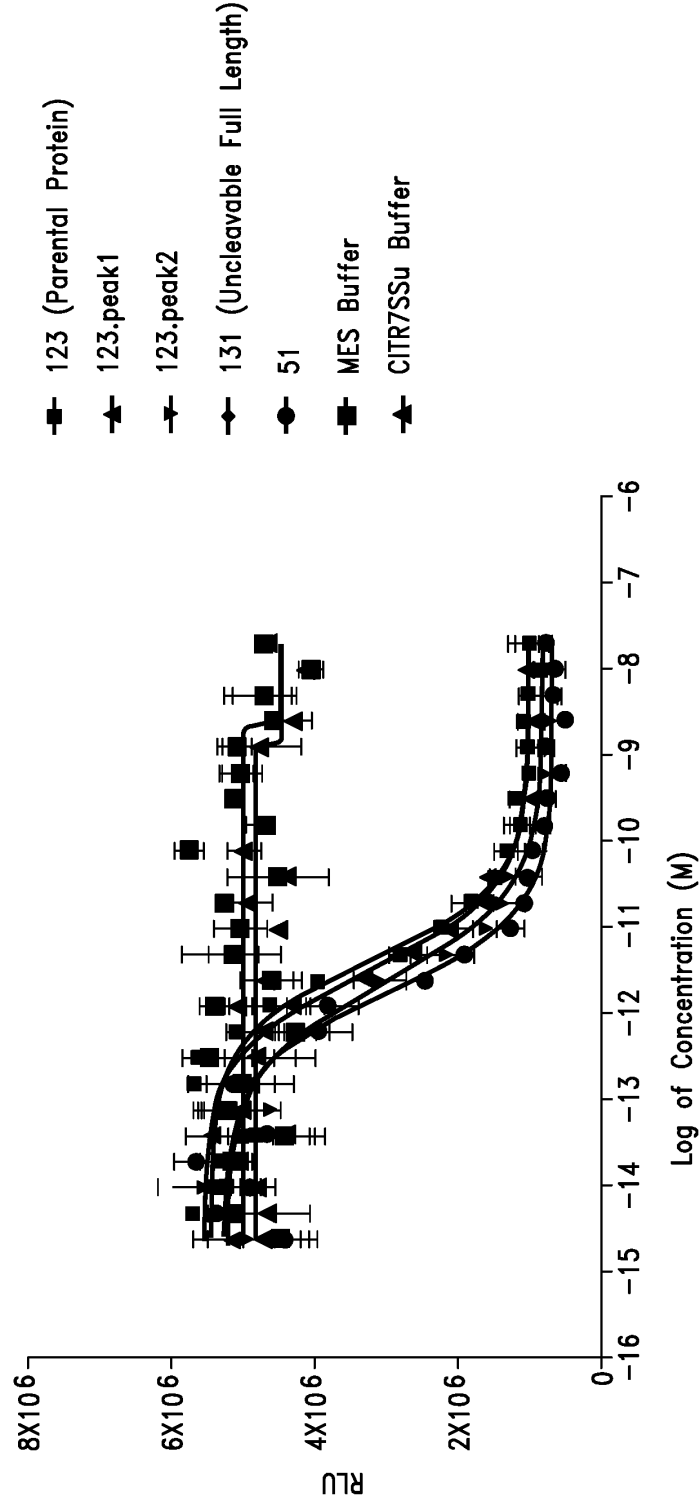


Figure 23A

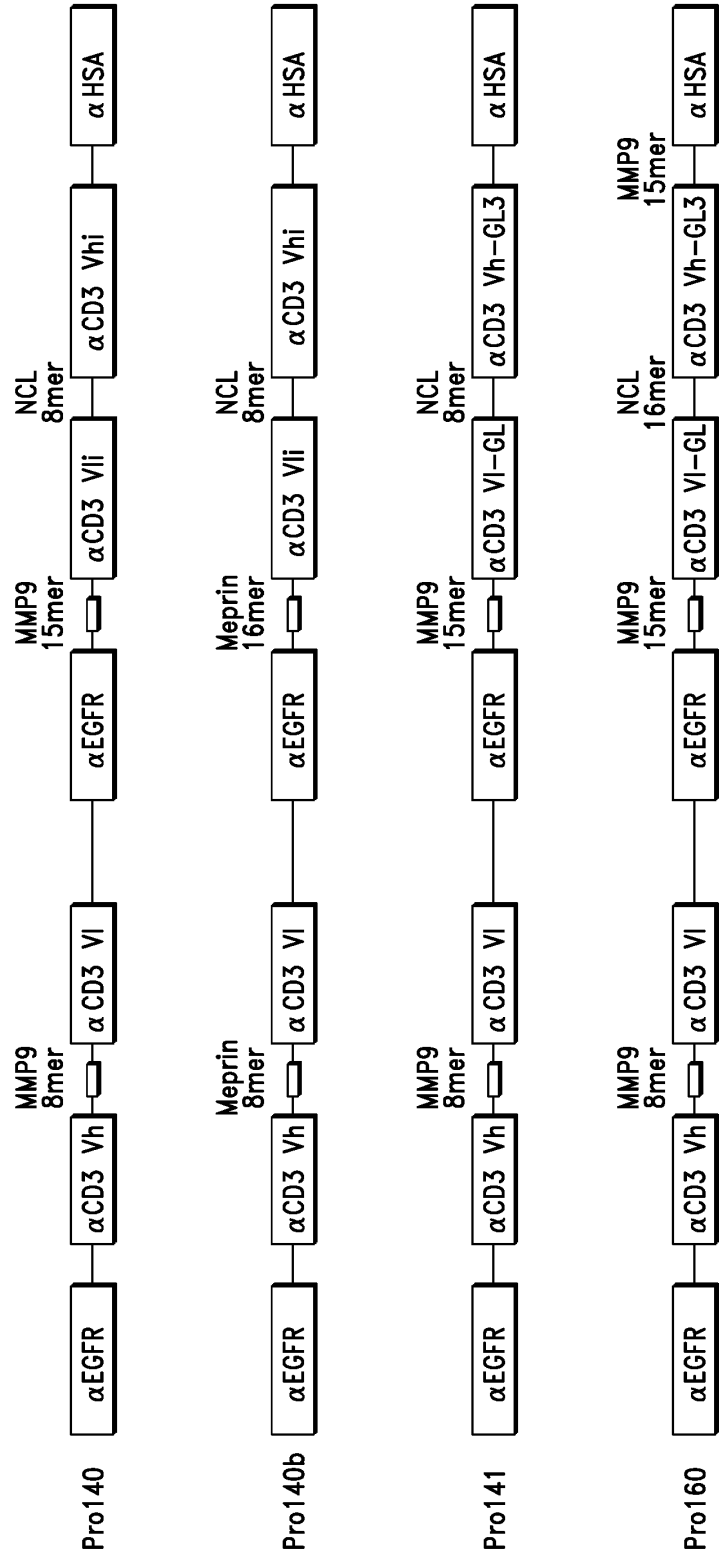


Figure 23B

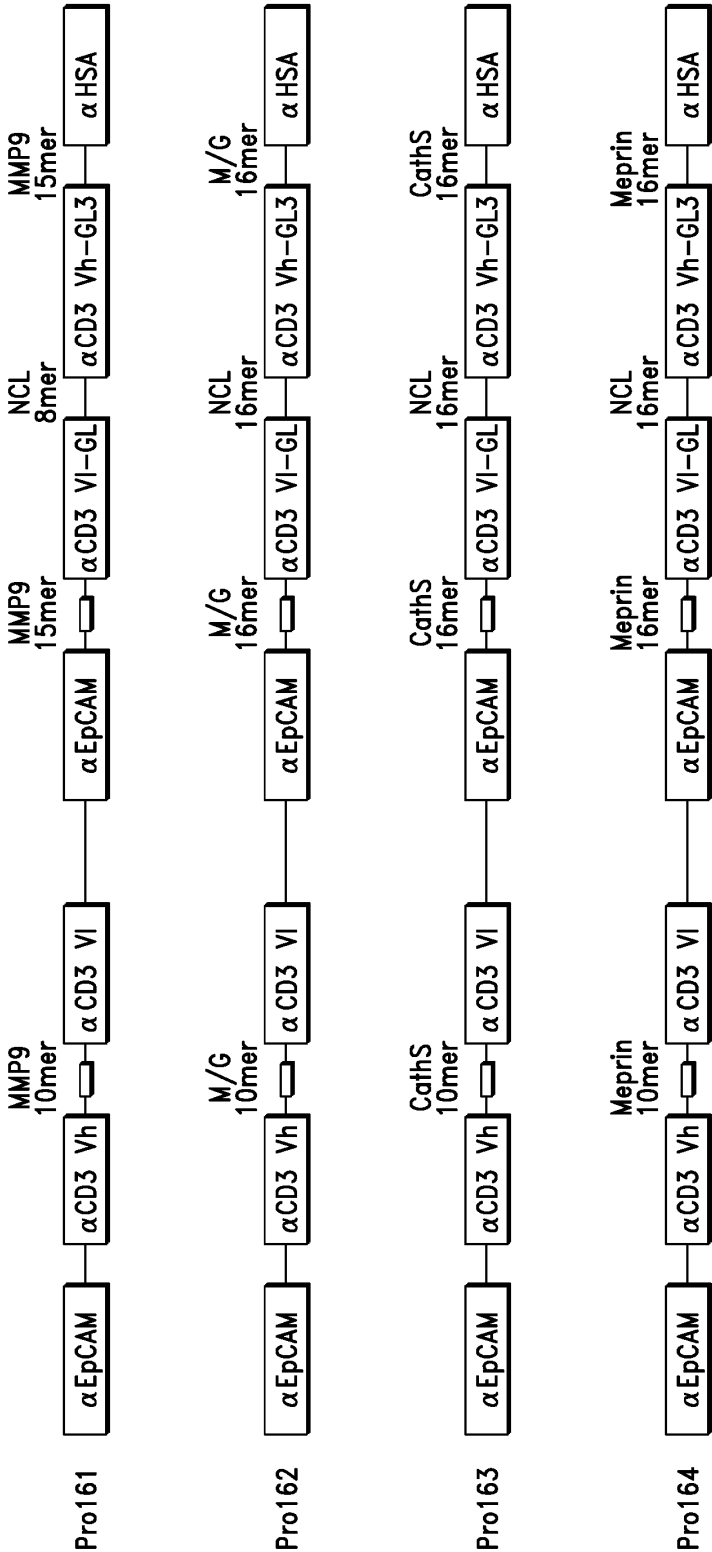


Figure 23C

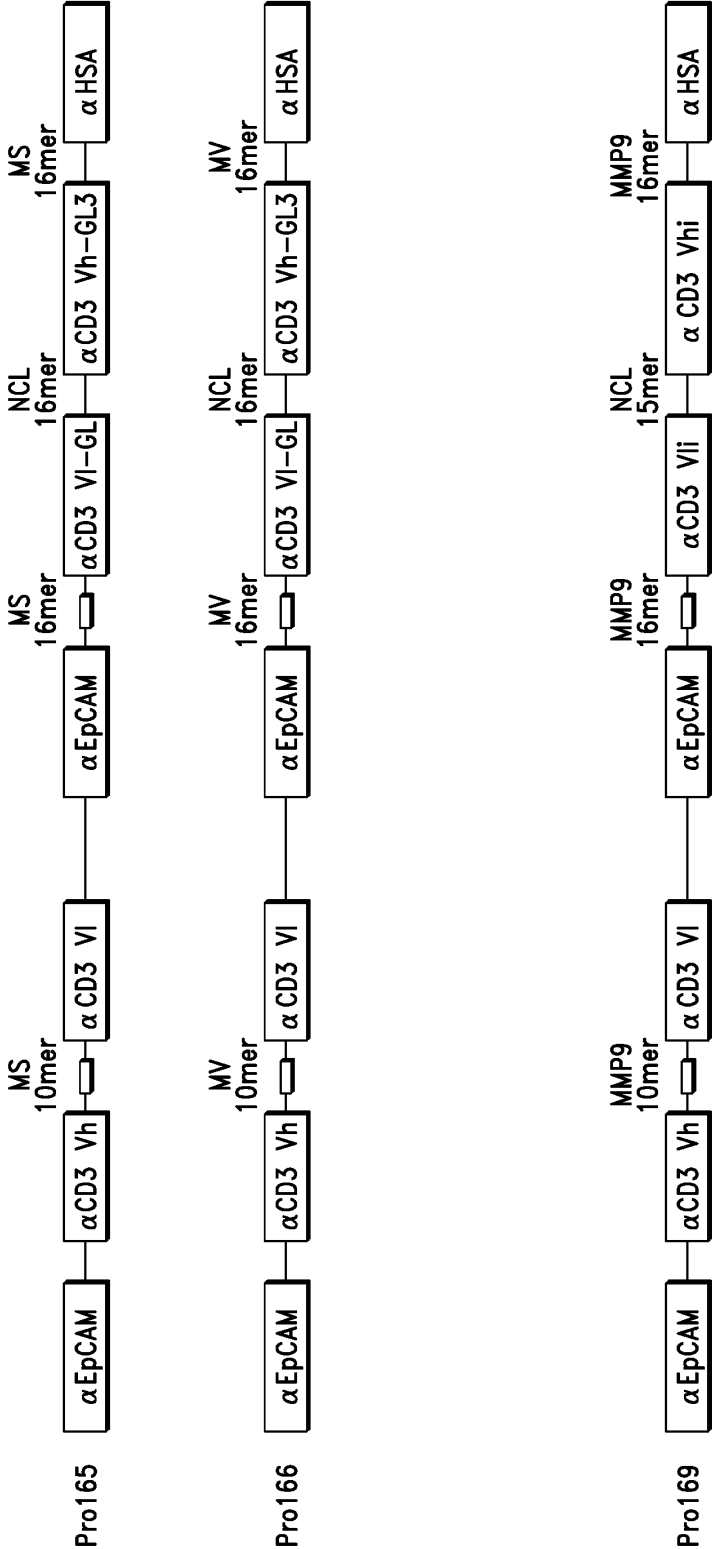


Figure 23D

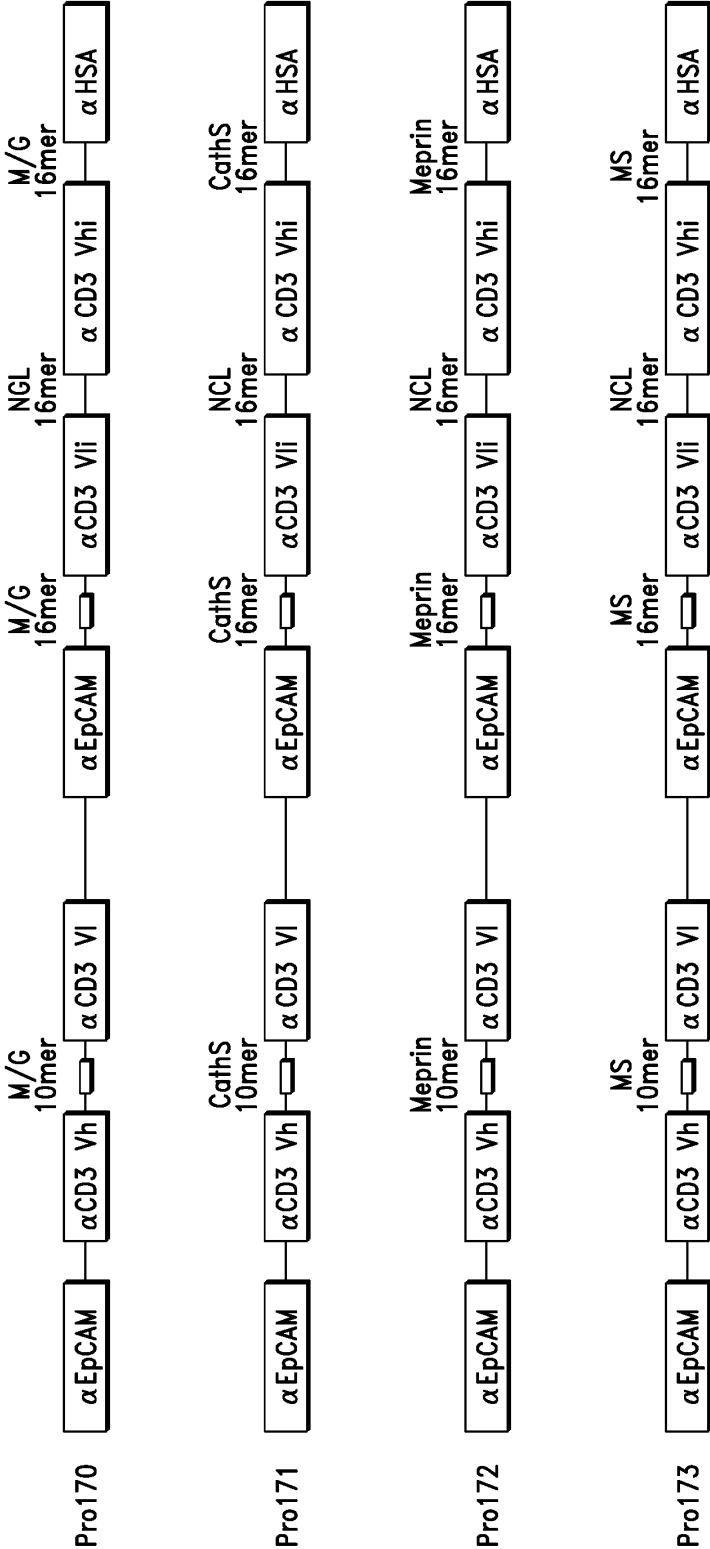


Figure 23E

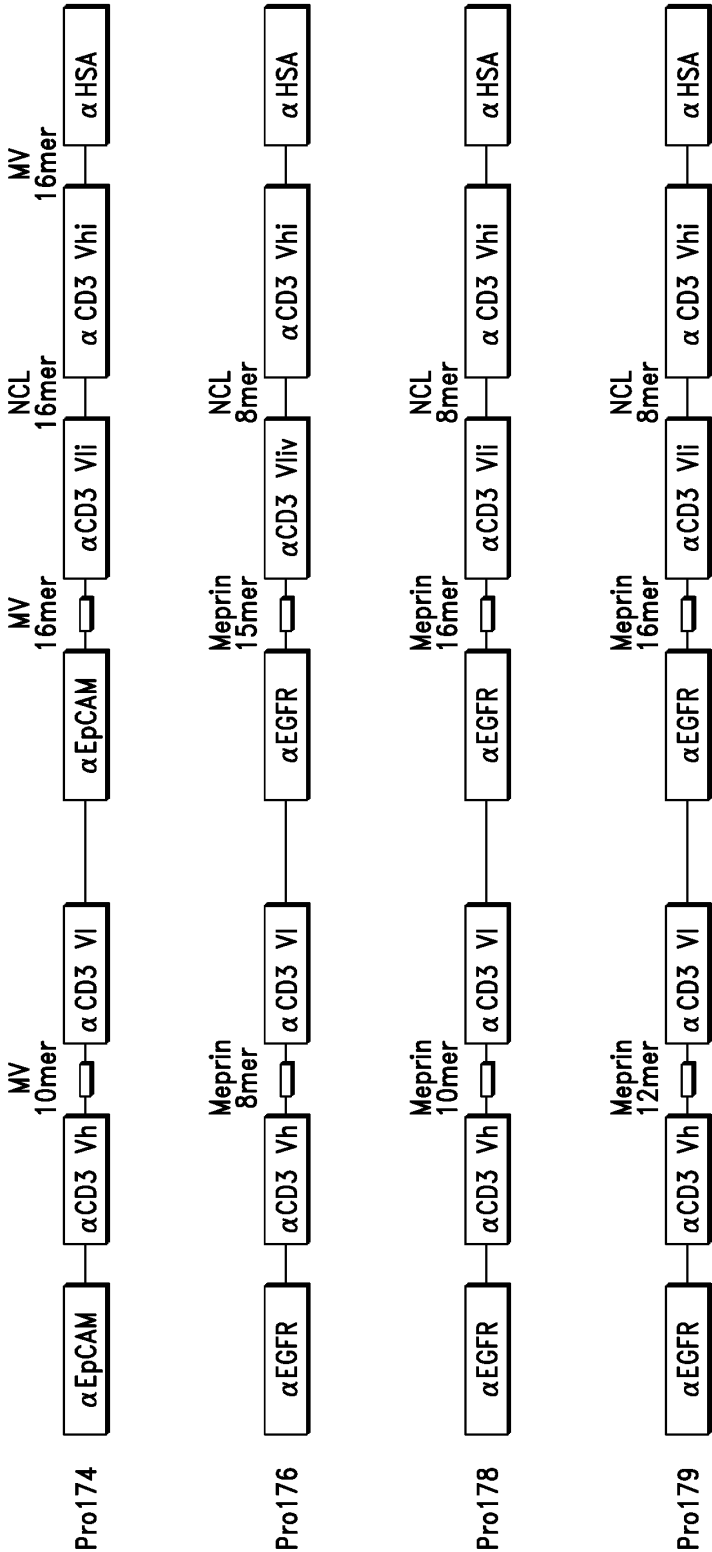


Figure 23F

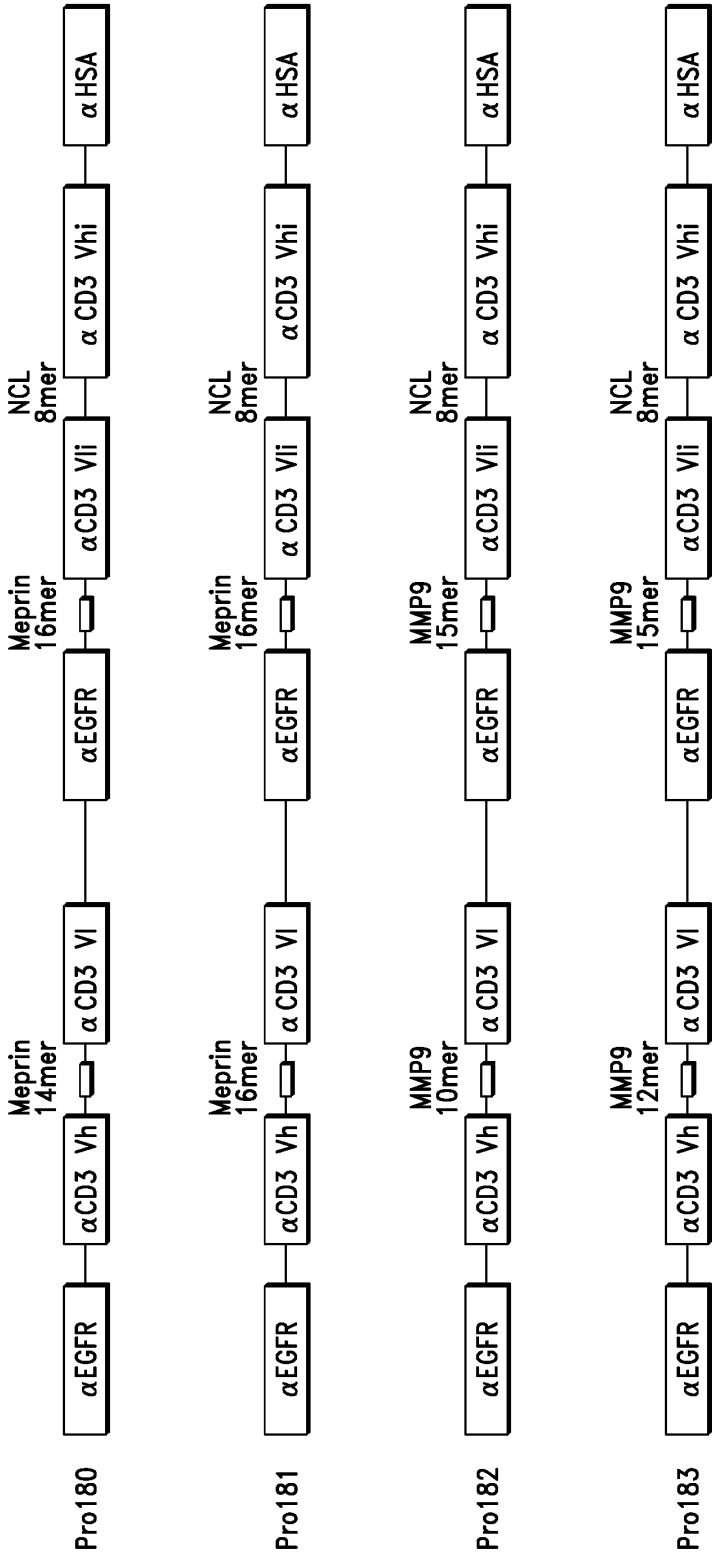


Figure 23G

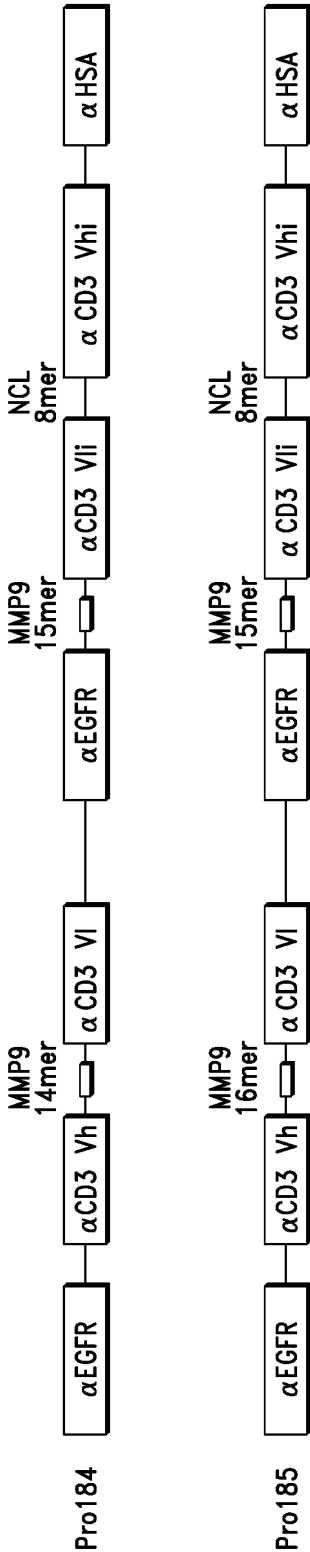


Figure 24

DAD1A,Sig=280,16 Ref=off(C:\CHEM32\...ATA\JK171027 SEC LOTS 503 TO 508\003-P1-A4PRO lot PL-0506.D0 4°C
DAD1A,Sig=280,16 Ref=off(JK17 1030 Pro140 and 41 and 42 at 37\003-P1-A4-Pro 140at 37 C.D) 37°C 72hrs

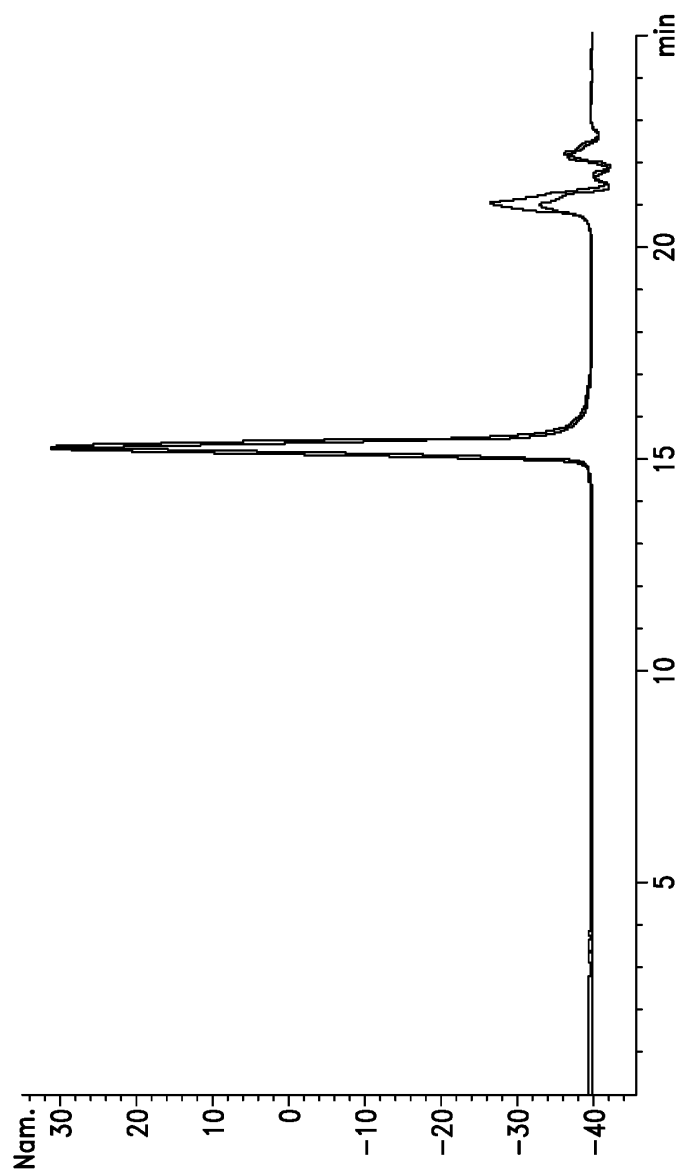


Figure 25

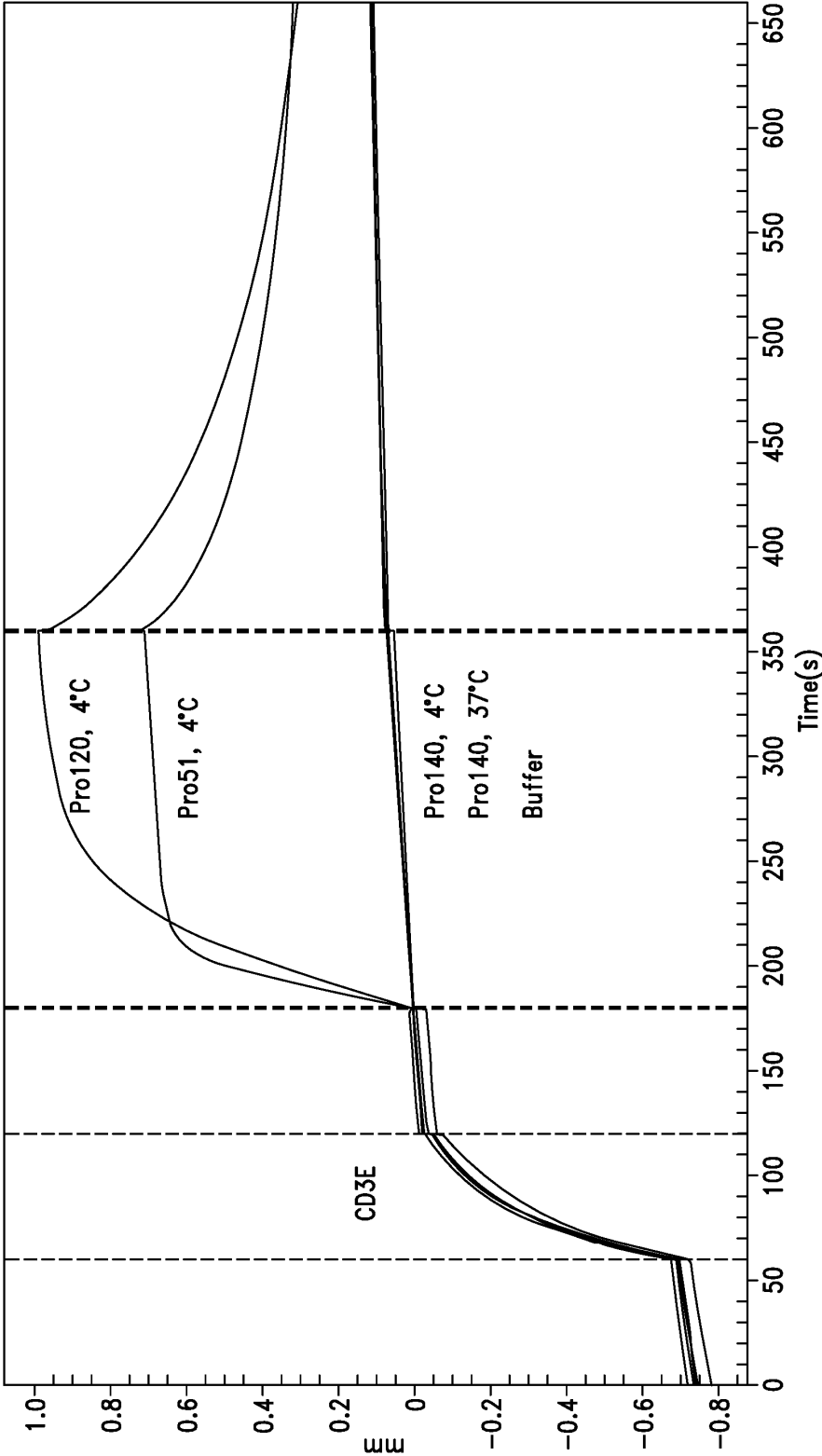


Figure 26

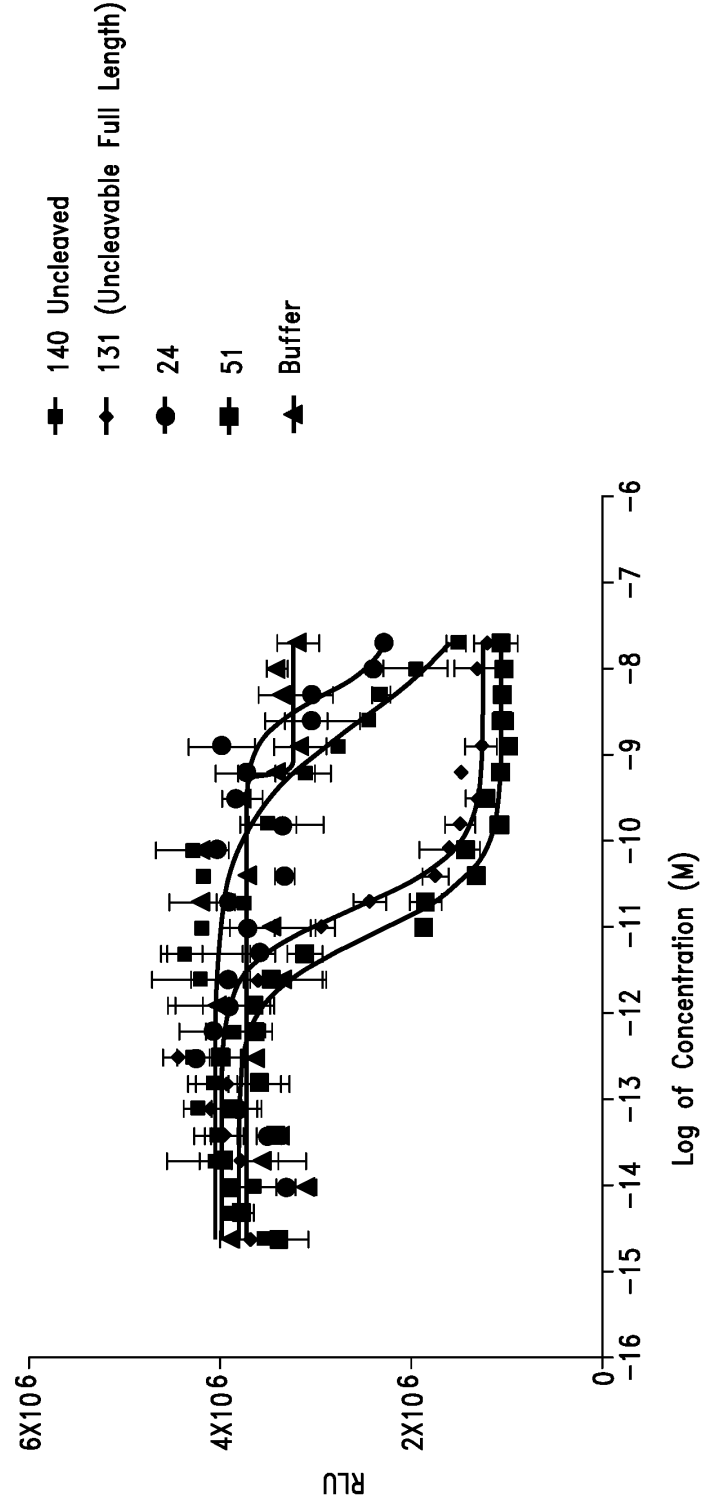
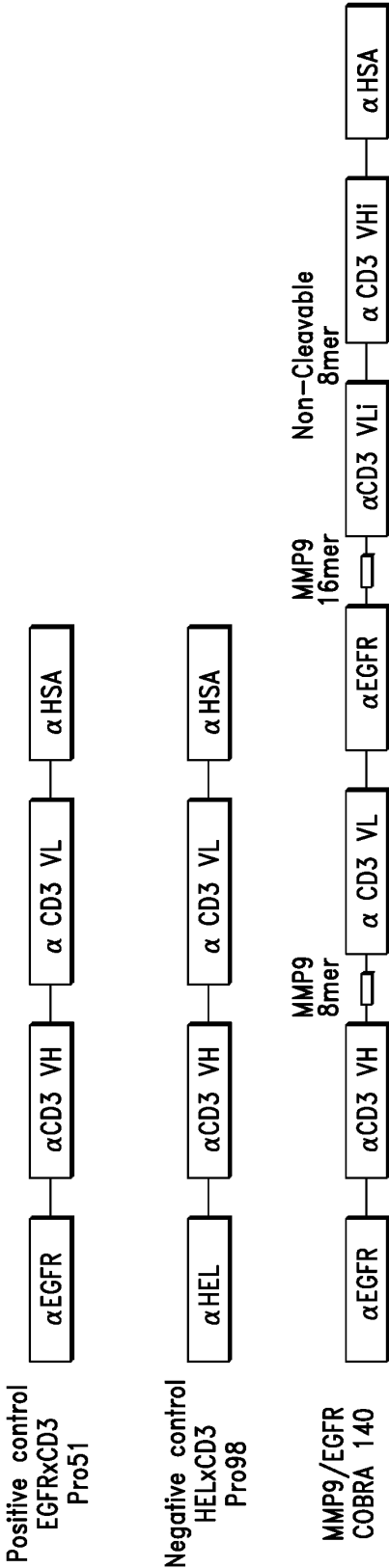


Figure 27

Groups:



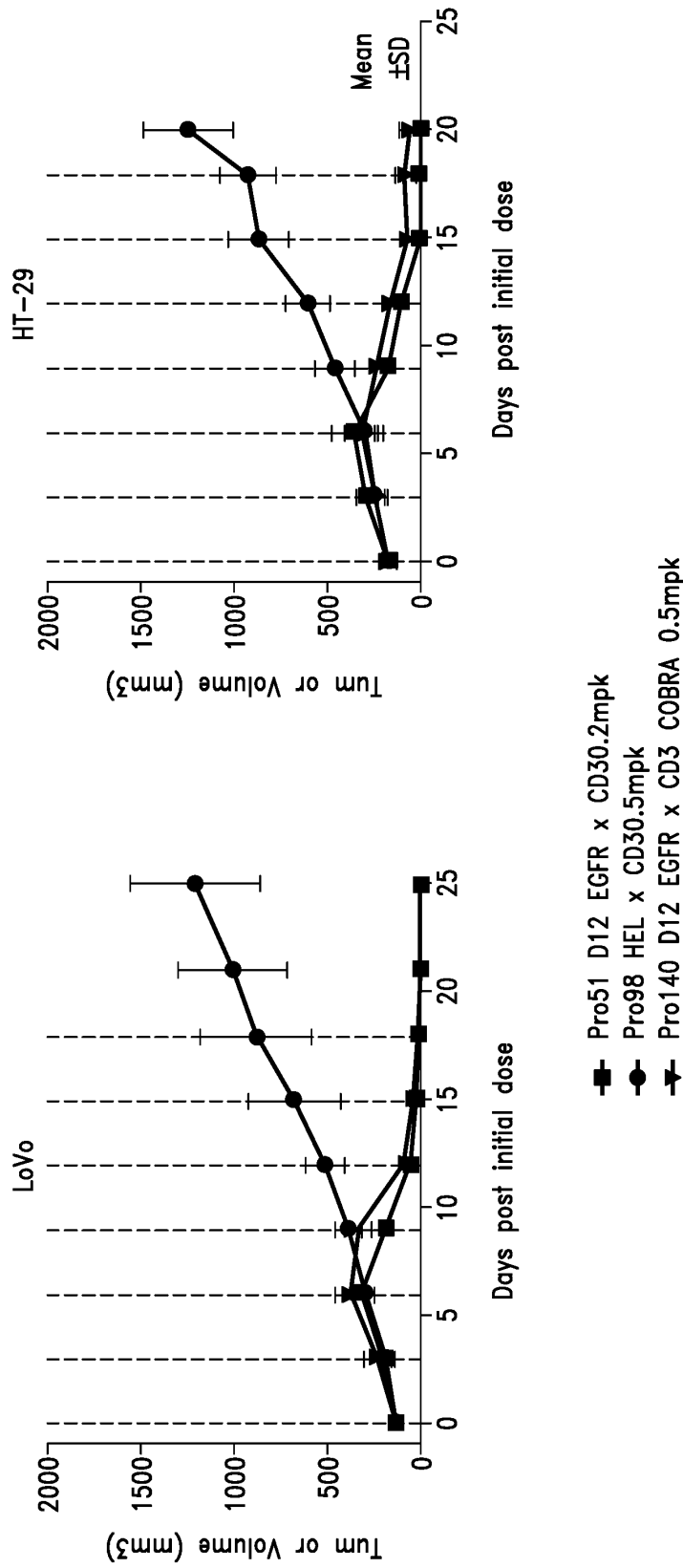
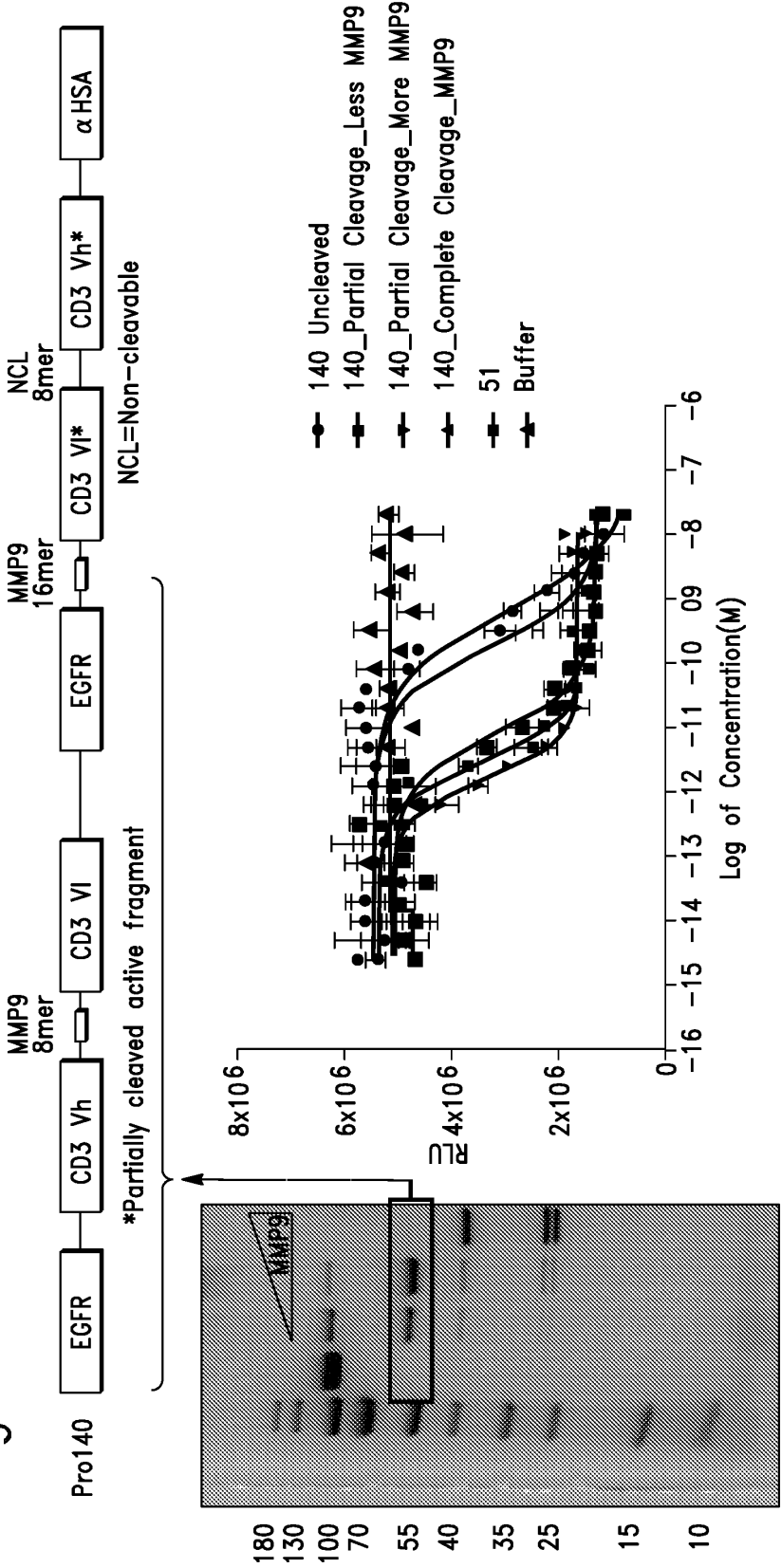


Figure 28A

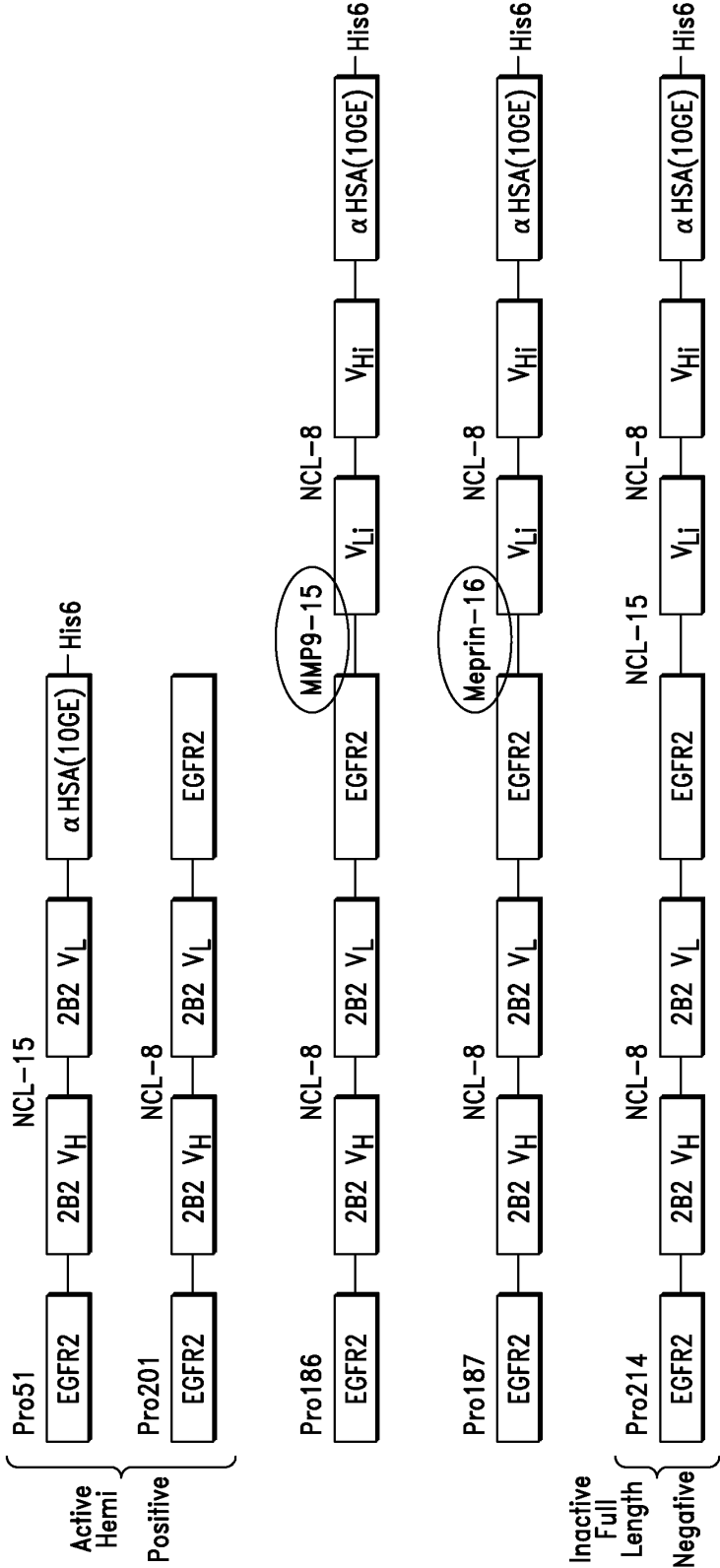
Figure 28B

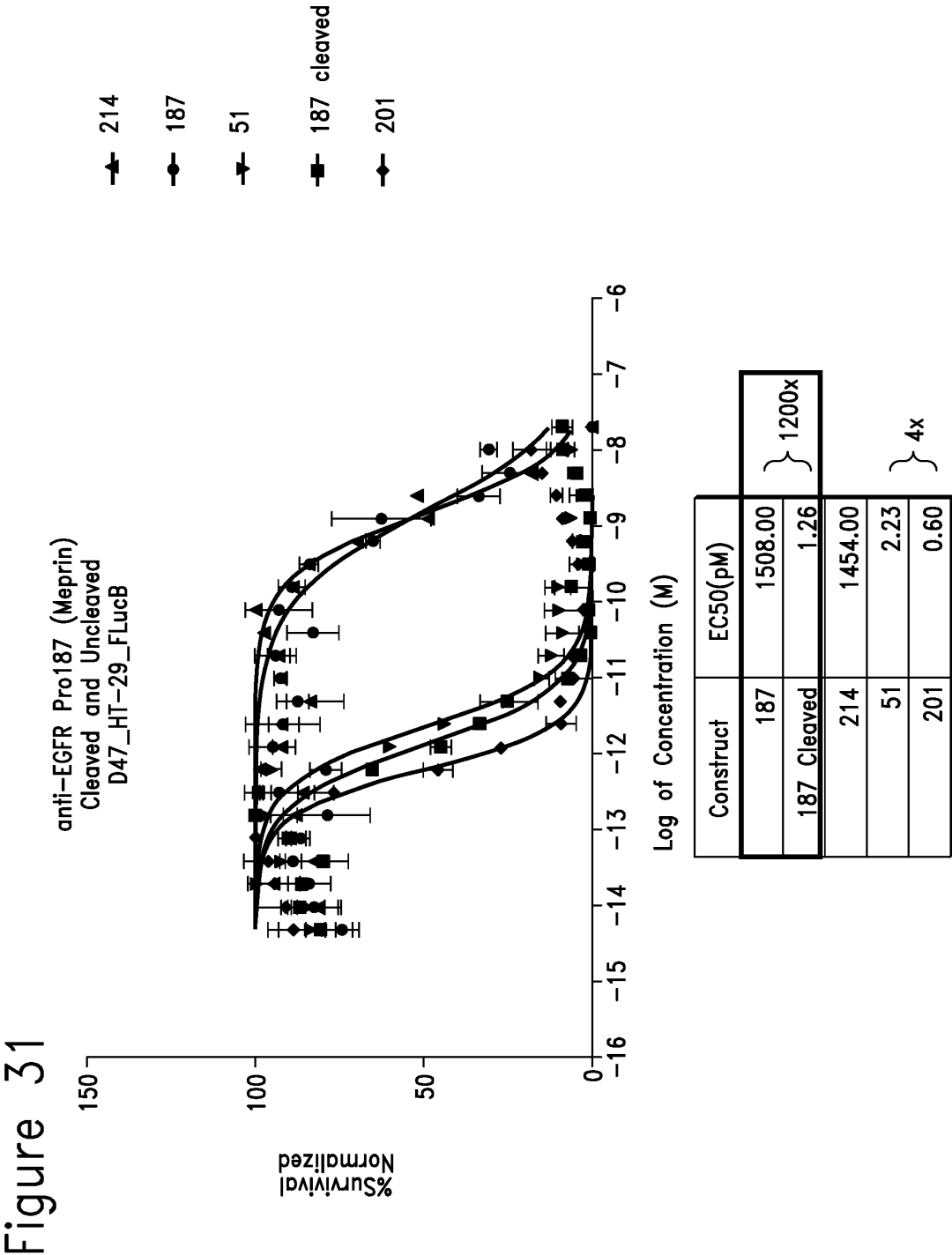
Figure 29

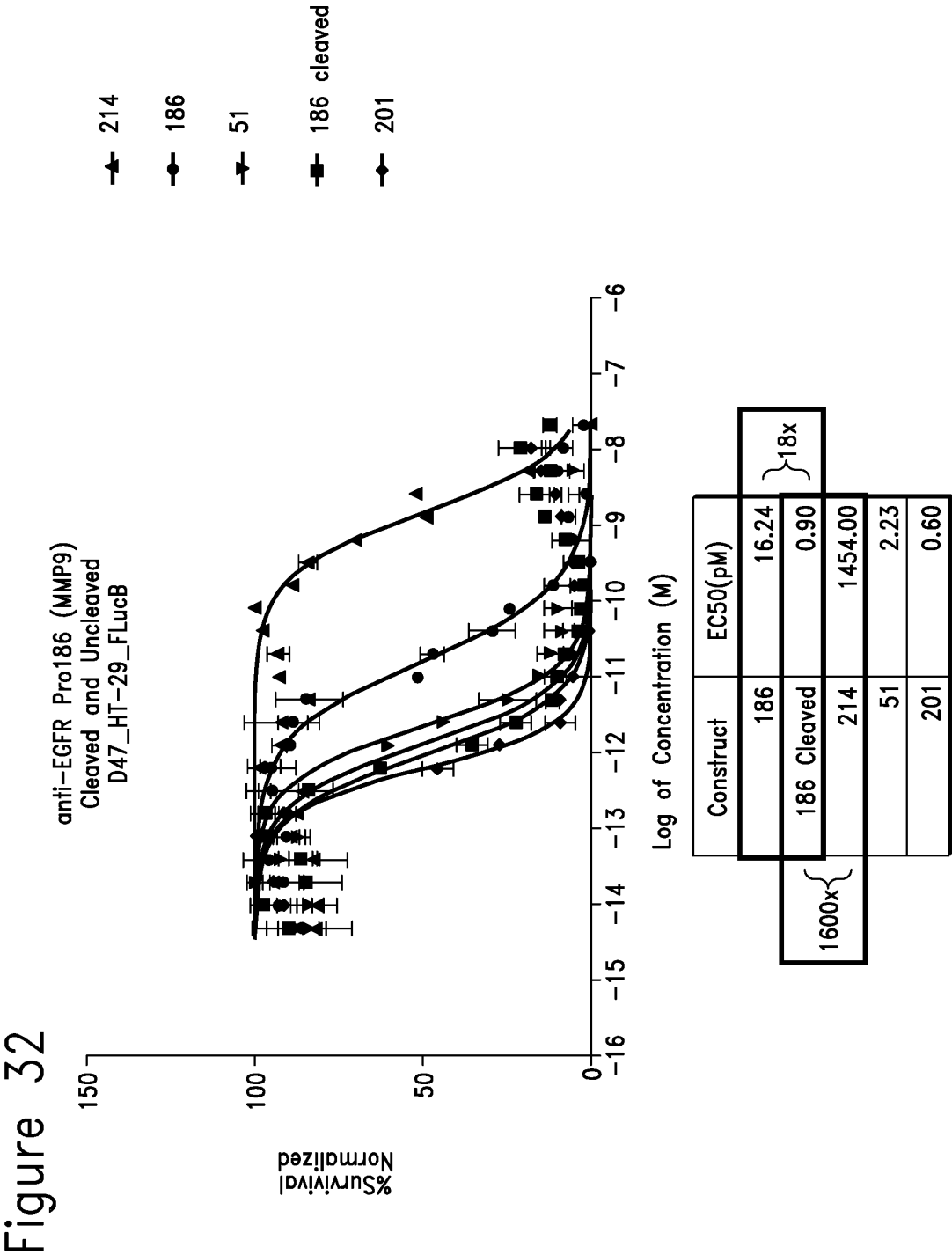


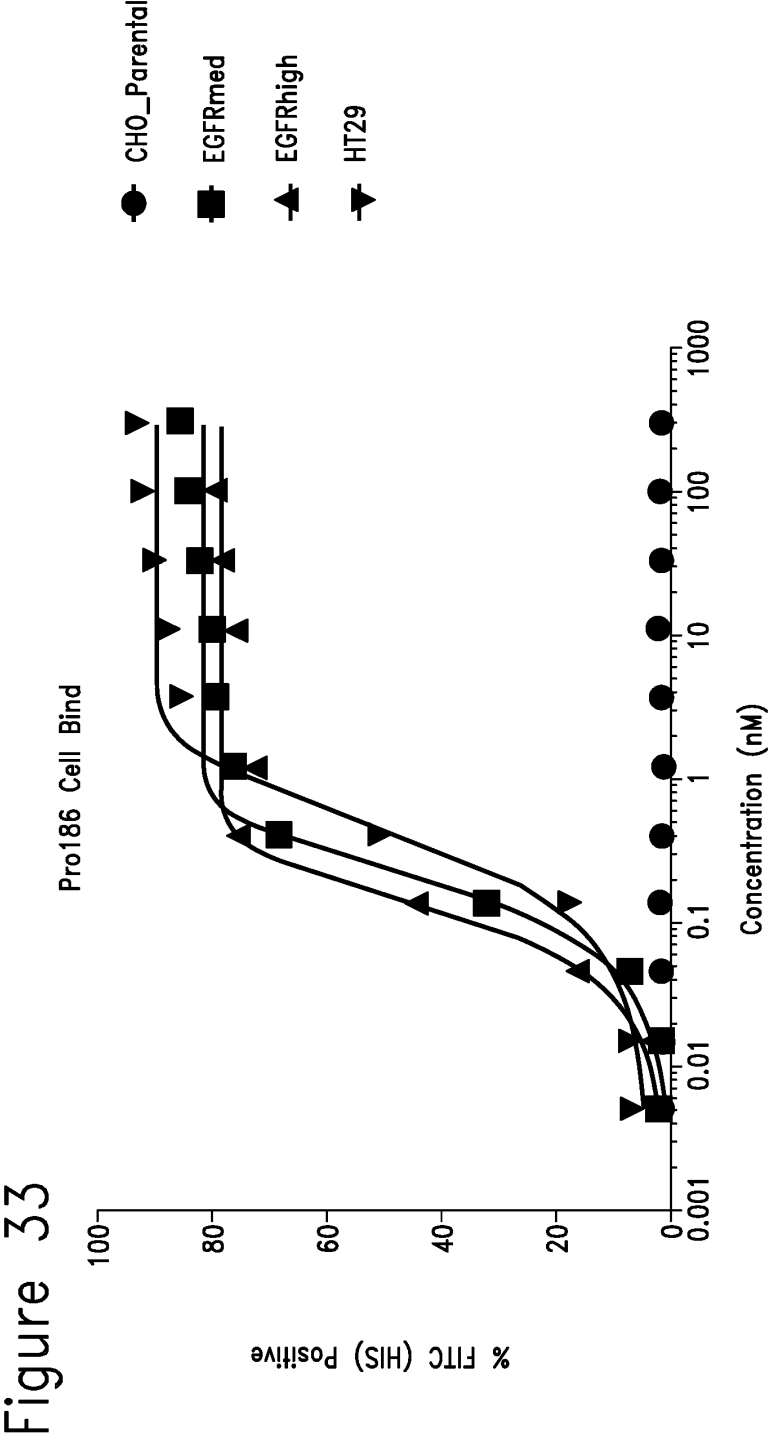
*16mer MMP9 linker is cleaved at a faster rate than the 8mer MMP9 linker

Figure 30









Groups:

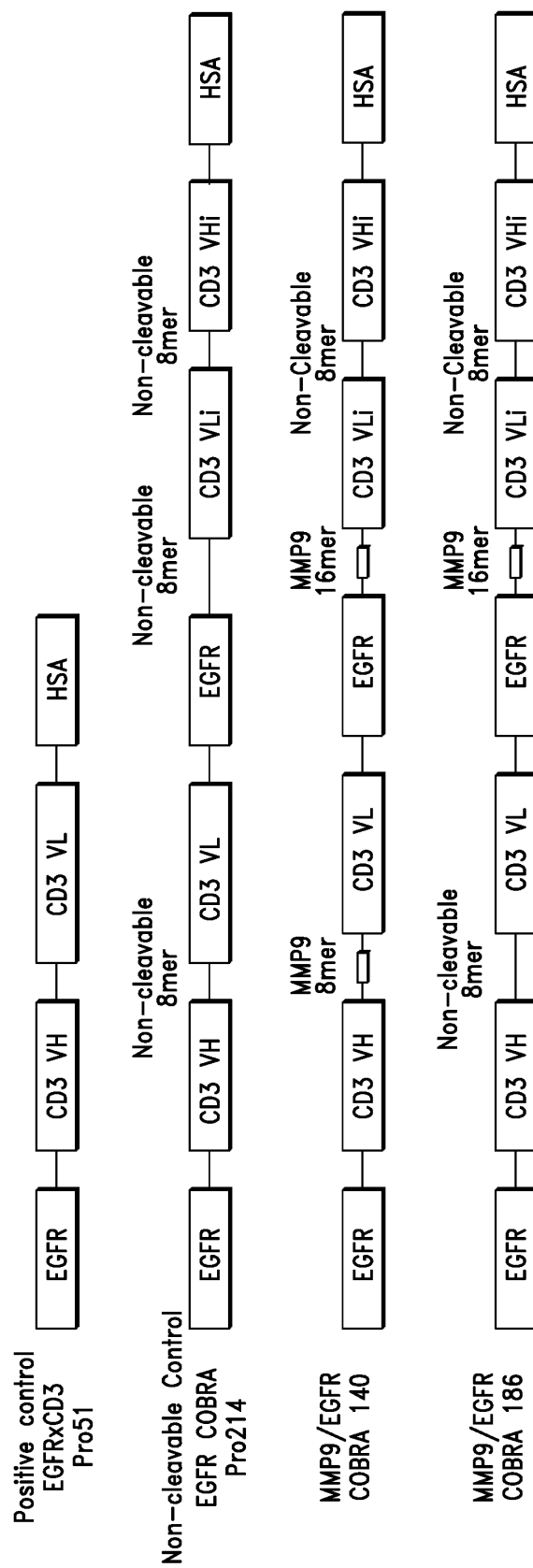


Figure 35

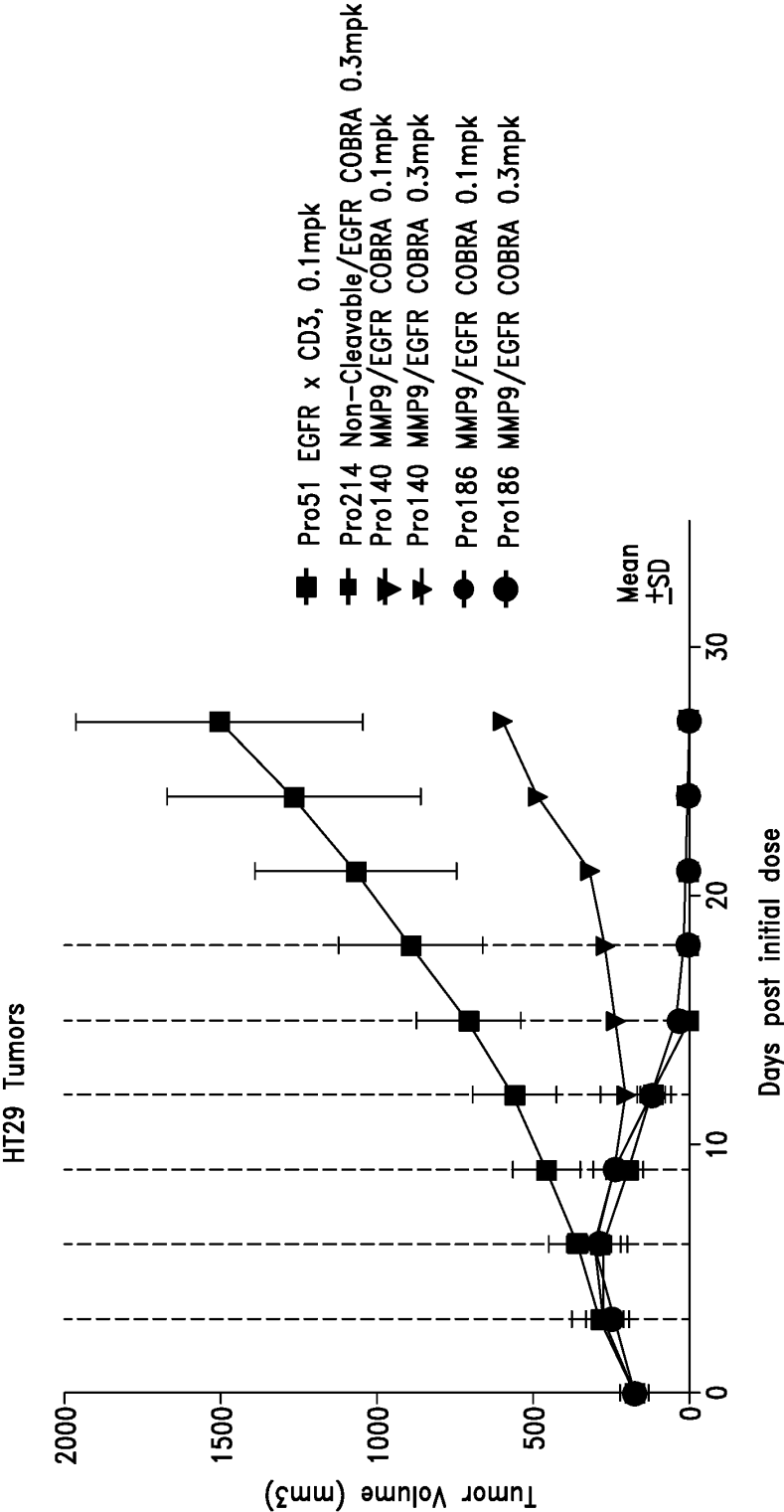


Figure 36

Pro186

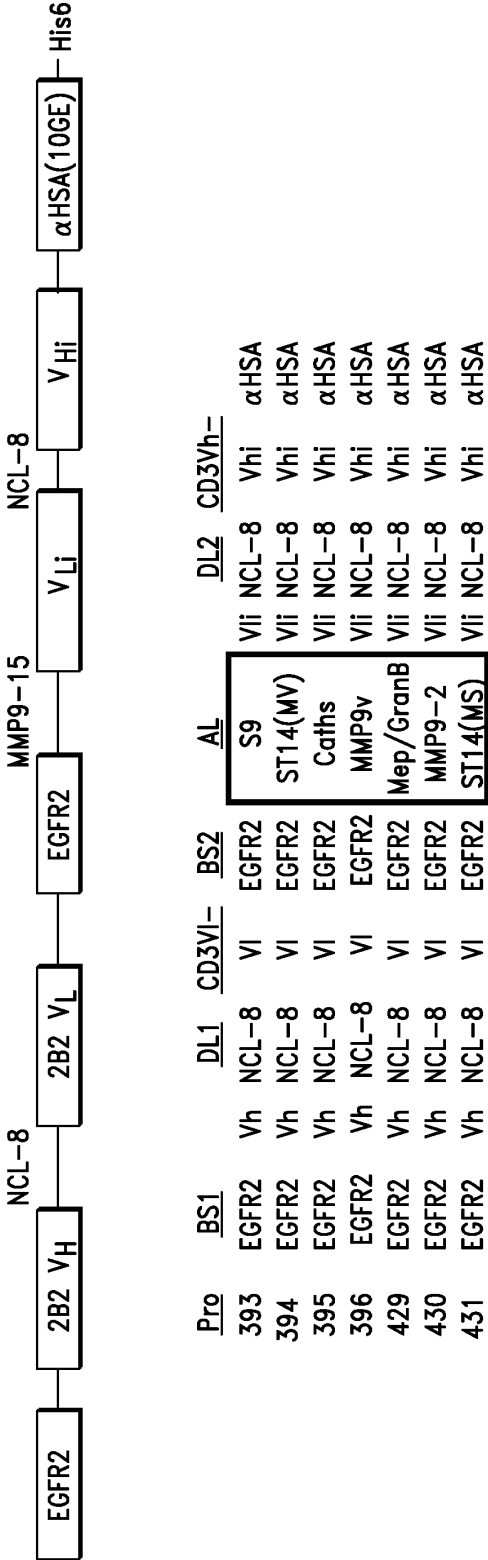


Figure 37

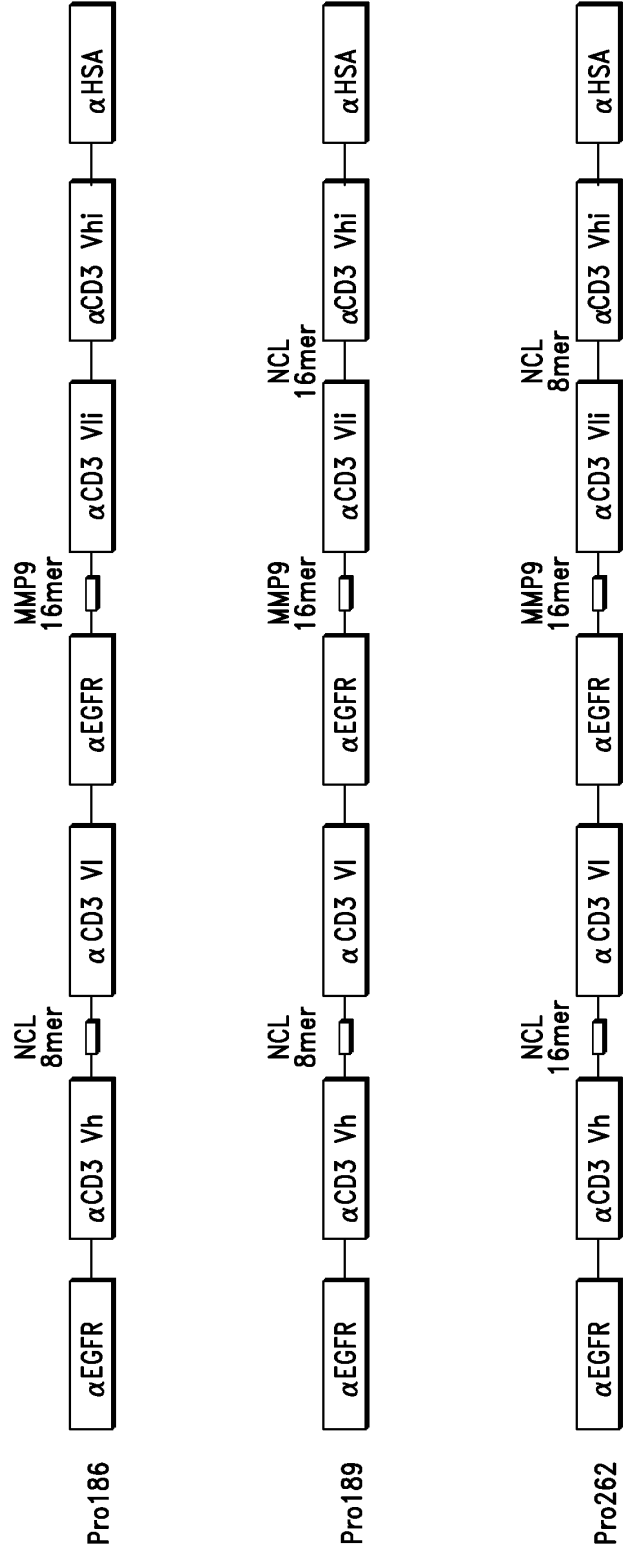
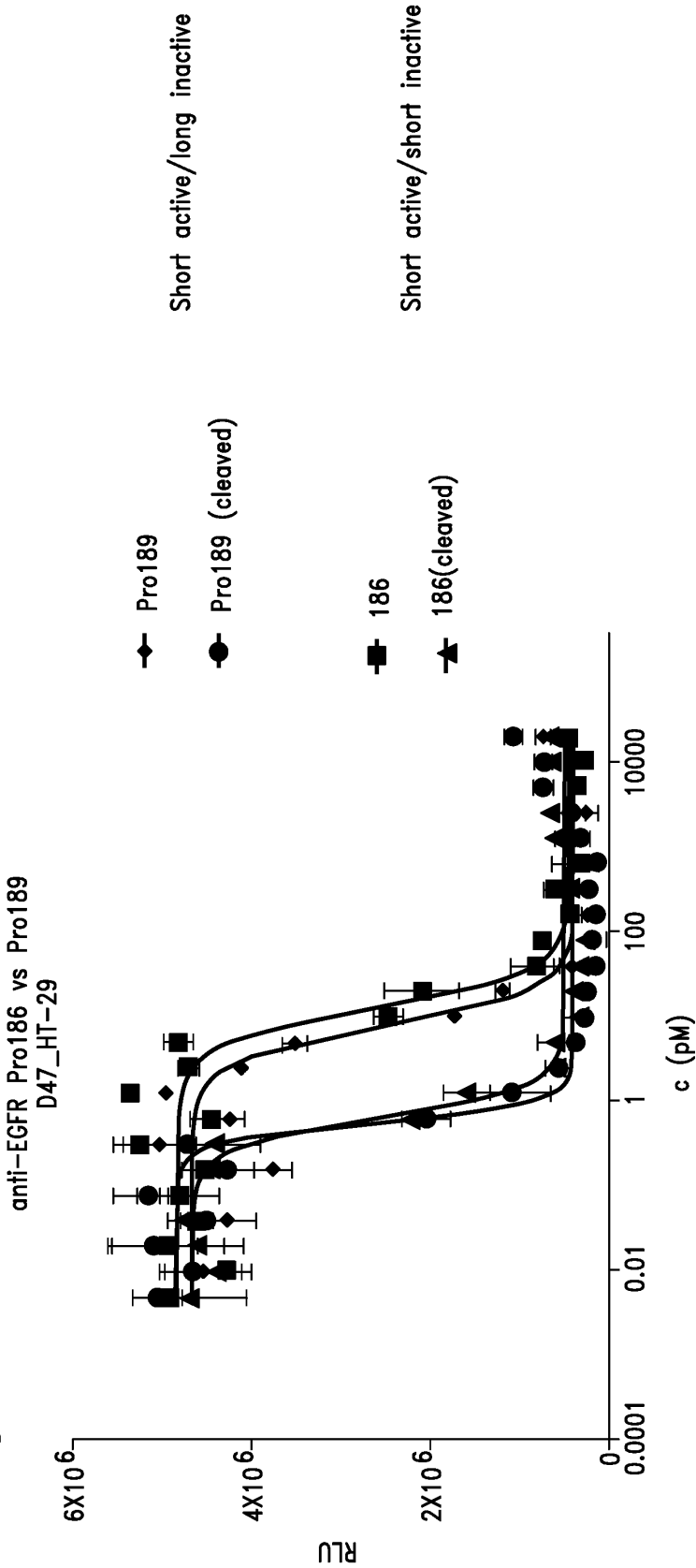


Figure 38



	EC50
Pro189	7.754
Pro189 (cleaved)	0.5528
186	12.41
186 (cleaved)	0.6232

Figure 39

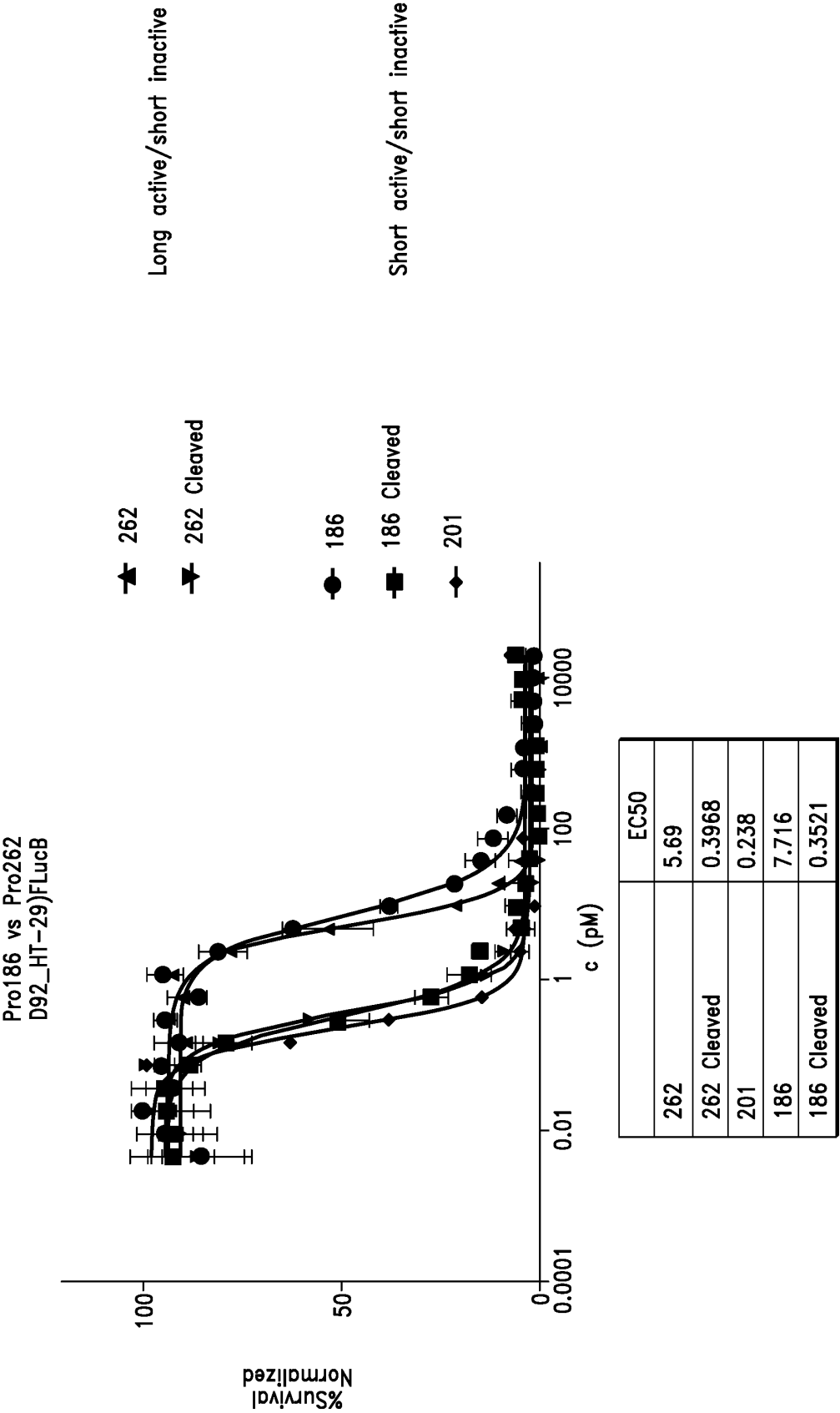


Figure 40A

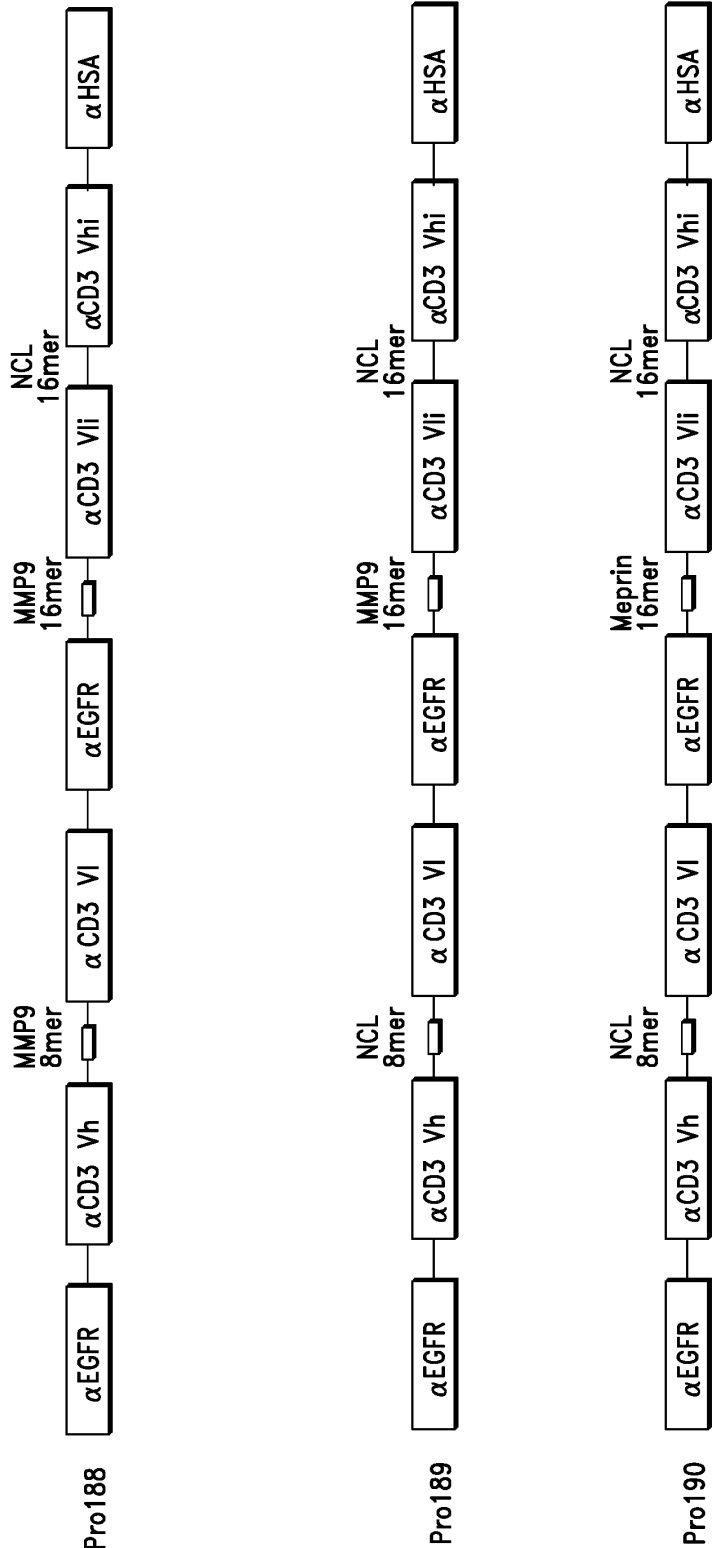


Figure 40B

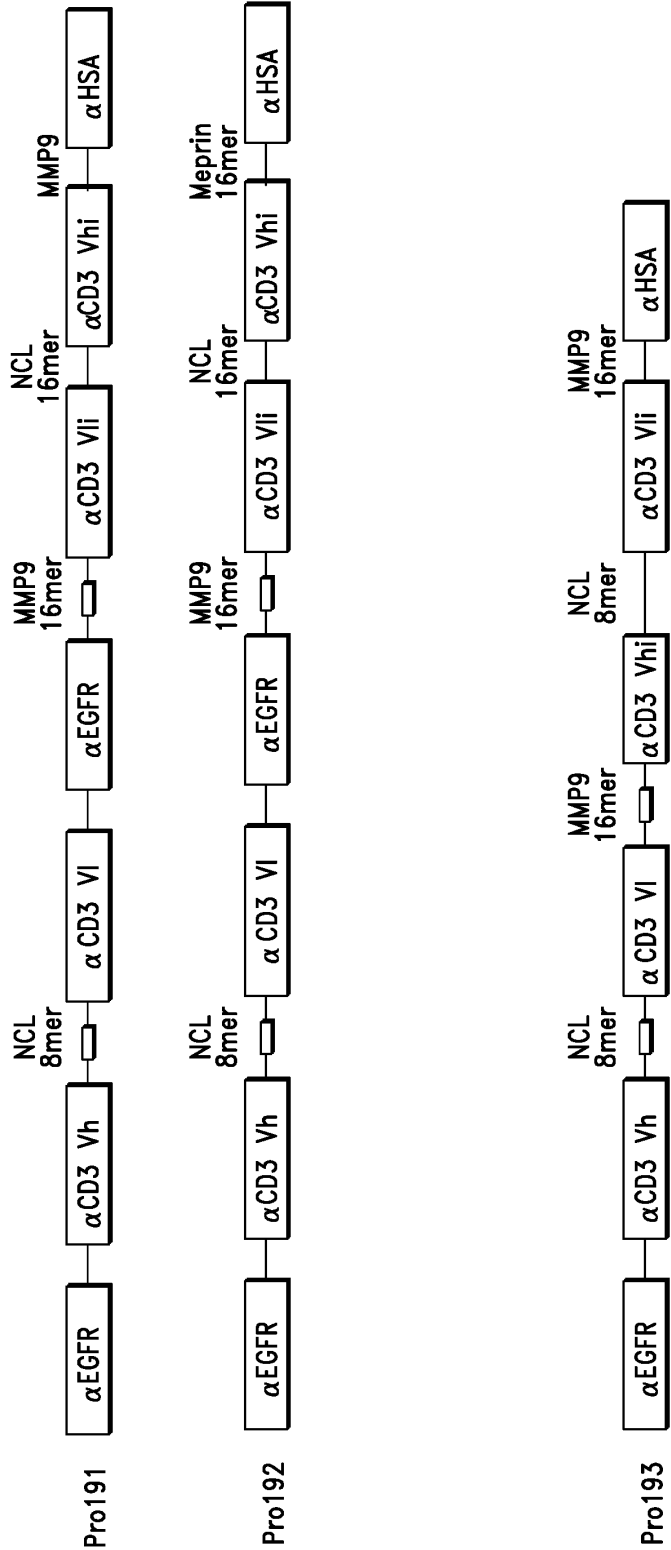


Figure 40C

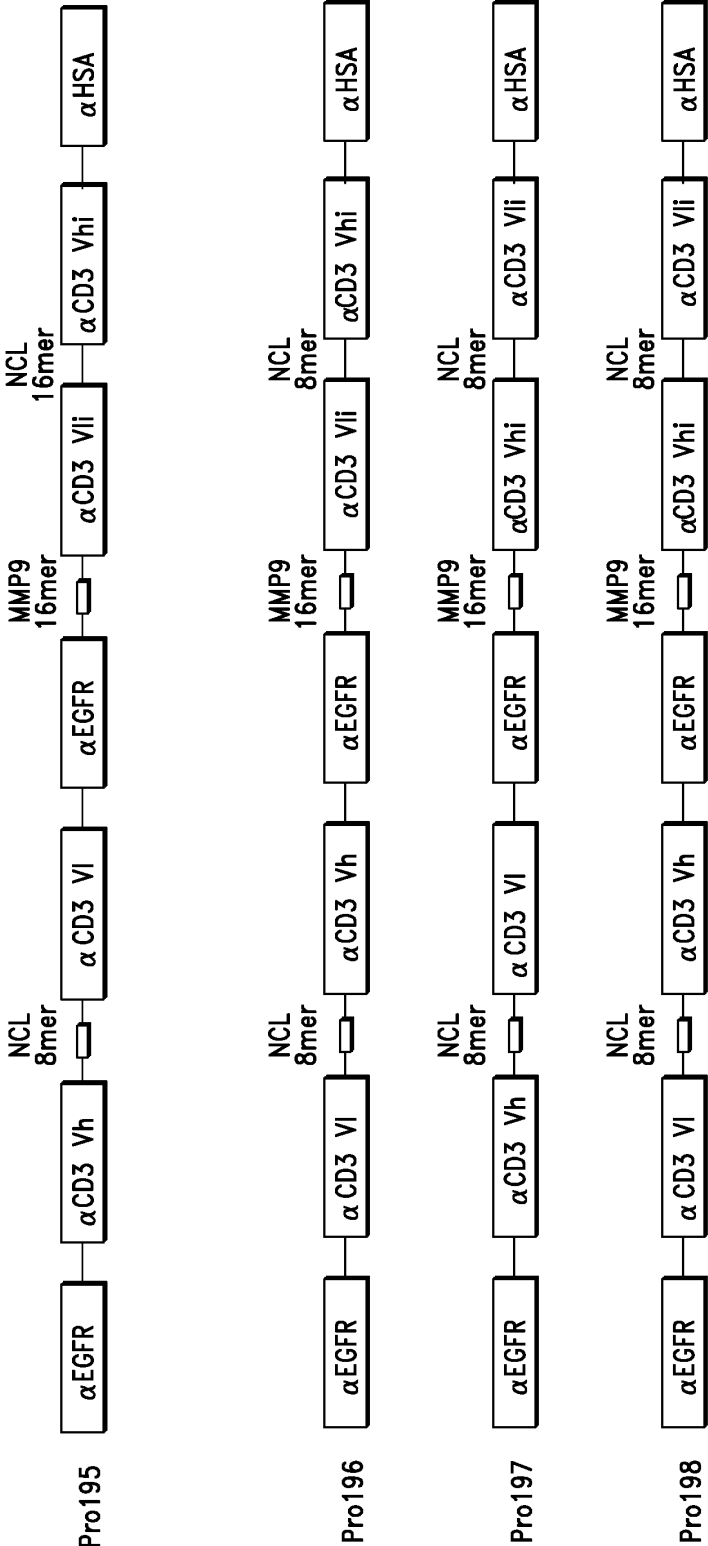


Figure 41

sdAb		Protein Binding: K_D (nM)			Cell Binding:		TDCC EC_{50} (pM)	
MVK ID	family	Human	Rhesus	Mouse	Human	Rhesus	IGROV1	OVAR8
77-2	2	2	3	7	+++	+++	2	0.2
59-3	3	15	53	NB	+++	+++	30	6
22-4	4	2	11	NB	+++	+++	8	1
Pro51							41	2

Figure 42

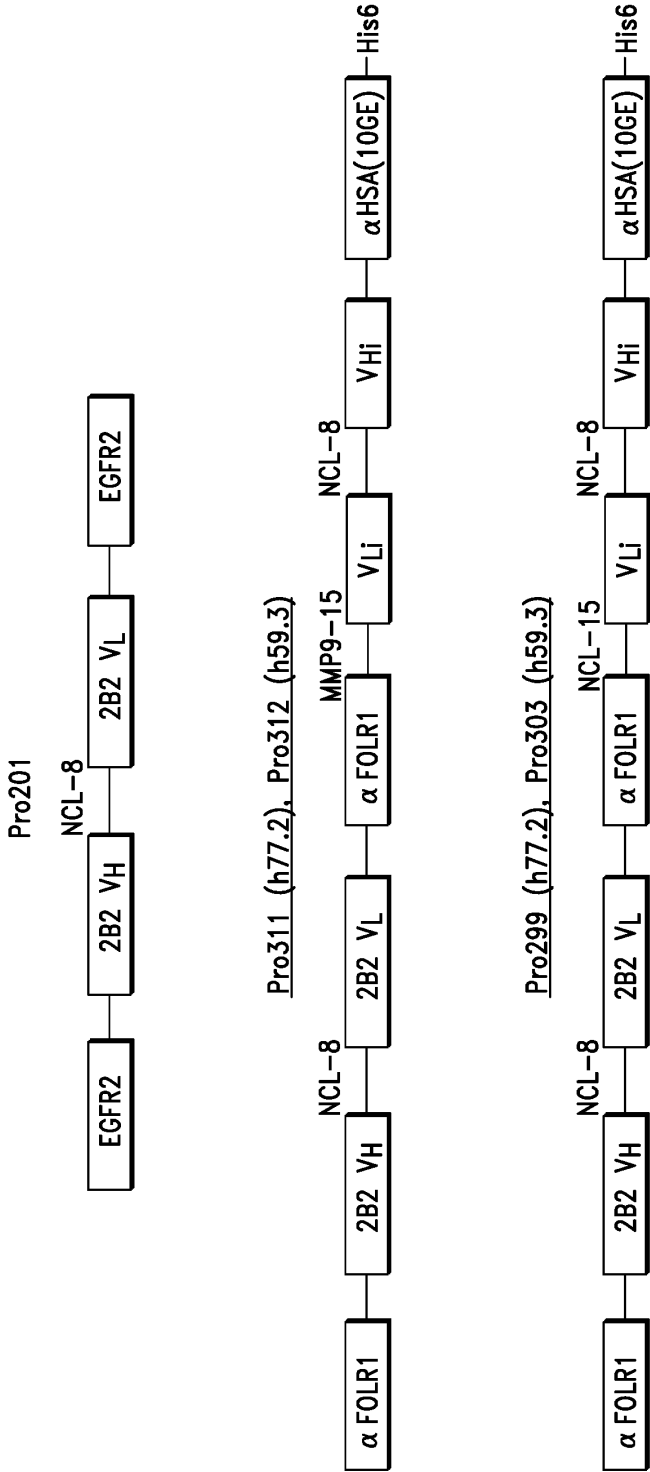


Figure 43

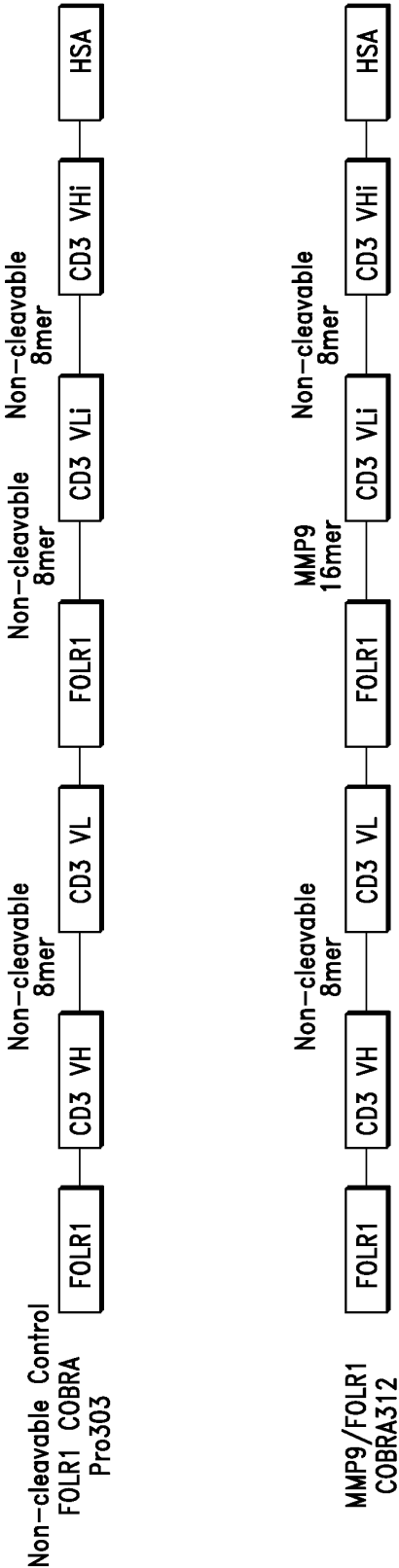


Figure 44

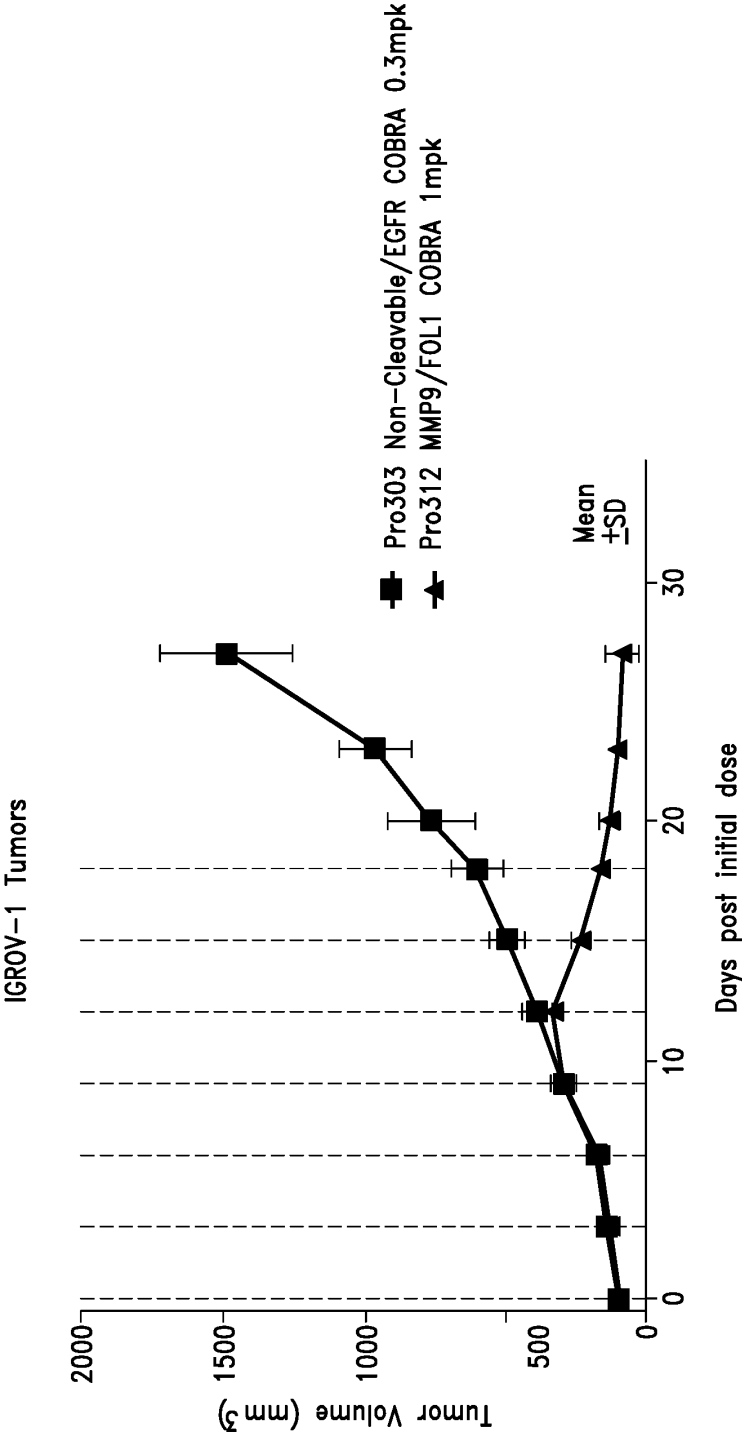
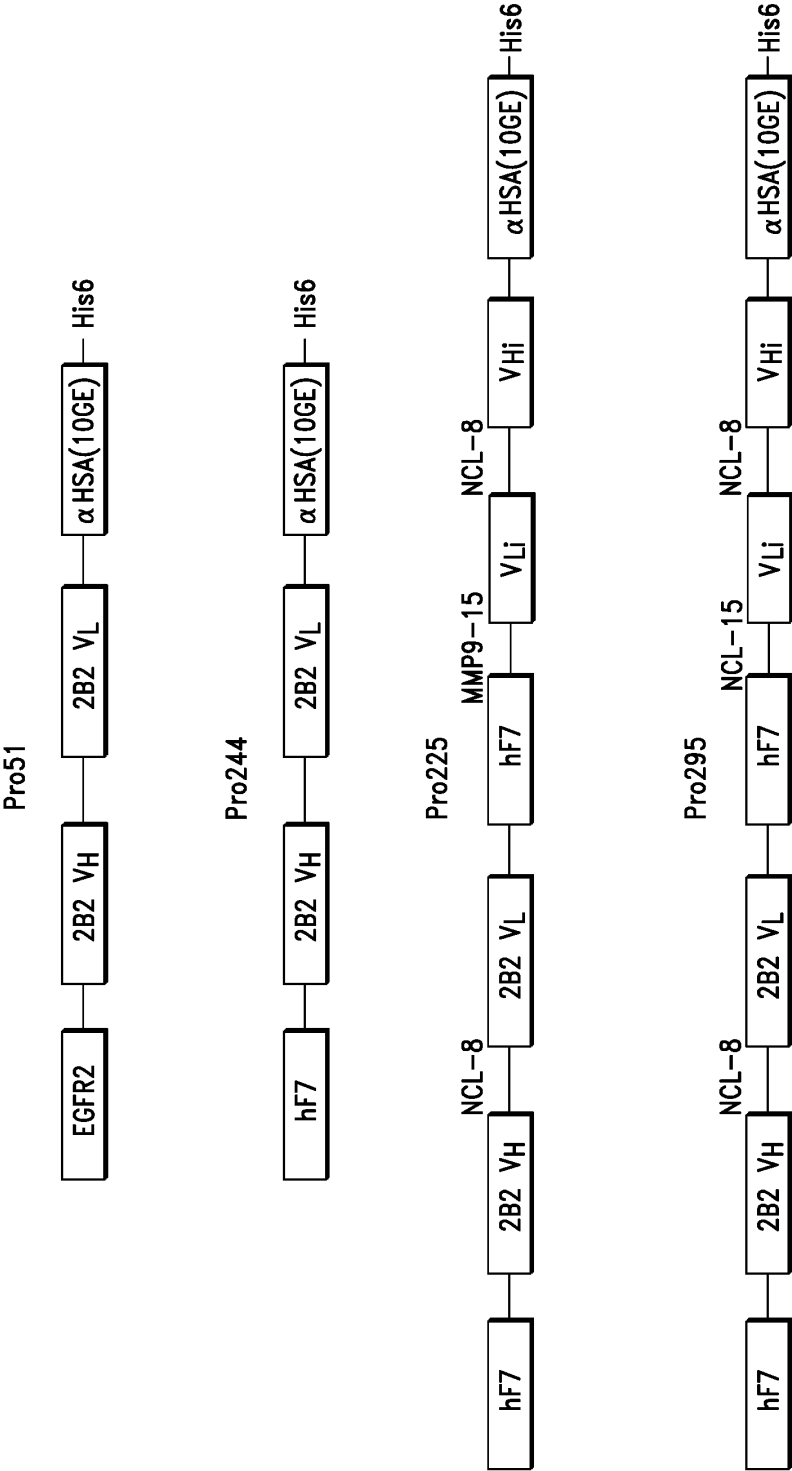


Figure 45



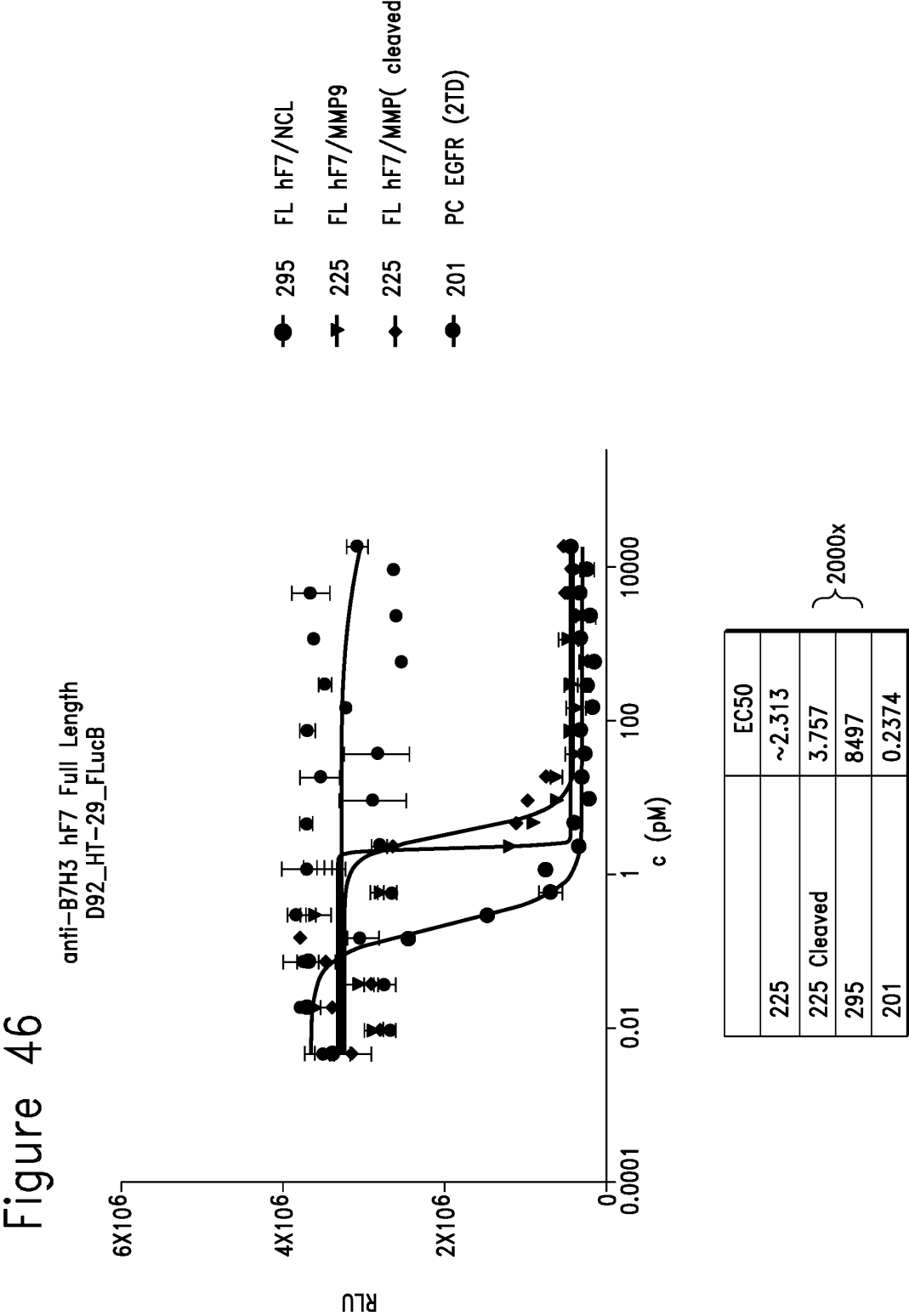


Figure 47

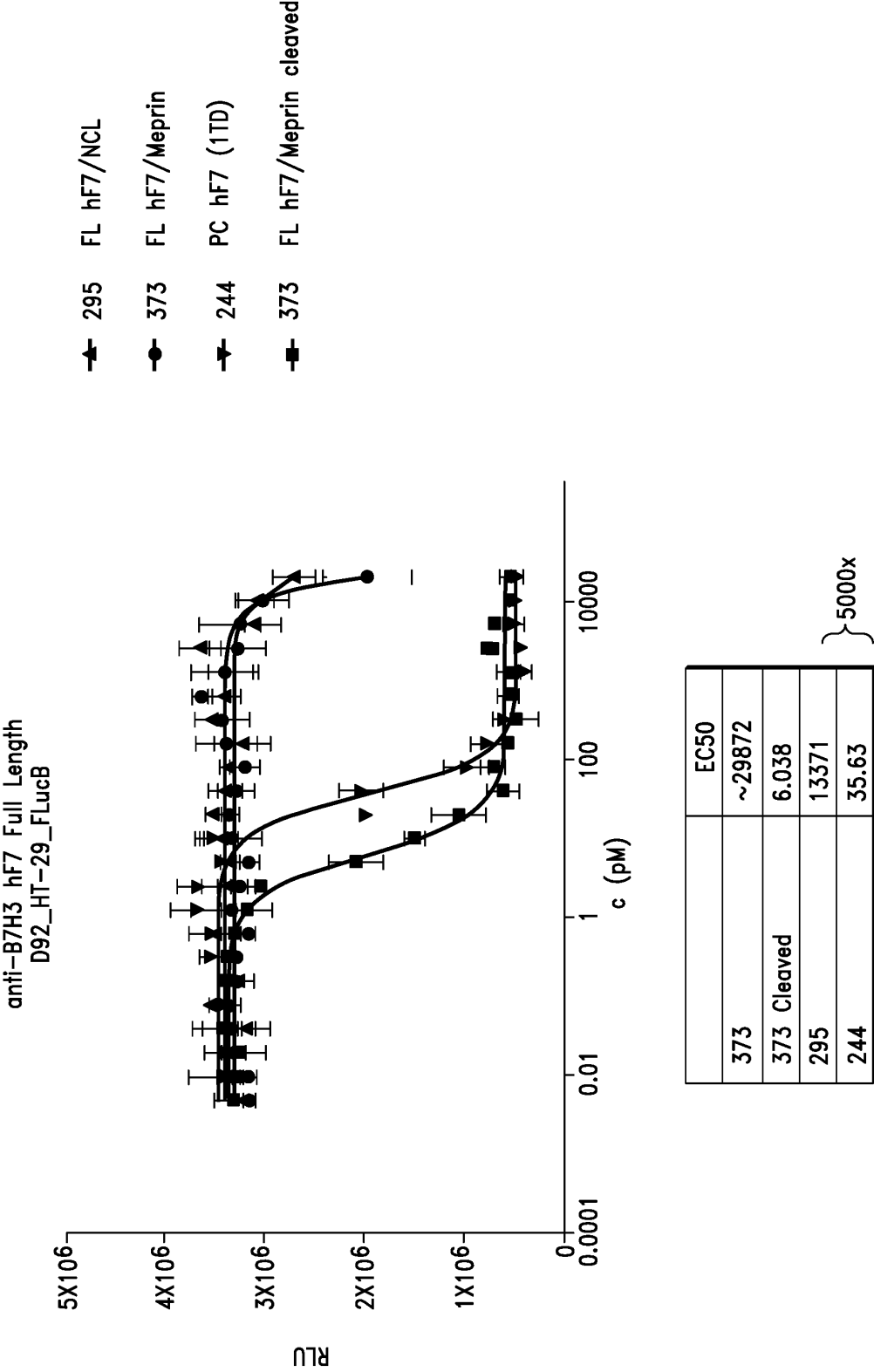


Figure 48

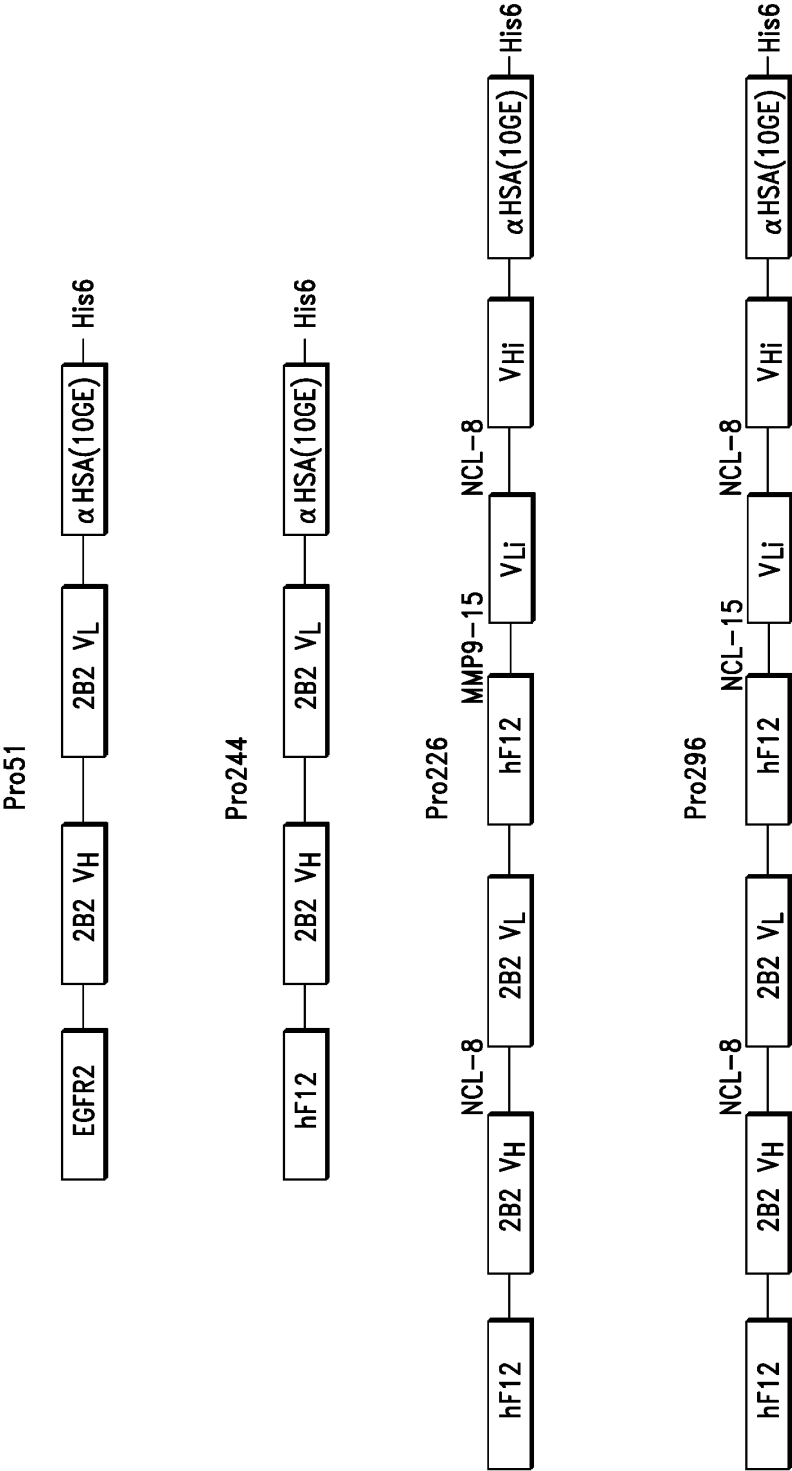
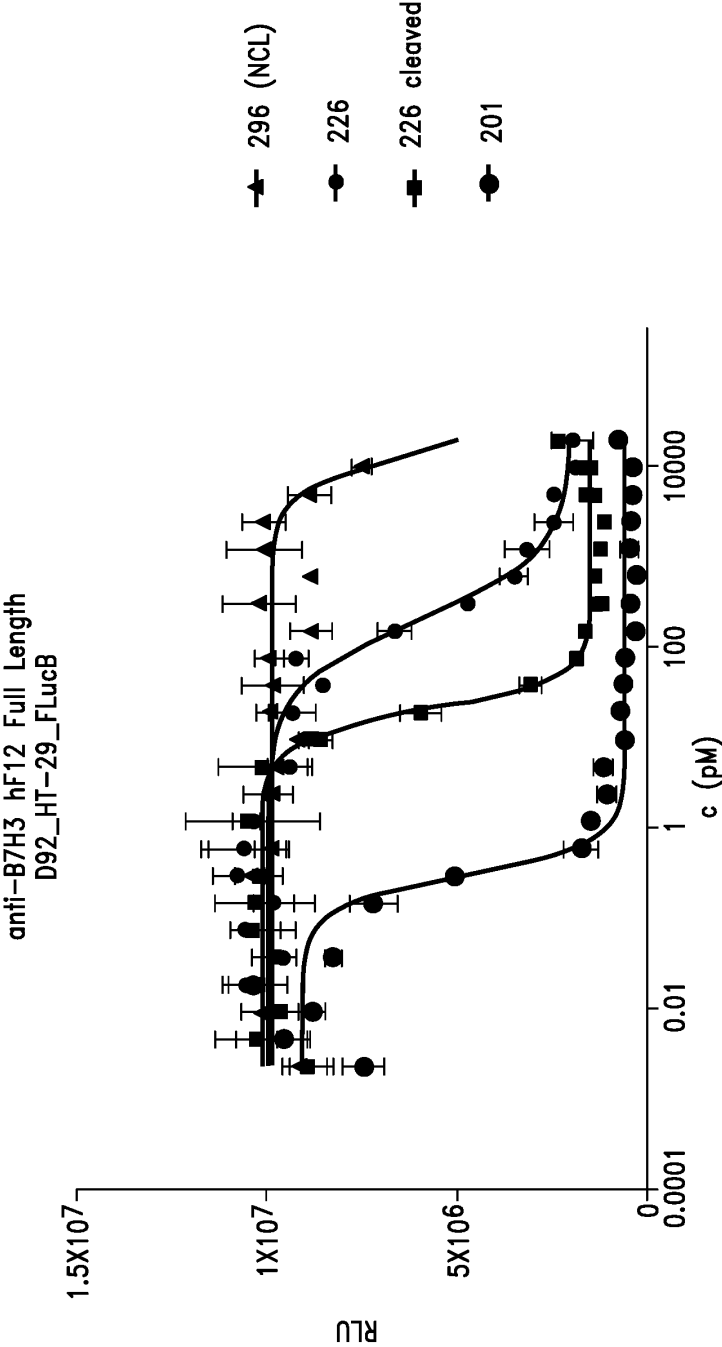


Figure 49

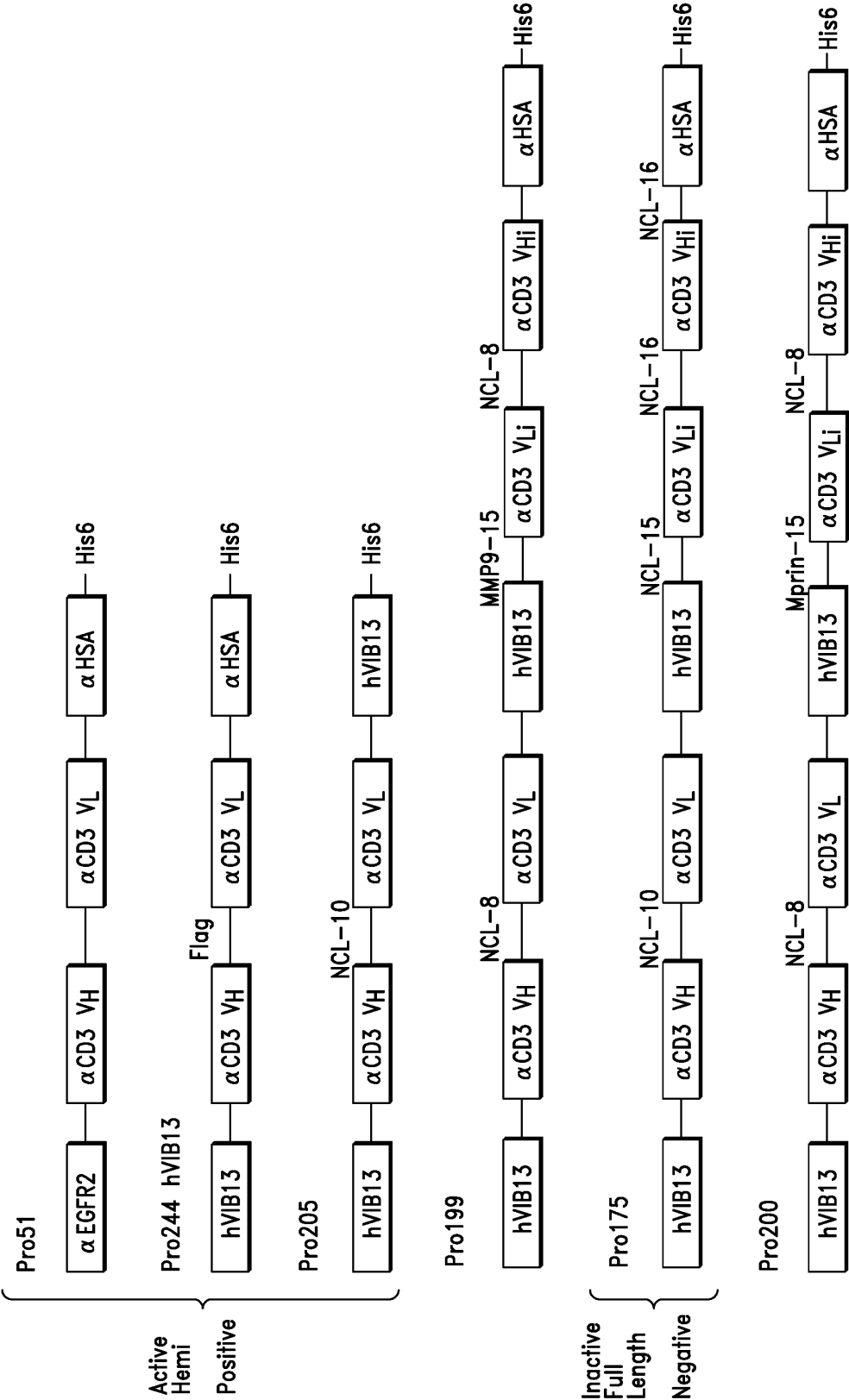


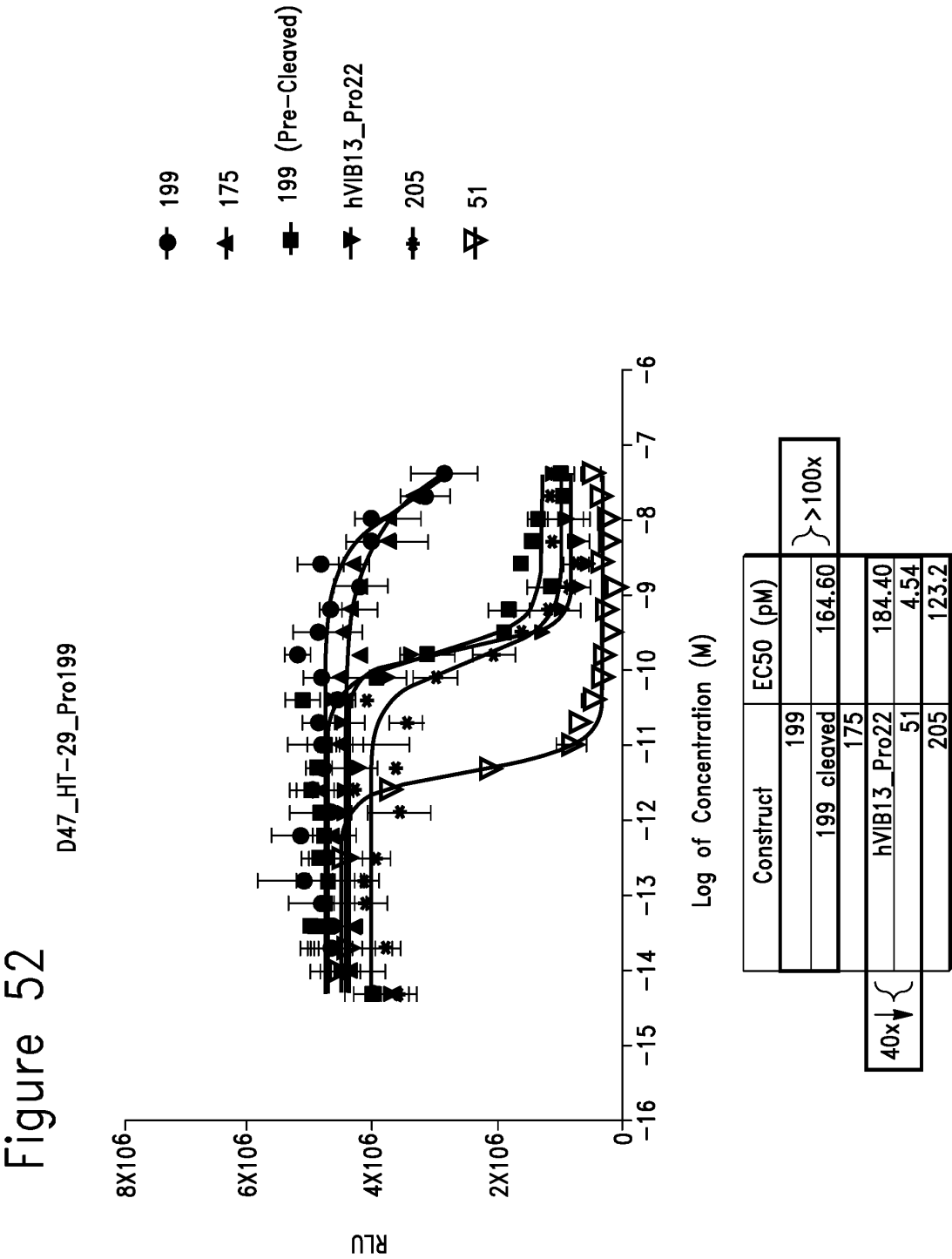
	EC50
226	211.7
226 cleaved	20.3
296 (NCL)	13075
201	0.3082

Figure 50

<u>Binding Affinity (nM)</u>		<u>Cross-Reactivity</u>	
<u>Clone</u>	<u>Human</u>	<u>Cyno</u>	<u>Cyno/Human</u>
VIB-13	2.3	11.6	5
hVIB-13	2.8	12.7	4.5
VIB-23	4.2	46.7	11.1
hVIB-23	4.1	51.8	12.6

Figure 51





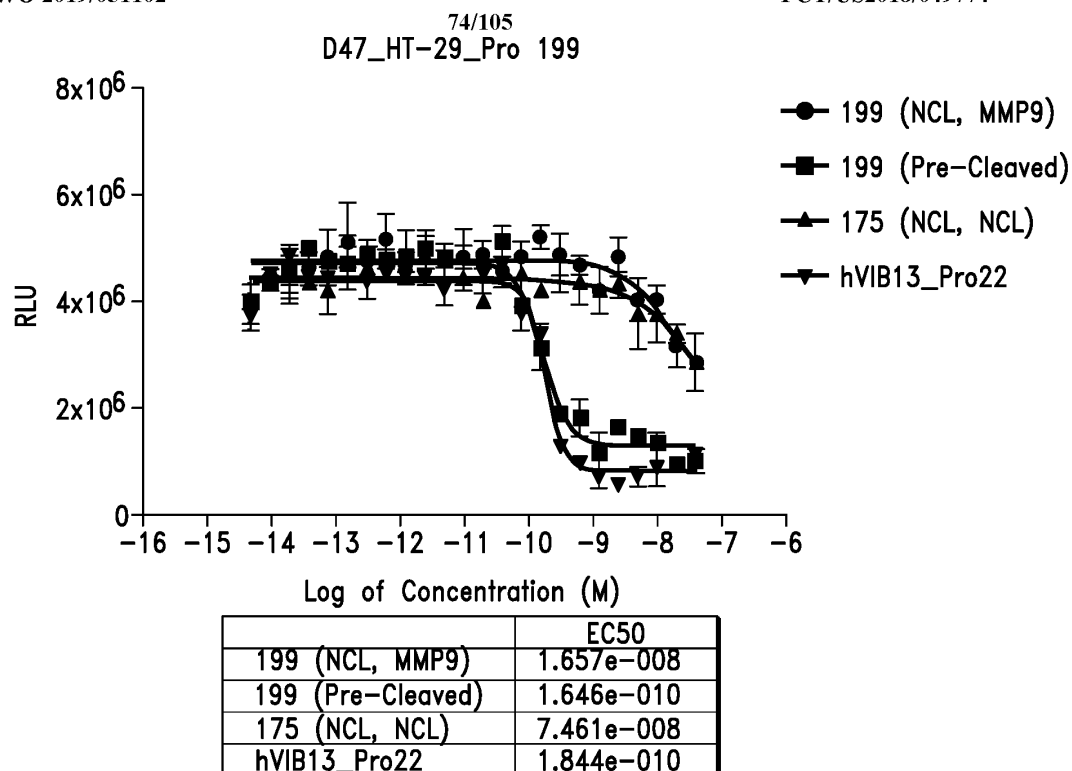


Figure 53A

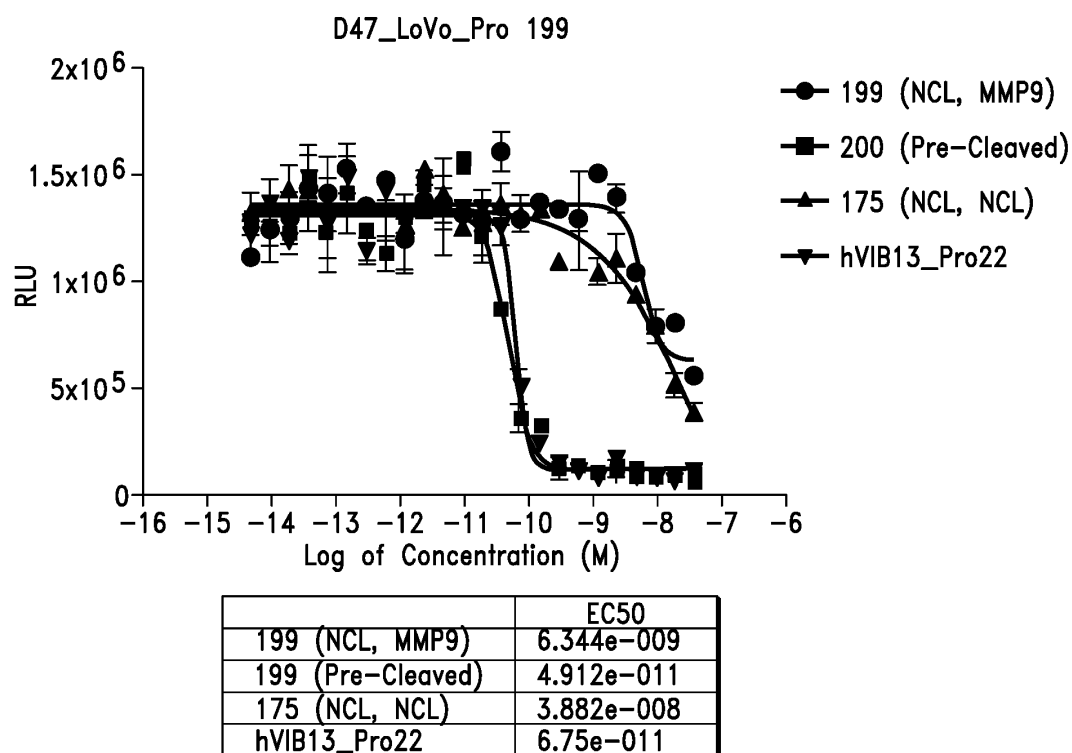


Figure 53B

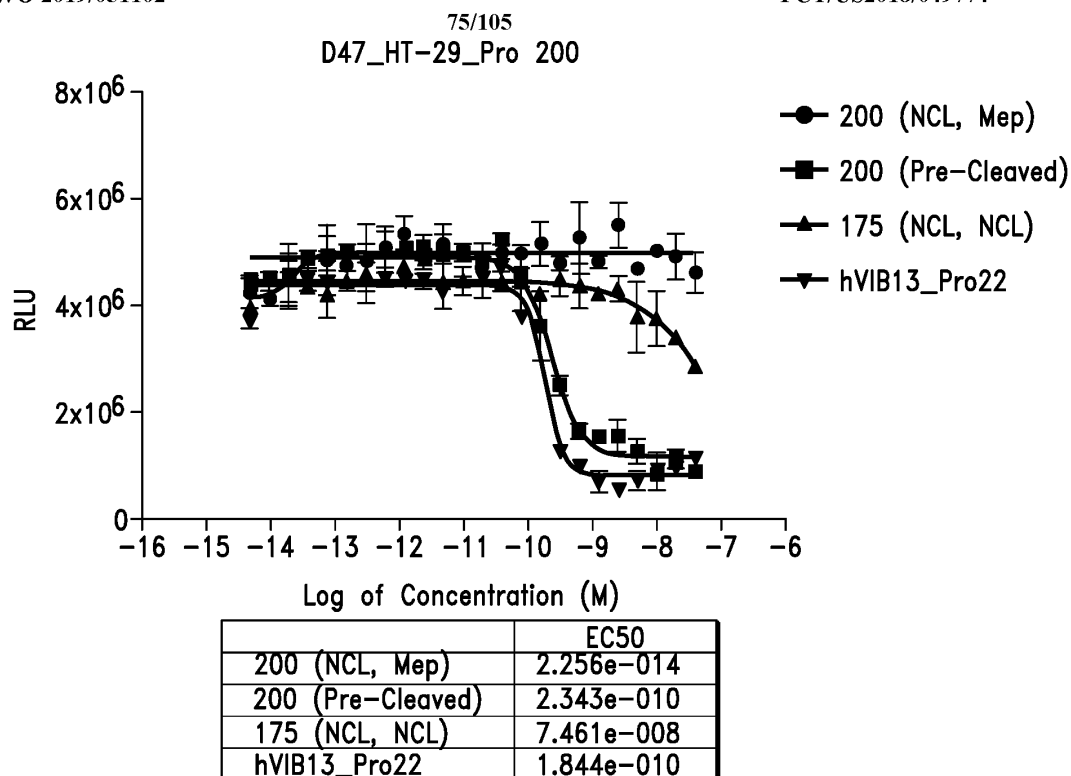


Figure 54A

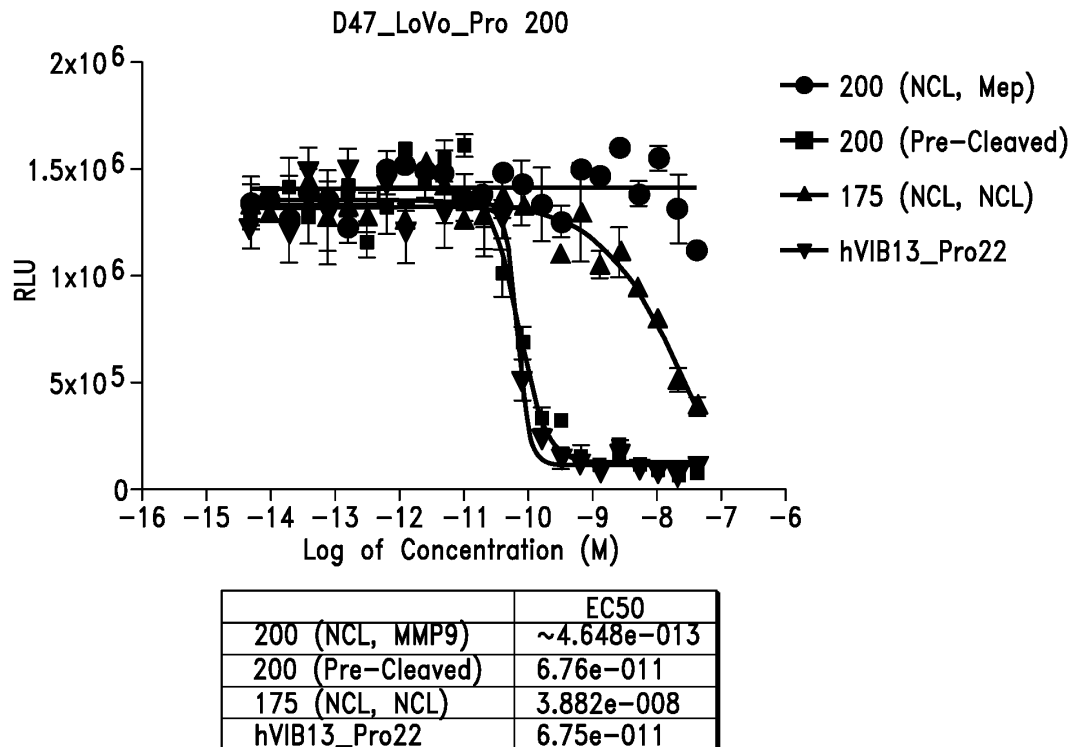
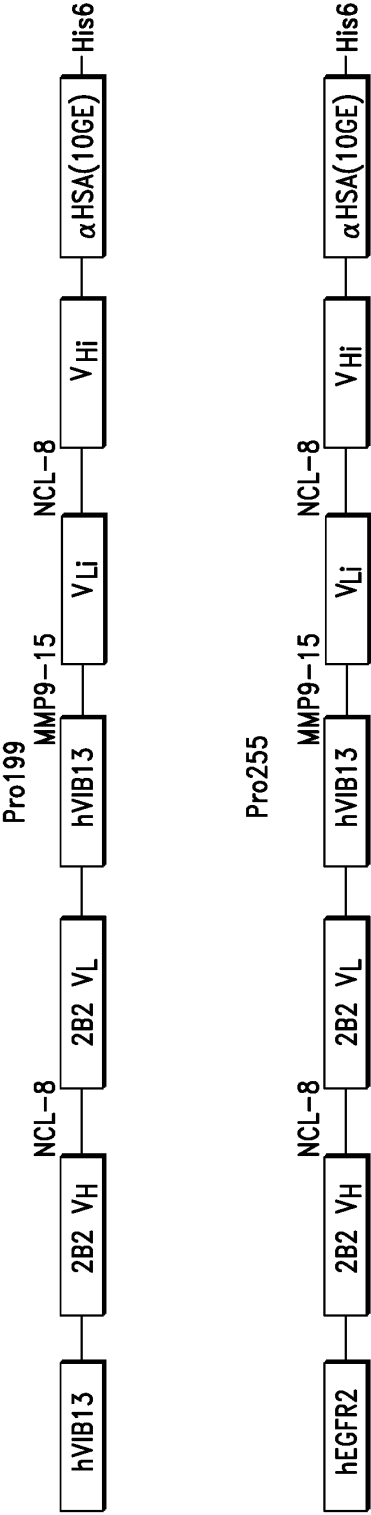


Figure 54B

Figure 55



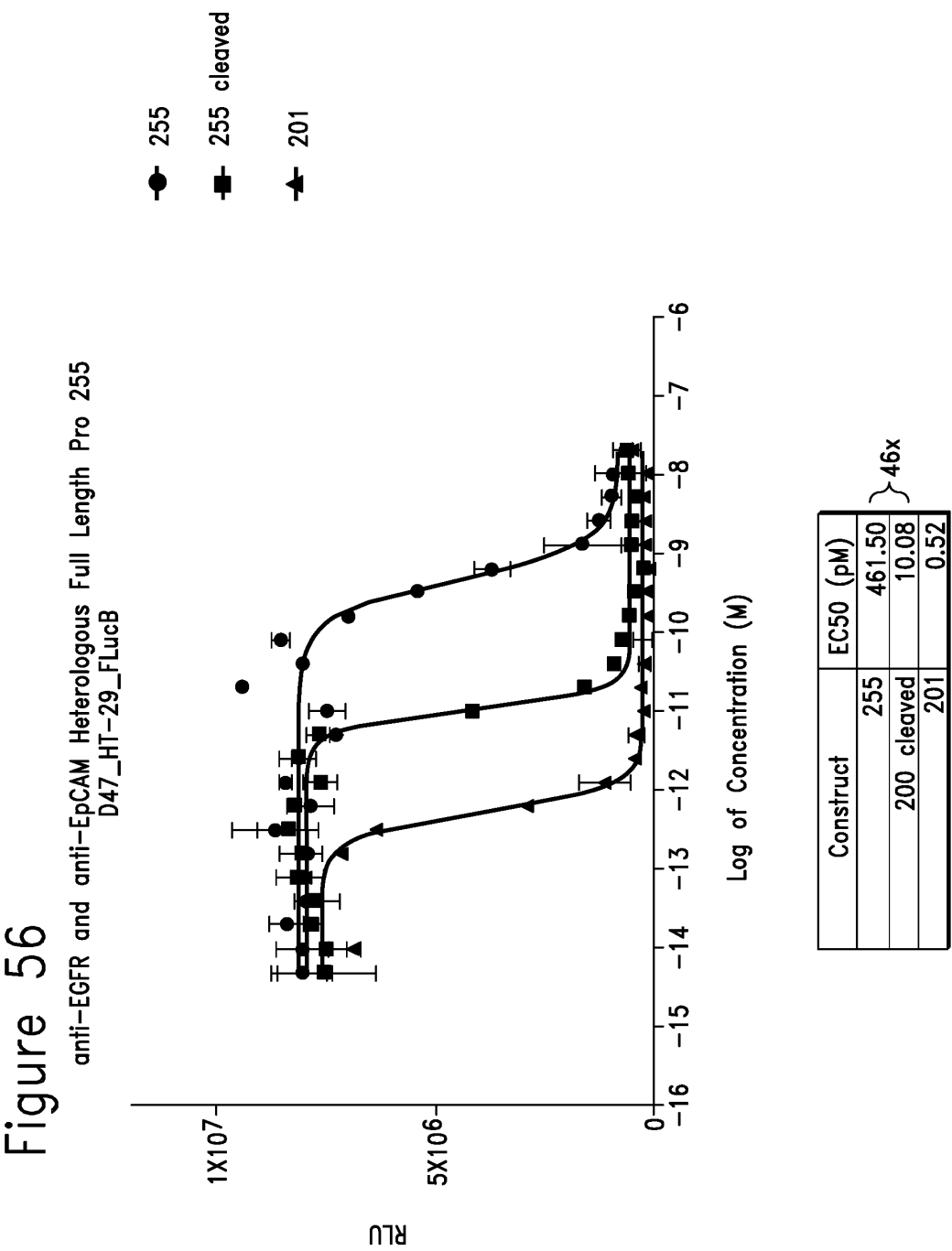
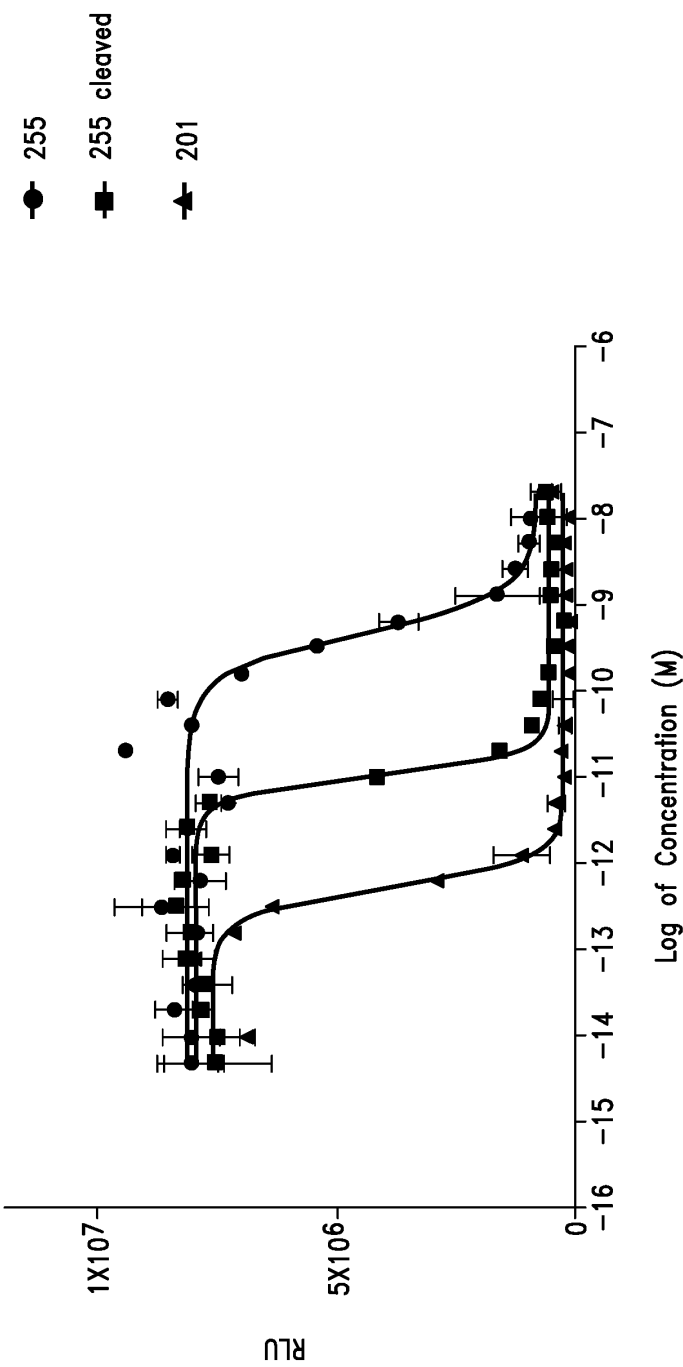


Figure 56

anti-EGFR and anti-EpCAM Heterologous Full Length Pro 255
D47_HT-29_FLucB



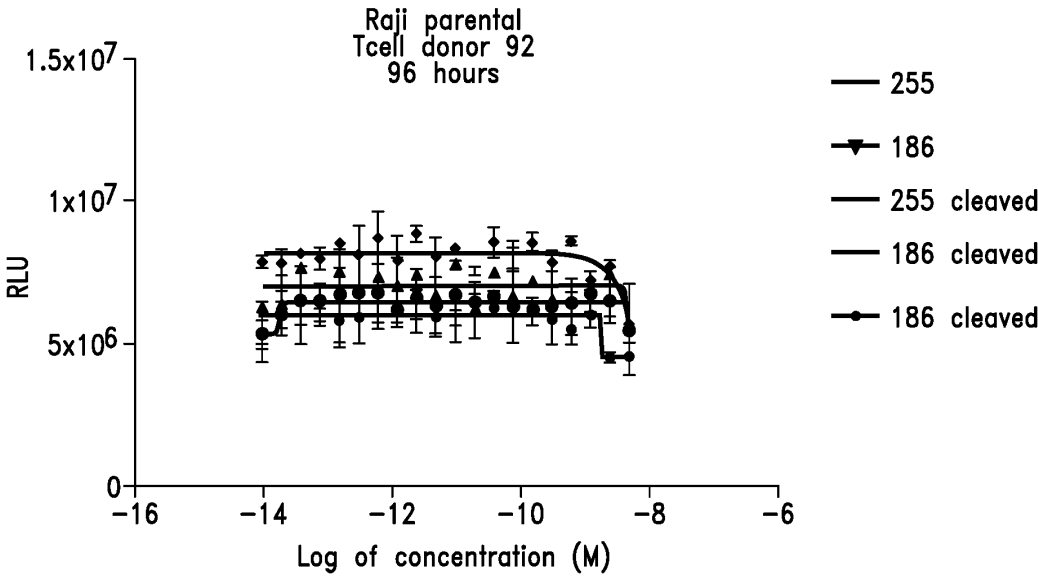
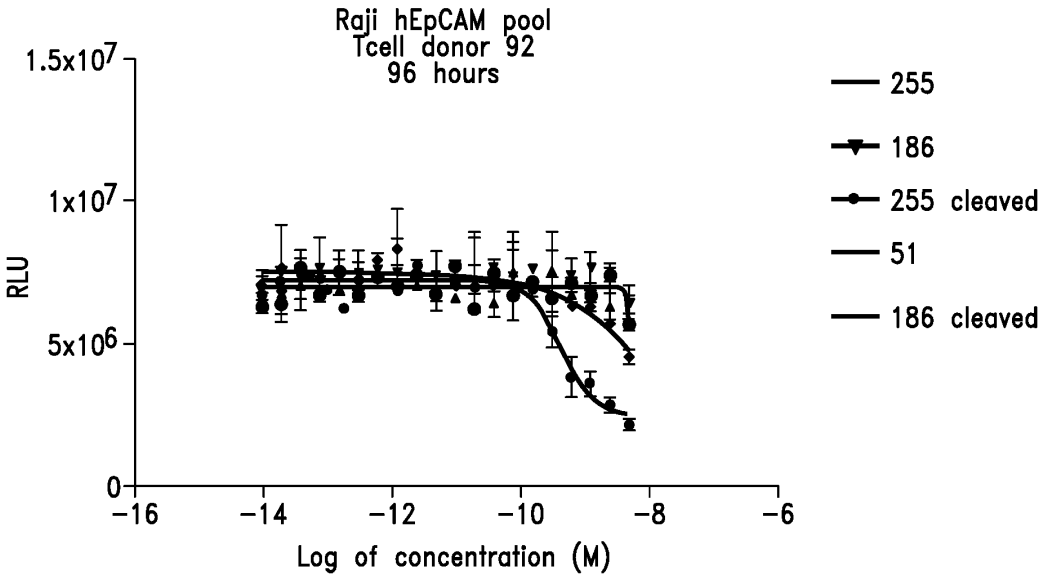
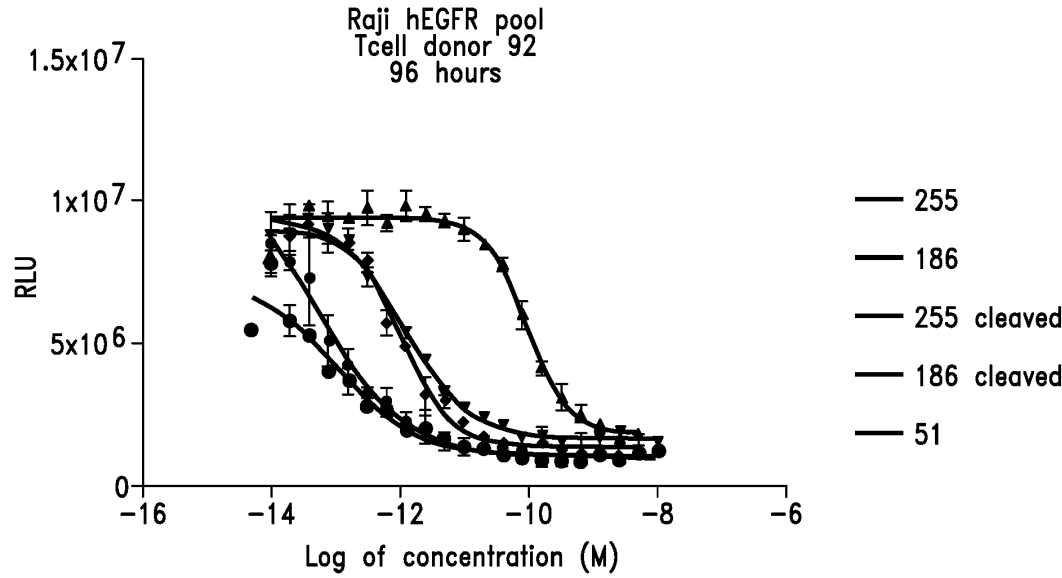


Figure 57A



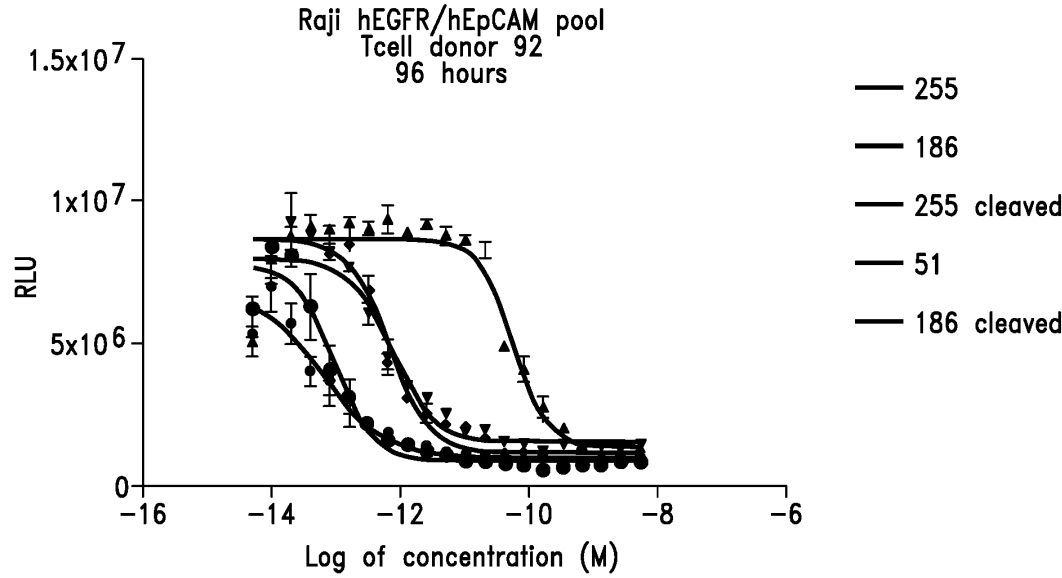
	IC50
255	~4.612e-009
255 cleaved	4.462e-010

Figure 57B



	IC50
255	9.205e-011
186	1.132e-012
255 cleaved	1.082e-012
186 cleaved	1.013e-013
51	5.329e-014

Figure 57C

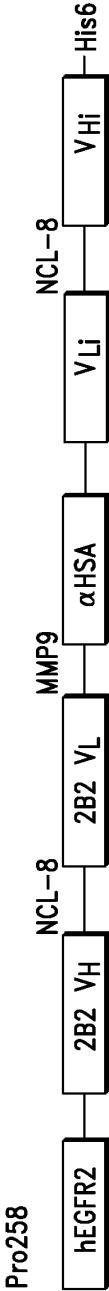


	IC50
255	5.29e-011
186	7.07e-013
255 cleaved	6.288e-013
51	9.237e-014
186 cleaved	5.862e-014

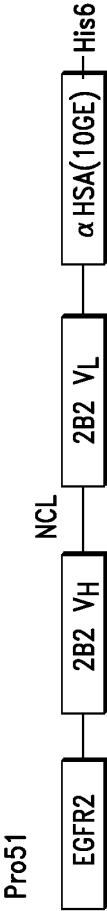
Figure 57D

Figure 58

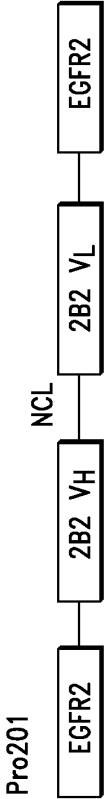
- Single Target COBRA



- αEGFR Positive Control



- Active Domain of Pro186



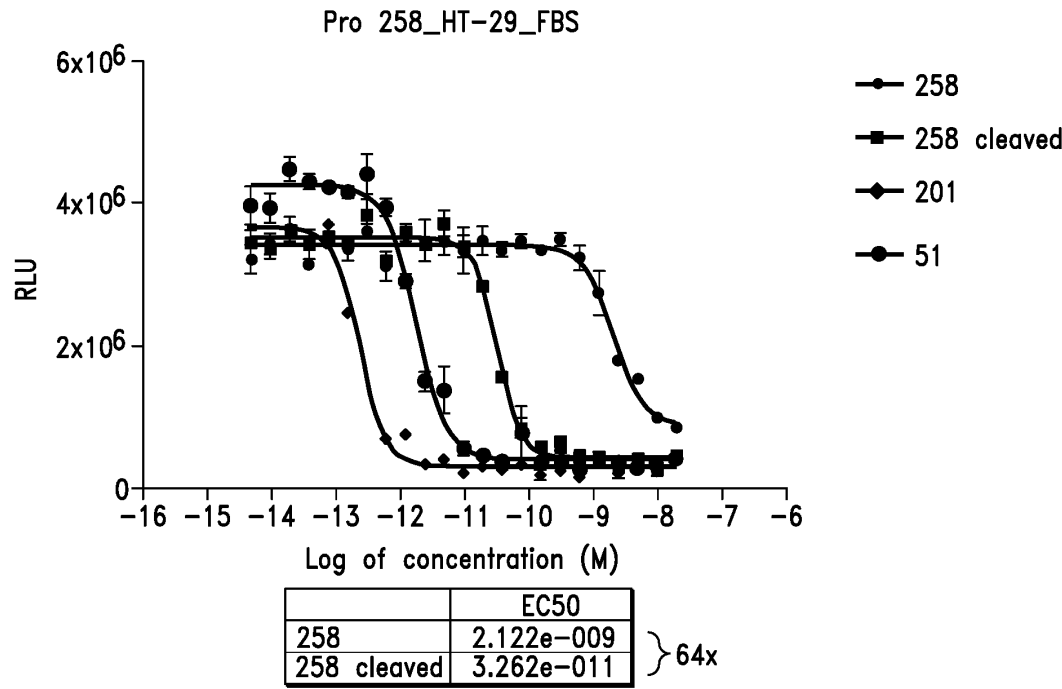


Figure 59A

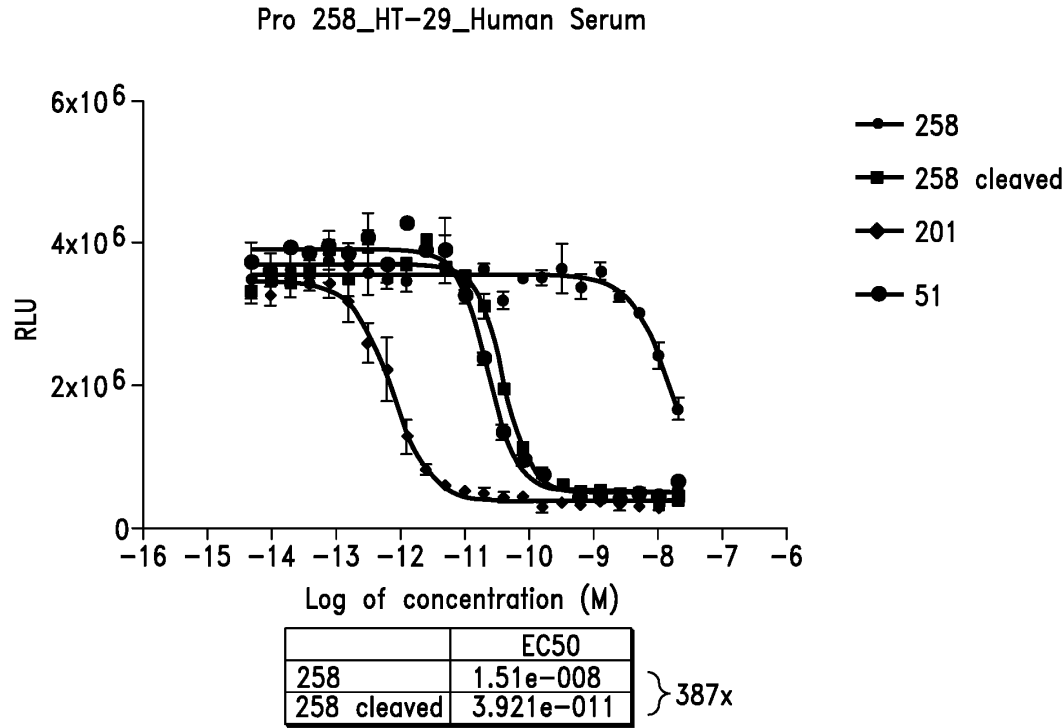


Figure 59B

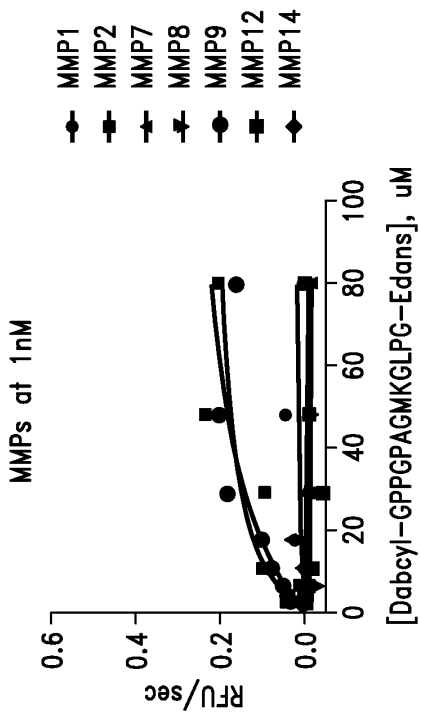


Figure 60B

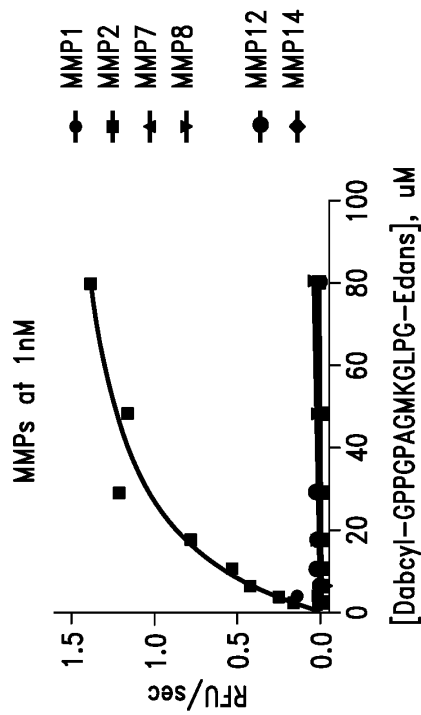


Figure 60C

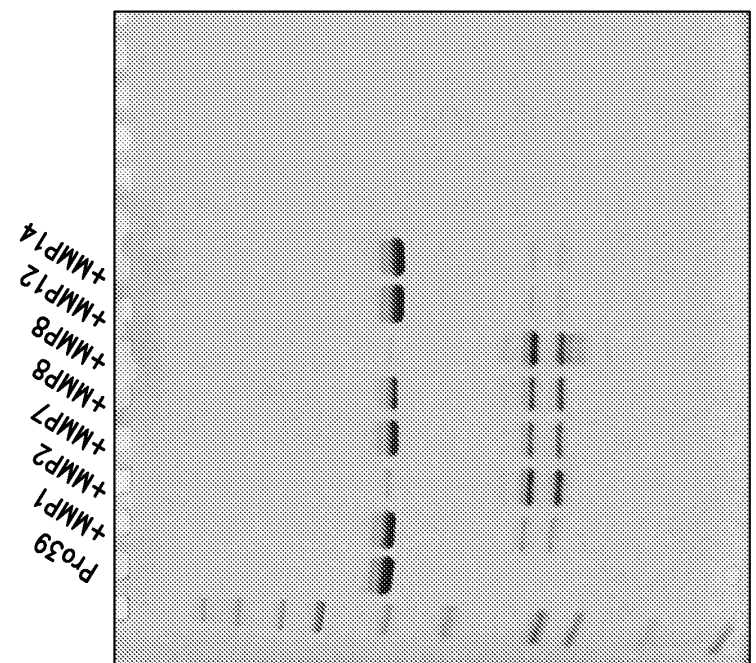


Figure 60A

Figure 61A

Format 2

Pro186 – EGFR2/MMP9 (aEGFR),
Pro225 – hF7/MMP9 (aB7H3)
Pro226 – hF12/MMP9 (aB7H3)
Pro233 – hEGFR2/MMP9 (aEGFR)
Pro311 – h77.2/MMP9 (aFOLR1)
Pro312 – h59.3/MMP9 (aFOLR1)
Pro313 – h22.4/MMP9 (aFOLR1)
Pro495 – hF7 MMP9 Vli2 + Vhi2 (aB7H3)

Format 2 - Heterologous

Pro246 – hEGFR1/hEGFR2 MMP9 (aEGFR)
Pro254 – hEGFR2/hEGFR1 MMP9 (aEGFR)
Pro255 – hEGFR2/h13 MMP9 (aEGFR/aEpCAM)
Pro256 – h13/hEGFR2 MMP9 (aEpCAM/aEGFR)
Pro420 – h77.2/hEGFR2 MMP9 (aFOLR1/aEGFR)
Pro421 – hEGFR2/h77.2 MMP9 (aEGFR/aFOLR1)
Pro432 - h13/hEGFR1 MMP9 (aEpCAM/aEGFR)
Pro479 – hF7/hF12 MMP9 (aB7H3)
Pro480 – hF12/hF7 MMP9 (aB7H3)

Dual Targeting Hemis (Format 3)

Pro448 – h77.2/hEGFR2 MMP9 VH (aFOLR1/aEGFR)
Pro449 – hEGFR2/h77.2 MMP9 VH (aEGFR/aFOLR1)
Pro450 – h77.2/hEGFR2 MMP9 VL (aFOLR1/aEGFR)
Pro451 – hEGFR2/h77.2 MMP9 VL (aEGFR/aFOLR1)

Figure 61B

Format 1

Pro140 – EGFR2 MMP9 (aEGFR)

Pro140b – EGFR2 Meprin (aEGFR)

Format 2 – Cleavable Linker Variants

Pro187 – EGFR2/Meprin (aEGFR)

Pro221 – EGFR2/KLK7-6 (aEGFR)

Pro222 – EGFR2/KLK7-13 (aEGFR)

Pro223 – EGFR2/KLK7-11 (aEGFR)

Pro224 – EGFR2/KLK7-10 (aEGFR)

Pro393 – EGFR2/S9 (aEGFR)

Pro394 – EGFR2/ST14MV (aEGFR)

Pro395 – EGFR2/CathS (aEGFR)

Pro396 – EGFR2/MMP9v (aEGFR)

Pro429 – EGFR2/Meprin/GranzymeB (aEGFR)

Pro430 – EGFR2/MMP9-2 (aEGFR)

Pro431 – EGFR2/ST14MS (aEGFR)

Format 4

Pro258 – hEGFR2 MMP9 (aEGFR)

Pro356 – hEGFR1 MMP9 (aEGFR)

Pro359 – hF7 MMP9 (aB7H3)

Pro388 – h77.2 MMP9 (aFOLR1)

Pro364 – h59.3 MMP9 (aFOLR1)

Figure 62A

Pro140 (Format 1)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GPAGMKGL/QTVVTQEPSLTVSPGGTVTLTCAASSTGA
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGR
TSSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNANTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV
TQEPSLTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA
RFGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDDD
DKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRRLSAASGFTFSKFGMSWVRQAPG
KGLEWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSQGTTLTVSS (SEQ ID NO:143)

Pro140b Format 1

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/KKLADEPE/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
TSGNYPNWWQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRT
SRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNANTVDLQMNSL
PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADEPEGGGS/QTVVT
QEPSLTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDDD
KADSVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRRLSAASGFTFSKFGMSWVRQAPGK
GLEWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSV
SSQGTTLTVSS (SEQ ID NO:144)

Figure 62B

Pro186 Format 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCAASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGR
TSRSGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNANTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV
TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD
DKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQAPG
KGLEWSSSISGSGRDTLYAESVKGRRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSQGTTLTVSS (SEQ ID NO:145)

Pro187 Format 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
TQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCAASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGR
TSRSGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNANTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADPEGGGS/QTVV
TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD
DKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQAPG
KGLEWSSSISGSGRDTLYAESVKGRRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSQGTTLTVSS (SEQ ID NO:146)

Figure 62C

Pro225 (FL aB7H3 hF7 MMP9 linker) Format 2

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT
FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
PARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:147)

Pro226 (FL aB7H3 hF12 MMP9 linker) Format 2

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTV
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEW
VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS
YISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG
NYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCTL
WYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPRTFSTY
SMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
VYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTV
SPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
PARFSGSLLG
GKAALTLSGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
VQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDR
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGG**
SGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWSSIS
GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTV
SS/HHHHHH (SEQ ID NO:148)

Figure 62D

Pro233 (humanized Pro186) Format 2

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRT
SRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNKNSLYLQMNSLR
AEDTALYYCAAAGSAWYGTLYEYDYWGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLTVTVSS/HHHHHH (SEQ ID NO:149)

Pro311 (FL aFOLR1 h77.2 MMP9 linker) format 2

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGGQGTTLTVTVSS/**GGGSGG**
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWWARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQK
PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWWFGG
GTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPG
NEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYW
GGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGN
YPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV
LWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQ
PGNSLRSLSCAASGFTFSKFGMSWVRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISR
NAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLTVTVSS/HHHHHH (SEQ ID NO:150)

Figure 62E

Pro312 (FL aFOLR1 h59.3 MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTN
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGLTVTVSS/**GGGS**
GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIRSKY
NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
GQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQ
KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWWF
GGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQA
PGKQREWWAVTHSDYSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGI
DYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVT
SGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEY
YCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTF
NKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNN
LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGL
VQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTIS
RDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID
NO:151)

Pro313 (FL aFOLR1 h22.4 MMP9 linker) format 2

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNY
ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGLTVTVSS/**G**
GGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIR
SKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW
AYWGQGLTVTVSS/**GGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW
VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
WWFGGGTKLTVL/**GGSGGGS**/QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWY
RQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAN
TATWGRVFWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLTCG
SSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGSGGGS**/EVQLVESGGGLVQPGGSLKLS
CAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKN
TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGSGGGS**/EV
QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYA
ESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH
(SEQ ID NO:152)

Figure 62F

Pro246 (FL haEGFR1/haEGFR2 heterologous COBRA with MMP9 linker)

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAINWSSGSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQ
GTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPG
KGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
NFGNSYISYWAYWGQGT LVT VSS/**GGGSGGGS**/QTVVTQEP SLTVSPGGTVTLTCASSTG
AVTSGNYPNWWQQKPGQAPRGLIGG TKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTLWYSNRWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRP GGS LTLSCAASGR
TSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSL
RAEDTALYYCAAAAGSAWYGTLYEYDYWGQGT LVT VSS/**SGGPGPAGMKGLPGS**/QTVV
TQEP SLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVT
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG
LEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLVTVSS/HHHHHH (SEQ ID NO:153)

Pro256 (FL haEpCAM VIB13/haEGFR1 heterologous COBRA MMP9 linker)

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
YADSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGT LVT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWW
ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
SYWAYWGQGT LVT VSS/**GGGSGGGS**/QTVVTQEP SLTVSPGGTVTLTCASSTGAVTSGNY
PNWWQQKPGQAPRGLIGG TKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
SNRWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRP GGS LTLSCAASGRTSRSYGM
GWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALY
YCAAAAGSAWYGTLYEYDYWGQGT LVT VSS/**SGGPGPAGMKGLPGS**/QTVVTQEP SLTV
SPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLG
GKAALTLSGVQPEDEAEYYCVLWYSNRWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
VQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDR
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVT VSS/**GGG
SGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWVSSIS
GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTV
SS/HHHHHH (SEQ ID NO:154)

Figure 62G

Pro420 (FL aFOLR1 h77.2/haEGFR1 heterologous COBRA MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGGGTLTVSS/**GGGSGG
GS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWWARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWWFGG
GTKLTVL/**GGGSGGGS**/QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPG
KREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAGS
AWYGTLYEYDYWGQGT LTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLT
CGSSTGAVTSGNYPNWWQKP GQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSG
VQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLK
LSCAASGFTFNKYAMN WWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDS
KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVSS/**GGGSGGGS**/
EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTL
YAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LTVSS/HHHHH
H (SEQ ID NO:155)

Pro421 (FL haEGFR1/aFOLR1 h77.2 heterologous COBRA MMP9 linker)

QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKREFVSGISWRGDST
GYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQ
TLTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGT LTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFT
VSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
AVYVCNRNFDRIYWGGGTLTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVT
LTCGSSTGAVTSGNYPNWWQKP GQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALT
SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGG
LKLSCAASGFTFNKYAMN WWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVSS/**GGGSGGGS**/
/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTL
YAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LTVSS/HHHHH
H (SEQ ID NO:156)

Figure 62H

Pro393 (Pro186 S9 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GARLQSAAPAGLKGAG**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSAAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTTLTVSS/HHHHHH (SEQ ID NO:157)

Pro394 (Pro186 ST14(MV) linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSFTRQARVVGGGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSAAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTTLTVSS/HHHHHH (SEQ ID NO:158)

Figure 62I

Pro395 (Pro186 CathS linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSARLQSAAPGGGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCWLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:159)

Pro396 (Pro186 MMP9v linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GSGGPGPAGMHGLPGGS**/QTVV
TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCWLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKG
LEWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:160)

Figure 62J

Pro429 (Pro186 Meprin/GranzymeB linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGGVYADSLEDGGGS**/QTVVTQ
EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARF
SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLV
ESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDKA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV
SS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKGLE
WVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GTLTVTVSS/HHHHHH (SEQ ID NO:161)

Pro430 (Pro186 MMP9-2 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGPGPAGLKGAPGS**/QTVVTQE
PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARF
GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLV
ESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDKA
DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV
SS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKGLE
WVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GTLTVTVSS/HHHHHH (SEQ ID NO:162)

Figure 62K

Pro431 (Pro186 ST14(MS) linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSLSGRSDNHGGGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTTLTVSS/HHHHHH (SEQ ID NO:163)

Pro258 (Pro186 with a single aEGFR domain and a central aHSA domain)

QVKLVESGGGVVRPGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANKSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQ
TLTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLS
CAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNANTTLYL
QMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQ
PGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSS/HHHHHH
(SEQ ID NO:164)

Figure 62L

Pro221

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNPYSAGRGGS/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTGLTVTVSS/HHHHHH (SEQ ID NO:165)

Pro222

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNPYSAGGSGG/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTGLTVTVSS/HHHHHH (SEQ ID NO:166)

Figure 62M

Pro223

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGRNVYSAGGSGG/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:167)

Pro224

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNTWSAGKGGGS/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:168)

Figure 62N

Pro254

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRT
FSSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNANKNTLYLQMNSLRA
EDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVV
TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPA
RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLV
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG
LEWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTTLVTVSS/HHHHHH (SEQ ID NO:169)

Pro255

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLTLSCAASGTG
SIFSINLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRFTISRDNANKNTLYLQMNSLRP
EDTAVYYCNLLLRSSPGATTPYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSL
TVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSL
LGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG
GLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/**G**
GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWS
SISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLV
TVSS/HHHHHH (SEQ ID NO:170)

Figure 62O

Pro262

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLT
CASSTGAVTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLT
CAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVD
LQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPG
S/QTVVTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDD
KGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGSGG
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYD
YKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW
GQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWR
QAPGKGLEWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:171)

Pro356

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAINWSSGSTY
YADSVKGRFTISRDNANTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQ
GTLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPG
KGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
NFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASSTG
AVTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCTLWYSNRWWFGGGTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGNSLRL
SCAASGFTFSKFGMSWWRQAPGKGLEWWSSISGSGRDTLYAESVKGRFTISRDNANTTLY
LQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/GGGSGGGS/QTVVTQEPSTVSPG
GTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPG
GGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/HHHHHH
(SEQ ID NO:172)

Figure 62P

Pro359

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGS**GGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGT LVT VSS/**GGGS**GGGS/QT VVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWFFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLS
CAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYL
QMNSLRPEDTAVYYCTIGGSLSVSSQGT LVT VSS/**GGGS**GGGS/QT VVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWFFGGGTKLTVL/**GGGS**GGGS/EVQLVESGGGLVQ
GGSLKLSCAASGFTFNKYAMN WWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVT VSS/HHHHHH
(SEQ ID NO:173)

Pro364

QVQLVESGGGLVQPGGSLRLSCAAPGN TFSISAMGWYRQAPGKQREWWAVTHSDYSTN
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGT LVT VSS/**GGGS**
GGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWWARIRSKY
NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
GQGT LVT VSS/**GGGS**GGGS/QT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQ
KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWFF
GGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGM
SWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGT LVT VSS/**GGGS**GGGS/QT VVTQEPSLTVSPGGTVTLTCGSSTGAV
TSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAE
YYCVLWYSNRWFFGGGTKLTVL/**GGGS**GGGS/EVQLVESGGGLVQPGGSLKLSCAASGF
TFNKYAMN WWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQM
NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVT VSS/HHHHHH (SEQ ID NO:174)

Figure 62Q

Pro388

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/**GGGSGG**
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWWARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWWFGG
GTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW
VRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCT
IGGSLSVSSQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG
NYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC
VLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK
YAMNWWVRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/HHHHHH (SEQ ID NO:175)

Figure 62R

Pro432

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
YADSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGLTVTV
SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWW
ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
SYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY
PNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
SNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAM
GWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY
YCAAGYQINSGNYNFKDYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSL
TVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSL
LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG
GLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**G**
GGGSGGGS/EVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWS
SISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV
TVSS/HHHHHH (SEQ ID NO:176)

Pro448

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGGQGLTVTVSS/**GGGGSG**
GGG/QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
DSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYW
GQGLTVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQ
APGKGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV
RHANFGNSYISYWAYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAAL
TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGGSGGGS**/EVQLVESGGGLVQP
GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWSISGSGRDTLYAESVKGRFTISRDN
AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLTVTVSS/HHHHHH (SEQ ID NO:177)

Figure 62S

Pro449

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/QVKLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTP
GNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
WGQGTTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR
QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHANFGNSYISYWAYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKA
ALTL SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLV
QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISR
DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLVTVSS/HHHHHH (SEQ ID
NO:178)

Pro450

QVKLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD
SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTTLVTVSS/**GGGSGG**
GS/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
DSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYW
GQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQ
QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCTLWYSNRWW
FGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA
MNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
DTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQ
GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN
AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLVTVSS/HHHHHH (SEQ ID NO:179)

Figure 62T

Pro451

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLVTVSS/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNVMAWYRQTP
GNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
WGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSTLVSPGGTVTLTCASSTGAVTSGNYPNW
VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
WVFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNK
YAMNWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/EVQLVESGGGLV
QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISR
DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLVTVSS/HHHHHH (SEQ ID
NO:180)

Pro479

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSTLVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPT
FSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNKNTLYLQMNSLRA
EDTAVYYCAAGGVLAHHNYEYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEP
STLVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTARFSG
SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVES
GGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYDYKDDDDKAD
SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVS
S/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW
VSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
LTVTVSS/HHHHHH (SEQ ID NO:181)

Figure 62U

Pro480

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNIEYDYWGQGLTVT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW
VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS
YISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG
NYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL
WYSNRWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTY
HMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
AVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPS
LTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGS
LLGGKAALTLSGVQPEDEAEYYCWLWYSNRWFGGGTKLTVL/**GGGSGGGS**/EVQLVESG
GGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYDYKDDDDKADSV
KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/
GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV
SSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
LTVTVSS/HHHHHH (SEQ ID NO:182)

Pro495

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQ
GLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT
FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLR
AEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGGTKDDAPGTPARF
SGSLLGGKAALTLSGVQPEDEAEYYCWLWYSNRWFGGGTKLTVL/**GGGSGGGS**/EVQLV
ESGGGLVQPGGSLKLSCAASGFTFNKHAMN WVRQAPGKGLEWVARIRSKYNNYATAYAD
SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS
S/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW
VSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
LTVTVSS/HHHHHH (SEQ ID NO:183)