

Figura 1

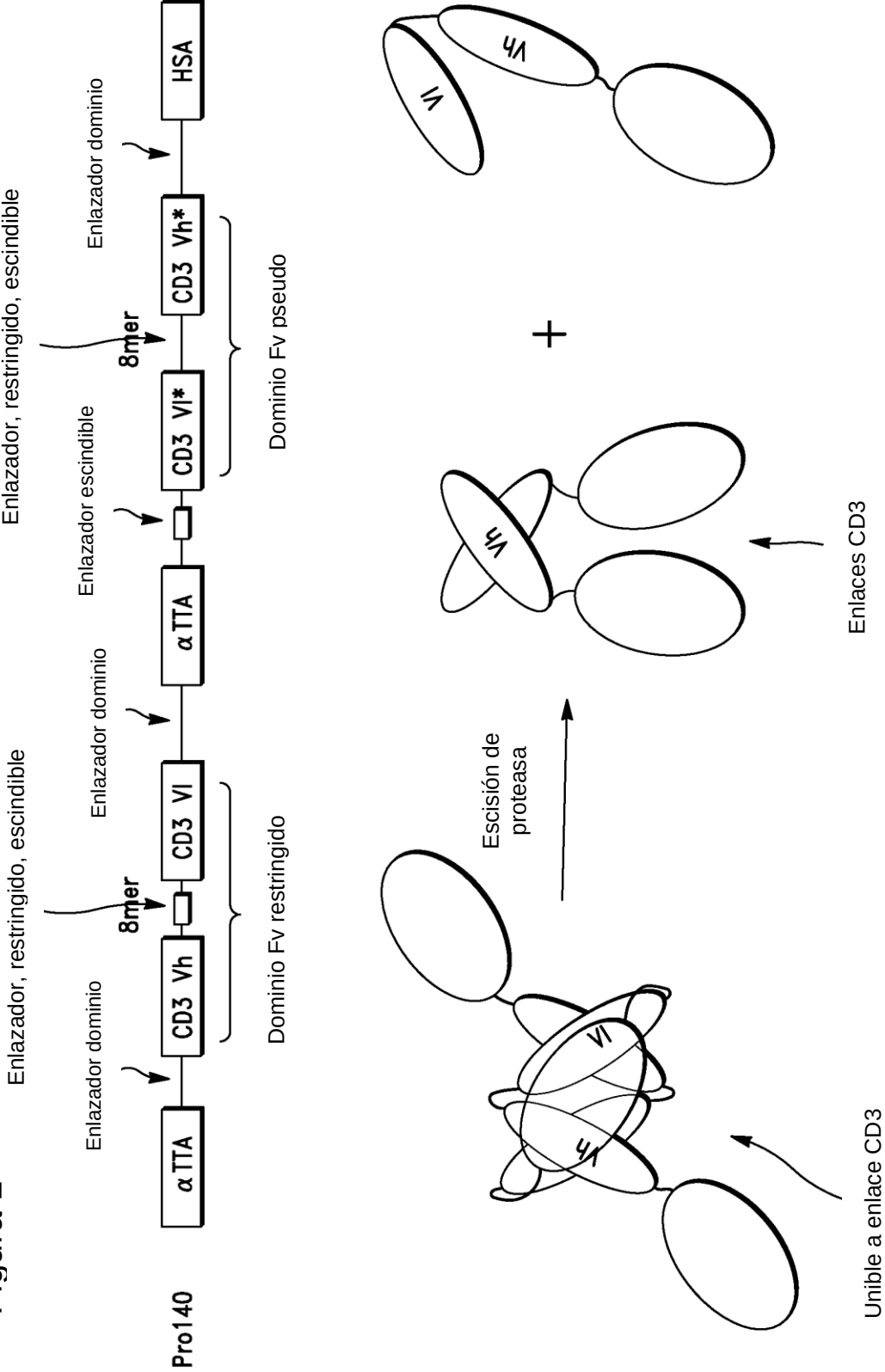


Figura 2

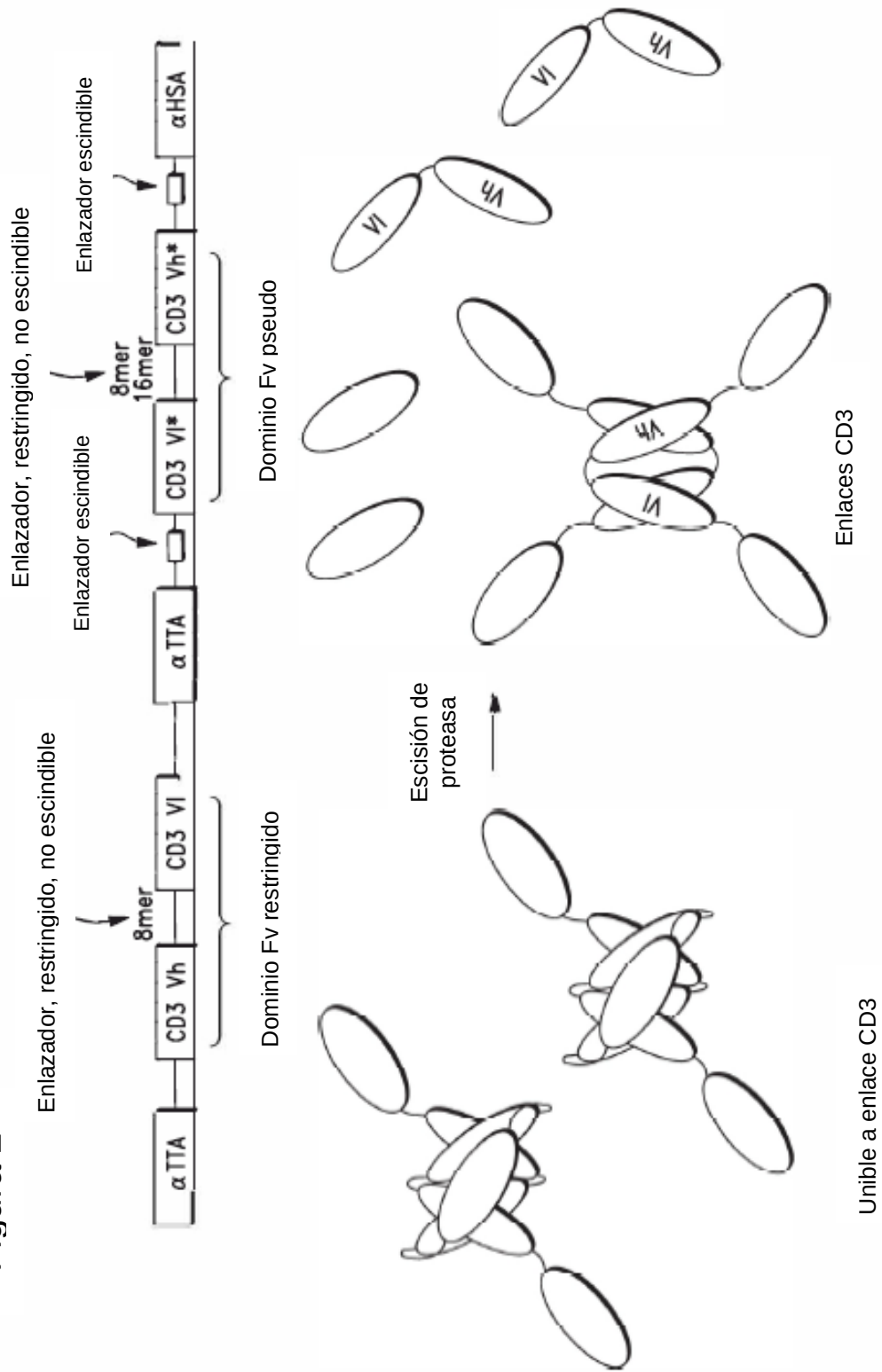


Figura 3A

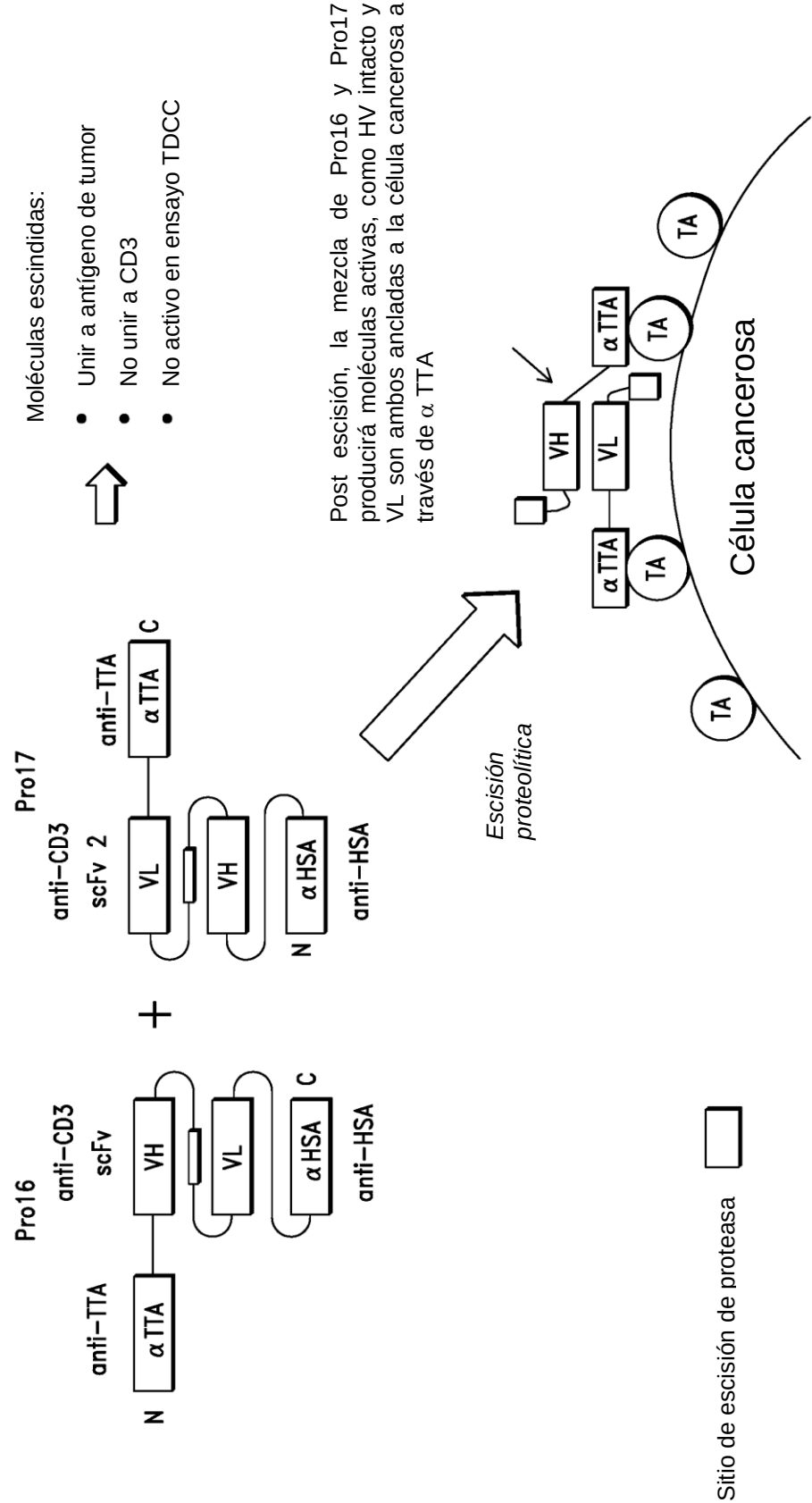


Figura 3B

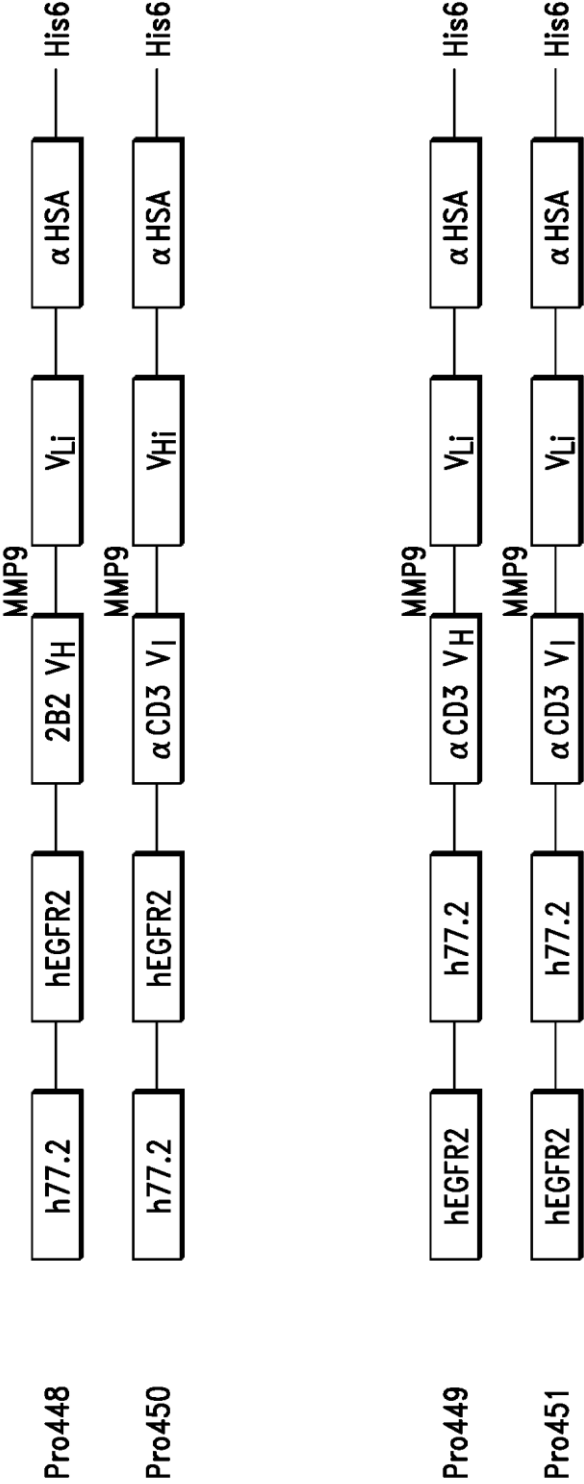


Figura 4

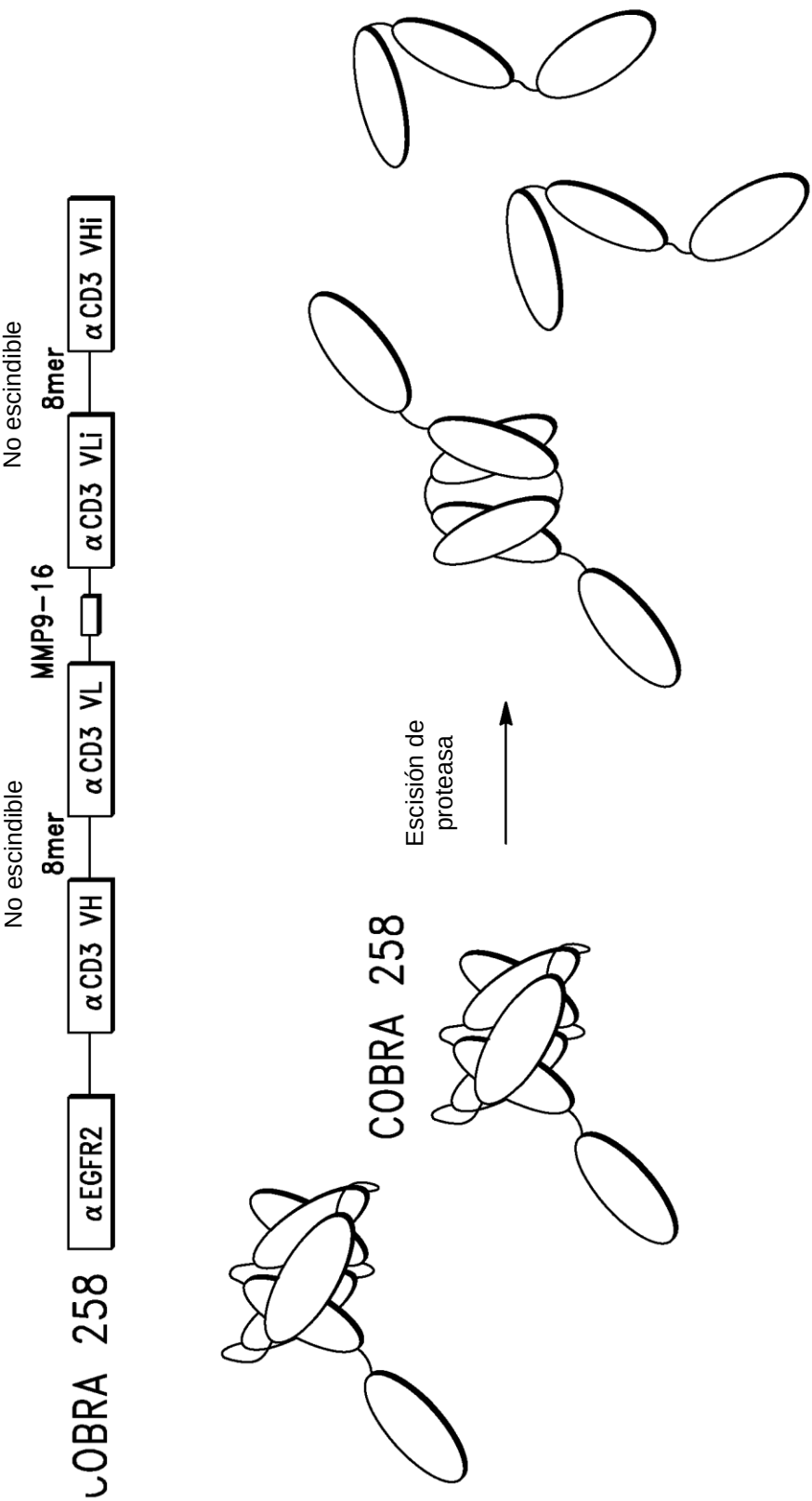


Figura 5A

sdAbs direccinada **α EGFR1**

EVQLVESGGGLVQAGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTYYADS**
VKGRFTISRDNKNTMYLQMNSLKPEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WGQGTQVTVS
 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

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYAD**
SVKGRFTISRDNKNTVDLQMNSLKPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS
 (SEQ ID NO:5)

sdCDR1 **GRTSRSYGMG** (SEQ ID NO:6)

sdCDR2 **GISWRGDSTGYADSVKG** (SEQ ID NO:7)

sdCDR3 **AAGSAWYGTLYEYDY** (SEQ ID NO:8)

haEGFR1

EVQLVESGGGLVQPGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTYYADS**
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WGQGTQVTVSS
 (SEQ ID NO:9)

sdCDR1 **GRTFSSYAMG** (SEQ ID NO:10)

sdCDR2 **INWSSGSTYYADSVKG** (SEQ ID NO:11)

sdCDR3 **GYQINSGNYNFKDYEYDY** (SEQ ID NO:12)

haEGFR2

QVKLVESGGGWRPGLSLTSCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYAD**
SVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAA**AAGSAWYGTLYEYDY**WGQGTQVTVSS
 (SEQ ID NO:13)

sdCDR1 **GRTSRSYGMG** (SEQ ID NO:14)

sdCDR2 **GISWRGDSTGYADSVKG** (SEQ ID NO:15)

sdCDR3 **AAGSAWYGTLYEYDY** (SEQ ID NO:16)

Figura 5B

sdAbs direccionada - Continuación**αFOLR1 h77-2**

QVQLVESGGGLVQPGGSLRLSCAAS**GFTVSN****SVMA**WYRQTPGNREFVA**IINSIGITNYADSVK**
GRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNR**NFDRIY**WGQGTLVTVSS (SEQ ID NO:17)

sdCDR1 **GFTVSN****SVMA** (SEQ ID NO:18)

sdCDR2 **IINSIGITNYADSVKG** (SEQ ID NO:19)

sdCDR3 **NFDRIY** (SEQ ID NO:20)

αFOLR1 h59.3

QVQLVESGGGLVQPGGSLRLSCAAP**GNTFSISAMG**WYRQAPGKQREWWA**VTHSDYSTNYADS**
VKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCKH****YGIDY**WGQGTLVTVSS (SEQ ID NO:21)

sdCDR1 **GNTFSISAMG** (SEQ ID NO:22)

sdCDR2 **VTHSDYSTNYADSVKG** (SEQ ID NO:23)

sdCDR3 **YGIDY** (SEQ ID NO:24)

αFOLR1 h22-4

QVQLVESGGGLVQPGGSLRLSCEAS**GTTFSRDVMG**WYRQAPGKQRELVA**IISRGGSTNYADSV**
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNAN**NTATWGRVF**WGQGTLVTVSS (SEQ ID NO:25)

sdCDR1 **GTTFSRDVMG** (SEQ ID NO:26)

sdCDR2 **IISRGGSTNYADSVKG** (SEQ ID NO:27)

sdCDR3 **NTATWGRVF** (SEQ ID NO:28)

αB7H3 hF7

QVQLQESGGGLVQPGGSLRLSCAPS**RRTFHTYHMG**WFRQAPGKEREFVA**VINWSGGSTVYAD**
SVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAG****GGATTQRATEASYDY**WGQGTLVTVSS (SEQ ID NO:29)

sdCDR1 **RRTFHTYHMG** (SEQ ID NO:30)

sdCDR2 **VINWSGGSTVYADSVKG** (SEQ ID NO:31)

sdCDR3 **GGATTQRATEASYDY** (SEQ ID NO:32)

Figura 5C

sdAbs direcccionada - Continuación α B7H3 hF12

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTSYADSVKG**RFTISRDNKNTLYLQMNSLRRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGLTVTVSS (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

QVQLVESGGGLVQPGGSLTLSCAAS**GTGSIFSINLMG**WYRQAPGKQRELVA**RITSGDSTVYADSVKG**RFTISRDNKNTLYLQMNSLRPEDTAVYYCN**LLRSPGATTPY**WGQGLTVTVSS (SEQ ID NO:37)

sdCDR1 **GTGSIFSINLMG** (SEQ ID NO:38)

sdCDR2 **RITSGDSTVYADSVKG** (SEQ ID NO:39)

sdCDR3 **LLRSPGATTPY** (SEQ ID NO:40)

 α EpCAM h23

QVQLVESGGGLVQPGGSLTLSCVIS**GSFSALWAMR**WYRQAPGQRELVA**SSRGGTTSYADSVKGR**RFTISRDNKNTLYLQMNSLRPEDTAVYYCNA**IDGHLAY**WGQGLTVTVSS (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

EVQLVESGGGLVQPGNSLRSLSCAAS**GFTFSKFGMS**WYRQAPGKGLEWVSS**SISGSGRDTLYAESVKG**RFTISRDNKNTLYLQMNSLRPEDTAVYYCTI**GGSLSV**VSSQGLTVTVSS (SEQ ID NO:45)

sdCDR1 **GFTFSKFGMS** (SEQ ID NO:46)

sdCDR2 **SISGSGRDTLYAESVKG** (SEQ ID NO:47)

sdCDR3 **GGSLSV** (SEQ ID NO:48)

EVQLVESGGGLVQPGNSLRSLSCAAS**GFTFSKFGMS**WYRQAPGKGLEWVSS**SISGSGRDTLYAESVKG**RFTISRDNKNTLYLQMNSLRPEDTAVYYCTI**GGSLSV**VSSQGLTVTVSS/HHHHHH (SEQ ID NO:142)

Figura 5D

Dominios α CD3 scFv **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_{Li}

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_{Li2}

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**WVRQAPGKGLEWVAR**RIRSKYNNYATYYA**
DQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS
(SEQ ID NO:61)

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

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

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

Figura 5E

Dominios α CD3 scFv - Continuación **α CD3 V_{Hi}**

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEWVA**RIRSKYDYKDDDD**
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGLTVTVSS
 (SEQ ID NO:65)

IVHsdCDR1 **GFTFNKYAMN** (SEQ ID NO:66)

IVHsdCDR2 **RIRSKYDYKDDDDKADSVKD** (SEQ ID NO:67)

IVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:68)

 α CD3 V_{Hi2}

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKHAMN**WVRQAPGKGLEWVA**RIRSKYNNYATAY**
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGLTVTVSS
 (SEQ ID NO:69)

IVHsdCDR1 **GFTFNKHAMN** (SEQ ID NO:70)

IVHsdCDR2 **RIRSKYNNYATAYADSVKD** (SEQ ID NO:71)

IVHsdCDR3 **HGNFGNSYISYWAY** (SEQ ID NO:72)

Enlazadores α CD3 scFv**Normal/No escindible**

GGGSGGGSGGGGS (SEQ ID NO:73)

Restringida

GGGSGGGGS (SEQ ID NO:74)

Figura 5F

Enlazadores escindibles (Sitio de reconocimiento en negritas, sitio de escisión - /)MMP 2/9**GPAG/MKGL** (SEQ ID NO:75)**SGGPGPAG/MKGLPGS** (SEQ ID NO:76)**SGGGPGPAG/MKGLPGGS** (SEQ ID NO:77)Meprina A/B**GGGGKKLA/DEPEGGS** (SEQ ID NO:78)**KKLA/DEPE** (SEQ ID NO:79)Meprina A/B (Variante, alta eficiencia)**GGGKFLA/DEPEGG** (SEQ ID NO:80)Catepsina S, K, L**SGGGARLQ/SAAPGGGS** (SEQ ID NO:81)**ARLQ/SAAP** (SEQ ID NO:82)Meprina/Granzima B**SGGGGVYADSLEDGGGS** (SEQ ID NO:83)**GVYADSLEDG** (SEQ ID NO:84)Matriptasa/uPA (MS)**GGGSLSGR/SDNHGGGS** (SEQ ID NO:85)**GLSGR/SDNHG** (SEQ ID NO:86)Matriptasa (MV)**SGGGSFTR/QARVVGGGS** (SEQ ID NO:87)**SFTR/QARVV** (SEQ ID NO:88)Catepsina S/MMP9/Meprina A**ARLQ/SAAPAG/LKGA** (SEQ ID NO:89)MMP9 (Variante, alta eficiencia)**GGPGPAG/MHGLPG** (SEQ ID NO:90)MMP9 (Variante, baja eficiencia)**GGPGPAG/MEGLPG** (SEQ ID NO:91)

Figura 5G

Enlazadores escindibles (Sitio de reconocimiento en negritas, sitio de escisión - /) - continuación**Trombina 1**GGGGLVPR/**GSL**GGGGS (SEQ ID NO:92)**Trombina 2**SSGGGMPR/**SFR**GGGS (SEQ ID NO:93)**Enteroquinasas/bandera**

GGGGDYKDDDDK/GGGS (SEQ ID NO:94)

KLK7-6SGGGQNPY/**SAGR**GGGS (SEQ ID NO:95)**KLK7-13**SGGGQNPY/**SAGGG**SGG (SEQ ID NO:96)**KLK7-11**SGGGRNVY/**SAGGG**SGG (SEQ ID NO:97)**KLK7-10**SGGGQNTW/**SAGK**GGGS (SEQ ID NO:98)**uPA**GGGSHTGR/**SAYF**GGGS (SEQ ID NO:99)**MMP9-2**

SGGPGPAG/LKGAPGS (SEQ ID NO:184)

Figura 6A

Proteasa	Secuencia de dominio de escisión	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
Activador de uroquinasa plasminógeno (upa)	DAFK	114
Activador de uroquinasa plasminógeno (upa)	GGGRR	115
Enzima lisosomal	GFLG	116
Enzima lisosomal	ALAL	117
Enzima lisosomal	FK	118
Catepsina B	NLL	119
Catepsina D	PIC(ET)FF	120
Catepsina K	GGPRGLPG	121
Antígeno específico de próstata	HSSKLQ	122
Antígeno específico de próstata	HSSKLQL	123
Antígeno específico de próstata	HSSKLQEDA	124
Proteasa de virus de herpes simple	LVLASSSFGY	125
Proteasa Hiv	GVSQNYPIVG	126
Proteasa Cmv	GVVQASCRLA	127

Figura 6B

Proteasa	Secuencia de dominio de escisión	Seq id no:
Trombina	F(PIP)RS	128
Trombina	DPRSFL	129
Trombina	PPRSFL	130
Caspasa-3	DEV D	131
Caspasa-3	DEVDP	132
Caspasa-3	KGSGDVEG	133
Enzima que convierte Interleucina 1 β	GWEHDG	134
Enteroquinasa	EDDDDKA	135
Fap	KQEQNPGST	136
Kalikeina 2	GKA FRR	137
Plasmina	DAFK	138
Plasmina	DVLK	139
Plasmina	DAFK	140
Superior	ALLLALL	141

Unión de Pro6 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

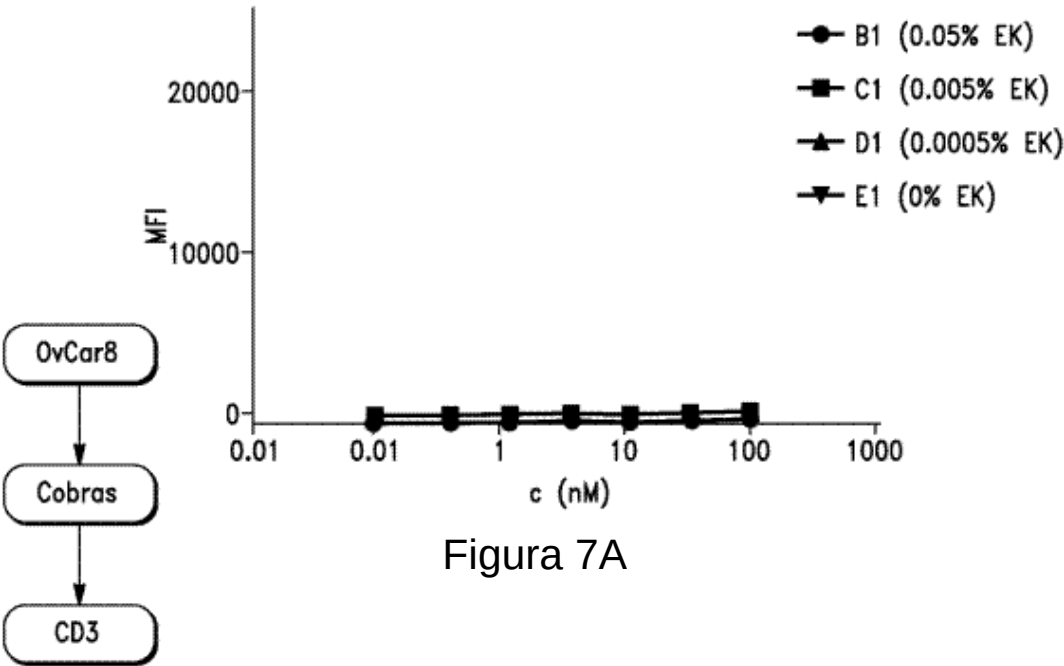


Figura 7A

Unión de Pro7 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

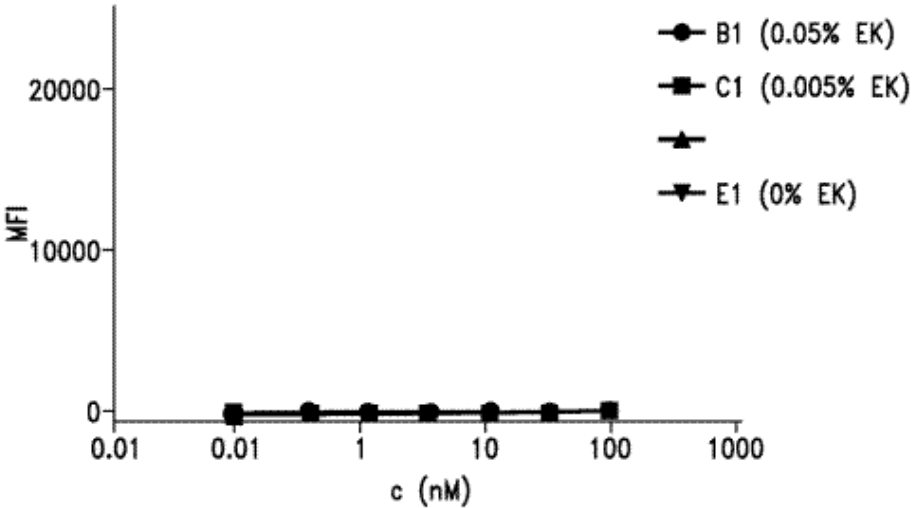


Figura 7B

Unión de Pro6+7 digerido con EK a OVCAR-8,
detectado con A488-cyCD3::Flag::hFC

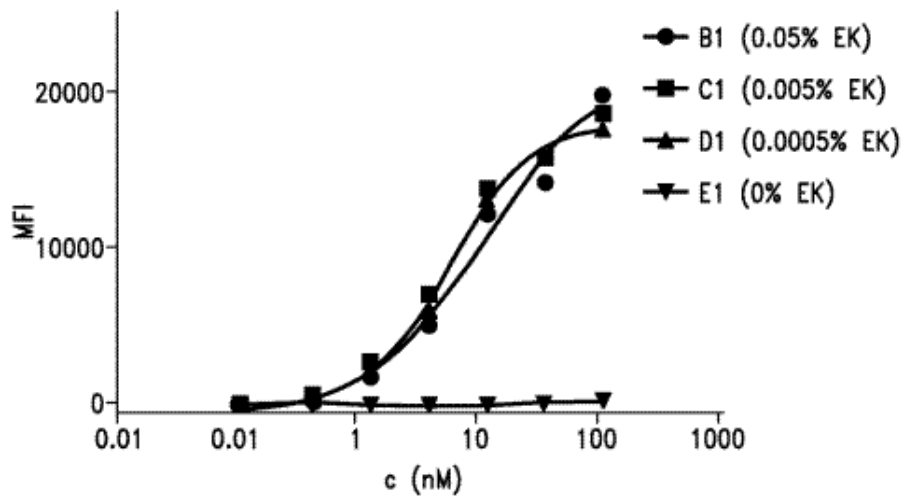


Figura 7C

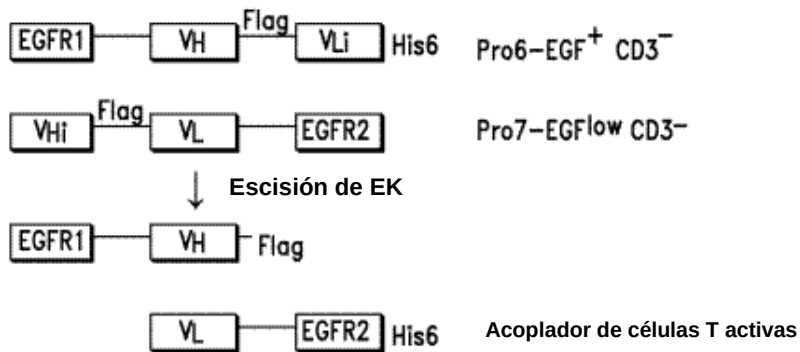


Figura 7D

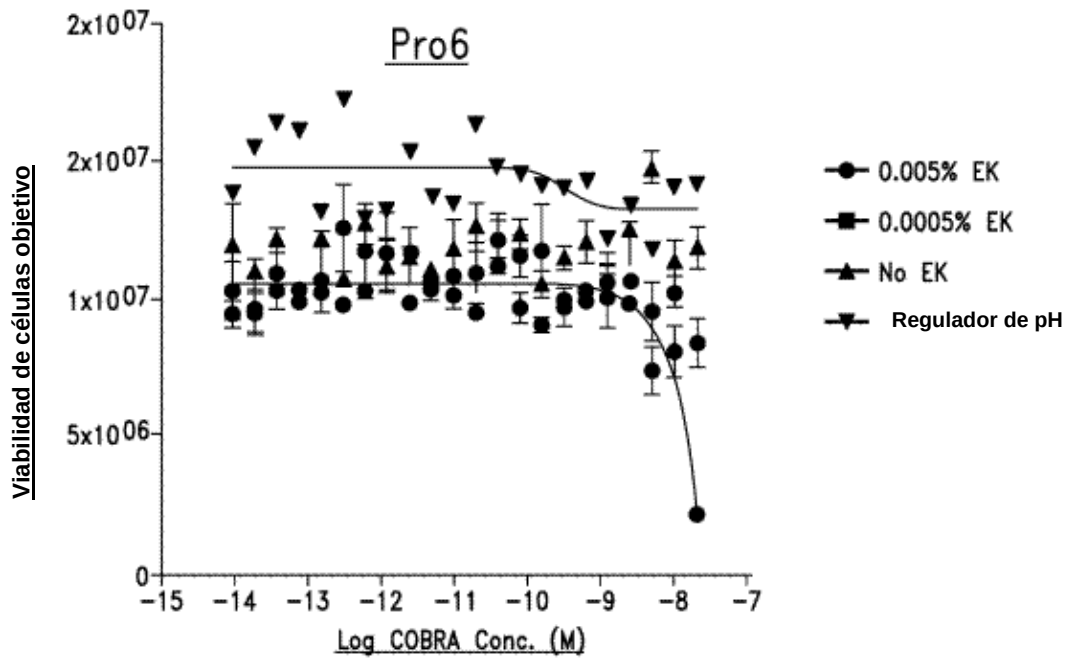


Figura 8A

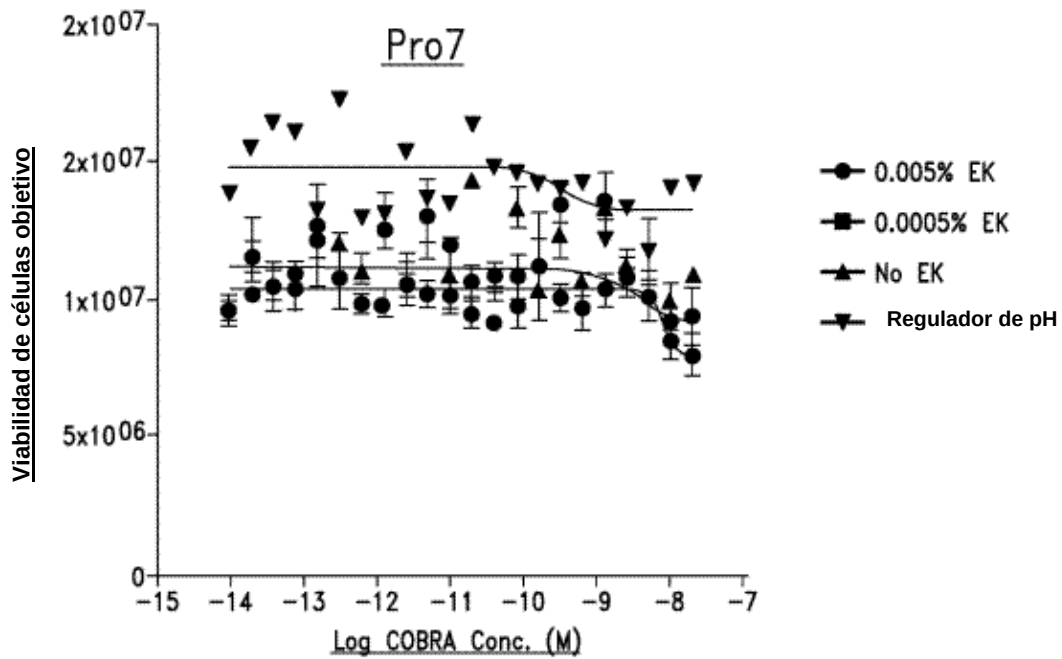


Figura 8B

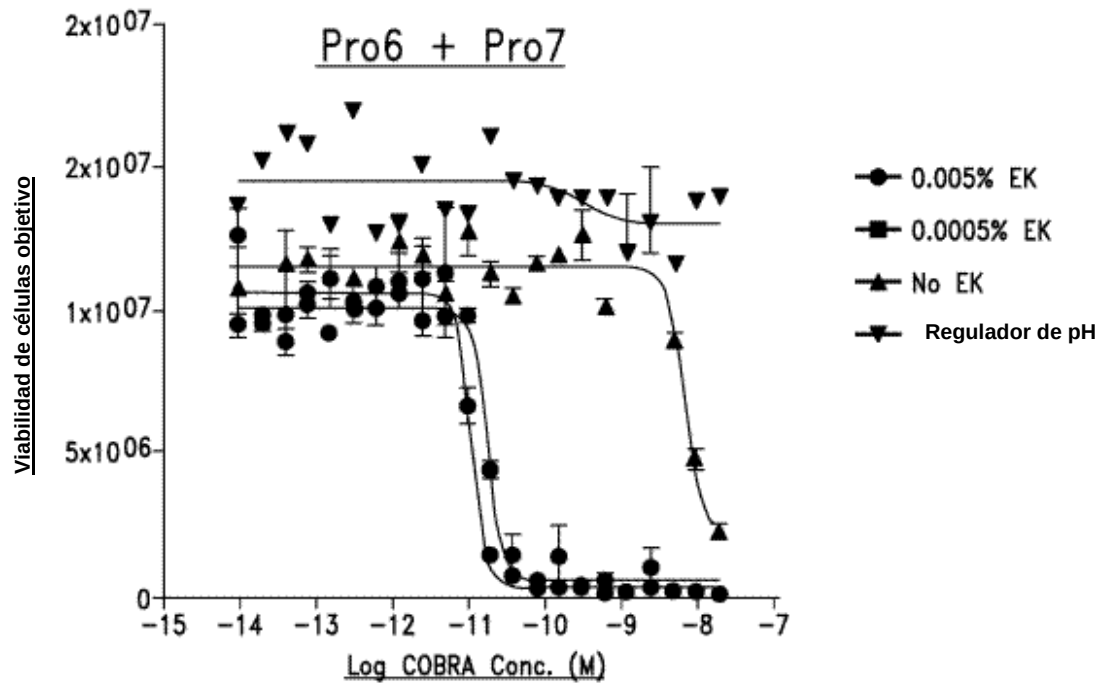


Figura 8C

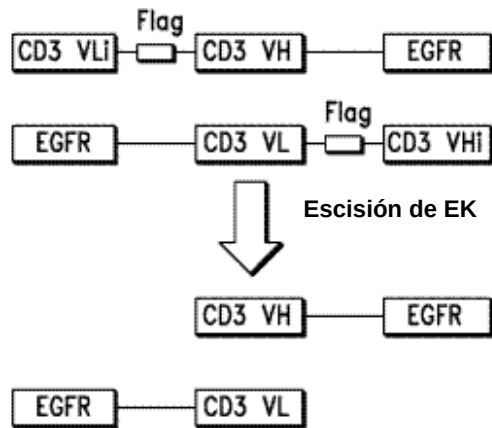
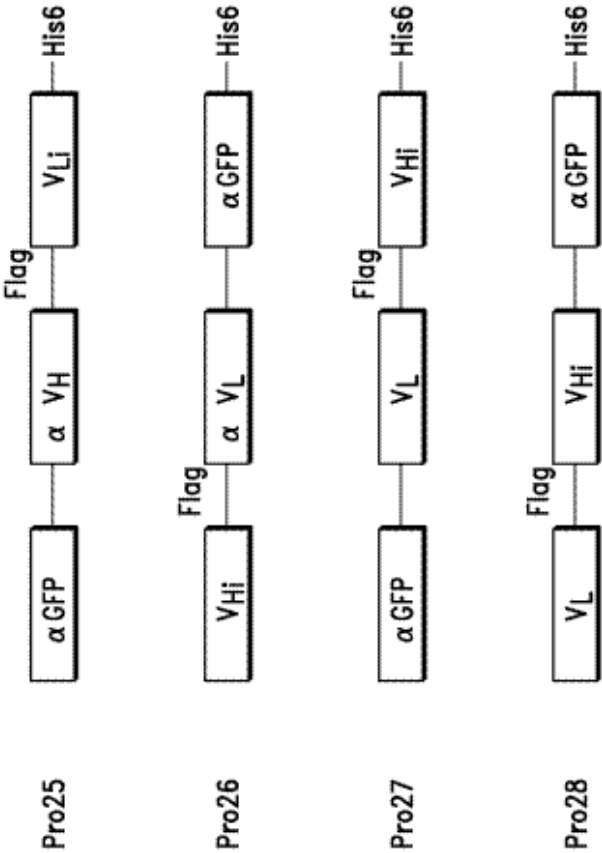


Figura 8D

Figura 9



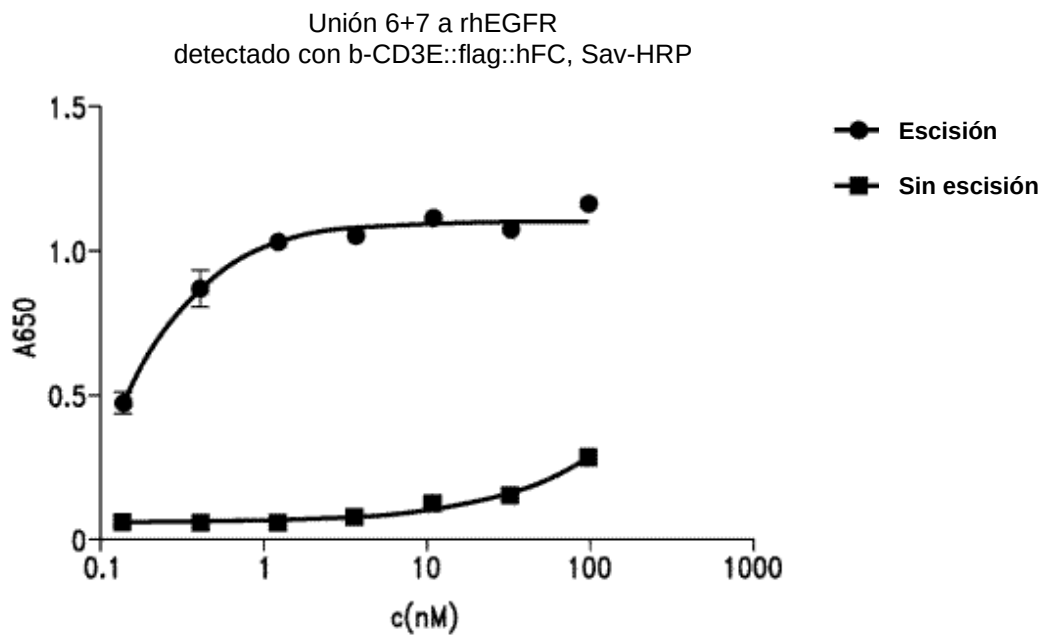


Figura 10A

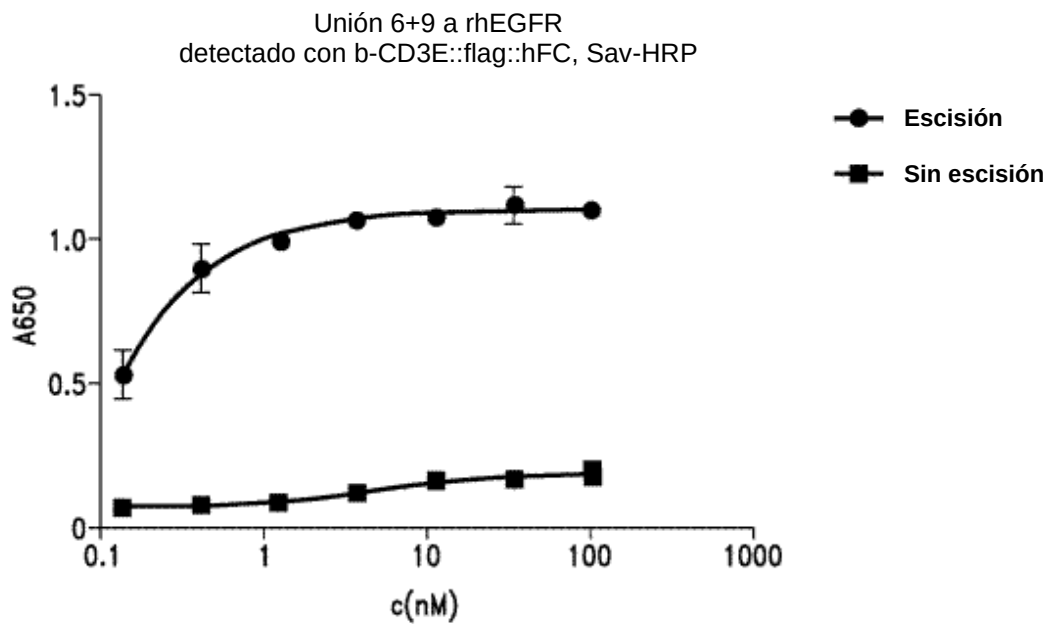


Figura 10B

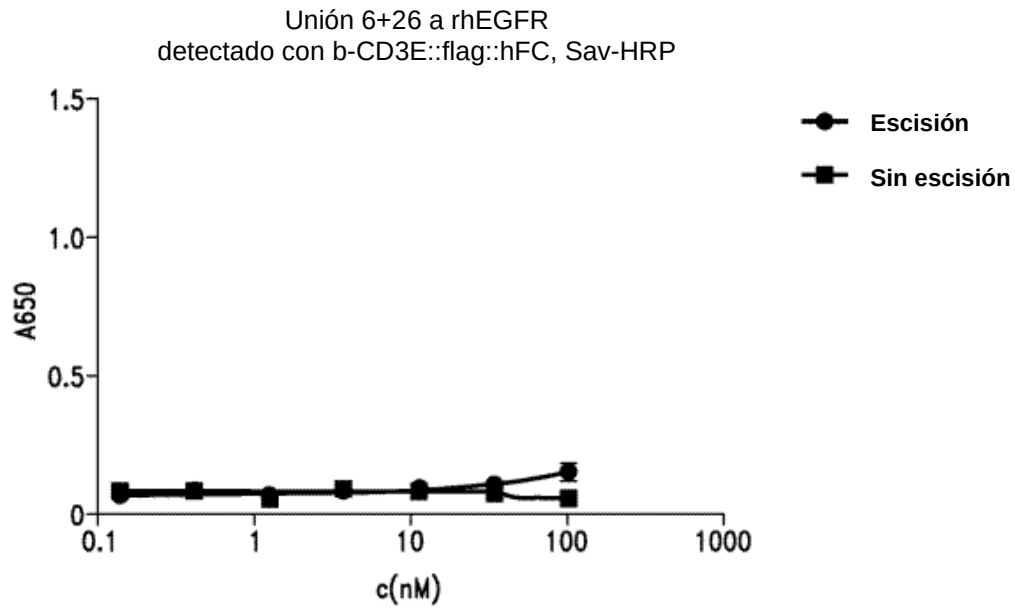


Figura 10C

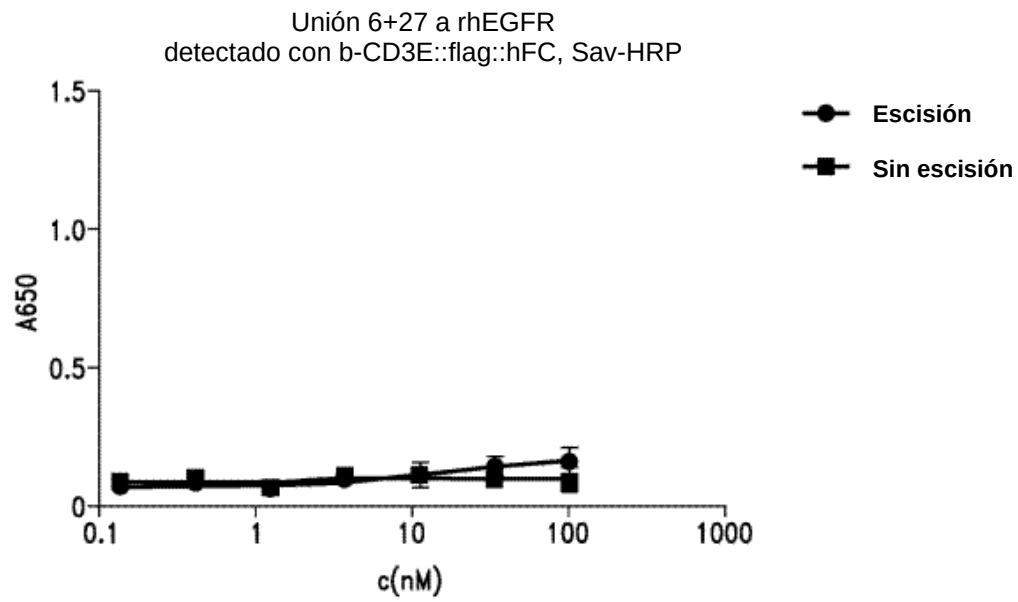


Figura 10D

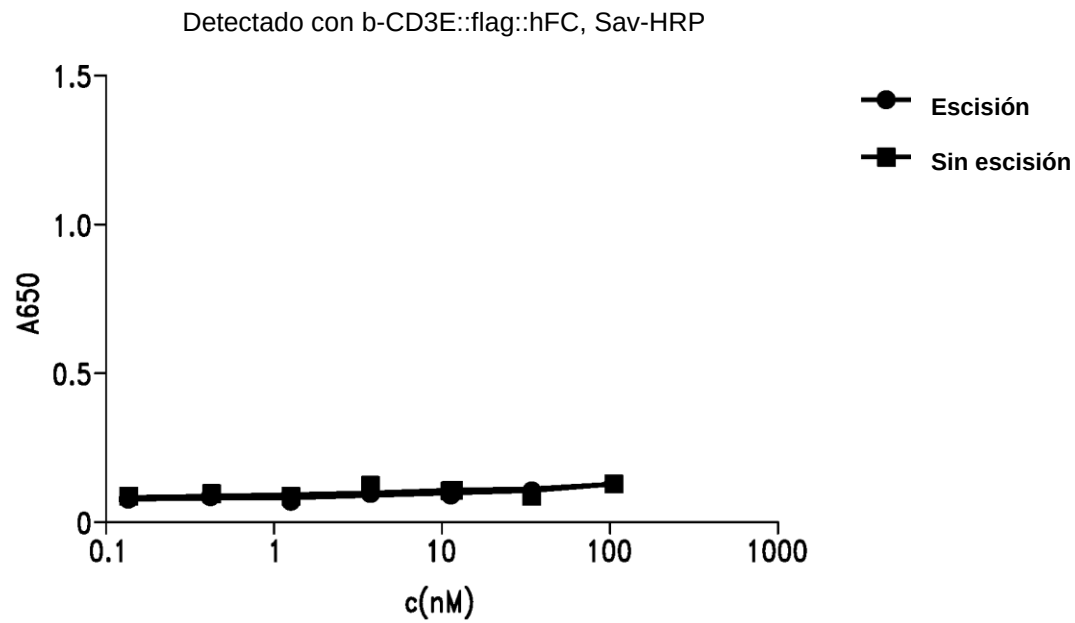


Figura 10E

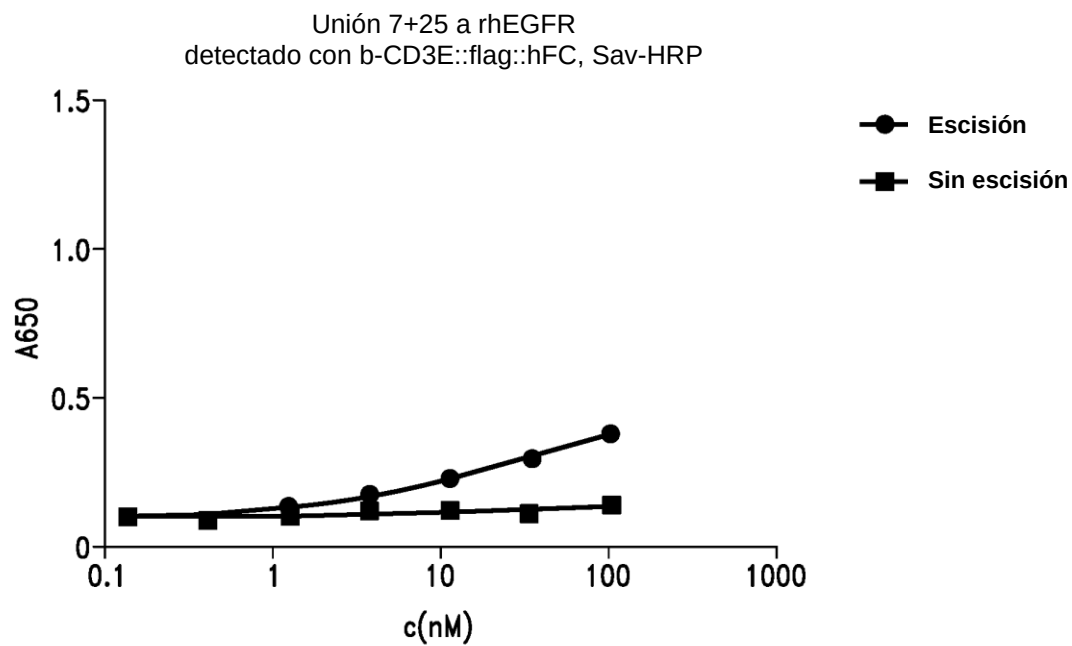
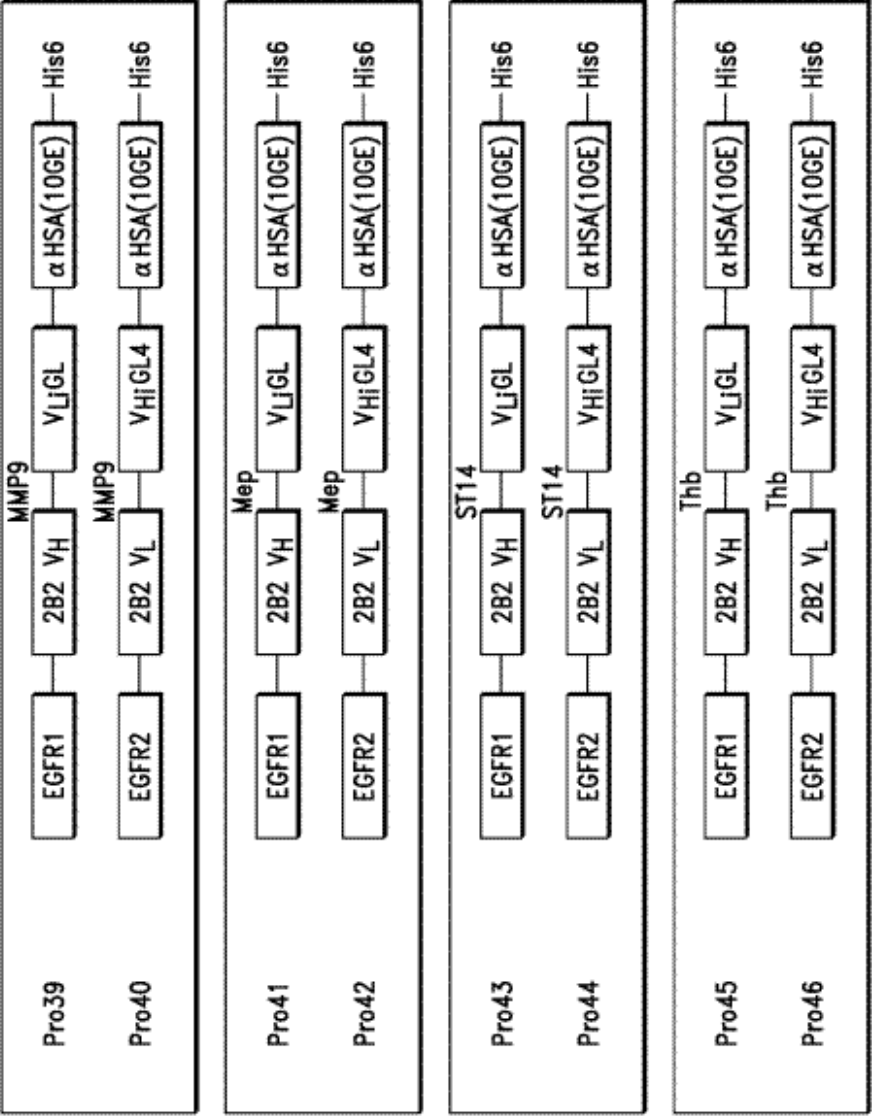


Figura 10F

Figura 11



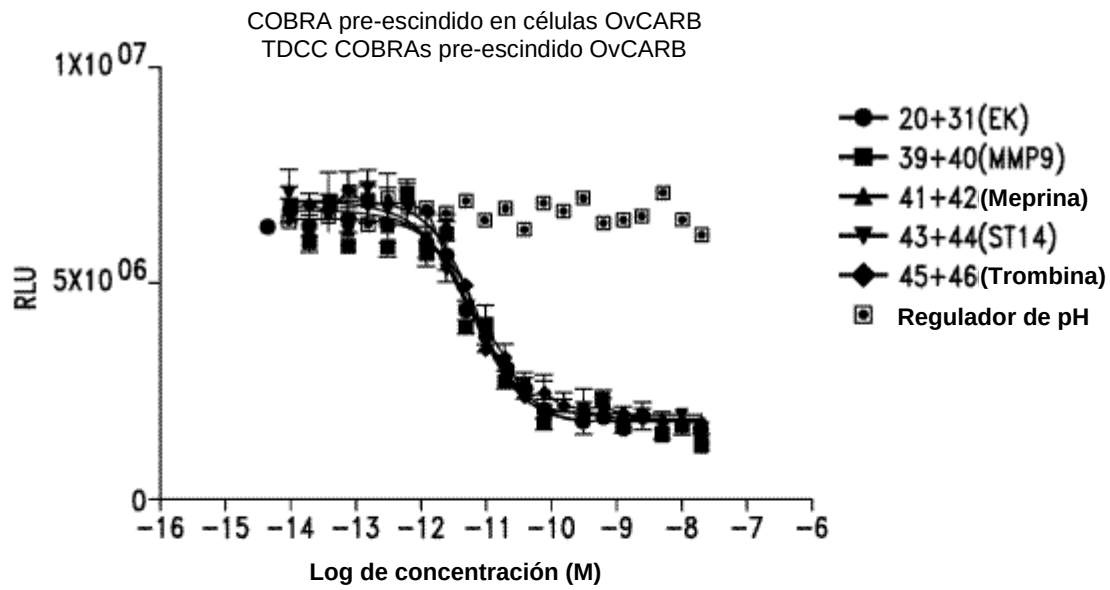


Figura 12A

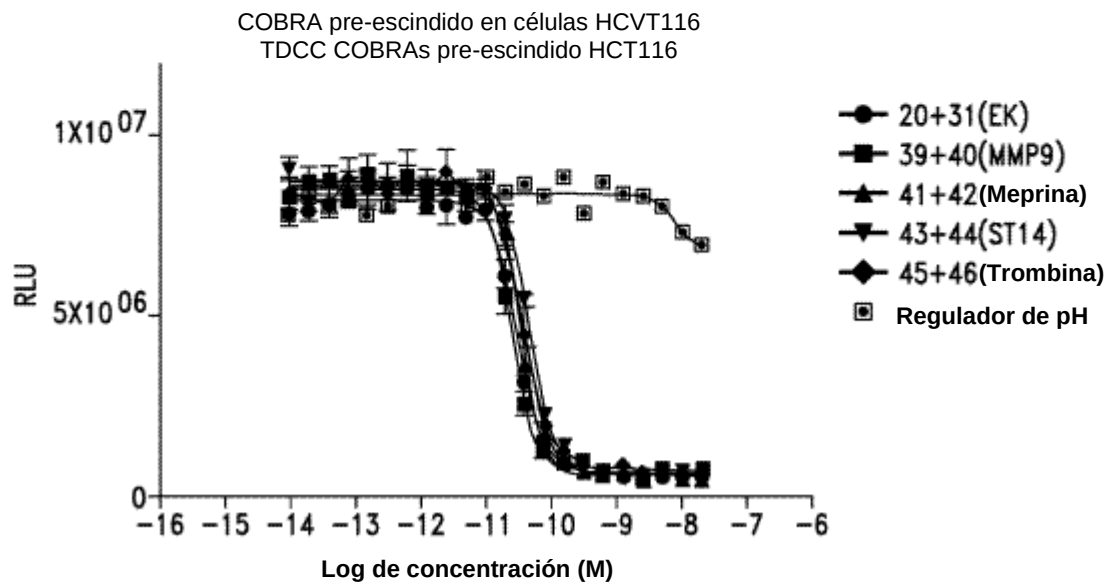


Figura 12B

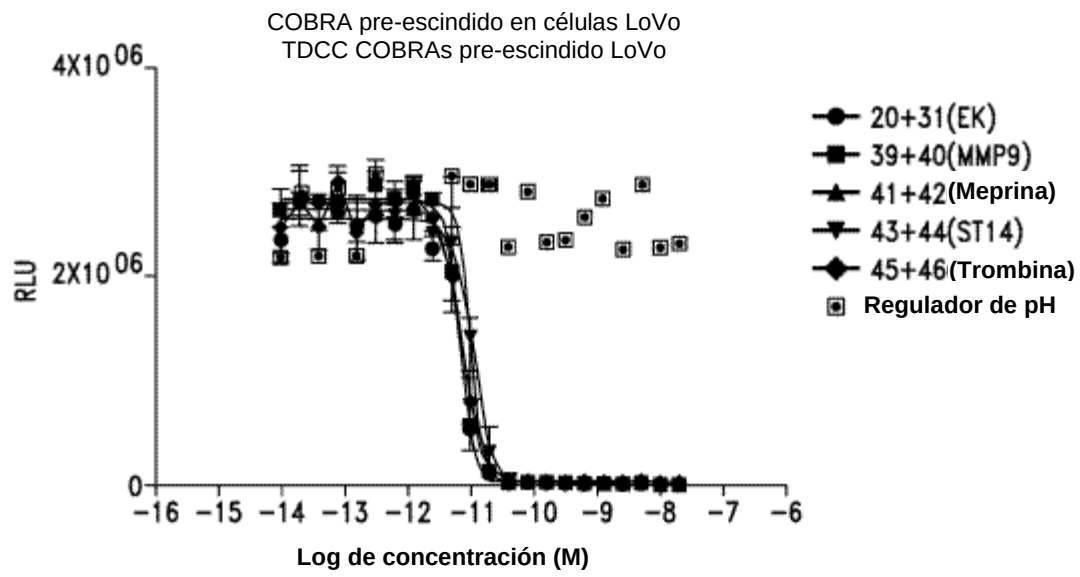


Figura 12C

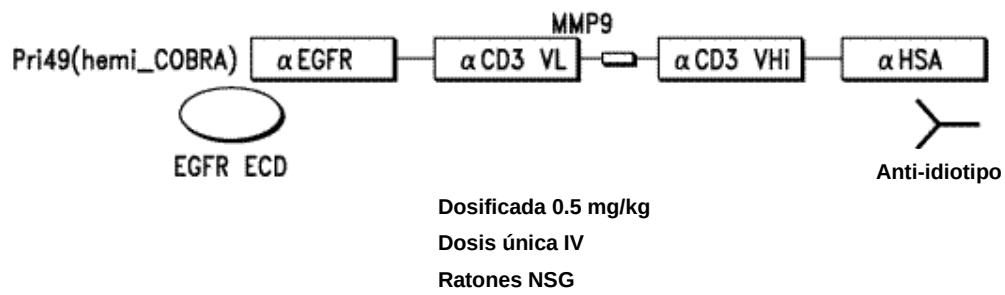


Figura 13A

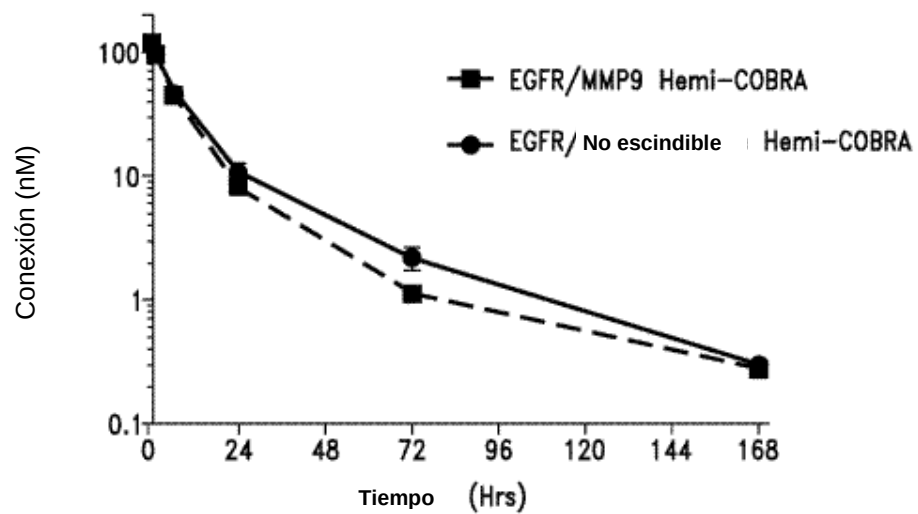


Figura 13B

Figura 14

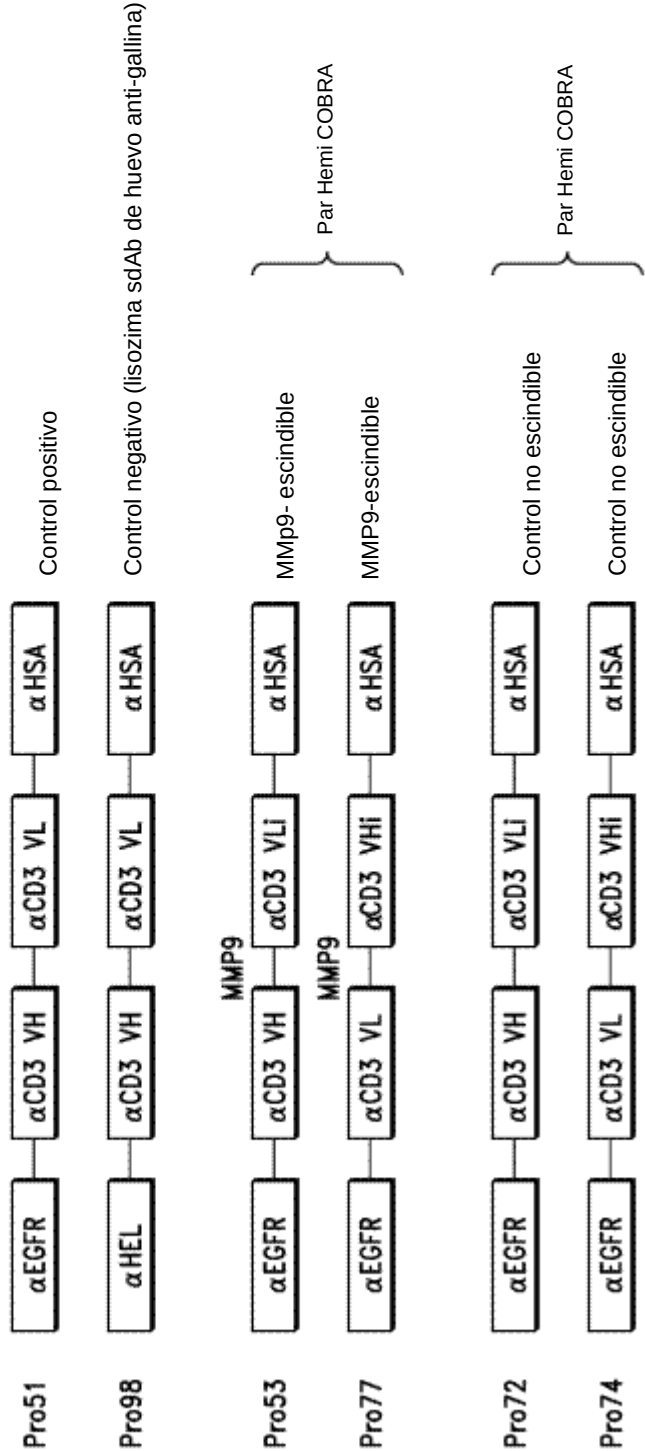


Figura 15

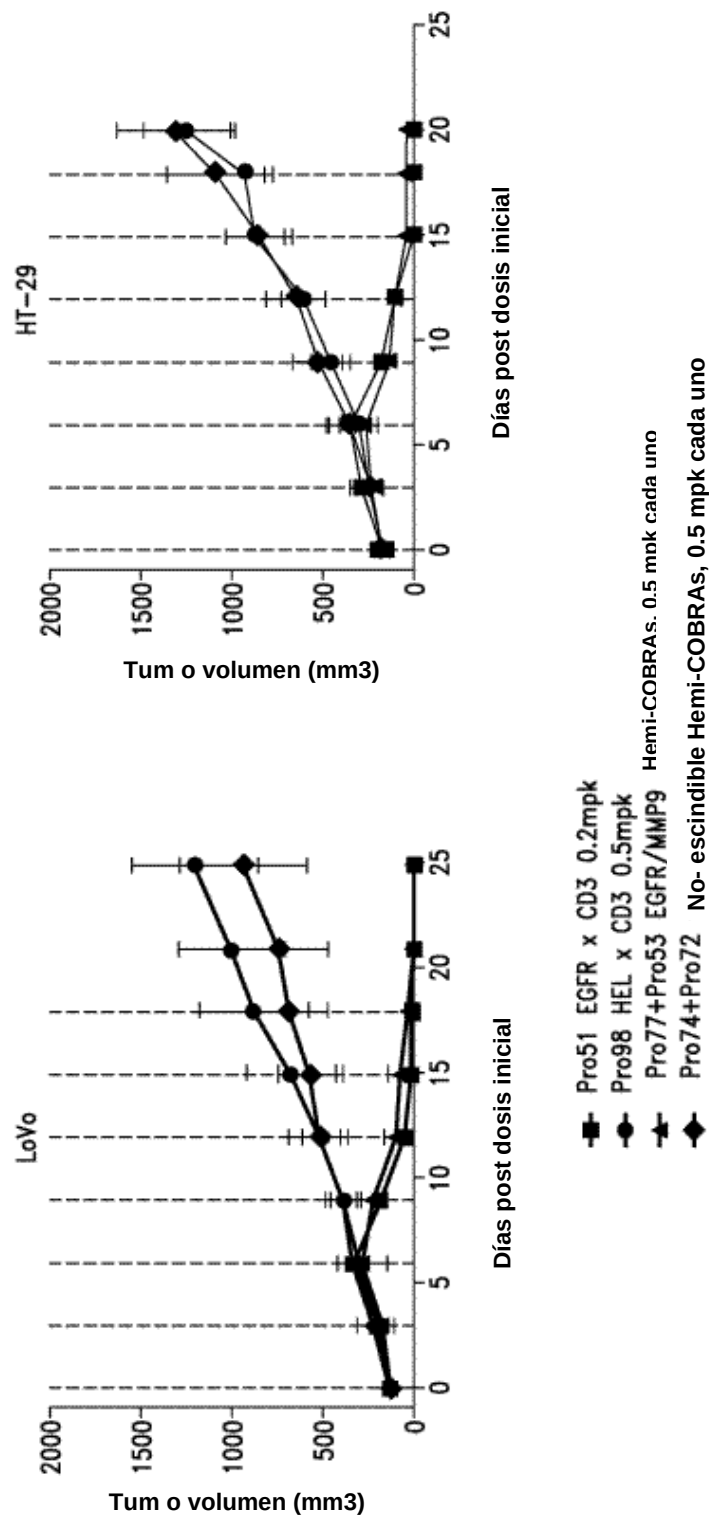


Figura 16

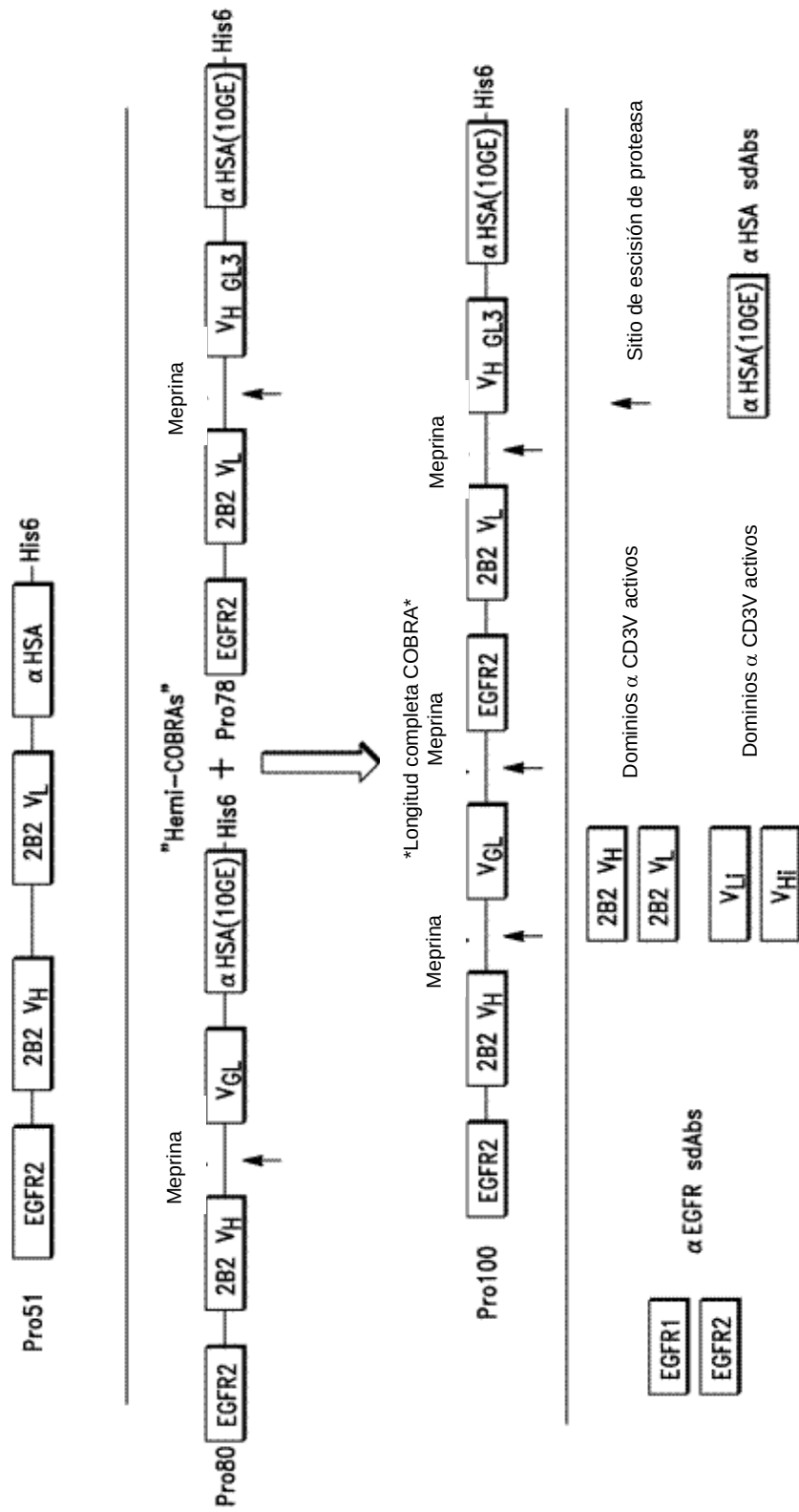


Figura 17

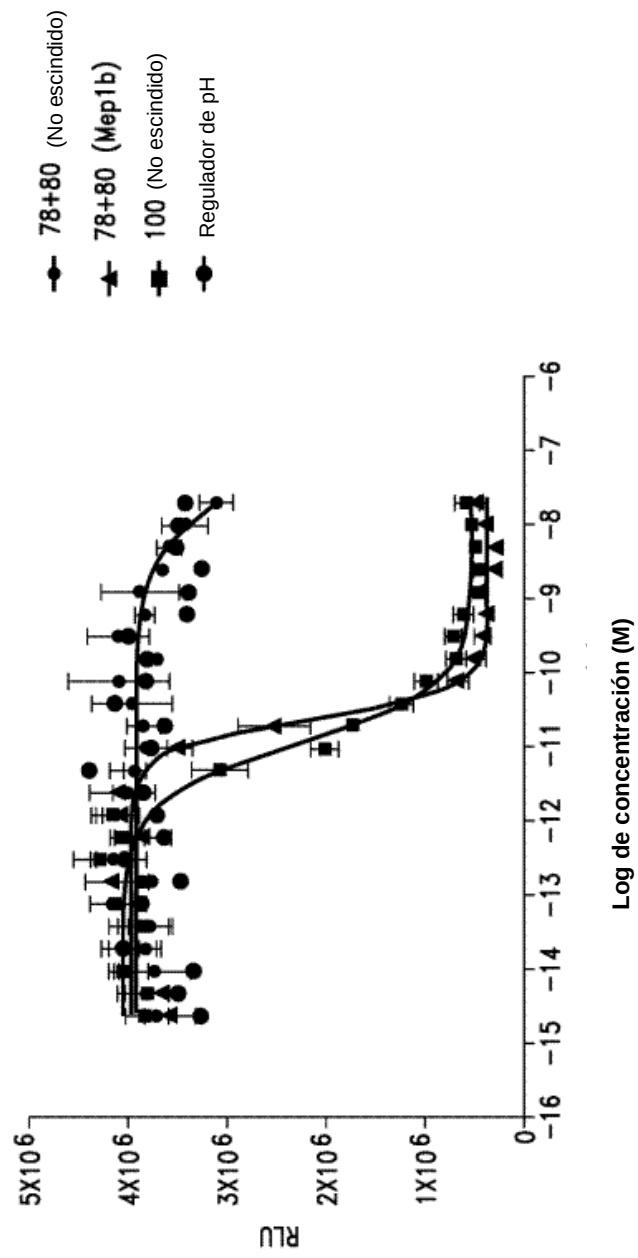


Figura 18

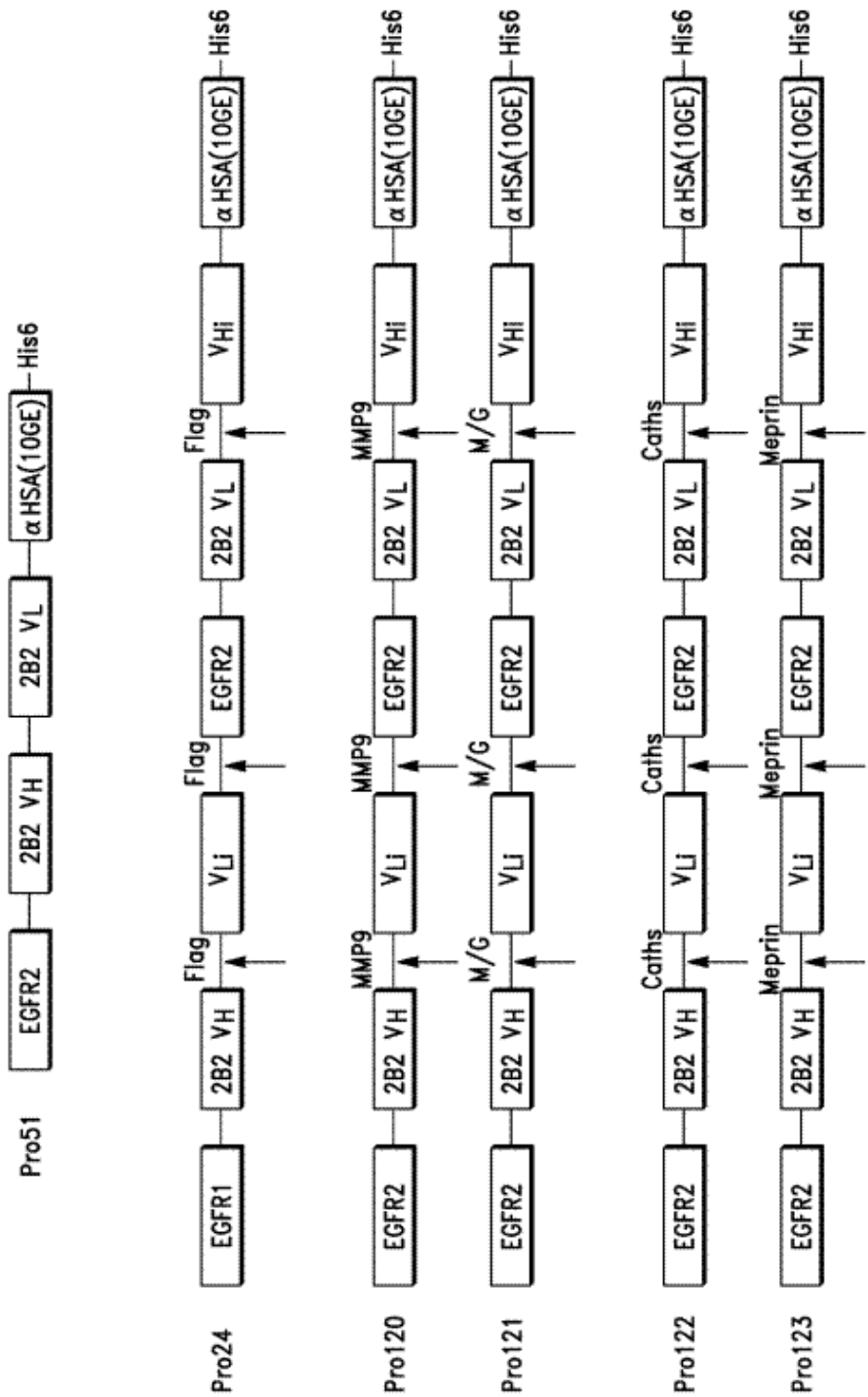


Figura 19

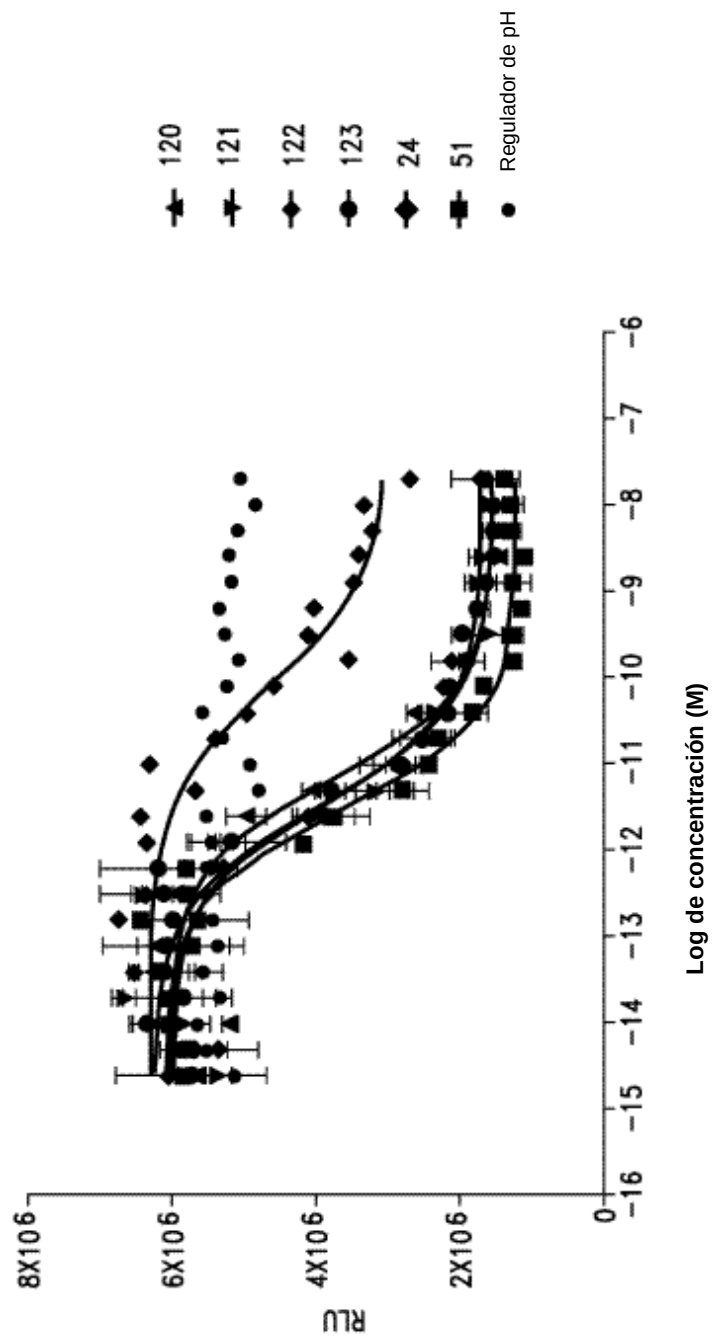


Figura 20

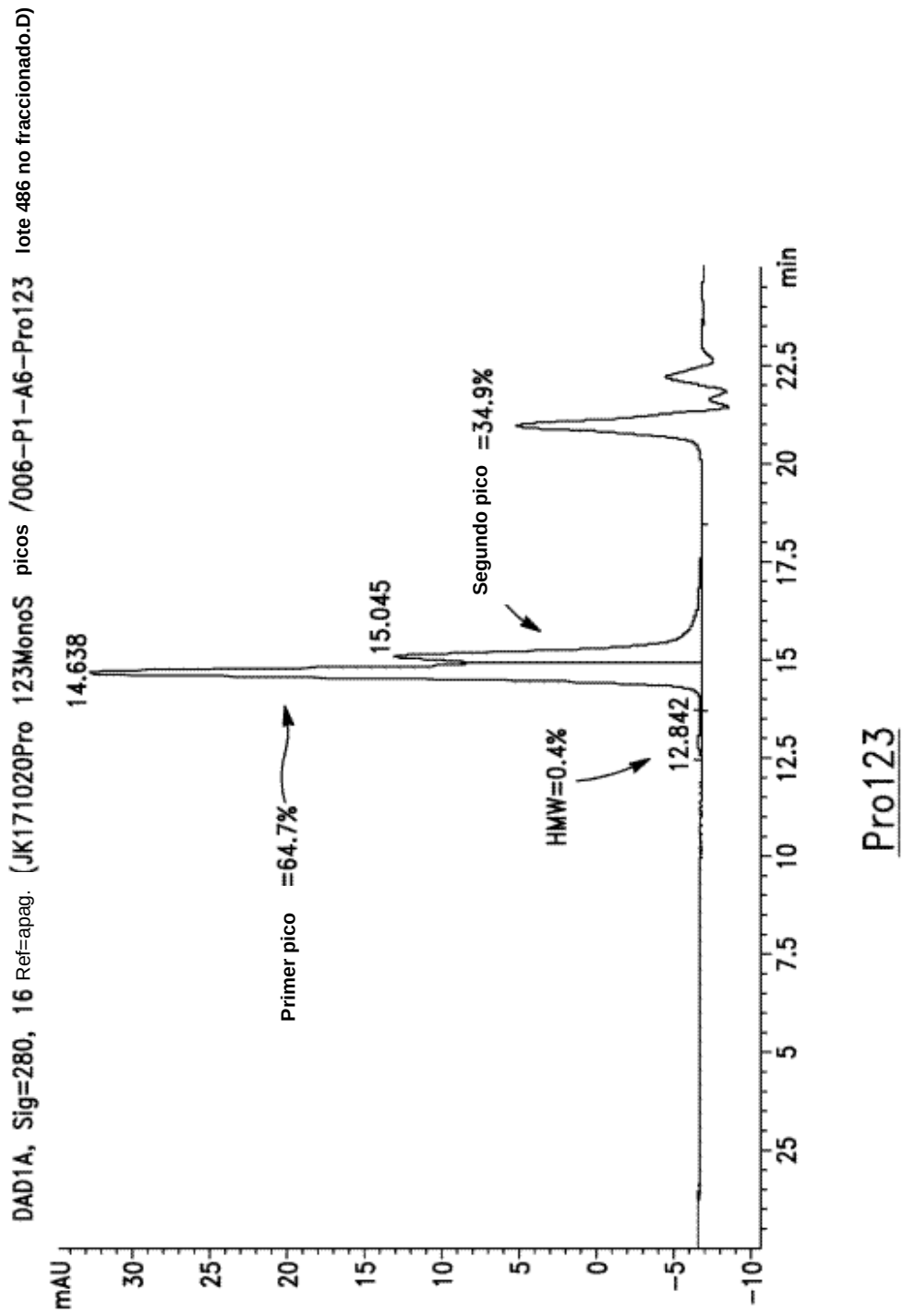


Figura 21

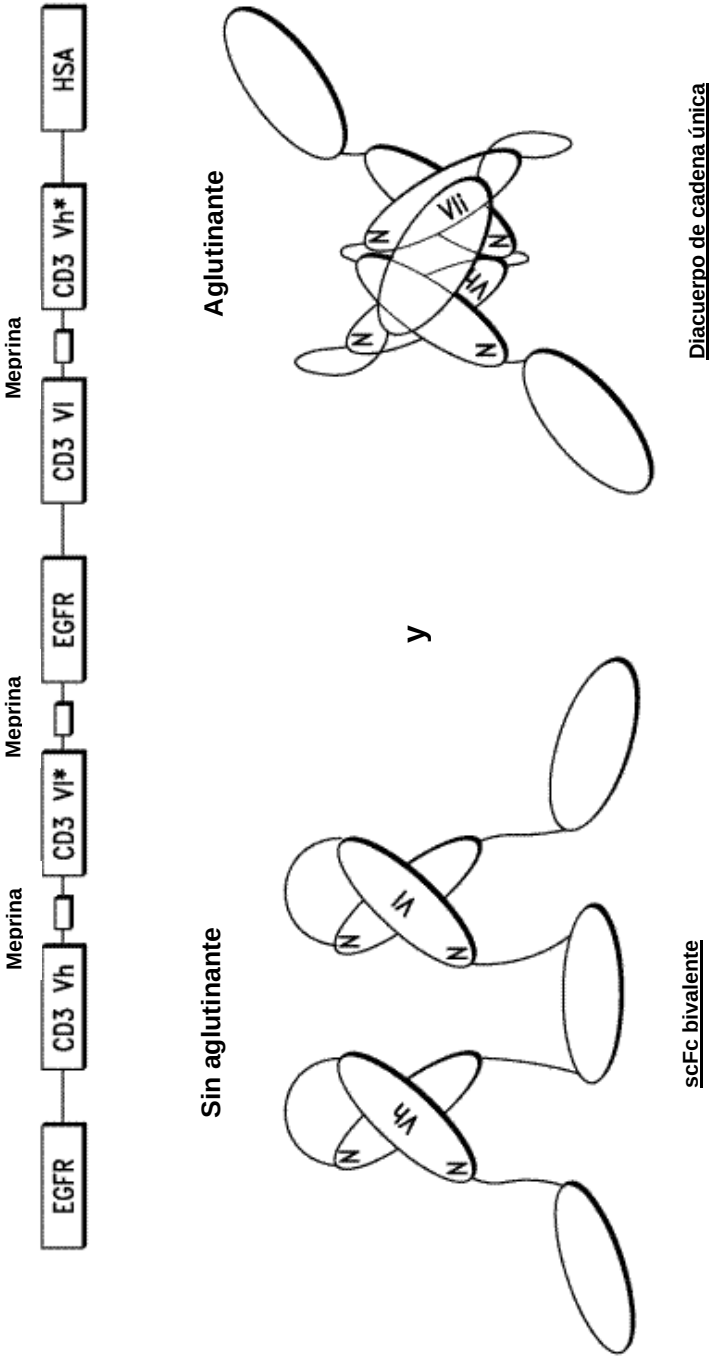


Figura 22

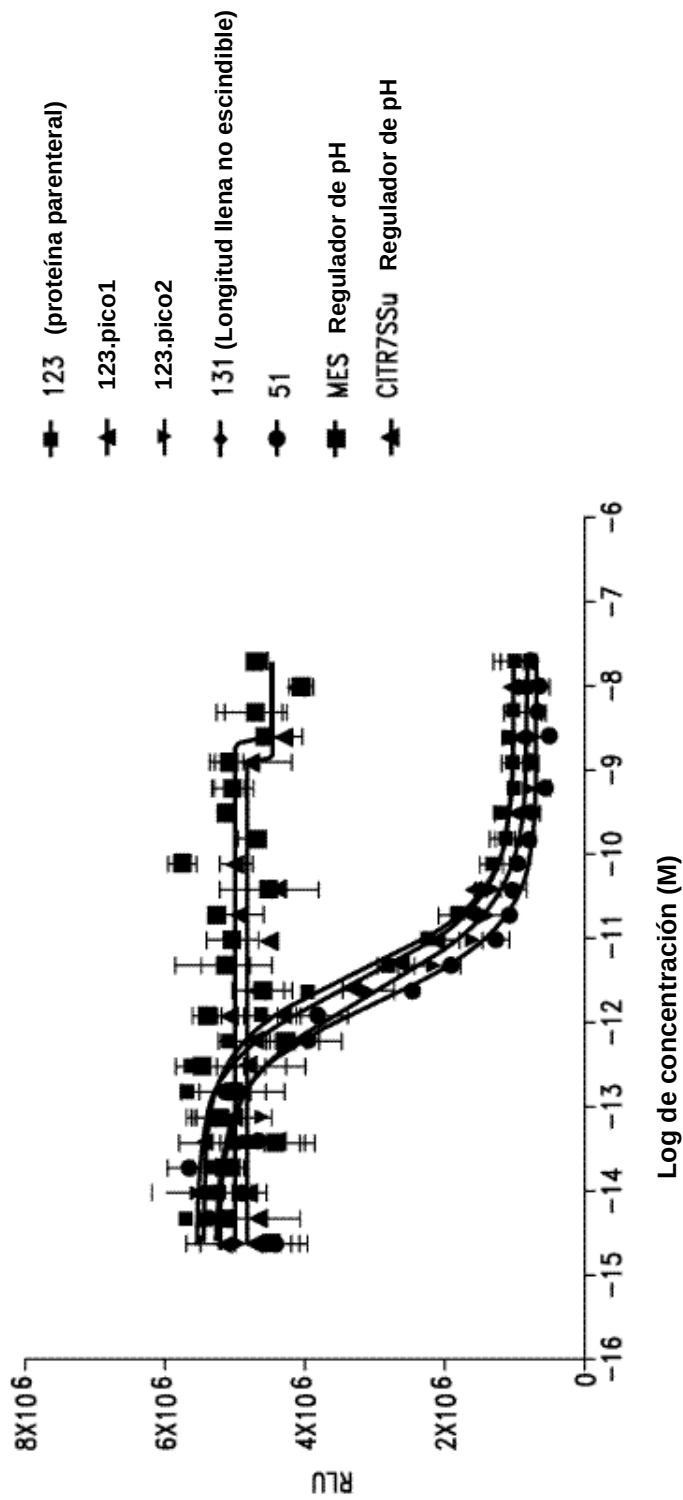


Figura 23A

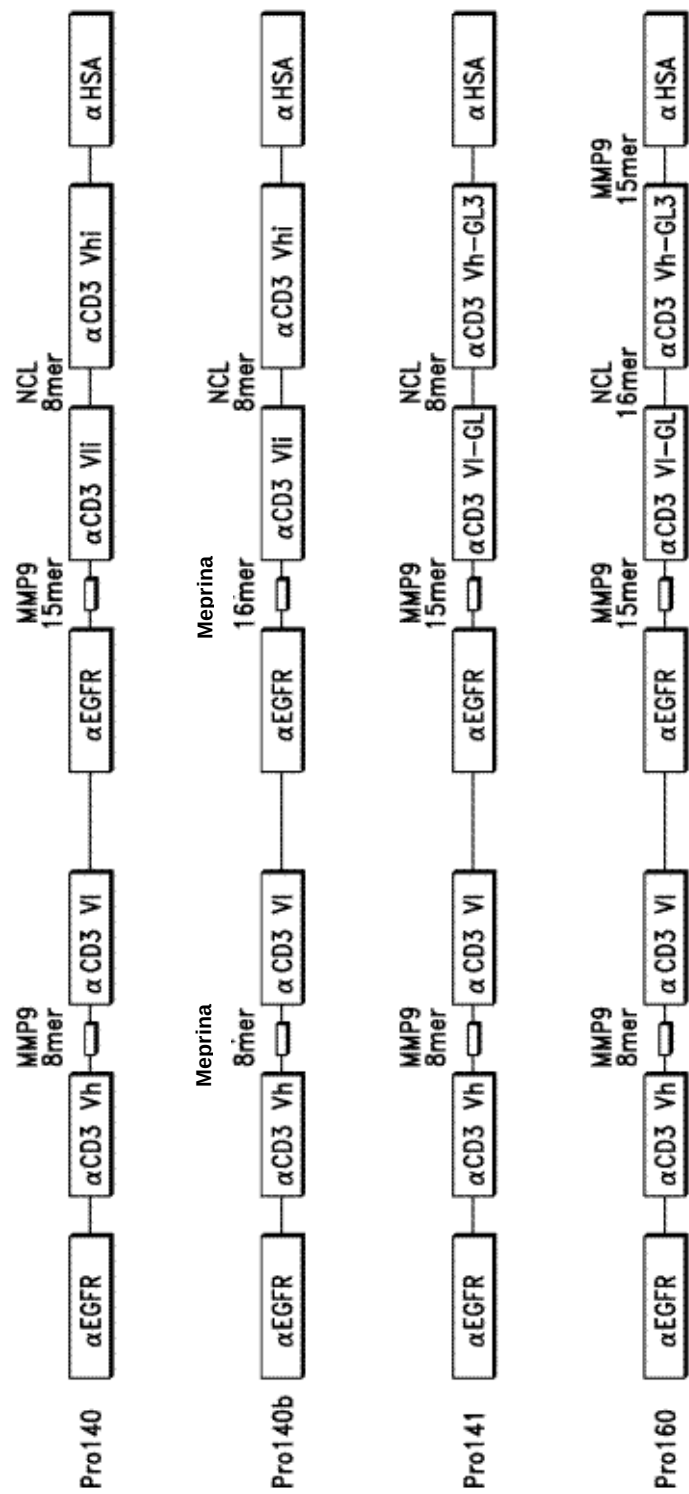


Figura 23B

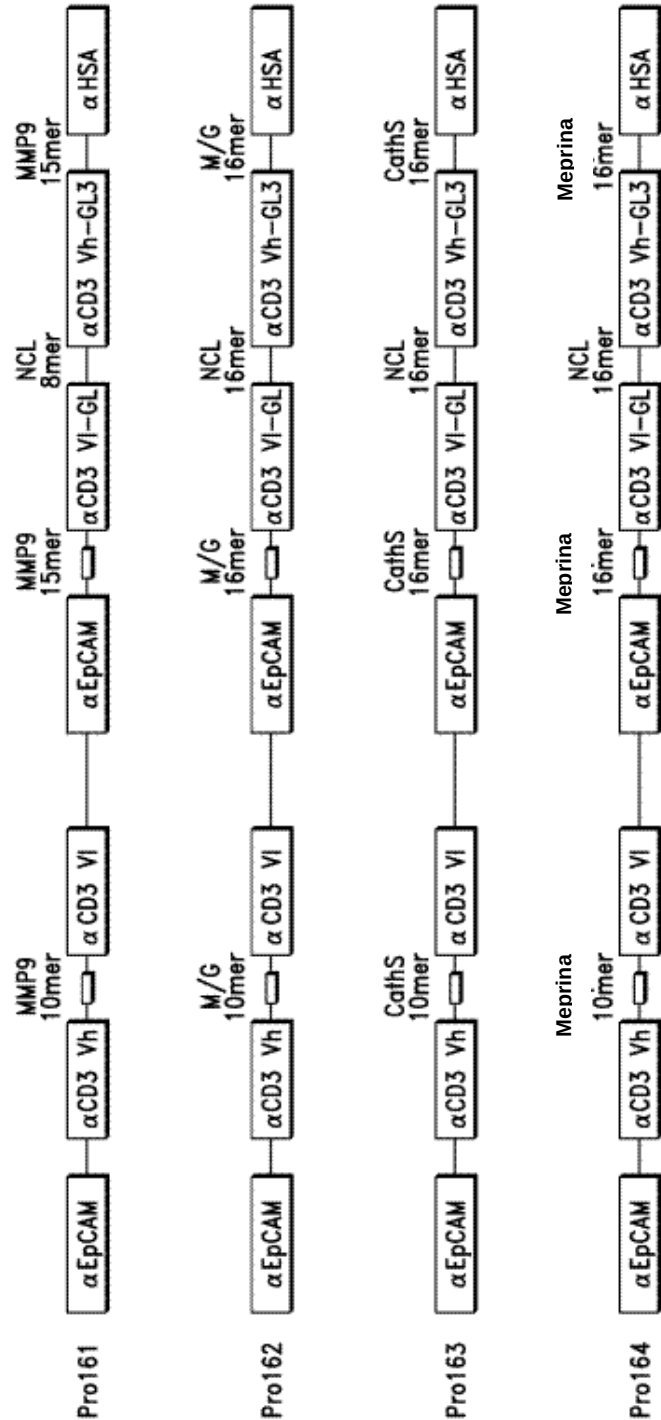


Figura 23C

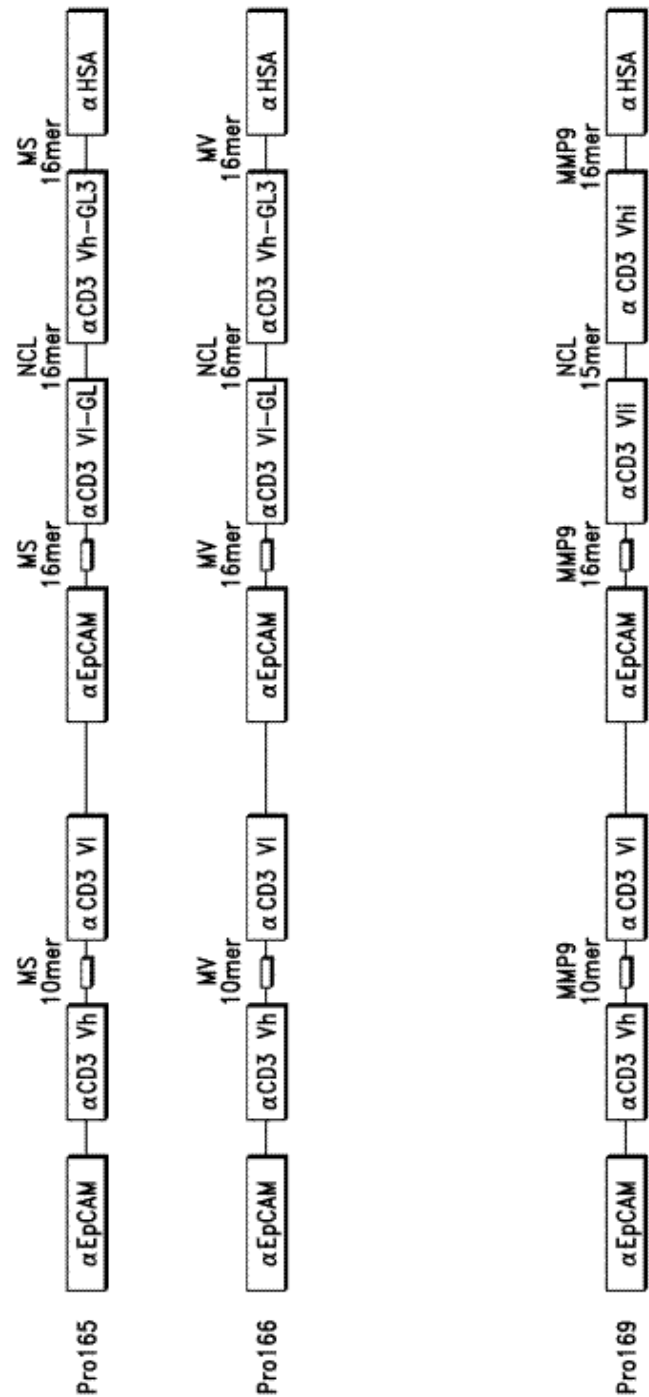


Figura 23D

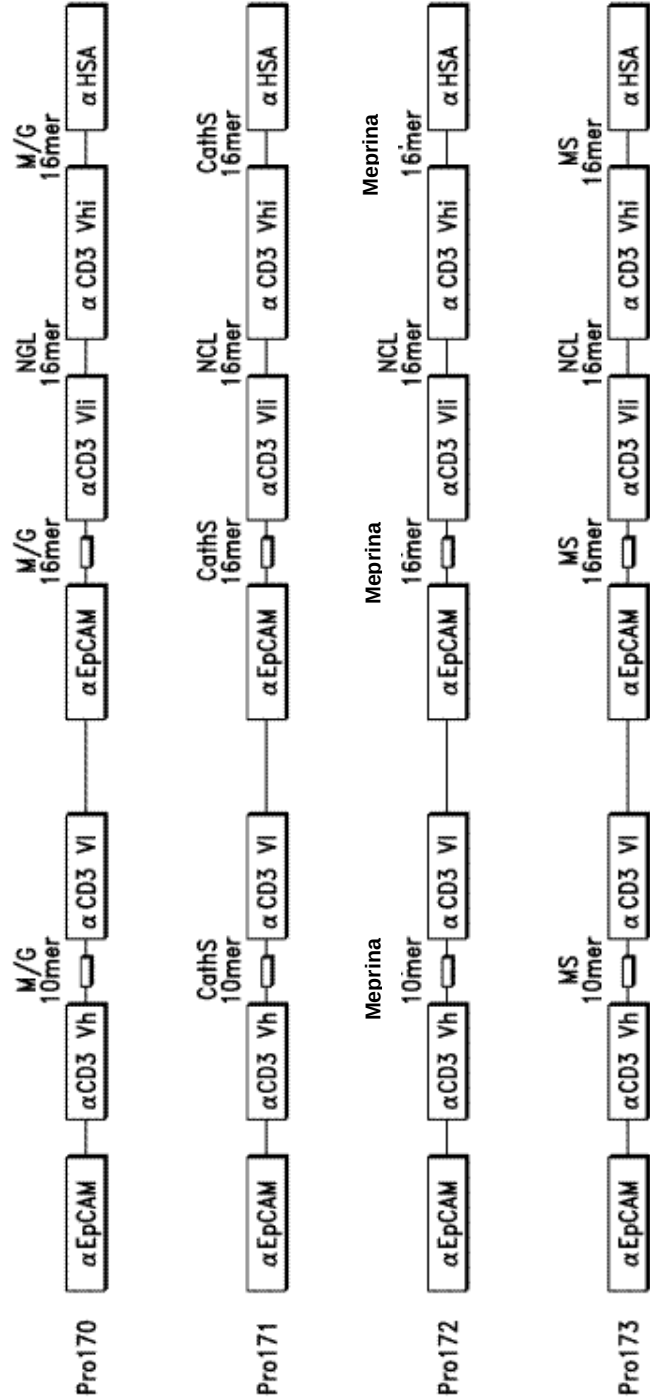


Figura 23E

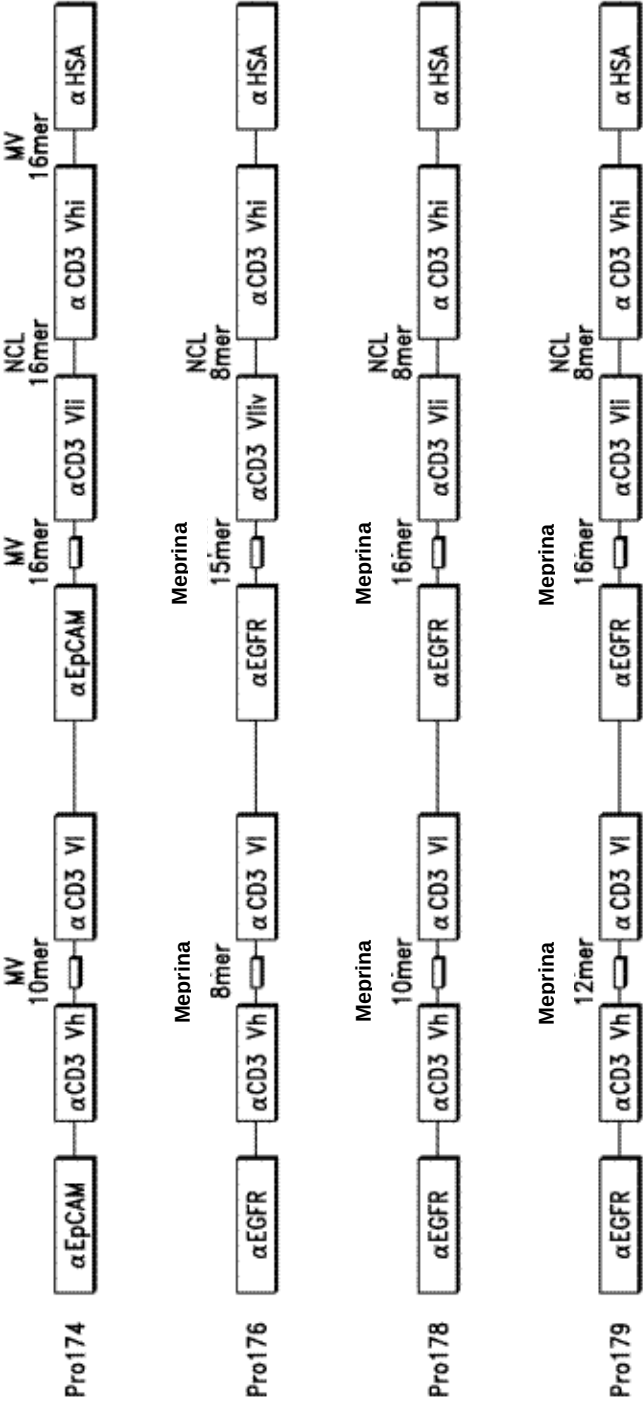


Figura 23F

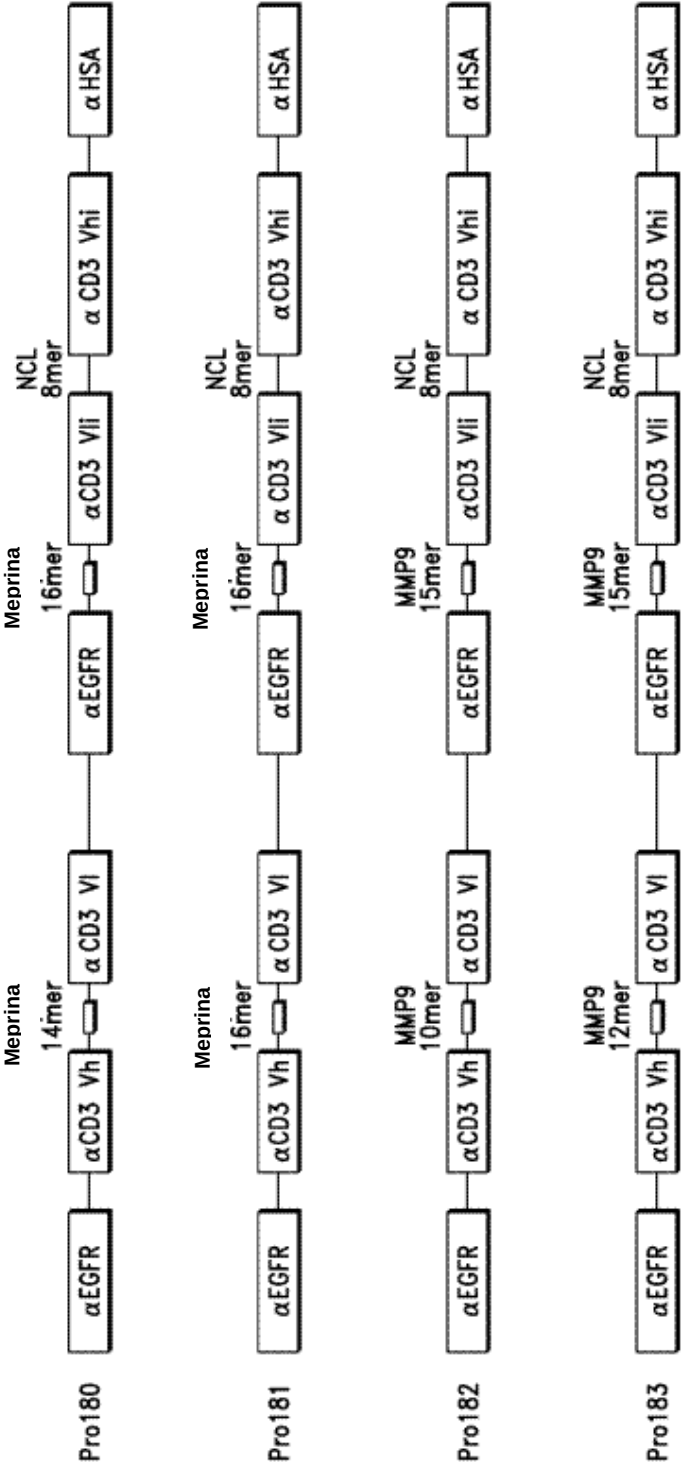


Figura 23G

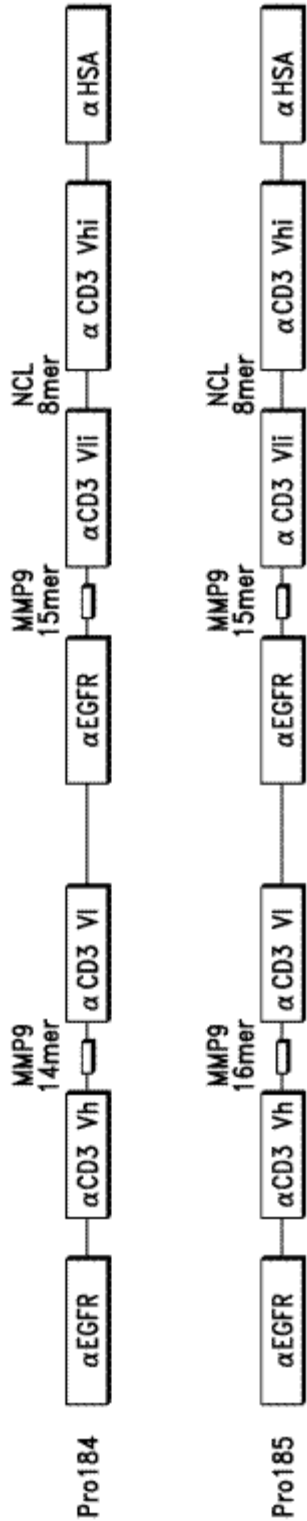


Figura 24

DAD1A, Sig=280,16 Ref= apag(C:\CHEM32\...ATAJK171027 SEC LOTES 503 a 508V003-P1-A4PRO Lote PL-0506.DO 4°C
DAD1A, Sig=280,16 Ref= apag(JK17 1030 Pro140 y 41 y 42 a 37V003-P1-A4-Pro 140 a 37 C.D) 37°C 72 hrs

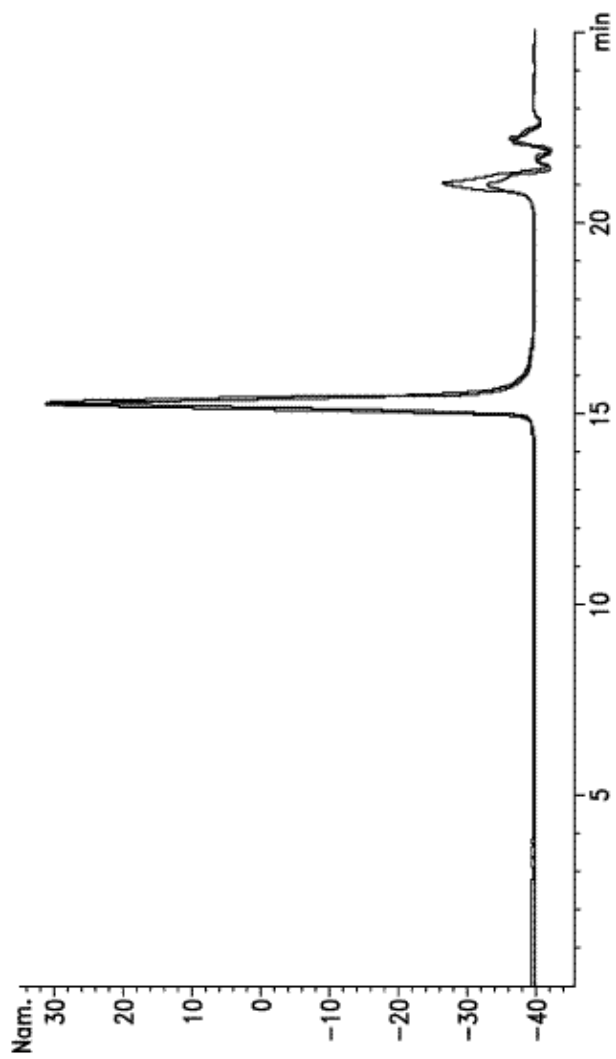


Figura 25

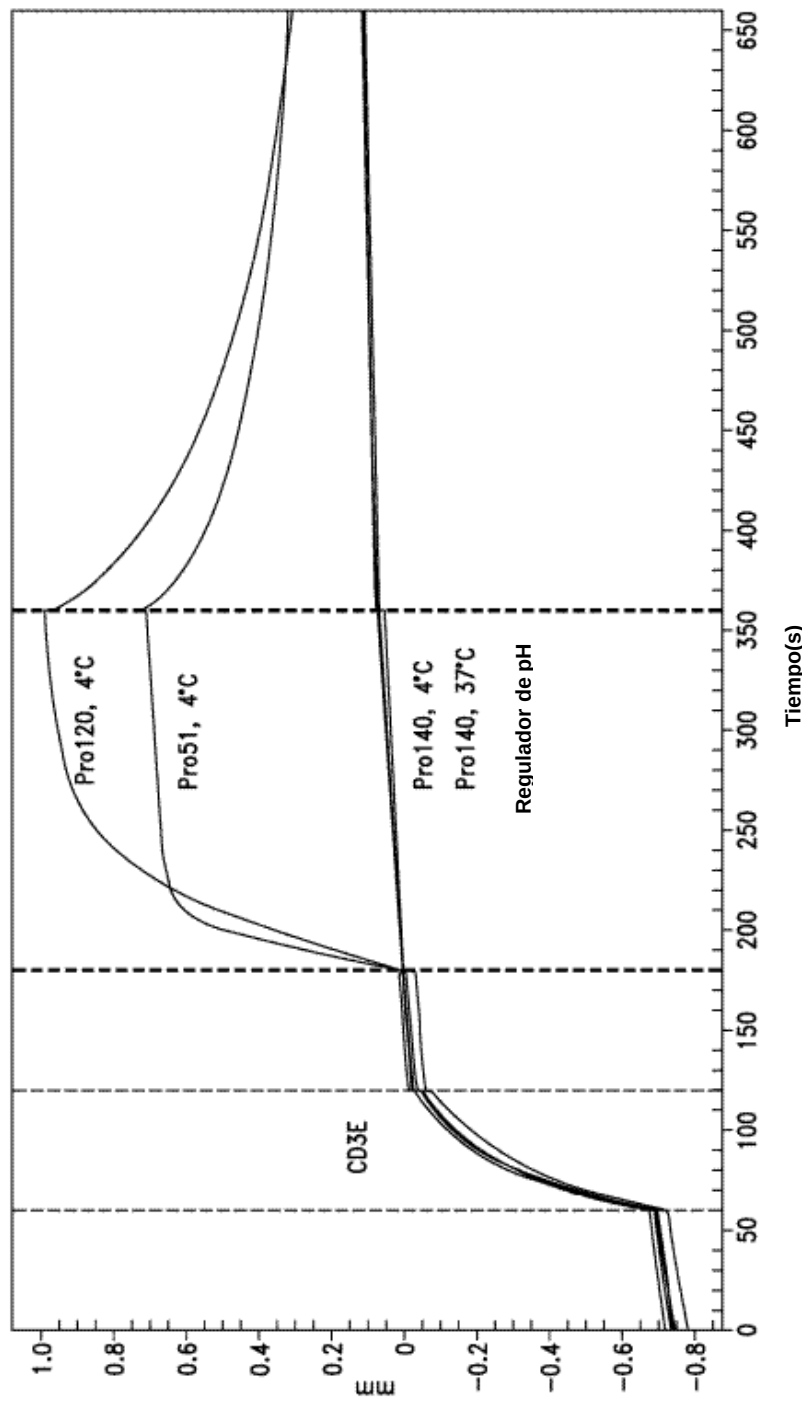


Figura 26

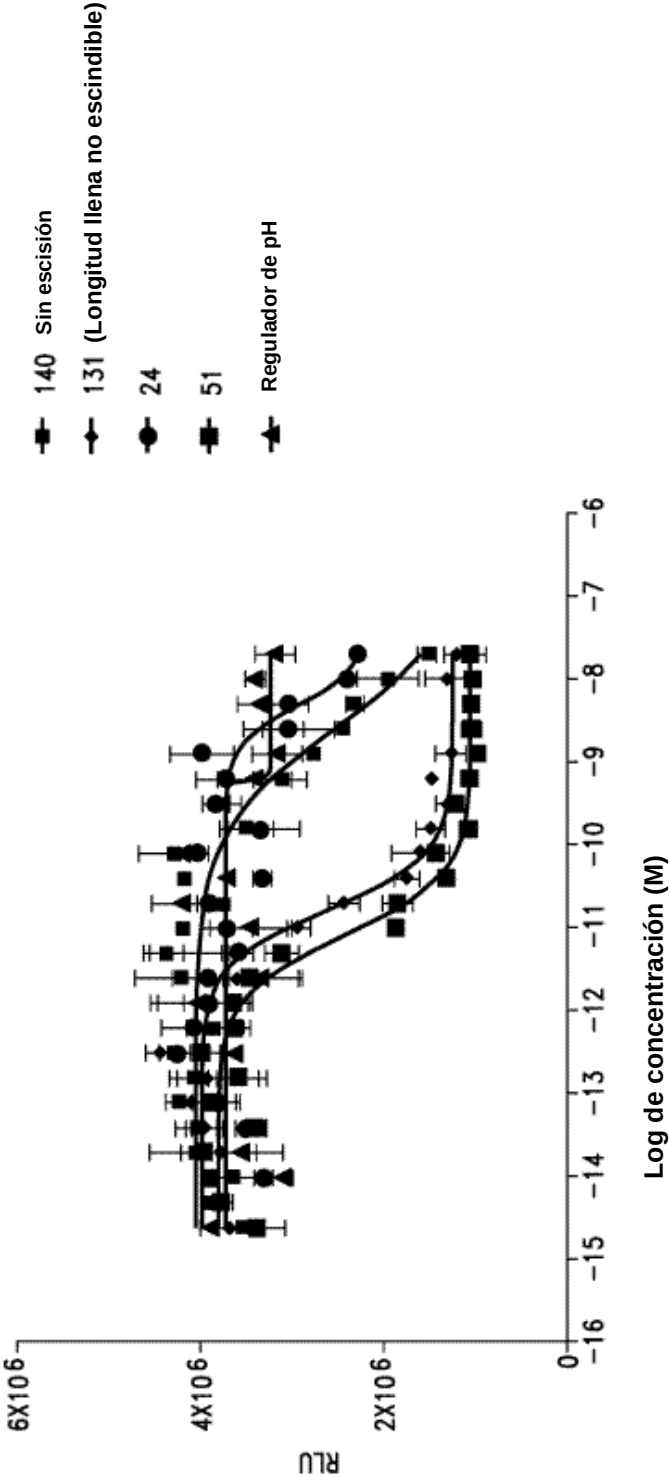
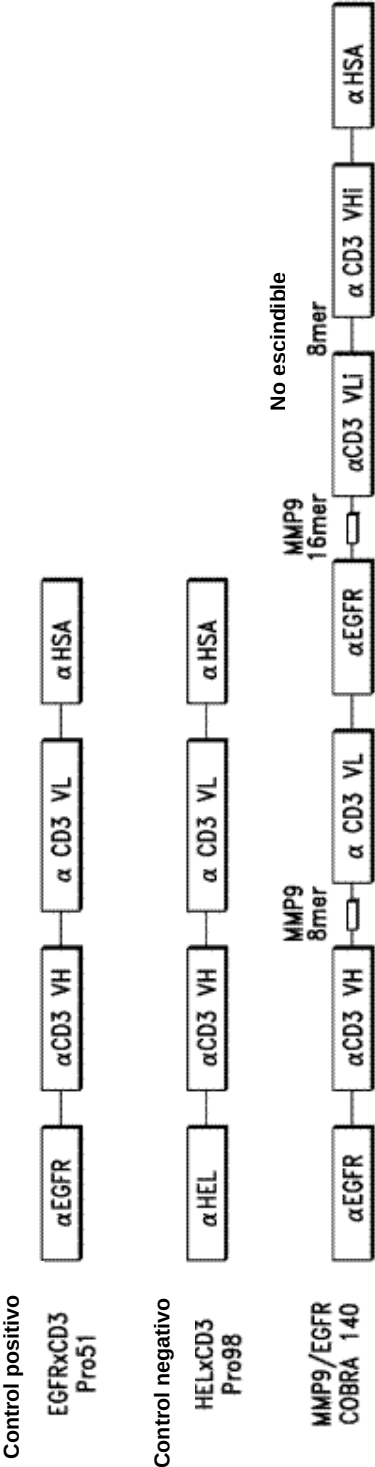


Figura 27

Grupos:



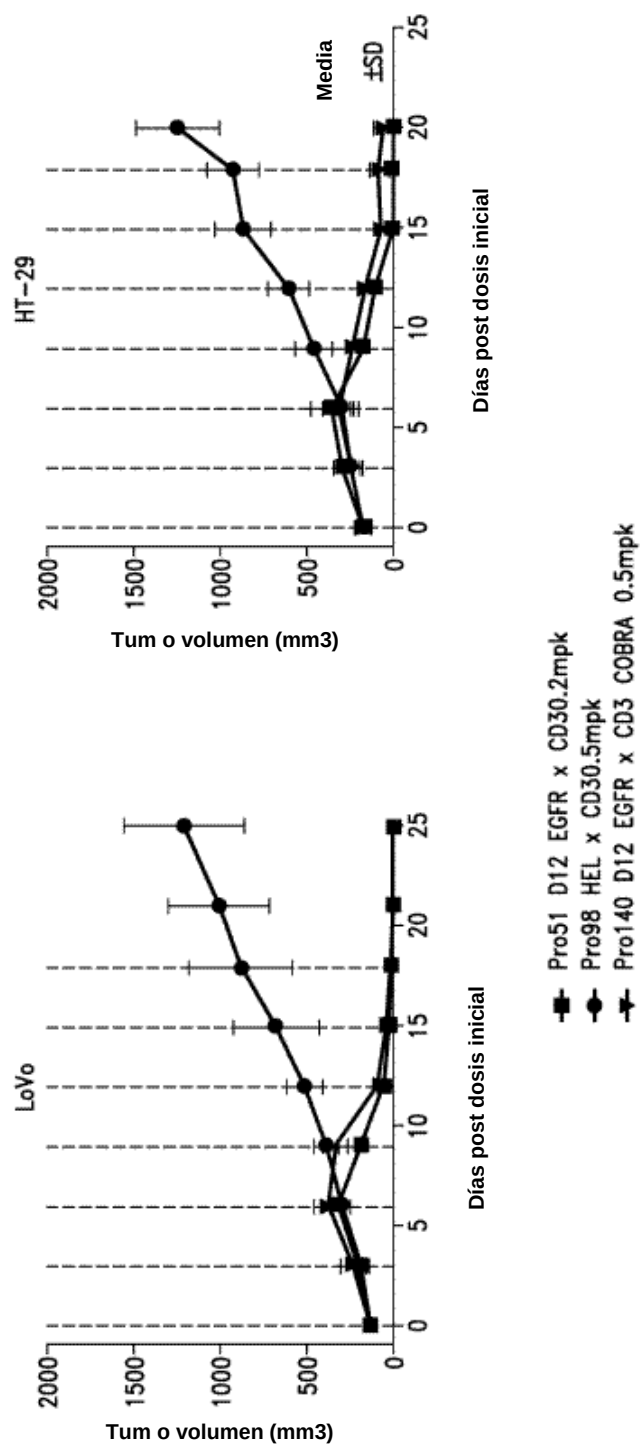
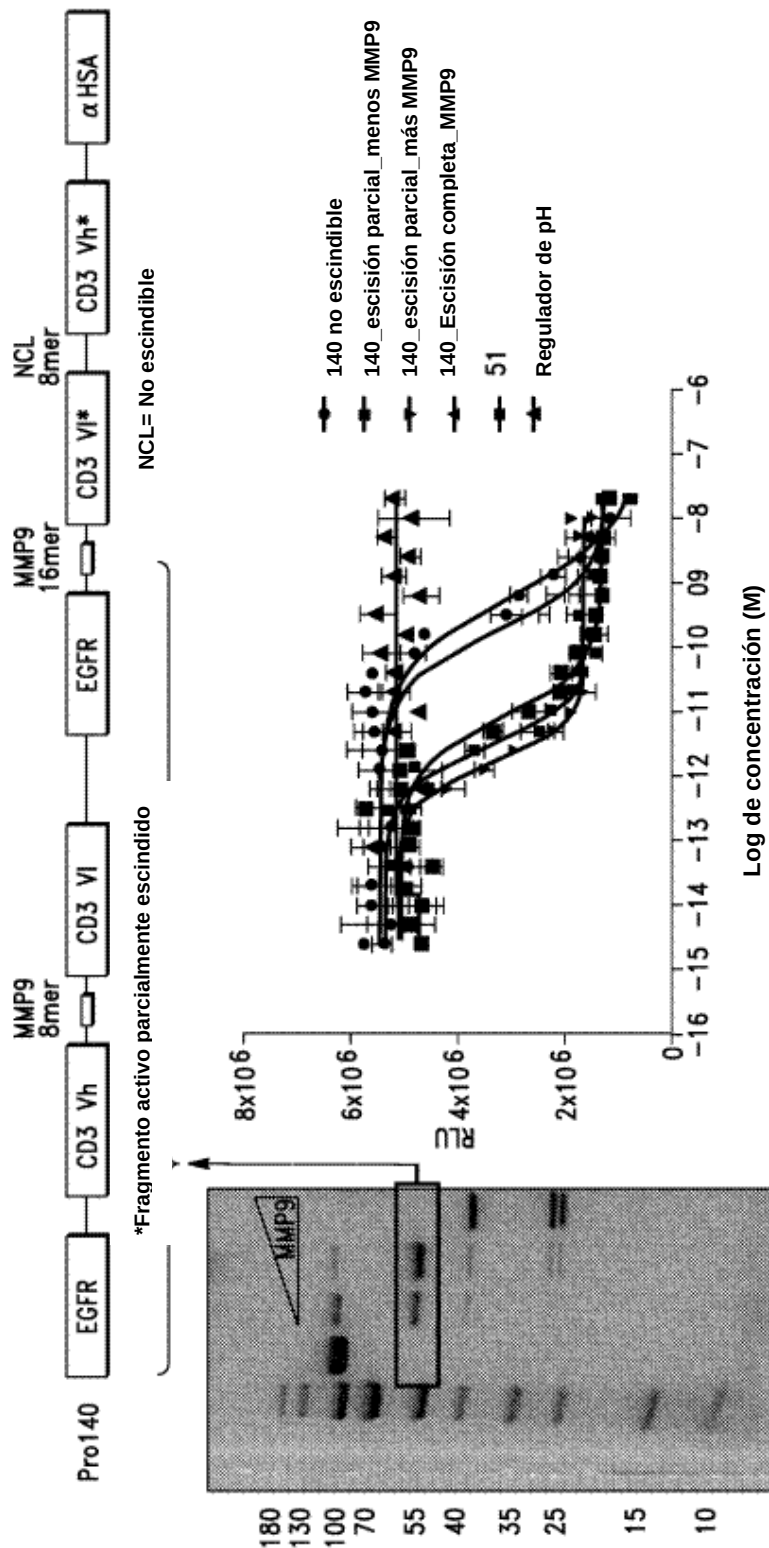


Figura 28B

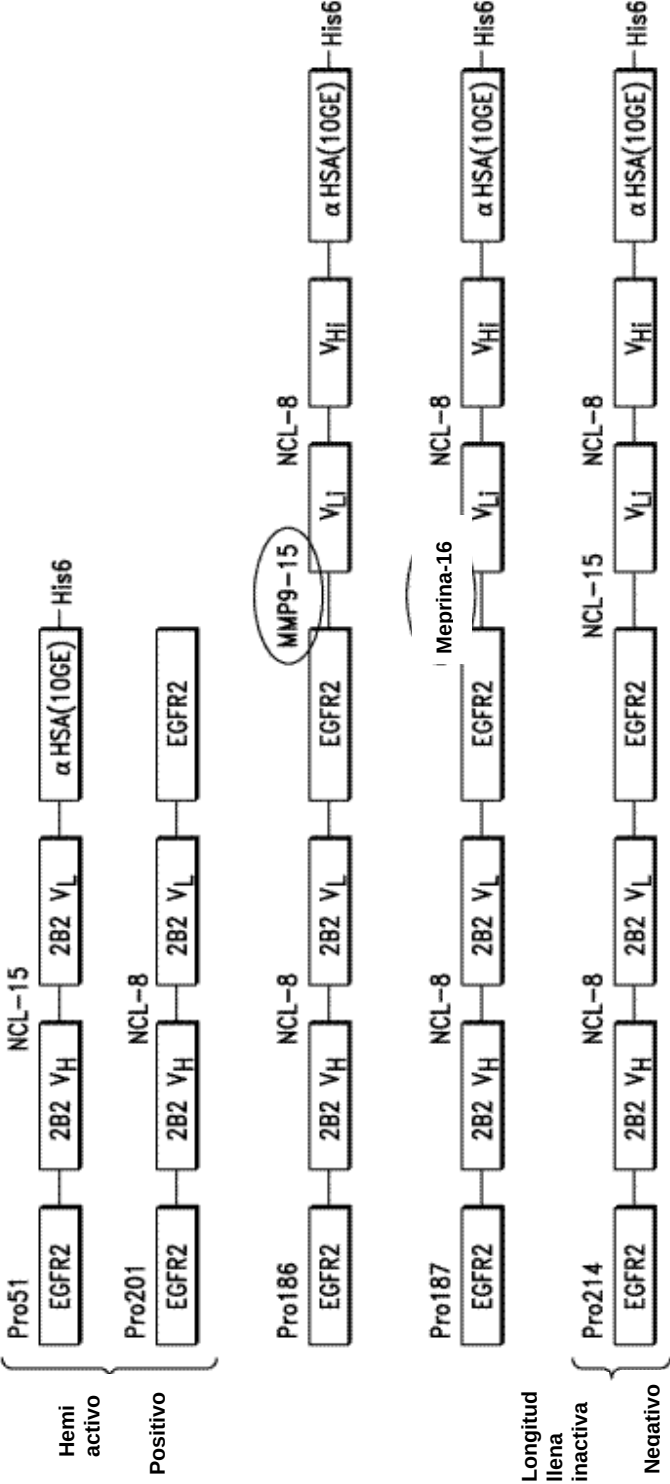
Figura 28A

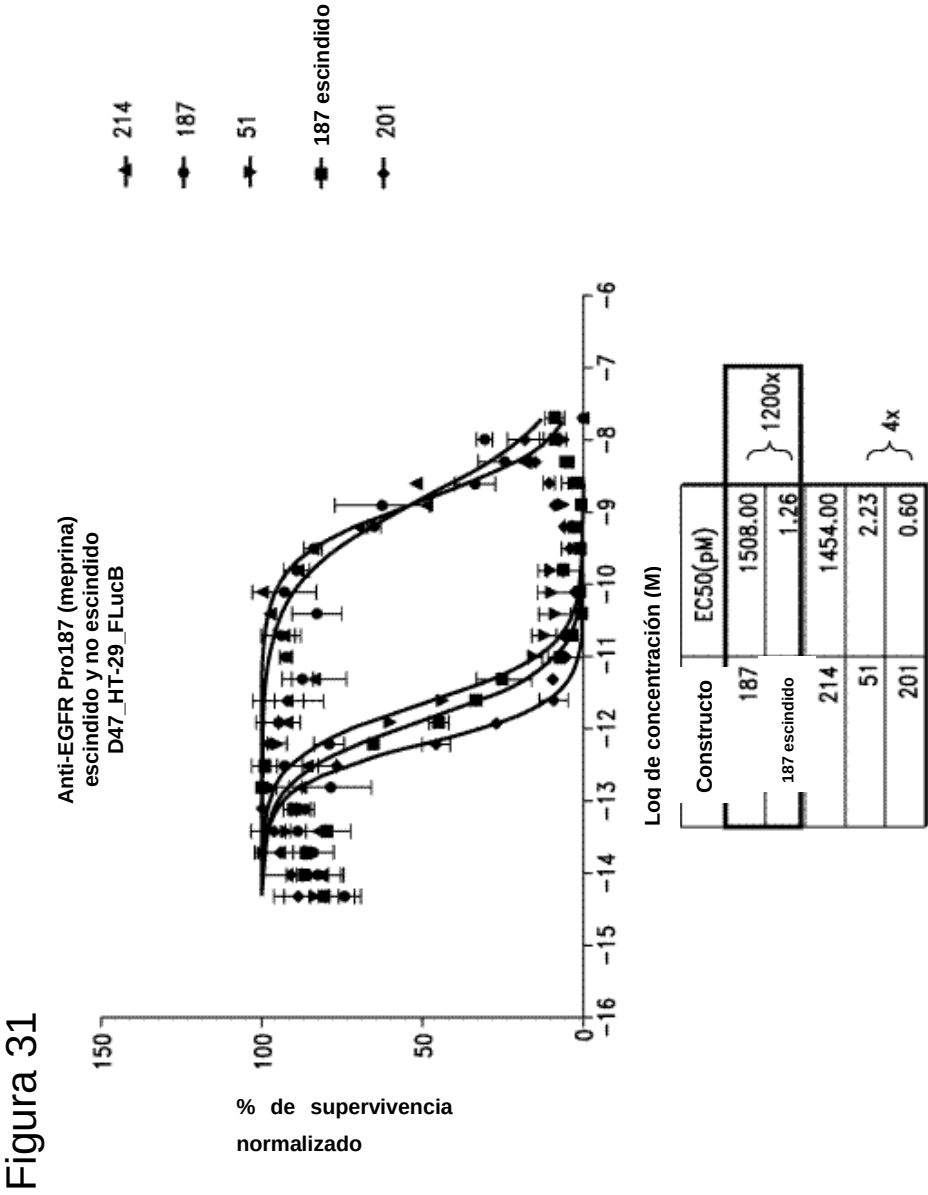
Figura 29

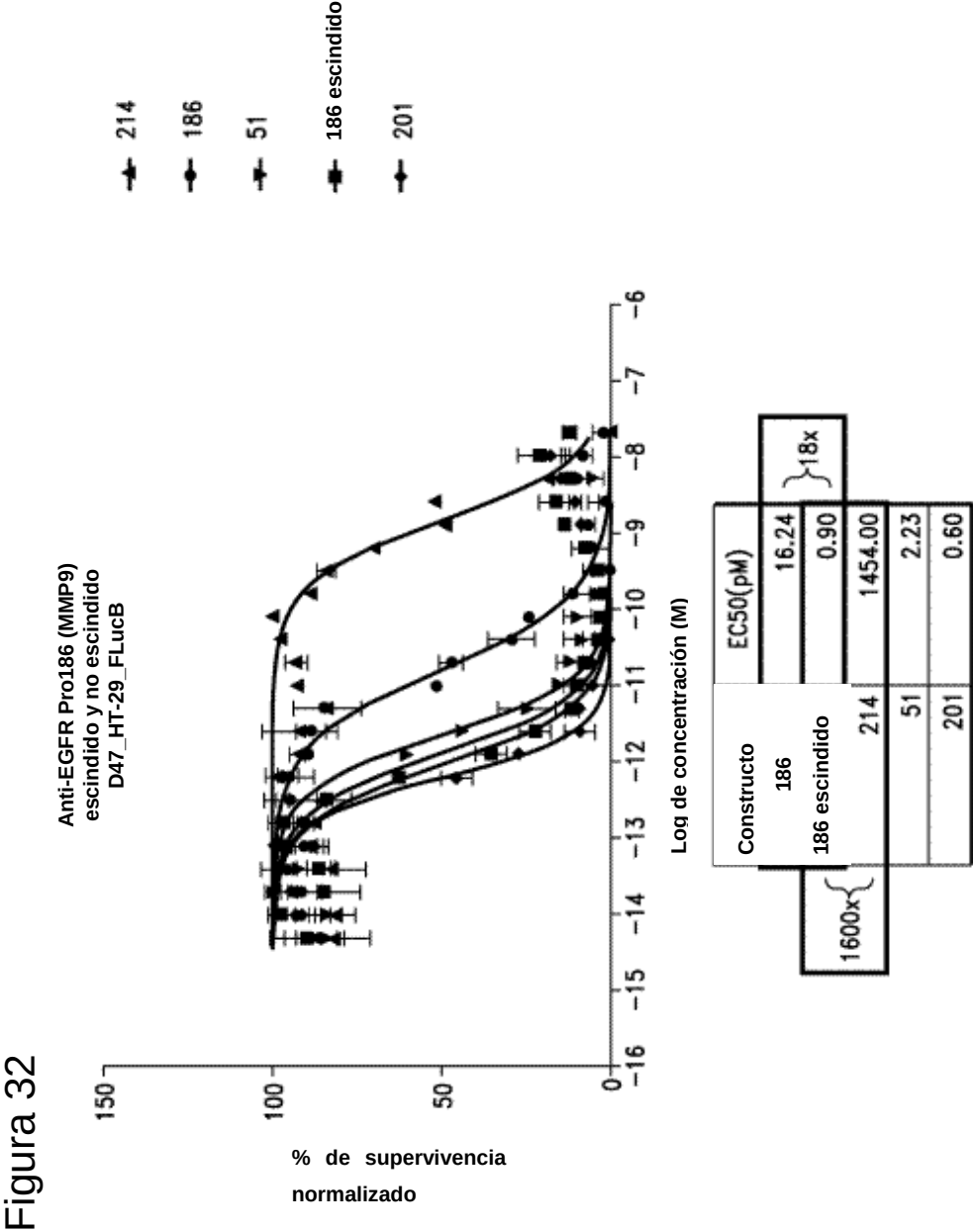


*Enlazador 16 mer MMP9 se escinde a una velocidad más rápida que el enlazador 8 mer MMP9

Figura 30







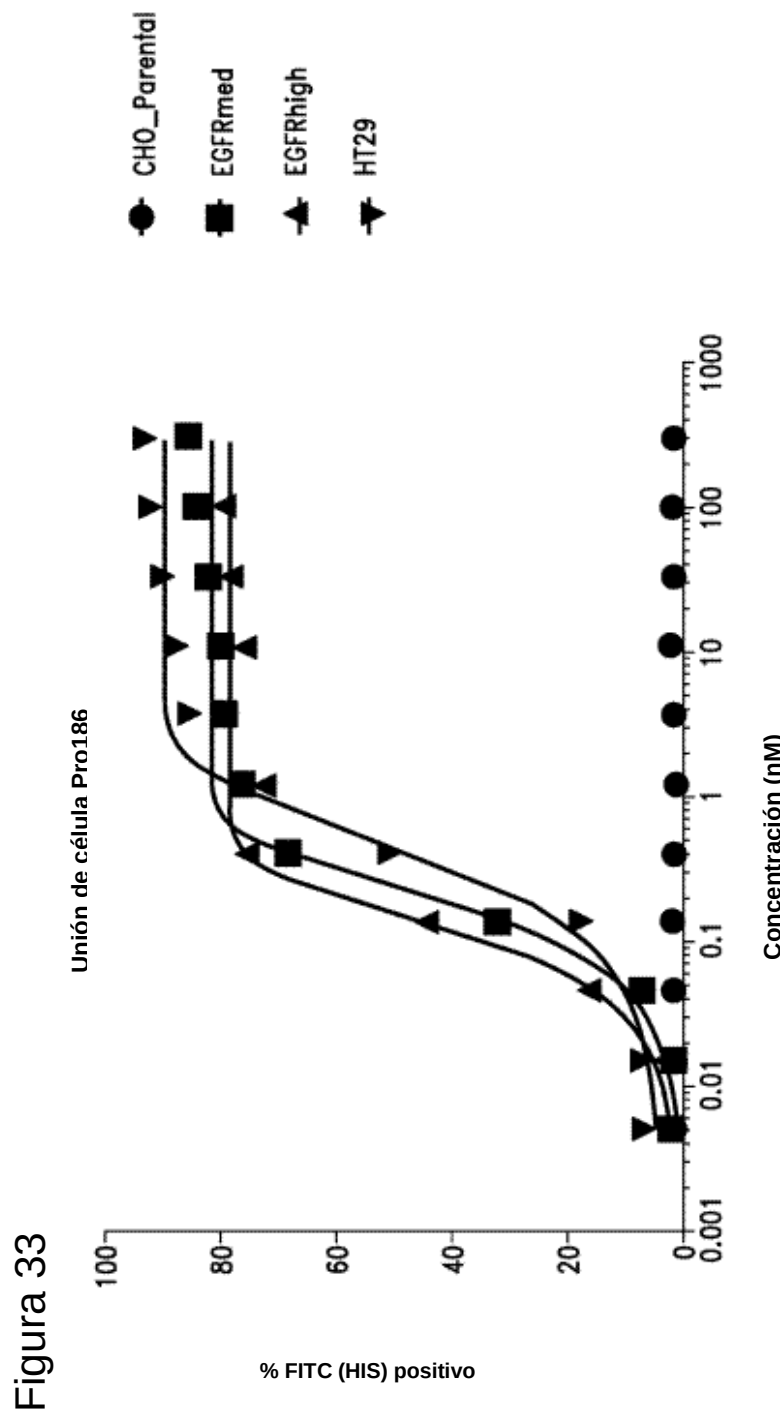


Figura 34

Grupos:

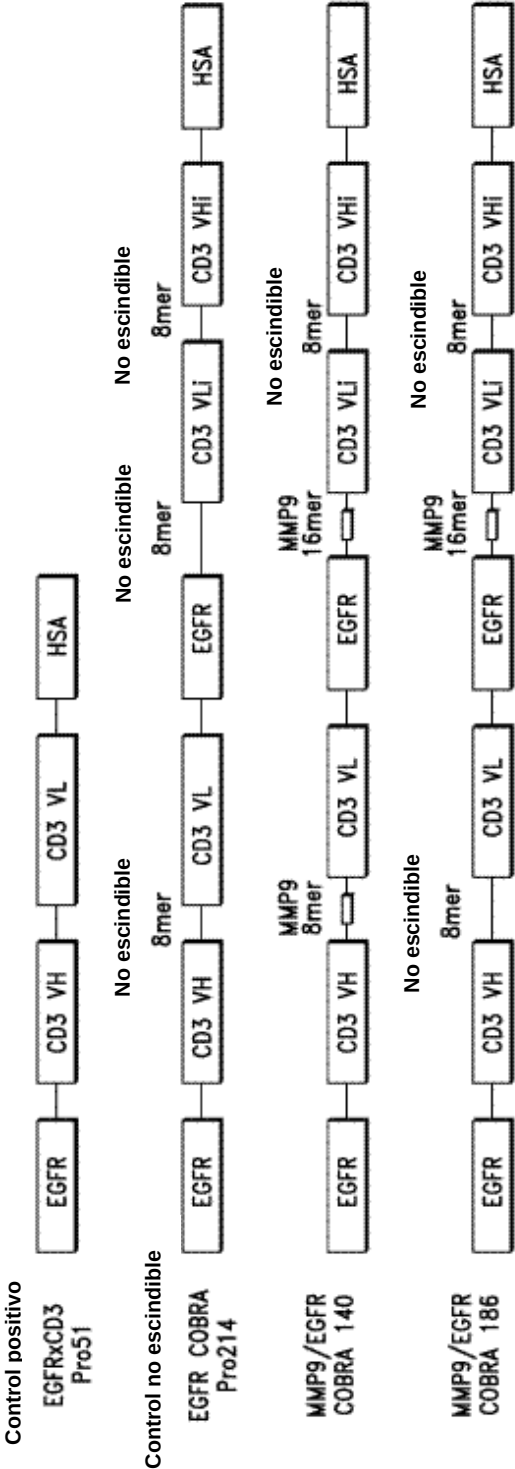


Figura 35

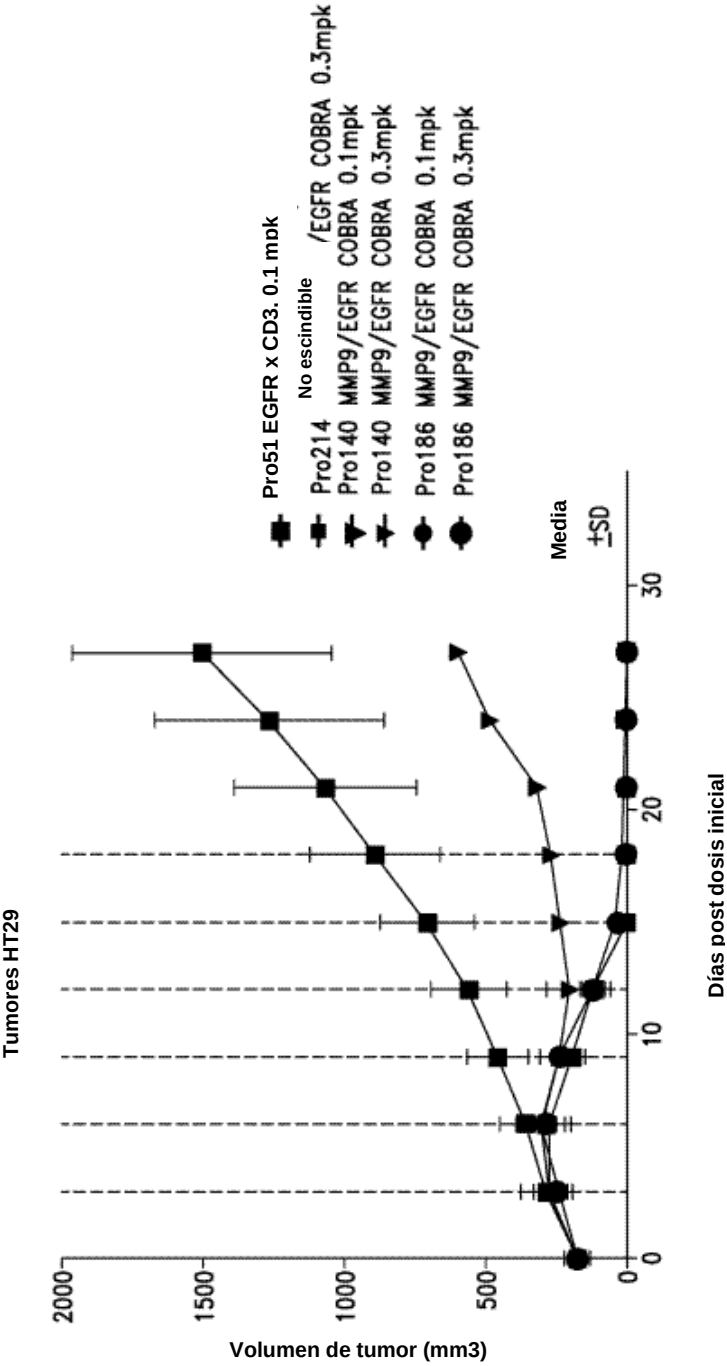
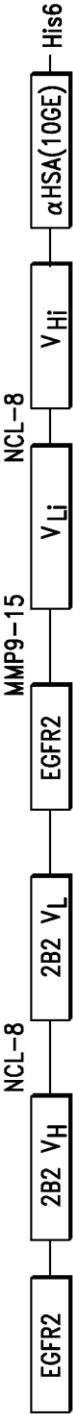


Figura 36

Pro186



Pro	BS1	DL1	CD3VI-	BS2	AL	DL2	CD3Vh-		
393	EGFR2	Vh	NCL-8	VI	S9 ST14(MV) Cats MMP9v	Vii	NCL-8	Vhi	αHSA
394	EGFR2	Vh	NCL-8	VI		Vii	NCL-8	Vhi	αHSA
395	EGFR2	Vh	NCL-8	VI		Vii	NCL-8	Vhi	αHSA
396	EGFR2	Vh	NCL-8	VI		Vii	NCL-8	Vhi	αHSA
429	EGFR2	Vh	NCL-8	VI	Mep/GrandB	Vii	NCL-8	Vhi	αHSA
430	EGFR2	Vh	NCL-8	VI	MMP9-2	Vii	NCL-8	Vhi	αHSA
431	EGFR2	Vh	NCL-8	VI	ST14(MS)	Vii	NCL-8	Vhi	αHSA

S9
ST14(MV)
Cats
MMP9v
Mep/GrandB
MMP9-2
ST14(MS)

Figura 37

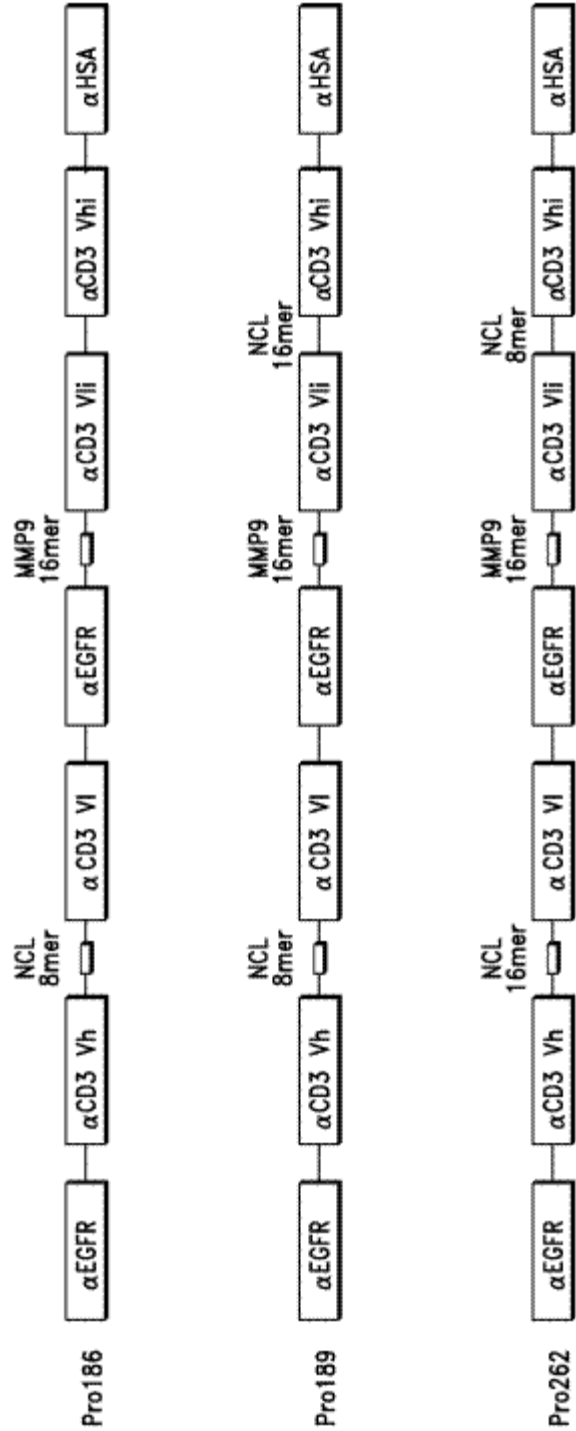


Figura 38

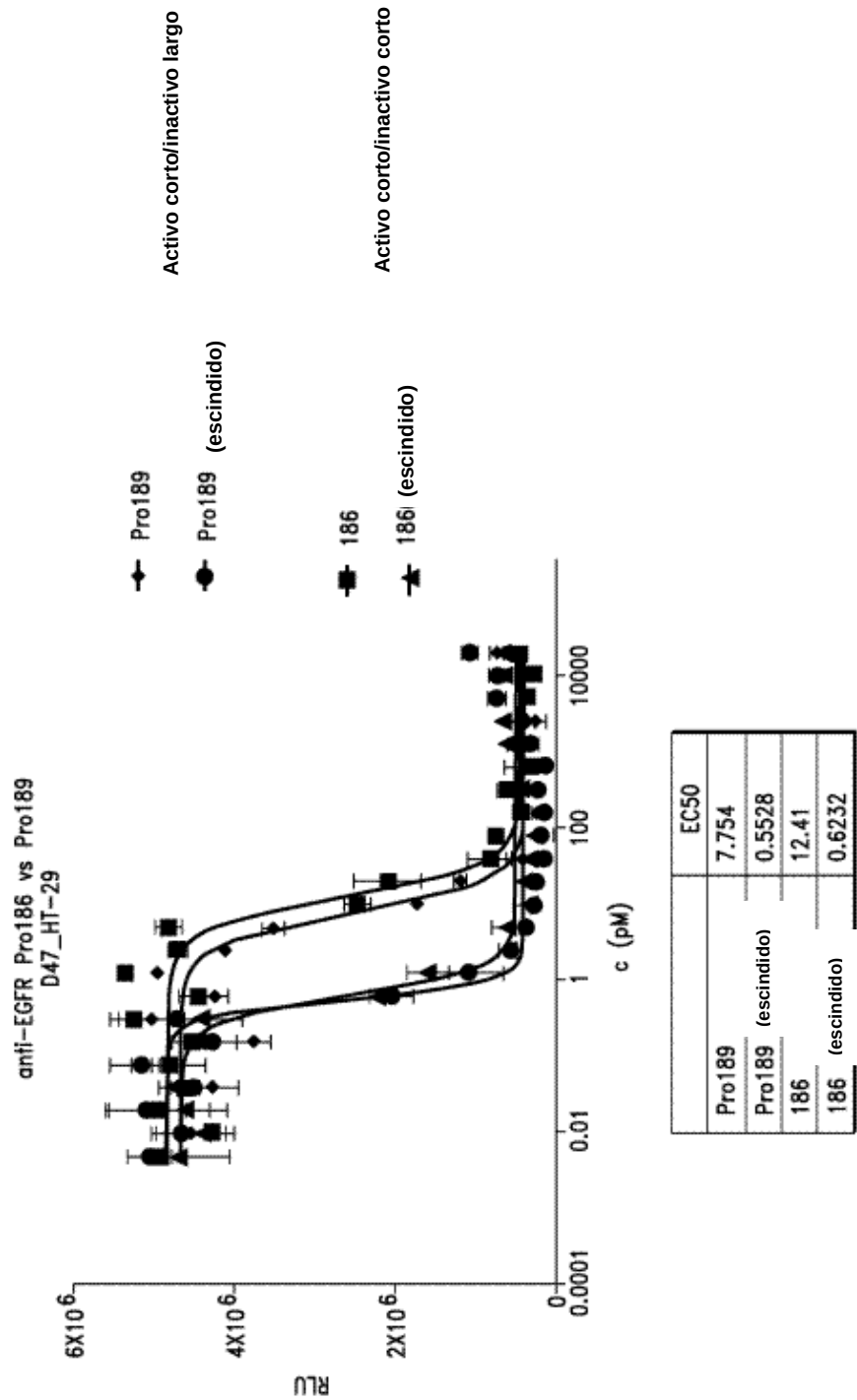


Figura 39

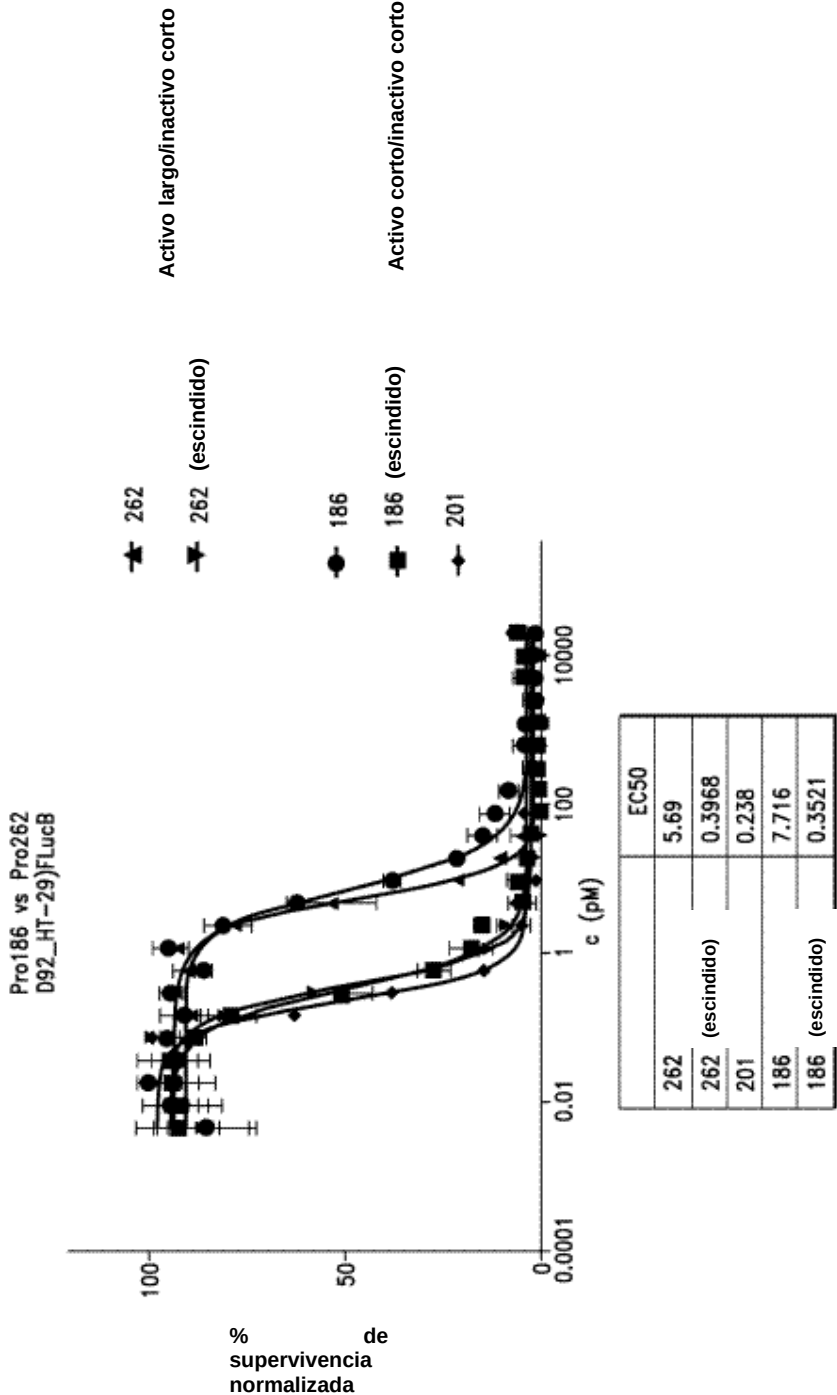


Figura 40A

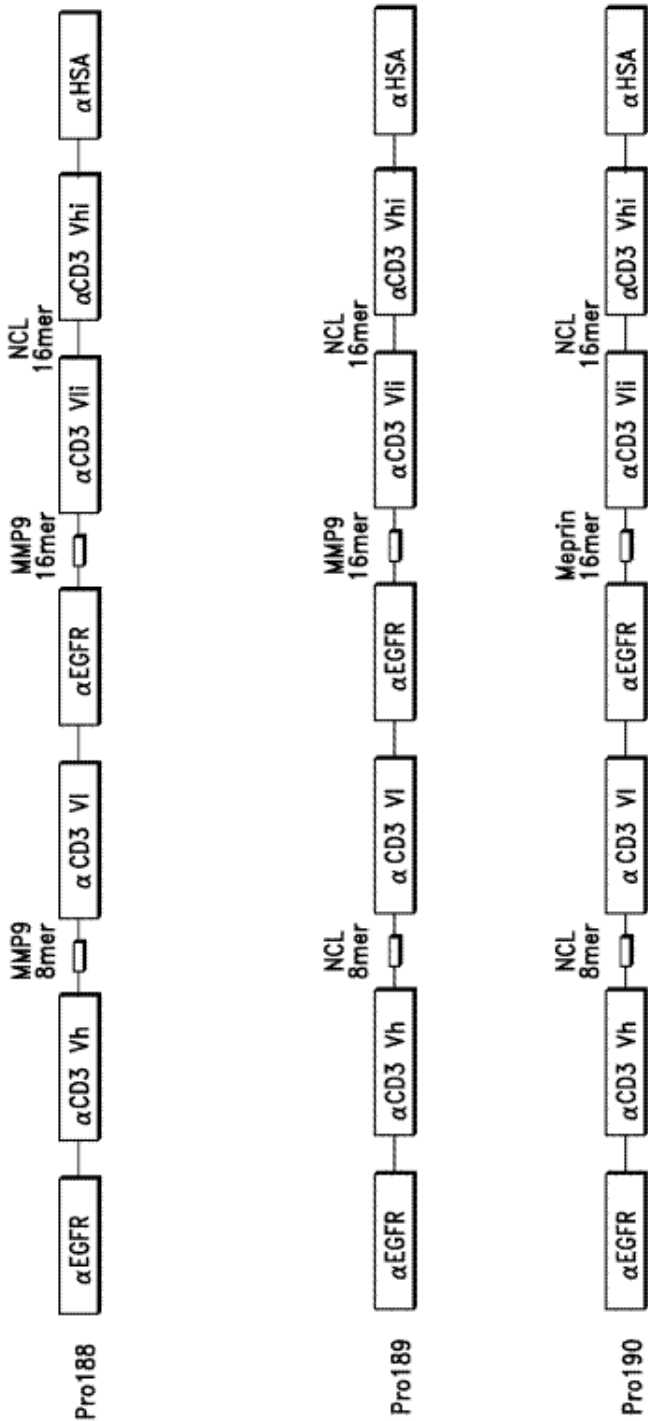


Figura 40B

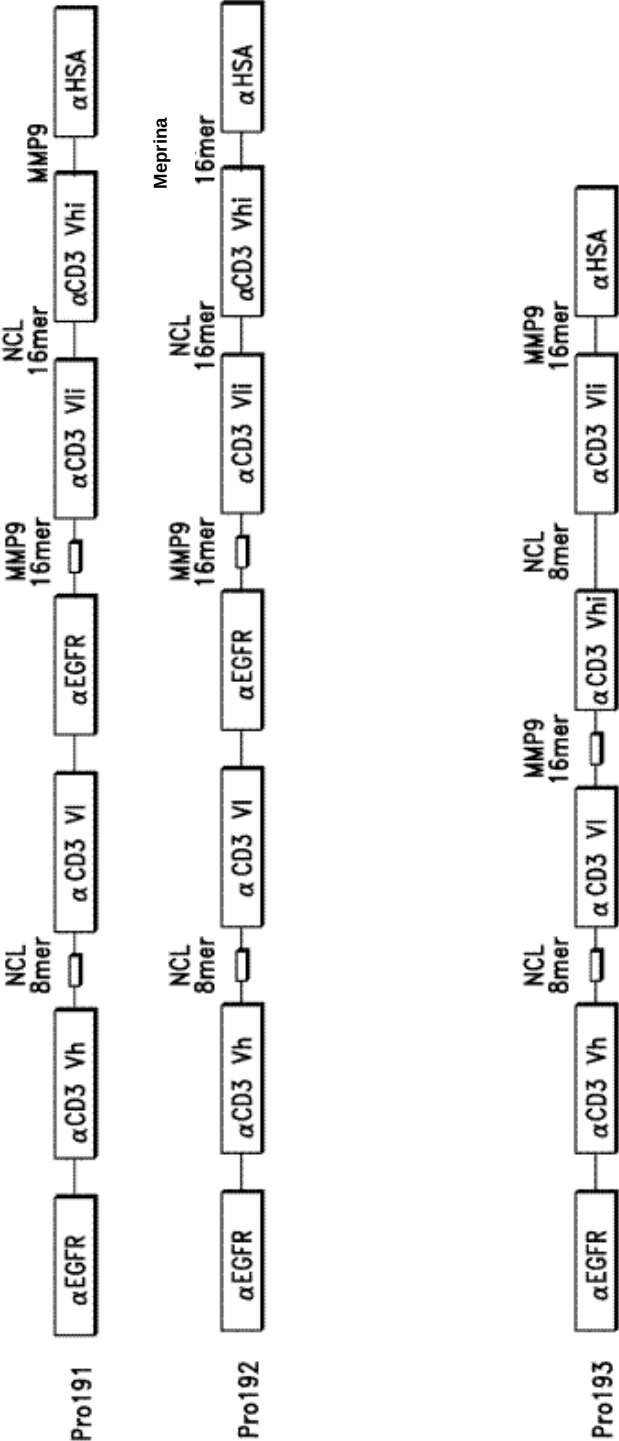


Figura 40C

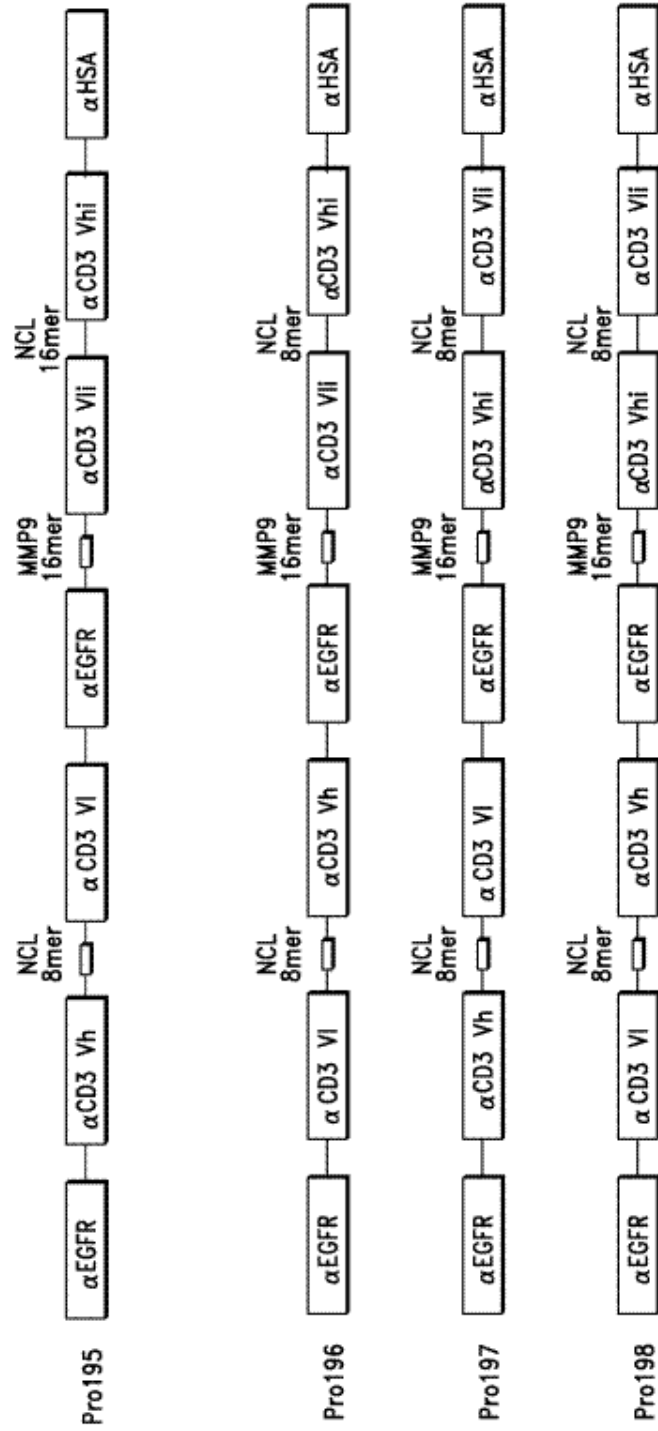


Figura 42

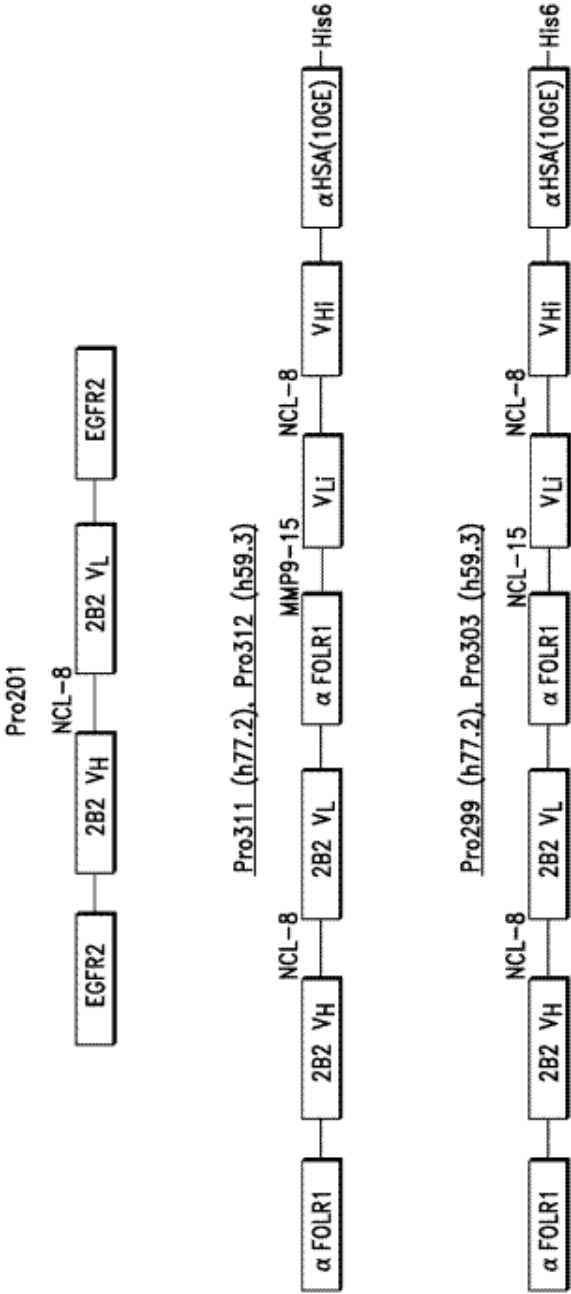


Figura 43

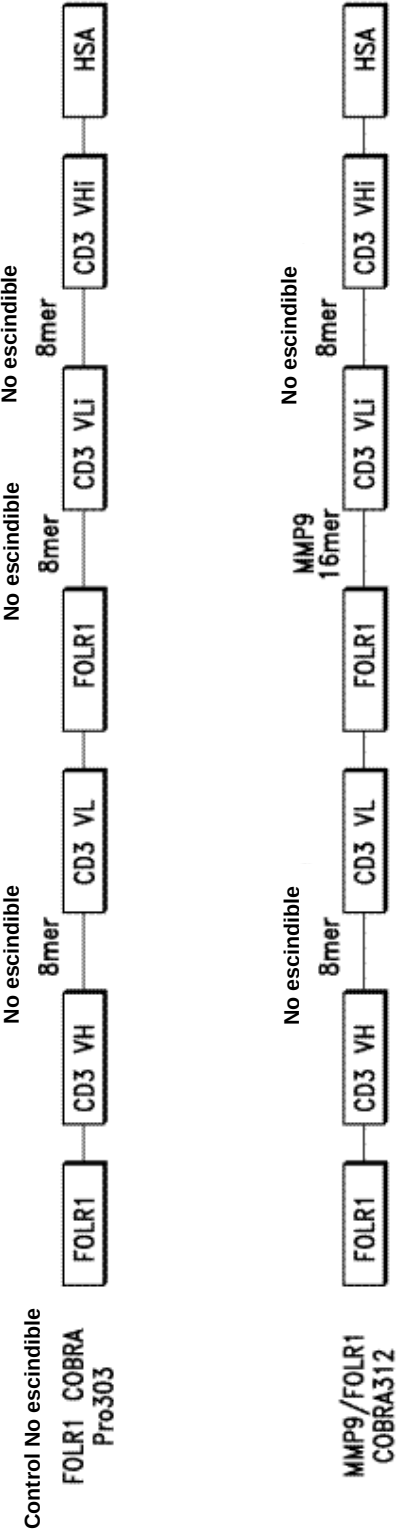


Figura 44

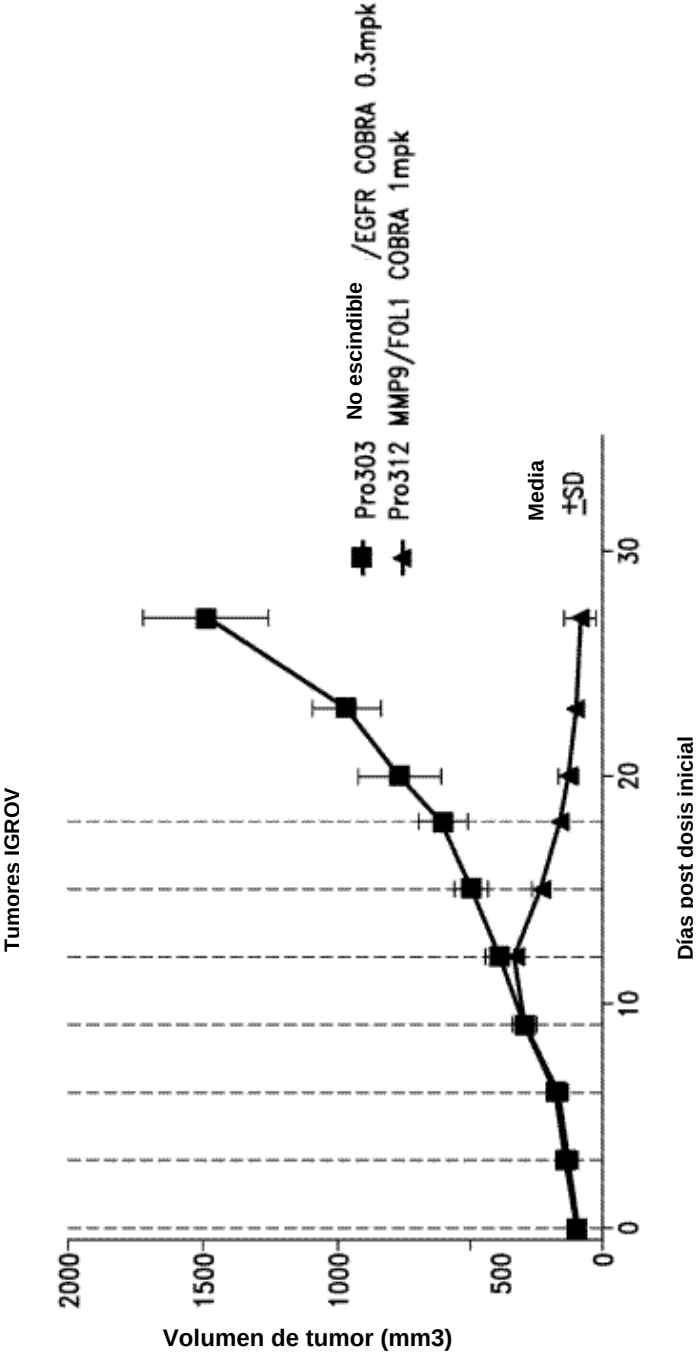


Figura 45

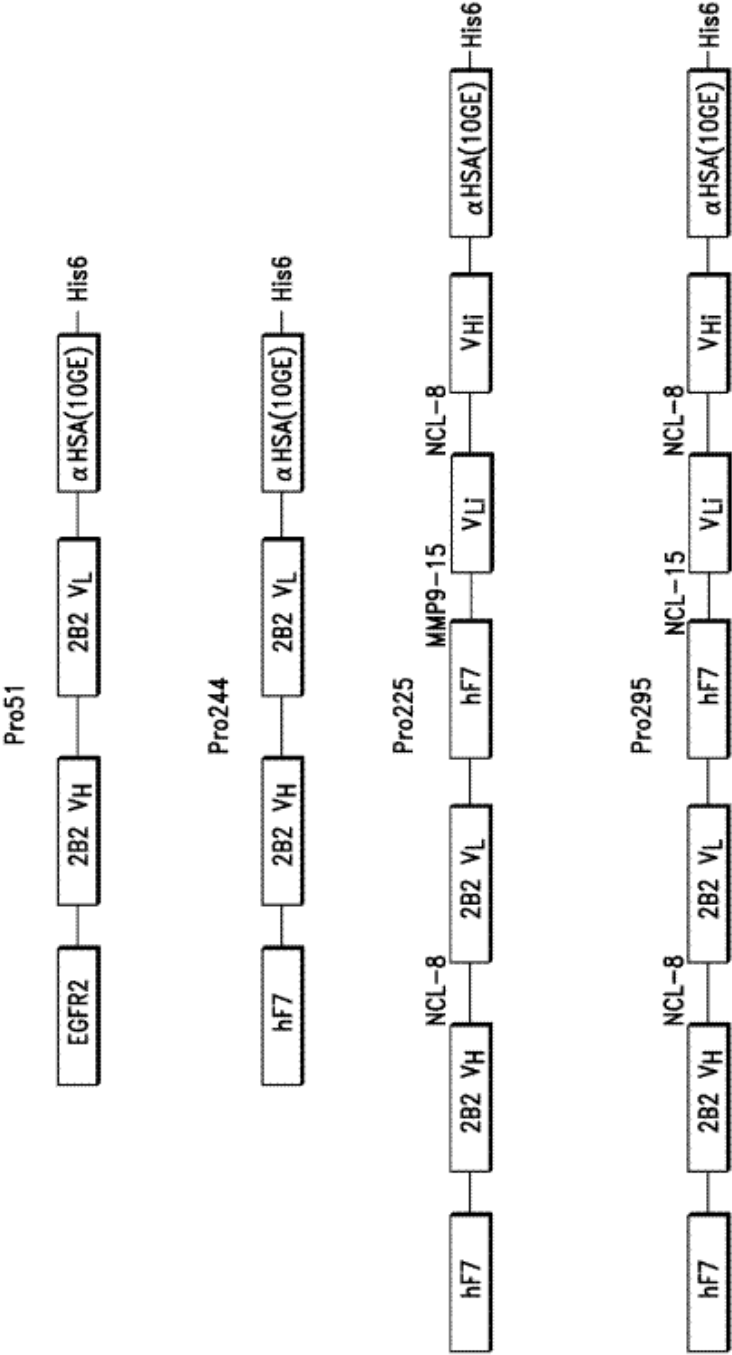


Figura 46

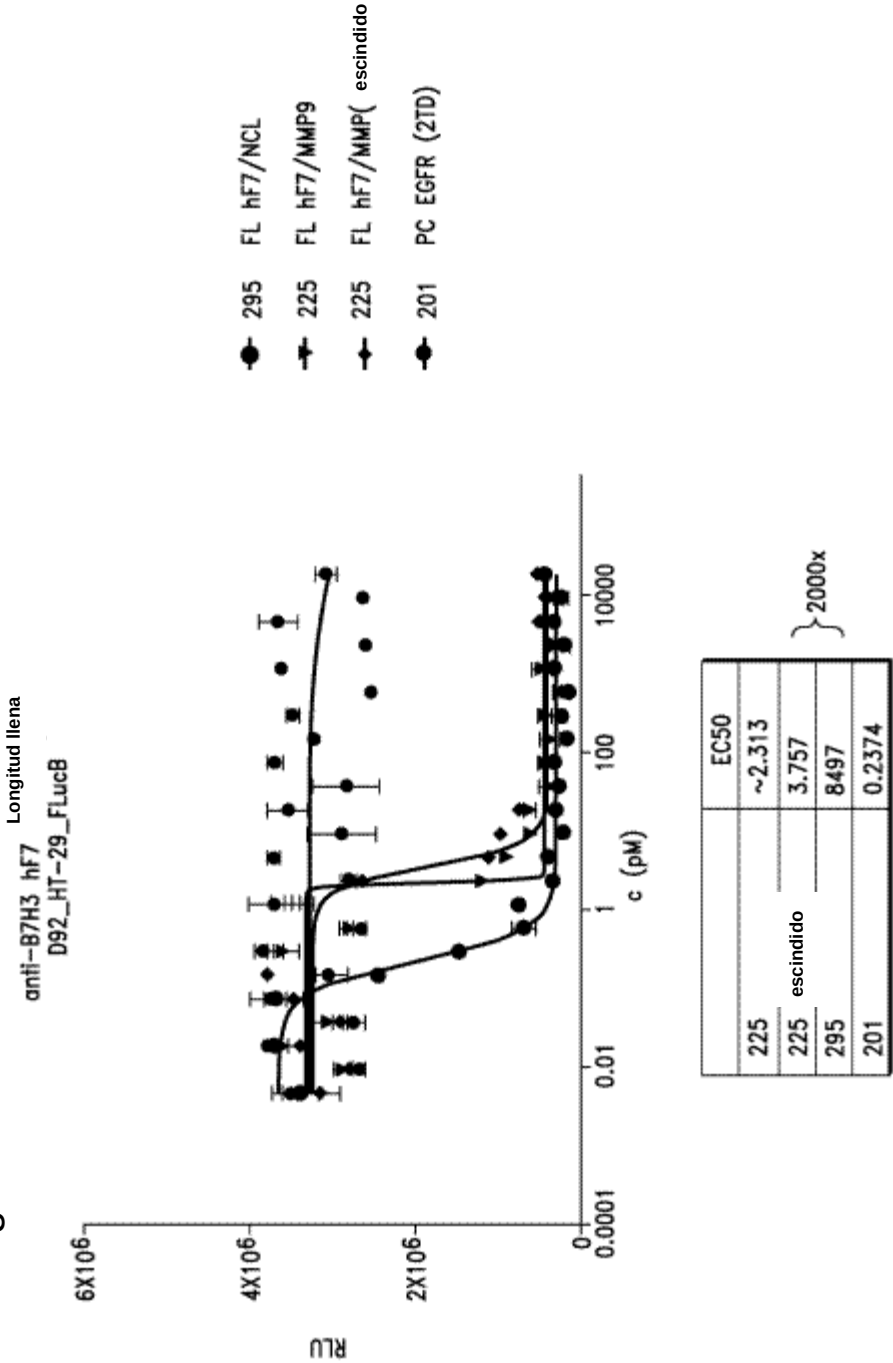


Figura 47

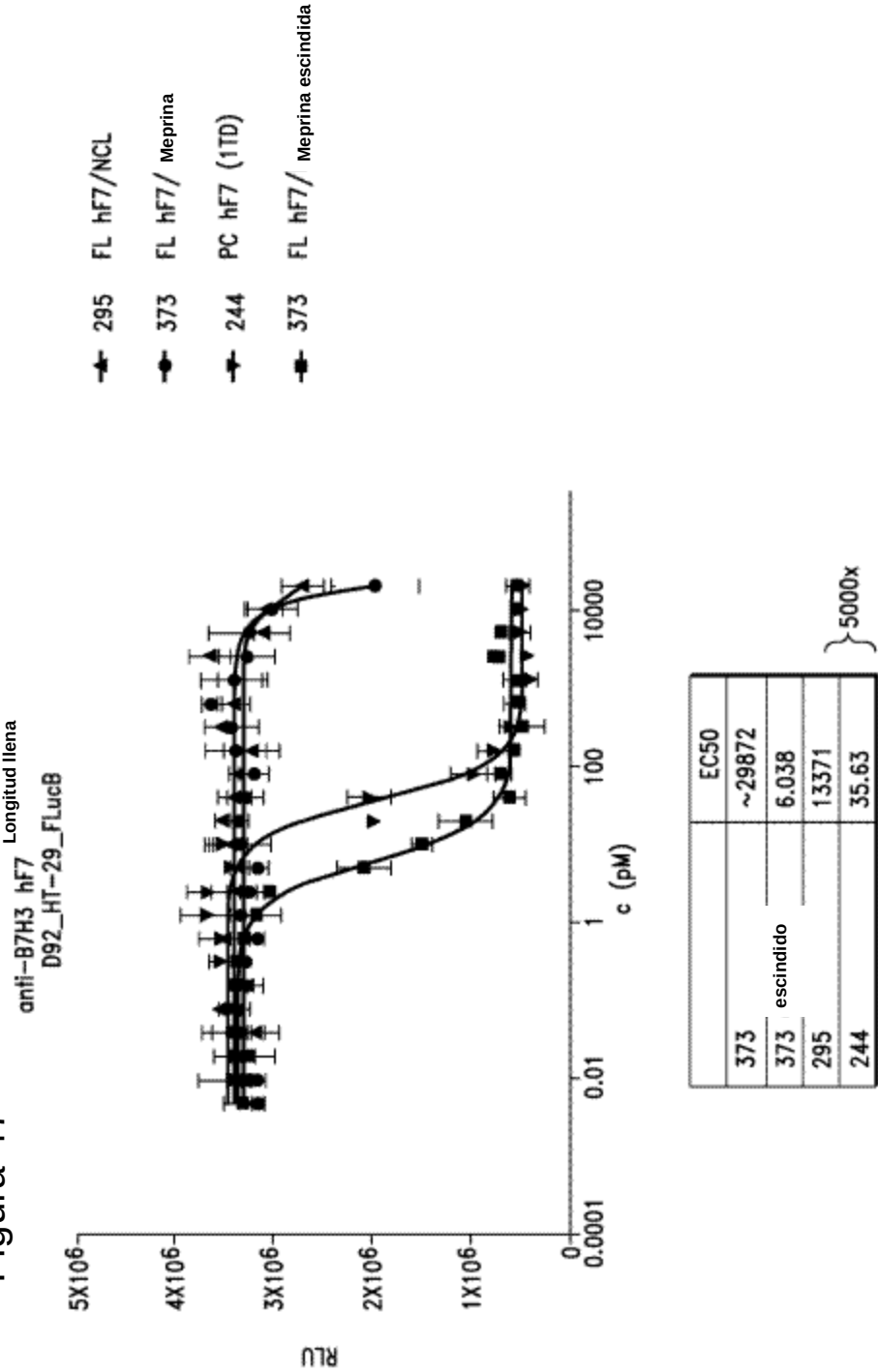


Figura 48

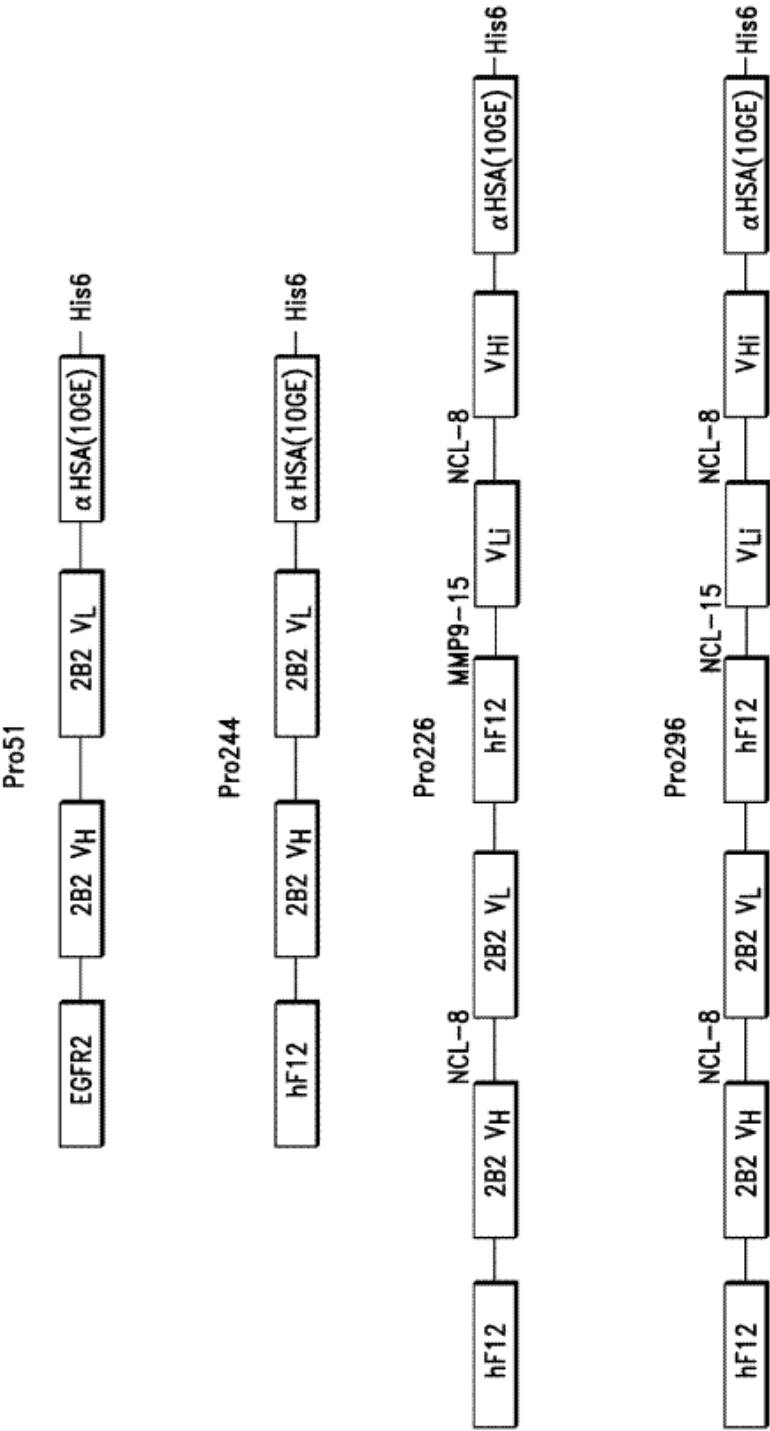
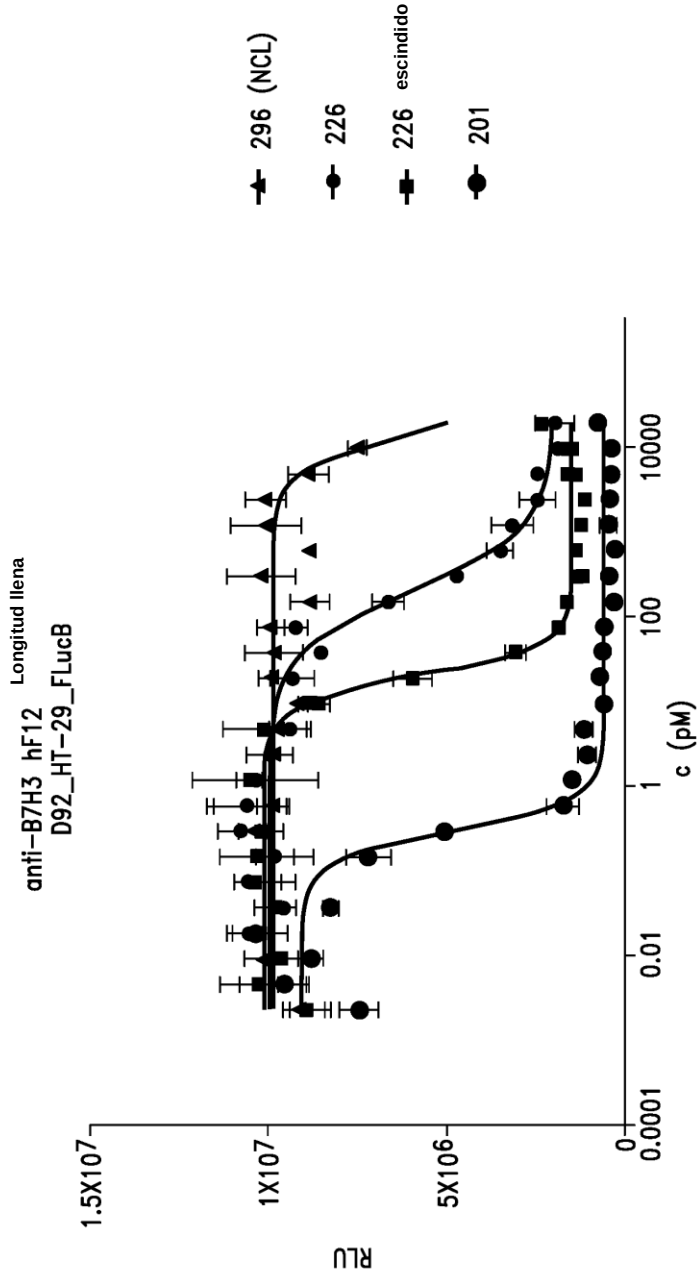


Figura 49



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

Figura 50

<u>Afinidad de unión (nM)</u>			<u>Reactividad cruzada</u>	
<u>Clon</u>	Humano	<u>Cino</u>	<u>Cino/humano</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	

Figura 51

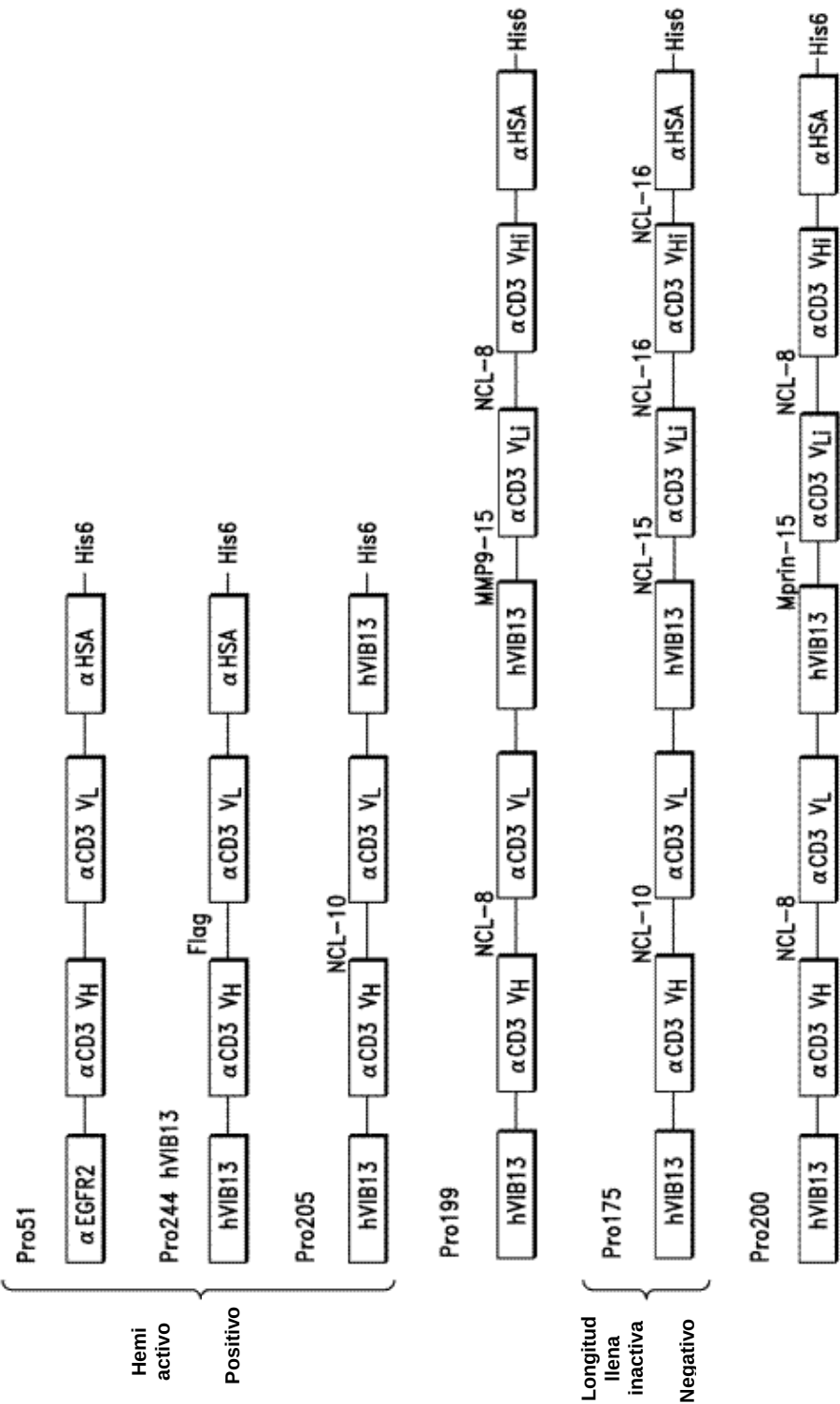
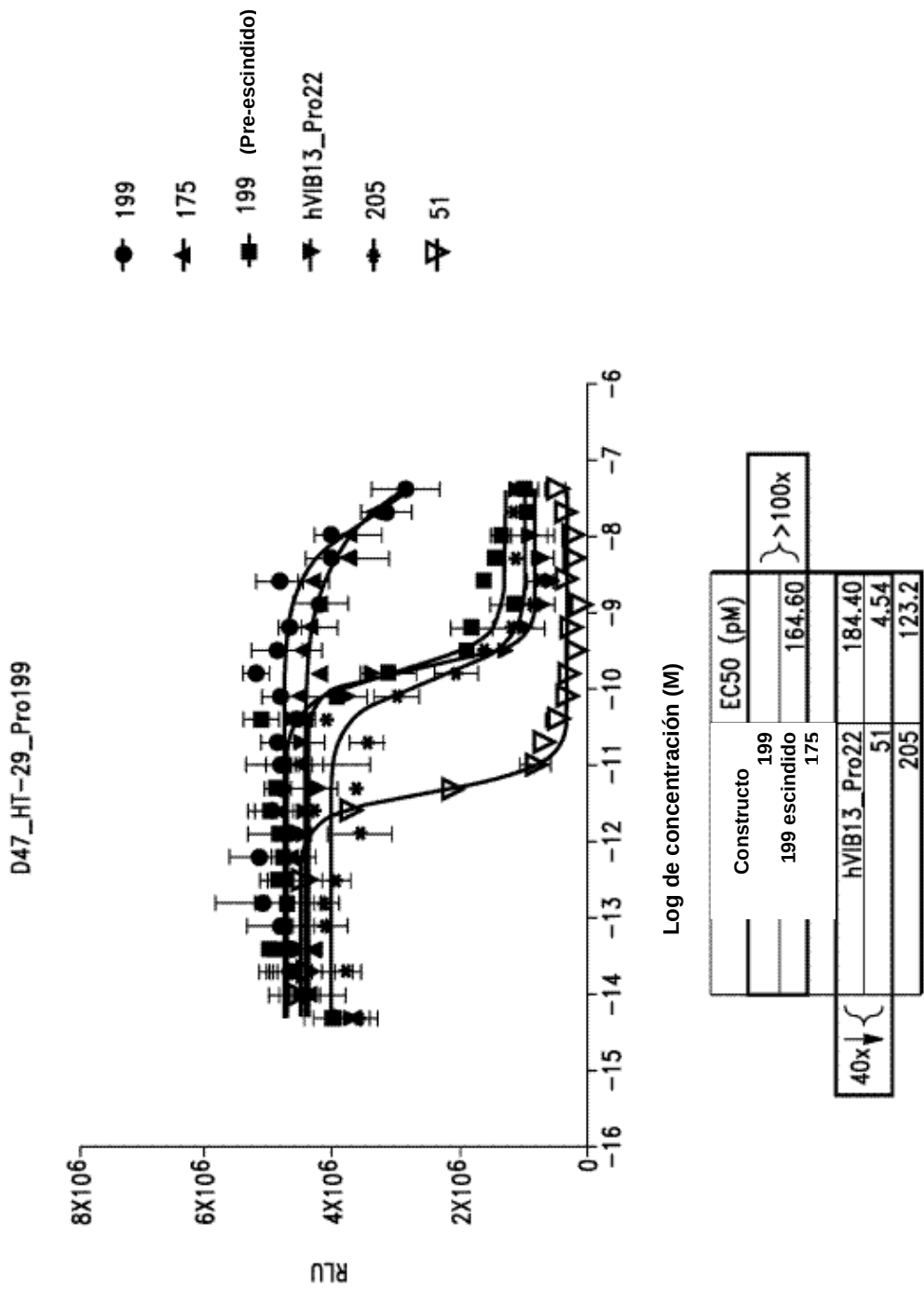


Figura 52



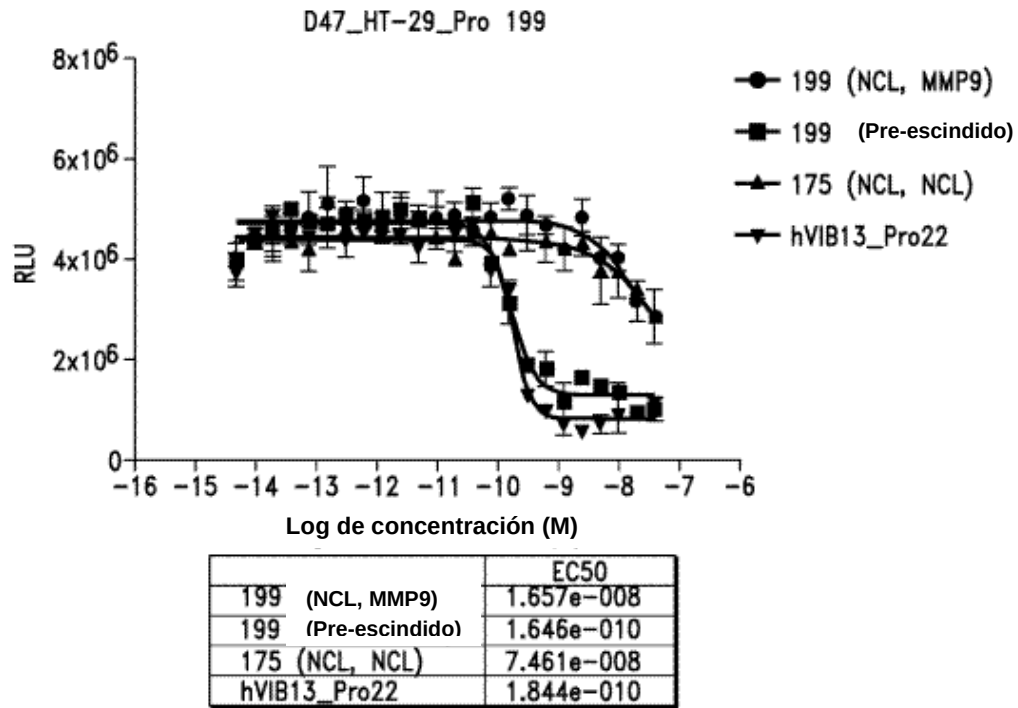


Figura 53A

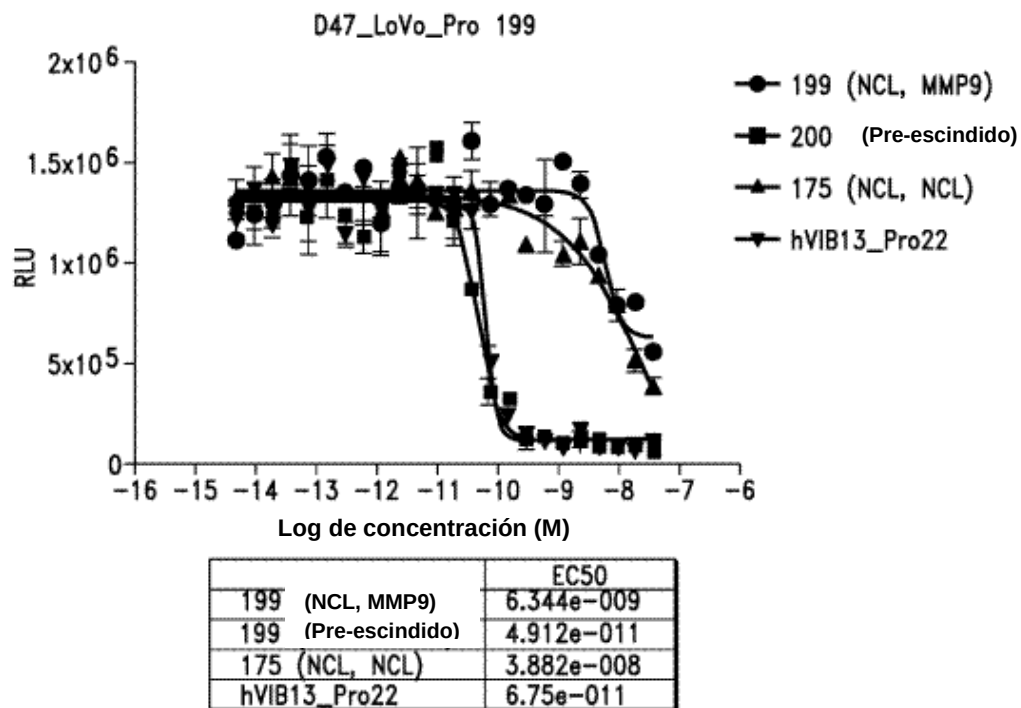


Figura 53B

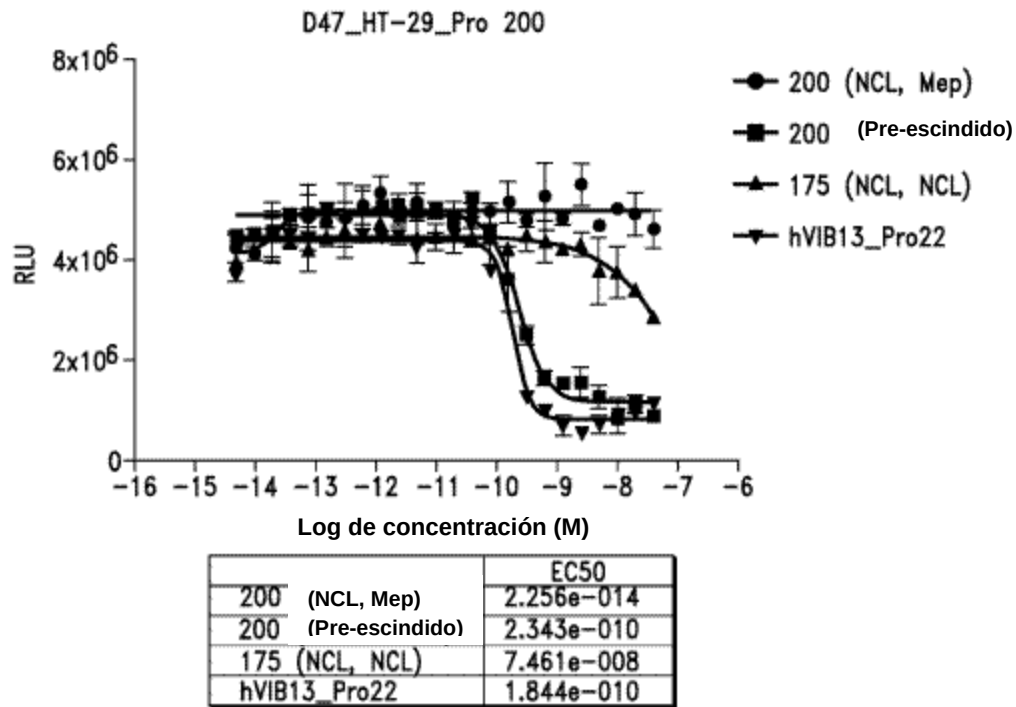


Figura 54A

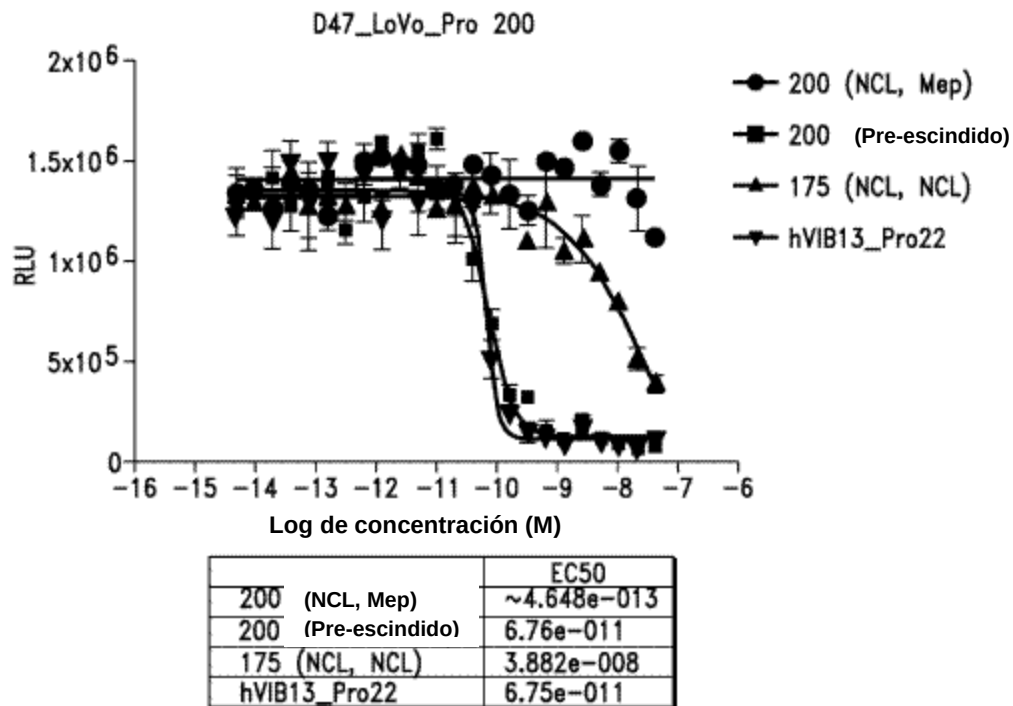


Figura 54B

Figura 55

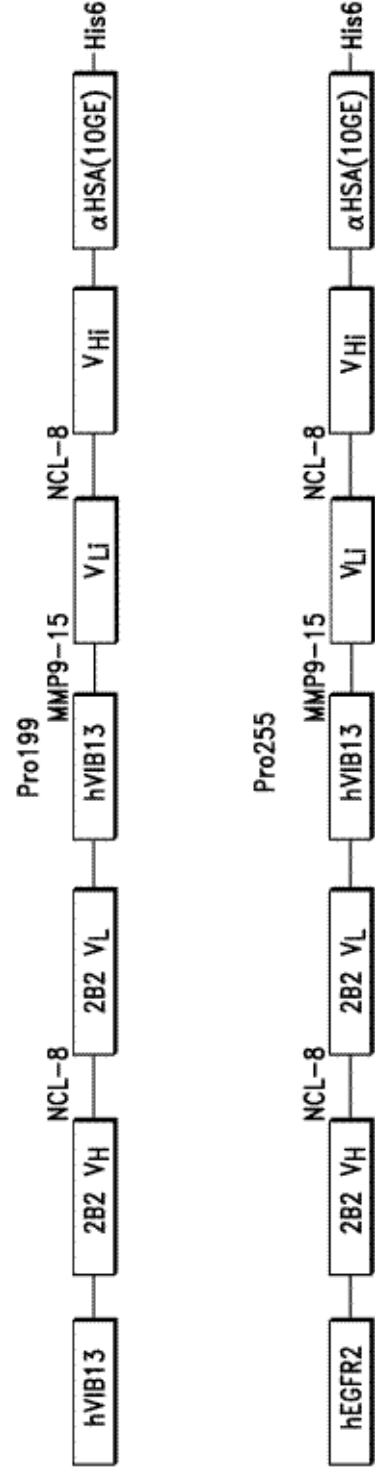
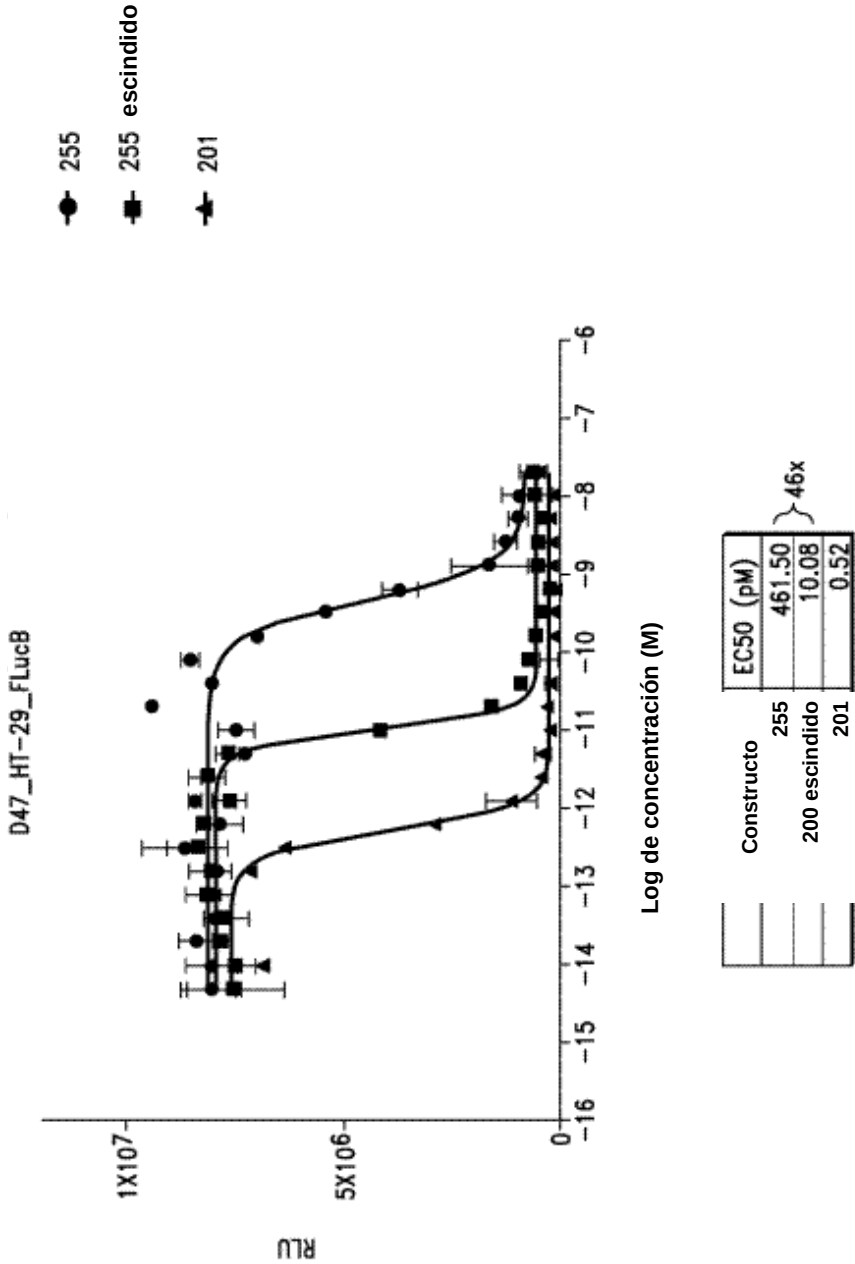


Figura 56

Anti-EGFR y anti-EpCAM Heterólogo Longitud Ilena Pro 255



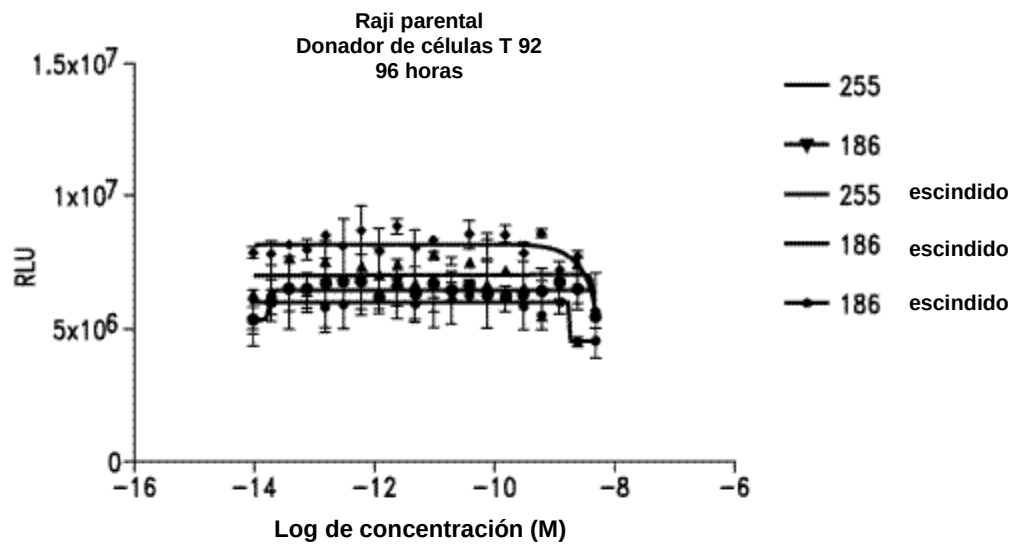


Figura 57A

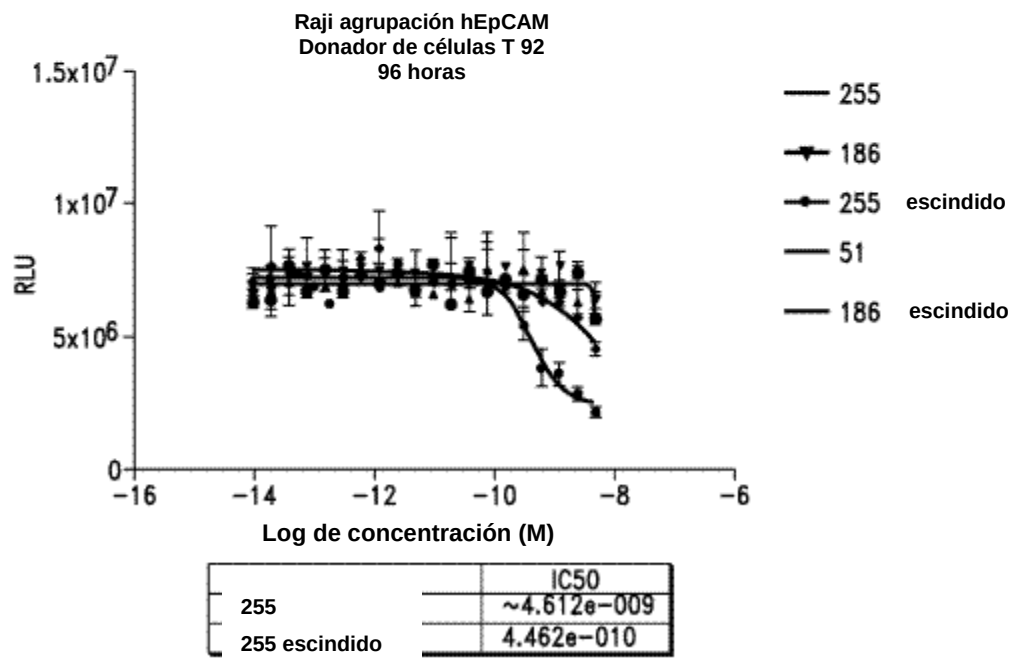


Figura 57B

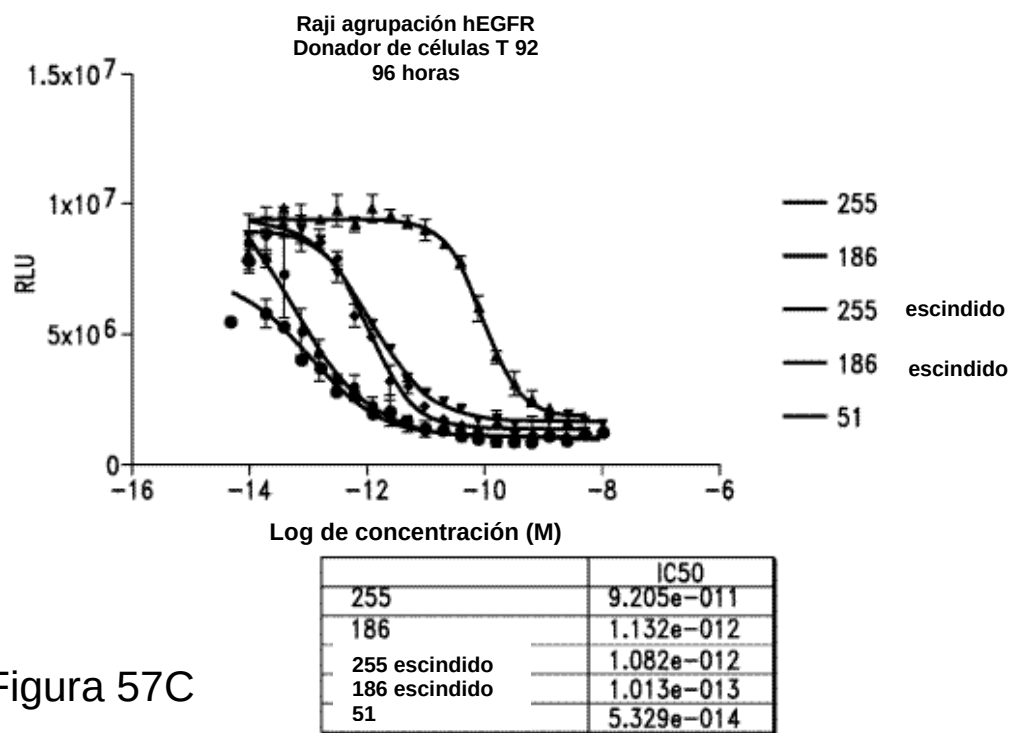


Figura 57C

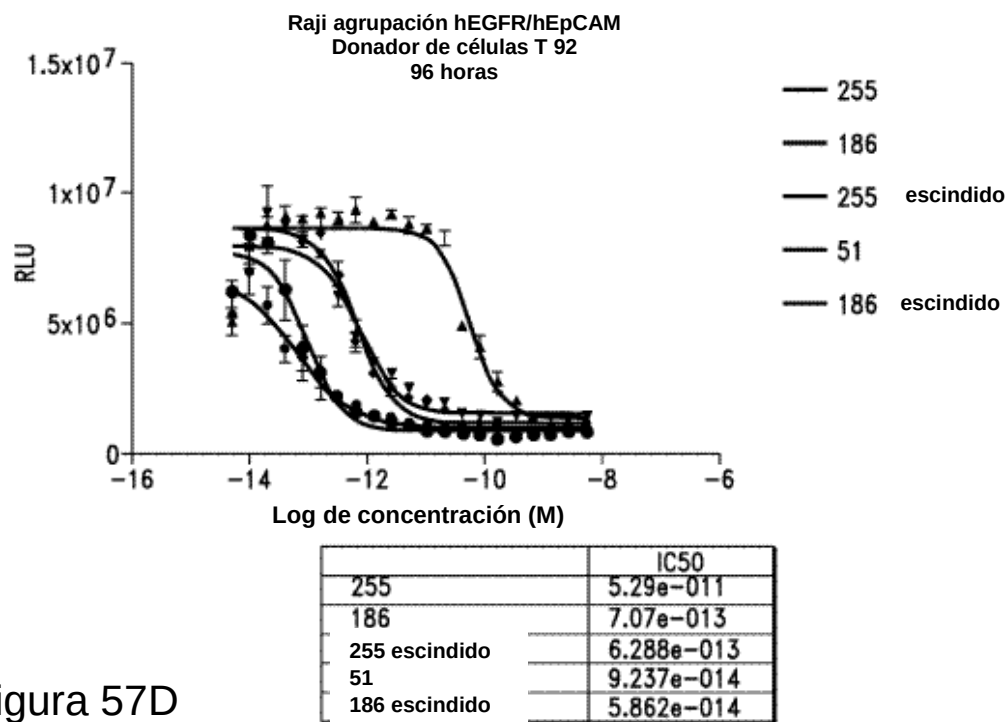
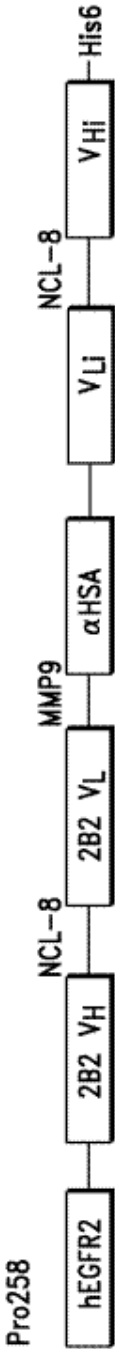


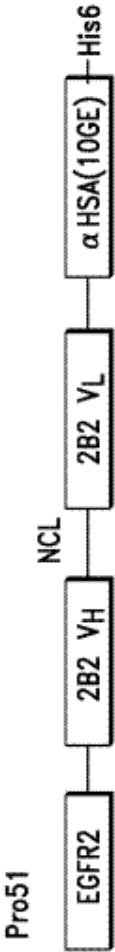
Figura 57D

Figura 58

- COBRA objetivo único



- Control positivo α EGFR



- Dominio activo de Pro186



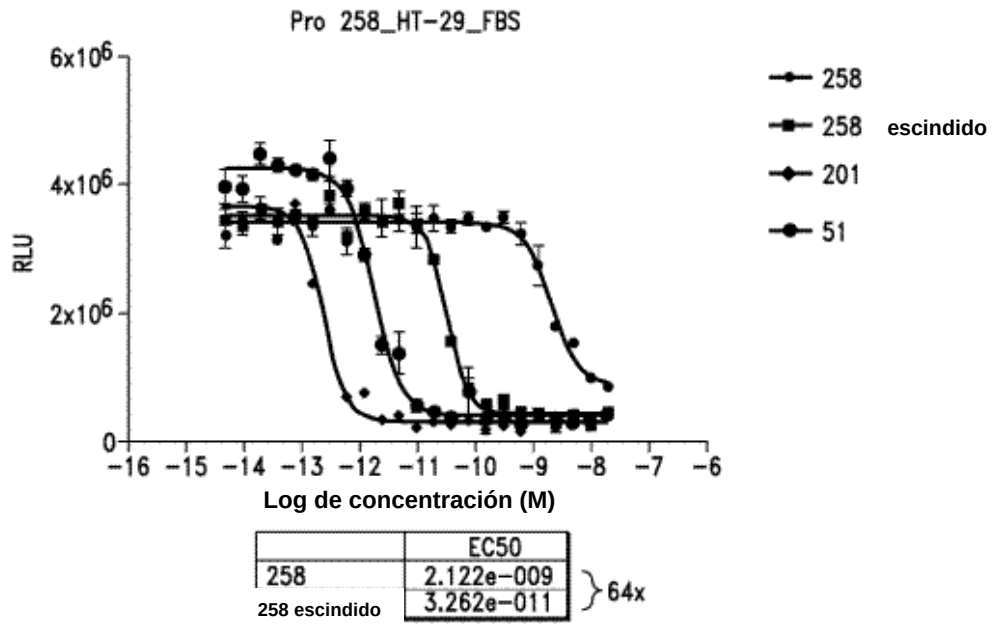


Figura 59A

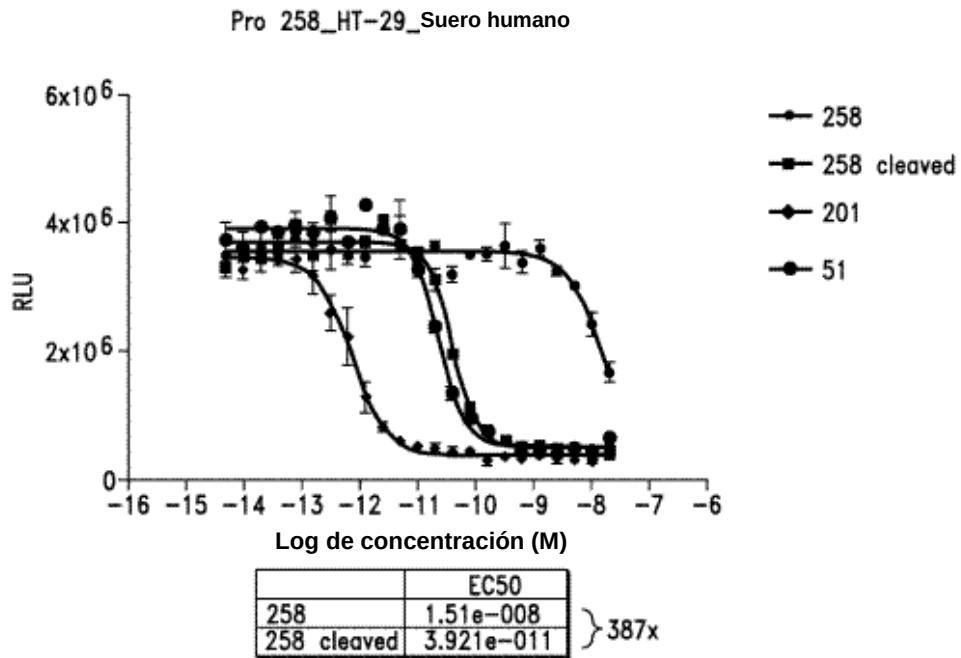


Figura 59B

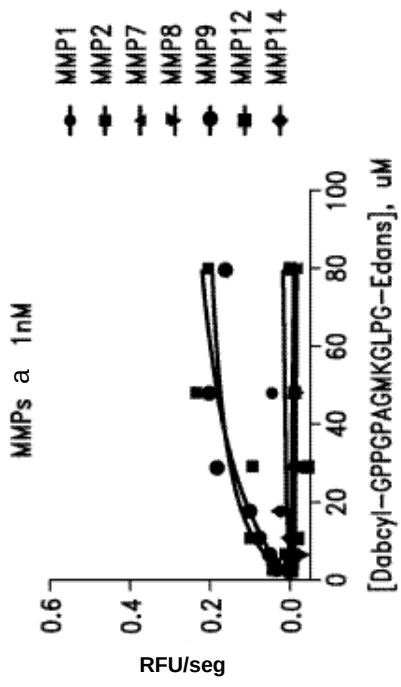


Figura 60B

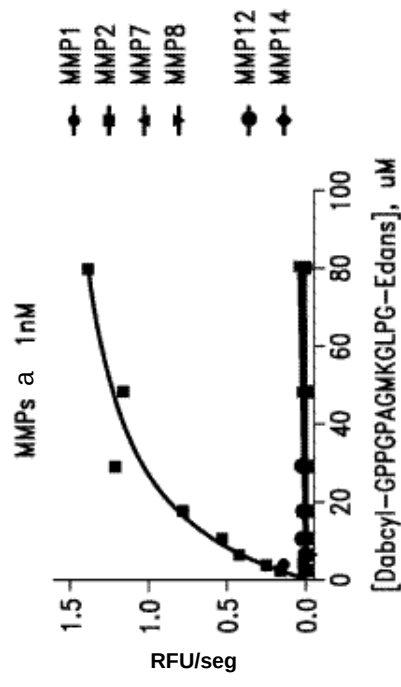


Figura 60C

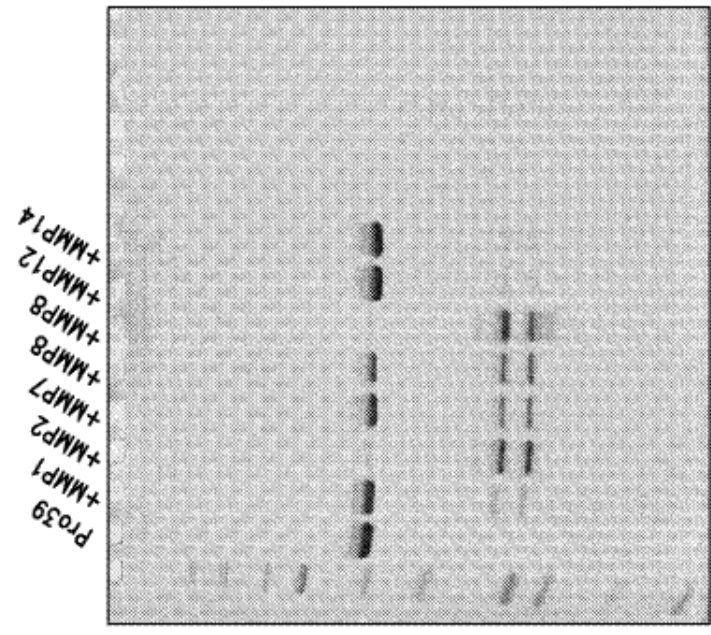


Figura 60A

Figura 61A

Formato 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)

Formato 2 - heterólogo

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)

Hemis de direccionamiento doble (Formato 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)

Figura 61B

Formato 1

Pro140 – EGFR2 MMP9 (aEGFR)

Pro140b – EGFR2 Meprin (aEGFR)

Formato 2 - Variantes del enlazador escindible

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)

Formato 4

Pro258 – hEGFR2 MMP9 (aEGFR)

Pro356 – hEGFR1 MMP9 (aEGFR)

Pro359 – hF7 MMP9 (aB7H3)

Pro388 – h77.2 MMP9 (aFOLR1)

Pro364 – h59.3 MMP9 (aFOLR1)

Figura 62A

Pro140 (Formato 1)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLTVTSS/GPAGMKGL/QTVVTQEPSTVSPGGTVTLTCAASSTGA
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
 YYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGGSVQTGGSLRLTCAASGR
TSRSGMGWFRQAPGKEREFSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV
 TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA
 RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLASASGFTFSKFGMSWVRQAPG
 KGLEWSSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNSLRPEDTAVYYCTIGGSL
VSSQGTLTVTSS (SEQ ID NO:143)

Pro140b Formato 1

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTLTVTSS/KKLADPE/QTVVTQEPSTVSPGGTVTLTCAASSTGAV
TSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGGSVQTGGSLRLTCAASGRT
SRSYGMGWFRQAPGKEREFSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLK
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADPEGGGGS/QTVVT
 QEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPAR
 FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 VTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLASASGFTFSKFGMSWVRQAPGK
 GLEWSSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNSLRPEDTAVYYCTIGGSLSV
SSQGTLTVTSS (SEQ ID NO:144)

Figura 62B

Pro186 Formato 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTVTLTCASSTGA
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
 YYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSVQTGGSLRLTCAASGR
TSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV
 TQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDD
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPG
 KGLEWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSGTTLTVSS (SEQ ID NO:145)

Pro187 Formato 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTVTLTCASSTGA
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
 YYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSVQTGGSLRLTCAASGR
TSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADPEGGGS/QTVV
 TQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDD
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPG
 KGLEWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSGTTLTVSS (SEQ ID NO:146)

Figura 62C

Pro225 (enlazador FL aB7H3 hF7 MMP9) Formato 2

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
 VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
 TLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGA
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT
 FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSL
 AEDTAVYYCAAGGATTQRATEASYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVT
 QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
 VESGGGLVQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTLVTVSS/HHHHHH (SEQ ID NO:147)

Pro226 (enlazador FL aB7H3 hF12 MMP9) Formato 2

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGT
 LVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG
 NYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL
 WYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPRTFSTY
 SMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
 AVYYCAAGGVLAHHNYEYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTV
 SPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
 VQPGGSLKLSAASGFTFNKYAMNWRQAPGKGLEWARIRSKYDYKDDDDKADSVKDR
 FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/**GGG**
GSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWRQAPGKGLEWSSIS
 GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVT
 VSS/HHHHHH (SEQ ID NO:148)

Figura 62D

Pro233 (Pro186 humanizado) Formato 2

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLVESGGGVVRPGGSLTSCAASGRT
SRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNKNSLYLQMNSLR
AEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVT
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
PARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
TVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSS/HHHHHH (SEQ ID NO:149)

Pro311 (enlazador FL aFOLR1 h77.2 MMP9) Formato 2

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGG
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWWARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQK
PQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYCTLWYSNRWWFGG
GTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPG
NEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
WGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGN
YPNWWQQKPGQAPRGLIGDYKDDDDKGT
PARFSGSLLGGKAALTLSGVQPEDEAEYCV
LWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQ
PGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGLEWWSSISGSGRDTLYAESVKGRFTISR
DNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:150)

Figura 62E

Pro312 (enlazador FL aFOLR1 h59.3 MMP9)

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTN
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGLTVTVSS/**GGGS**
GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIRSKY
 NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
 GQGLTVTVSS/**GGSGGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWWQQ
 KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWFF
 GGGTKLTVL/**GGSGGGGS**/QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQA
 PGKQREWWAVTHSDYSTNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCKHYGI
 DYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGTVTLTCGSSTGAVT
 SGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCVLWYSNRWFFGGGTKLTVL/**GGSGGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTF
 NKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNN
 LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGGSGGGGS**/EVQLVESGGGL
 VQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTIS
 RDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID
 NO:151)

Pro313 (enlazador FL aFOLR1 h22.4 MMP9) formato 2

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNY
 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGLTVTVSS/**G**
GGSGGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIR
 SKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW
 AYWGQGLTVTVSS/**GGSGGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNW
 VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
 WFFGGGTKLTVL/**GGSGGGGS**/QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWY
 RQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCNAN
 TATWGRVFWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGTVTLTCG
 SSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
 PEDEAEYYCVLWYSNRWFFGGGTKLTVL/**GGSGGGGS**/EVQLVESGGGLVQPGGSLKLS
 CAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKN
 TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGGSGGGGS**/EV
 QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYA
 ESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH
 (SEQ ID NO:152)

Figura 62F

Pro246 (FL haEGFR1/haEGFR2 heterólogo COBRA con enlazador MMP9)

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAIWSSGSTY
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDWGQ
 GTLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPG
 KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
 NFGNSYISYWAYWGQGTTLTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTG
 AVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE
 YYCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGR
 TRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSL
 RAEDTALYYCAAAGSAWYGTLYEYDWGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVV
 TQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA
 RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKLEWVARIRSKYDYKDDDD
 KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLV
 TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWWRQAPGKG
 LEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTTLTVTVSS/HHHHHH (SEQ ID NO:153)

Pro256 (FL haEpCAM VIB13/haEGFR1 heterólogo COBRA enlazador MMP9)

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
 YADSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGTTLTV
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKLEWV
 ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
 SYWAYWGQGTTLTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNY
 PNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
 SNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGM
 GWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALY
 YCAAAGSAWYGTLYEYDWGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTV
 SPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL
 VQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKLEWVARIRSKYDYKDDDDKADSVKDR
 FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSS/**GGG**
GSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWWRQAPGKLEWSSIS
 GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTV
 SS/HHHHHH (SEQ ID NO:154)

Figura 62G

Pro420 (FL aFOLR1 h77.2/haEGFR1 heterólogo COBRA enlazador MMP9)

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGG
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLTVTVSS/GGGSGGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQQKP
GQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCTLWYSNRWWFGG
GTKLTVL/GGGSGGGGS/QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPG
KREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAGS
AWYGTLYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLT
CGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTL SG
VQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGGS/EVQLVESGGGLVQPGGSLK
LSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDS
KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/
EVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWRQAPGKGLEWSSISGSGRDTL
YAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHH
H (SEQ ID NO:155)

Pro421 (FL haEGFR1/aFOLR1 h77.2 heterólogo COBRA enlazador MMP9)

QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKREFVSGISWRGDST
GYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLTVTVSS/GGGSGGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGA
VTSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/GGGSGGGGS/QVQLVESGGGLVQPGGSLRLSCAASGFT
VSNSVMAWYRQTPGNREFVAIINSIGITNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
AVYVCNRNFDRIYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVT
LTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTL
SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGGS/EVQLVESGGGLVQPGG
SLKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS
/EVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWRQAPGKGLEWSSISGSGRDTL
YAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHH
H (SEQ ID NO:156)

Figura 62H

Pro393 (enlazador Pro186 S9)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFEVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFEVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GARLQSAAPAGLKGAG/QTVVT
 QEPSTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPAR
 FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
 VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTTLTVSS/HHHHHH (SEQ ID NO:157)

Pro394 (enlazador Pro186 ST14(MV))

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFEVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFEVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSFTRQARVVGGGS/QTVVT
 QEPSTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPAR
 FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
 VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTTLTVSS/HHHHHH (SEQ ID NO:158)

Figura 62l

Pro395 (enlizador Pro186 CatS)

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGVSQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSARLQSAAPGGGS**/QTVVT
 QEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
 VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTLTVTVSS/HHHHHH (SEQ ID NO:159)

Pro396 (enlizador Pro186 MMP9v)

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGVSQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GSGGPGPAGMHGLPGGS**/QTVV
 TQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDD
 KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
 TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG
 LEWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTLTVTVSS/HHHHHH (SEQ ID NO:160)

Figura 62J

Pro429 (enlazador Pro186 Meprina/granzimaB)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGGVYADSLEDGGGS**/QTVVTQ
 EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARF
 SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLV
 ESGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKA
 DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGLE
 WSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSSQ
 GTLTVTVSS/HHHHHH (SEQ ID NO:161)

Pro430 (enlazador Pro186 MMP9-2)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGPGPAGLKGAPGS**/QTVVTQ
 PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARF
 GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLV
 SGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKA
 DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGLE
 WSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSSQ
 GTLTVTVSS/HHHHHH (SEQ ID NO:162)

Figura 62K

Pro431 (enlazador Pro186 ST14(MS))

QVKLEESGGGVSQVTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANKNTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
TSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGVSQVTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANKNTVDLQMNSLKP
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSLSGRSDNHGGGS/QTVVT
QEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTTLTVSS/HHHHHH (SEQ ID NO:163)

Pro258 (Pro186 con un dominio aEGFR sencillo y un dominio aHSA central)

QVKLVESGGGVVRPGGSLTSLCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
GYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
TLTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGA
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
YCTLWYSNRWWFGGGTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGNSLRSL
CAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYL
QMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPG
GGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSS/HHHHHH
(SEQ ID NO:164)

Figura 62L

Pro221

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAV
TSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGGQNPYSAGGGGS**/QTVVT
QEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCWLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLTVTVSS/HHHHHH (SEQ ID NO:165)

Pro222

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAV
TSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY
CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGGQNPYSAGGGSGG**/QTVVT
QEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPAR
FSGSLLGGKAALTLSGVQPEDEAEYYCWLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLT
VSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL
EWWSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGTLTVTVSS/HHHHHH (SEQ ID NO:166)

Figura 62M

Pro223

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLGVPQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNTWSAGKGGGS/QTVVT
 QEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPGLSLRLSCAASGFTFSKFGMSWWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNLSRPEDTAVYYCTIGGSLSVSS
 QGTTLTVSS/HHHHHH (SEQ ID NO:167)

Pro224

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV
 TSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLGVPQPEDEAEYY
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS
 RSYGMGWFQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNTWSAGKGGGS/QTVVT
 QEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK
 ADSVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPGLSLRLSCAASGFTFSKFGMSWWRQAPGKGL
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNLSRPEDTAVYYCTIGGSLSVSS
 QGTTLTVSS/HHHHHH (SEQ ID NO:168)

Figura 62N

Pro254

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFQRQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
 TLVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGTTLVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASSTGA
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLRLSCAASGRT
 FSSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRA
 EDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTTLVTVSS/SGGPGPAGMKGLPGS/QTVV
 TQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTGA
 RFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDD
 KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLV
 TVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG
 LEWSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTTLVTVSS/HHHHHH (SEQ ID NO:169)

Pro255

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFQRQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
 TLVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGTTLVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASSTGA
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLTLSCAASGTG
 SIFSINLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRFTISRDNKNTLYLQMNSLRP
 EDTAVYYCNLLLRSSPGATTPYWGQGTTLVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPST
 TVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTGA
 RFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGG
 GLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/G
GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWS
 SISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLV
 TVSS/HHHHHH (SEQ ID NO:170)

Figura 62O

Pro262

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST
 GYADSVKGRFTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGT
 QVTVSS/**GGGS**GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF
 GNSYISYWAYWGQGLTVTVSS/**GGGS**GGGS**GGGS**GGGS/QTVVTQEPSLTVSPGGTVTLT
 CASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQ
 PEDEAEYYCTLWYSNRWWFGGGTKLTVL/**GGGS**GGGS/QVKLEESGGGSVQTGGSLRLT
 CAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNKNTVD
 LQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGPGPAGMKGLPG**
S/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDD
 KGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGS**GG
GS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYD
 YKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW
 GQGLTVTVSS/**GGGS**GGGS/EVQLVESGGGLVQPGNSLRLS AASGFTFSKFGMSWVR
 QAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIG
 GSLSVSSQGLTVTVSS/HHHHH (SEQ ID NO:171)

Pro356

EVQLVESGGGLVQPGGSLRLS AASGRTFSSYAMGWFRQAPGKEREFSVAINWSSGSTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYDYWGQ
 GTLTVTVSS/**GGGS**GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPG
 KGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA
 NFGNSYISYWAYWGQGLTVTVSS/**GGGS**GGGS/QTVVTQEPSLTVSPGGTVTLTCASSTG
 AVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAE
 YYCTLWYSNRWWFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRL
 SCAASGFTFSKFGMSWVRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNKNTLY
 LQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/**GGGS**GGGS/QTVVTQEPSLTVSPG
 GTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
 ALTL SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGS**GGGS/EVQLVESGGGLVQPG
 GSKL SCAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
 RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/HHHHH
 (SEQ ID NO:172)

Figura 62P

Pro359

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
 VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
 TLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGT LTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGA
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWWFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRSL
 CAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYL
 QMNSLRPEDTAVYYCTIGGSLSVSSQGT LTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPG
 GTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKA
 ALTLSGVQPEDEAEYCYLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPG
 GSKLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS
 RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSS/HHHHHH
 (SEQ ID NO:173)

Pro364

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTN
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGT LTVTVSS/**GGGS**
GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIRSKY
 NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW
 GGGLTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWWQK
 KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCYLWYSNRWWF
 GGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRSLSCAASGFTFSKFGM
 SWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGT LTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCGSSTGAV
 TSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAE
 YCYLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGF
 TFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQM
 NNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LTVTVSS/HHHHHH (SEQ ID NO:174)

Figura 62Q

Pro388

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGG
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ
GTLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQKP
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCTLWYSNRWWFGG
GTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW
VRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCT
IGGSLSVSSQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG
NYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTL SGVQPEDEAEYYC
VLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK
YAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
TEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/HHHHHH (SEQ ID NO:175)

Figura 62R

Pro432

QVQLVESGGGLVQPGGSLTSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
 YADSVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCNLLRSPGATTPYWGQGLTVTV
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWW
 ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI
 SYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY
 PNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY
 SNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAM
 GWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVY
 YCAAGYQINSGNYNFKDYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSL
 TVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSL
 LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG
 GLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**G**
GGGSGGGS/EVQLVESGGGLVQPNSLRRLSCAASGFTFSKFGMSWWRQAPGKGLEWWS
 SISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTV
 TVSS/HHHHHH (SEQ ID NO:176)

Pro448

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
 SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/**GGGSGG**
GS/QVQLVESGGGVWRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
 DSTGYADSVKGRFTISRDNKNTLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYW
 GQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQ
 APGKGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV
 RHANFGNSYISYWAYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
 VTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAAL
 TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP
 GNSLRRLSCAASGFTFSKFGMSWWRQAPGKGLEWWSISGSGRDTLYAESVKGRFTISRDN
 AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:177)

Figura 62S

Pro449

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
 TLTVTVSS/**GGGGS**GGGS/QVQLVESGGGLVQPGGSLRSLCAASGFTVSNSVMAWYRQTP
 GNREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
 WGQGTTLTVTVSS/**GGGGS**GGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWR
 QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
 VRHANFGNSYISYWAYWGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPG
 GTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKA
 ALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGGS**GGGS/EVQLVESGGGLV
 QPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISR
 DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVTVSS/HHHHHH (SEQ ID
 NO:178)

Pro450

QVQLVESGGGLVQPGGSLRSLCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD
 SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTTLTVTVSS/**GGGGS**
GGG/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG
 DSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYW
 GGQGTTLTVTVSS/**GGGGS**GGGS/QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQ
 QKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWW
 FGGGTCLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYA
 MNWWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
 DTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSS/**GGGGS**GGGS/EVQLVESGGGLVQP
 GNSLRSLCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN
 AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVTVSS/HHHHHH (SEQ ID NO:179)

Figura 62T

Pro451

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFEVSGISWRGDST
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG
 TLVTVSS/**GGGSGGGG**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNVMAWYRQTP
 GNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
 WGQGTTLVTVSS/**GGGSGGGG**/QTVVTQEPSTLVSPGGTVTLTCASSTGAVTSGNYPNW
 VQKPGQAPRGLIGGKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR
 WFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK
 YAMNWRQAPGKGLEWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGG**/EVQLVESGGGLV
 QPGLNSRLSCAASGFTFSKFGMSWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISR
 DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLVTVSS/HHHHHH (SEQ ID
 NO:180)

Pro479

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFEVAVINWSGGST
 VYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG
 TLVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQAPGK
 GLEWARIRSKYNNTAYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGTTLVTVSS/**GGGSGGGG**/QTVVTQEPSTLVSPGGTVTLTCASSTGA
 VTSNYPNWWQKPGQAPRGLIGGKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWFGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLSCEASPRT
 FSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNKNTLYLQMNSLRA
 EDTAVYYCAAGGVLAHHNYEYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEP
 SLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTARFSG
 SLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWFGGGTKLTVL/**GGGSGGGG**/EVQLVES
 GGGLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWARIRSKYDYKDDDDKAD
 SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLVTS
 S/**GGGSGGGG**/EVQLVESGGGLVQPGLNSRLSCAASGFTFSKFGMSWRQAPGKGLEW
 VSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
 LVTVSS/HHHHHH (SEQ ID NO:181)

Figura 62U

Pro480

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVT
 VSS/**GGGS**GGGS/ EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEW
 VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS
 YISYWAYWGQGLTVTVSS/**GGGS**GGGS/ QTVVTQEPLTVSPGGTVTLTCASSTGAVTSG
 NYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL
 WYSNRWWFGGGTKLTVL/**GGGS**GGGS/ QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTY
 HMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
 AVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/ QTVVTQEPL
 LTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGS
 LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGS**GGGS/ EVQLVESG
 GGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSV
 KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/
GGGSGGGS/ EVQLVESGGGLVQPGNSLRLS AASGFTFSKFGMSWWRQAPGKGLEWW
 SSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGL
 VTVSS/HHHHHH (SEQ ID NO:182)

Pro495

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST
 VYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQ
 GLTVTVSS/**GGGS**GGGS/ EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN
 FGNSYISYWAYWGQGLTVTVSS/**GGGS**GGGS/ QTVVTQEPLTVSPGGTVTLTCASSTGA
 VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCTLWYSNRWWFGGGTKLTVL/**GGGS**GGGS/ QVQLQESGGGLVQPGGSLRLSCAPSRR
 FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLR
 AEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/ QTVVT
 QEPLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGGTKDDAPGTPARF
 SGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGS**GGGS/ EVQLV
 ESGGGLVQPGGSLKLSAASGFTFNKHAMNWWWRQAPGKGLEWWARIRSKYNNYATAYAD
 SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVS
 S/**GGGS**GGGS/ EVQLVESGGGLVQPGNSLRLS AASGFTFSKFGMSWWRQAPGKGLEW
 VSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT
 LTVTVSS/HHHHHH (SEQ ID NO:183)