

Figura 1

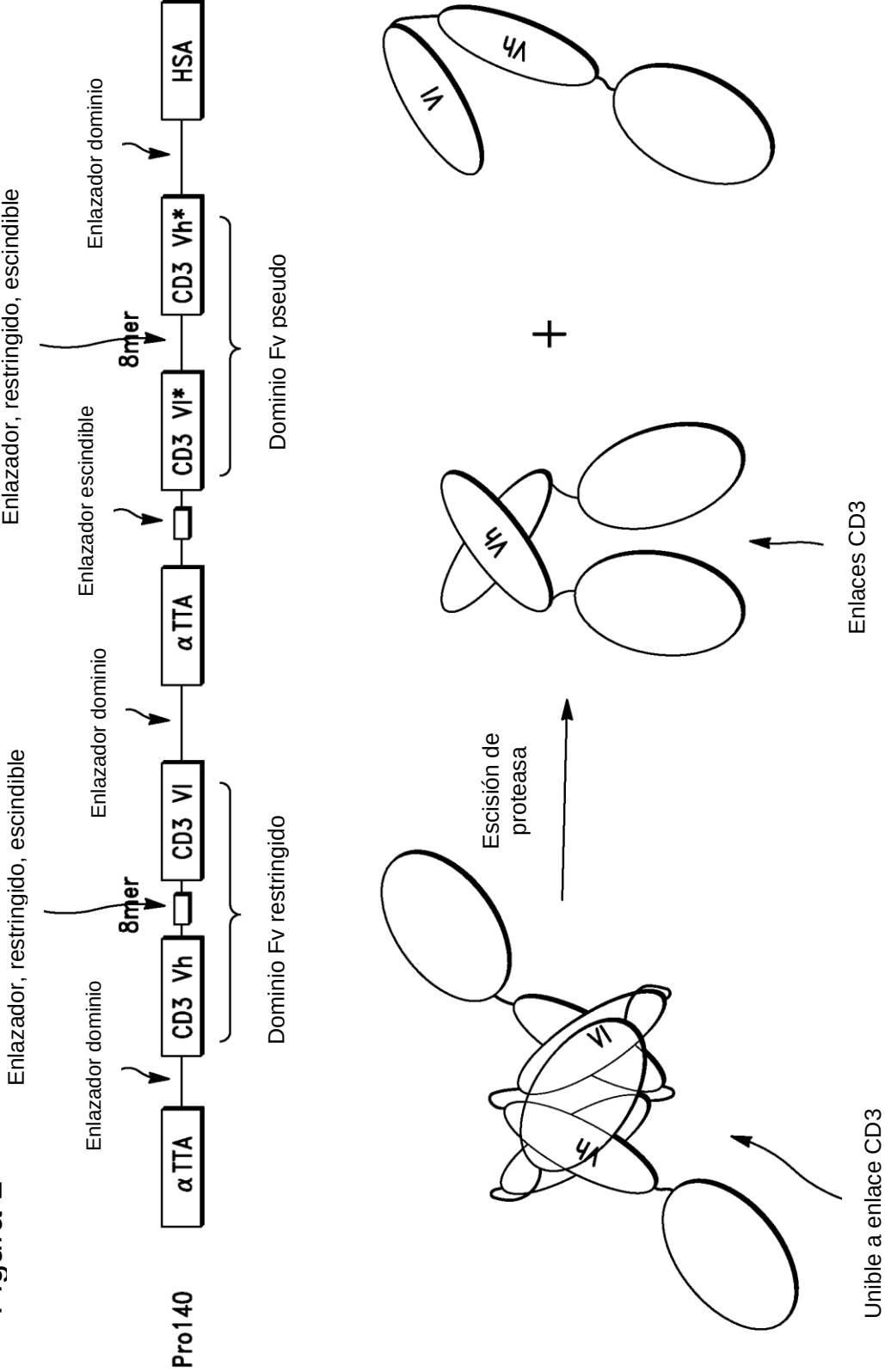




Figura 3A

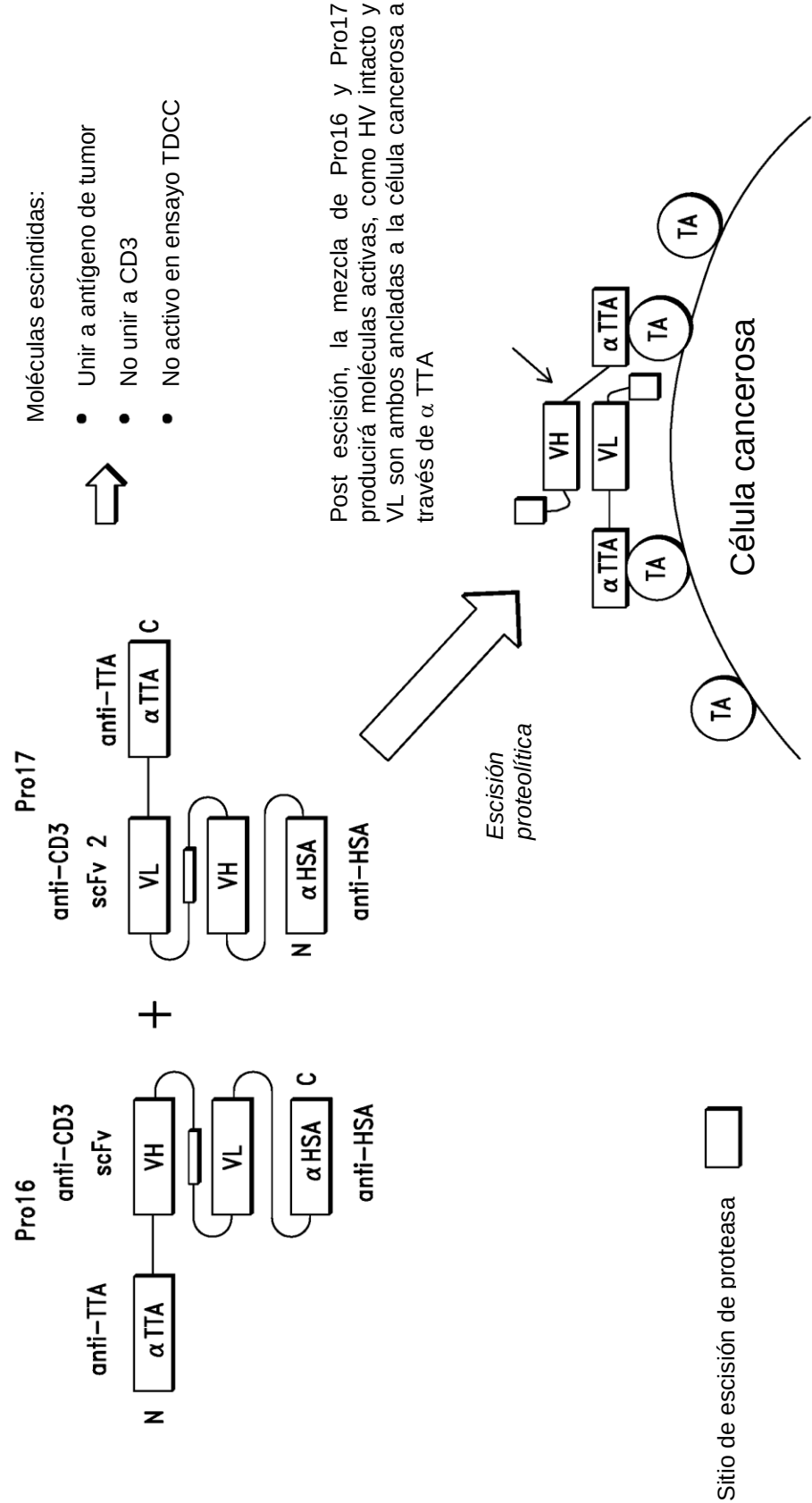


Figura 3B

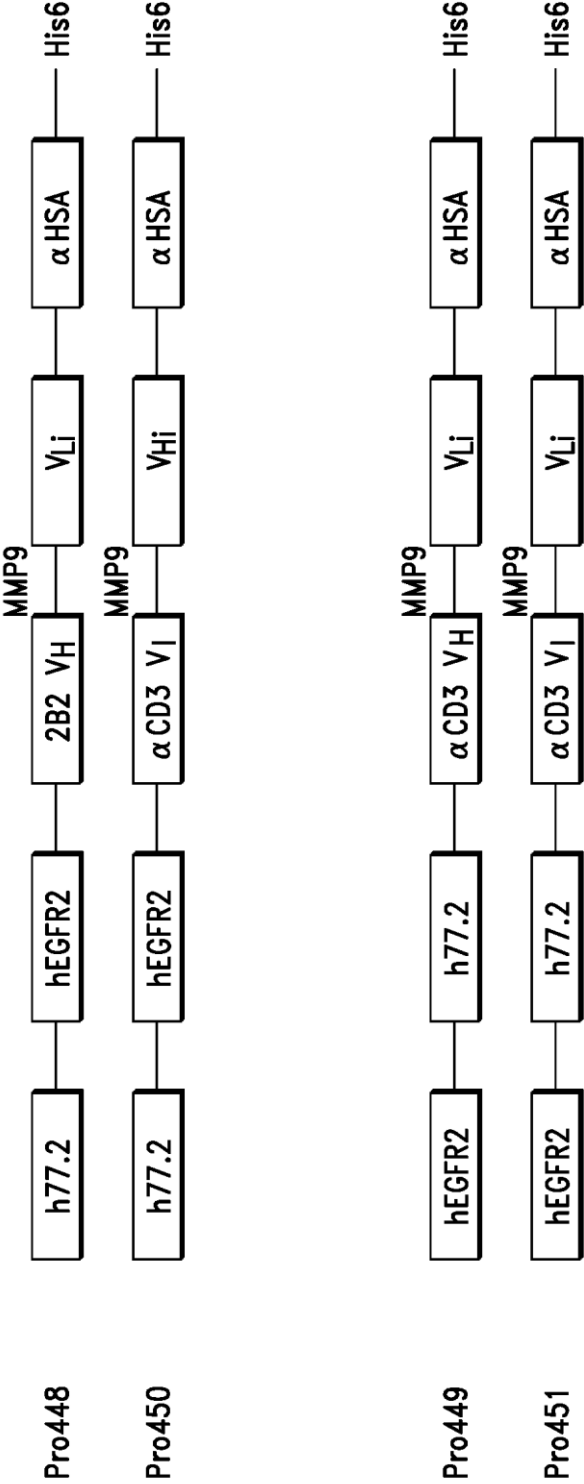
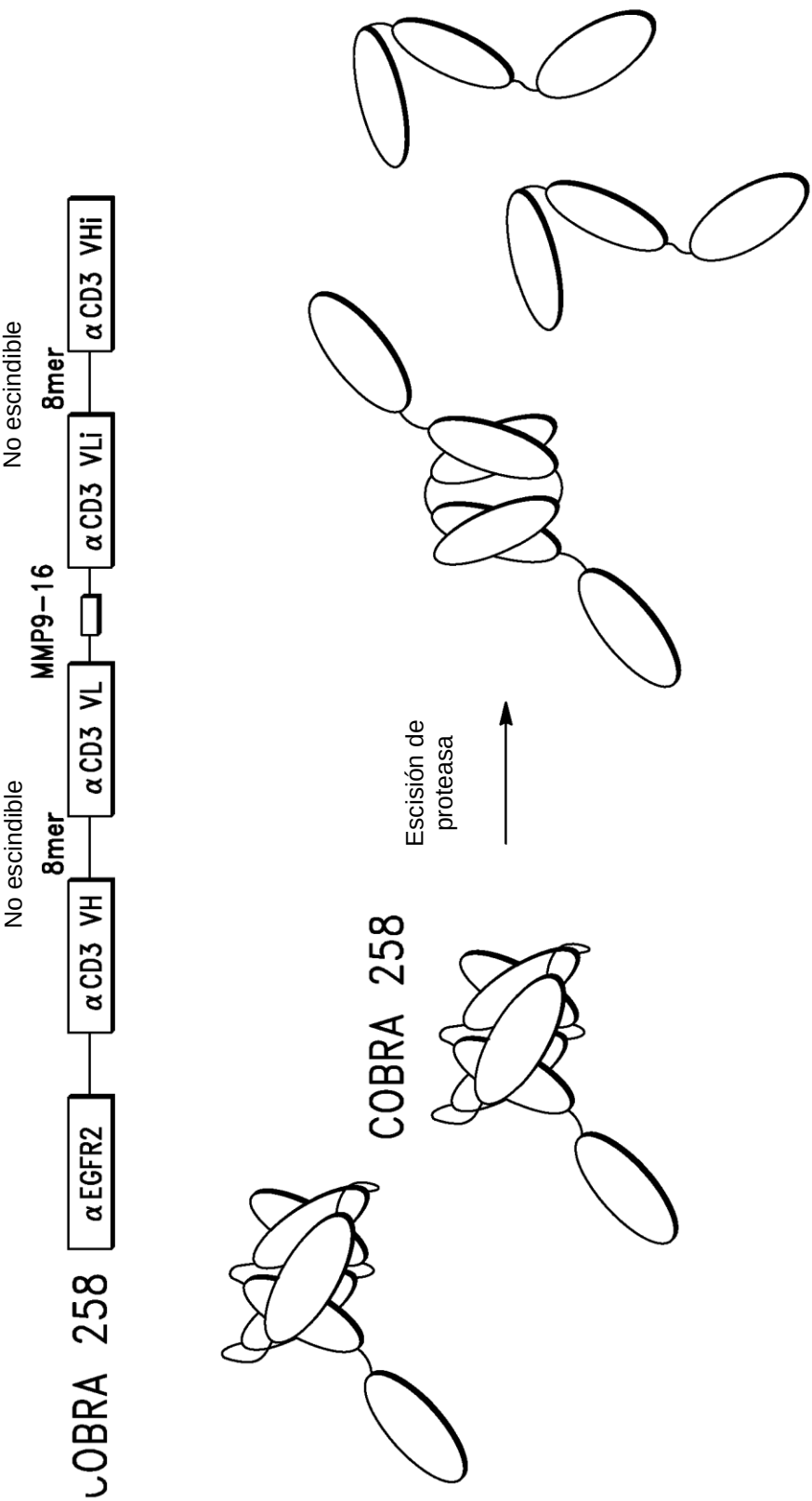


Figura 4



## Figura 5A

**sdAbs direccinada** **$\alpha$ EGFR1**

EVQLVESGGGLVQAGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTYYADS**  
**VKG**RFTISRDNKNTMYLQMNSLKPEDTAVYYCAA**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)

 **$\alpha$ EGFR2**

QVKLEESGGGSVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFVS**GISWRGDSTGYAD**  
**SVKG**RFTISRDNKNTVDLQMNSLKPEDTAIYYCAA**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**  
**VKG**RFTISRDNKNTLYLQMNSLRAEDTAVYYCAA**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**  
**SVKG**RFTISRDNKNSLYLQMNSLRAEDTALYYCAA**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 $\alpha$ FOLR1 h77-2

QVQLVESGGGLVQPGGSLRLSCAAS**GFTVSNSVMA**WYRQTPGNEREFVA**IINSIGITNYADSVK**  
**GRFTISRDNSKNTLYLQMNSLRAEDTAVYVCNRRNFDRIY**WGQGTLVTVSS (SEQ ID NO:17)

sdCDR1 **GFTVSNSVMA** (SEQ ID NO:18)

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

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

 $\alpha$ FOLR1 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)

 $\alpha$ FOLR1 h22-4

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

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

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

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

 $\alpha$ B7H3 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 direccinada - Continuación $\alpha$ 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)

 $\alpha$ 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)

 $\alpha$ 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)

 $\alpha$ 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  $\alpha$ CD3 scFv $\alpha$ CD3 V<sub>L</sub>

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)

 $\alpha$ CD3 V<sub>L1</sub>

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)

 $\alpha$ CD3 V<sub>L2</sub>

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)

 $\alpha$ CD3 V<sub>H</sub>

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**RIRSKYNNYATYYA**  
**DQVKDR**FTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**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  $\alpha$ CD3 scFv - Continuación** **$\alpha$ CD3 V<sub>Hi</sub>**

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

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

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

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

 **$\alpha$ CD3 V<sub>Hi2</sub>**

EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKHAMN**WVRQAPGKGLEWVA**RIRSKYNNYATAY**  
**ADSVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**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  $\alpha$ 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/QARVVGGS** (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)

**KLK7-6**SGGGQNPY/**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) <sub>8</sub> RPLALWRS(DR) <sub>8</sub> | 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 $\beta$ | GWEHDG                           | 134        |
| Enteroquinasa                               | EDDDDKA                          | 135        |
| Fap                                         | KQEQNPGST                        | 136        |
| Kalikeina 2                                 | GKAFRR                           | 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

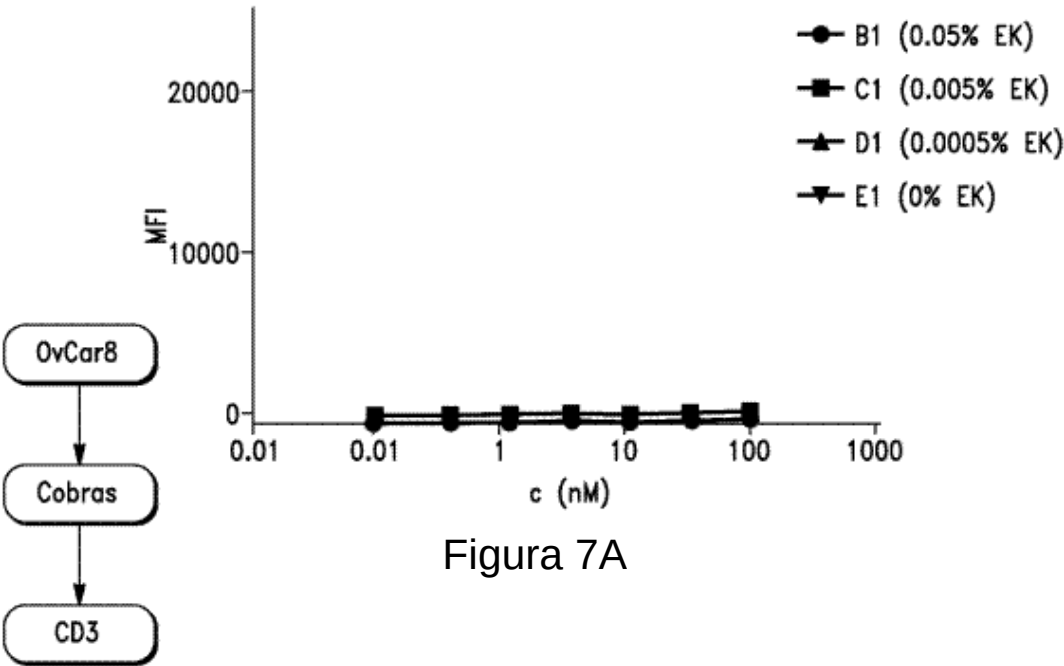


Figura 7A

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

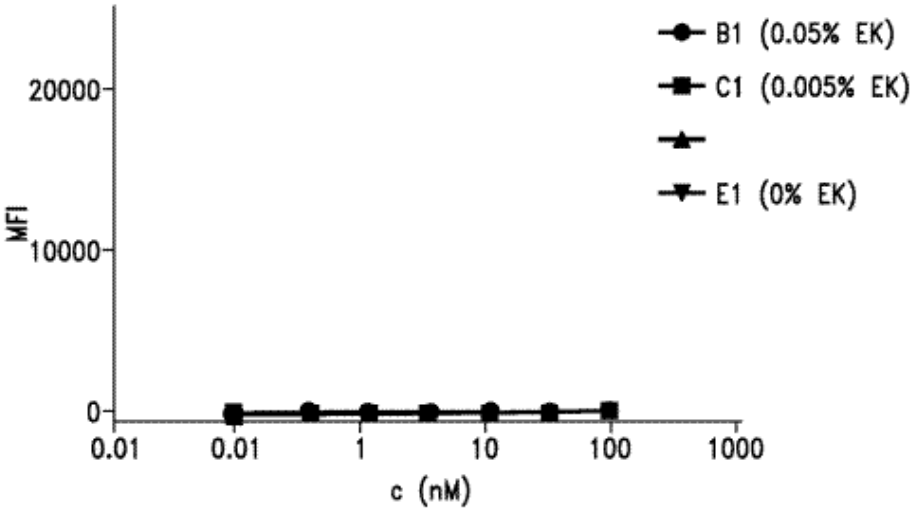


Figura 7B

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

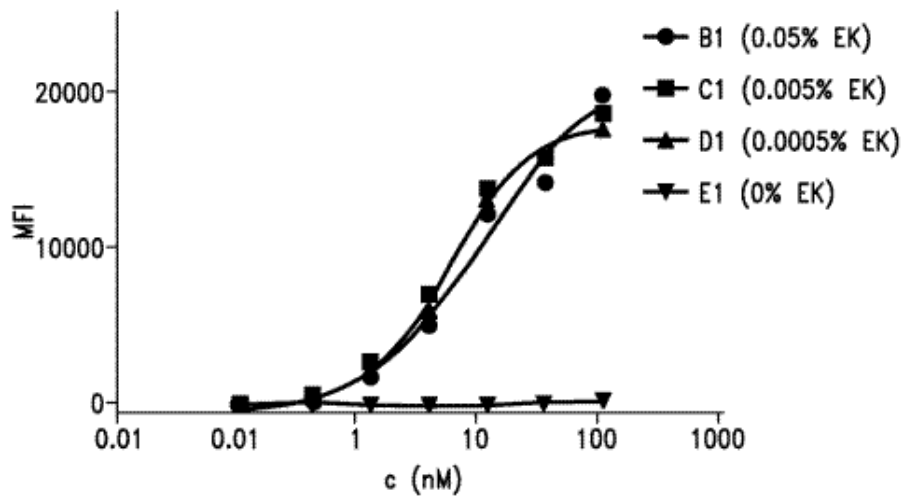


Figura 7C

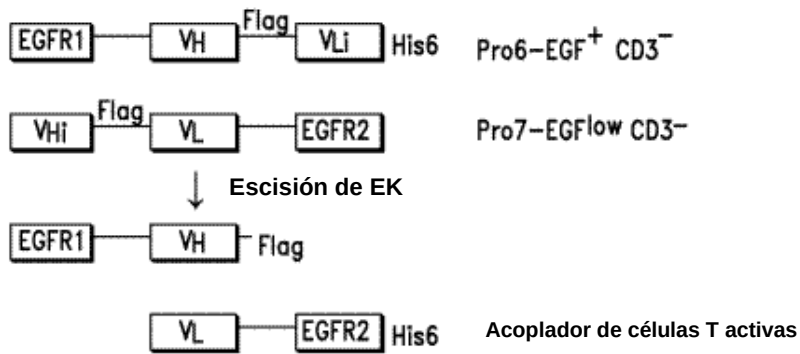


Figura 7D

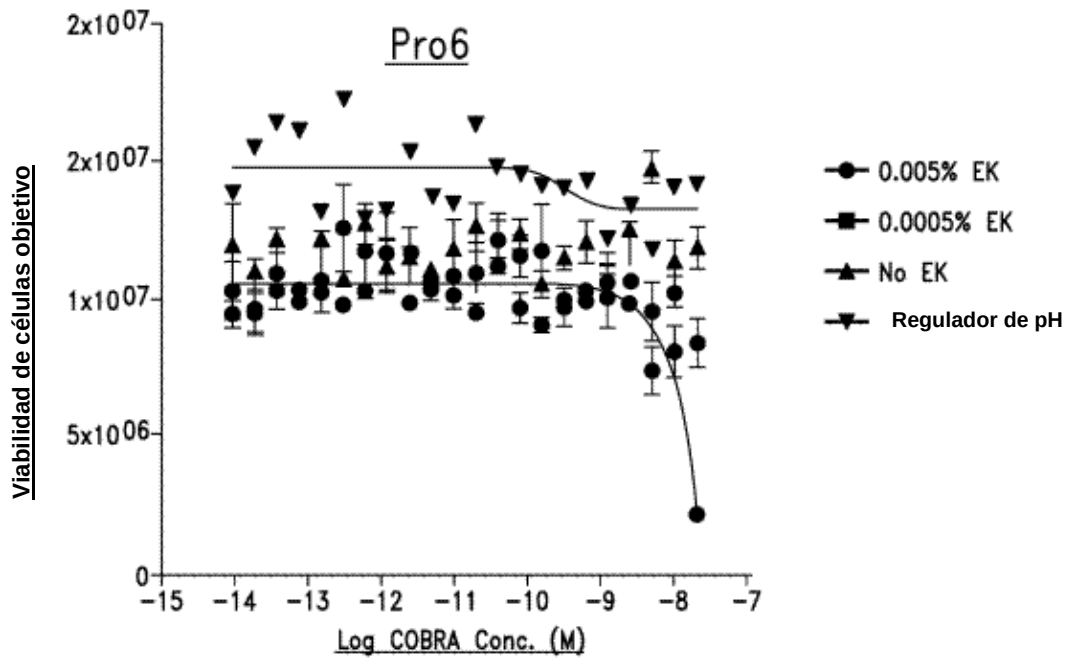


Figura 8A

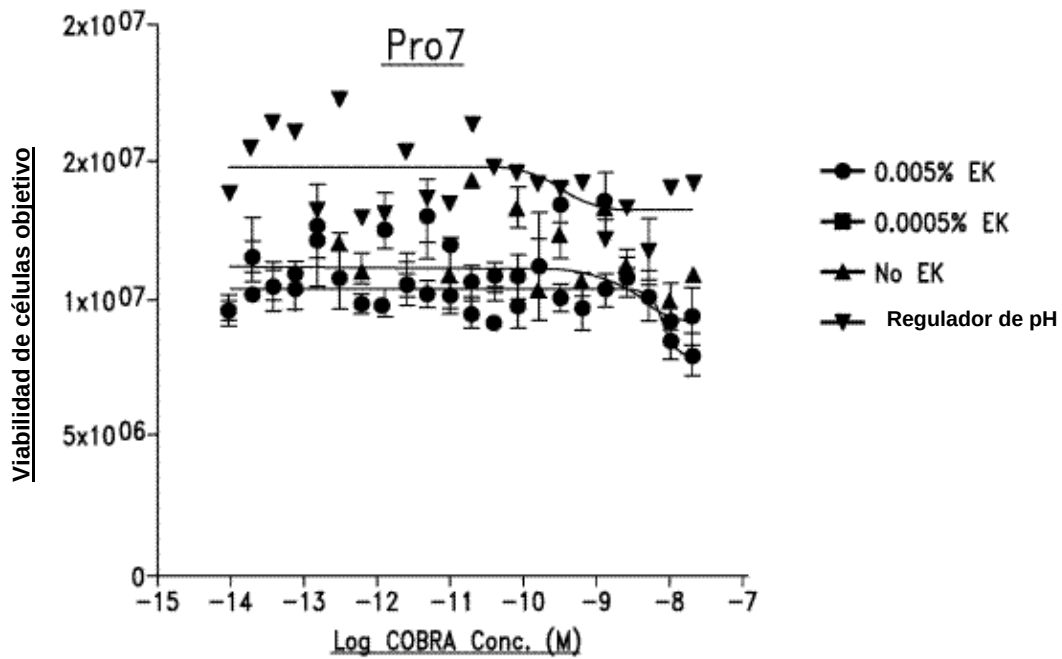


Figura 8B

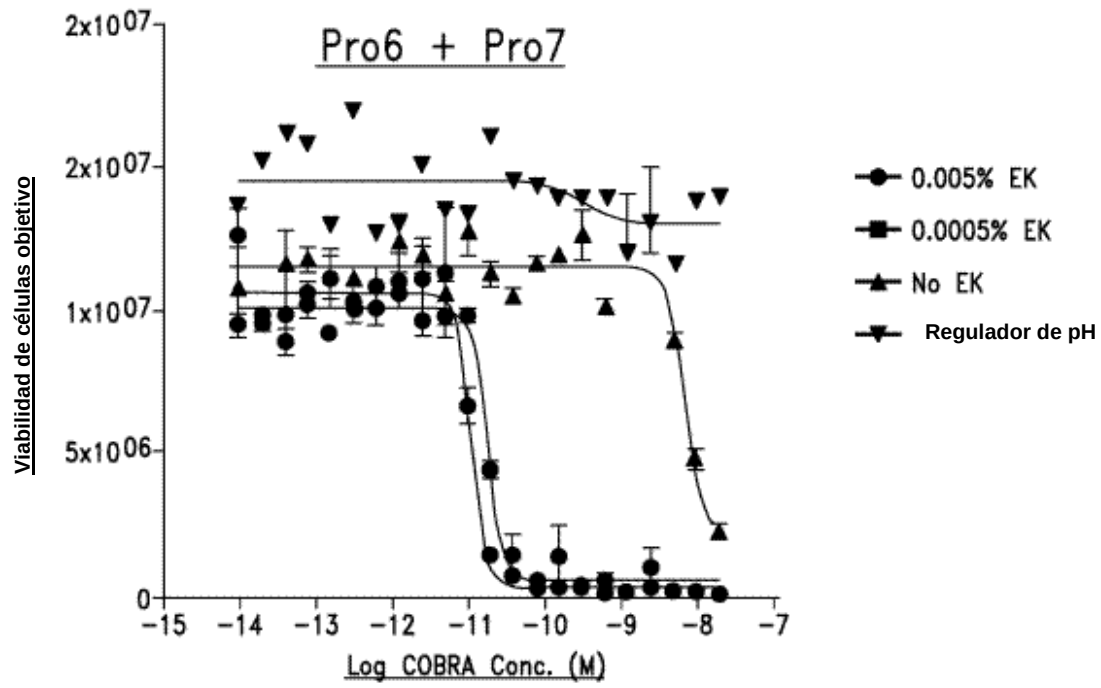


Figura 8C

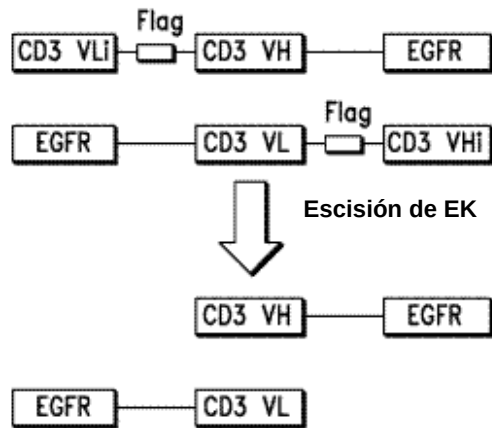
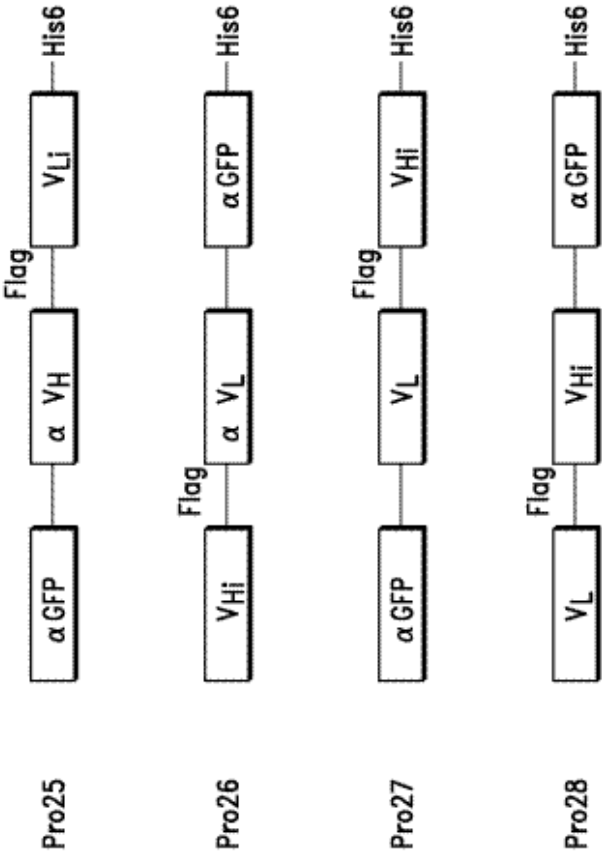


Figura 8D

Figura 9



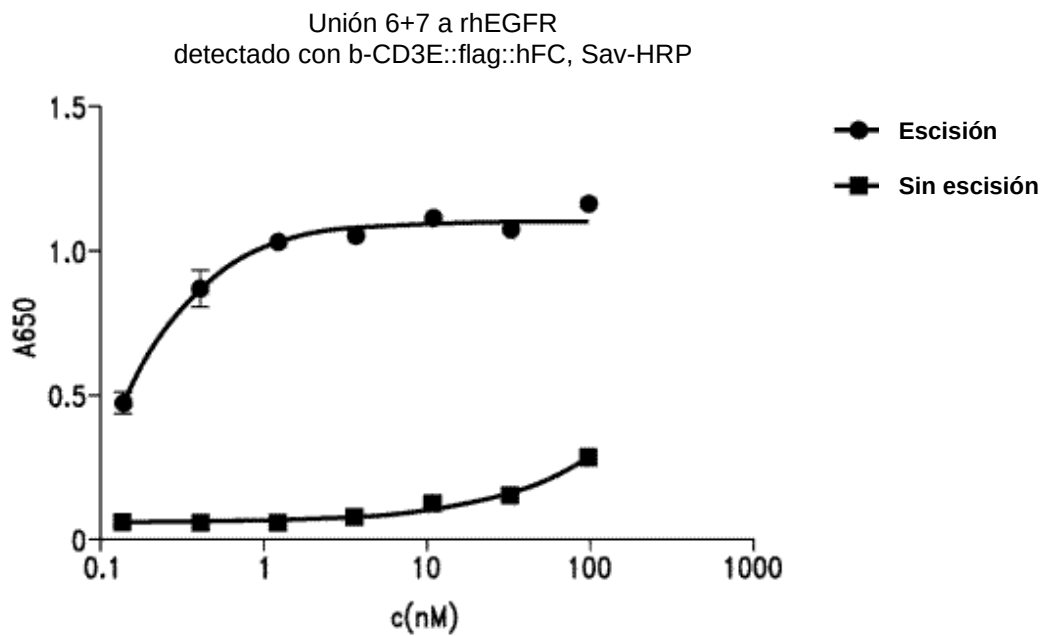


Figura 10A

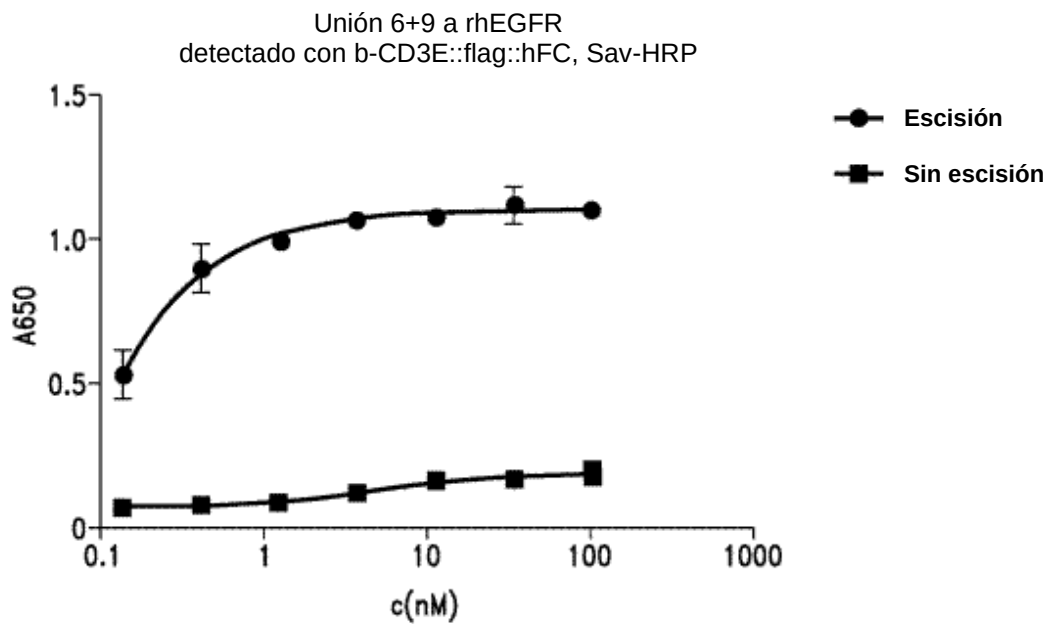


Figura 10B

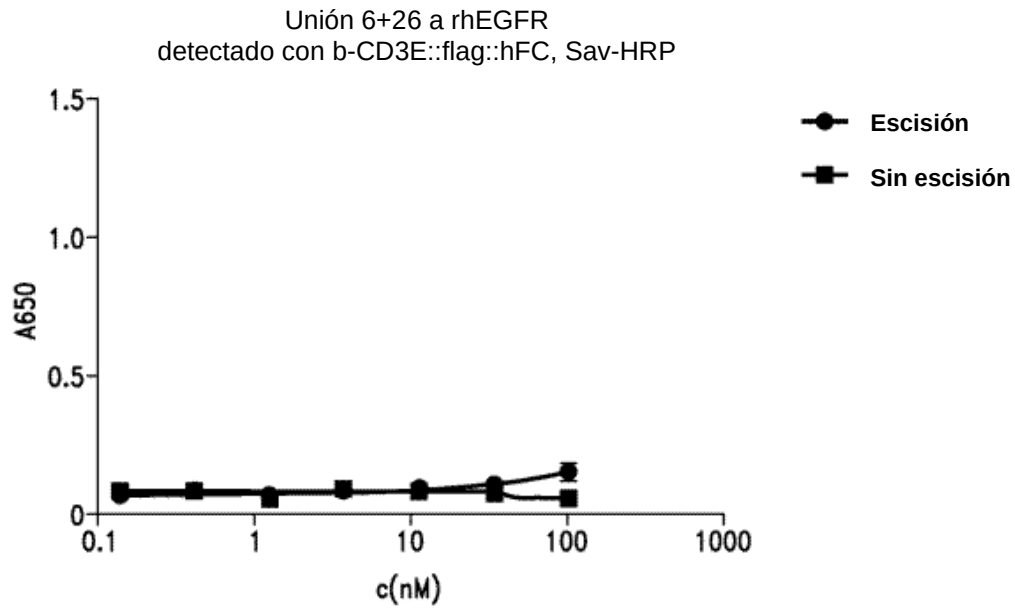


Figura 10C

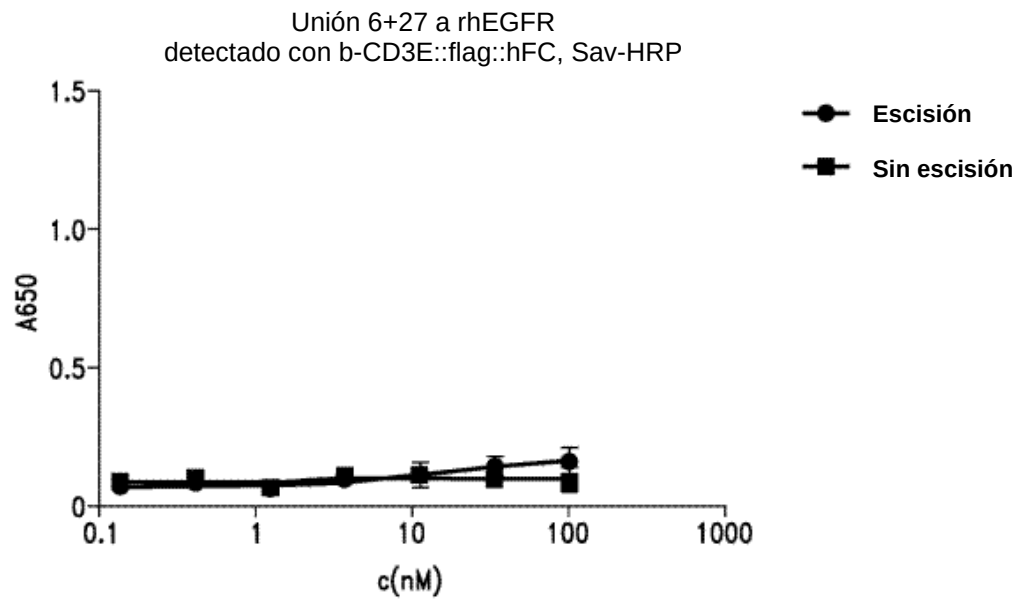


Figura 10D

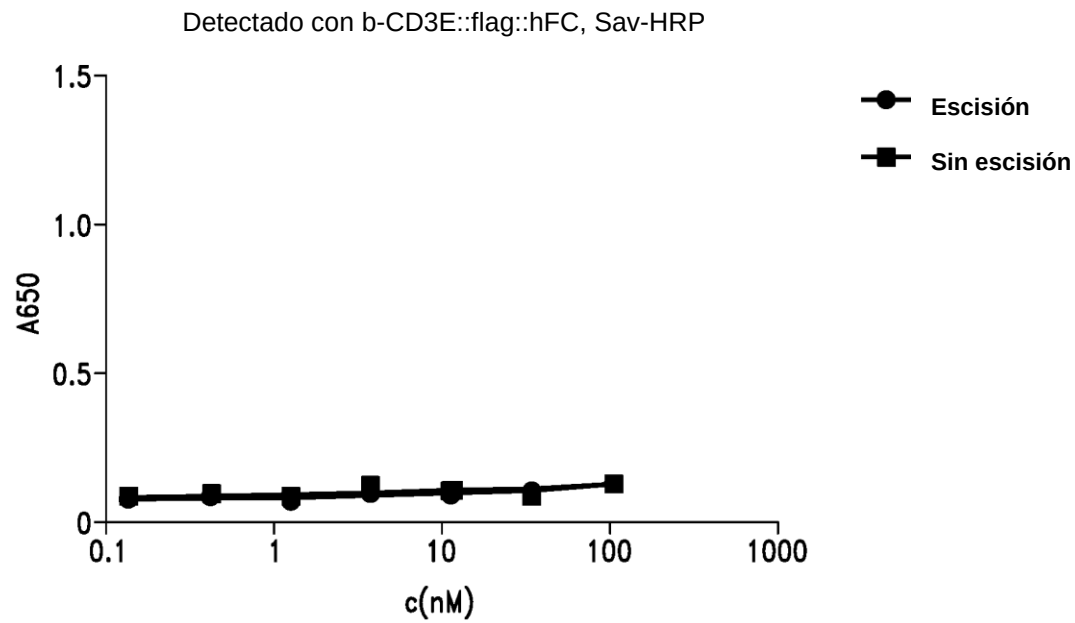


Figura 10E

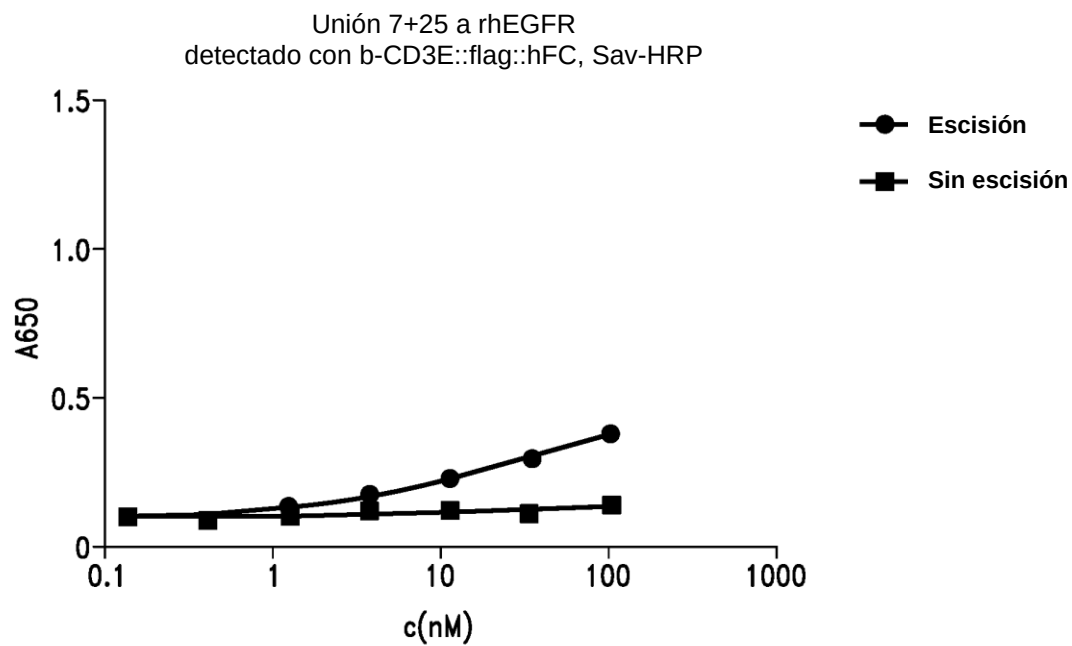
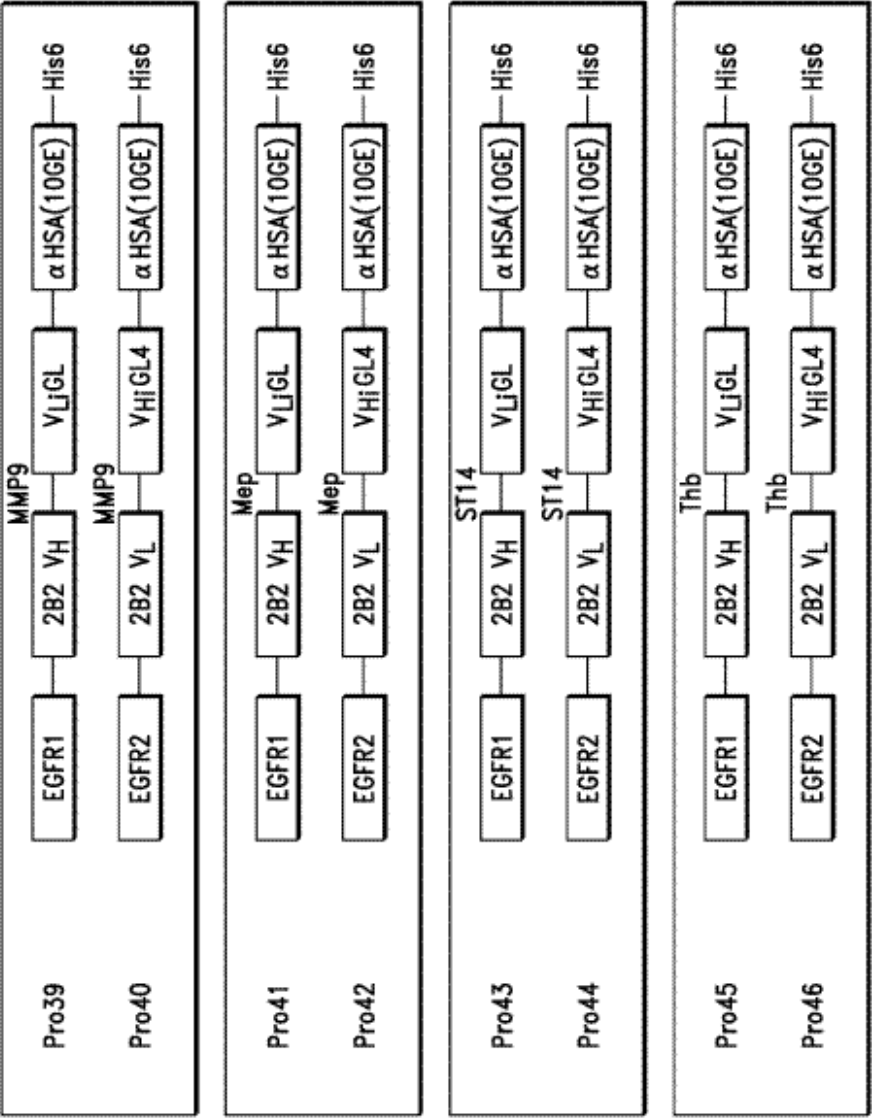


Figura 10F

Figura 11



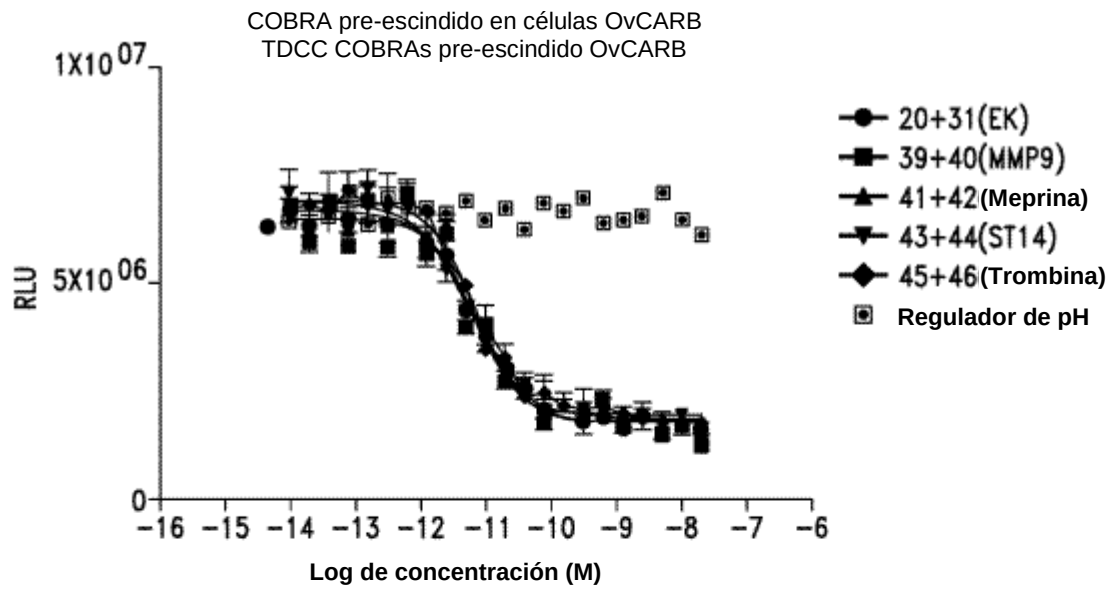


Figura 12A

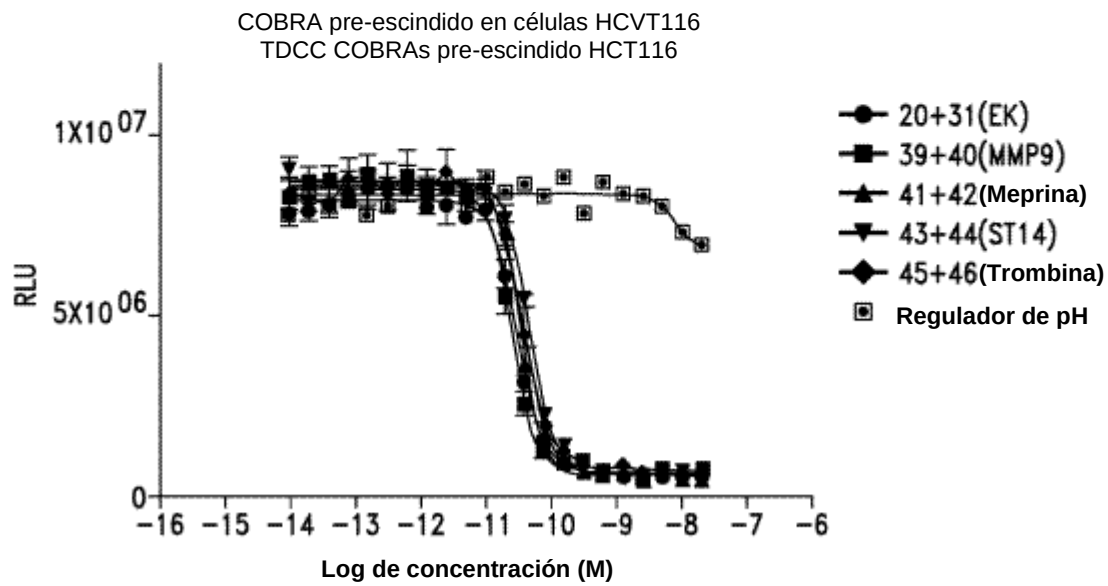


Figura 12B

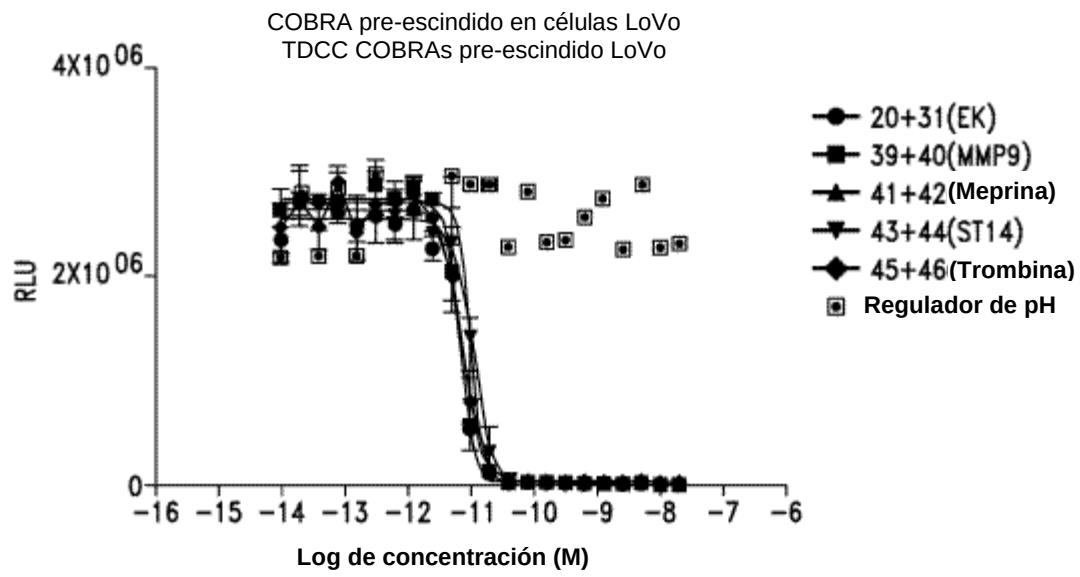


Figura 12C

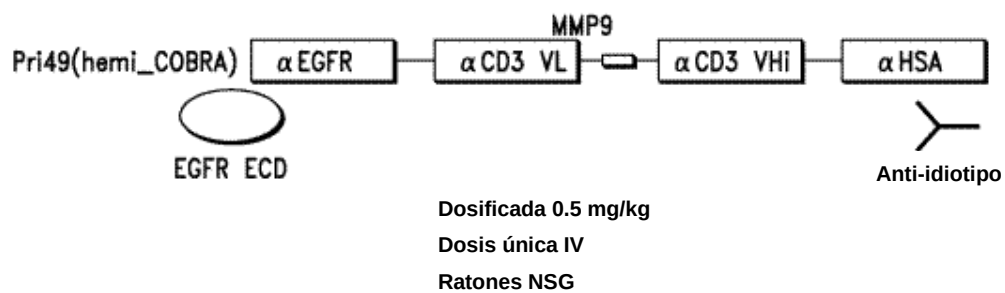


Figura 13A

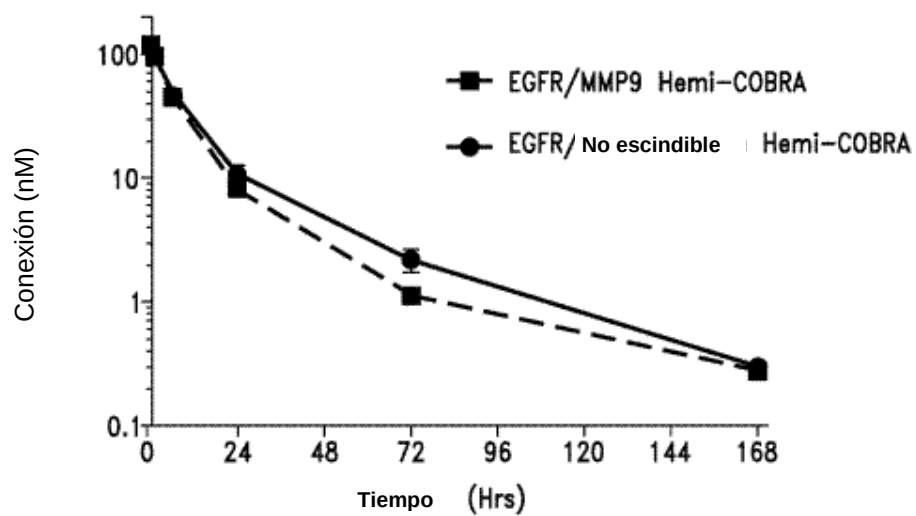
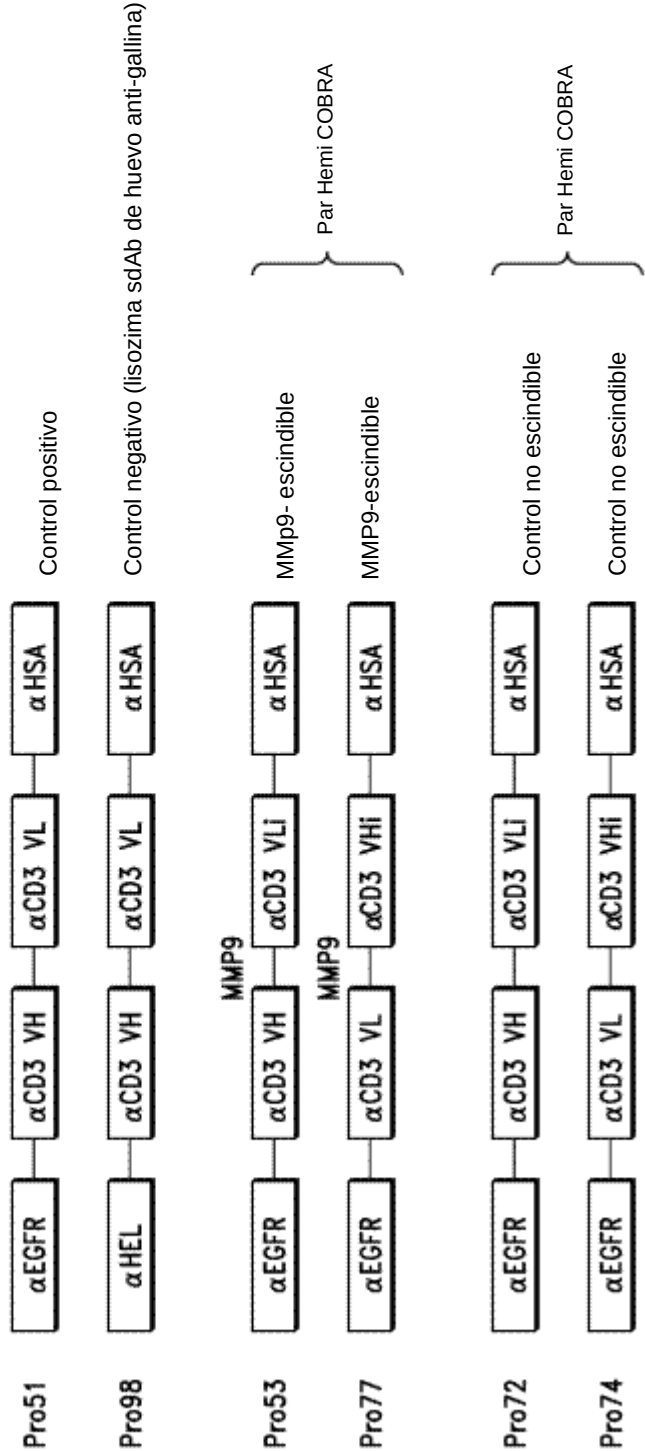


Figura 13B

Figura 14



## Figura 15

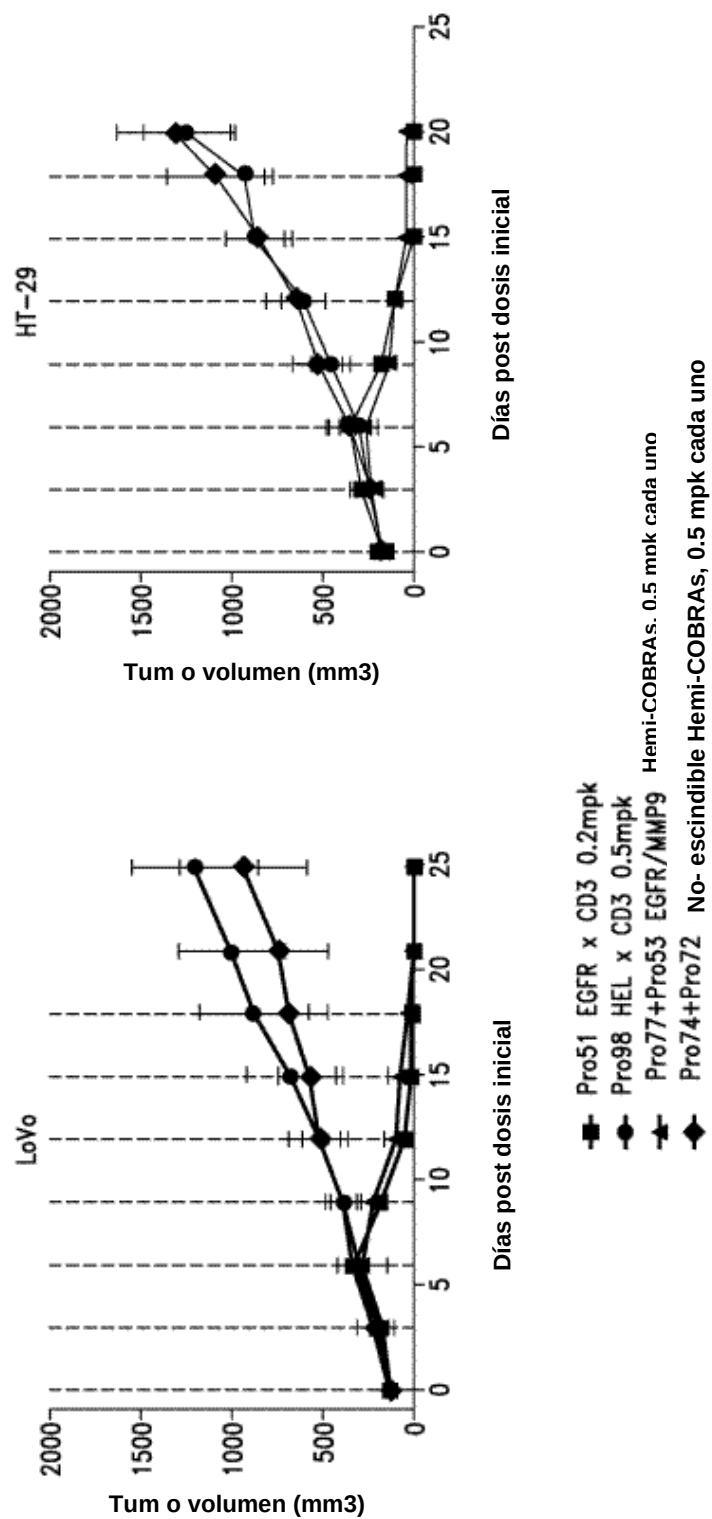


Figura 16

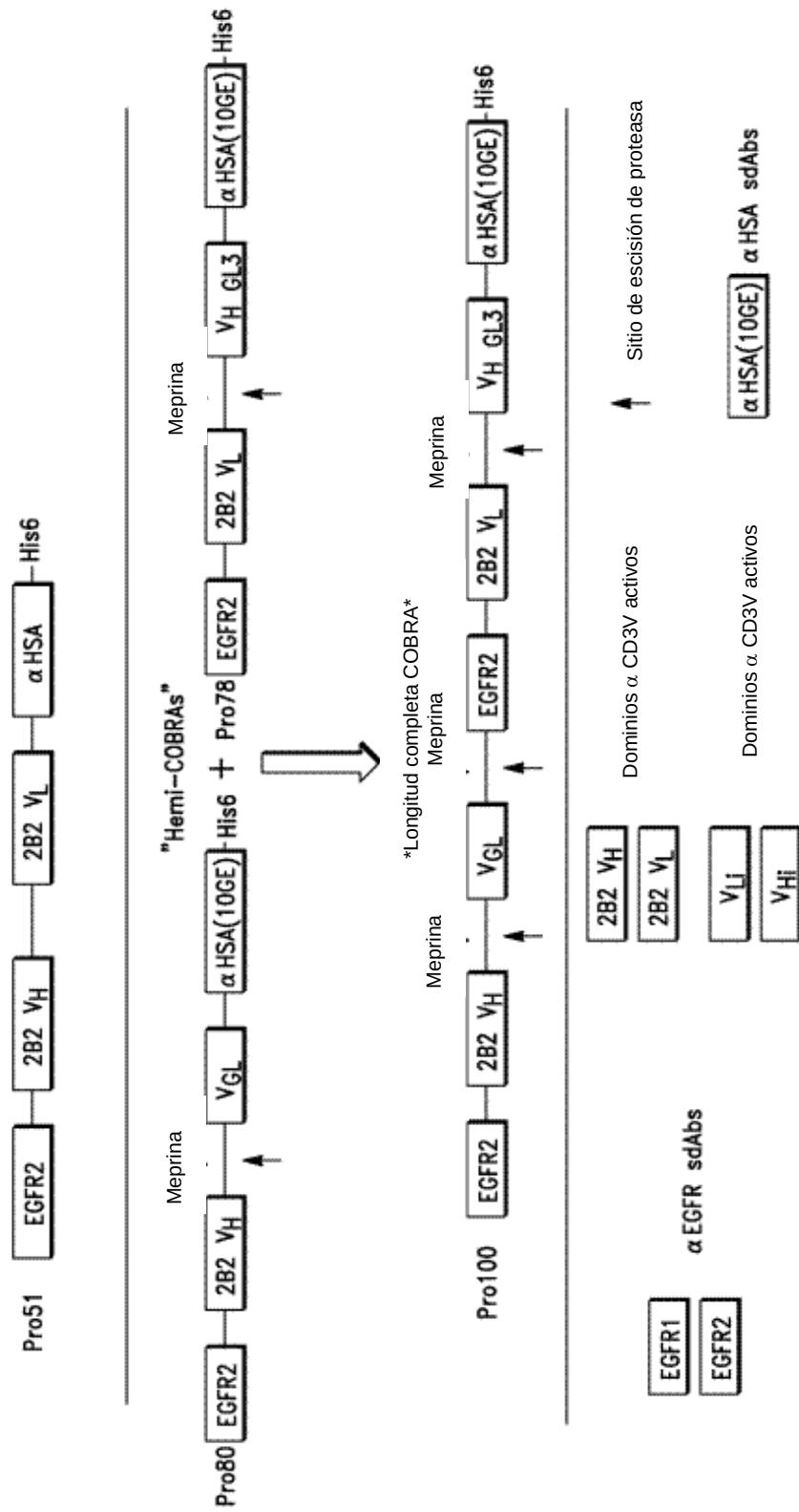


Figura 17

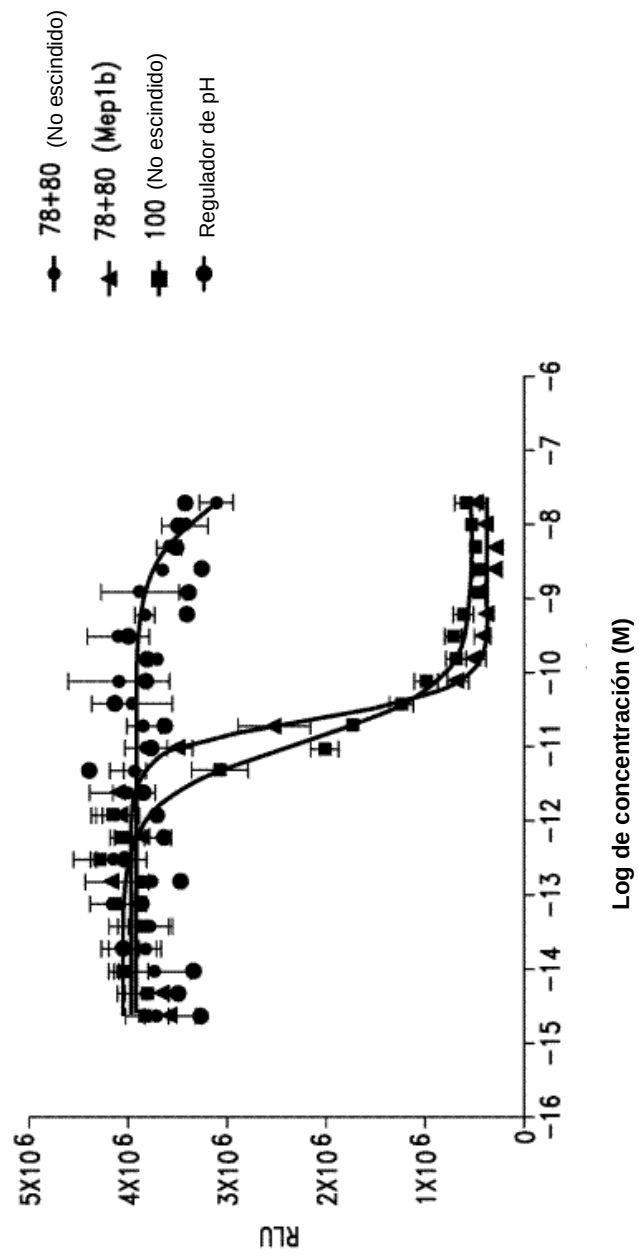


Figura 18

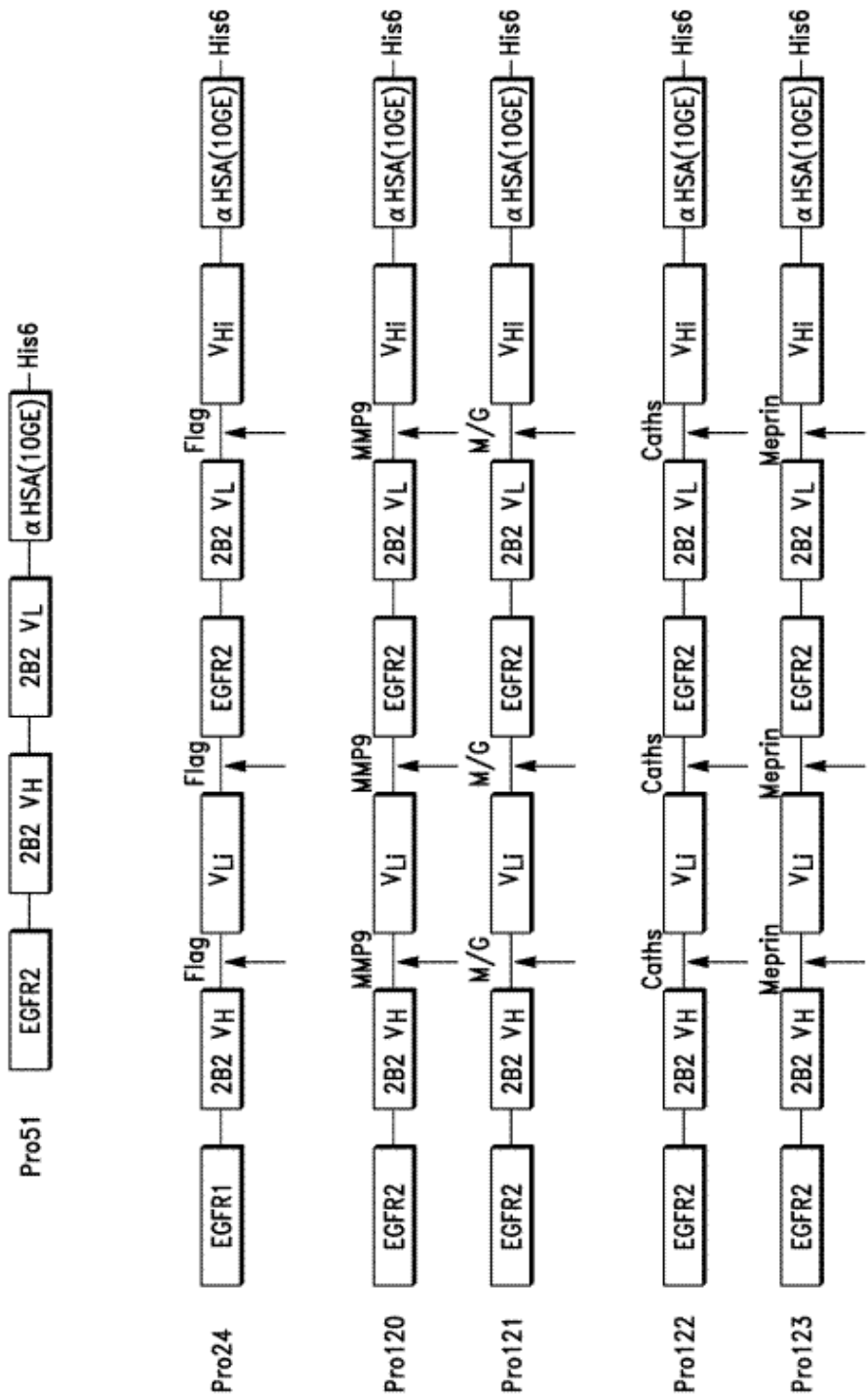


Figura 19

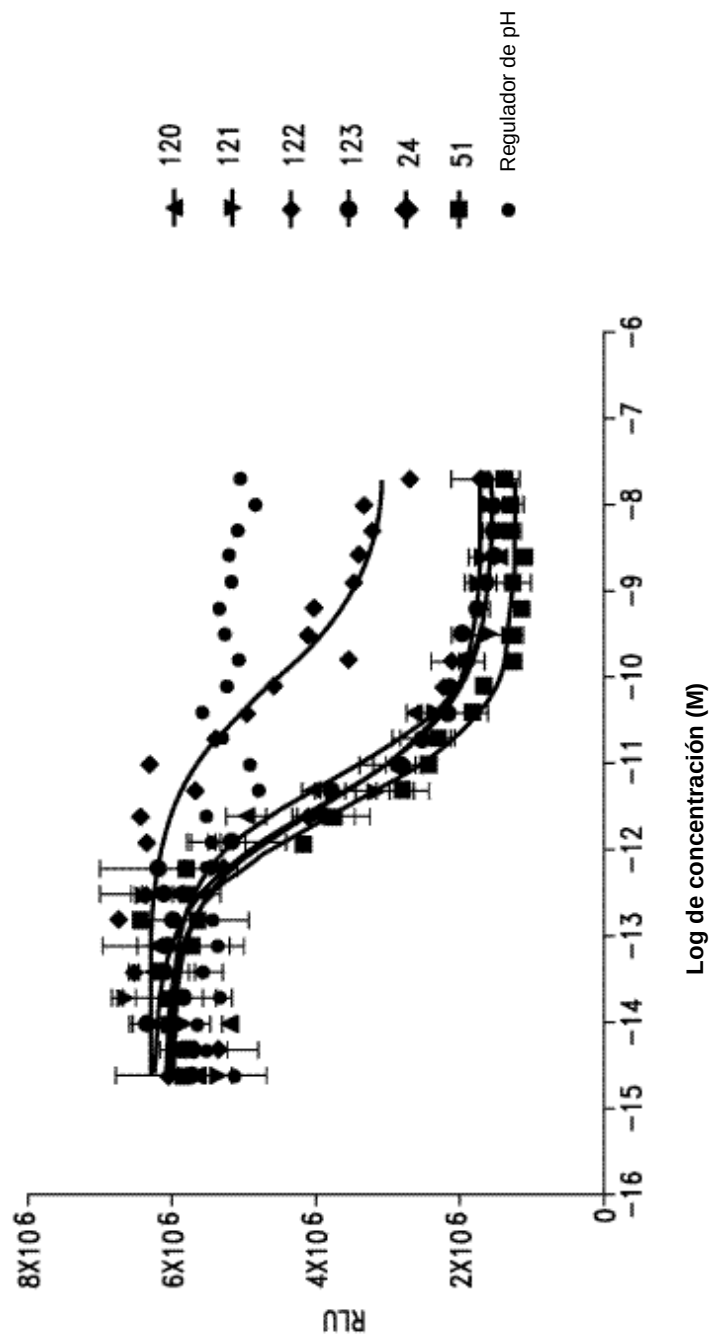


Figura 20

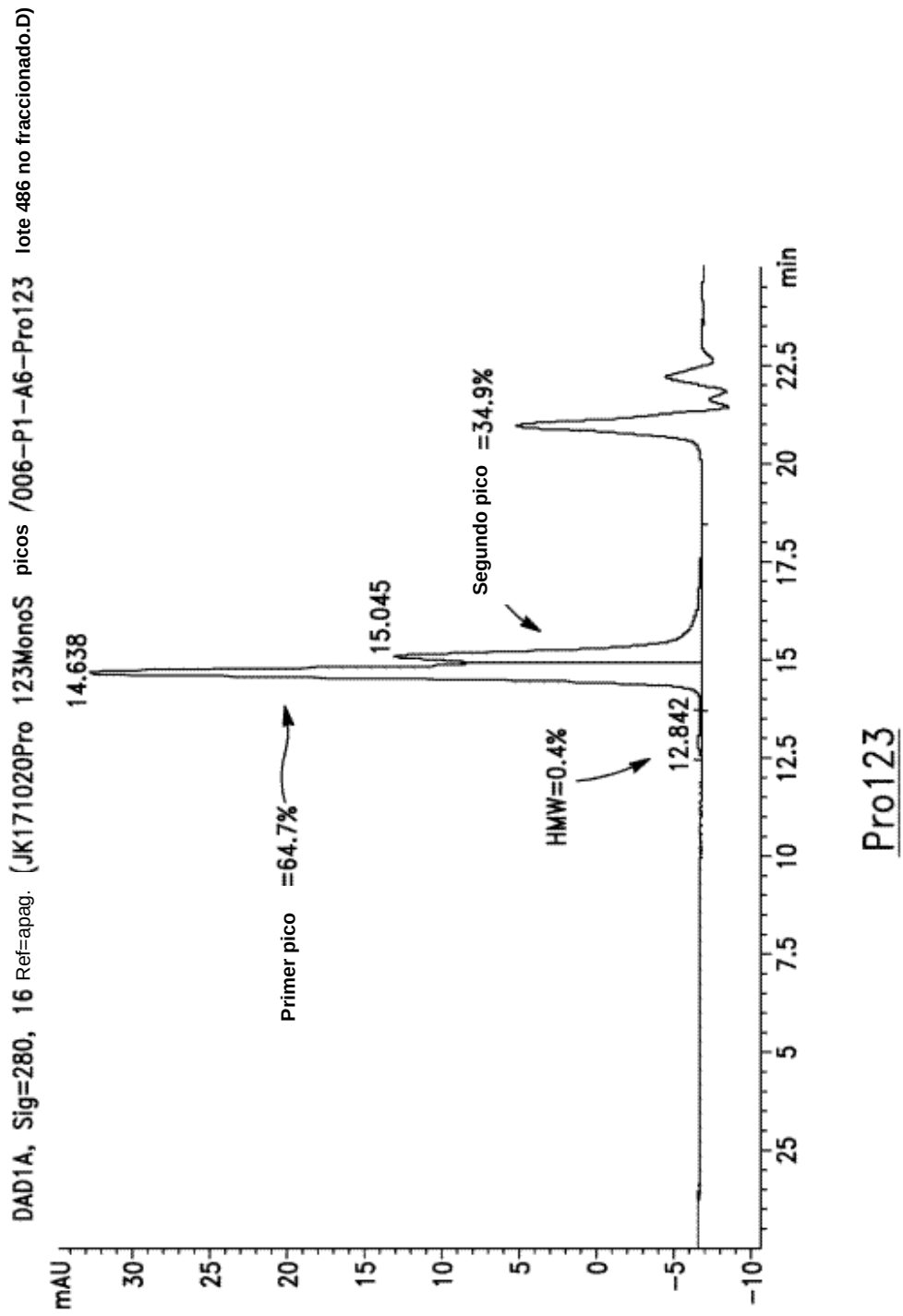


Figura 21

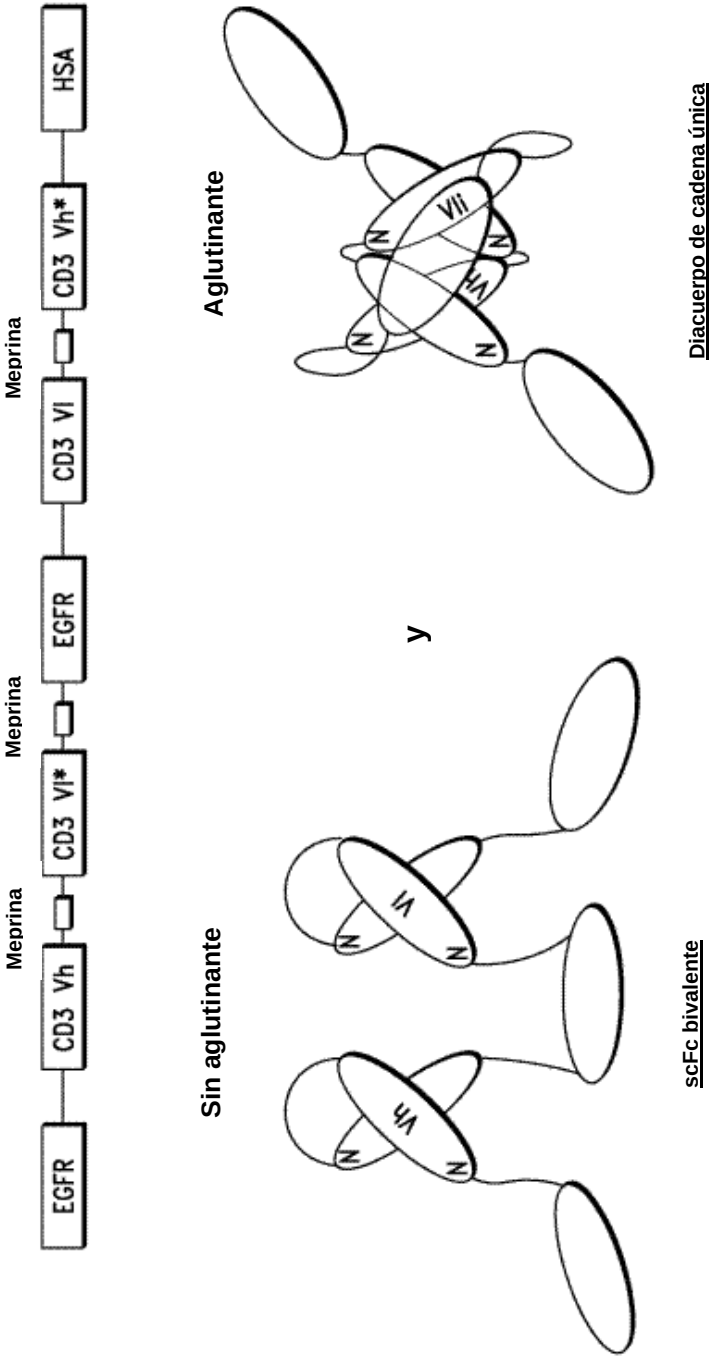


Figura 22

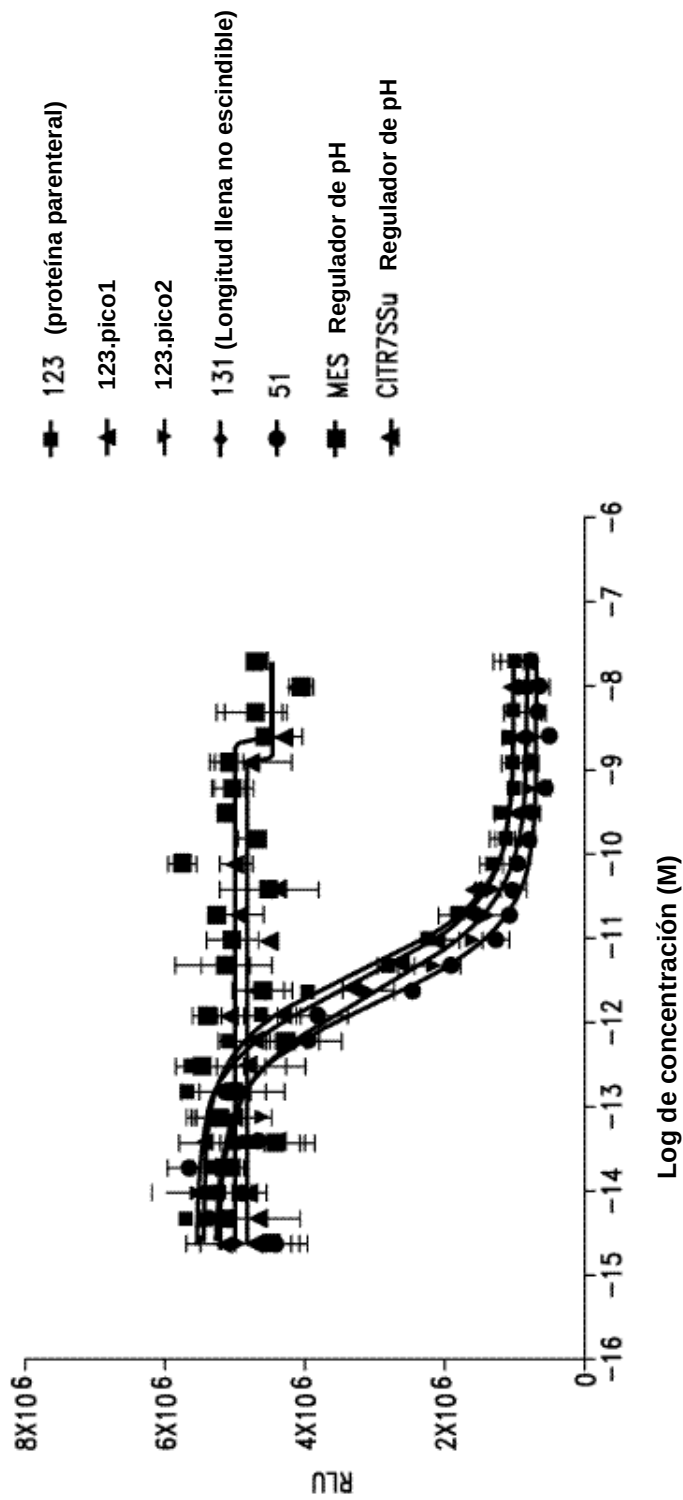


Figura 23A

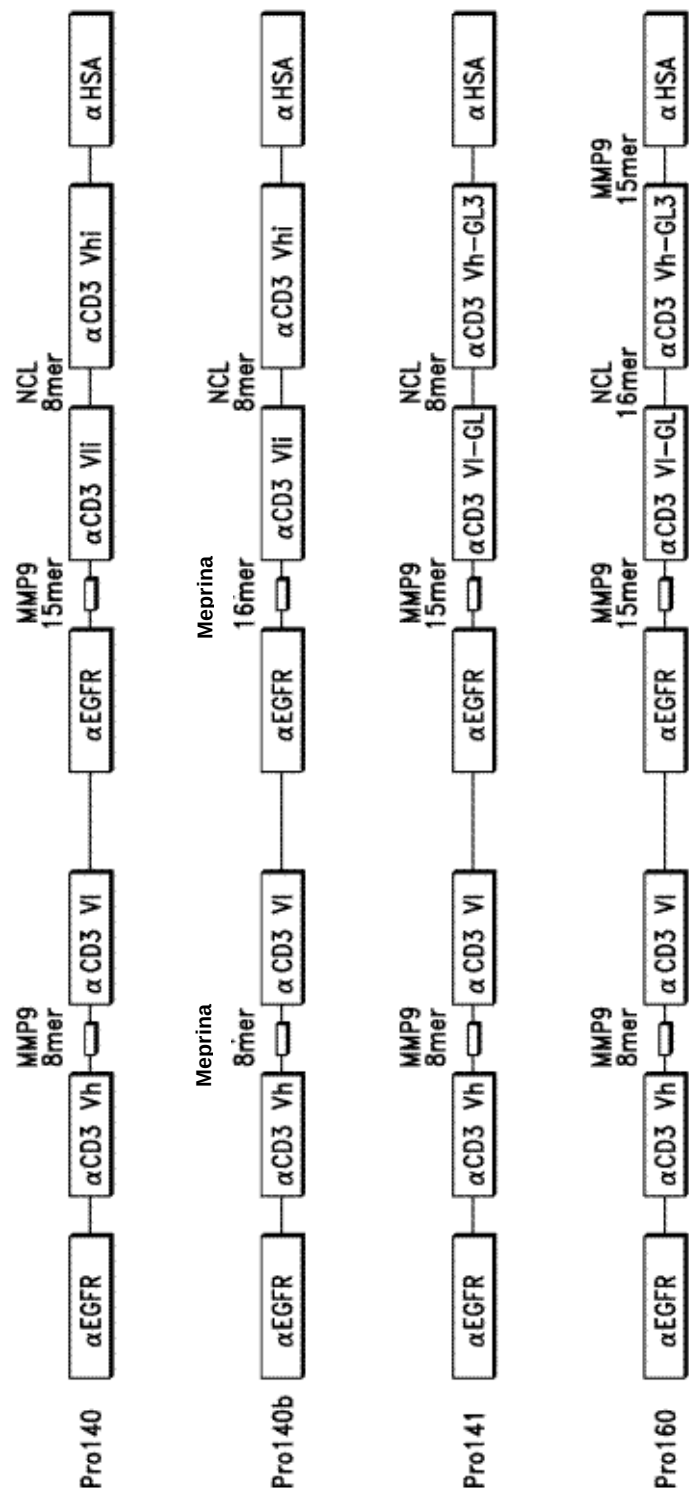


Figura 23B

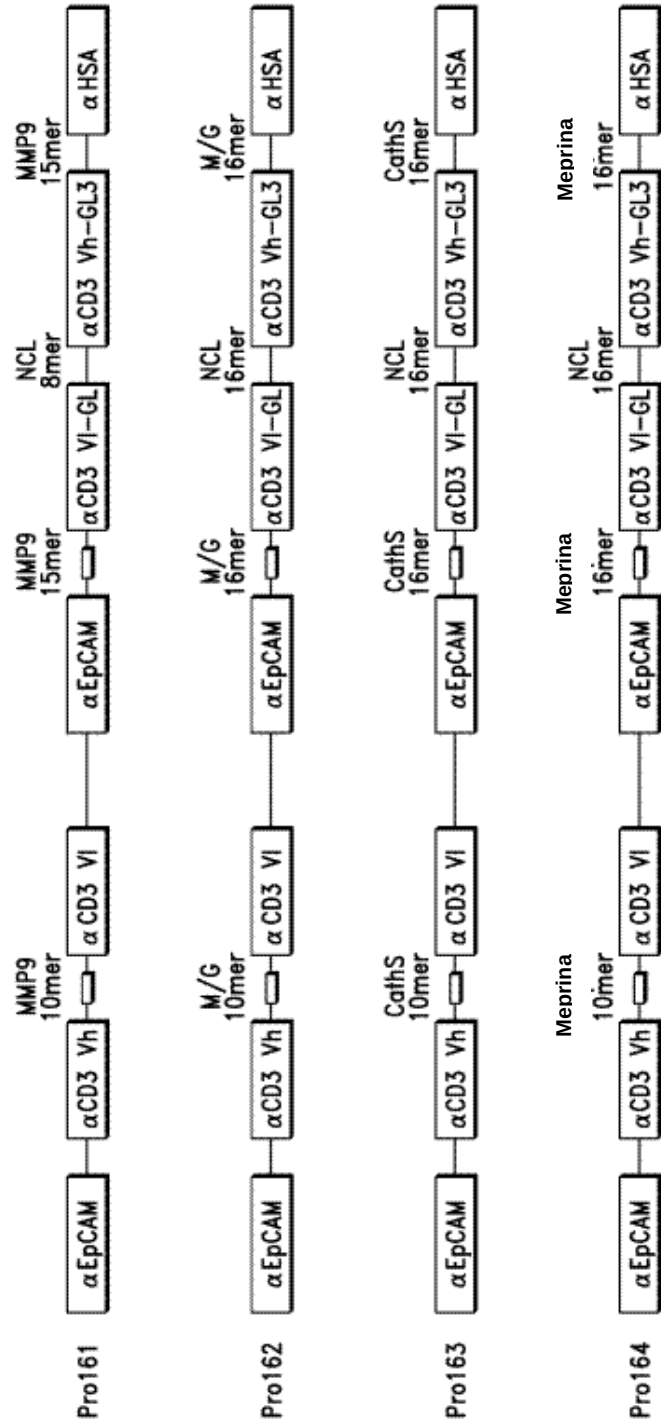


Figura 23C



Figura 23D

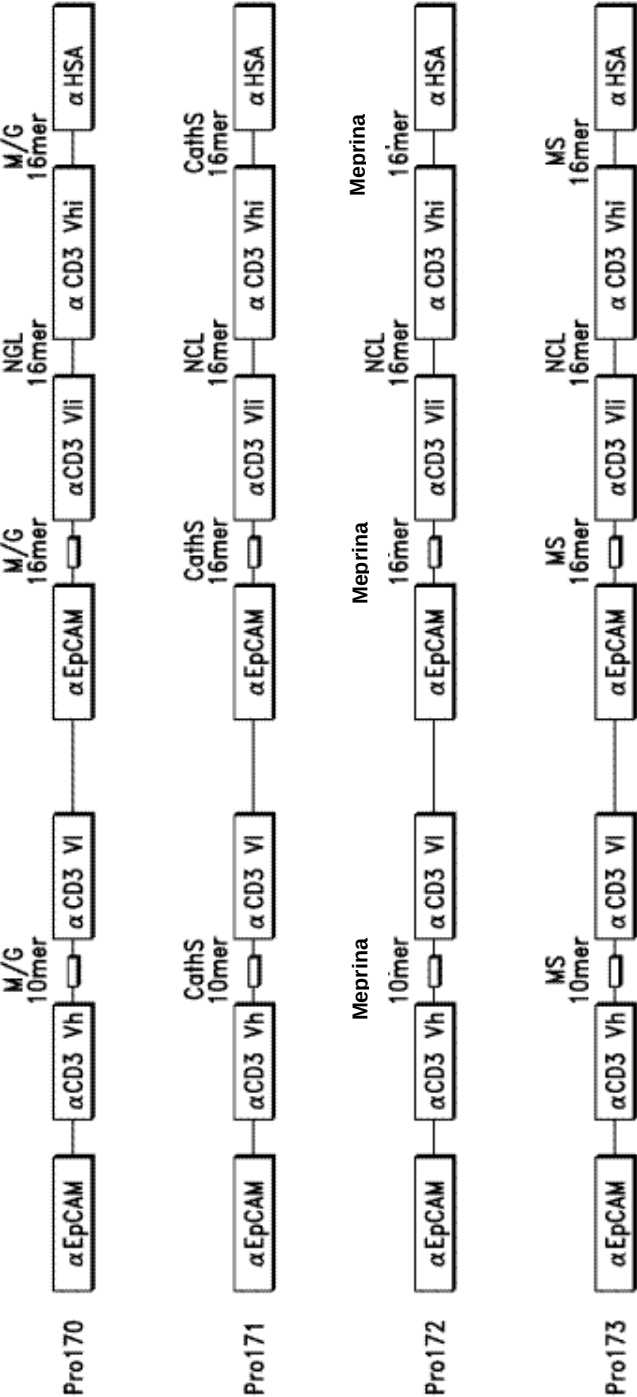


Figura 23E

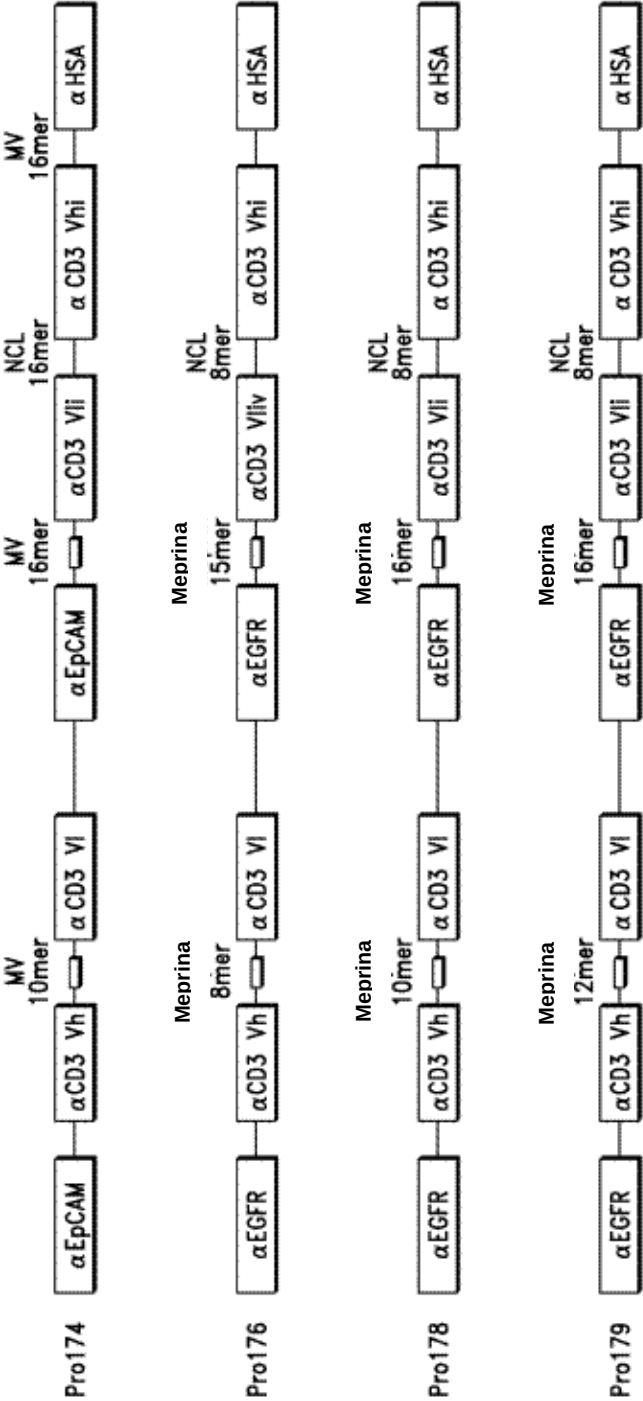


Figura 23F

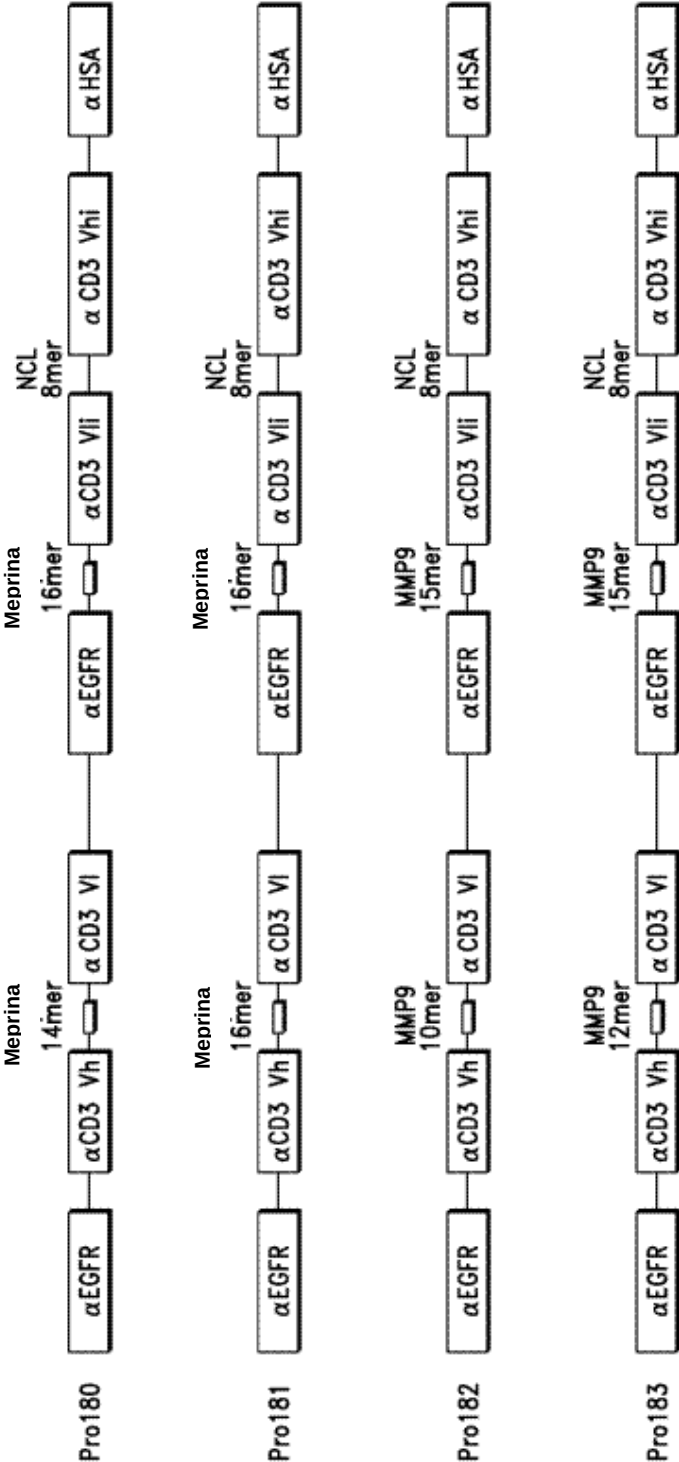


Figura 23G

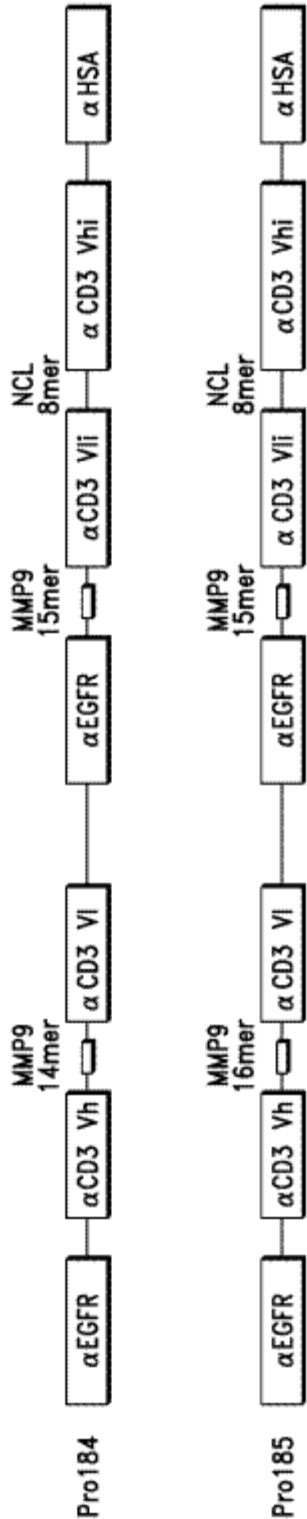


Figura 24

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 37\003-P1-A4-Pro 140 a 37 C.D) 37°C 72 hrs

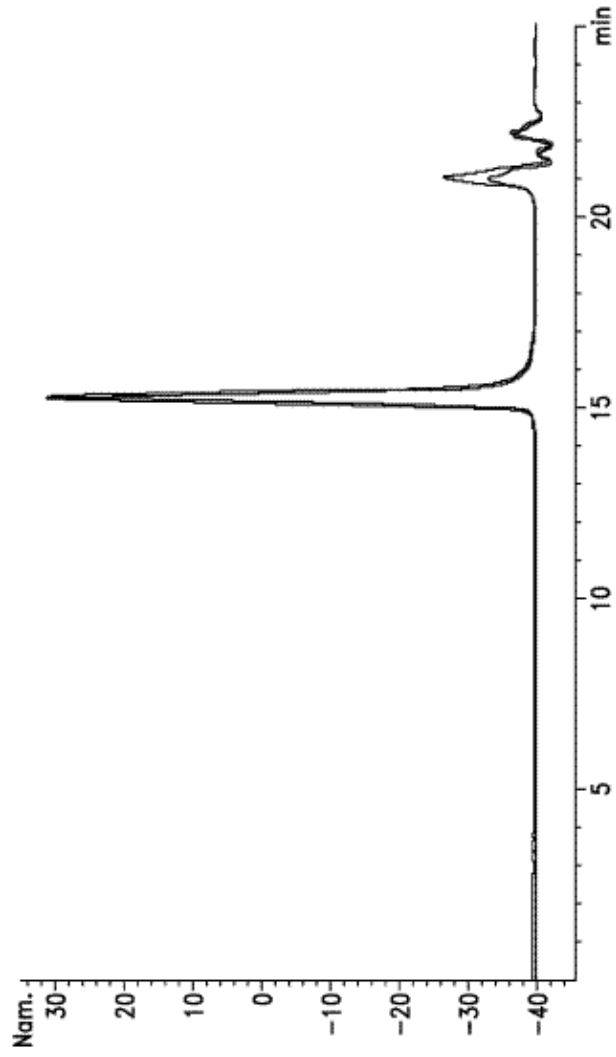


Figura 25

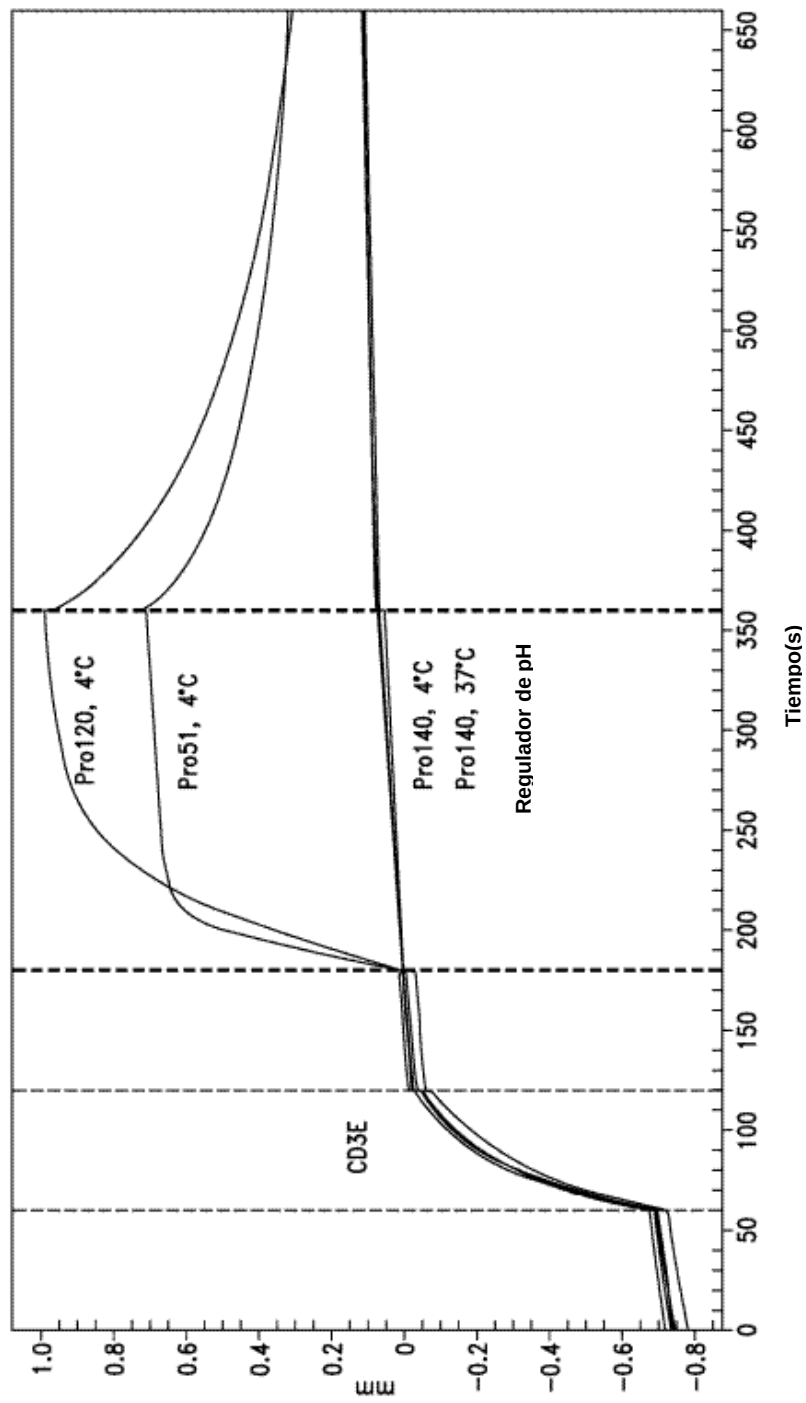


Figura 26

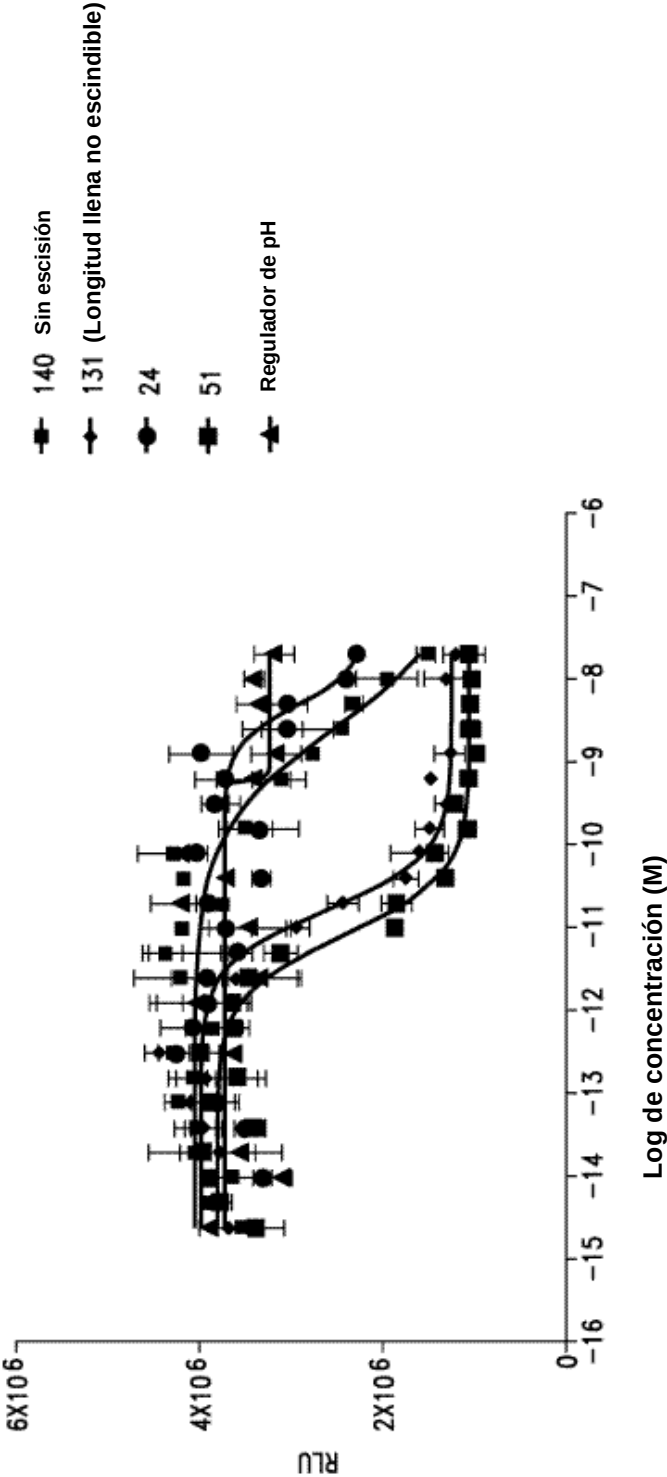
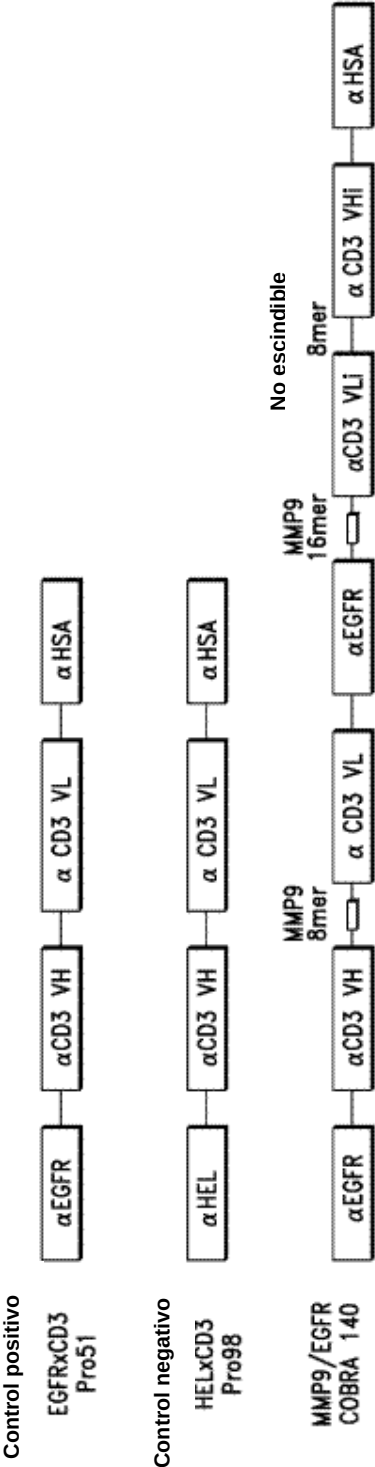


Figura 27

Grupos:



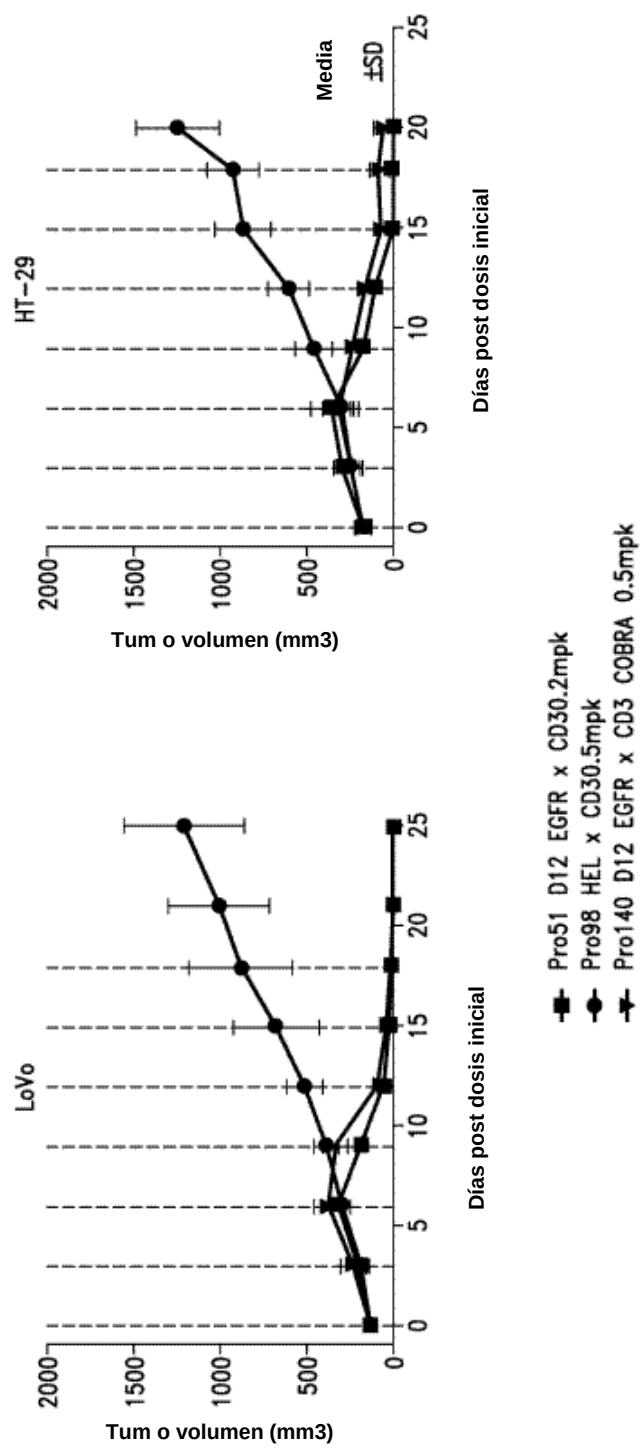
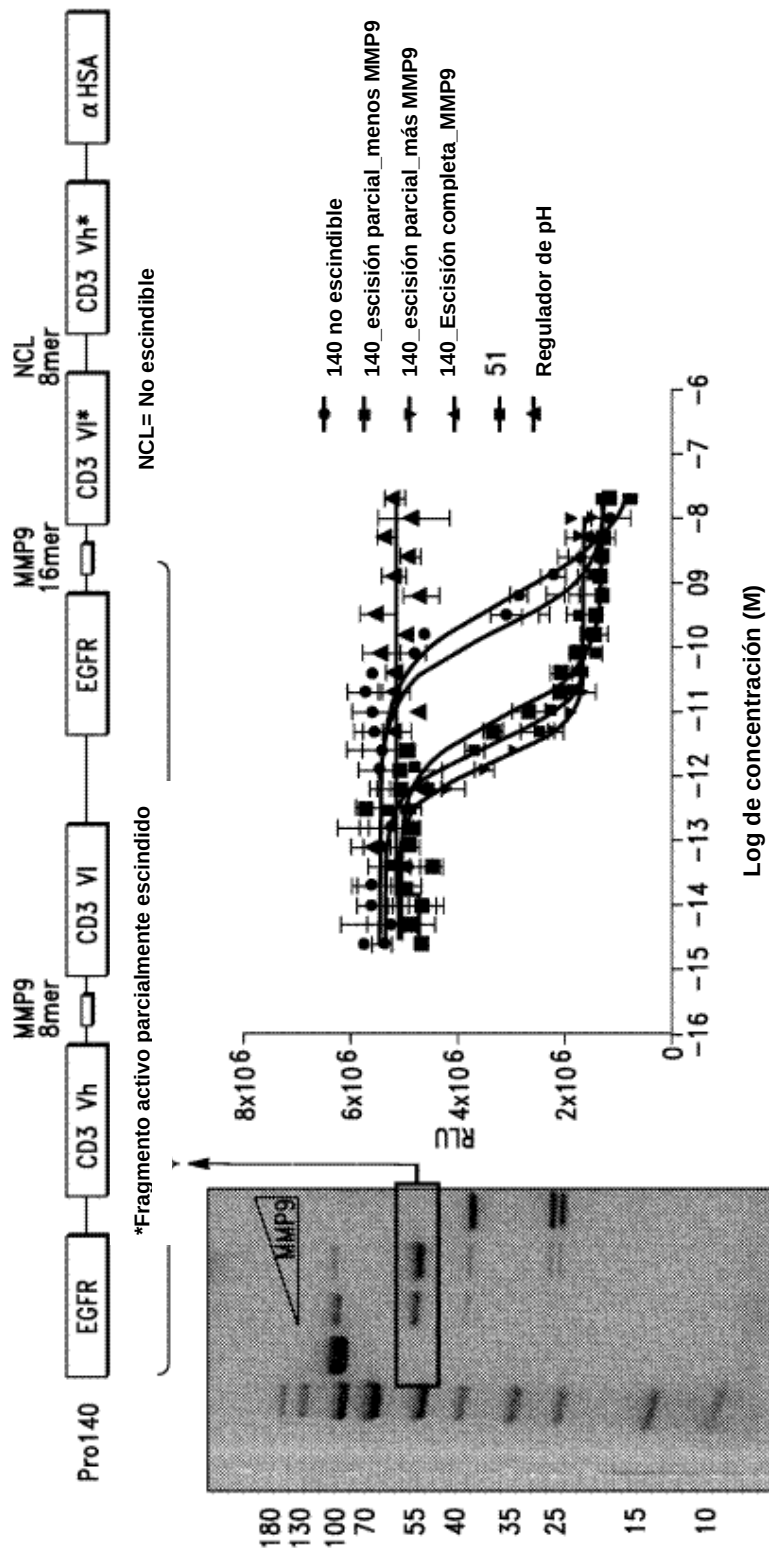


Figura 28B

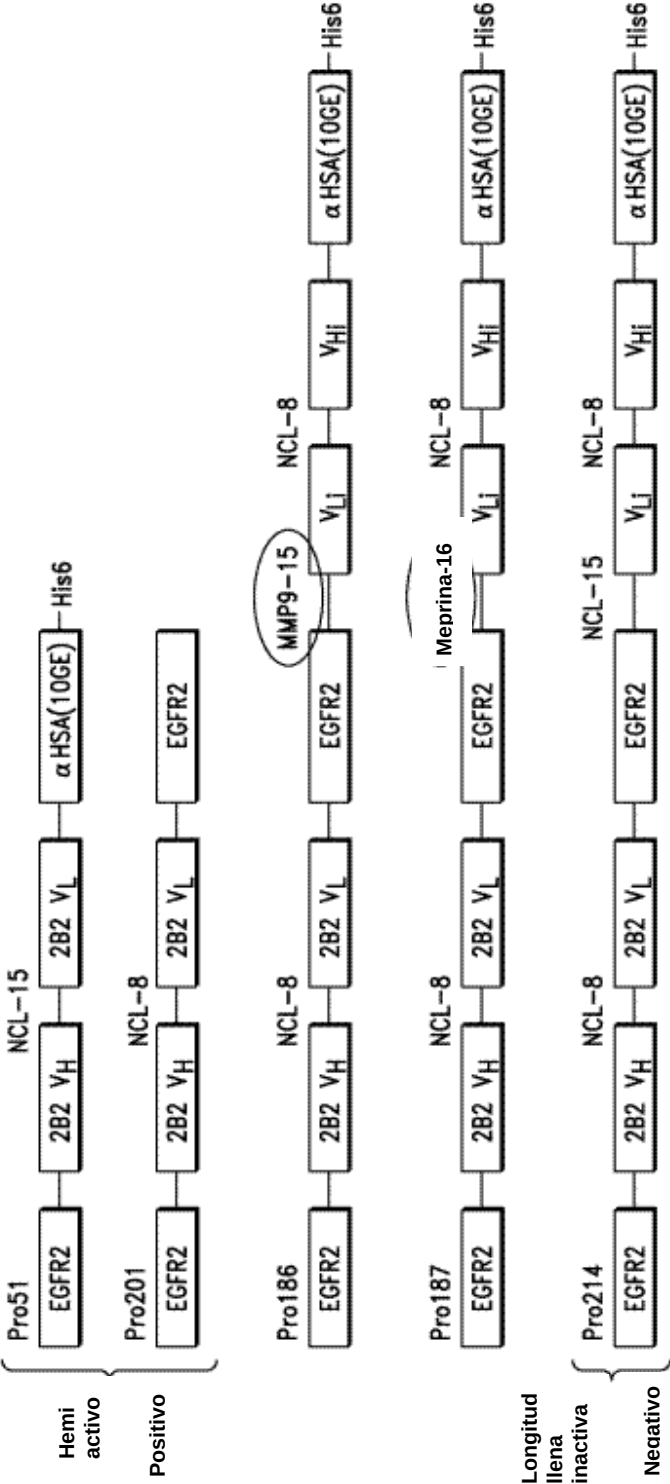
Figura 28A

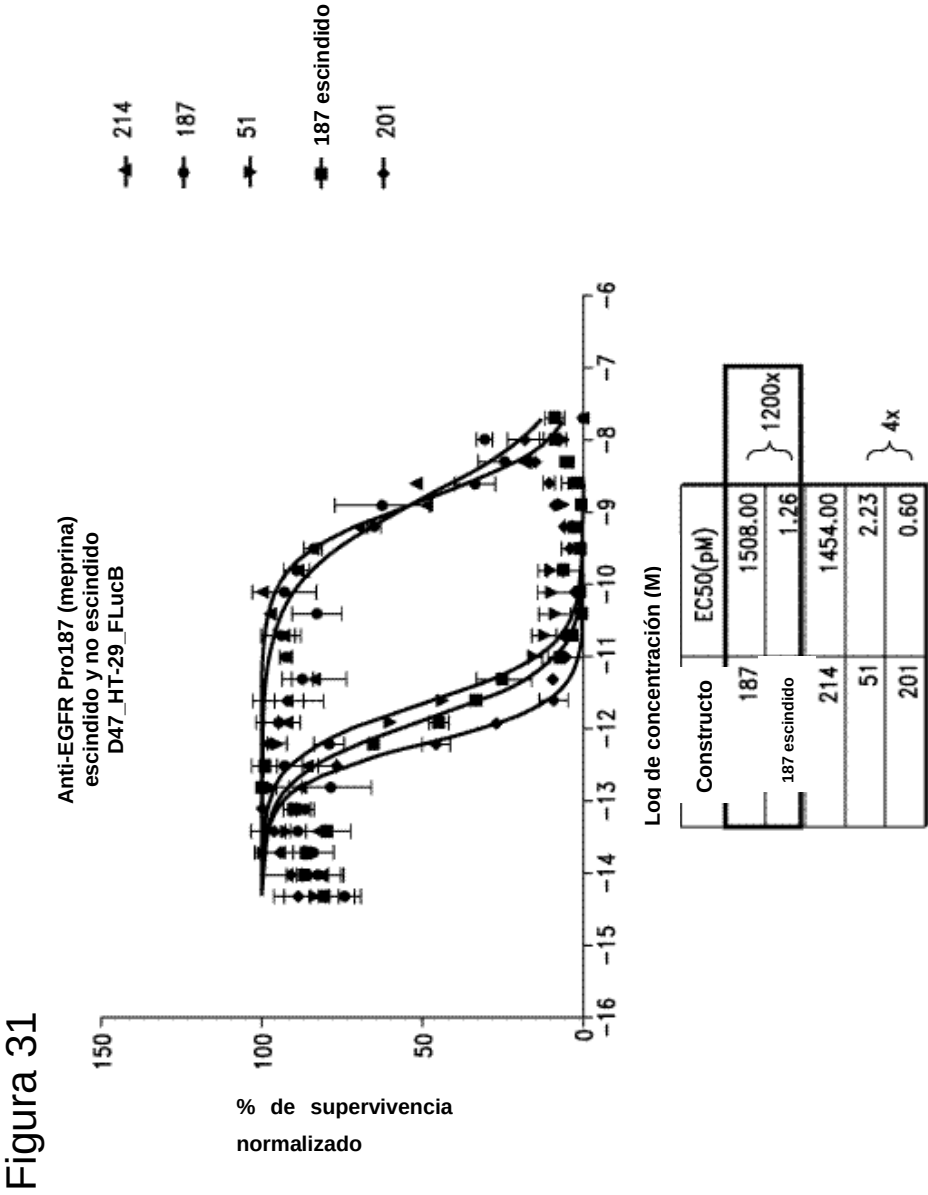
Figura 29

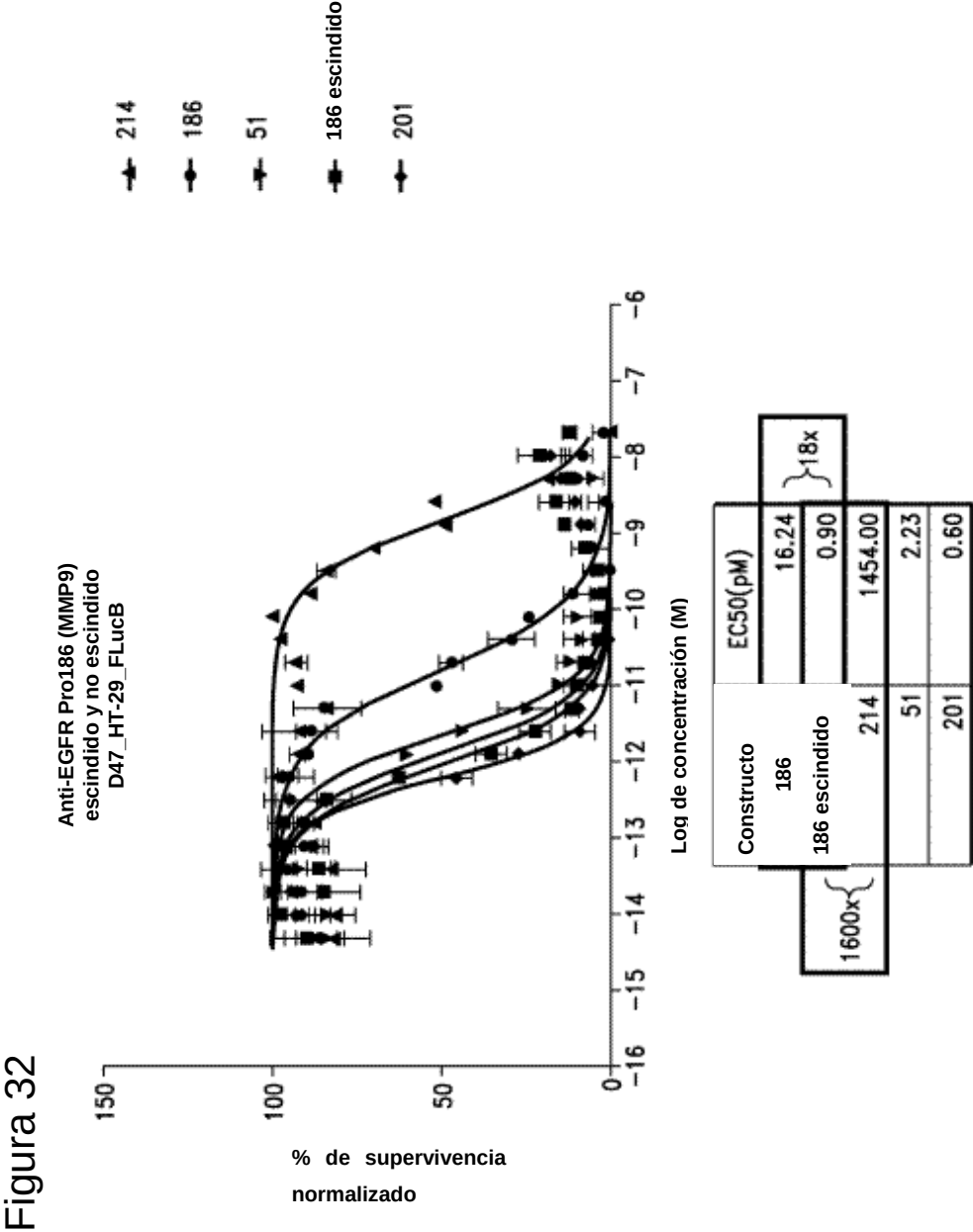


\*Enlazador 16 mer MMP9 se escinde a una velocidad más rápida que el enlazador 8 mer MMP9

Figura 30







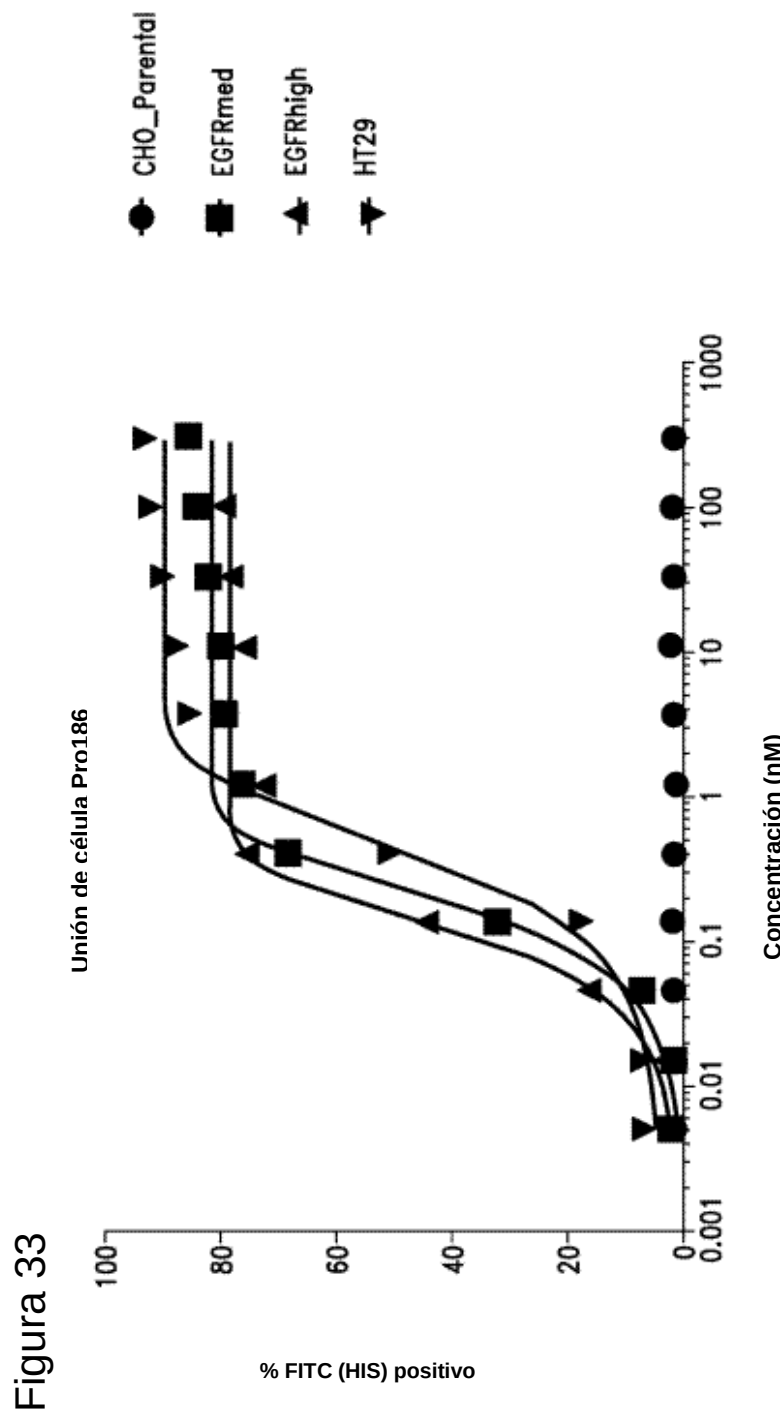


Figura 34

Grupos:

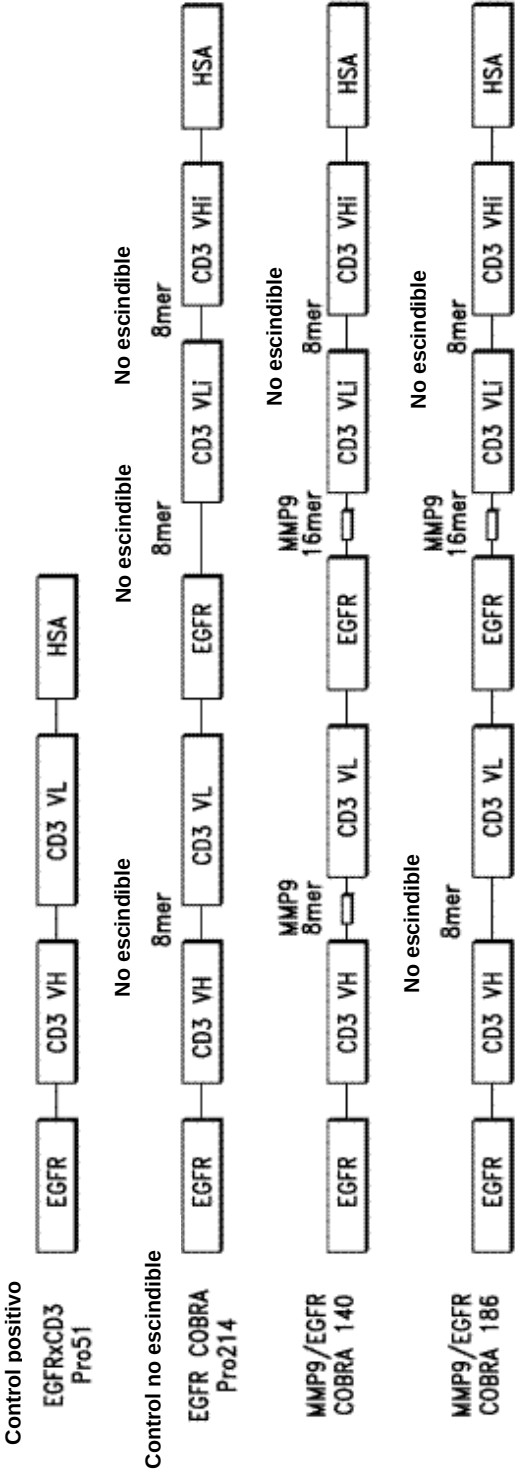




Figura 36

Pro186

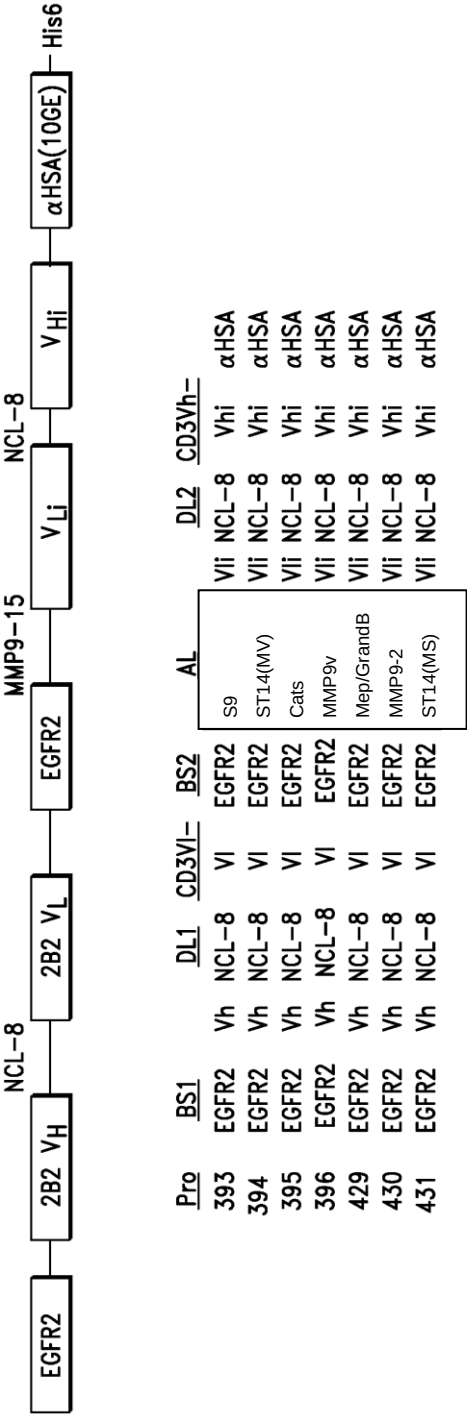


Figura 37

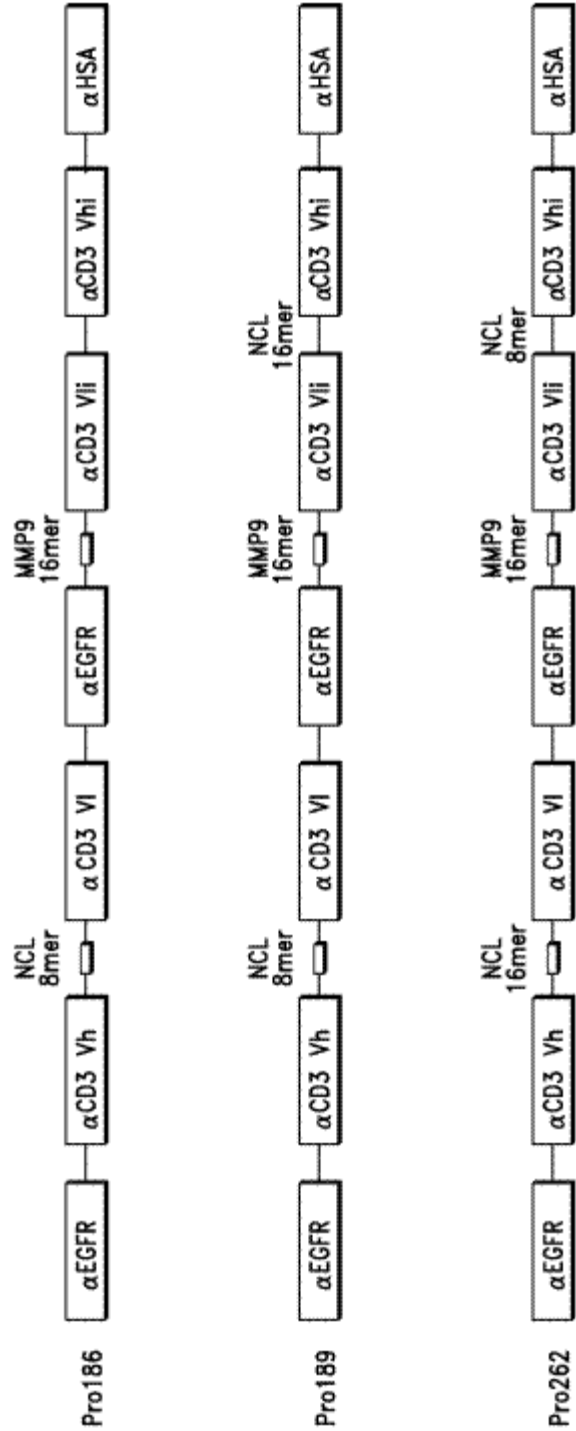


Figura 38

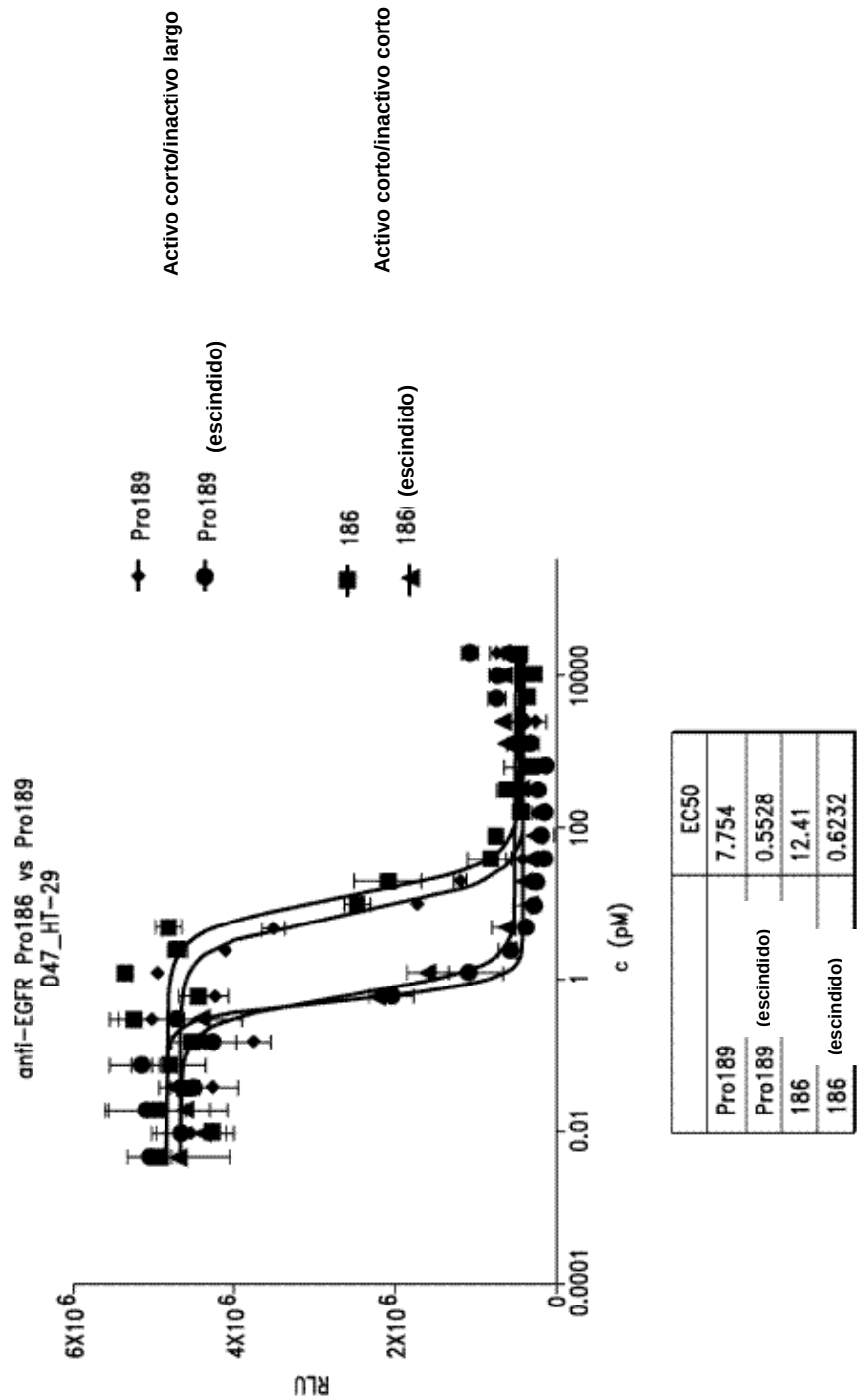


Figura 39

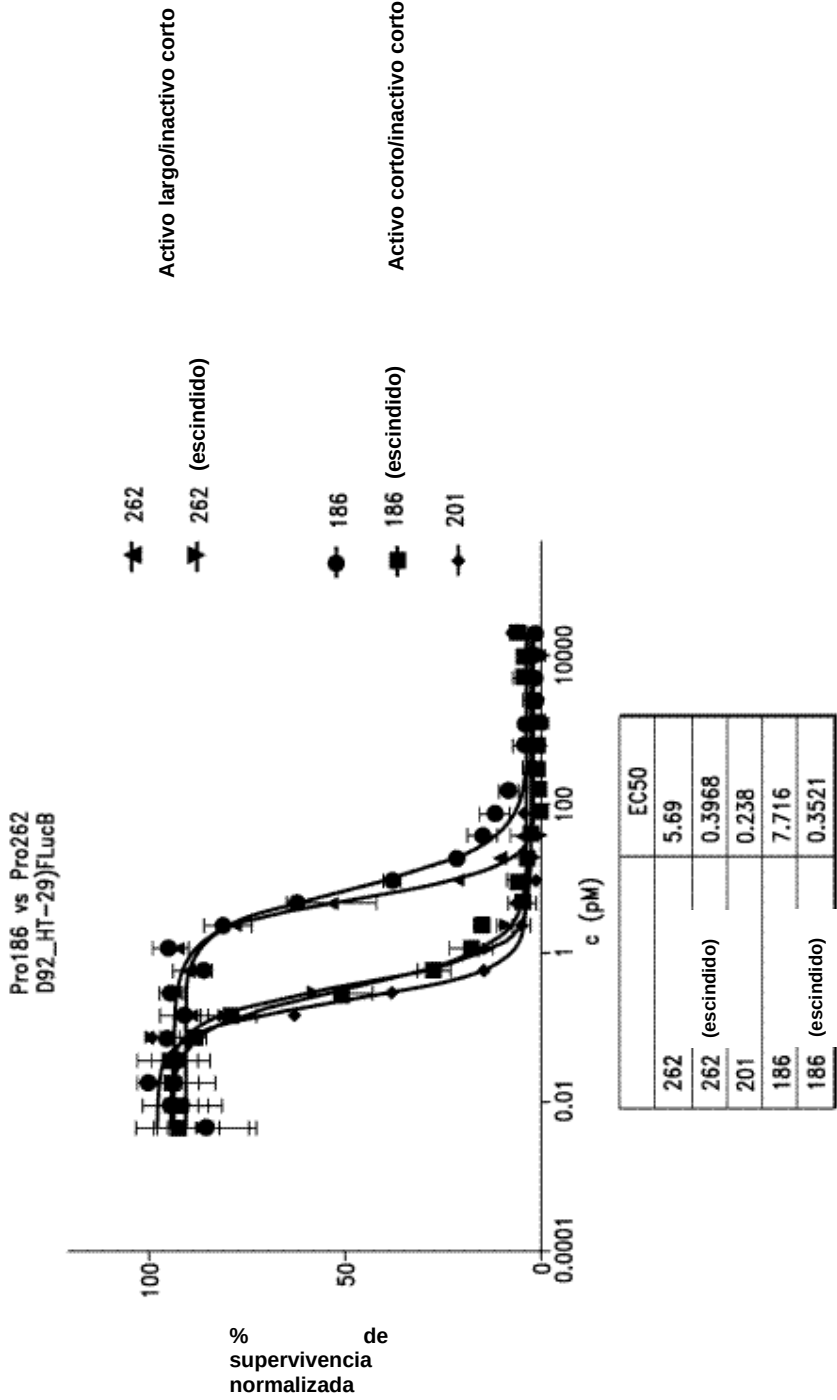


Figura 40A

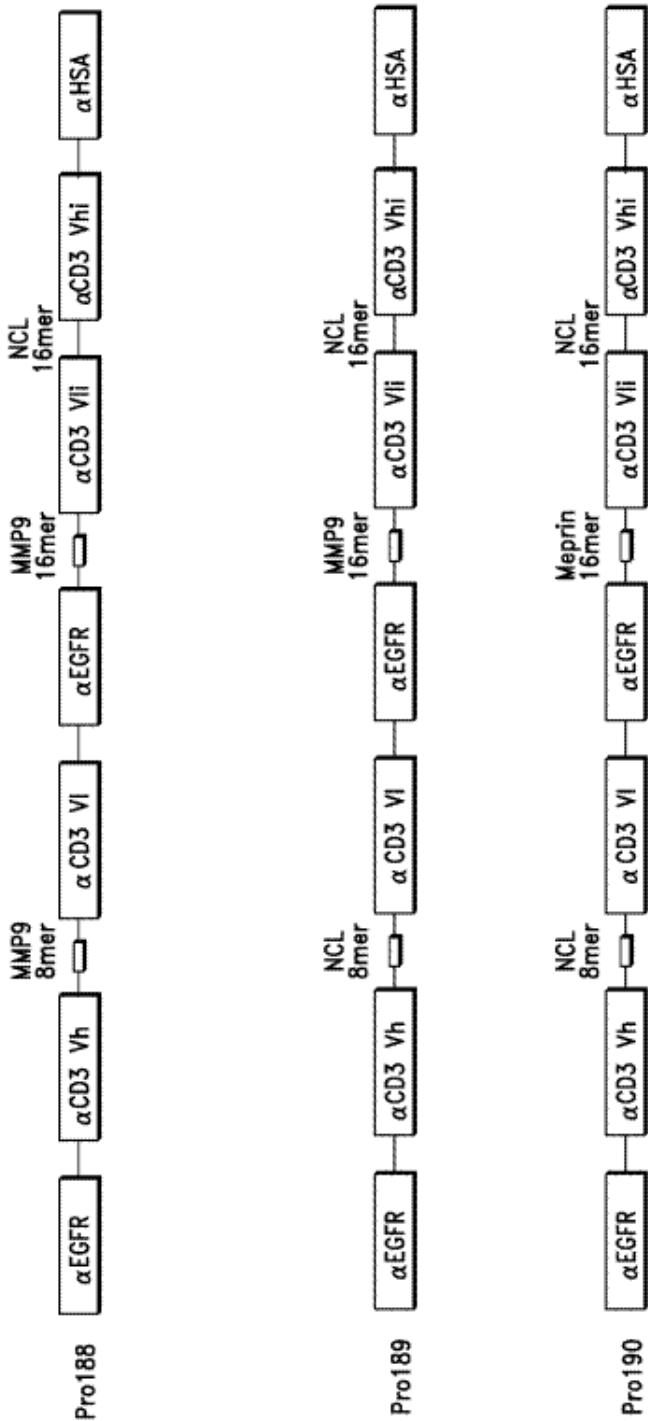


Figura 40B

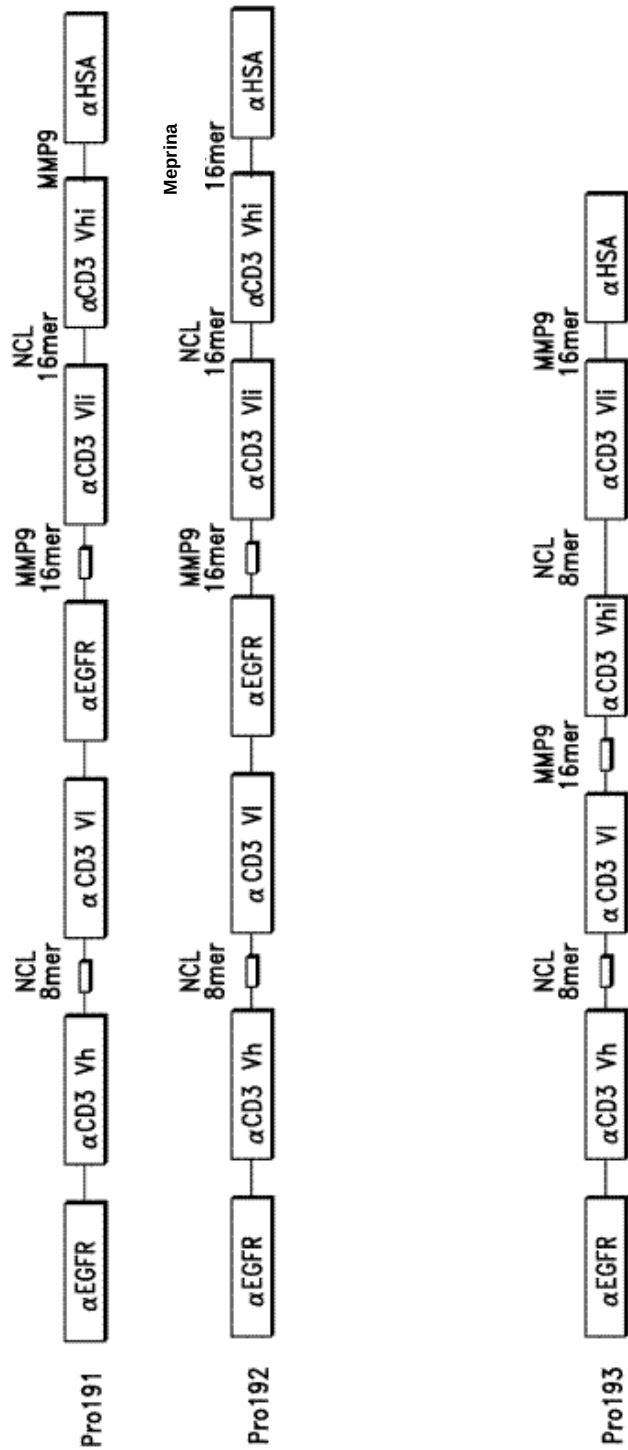


Figura 40C

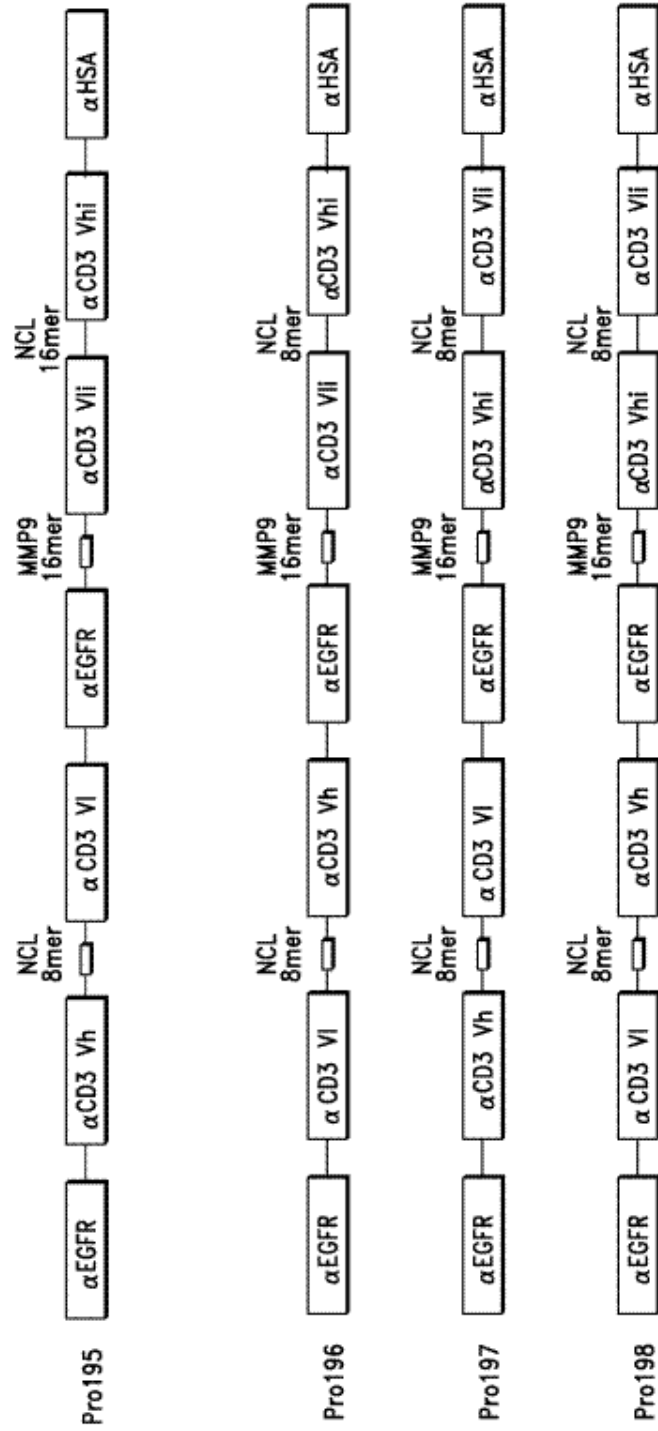




Figura 42

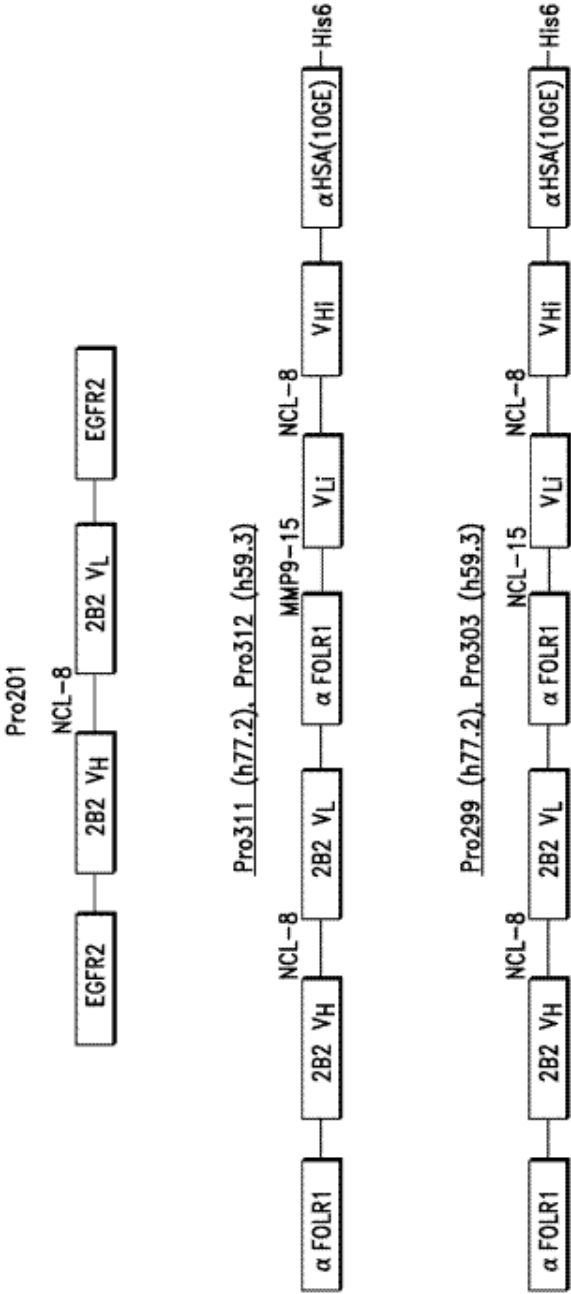


Figura 43

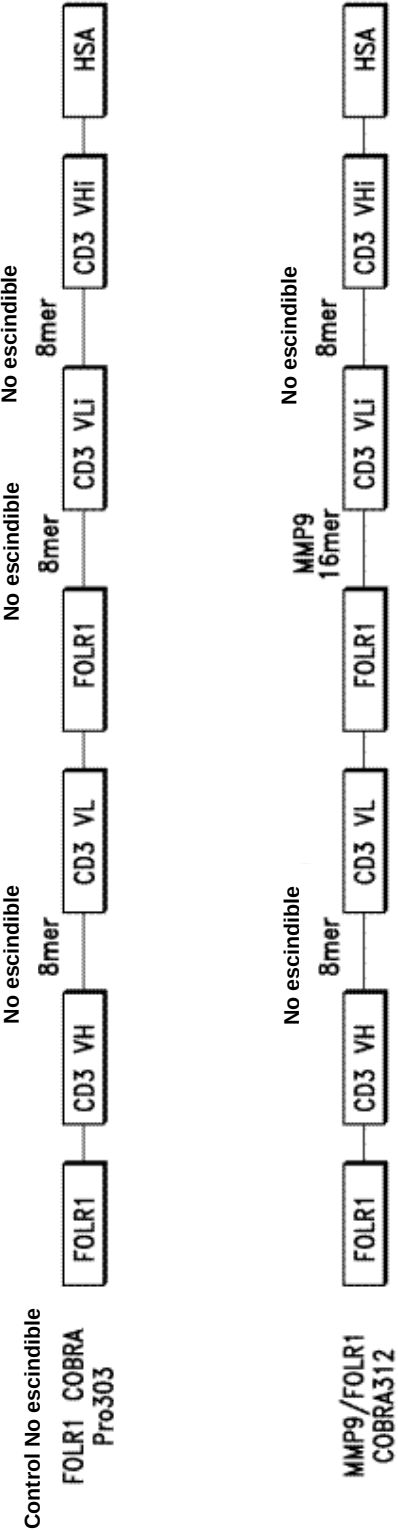


Figura 44

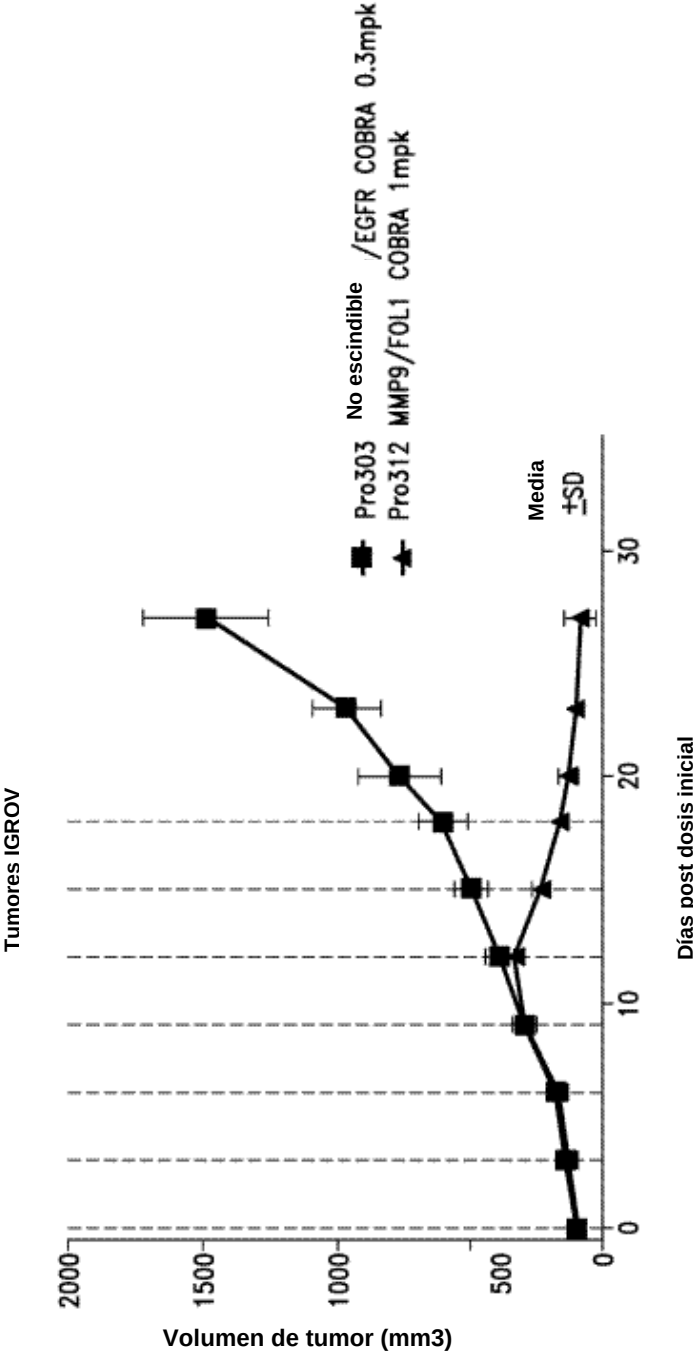


Figura 45

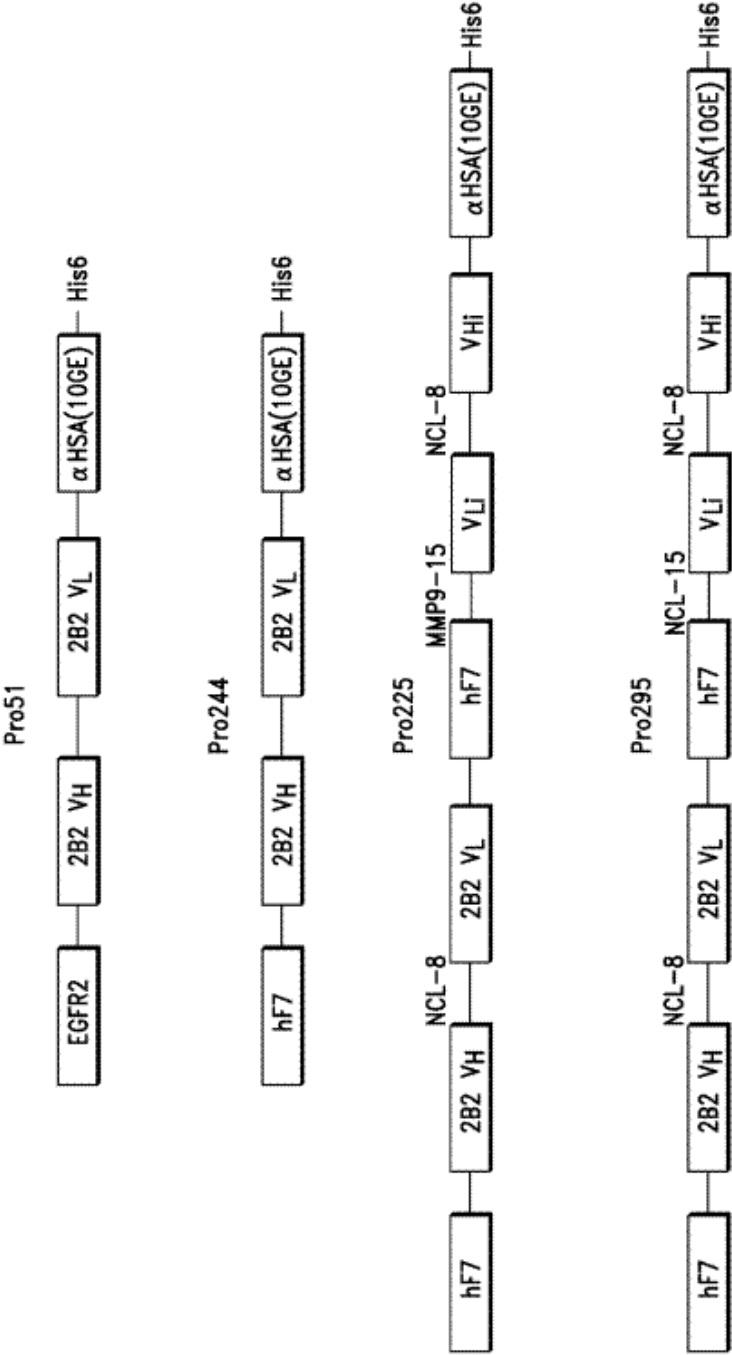


Figura 46

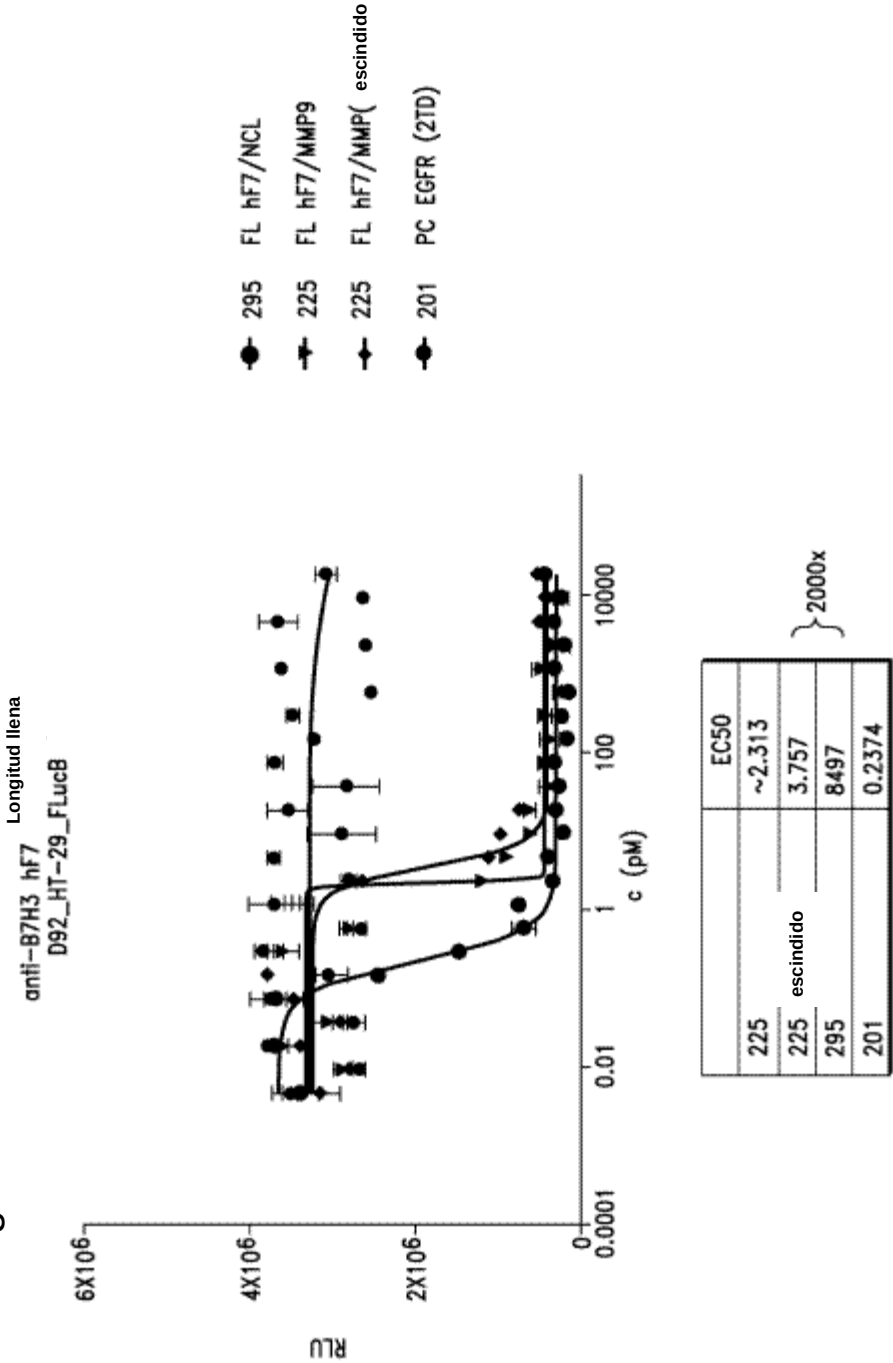


Figura 47

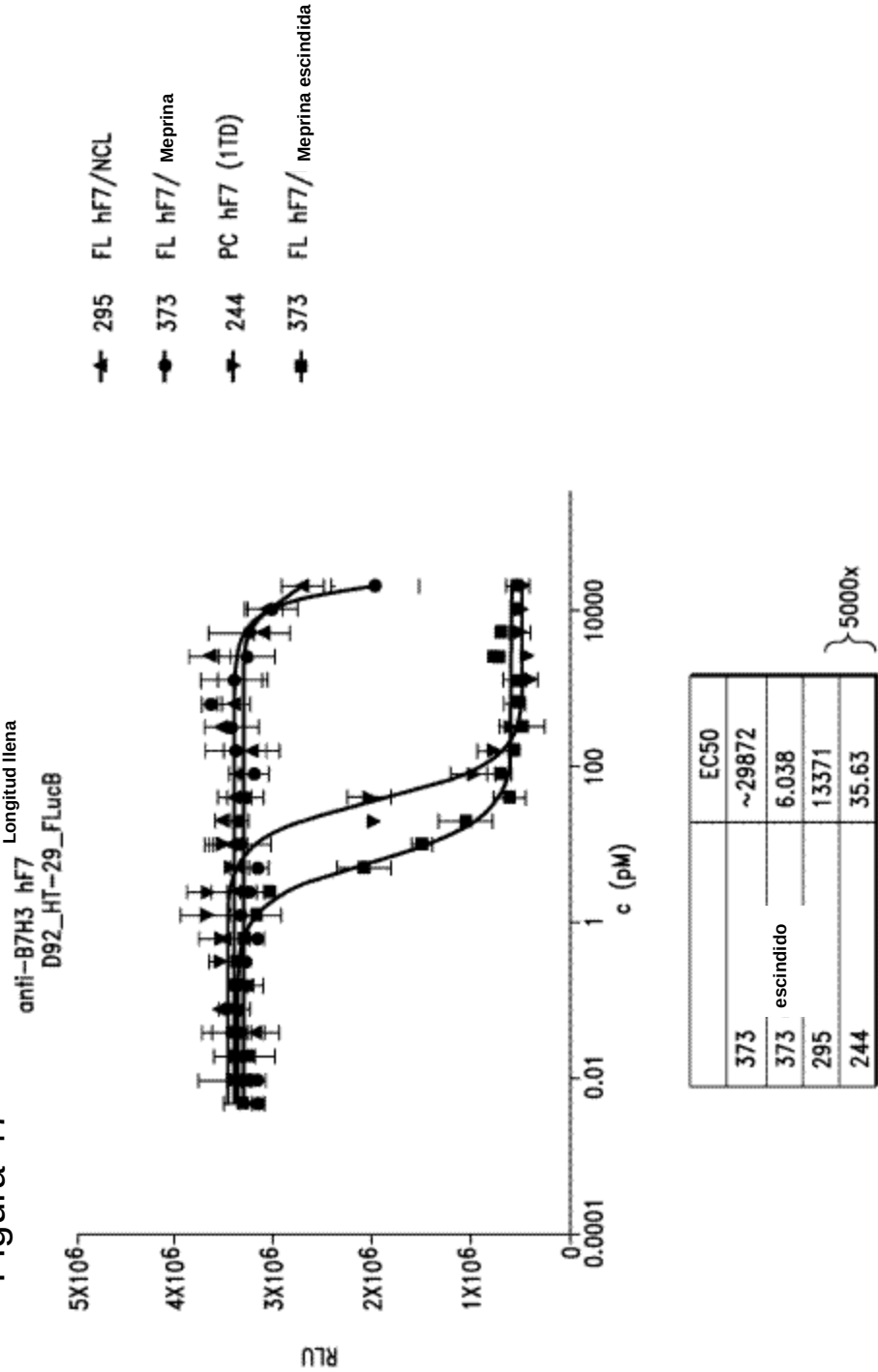


Figura 48

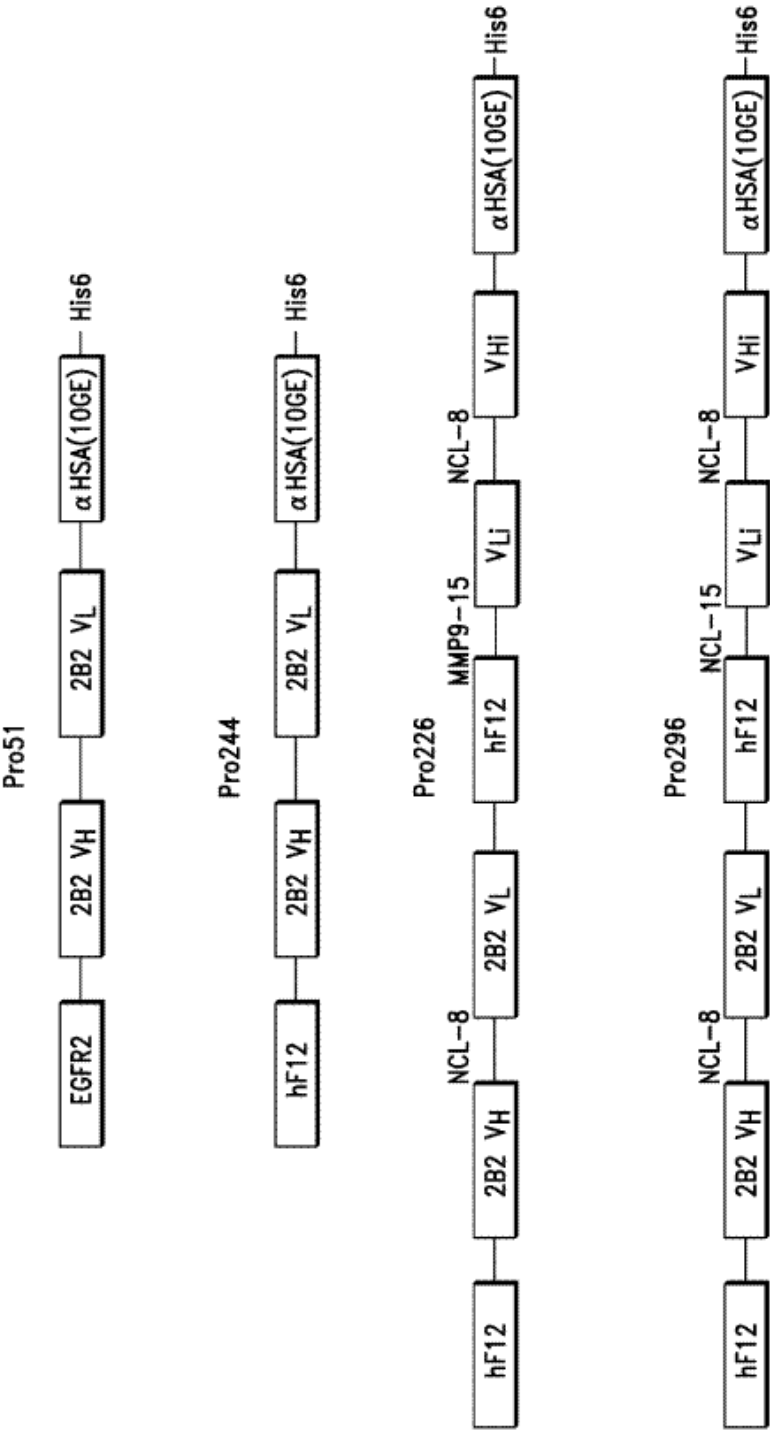
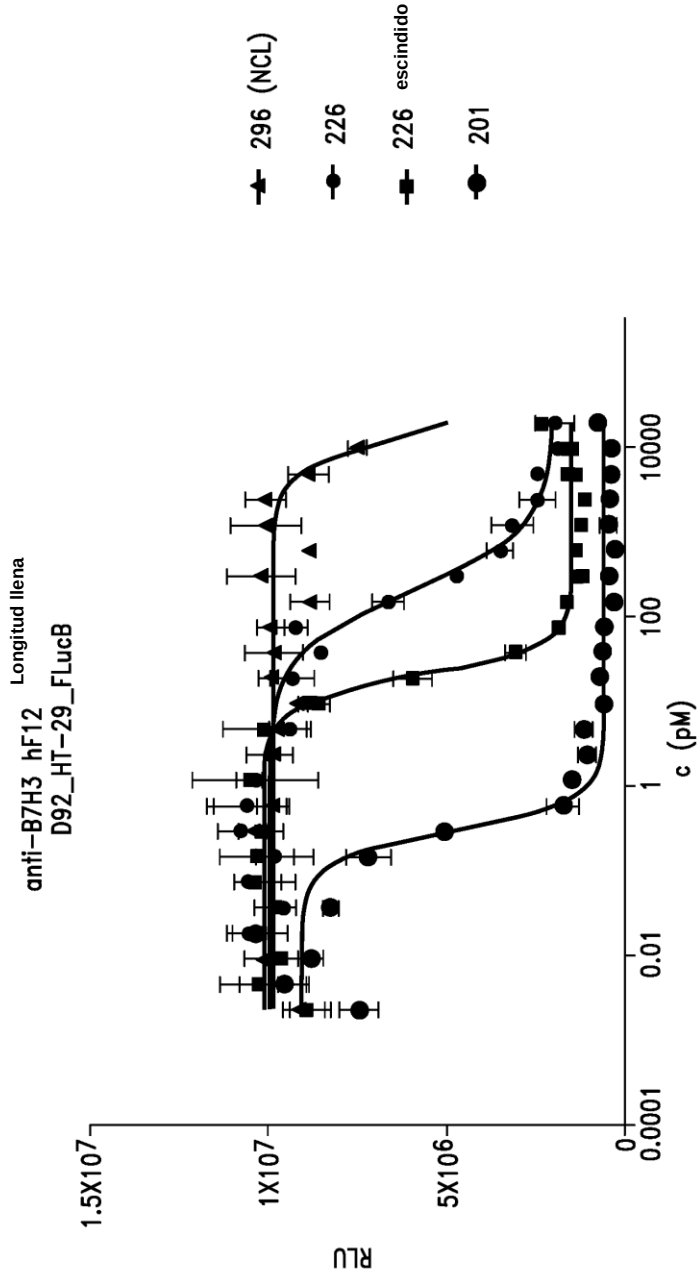


Figura 49



|               | 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

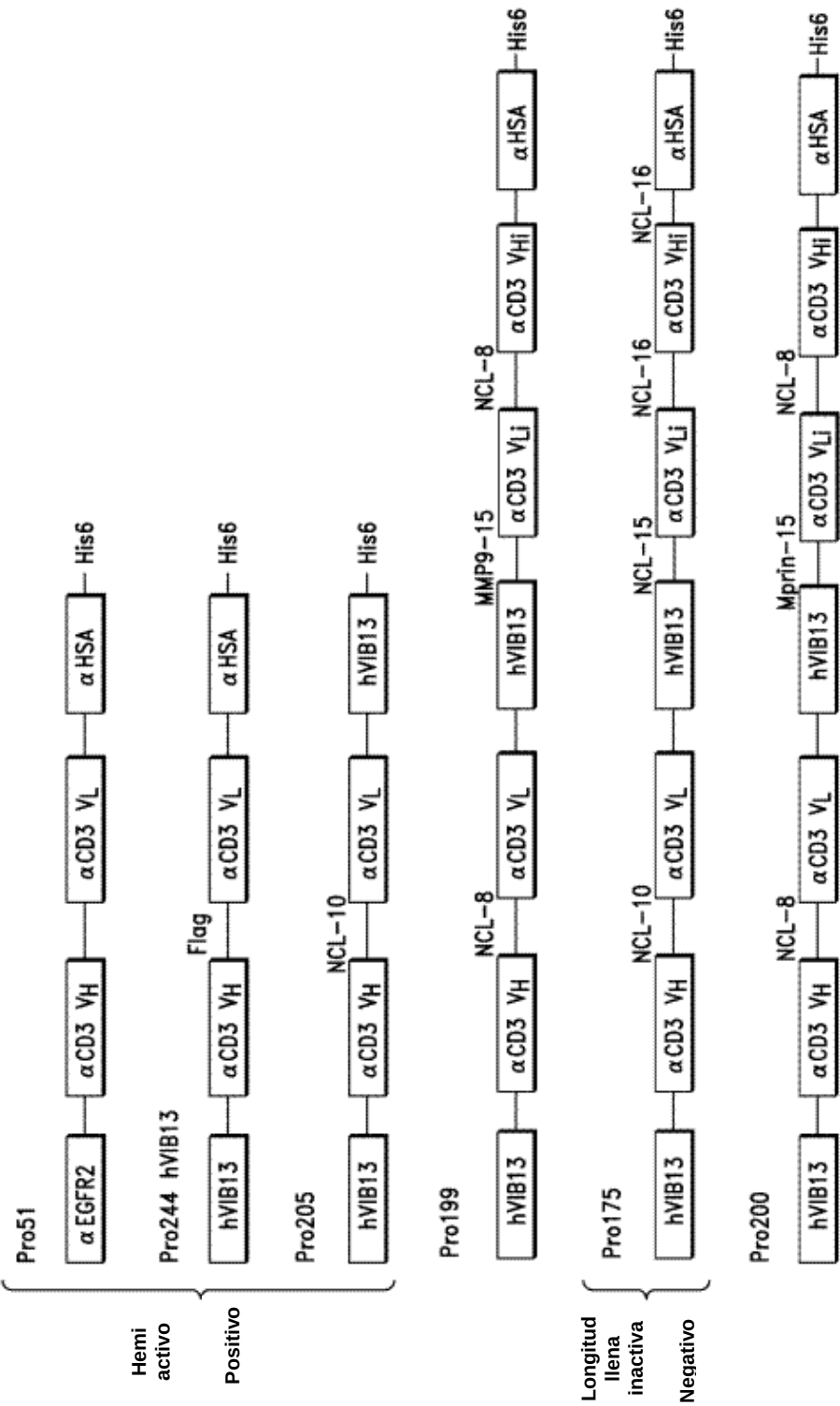
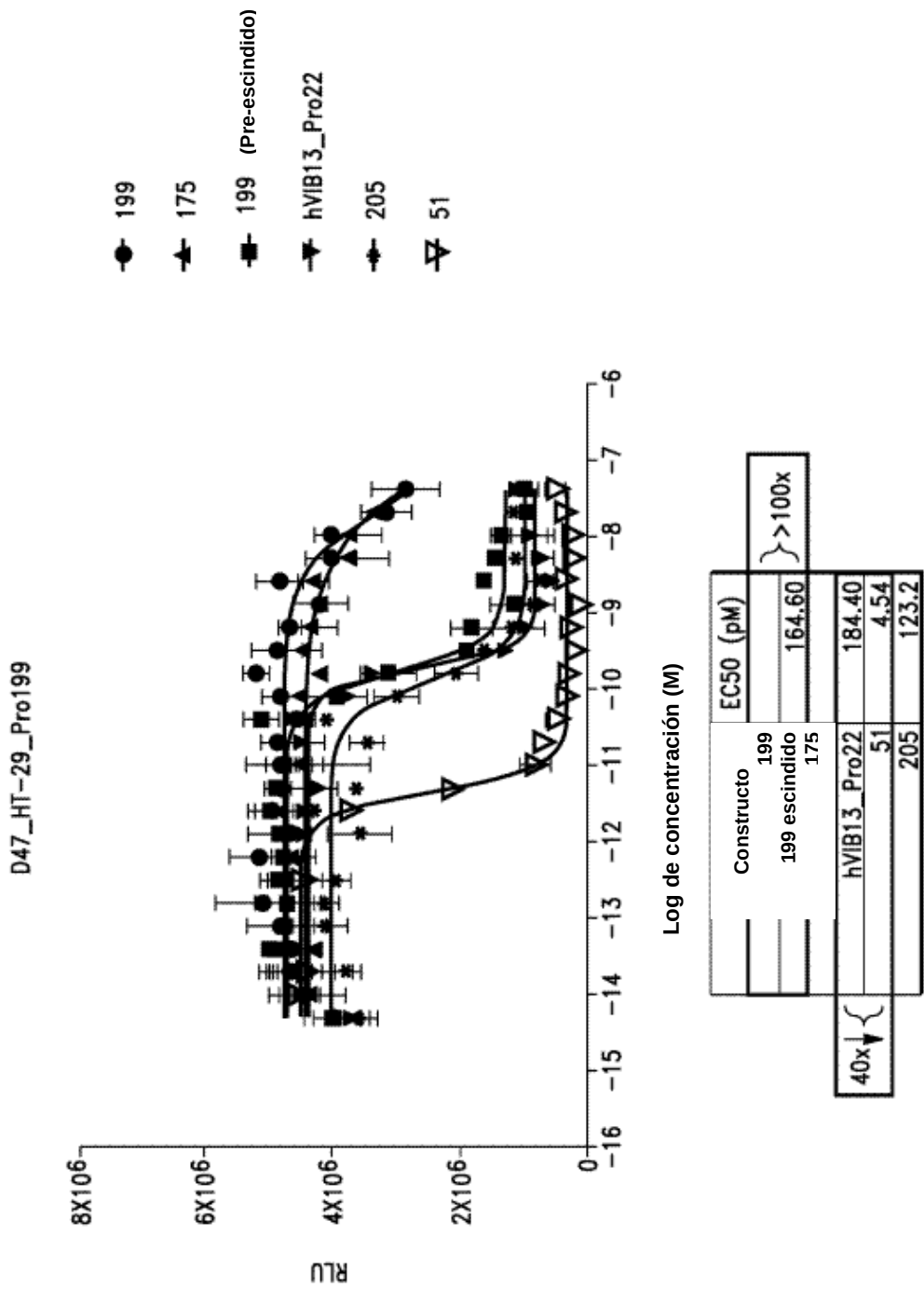


Figura 52



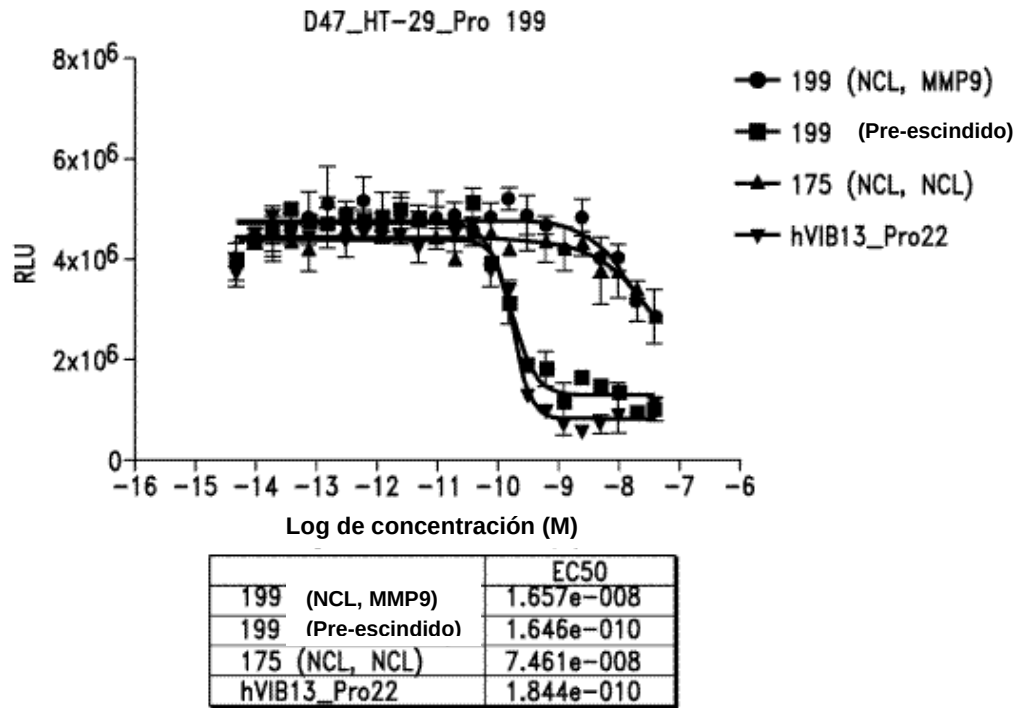


Figura 53A

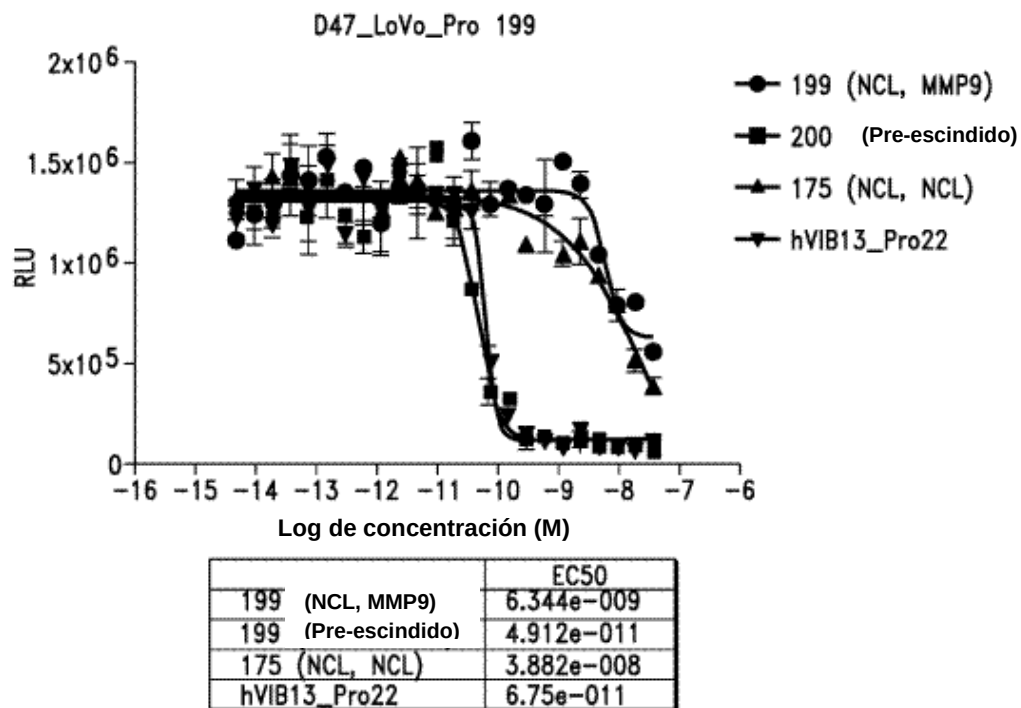


Figura 53B

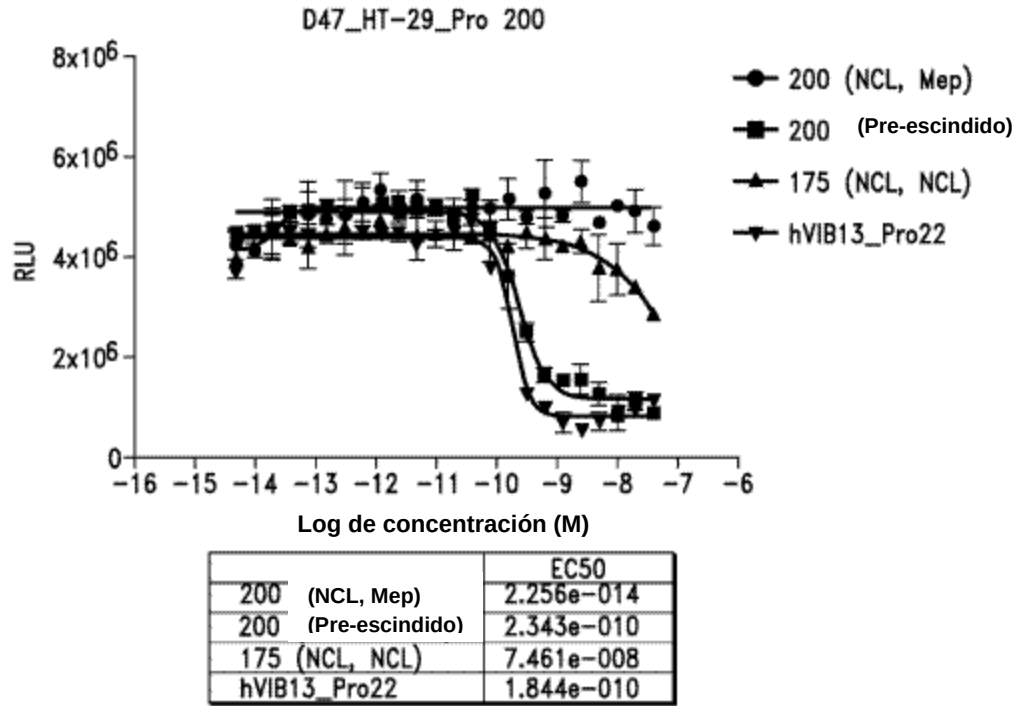


Figura 54A

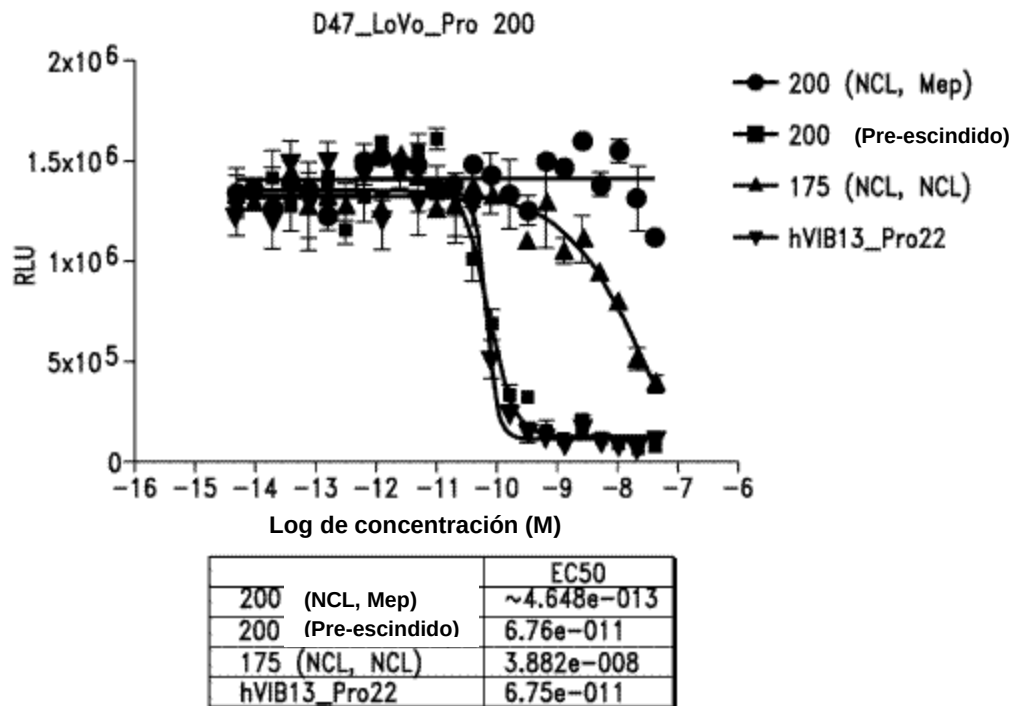


Figura 54B

Figura 55

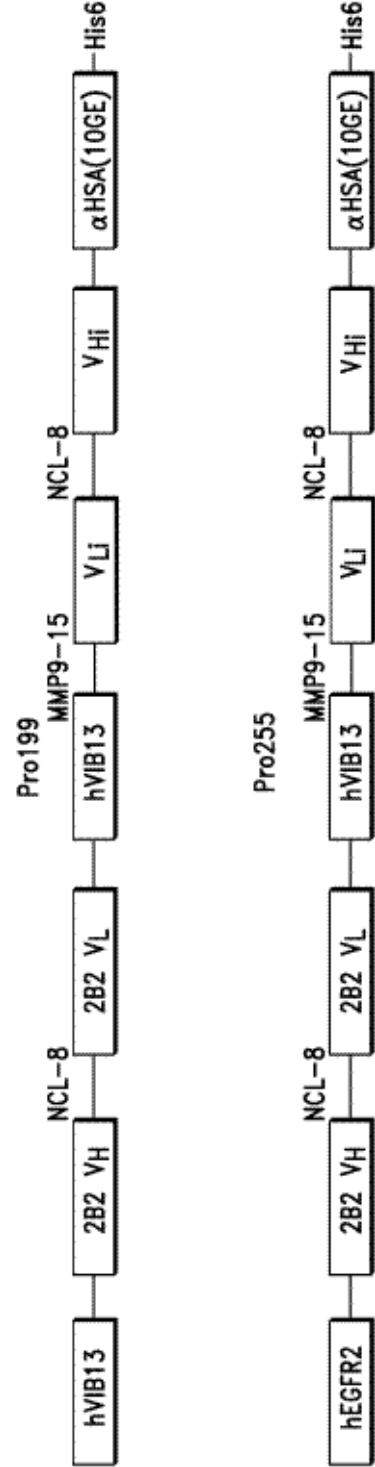
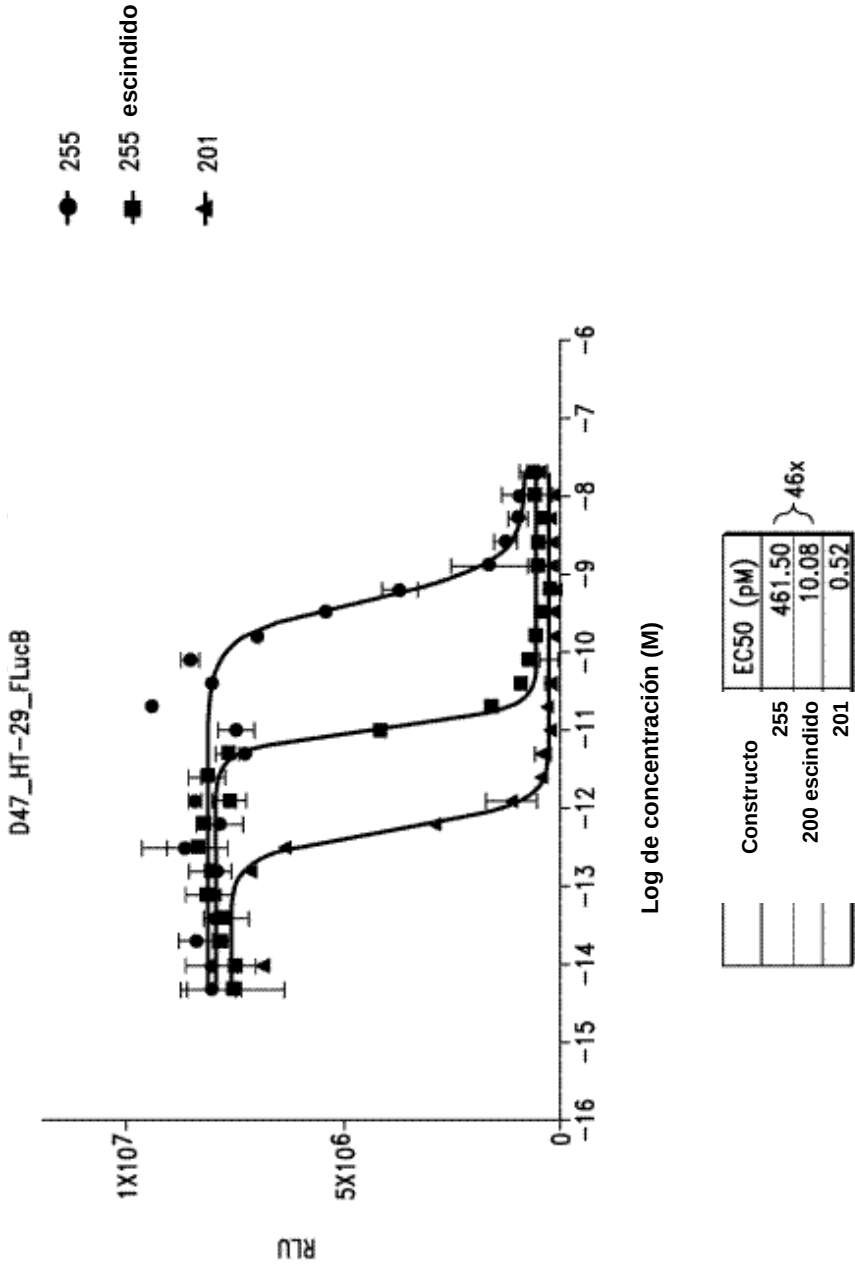


Figura 56

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



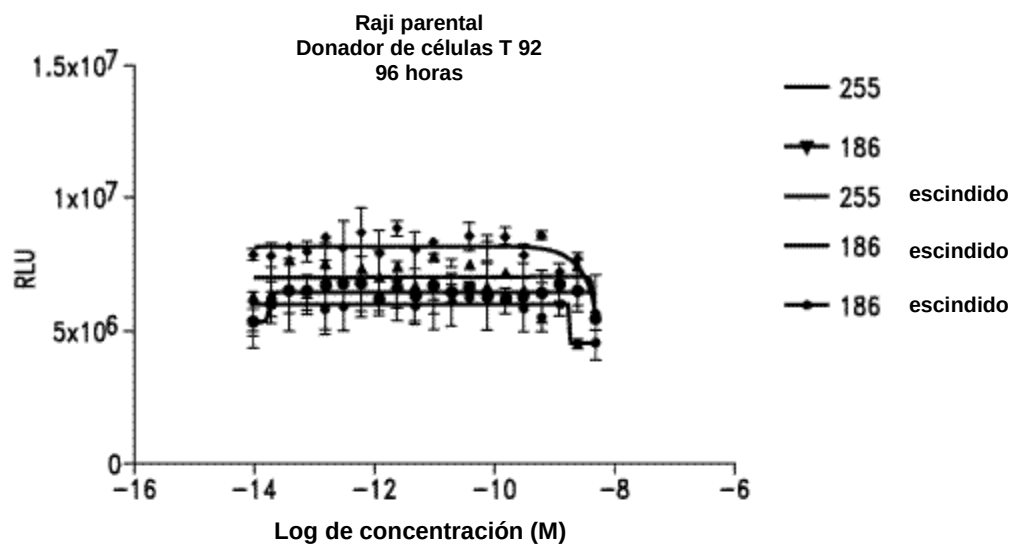


Figura 57A

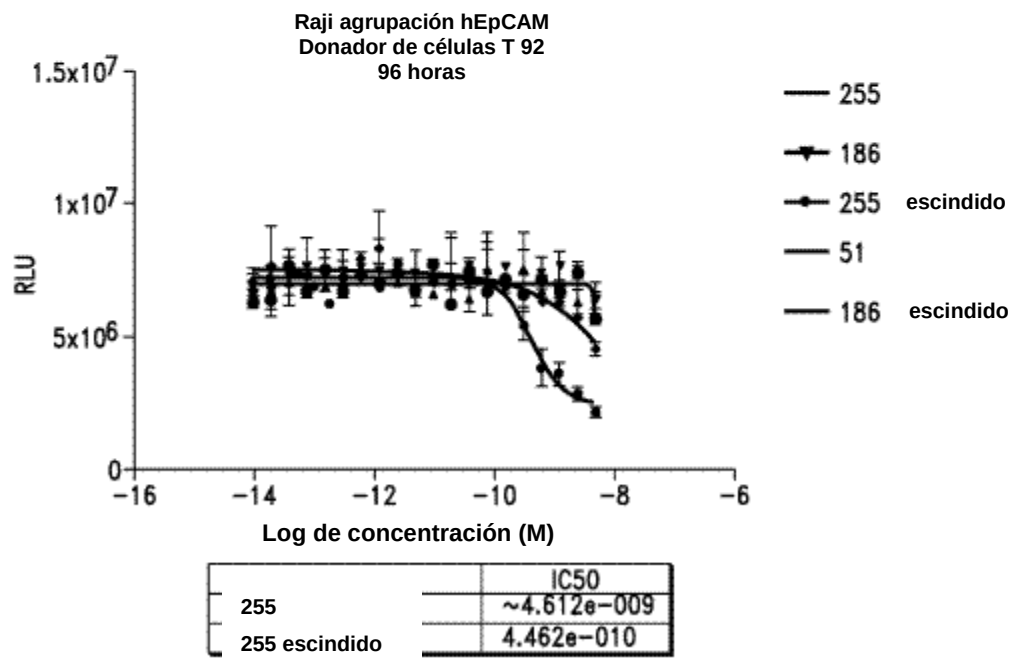


Figura 57B

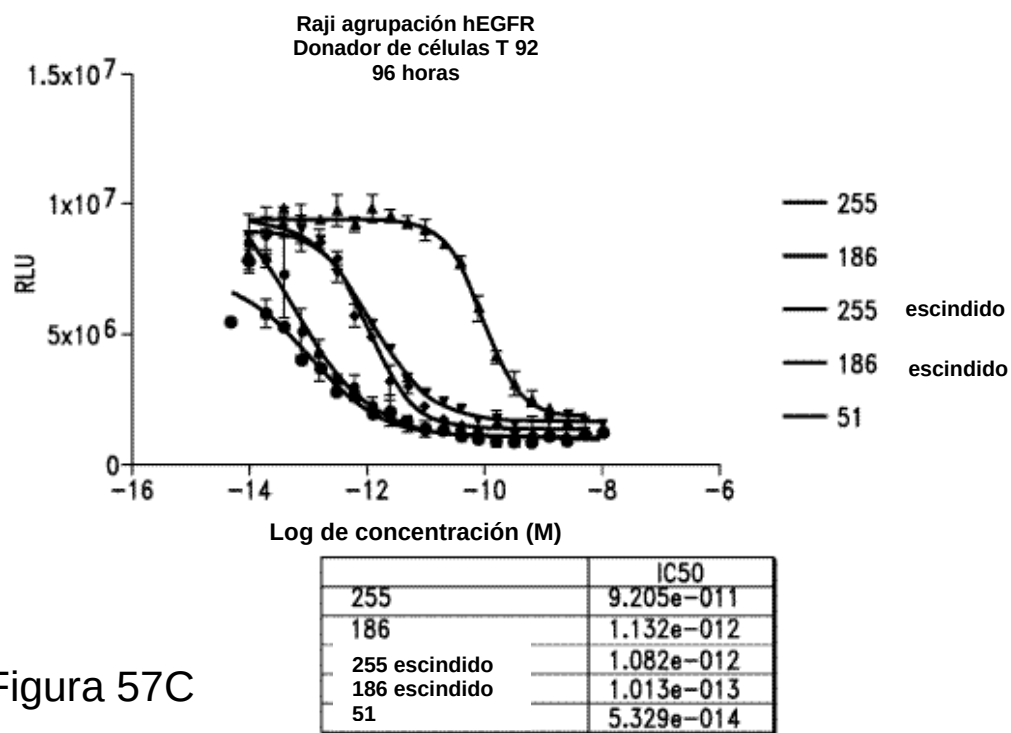


Figura 57C

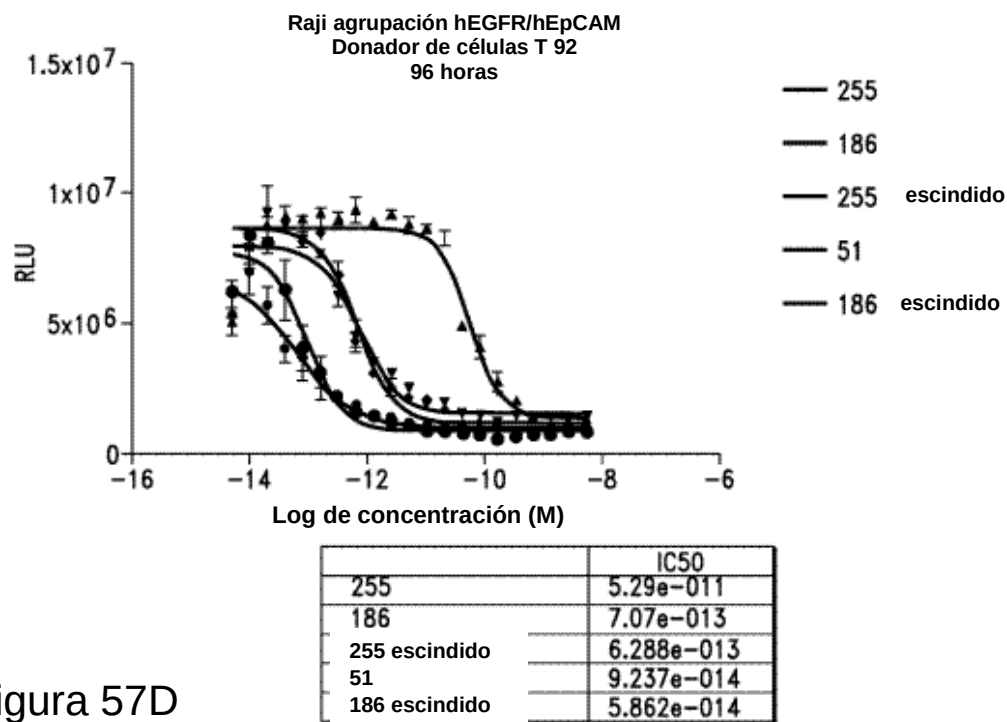
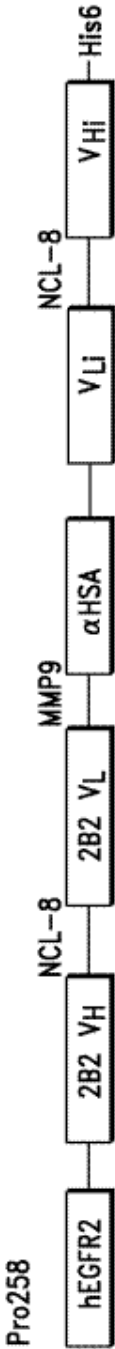


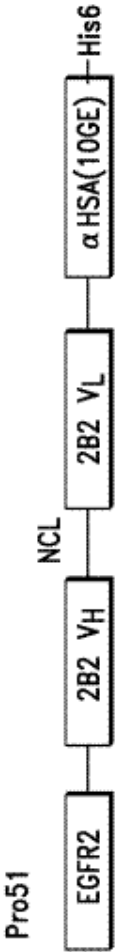
Figura 57D

Figura 58

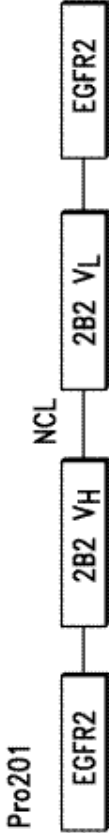
- COBRA objetivo único



- Control positivo α EGFR



- Dominio activo de Pro186



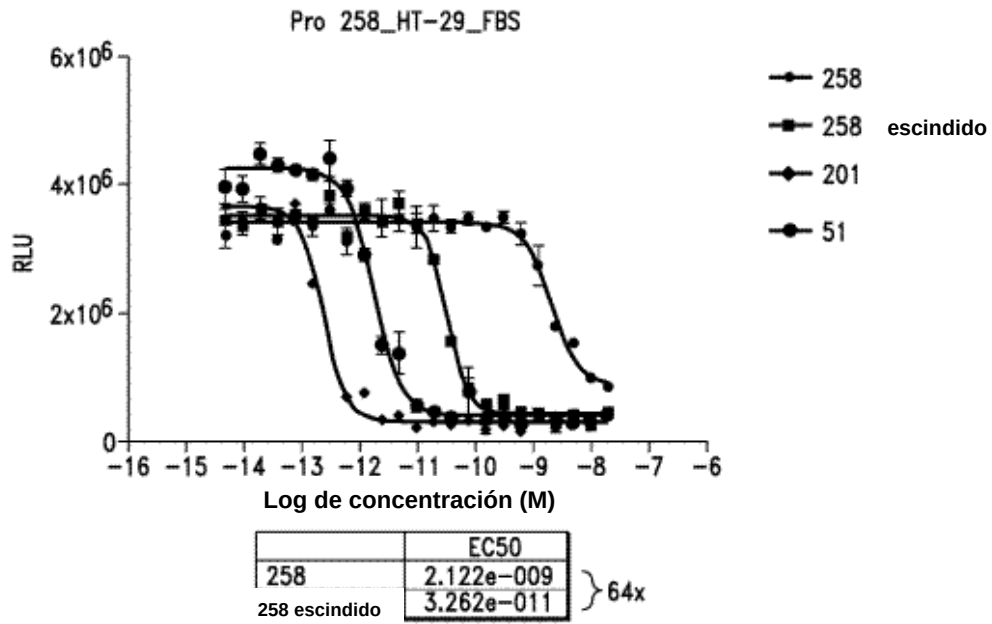


Figura 59A

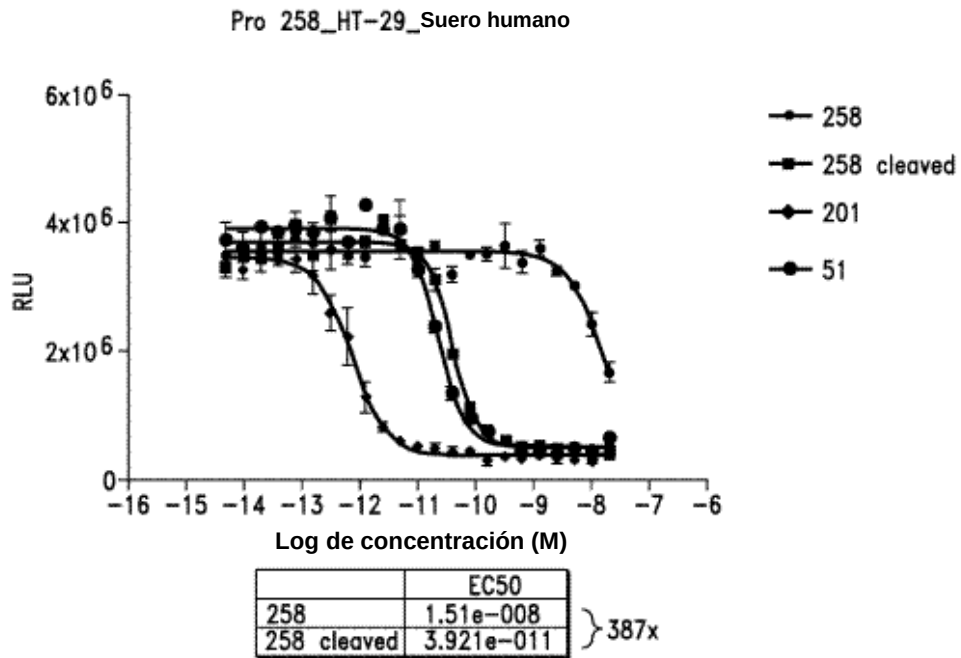


Figura 59B

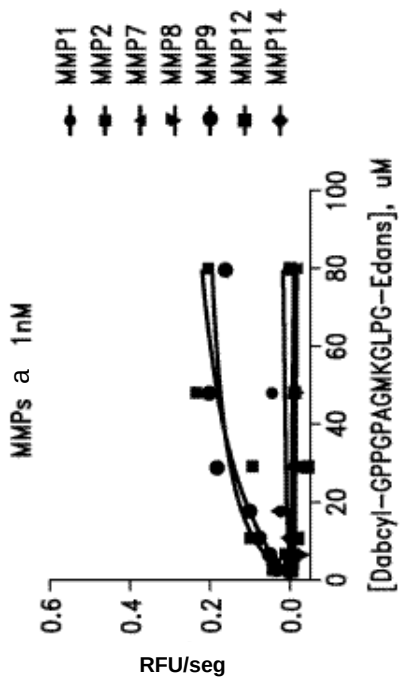


Figura 60B

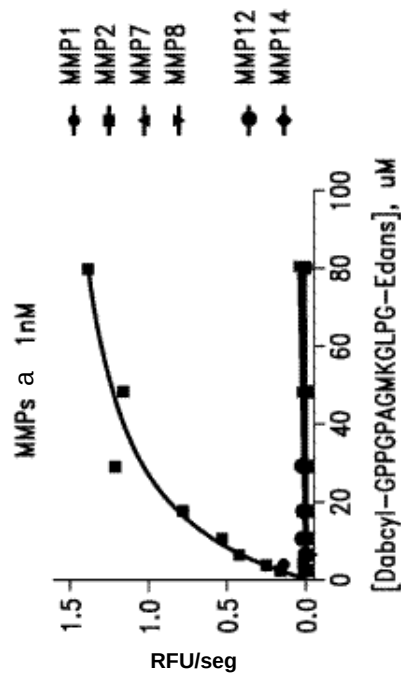


Figura 60C

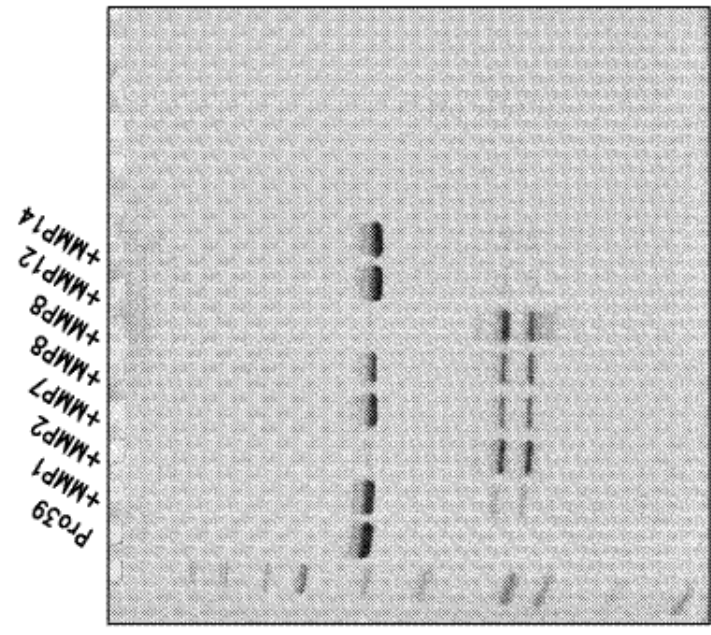


Figura 60A

## 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)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST  
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG  
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK  
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGTLTVTSS/GPAGMKGL/QTVVTQEPSTVSPGGTVTLTCAASSTGA  
VTSGNYPNWWQKPGQAPRGLIGGGTKFLVPGTPARFSGSLLGGKAALTLGVPQPEDEAE  
 YYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGGSVQTGGSLRLTCAASGR  
TSRSGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL  
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV  
 TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA  
 RFSGSLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ  
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD  
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LVTSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLASGFTFSKFGMSWVRQAPG  
 KGLEWSSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNSLRPEDTAVYYCTIGGSL  
SVSSQGTLTVTSS (SEQ ID NO:143)

Pro140b Formato 1

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST  
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG  
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK  
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGTLTVTSS/KKLADEPE/QTVVTQEPSTVSPGGTVTLTCAASSTGAV  
TSGNYPNWWQKPGQAPRGLIGGGTKFLVPGTPARFSGSLLGGKAALTLGVPQPEDEAEY  
 YCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGGSVQTGGSLRLTCAASGRT  
SRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLK  
 PEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADEPEGGG/QTVVT  
 QEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPAR  
 FSGSLLGGKAALTLGVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ  
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWWARIRSKYDYKDDD  
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LVTSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLASGFTFSKFGMSWVRQAPG  
 KGLEWSSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNSLRPEDTAVYYCTIGGSL  
SVSSQGTLTVTSS (SEQ ID NO:144)

## Figura 62B

Pro186 Formato 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST  
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG  
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK  
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTVTLTCAASSTGA  
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE  
 YYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSVQTGGSLRLTCAASGR  
TSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL  
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVV  
 TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA  
 RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ  
 LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDD  
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPG  
 KGLEWSSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL  
VSSGTTLTVSS (SEQ ID NO:145)

Pro187 Formato 2

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST  
GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQG  
 TQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK  
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTVTLTCAASSTGA  
VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE  
 YYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSVQTGGSLRLTCAASGR  
TSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSL  
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADPEGGGS/QTVV  
 TQEPSTVSPGGTVTLTCAGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPA  
 RFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQ  
 LVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDD  
DKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPG  
 KGLEWSSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIGGSL  
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  
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEY  
 YCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCAPSRRT  
FHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSL  
AEDTAVYYCAAGGATTQRATEASYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVT  
QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT  
PARFSGSLLGGKAALTL SGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQL  
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWARIRSKYDYKDDDDK  
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
LVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGL  
EWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS  
QGTTLVTVSS/HHHHHH (SEQ ID NO:147)

**Pro226 (enlazador FL aB7H3 hF12 MMP9) Formato 2**

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTS  
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGT  
LVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEW  
VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS  
YISYWAYWGQGTTLVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG  
NYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEYCTL  
WYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCEASPRTFSTY  
SMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTA  
VYYCAAGGVLAHHNYEYDYWGQGTTLVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTV  
SPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT  
PARFSGSLLG  
GKAALTL SGVQPEDEAEYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL  
VQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWARIRSKYDYKDDDDKADSVKDR  
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
LVTVSS/**GGG**  
GSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSIS  
GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT  
LVTVSS/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  
PARFSGSLLGGKAALTLSGVQPEDEAEYCYVLWYSNRWWFGGGTKLTVL/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  
PARFSGSLLGGKAALTLSGVQPEDEAEYCY  
VLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY  
AMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK  
TEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQ  
PNSLRSLSCAASGFTFSKFGMSWWRQAPGKGLEWWSSISGSGRDTLYAESVKGRFTISR  
DNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:150)

## Figura 62E

**Pro312 (enlazador FL aFOLR1 h59.3 MMP9)**

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTN  
 YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGLTVTVSS/**GGGS**  
**GGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIRSKY  
 NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW  
 GQGLTVTVSS/**GGSGGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWWQQ  
 KPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWFF  
 GGGTKLTVL/**GGSGGGGS**/QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQA  
 PGKQREWWAVTHSDYSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGI  
 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  
 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGLTVTVSS/**G**  
**GGSGGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEWWARIR  
 SKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW  
 AYWGQGLTVTVSS/**GGSGGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNW  
 VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNR  
 WFFGGGTKLTVL/**GGSGGGGS**/QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWY  
 RQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAN  
 TATWGRVFWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGTVTLTCG  
 SSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ  
 PEDEAEYYCVLWYSNRWFFGGGTKLTVL/**GGSGGGGS**/EVQLVESGGGLVQPGGSLKLS  
 CAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTISRDDSKN  
 TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGGSGGGGS**/EV  
 QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYA  
 ESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH  
 (SEQ ID NO:152)

## Figura 62F

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

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAINWSSGSTY  
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDWGQ  
GTLVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPG  
KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA  
NFGNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTG  
AVTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE  
YYCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTSCAASGR  
TSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSL  
RAEDTALYYCAAAGSAWYGTLYEYDWGQGTTLTVSS/**SGGPGPAGMKGLPGS**/QTVV  
TQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPA  
RFGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQ  
LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKLEWVARIRSKYDYKDDDD  
KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLV  
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG  
LEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS  
QGTLVTVSS/HHHHHH (SEQ ID NO:153)

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

QVQLVESGGGLVQPGGSLTSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV  
YADSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLLRSSPGATTPYWGQGTTLTV  
SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKLEWV  
ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI  
SYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNY  
PNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY  
SNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGM  
GWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALY  
YCAAAGSAWYGTLYEYDWGQGTTLTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTV  
SPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLG  
GKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGL  
VQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKLEWVARIRSKYDYKDDDDKADSVKDR  
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSS/**GGG**  
**GSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKLEWSSIS  
GSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTV  
SS/HHHHHH (SEQ ID NO:154)

## Figura 62G

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

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

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

QVQLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKREFVSGISWRGDSY  
GYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQ  
GLTVTVSS/GGGSGGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK  
GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGA  
VTSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEY  
YCTLWYSNRWWFGGGTKLTVL/GGGSGGGGS/QVQLVESGGGLVQPGGSLRLSCAASGFT  
VSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT  
AVYVCNRNFDRIYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVT  
LTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTL  
SGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGGS/EVQLVESGGGLVQP GGS  
LKLSCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDD  
SKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS  
/EVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTL  
YAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHH  
H (SEQ ID NO:156)

## Figura 62H

### Pro393 (enlazador Pro186 S9)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFEVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFRQAPGKEREFEVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GARLQSAAPAGLKGAG/QTVVT  
 QEPSTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL  
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL  
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNLSRPEDTAVYYCTIGGSLSVSS  
 QGTTLTVSS/HHHHHH (SEQ ID NO:157)

### Pro394 (enlazador Pro186 ST14(MV))

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFEVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFRQAPGKEREFEVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSFTRQARVVGGGS/QTVVT  
 QEPSTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL  
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPNSLRSLSCAASGFTFSKFGMSWWRQAPGKGL  
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLYLQMNLSRPEDTAVYYCTIGGSLSVSS  
 QGTTLTVSS/HHHHHH (SEQ ID NO:158)

## Figura 62l

**Pro395 (enlazador Pro186 CatS)**

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGLTVTVSS/**GGGSGGGG**/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGG**/QVKLEESGGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSARLQSAAPGGG**/QTVVT  
 QEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGG**/EVQL  
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
 ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV  
 VSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGL  
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSS  
 QGTLTVTVSS/HHHHHH (SEQ ID NO:159)

**Pro396 (enlazador Pro186 MMP9v)**

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGLTVTVSS/**GGGSGGGG**/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGG**/QVKLEESGGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GSGGPGPAGMHGLPGG**/QTVV  
 TQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGG**/EVQ  
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDD  
 KADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV  
 TVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWWRQAPGKG  
 LEWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSS  
 QGTLTVTVSS/HHHHHH (SEQ ID NO:160)

## Figura 62J

**Pro429 (enlazador Pro186 Meprina/granzimaB)**

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

**Pro430 (enlazador Pro186 MMP9-2)**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGTTLTVSS/**GGGSGGGS**/QTVVTQEPLSLTVSPGGTVTLTCASSTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGPGPAGLKGAPGS**/QTVVTQE  
 PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARFS  
 GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVE  
 SGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKA  
 DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV  
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGLE  
 WSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIGGSLSVSSQ  
 GTLTVTVSS/HHHHHH (SEQ ID NO:162)

## Figura 62K

### Pro431 (enlazador Pro186 ST14(MS))

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST  
GYADSVKGRFTISRDNANKNTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG  
LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV  
TSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY  
CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTCAASGRTS  
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANKNTVDLQMNSLKP  
EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSLSGRSDNHGGGS/QTVVT  
QEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPAR  
FSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL  
VESGGGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTV  
VSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGL  
EWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS  
QGTTLTVSS/HHHHHH (SEQ ID NO:163)

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

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST  
GYADSVKGRFTISRDNANKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG  
TLTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGK  
GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGA  
VTSGNYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY  
YCTLWYSNRWWFGGGTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGNSLRSL  
CAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNAKTTLYL  
QMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPG  
GTVTLTCSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKA  
ALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQP  
GGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS  
RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVSS/HHHHHH  
(SEQ ID NO:164)

## Figura 62L

**Pro221**

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

**Pro222**

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

## Figura 62M

**Pro223**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFQAPGKEREFSVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNTWSAGKGGGS/QTVVT  
 QEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL  
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
 ADSVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGL  
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNLSRPLEDTAVYYCTIGGSLSVSS  
 QGTTLTVSS/HHHHHH (SEQ ID NO:167)

**Pro224**

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFQAPGKEREFSVSGISWRGDST  
 GYADSVKGRFTISRDNANTVDLQMNLSKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGT  
 QVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCAASSTGAV  
 TSGNYPNWWQQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLGSGVQPEDEAEYY  
 CTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTS  
 RSYGMGWFQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNLSK  
 EDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNTWSAGKGGGS/QTVVT  
 QEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT  
 PARFSGSLLGGKAALTLGSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQL  
 VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDK  
 ADSVKDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT  
 LTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWWRQAPGKGL  
 EWWSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNLSRPLEDTAVYYCTIGGSLSVSS  
 QGTTLTVSS/HHHHHH (SEQ ID NO:168)

## Figura 62N

### Pro254

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

### Pro255

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFQAPGKEREFEVSGISWRGDST  
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG  
 TLVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGK  
 GLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
 FGNSYISYWAYWGQGTTLVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASSTGA  
 VTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY  
 YCTLWYSNRWWFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLTSCAASGTG  
 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/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKG  
 LEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF  
 GNSYISYWAYWGQGLTVTVSS/**GGGSGGGGSGGGGS**/QTVVTQEPSLTVSPGGTVTLT  
 CASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLGVSQ  
 PEDEAEYYCTLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGSVQTGGSLRLT  
 CAASGRTSRSYGMGWFRQAPGKEREFSVSGISWRGDSTGYADSVKGRFTISRDNKNTVD  
 LQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**SGGPGPAGMKGLPG**  
**S**/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDD  
 KGTPARFSGSLLGGKAALTLGVSQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGG**  
**GS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYD  
 YKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYW  
 GQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR  
 QAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIG  
 GSLSVSSQGLTVTVSS/HHHHH (SEQ ID NO:171)

**Pro356**

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFSVAINWSSGSTY  
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQ  
 GTLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPG  
 KGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA  
 NFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCASSTG  
 AVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLGVSQPEDEAE  
 YYCTLWYSNRWWFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRL  
 SCAASGFTFSKFGMSWVRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDNKNTLY  
 LQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG  
 GTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA  
 ALTLGVSQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPG  
 GSKLSCAASGFTFNKYAMNWWRQAPGKGLEWWARIRSKYDYKDDDDKADSVKDRFTIS  
 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

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYAD  
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGG  
GS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNN  
YATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ  
GTLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWWQKP  
GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWWFGG  
GTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW  
VRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCT  
IGGSLSVSSQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG  
NYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYYC  
VLWYSNRWWFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNK  
YAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK  
TEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/HHHHHH (SEQ ID NO:175)

## Figura 62R

**Pro432**

QVQLVESGGGLVQPGGSLTSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV  
 YADSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCNLLRSPGATTPYWGQGLTVTV  
 SS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQAPGKGLEWW  
 ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI  
 SYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNY  
 PNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY  
 SNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAM  
 GWFRQAPGKEREFVWAINWSSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY  
 YCAAGYQINSGNYNFKDYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTV  
 SPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSL  
 LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGG  
 GLVQPGGSLKLSCAASGFTFNKYAMNWRQAPGKGLEWWARIRSKYDYKDDDDKADSVK  
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**G**  
**GGGSGGGS**/EVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWS  
 SISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV  
 TVSS/HHHHHH (SEQ ID NO:176)

**Pro448**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD  
 SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/**GGGSGG**  
**GS**/QVQLVESGGGVWRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG  
 DSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYW  
 GQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWRQ  
 APGKGLEWWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV  
 RHANFGNSYISYWAYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGT  
 VTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAAL  
 TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP  
 GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWWSSISGSGRDTLYAESVKGRFTISRDN  
 AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHHH (SEQ ID NO:177)

## Figura 62S

**Pro449**

QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDST  
 GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQG  
 TLTVTVSS/**GGGGS**GGGS/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTP  
 GNREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY  
 WGQGTTLTVTVSS/**GGGGS**GGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWWR  
 QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC  
 VRHANFGNSYISYWAYWGQGTTLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPG  
 GTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKA  
 ALTLGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGGS**GGGS/EVQLVESGGGLV  
 QPGNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISR  
 DNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVTVSS/HHHHHH (SEQ ID  
 NO:178)

**Pro450**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYAD  
 SVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTTLTVTVSS/**GGGGS**  
**GGGS**/QVKLVESGGGVVRPGGSLTLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRG  
 DSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYW  
 GGQGTTLTVTVSS/**GGGGS**GGGS/QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQ  
 QKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLGVQPEDEAEYYCTLWYSNRWW  
 FGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA  
 MNWWRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE  
 DTAVYYCVRHGNFGNSYISYWAYWGQGTTLTVTVSS/**GGGGS**GGGS/EVQLVESGGGLVQP  
 GNSLRLSCAASGFTFSKFGMSWWRQAPGKGLEWSSISGSGRDTLYAESVKGRFTISRDN  
 AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTTLTVTVSS/HHHHHH (SEQ ID NO:179)

## Figura 62T

### Pro451

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

### Pro479

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGST  
 VYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQG  
 TLVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWRQAPGK  
 GLEWARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN  
 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/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWWRQAPGKGLEW  
 VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS  
 YISYWAYWGQGLTVTVSS/**GGGSGGGG**/QTVVTQEPLTVSPGGTVTLTCASSTGAVTSG  
 NYPNWWQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL  
 WYSNRWWFGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTY  
 HMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT  
 AVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPL  
 TVSPGGTVTLTCGSSTGAVTSGNYPNWWQQKPGQAPRGLIGDYKDDDDKGT PARFSGS  
 LLGGKAALTLSGVQPEDEAEYYCVLWYSNRWWFGGGTKLTVL/**GGGSGGGG**/EVQLVESG  
 GGLVQPGGSLKLSAASGFTFNKYAMNWWWRQAPGKGLEWWARIRSKYDYKDDDDKADSV  
 KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/  
**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLS AASGFTFSKFGMSWWRQAPGKGLEWW  
 SSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGL  
 TVTVSS/HHHHHH (SEQ ID NO:182)

### **Pro495**

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