

Figure 2

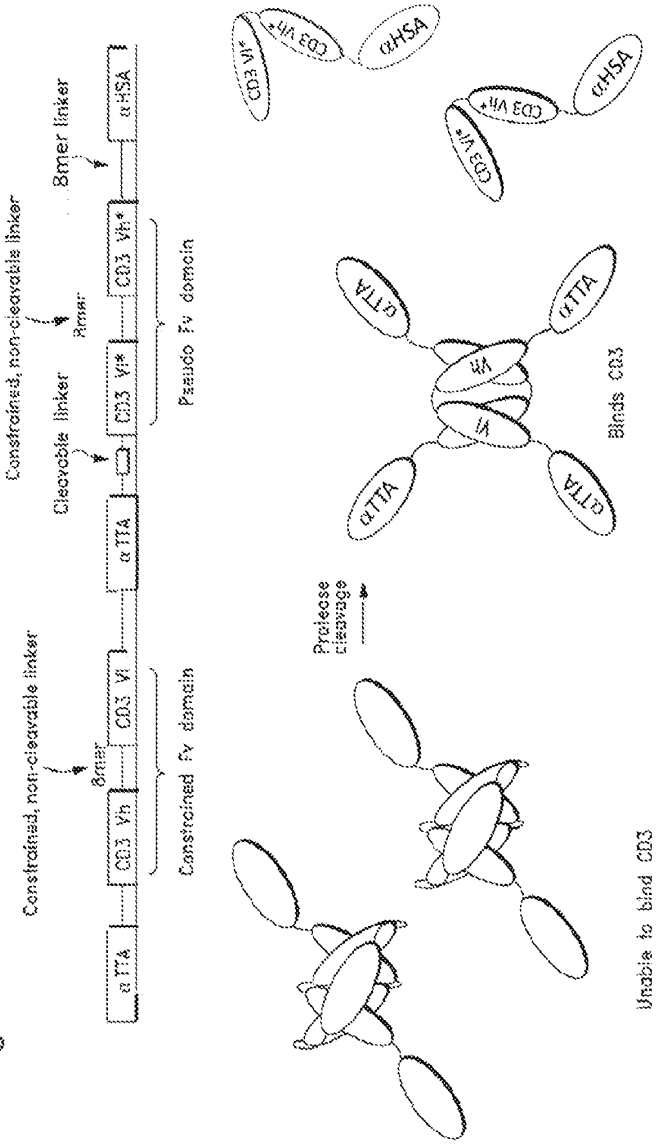


Figure 3A

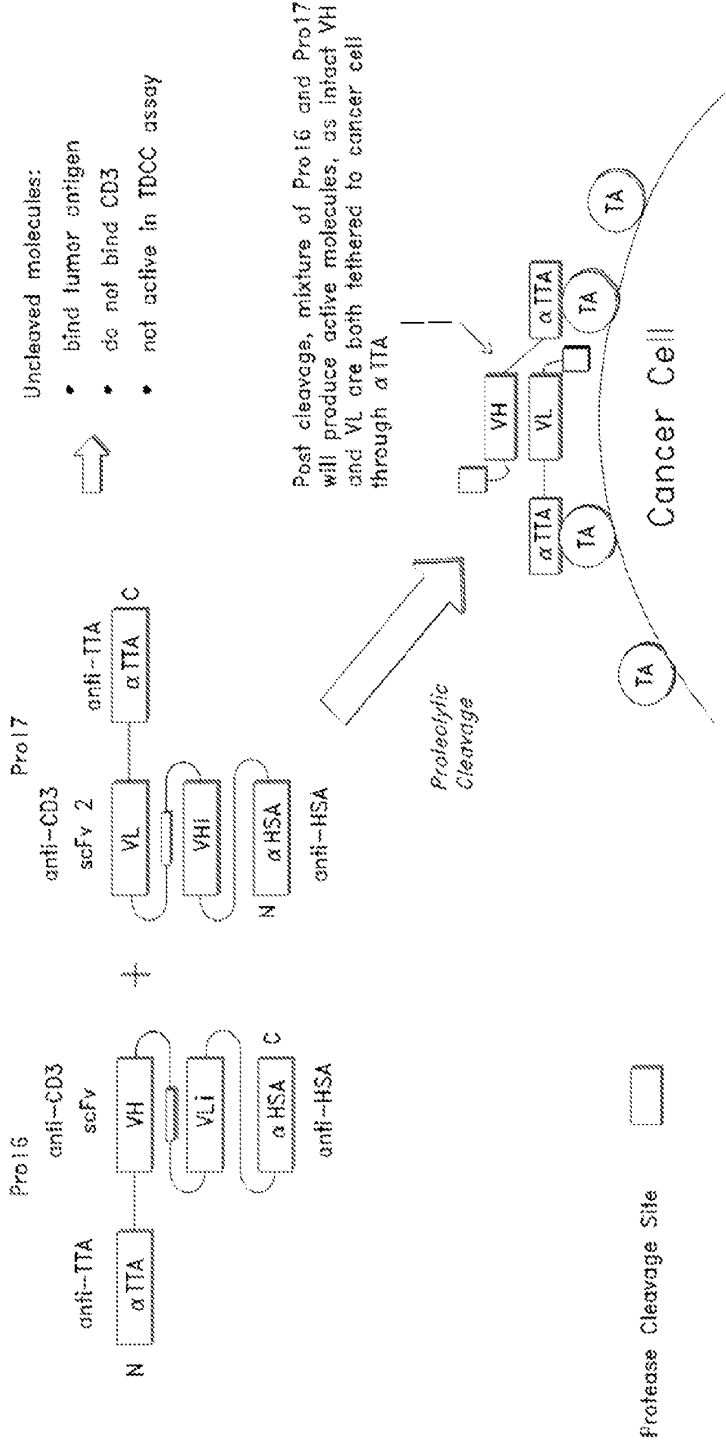


Figure 3B

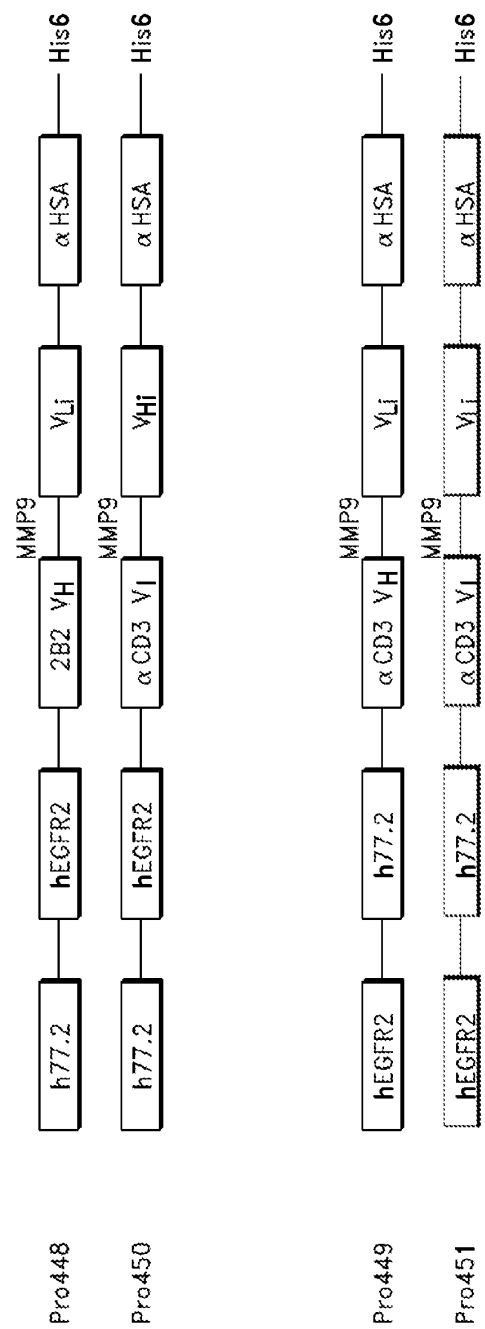


Figure 4

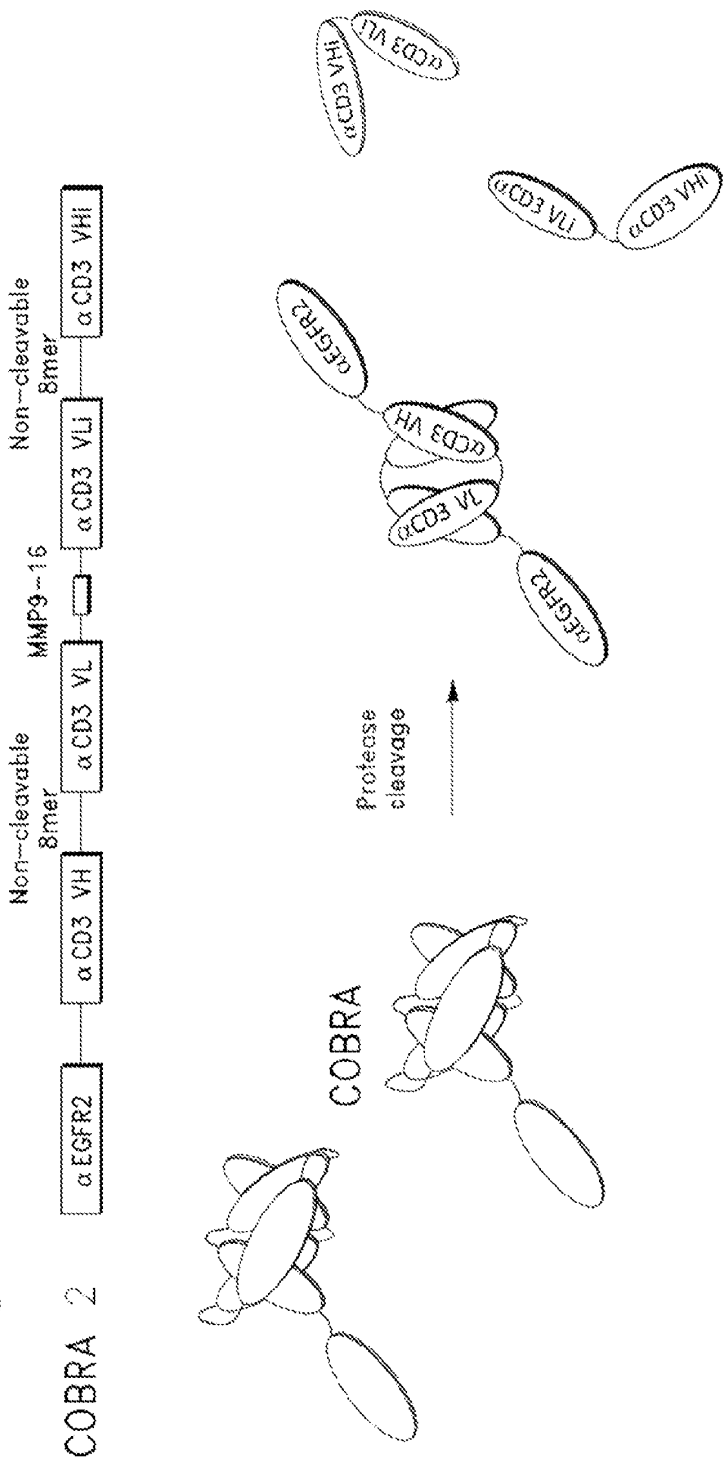


Figure 5A

 α EGFR1

EVQLVESGGGLVQAGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTY**
YADSVKGRFTISRDNKNTMYLQMNSLPEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WG
QGTQVTSS (SEQ ID NO:1)

sdCDR1 **GRTFSSYAMG** (SEQ ID NO:2)

sdCDR2 **INWSSGSTYADSVKG** (SEQ ID NO:3)

sdCDR3 **GYQINSGNYNFKDYEYDY** (SEQ ID NO:4)

 α EGFR2

QVKLEESGGGSGVQTGGSLRLTCAAS**GRTSRSYGMG**WFRQAPGKEREFV**SGISWRGDST**
GYADSVKGRFTISRDNKNTVDLQMNSLPEDTAIYYCAA**AAGSAWYGTLYEYDY**WGQ
TQVTSS (SEQ ID NO:5)

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

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

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

h α EGFR1

EVQLVESGGGLVQPGGSLRLSCAAS**GRTFSSYAMG**WFRQAPGKEREFVVA**INWSSGSTY**
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAA**GYQINSGNYNFKDYEYDY**WGQ
GTLVTSS (SEQ ID NO:9)

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

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

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

aEGFR2a sdAb

EVQLVESGGGVVRPGGSLRLSCAAS**GRTSRSYGMG**WFRQAPGKEREFV**SGISWRGDST**
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAA**AAGSAWYGTLYEYDY**WGQ
TLVTSS (SEQ ID NO:13)

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

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

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

h α EGFR2d

QVKLVESGGGVVRPGGSLTLSCAAS**GRTSRSYGMG**WFRQAPGKEREFV**SGISWRGDST**
GYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAA**AAGSAWYGTLYEYDY**WGQ
TLVTSS (SEQ ID NO:17)

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

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

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

Figure 5B

αFOLR1 h77-2

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGT LVT VSS (SEQ ID NO:21)

sdCDR1 GFTVSNSVMA (SEQ ID NO:22)

sdCDR2 IINSIGITNYADSVKG (SEQ ID NO:23)

sdCDR3 NFDRIY (SEQ ID NO:24)

αFOLR1 h59.3

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWWAVTHSDYSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYYGIDYWGQGT LVT VSS (SEQ ID NO:25)

sdCDR1 GNTFSISAMG (SEQ ID NO:26)

sdCDR2 VTHSDYSTNYADSVKG (SEQ ID NO:27)

sdCDR3 YGIDY (SEQ ID NO:28)

αFOLR1 h22-4

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNANNTATWGRVFWGQGT LVT VSS (SEQ ID NO:29)

sdCDR1 GTTFSRDVMG (SEQ ID NO:30)

sdCDR2 IISRGGSTNYADSVKG (SEQ ID NO:31)

sdCDR3 NTATWGRV (SEQ ID NO:32)

αB7H3 hF7

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGT LVT VSS (SEQ ID NO:33)

sdCDR1 RRTFHTYHMG (SEQ ID NO:34)

sdCDR2 VINWSGGSTVYADSVKG (SEQ ID NO:35)

sdCDR3 GGATTQRATEASYDY (SEQ ID NO:36)

Figure 5C

αB7H3 hF12

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTS**
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGT LVT
VSS (SEQ ID NO:37)

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

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

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

αB7H3 hF12 (N57Q)

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGQTS**
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGT LVT
VSS (SEQ ID NO:41)

sdCDR1 **PRTFSTYSMA** (SEQ ID NO:42)

sdCDR2 **AINWSGGQTSYADSVKG** (SEQ ID NO:43)

sdCDR3 **GGVLAHHNYEYDY** (SEQ ID NO:44)

αB7H3 hF12 (N57E)

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGETS**
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGT LVT
VSS (SEQ ID NO:45)

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

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

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

αB7H3 hF12 (N57D)

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGDTS**
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNYEYDY**WGQGT LVT
VSS (SEQ ID NO:49)

sdCDR1 **PRTFSTYSMA** (SEQ ID NO:50)

sdCDR2 **AINWSGGDTSYADSVKG** (SEQ ID NO:51)

sdCDR3 **GGVLAHHNYEYDY** (SEQ ID NO:52)

Figure 5D

αB7H3 hF12 (S59A)

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTA
YADSVKGRRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAAGGVLAHHNYEYDYWGQGT LVT
 VSS (SEQ ID NO:53)

sdCDR1 PRTFSTYSMA (SEQ ID NO:54)

sdCDR2 AINWSSGGNTAYADSVKG (SEQ ID NO:55)

sdCDR3 GGVLAHHNYEYDY (SEQ ID NO:56)

αB7H3 hF12 (S59Y)

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTY
YADSVKGRRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAAGGVLAHHNYEYDYWGQGT LVT
 VSS (SEQ ID NO:57)

sdCDR1 PRTFSTYSMA (SEQ ID NO:58)

sdCDR2 AINWSSGGNTYYADSVKG (SEQ ID NO:59)

sdCDR3 GGVLAHHNYEYDY (SEQ ID NO:60)

αEpCAM h13

QVQLVESGGGLVQPGGSLTLSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTV
YADSVKGRRFTISRDN SKNTLYLQMNSLR PEDTAVYYCNLLRSSPGATTPYWGQGT LVT
 VSS (SEQ ID NO:61)

sdCDR1 GTGSIFSINLMG (SEQ ID NO:62)

sdCDR2 RITSGDSTVYADSVKG (SEQ ID NO:63)

sdCDR3 LLRSSPGATTPY (SEQ ID NO:64)

αEpCAM h23

QVQLVESGGGLVQPGGSLTLSCVISGSFSALWAMRWYRQAPGQQRELVASSRGGTTSYA
DSVKGRRFTISRDN SKNTLYLQMNSLR PEDTAVYYCNAIDGHLAYWGQGT LVT
 VSS (SEQ ID NO:65)

sdCDR1 GSFSALWAMR (SEQ ID NO:66)

sdCDR2 SSRGGTTSYADSVKG (SEQ ID NO:67)

sdCDR3 IDGHLAY (SEQ ID NO:68)

Figure 5E

acEpCAM hVIB665

QVQLLESGGGLVQPGGSLRLSCAAS**GRTFSDYDMG**WFRQGPGKEREFFVA**AISWSSGGHT**
NYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**DLRFTGGDTTTPETYDY**WGQ
 GTLVTVSS (SEQ ID NO:69)

sdCDR1 **GRTFSDYDMG** (SEQ ID NO:70)

sdCDR2 **AISWSSGGHTNYADSVKG** (SEQ ID NO:71)

sdCDR3 **DLRFTGGDTTTPETYDY** (SEQ ID NO:72)

acEpCAM hVIB666

QVQLVESGGGLVQPGGSLRLSCAAS**GRTL DNYDMG**WFRQGPGKEREFFVA**AISWSSGGST**
DYAYSVTGRFTISRDN AKNSLYLQMNSLRAEDTALYYCAA**DLRFTGGDTMTPEYDY**WGQ
 GTLVTVSS (SEQ ID NO:73)

sdCDR1 **GRTL DNYDMG** (SEQ ID NO:74)

sdCDR2 **AISWSSGGSTDYAYSVTG** (SEQ ID NO:75)

sdCDR3 **DLRFTGGDTMTPEYDY** (SEQ ID NO:76)

aTrop2 hVIB557

QVQLLESGGGLVQPGGSLRLSCAAS**GRTFSSQSMG**WFRQAPGKEREFFV**SAISWTGANPT**
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**DTSGGSYYYERATAETSYDY**W
 QGTLTVSS (SEQ ID NO:77)

sdCDR1 **GRTFSSQSMG** (SEQ ID NO:78)

sdCDR2 **AISWTGANPTYADSVKG** (SEQ ID NO:79)

sdCDR3 **DTSGGSYYYERATAETSYDY** (SEQ ID NO:80)

aTrop2 hVIB565

QVQLLESGGGLVQPGGSLRLSCAAS**GFTFDYYAIG**WFRQAPGKEREGV**SCISSSHGSTYY**
ADSVKGRFTISRDN SKNTVYLQMNSLRAEDTAVYYCAT**AGDGGDYHCSGLVDYGM DY**WG
 KGLTVTVSS (SEQ ID NO:81)

sdCDR1 **GFTFDYYAIG** (SEQ ID NO:82)

sdCDR2 **CISSSHGSTYYADSVKG** (SEQ ID NO:83)

sdCDR3 **AGDGGDYHCSGLVDYGM DY** (SEQ ID NO:84)

Figure 5F

aTrop2 hVIB575

QVQLLESGGGLVQPGGSLRLSCLAS**GRTVGRTAMG**WFRQPPGKEREFFV**ATISWAGGTTY**
YADFVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA**SEPYS DYDP SGMVY**WGKGLTV
 TVSS (SEQ ID NO:85)

sdCDR1 **GRTVGRTAMG** (SEQ ID NO:86)

sdCDR2 **TISWAGGTTYADFVKG** (SEQ ID NO:87)

sdCDR3 **SEPYS DYDP SGMVY** (SEQ ID NO:88)

aTrop2 hVIB578

QVQLLESGGGLVQPGGSLRLSCAASGRTFGRAAMGWFRQPPGKEREFATTISWSGSNTY
YADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAASEPYSDYDPSGMVYWGKGTLV
TVSS (SEQ ID NO:89)

sdCDR1 GRTFGRAAMG (SEQ ID NO:90)
sdCDR2 TISWSGSNTYYADSVKG (SEQ ID NO:91)
sdCDR3 SEPYSDYDPSGMVY (SEQ ID NO:92)

aTrop2 hVIB609

QVQLLESGGGLVQPGGSLRLSCALSGLTFTNYPMAWFRQPPGQEREFVADDMSWSGTNTY
YADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGWPYSGTGRSTTDYTYWGQG
TLVTVSS (SEQ ID NO:93)

sdCDR1 LTFTNYPMA (SEQ ID NO:94)
sdCDR2 DMSWSGTNTYYADSVKG (SEQ ID NO:95)
sdCDR3 GWPYSGTGRSTTDYTY (SEQ ID NO:96)

aTrop2 hVIB619

QVQLLESGGGLVQPGGSLRLSCAASGRSFSRYGMGWLRQAPGKERELVASSISWSGHSTY
YADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAESLPYESGSPRLTDFASWGQG
TLVTVSS (SEQ ID NO:97)

sdCDR1 GRSFSRYGMG (SEQ ID NO:98)
sdCDR2 SISWSGHSTYYADSVKG (SEQ ID NO:99)
sdCDR3 ESLPYESGSPRLTDFAS (SEQ ID NO:100)

aCA9 hVIB456 sdAb

QVQLVESGGGLVQPGGSLRLSCAASGSALIINAMGWYRQAPGKQRELVATVTRSGRTNY
ADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNVALWIADGEYDYWGQGTTLVTVSS
(SEQ ID NO:101)

sdCDR1 GSALIINAMG (SEQ ID NO:102)
sdCDR2 TVTRSGRTNYADSVKG (SEQ ID NO:103)
sdCDR3 ALWIADGEYDY (SEQ ID NO:104)

Figure 5G

aCA9 hVIB476 sdAb

QVQLVESGGGLVQPGGSLRLSCAASGNIFIINVMGWYRQAPGKQRELVATITNGGRTHYA
DSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNANHIELGDYWGQGT LVT VSS (SEQ
ID NO:105)

sdCDR1 GNIFIINVMG (SEQ ID NO:106)

sdCDR2 TITNGGRTHYADSVKG (SEQ ID NO:107)

sdCDR3 NHIELGDY (SEQ ID NO:108)

aCA9 hVIB407 sdAb

QVQLVESGGGLVQPGGSLRLSCTASGIIFSVYDMGWYRQTPGKQREFVARITAGGGTYLT
DSVKGRRFTISRDN SKNTLYLQMNSLRAEDTGVYYCNAAWIGDDYWGQGT LVT VSS (SEQ
ID NO:109)

sdCDR1 GIIFSVYDMG (SEQ ID NO:110)

sdCDR2 RITAGGGTYLTDSVKG (SEQ ID NO:111)

sdCDR3 AWIGDDY (SEQ ID NO:112)

aCA9 hVIB445 sdAb

QVQLVESGGGLVKPGGSLRLSCAASGITFNLHAMRWYRRAPGKQRELVAYISARDWTNY
ADSVKGRRFTISRDN AKNSLYLQMNSLRAEDTAVYYCNTDLVGEDYWGRGT LVT VSS (SEQ
ID NO:113)

sdCDR1 GITFNLHAMR (SEQ ID NO:114)

sdCDR2 YISARDWTNYADSVKG (SEQ ID NO:115)

sdCDR3 DLVGEDY (SEQ ID NO:116)

αLyPD3 h787 sdAb

QVQLLES GGGLVQP GGSLRLSCAASGFTLDYYAIGWFRQAPGKEHEAVSCISSSDGSTYY
ADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATVKSCYSDGYALWGSWGQGT LVT
TVSS (SEQ ID NO:117)

sdCDR1 GFTLDYYAIG (SEQ ID NO:118)

sdCDR2 CISSSDGSTYYADSVKG (SEQ ID NO:119)

sdCDR3 VKSCYSDGYALWGS (SEQ ID NO:120)

αLyPD3 h790 sdAb

QVQLLES GGGLVQP GGSLRLSCAASGFTLDYYSIGWFRQAPGKEREGVSCISSSDGSTYY
ADSVKGRRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATVKSCYVDGYILWGSWGQGT LVT
VSS (SEQ ID NO:121)

sdCDR1 GFTLDYYSIG (SEQ ID NO:122)

sdCDR2 CISSSDGSTYYADSVKG (SEQ ID NO:123)

sdCDR3 VKSCYVDGYILWGS (SEQ ID NO:124)

Figure 5H

αLyPD3 H804 sdAb

QVQLLES GGGGLVQP GGSRLRLSCAAS **GFTLDYYAIG**WFRQAPGKEHEGVS **CISSSDGSTYYADSVKGR**FTI
SRDNSKNTLYLQMNSLRAEDTAVYYCAT **VRSCASPYELGS**WGQGTLLTVSS (SEQ ID NO:125)

sdCDR1 **GFTLDYYAIG** (SEQ ID NO:126)

sdCDR2 **CISSSDGSTYYADSVKG** (SEQ ID NO:127)

sdCDR3 **VRSCASPYELGS** (SEQ ID NO:128)

αLyPD h773 sdAb (Pro929)

QVQLVES GGGGLVQP GGSRLRLSCAAS **GRSFSSYGMG**WFRQAPGKEREIVA **AISWGGS**AVYYANS **SVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAA **NRQGRALVRKEFYDY**WGQGTLLTVSS (SEQ ID
NO:129)

sdCDR1 **GRSFSSYGMG** (SEQ ID NO:130)

sdCDR2 **AISWGGS**AVYYANS **SVKGR** (SEQ ID NO:131)

sdCDR3 **NRQGRALVRKEFYDY** (SEQ ID NO:132)

αLyPD3 h840 sdAb (Pro980)

QVQLLES GGGGKVQP GGSRLRLSCVVS **GDTSSIYLMG**WYRQTPGKQRELVA **HIRGN**GRTNYADSVKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCNV **RNFWGSAEY**WGQGTLLTVSS (SEQ ID NO:133)

sdCDR1 **GDTSSIYLMG** (SEQ ID NO:134)

sdCDR2 **HIRGN**GRTNYADSVKGR (SEQ ID NO:135)

sdCDR3 **RNFWGSAEY** (SEQ ID NO:136)

αLyPD3 h885 sdAb (Pro981)

QVQLLES GGGGLVQP GGSRLRLSCVAS **RGTF**SRYS **MG**WFRQAPGKEREFV **GRISW**SGDMTYADSVKGR
FTISRDNKNTLYLQMNSLRAEDTAVYYCAA **STLGYVWNHPNMYGY**WGHGTLTVSS (SEQ ID
NO:137)

sdCDR1 **RGTF**SRYS **MG** (SEQ ID NO:138)

sdCDR2 **RISW**SGDMTYADSVKGR (SEQ ID NO:139)

sdCDR3 **STLGYVWNHPNMYGY** (SEQ ID NO:140)

αHer-2 1054 sdAb

QVQLQES GGGGLVQAGGSLILSCAAS **GRTFS**NYAMG WFRQAPGKEREFVA **AINW**SGTHTDYADSVKGR
RFTISRDNVKTLYLQMNSLPEDTATYFCSR **GWSV**FDPDYRGQGTQVTVSS (SEQ ID NO:141)

sdCDR1 **GRTFS**NYAMG (SEQ ID NO:142)

sdCDR2 **AINW**SGTHTDYADSVKGR (SEQ ID NO:143)

sdCDR3 **GWSV**FDPDY (SEQ ID NO:144)

Figure 5I

αHer-2 1055 sdAb

QVQLQESGGGLVQPGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKNTVYLQMNSLKPEDTATYFCSRGWSVFDPDYRGQGTQVTSS (SEQ ID NO:145)
sdCDR1 GRAISSYAI (SEQ ID NO:146)
sdCDR2 AINWSGTHTNYADSVKG (SEQ ID NO:147)
sdCDR3 GWSVFDPDYR (SEQ ID NO:148)

αHer-2 1058 sdAb

QVQLQESGGGLVQPGGSLRLTCAASGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKNTVYLQMNSLKPEDTATYFCSRGWSVFDPDYRGQGTQVTSS (SEQ ID NO:149)
sdCDR1 GRAISSYAI (SEQ ID NO:150)
sdCDR2 AINWSGTHTNYADSVKG (SEQ ID NO:151)
sdCDR3 GWSVFDPDY (SEQ ID NO:152)

αHer-2 1059 sdAb

QVQLQESGGGLVQPGGSLRLTCAASGRAISSYAIWFRQAPGEEREFVAAINWSGTHTDYADSVKGRF
TISRDNKNTVYLQMNSLKPEDTAVYFCSRGWSVFDPDYRGQGTQVTSS (SEQ ID NO:153)
sdCDR1 GRAISSYAI (SEQ ID NO:154)
sdCDR2 AINWSGTHTDYADSVKG (SEQ ID NO:155)
sdCDR3 GWSVFDPDY (SEQ ID NO:156)

αHer-2 1065 sdAb

QVQLQESGGGLVQPGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKRTVYLQMNSLKPEDTATYFCSRGWSVFDPDYRGQGTQVTSS (SEQ ID NO:157)
sdCDR1 GRAISSYAI (SEQ ID NO:158)
sdCDR2 AINWSGTHTNYADSVKG (SEQ ID NO:159)
sdCDR3 GWSVFDPDY (SEQ ID NO:160)

αHer-2 1090 sdAb

QVQLQESGGGLVQTGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKNTVYLQMNSLKPEDTATYFCSRGWSLFDPDYRGQGTQVTSS (SEQ ID NO:161)
sdCDR1 GRAISSYAI (SEQ ID NO:162)
sdCDR2 AINWSGTHTNYADSVKG (SEQ ID NO:163)
sdCDR3 GWSLFDPDY (SEQ ID NO:164)

Figure 5J

αHer-2 1091 sdAb

QVQLQESGGGLVQPGGSLRLSCAAS**GFTFDDYAMS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**
RFTISRDNAKNTLYLQMNSLKSEDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTSS (SEQ ID NO:165)
sdCDR1 **GFTFDDYAMS** (SEQ ID NO:166)
sdCDR2 **SINWSGTHTDYADSVKG** (SEQ ID NO:167)
sdCDR3 **GWRLTGGYYDSV** (SEQ ID NO:168)

αHer-2 1092 sdAb

QVQLQESGGGLVQAGASRLSCAAS**GFTFDDYALS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**
RFTISRDNAKNTLYLQMNSLKSEDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTSS (SEQ ID NO:169)
sdCDR1 **GFTFDDYALS** (SEQ ID NO:170)
sdCDR2 **SINWSGTHTDYADSVKG** (SEQ ID NO:171)
sdCDR3 **GWRLTGGYYDSV** (SEQ ID NO:172)

αHer-2 1097 sdAb

QVQLQESGGGLVQPGGSLRLSCAAS**GFIFDDYAMT**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**
RFTISRDNAKNTLYLQMNSLKSEDSAVYYCVK**GWRHTDNYYAGV**QGQGTQVTSS (SEQ ID NO:173)
sdCDR1 **GFIFDDYAMT** (SEQ ID NO:174)
sdCDR2 **SINWSGTHTDYADSVKG** (SEQ ID NO:175)
sdCDR3 **GWRHTDNYYAGV** (SEQ ID NO:176)

αHer-2 1118 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GFTFDDYAMS**WVRQTPGKGLEWVSS**SINWSGHTNYADSVKG**
RFTISRDNAKNTLYLQMNSLKSEDTAVYYCARG**GWMVVPDST**RGQGTQVTSS (SEQ ID NO:177)
sdCDR1 **GFTFDDYAMS** (SEQ ID NO:178)
sdCDR2 **SINWSGHTNYADSVKG** (SEQ ID NO:179)
sdCDR3 **GWMVVPDST** (SEQ ID NO:180)

αHer-2 1121 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GFIFSDYAMT**WVRQAPGKGLEWVSS**SINWSGHTNYADSVKG**
RFTISRDNAKNTLYLQMNSLKSEDTAVYYCARG**GWMVVPDST**RGQGTQVTSS (SEQ ID NO:181)
sdCDR1 **GFIFSDYAMT** (SEQ ID NO:182)
sdCDR2 **SINWSGHTNYADSVKG** (SEQ ID NO:183)
sdCDR3 **GWMVVPDST** (SEQ ID NO:184)

Figure 5K

αHer-2 1134 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFSAAVMA**WYRQPPGEQRELVA**SITHRGFTRYADSVK**DRFT
ISRDNVNNTMYLQMNRLSPEDTAIYYCRL**LNGDY**WGQGTQVTSS (SEQ ID NO:185)
sdCDR1 **GRIFSAAVMA** (SEQ ID NO:186)
sdCDR2 **SITHRGFTRYADSVK** (SEQ ID NO:187)
sdCDR3 **LNGDY** (SEQ ID NO:188)

αHer-2 1138 sdAb

QVQLQESGGGLVQPGGSLRLSCAAS**GFTFDDYAMS**WVRQAPGKEMEWVS**GINWSGTHTRYADSVK**
GRFTISRDNAKNTLDLQMNLSIEDTAVYYCARGFAADSRSTRGQGTQVTSS (SEQ ID NO:189)
sdCDR1 **GFTFDDYAMS** (SEQ ID NO:190)
sdCDR2 **GINWSGTHTRYADSVK** (SEQ ID NO:191)
sdCDR3 **GFAADSRST** (SEQ ID NO:192)

αHer-2 1139 sdAb

QVQLQESGGGLVQPGGSLRLSCAAS**GFTFDDYAMS**WIRQAPGKEMEWVS**GINWSGTHTRYADSVK**
GRFTISRDNAKNTLDLQMNLSIEDTAVYYCARGFAADSRSTRGQGTQVTSS (SEQ ID NO:193)
sdCDR1 **GFTFDDYAMS** (SEQ ID NO:194)
sdCDR2 **GINWSGTHTRYADSVK** (SEQ ID NO:195)
sdCDR3 **GFAADSRST** (SEQ ID NO:196)

αHer-2 1140 sdAb

QVQLQESGGGLVQPGGSLRLSCVAS**GFTFDDYAMS**WVRQAPGKEMEWVS**GINWSGTHTRYADSVK**
GRFTISRDNAKNTLDLQMNLSIEDTAVYYCARGFAADSRSTRGQGTQVTSS (SEQ ID NO:197)
sdCDR1 **GFTFDDYAMS** (SEQ ID NO:198)
sdCDR2 **GINWSGTHTRYADSVK** (SEQ ID NO:199)
sdCDR3 **GFAADSRST** (SEQ ID NO:200)

αHer-2 1145 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFKNYPMG**WFRQPPGKDEFVAAITSSGGTTHYRDSVKGR
FTISRDNANTVYLQMNLSKPDATVYYCAG**SSTPWDIPLGPNEVG**YWGQGTQVTSS (SEQ ID
NO:201)
sdCDR1 **GRIFKNYPMG** (SEQ ID NO:202)
sdCDR2 **AITSSGGTTHYRDSVK**G (SEQ ID NO:203)
sdCDR3 **SSTPWDIPLGPNEVG**Y (SEQ ID NO:204)

Figure 5L

αHer-2 1146 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFKNYPMG**WFRQPPGKDRFVA**AITSSGGTTPYRDSVKGRF**
TISRDNAKNTVYLQMNSLKPEDTAVYYCAG**SSTPWDIPLGPNEVGF**WGQGTQVTVSS (SEQ ID NO:205)

sdCDR1 **GRIFKNYPMG** (SEQ ID NO:206)

sdCDR2 **AITSSGGTTPYRDSVKG** (SEQ ID NO:207)

sdCDR3 **SSTPWDIPLGPNEVGF** (SEQ ID NO:208)

αHer-2 1149 sdAb

QVQLQESGGGLVQAGGSLRLSCVAS**GNIFGFNVMG**WYRQVPGKQRELVA**ISTGGRSTDYADSAKGRF**
TISRNNAKDVTYLMNSLKPEDTAVYYCKM**TMASSDY**WGQGTQVTVSS (SEQ ID NO:209)

sdCDR1 **GNIFGFNVMG** (SEQ ID NO:210)

sdCDR2 **ISTGGRSTDYADSAKG** (SEQ ID NO:211)

sdCDR3 **TMASSDY** (SEQ ID NO:212)

αHer-2 1150 sdAb

QVQLQESGGGLVQAGGSLRLSCVAS**GNIFGFNVMG**WYRQVPGKQRELVA**ISTGGGSTNYADSAKGRF**
TVSRNNAKDVTYLMNSLKPEDTAVYYCKM**TMASVDY**WGQGTQVTVSS (SEQ ID NO:213)

sdCDR1 **GNIFGFNVMG** (SEQ ID NO:214)

sdCDR2 **ISTGGGSTNYADSAKG** (SEQ ID NO:215)

sdCDR3 **TMASVDY** (SEQ ID NO:216)

αHer-2 1156 sdAb

QVQLQESGGGLVQAGGSLKVSCAAS**RNIGSNYAVG**WFRQAPGKEREPVA**ALRWTGSIIGYDDSLRGR**
FTISKDDAKNTVYLQMNSLKPEDTGYYCAA**RILDRSSYDY**WGQGTQVTVSS (SEQ ID NO:217)

sdCDR1 **RNIGSNYAVG** (SEQ ID NO:218)

sdCDR2 **ALRWTGSIIGYDDSLRG** (SEQ ID NO:219)

sdCDR3 **RILDRSSYDY** (SEQ ID NO:220)

αHer-2 1158 sdAb

QVQLQESGGGLVQAGGSLRLSCTAS**GRTFSSYAMG**WFRQAPEKEREFVA**AITWSGGTTHYAESVKGR**
FTISRDNAKNTVYLQMTLEPEDTAVYYCAA**RINYSTISSNEKMYHY**WGQGTQVTVSS (SEQ ID NO:221)

sdCDR1 **GRTFSSYAMG** (SEQ ID NO:222)

sdCDR2 **AITWSGGTTHYAESVKG** (SEQ ID NO:223)

sdCDR3 **RINYSTISSNEKMYHY** (SEQ ID NO:224)

Figure 5M

 α Her-2 1159 sdAb

QVQLQESGGGLVQAGGSLRLSCATS**GRTFSSLAMG**WFRQAPGKERELVA**GISWSGSTTYYADSVKGR**
FAISRDNAKNTVYLQMNSLPEDTAVYYCAART**SSSIATIGREYDY**WGQGTQVTVSS (SEQ ID
NO:225)
sdCDR1 **GRTFSSLAMG** (SEQ ID NO:226)
sdCDR2 **GISWSGSTTYYADSVKG** (SEQ ID NO:227)
sdCDR3 **RTSSSIATIGREYDY** (SEQ ID NO:228)

 α Her-2 1160 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRTFSNERLG**WFRQAPGKERELVA**AIRWSGVIIGYADSVRGRF**
TISRDNASTVYLQMNSLRPEDTAVYFCAAD**DRGVYGTWDY**WGQGTQVTVSS (SEQ ID NO:229)
sdCDR1 **GRTFSNERLG** (SEQ ID NO:230)
sdCDR2 **AIRWSGVIIGYADSVRG** (SEQ ID NO:231)
sdCDR3 **DRGVYGTWDY** (SEQ ID NO:232)

 α Her-2 1161 sdAb

QVQLQESGGGLVQPGKSLRLSCAVS**GDIFGTYGMA**WYRQAPGKQREPVA**SISIGGIINYADSVKGRFTI**
SRDNVKNNTVYLQMNSLPEDTAVYYCKL**LDWNY**WGRGTQVTVSS (SEQ ID NO:233)
sdCDR1 **GDIFGTYGMA** (SEQ ID NO:234)
sdCDR2 **SISIGGIINYADSVKG** (SEQ ID NO:235)
sdCDR3 **LDWNY** (SEQ ID NO:236)

 α Her-2 1162 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRPFSGNAMG**WFRQAPGKEREFVA**AISWSGDSTYYADSVKG**
RFTISRDNENTAYLQMNSLPEDTAVYYCAART**RSFYSRYYTRPSDYN**WGPGTQVTVSS (SEQ ID
NO:237)
sdCDR1 **GRPFSGNAMG** (SEQ ID NO:238)
sdCDR2 **AISWSGDSTYYADSVKG** (SEQ ID NO:239)
sdCDR3 **TRSFYSRYYTRPSDYN** (SEQ ID NO:240)

 α Her-2 1163 sdAb

QVQLQESGGGLVQAGGSLRLSCAAS**GRRFNNYFMG**WFRQAPGKEREFV**ALLRESGDNTYYTNSVKGR**
FTISRDNARNNTVYLQMNSLPEDTAVYYCAAR**RLDTGFVLYSANSYAY**WGQGTQVTVSS (SEQ ID
NO:241)
sdCDR1 **GRRFNNYFMG** (SEQ ID NO:242)
sdCDR2 **LLRESGDNTYYTNSVKG** (SEQ ID NO:243)
sdCDR3 **RLDTGFVLYSANSYAY** (SEQ ID NO:244)

Figure 6

αHSA half-life extension domain (αHSA (10GE))

EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL
YAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS (SEQ ID
NO:245)

sdCDR1 GFTFSKFGMS (SEQ ID NO:246)
sdCDR2 SISGSGRDTLYAESVKG (SEQ ID NO:247)
sdCDR3 GGSLSV (SEQ ID NO:248)

αHSA half-life extension domain with His tag

EVQLVESGGGLVQPGNSLRRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL
YAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS/HHHHH
H (SEQ ID NO:249)

sdCDR1 GFTFSKFGMS (SEQ ID NO:250)
sdCDR2 SISGSGRDTLYAESVKG (SEQ ID NO:251)
sdCDR3 GGSLSV (SEQ ID NO:252)

Figure 7A

αCD3 scFv domains**αCD3 V_L**

QTVVTQEPSLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WVQQKPGQAPRGLIG**GTKFLVP**GT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL (SEQ ID
 NO:254)

aVLCDR1 **ASSTGAVTSGNYPN** (SEQ ID NO:255)

aVLsdCDR2 **GTKFLVP** (SEQ ID NO:256)

aVLsdCDR3 **TLWYSNRWV** (SEQ ID NO:257)

αCD3 V_{Li}

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**DYKDDDDK**
 GTPARFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID
 NO:258)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:259)

iVLsdCDR2 **DYKDDDDK** (SEQ ID NO:260)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:261)

αCD3 V_{Li2}

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGNYPN**WVQQKPGQAPRGLIG**GTKDDAPG**
 TPARFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL (SEQ ID
 NO:262)

iVLCDR1 **GSSTGAVTSGNYPN** (SEQ ID NO:263)

iVLsdCDR2 **GTKDDAP** (SEQ ID NO:264)

iVLsdCDR3 **VLWYSNRWV** (SEQ ID NO:265)

αCD3 V_{LiGL}

QTVVTQEPSLTVSPGGTVTLTC**GSSTGAVTSGHYPN**WVQQKPGQAPRGLIG**GTSNKHSW**
 TPARFSGSLLGGKAALTLSGVQPEDEAEYYC**VLWGSRRWV**FGGGTKLTVL (SEQ ID
 NO:266)

aV_{Li}GLCDR1 **GSSTGAVTSGHYPN** (SEQ ID NO:267)

aV_{Li}GLCDR2 **GTSNKHS** (SEQ ID NO:268)

aV_{Li}GLCDR3 **VLWGSRRWV** (SEQ ID NO:269)

Figure 7B **α CD3 V_H**

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYAT
YYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGT
 LTVSS (SEQ ID NO:270)

aVHCDR1 GFTFNKYAIN (SEQ ID NO:271)

aVHsdCDR2 RIRSKYNNYATYYADQVKD (SEQ ID NO:272)

aVHsdCDR3 HANFGNSYISYWAY (SEQ ID NO:273)

 α CD3 V_{Hi}

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARRIRSKYDYKD
DDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ
 GTLVTVSS (SEQ ID NO:274)

iVHsdCDR1 GFTFNKYAMN (SEQ ID NO:275)

iVHsdCDR2 RIRSKYDYKDDDDKADSVKD (SEQ ID NO:276)

iVHsdCDR3 HGNFGNSYISYWAY (SEQ ID NO:277)

 α CD3 V_{Hi2}

EVQLVESGGGLVQPGGSLKLSCAASGFTFNKHAMNWVRQAPGKGLEWVARRIRSKYNNYA
TAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
 LTVTVSS (SEQ ID NO:278)

iVHsdCDR1 GFTFNKHAMN (SEQ ID NO:279)

iVHsdCDR2 RIRSKYNNYATAYADSVKD (SEQ ID NO:280)

iVHsdCDR3 HGNFGNSYISYWAY (SEQ ID NO:281)

 α CD3 V_{HiGL4}

EVQLVESGGGLVQPGGSLKLSCAASGFTFSGYAMNWVRQAPGKGLEWVARRIRSKANSYA
TEYAASVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNAGNSAISYWAYWGQG
 TLTVTVSS (SEQ ID NO:282)

aVHiGL4CDR1 GFTFSGYAMN (SEQ ID NO:283)

aVHiGL4CDR2 RIRSKANSYATEYAASVKD (SEQ ID NO:284)

aVHiGL4CDR3 HGNAGNSAISYWAY (SEQ ID NO:285)

 α CD3 scFv linkers**Normal/Non-cleavable linker**

GGGSGGGSGGGSGGGGS (SEQ ID NO:286)

Constrained linker

GGGSGGGGS (SEQ ID NO:287)

Figure 8A

Cleavable Linkers (Recognition site in bold, cleavage site marked with"/")**MMP 2/9**

GPAG/MKGL (SEQ ID NO:339)

SGGPGPAG/MKGLPGS (SEQ ID NO:340)

SGGGPGPAG/MKGLPGGS (SEQ ID NO:341)

Meprin A/B

GGGGKKLA/DEPEGGS (SEQ ID NO:342)

SGGGKKLA/DEPEGGS (SEQ ID NO:343)

KKLA/DEPE (SEQ ID NO:344)

Meprin A/B (Variant, high efficiency)

GGGKFLA/DEPEGG (SEQ ID NO:345)

Cathepsin S, K, L

GGGARLQ/SAAPGGGS (SEQ ID NO:346)

SGGGARLQ/SAAPGGGS (SEQ ID NO:347)

ARLQ/SAAP (SEQ ID NO:348)

Meprin/Granzyme B

SGGGGVYADSLEDGGGS (SEQ ID NO:349)

GVYADSLEDG (SEQ ID NO:350)

Matriptase/uPA (MS)

GGGSLSGR/SDNHGGGS (SEQ ID NO:351)

GLSGR/SDNHG (SEQ ID NO:352)

Matriptase (MV)

SGGGSFTR/QARVVGGS (SEQ ID NO:353)

SFTR/QARVV (SEQ ID NO:354)

CathepsinS/MMP9/Meprin A

ARLQ/SAAPAG/LKGA (SEQ ID NO:355)

GARLQ/SAAPAG/LKGAG (SEQ ID NO:356)

Figure 8B**MMP9 (Variant, high efficiency)**

GGPGPAG/MHGLPG (SEQ ID NO:357)

GSGGPGPAG/MHGLPGGS (SEQ ID NO:358)

MMP9 (Variant, low efficiency)

GGPGPAG/MEGLPG (SEQ ID NO:359)

MMP9-15 (K>E)

SGGPGPAG/MEGLPGS (SEQ ID NO:360)

MMP9-15 (M>P)

SGGPGPAG/PKGLPGS (SEQ ID NO:361)

Cleavable Linkers (Recognition site in bold, cleavage site marked with"/")**Thrombin 1**

GGGGLVPR/GSLGGGS (SEQ ID NO:362)

Thrombin 2

SSGGMPR/SFRGGGS (SEQ ID NO:363)

Enterokinase/Flag

GGGGDYKDDDDK/GGGS (SEQ ID NO:364)

KLK7-6

SGGGQNPY/SAGRGGGS (SEQ ID NO:365)

KLK7-13

SGGGQNPY/SAGGGSGG (SEQ ID NO:366)

KLK7-11

SGGGRNVY/SAGGGSGG (SEQ ID NO:367)

KLK7-10

SGGGQNTW/SAGKGGGS (SEQ ID NO:368)

uPA

GGGSH TGR/SAYFGGGS (SEQ ID NO:369)

MMP9-2

SGGPGPAG/LKGAPGS (SEQ ID NO:370)

Figure 8C

Protease	Cleavage domain sequence	SEQ ID NO:
MMP7	KRALGLPG	371
MMP7	(DE) ₈ RPLALWRS(DR) ₈	372
MMP9	PR(S/T)(L/I)(S/T)	373
MMP9	LEATA	374
MMP11	GGAANLVRGG	375
MMP14	SGRIGFLRTA	376
MMP	PLGLAG	532
MMP	PLGLAX	533
MMP	PLGC(ME)AG	534
MMP	ESPAYYTA	535
MMP	RLQLKL	377
MMP	RLQLKAC	378
MMP2, MMP9, MMP14	EP(CIT)G(HOF)YL	379
Urokinase plasminogen activator (upa)	SGRSA	380
Urokinase plasminogen activator (upa)	DAFK	381
Urokinase plasminogen activator (upa)	GGGRR	382
Lysosomal enzyme	GFLG	383
Lysosomal enzyme	ALAL	384
Lysosomal enzyme	FK	385
Cathepsin B	NLL	386
Cathepsin D	PIC(ET)FF	387
Cathepsin K	GGPRGLPG	388
Prostate specific antigen	HSSKLQ	389
Prostate specific antigen	HSSKLQL	390
Prostate specific antigen	HSSKLQEDA	391
Herpes simplex virus protease	LVLASSSFGY	392
HIV protease	GVSQNYPIVG	393
CMV protease	GVVQASCRLA	394

Figure 8D

Protease	Cleavage domain sequence	SEQ ID NO:
Thrombin	F(PIP)RS	395
Thrombin	DPRSFL	396
Thrombin	PPRSFL	397
Caspase-3	DEVD	398
Caspase-3	DEVDP	399
Caspase-3	KGSGDVEG	400
Interleukin 1 β converting enzyme	GWEHDG	401
Enterokinase	EDDDDKA	402
Fap	KQEQNPGST	403
Kallikrein 2	GKAFRR	404
Plasmin	DAFK	405
Plasmin	DVLK	406
Plasmin	DAFK	407
Top	ALLLALL	408

Figure 9A

Pro140 (Mono-specific with two aEGFR/D12, Two MMP9 linkers) Format 1

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQVTVSS/GGGSGGGGS/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GPAGMKGL/Q
TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTSGVQPEDEAEYYCTWLWYSNRWVFGGGTKLTVL/GGGSGGGGS/QVKLEESGGGSVQTGGSLR
LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVS
PGGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSG
VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
AVYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGGS/EVQLVESGGGLVQPGNSLRLSAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTQVTVSS (SEQ ID NO:409)

Pro140b (Mono-specific with two aEGFR/D12, Two Meprin linkers) Format 1

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQVTVSS/GGGSGGGGS/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/KKLADEPE/QT
VVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG
KAALTSGVQPEDEAEYYCTWLWYSNRWVFGGGTKLTVL/GGGSGGGGS/QVKLEESGGGSVQTGGSLRLT
CAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSLK
PEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQVTVSS/GGGSKLADEPEGGGS/QTVVTQEPSLTVSP
GGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGV
QPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTF
NKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
VYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGGS/EVQLVESGGGLVQPGNSLRLSAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTQVTVSS (SEQ ID NO:410)

Figure 9B

Pro186 (Mono-specific with two aEGFR/D12, MMP9 linker) Format 2

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGG/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/Q
TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGVSQTGGSLR
LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVS
PGGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSG
VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDT
AVYYCVRHGNGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTQVTVSS (SEQ ID NO:411)

Pro187 (Mono-specific with two aEGFR/D12, Meprin linker) Format 2

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGG/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/Q
TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGVSQTGGSLR
LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSKKLADPEGGG/QTVVTQEPSLTV
SPGGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSG
VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDT
AVYYCVRHGNGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTQVTVSS (SEQ ID NO:412)

Figure 9C

Pro225 (Mono-specific FL aB7H3 hF7 MMP9 linker) Format 2

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLS
CAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGG
TVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAAALTSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:413)

Pro226 (Mono-specific FL aB7H3 hF12 MMP9 linker) format 2

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/**GGGSGGGS**/EVQL
VESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVT
QEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA
LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLQESGGGLVQPGGSLRLSCE
ASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA
VYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLT
CGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAAALTSGVQPEDEAEY
YCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNW
VRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN
FGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS
WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVS
SQGLTVTVSS/HHHHHH (SEQ ID NO:414)

Figure 9D

Pro233 (humanized Pro186, mono-specific with two aEGFR/D12, MMP9 linker) format 2

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNAKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTSC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAED
TALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTSGVQPED
EAEEYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYA
MNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV
RHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFSK
FGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG
SLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:415)

Pro311 (FL mono-specific aFOLR1 h77.2 MMP9 linker) format 2

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTIS
RDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQ
GGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL
QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTSGVQPED
EAEEYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSV
MAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFDRIY
WGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQ
QKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTSGVQPEDEAEYCVLWYSNRWVFGGGTKL
TVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKY
DYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTV
TVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVRQAPGKGLEWVSSISG
SGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH
(SEQ ID NO:416)

Figure 9E

Pro312 (FL mono-specific aFOLR1 h59.3 MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGRF
TISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGT LVTVSS/GGGSGGGS/EVQLVESGGGLVQ
PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY
LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGT LVTVSS/GGGSGGGS/QTVVTQEPSLTVSPG
GTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED
EAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISA
MGWYRQAPGKQREWVAVTHSDYSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCKHYGI
DYWGQGT LVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNW
VQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGG
TKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIR
SKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ
TLTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI
SGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LVTVSS/HHHHHH
(SEQ ID NO:417)

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

QVQLVESGGGLVQPGGSLRLSCEASGTTFSRDVMGWYRQAPGKQRELVAIISRGGSTNYADSVKGRFTI
SRDN SKNTLYLQMNSLRAEDTAVYYCNANTATWGRVFWGQGT LVTVSS/GGGSGGGS/EVQLVESGG
GLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSK
NTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGT LVTVSS/GGGSGGGS/QTVVTQEPSLTV
VSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV
QPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLRLSCEASGTTFS
RDVMGWYRQAPGKQRELVAIISRGGSTNYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCNAN
TATWGRVFWGQGT LVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG
NYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRW
VFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE
WVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA
YWGQGT LVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAPGKG
LEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LVTVSS/
HHHHHH (SEQ ID NO:418)

Figure 9F

Pro246 (FL haEGFR1/haEGFR2 hetero-specific COBRA MMP9 linker)

EVQLVESGGGLVQPGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVVAINWSSGSTYYADSVKGRF
TISRDN SKNTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEDYWGQGLTVTVSS/**GGGSGGGS**/
EVQLVESGGGLVQPGGSLRLSCAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADQVKD
RFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/Q
TVVTQEPSLT VSPGGTVTLT CASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVP GTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRP GGS
LSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLR
AEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLT VSP
GGTVTLT CGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP GGSLRLSCAASGFTFNK
YAMNWVRQAPGKLEWVARIRSKYDYKDDDDKADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSRLSCAASGFTF
SKFGMSWVRQAPGKLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:419)

Pro256 (FL haEpCAM VIB13/haEGFR1 hetero-specific COBRA MMP9 linker)

QVQLVESGGGLVQPGGSLTSCAASGTGSIFSNLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRF
TISRDN SKNTLYLQMNSLRPEDTAVYYCNLLRSPGATTPYWGQGLTVTVSS/**GGGSGGGS**/EVQLVES
GGGLVQP GGSLRLSCAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEP
SLTVSPGGTVTLT CASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRP GGS
LSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTALYY
CAAAGSAWYGTLYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLT VSPGGTVTLT
GSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYY
CVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQP GGSLRLSCAASGFTFNKYAMNW
VRQAPGKLEWVARIRSKYDYKDDDDKADSVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHGNF
GNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSW
VRQAPGKLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GLTVTVSS/HHHHHH (SEQ ID NO:420)

Figure 9G

Pro420 (FL aFOLR1 h77.2/haEGFR1 hetero-specific COBRA MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQP
 GGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL
 QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG
 GTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLSGVQPED
 EAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLVESGGGVVRPGGSLTSCAASGRTSRSYG
 MGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAAAG
 SAWYGTLYEYDYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTTLTCSSTGA
 VTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS
 NRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK
 GLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
 WAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
 GKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVT
 VSS/HHHHHH (SEQ ID NO:421)

Pro421 (FL haEGFR1/aFOLR1 h77.2 hetero-specific COBRA MMP9 linker)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**GGGSGGGS**/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGS**/QTV
 VTQEPSLTVSPGGTTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVQLVESGGGLVQPGGSLRLS
 CAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDT
 VYVCNRNFDRIYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGTTLTCSSTGA
 VTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS
 NRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK
 GLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
 WAYWGQGLTVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
 GKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVT
 VSS/HHHHHH (SEQ ID NO:422)

Figure 9H

Pro393 (Pro186, mono-specific single target with two aEGFR/D12 COBRA S9 linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GARLQSAAPAGLKGAG/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:423)

Pro394 (Pro186, mono-specific single target with two aEGFR/D12 COBRA ST14(MV) linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSFTRQARVVGGGS/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:424)

Figure 9I

Pro395 (Pro186, mono-specific single target with two aEGFR/D12 COBRA CathS linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSARLQSAAPGGGS/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:425)

Pro396 (Pro186, mono-specific single target with two aEGFR/D12 COBRA MMP9v linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPSLTVS
PGGTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGV
QPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTF
NKYAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV
YYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGF
TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYC
TIGGSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:426)

Figure 9J

Pro429 (Pro186, mono-specific single target with two aEGFR/D12 COBRA Meprin/GranzymeB linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGVYADSLEDGGGS/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:427)

Pro430 (Pro186, mono-specific single target with two aEGFR/D12 COBRA MMP9-2 linker)

QVKLEESGGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKP
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGLKAGAPGS/QTVVTQEPSLTVSPGG
TVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTLTLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:428)

Figure 9K**Pro431 (Pro186, mono-specific single target with two aEGFR/D12 COBRA ST14(MS) linker)**

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGVSQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNTVDLQMNSLKPE
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSLSGRSDNHGGGS**/QTVVTQEPSLTVSPG
GTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:429)

Pro258 (Pro186, mono-specific single target with two aEGFR/D12 COBRA with a single aEGFR domain and a central aHSA domain)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPG
NSLRSLCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQM
NSLRPEDTAVYYCTIGGSLSVSSQGTQVTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTVTLTCSSTGA
VTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS
NRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK
GLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGTQVTVSS/HHHHHH (SEQ ID NO:430)

Figure 9L

Pro221 (Pro186, mono-specific with two aEGFR/D12 COBRA, kallikrein 7-6 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKPE
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNPYSAGRGGGS/QTVVTQEPSLTVSP
GGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNK
YAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSLSAASGFTF
SKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:431)

Pro222 (Pro186, mono-specific with two aEGFR/D12 COBRA, kallikrein 7-13 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKPE
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNPYSAGGGSGG/QTVVTQEPSLTVSP
GGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNK
YAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSLSAASGFTF
SKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:432)

Figure 9M

Pro223 (Pro186, mono-specific with two aEGFR/D12, kallikrein 7-11 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN
 KNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQP
 GGSLLKSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV
 TSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG
 TKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTG
 YADSVKGRFTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGRNIVY
SAGGSGGG/QTVVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLK
 LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
 DAVYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSCAASGFTFS
 FGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
 GTLTVTVSS/HHHHHH (SEQ ID NO:433)

Pro224 (Pro186, mono-specific with two aEGFR/D12, kallikrein 7-10 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDN
 KNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQP
 GGSLLKSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLK
 TEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTVVTQEPSTVSPGGTVTLTCASTGAV
 TSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG
 TKLTVL/GGGSGGGS/QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTG
 YADSVKGRFTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGGQNT
WSAGKGGGS/QTVVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSL
 KLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
 DAVYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSCAASGFTFS
 KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
 QGTQVTVSS/HHHHHH (SEQ ID NO:434)

Figure 9N

Pro254 (Hetero-specific with aEGFR/hD12d and aEGFR/hG8, MMP9 linker)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNANKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/GGGSGGGG/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLRLSC
 AASGRTFSSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDT
 AVYYCAAGYQINSGNYNFKDYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPG
 GTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
 DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
 AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
 VRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFS
 KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG
 GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:435)

Pro255 (Hetero-specific with aEGFR/hD12d and aEpCAM hVIB12, MMP9 linker)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNANKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/GGGSGGGG/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGLVQPGGSLTSC
 AASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRFTISRDNKNTLYLQMNSLRPED
 TAVYYCNLLRSPGATTPYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLT
 CGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNW
 VRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN
 FGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS
 WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVS
 SQGLTVTVSS/HHHHHH (SEQ ID NO:436)

Figure 90

Pro262 (mono-specific w/ two aEGFR/D12, NCL15 active domain linker, MMP9 linker)

QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNANTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS
GGGS/QTVVTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGP
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSVQT
 GGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQ
 MNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEP
 SLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAAL
 TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAA
 SGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLK
 EDTAVYYCVRHGFNGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSC
 AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNATTLYLQMNSLRPEDT
 AVYYCTIGGSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:437)

Pro356 (mono-specific with one aEGFR/hG8, MMP9 linker)

EVQLVESGGGLVQPGGSLRLSAAASGRTFSSYAMGWFRQAPGKEREFVAINWSSGSTYYADSVKGRF
 TISRDNANTLYLQMNSLRAEDTAVYYCAAGYQINSGNYNFKDYEYDYWGQGTQVTVSS/GGGSGGGS/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGP
 PARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLV
 QPGNSLRLSAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNATTLYLQ
 MNSLRPEDTAVYYCTIGGSLSVSSQGTQVTVSS/GGGSGGGS/QTVVTQEPSLTVSPGGTVTLTCSST
 GAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL
 WYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ
 APGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGFNGN
 SYISYWAYWGQGTQVTVSS/HHHHHH (SEQ ID NO:438)

Figure 9P

Pro359 (mono-specific with one aB7H3/hF7, MMP9 linker)

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGTLLTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQ
GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQM
NSLRPEDTAVYYCTIGGSLSVSSQGTLLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTTLTCGSSTGA
VTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYS
NRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGK
GLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGTLLTVSS/HHHHHH (SEQ ID NO:439)

Pro364 (mono-specific with one aFOLR1/h59.3, MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGTLLTVSS/**GGGSGGGS**/EVQLVESGGGLVQ
PGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY
LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED
EAEYYCTLWYSNRWVFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLSCAASG
FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYY
CTIGGSLSVSSQGTLLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTTLTCGSSTGAVTSGNYPNW
VQQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTK
LTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK
YDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLL
TVSS/HHHHHH (SEQ ID NO:440)

Figure 9Q

Pro388 (Mono-specific with one aFOLR1/h77-2, MMP9 linker)

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTIS
RDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGTLLTVSS/**GGGSGGGS**/EVQLVESGGGLVQP
GGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL
QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPG
GTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED
EAEYYCTLWYSNRWVFGGGTKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGNSLRLSCAASG
FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYY
CTIGGSLSVSSQGTLLTVSS/**GGGSGGGS**/QTVVTQEPSLTVSPGGTTLTCGSSTGAVTSGNYPNWV
QKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTK
LTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSK
YDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT
LTVSS/HHHHHH (SEQ ID NO:441)

Pro429 (Pro186, mono-specific with two aEGFR/D12, Meprin/GranzymeB linker)

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/**GGGSGGGS**/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLLTVSS/**GGGSGGGS**/QTV
VTQEPSLTVSPGGTTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/QVKLEESGGGVSQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNKNTVDLQMNSLKP
DTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/**SGGGVYADSLEDGGGS**/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGS**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTLLTVSS/**GGGSGGGS**/EVQLVESGGGLVQPGNSLRLSCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTLLTVSS/HHHHHH (SEQ ID NO:442)

Figure 9R

Pro430 (Pro186, mono-specific with two aEGFR/D12, MMP9-2 linker)

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSGVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKPE
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGLKGAPGS/QTVVTQEPSLTVSPGG
TVTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:443)

Pro431 (Pro186, mono-specific with two aEGFR/D12, ST14(MS) linker)

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
TISRDNANTVDLQMNSLKPEDTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSGVQTGGSLRLTC
AASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNANTVDLQMNSLKPE
DTAIYYCAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSLSGRSDNHGGGS/QTVVTQEPSLTVSPG
GTVTLTCGSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
VRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLCAASGFTFS
KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNANTTLYLQMNSLRPEDTAVYYCTIG
GSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:444)

Figure 9S

Pro432 (Hetero-specific with aEpCAM/hVIB13 and aEGFR/hG8, MMP9 linker)

QVQLVESGGGLVQPGGSLTSCAASGTGSIFSINLMGWYRQAPGKQRELVARITSGDSTVYADSVKGRF
TISRDN SKNTLYLQMNSLRPEDTAVYYCNLLRSPGATTPYWGGQTLTVSS/**GGGSGGGG**/EVQLVES
GGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQTLTVSS/**GGGSGGGG**/QTVVTQEP
SLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLS
GVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLRLSCAASGR
TFSSYAMGWFRQAPGKEREFFVAINWSSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC
AAGYQINSGNYPNFKDYEYDYWGQTLTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEP SLTVSPGGTVTL
TCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAE
YYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN
WVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH
GNFGNSYISYWAYWGQTLTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRSCAASGFTFSKFG
MSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSL
VSSQGT LTVSS/HHHHHH (SEQ ID NO:445)

**Pro448 (Hetero-specific with aFOLR1/h77-2, aEGFR/hD12, MMP9 linker, VH-VLi
HemiCOBRA)**

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTIS
RDNSKNTLYLQMNSLRAEDTAVYYCNRNFDRIYWGQTLTVSS/**GGGSGGGG**/QVKLVESGGGVV
RPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFFVSGISWRGDSTGYADSVKGRFTISRDN AKNSLYL
QMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQTLTVSS/**GGGSGGGG**/EVQLVESGGGLVQ
PGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY
LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQTLTVSS/**SGGPGPAGMKGLPGS**/QTVVTQE
PSLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRSC
AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDT
AVYYCTIGGSLSVSSQGT LTVSS/HHHHHH (SEQ ID NO:446)

Figure 9T

Pro449 (Hetero-specific with aEGFR/hD12, aFOLR1/h77-2, MMP9 linker, VH-VLi HemiCOBRA)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNAKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**GGGGSGGGS**/Q
 VQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISR
 DNSKNTLYLQMNSLRAEDTAVYVCNRFDRYWGQGLTVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQPG
 GSKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL
 QMNNLKTEDTAVYVCVRHANFGNSYISYWAYWGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEP
 SLTVSPGGTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAAL
 TSGVQPEDEAEYCVLWYSNRWVFGGSKLTVL/**GGGGSGGGS**/EVQLVESGGGLVQPGNSLRLS
 ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTA
 VYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:447)

Pro450 (Hetero-specific with aFOLR1/h77-2, aEGFR/hD12, MMP9 linker, VL-VHi HemiCOBRA)

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYVCNRFDRYWGQGLTVTVSS/**GGGGSGGGS**/QVKLVESGGGV
 RPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRDNAKNSLYL
 QMNSLRAEDTALYYCAAAGSAWYGTLYEYDYWGQGLTVTVSS/**GGGGSGGGS**/QTVVTQEP
 SLTVSPGGTVTLTCSSTGAVTSGNYPNWWVQKPGQAPRGLIGTKFLVPGTPARFSGSLLGGKAALT
 TSGVQPEDEAEYCTLWYSNRWVFGGSKLTVL/**SGGPGPAGMKGLPGS**/EVQLVESGGGLVQPGGSLK
 LSCAASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQ
 MNNLKTEDTAVYVCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGGSGGGS**/EVQLVESGGGLVQ
 PGNSLRLSASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQ
 MNSLRPEDTA VYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:448)

Figure 9U

Pro451 (Hetero-specific with aEGFR/hD12, aFOLR1/h77-2, MMP9 linker, VL-VHi HemiCOBRA)

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRF
 TISRDNAKNSLYLQMNSLRAEDTALYYCAAAGSAWYGTLYEYDWGQGLTVTVSS/GGGSGGGG/Q
 VQLVESGGGLVQPGGSLRLSCAASGFTVSNVMAWYRQTPGNREFVAIINSIGITNYADSVKGRFTISR
 DNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGGGG/QTVVTQEPLTVSP
 GGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPE
 DEAEYYCTLWYSNRWVFGGGTKLTVL/SGGPGPAGMKGLPGS/EVQLVESGGGLVQPGGSLKLSAAS
 GFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
 DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCA
 ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTA
 VYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:449)

Pro479 (Hetero-specific, one target, two epitopes, haB7H3/F7 and haB7H3/F12, MMP9 linker)

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGR
 FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRFTISRDNKNTLYLQMNSLRAED
 TAVYYCAAGGVLAHHNNEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGTVT
 LTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEA
 EYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN
 WVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH
 GNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFG
 MSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSL
 VSSQGLTVTVSS/HHHHHH (SEQ ID NO:450)

Figure 9V

Pro480 (Hetero-specific, one target, two epitopes, haB7H3/F12 and haB7H3/F7, MMP9 linker)

QVQLQESGGGLVQPGGSLRLSCEASPRFTSTYSMAWFRQAPGKERSFVAAINWSGGNTSYADSVKGRF
 TISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQL
 VESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS
 RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVT
 QEPSTLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAA
 LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 PSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDT
 AVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTLTVSPGGTV
 TLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAA LTLSGVQPEDE
 AEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAM
 NWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR
 HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLS AASGFTFSKF
 GMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGS
 LSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:451)

Pro495 (Mono-specific with two haB7H3/F7, MMP9 linker, Vli2-Vhi2)

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGR
 FTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/EV
 QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRF
 TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSTLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAE
 DTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTLTVSPGG
 TVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTDKDDAPGT PARFSGSLLGGKAA LTLSGVQPED
 EAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKHA
 MNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR
 HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLS AASGFTFSKF
 GMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGS
 LSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:452)

Figure 10A

Pro601

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb
– MMP9-15 - aCD3Vli2 –NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGR
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGT LTVSS/ GGGSGGGG/
EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGT LTVSS/ GGGSGGGG/
QTVVTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/ GGGSGGGG/ QVQLQESGGGLVQPGGS
LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
LRAEDTAVYYCAAGGATTQRATEASYDYWGQGT LTVSS/ SGGPGPAGMKGLPGS/ QTVVTQEPSLTV
SPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGV
QPEDEAEYYCVLWYSNRWVFGGGTKLTVL/ GGGSGGGG/ EVQLVESGGGLVQPGGSLKLSAASGFTF
NKHAMN WVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV
YYCVRHGNFGNSYISYWAYWGQGT LTVSS/ GGGSGGGG/ EVQLVESGGGLVQPGNSLRLSCAASGF
TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYC
TIGGSLSVSSQGT LTVSS/ HHHHHH (SEQ ID NO:522)

Pro602

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb
– MMP9-15 - aCD3Vli2 –NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGR
FTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGT LTVSS/ GGGSGGGG/ EVQ
LVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT
ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGT LTVSS/ GGGSGGGG/ QTV
VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/ GGGSGGGG/ QVQLQESGGGLVQPGGSLRLS
CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAE
DTAVYYCAAGGVLAHHNYEYDYWGQGT LTVSS/ SGGPGPAGMKGLPGS/ QTVVTQEPSLTVSPGGT
VTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGVQPEDE
AEYYCVLWYSNRWVFGGGTKLTVL/ GGGSGGGG/ EVQLVESGGGLVQPGGSLKLSAASGFTFNKHA
MNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV
RHGNFGNSYISYWAYWGQGT LTVSS/ GGGSGGGG/ EVQLVESGGGLVQPGNSLRLSCAASGFTFSK
FGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGG
SLSVSSQGT LTVSS/ HHHHHH (SEQ ID NO:523)

Figure 10B

V3

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9-15 - aCD3Vli2 –NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGR
 RFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGRFTISRDNKNTLYLQMNS
 LRAEDTAVYYCAAGGVLAAHHNYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSP
 GGTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGVQ
 PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFN
 KHAMNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY
 YCVRHGNGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCEASGFT
 FSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCT
 IGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:524)

V4

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– MMP9-15 - aCD3Vli2 –NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGR
 FTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGVLAAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT
 ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDNKNTLYLQMNSLRA
 EDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPG
 GTVTLTCSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGVQPE
 DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKH
 AMNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
 VRHGNGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCEASGFTFS
 KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIG
 GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:525)

Figure 10C

Pro664

aB7H3 hF12 (S59Y) sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFT
ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTV
VTQEPLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLS
CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGT
VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCLCAASGFTF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:526)

Pro665

aB7H3 hF12 (N57Q) sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGQTSYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGS/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFT
ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTV
VTQEPLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLS
CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGQTSYADSVKGRFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGT
VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCLCAASGFTF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:527)

Figure 10D

Pro667

aB7H3 hF12 (N57E) sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGGETSYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNIEYDY**WGQGLTVTVSS/**GGGSGGGG**/EVQ
LVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**RIRSKYNNYATYYADQVKDRFT**
ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/**GGGSGGGG**/QTV
VTQEPSLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
AALTSGVQPEDEAEYYCT**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLS
CEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGGETSYADSVKGR**RFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAA**GGVLAHHNIEYDY**WGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLTC**GSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPE
DEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKY**
AMNWVRQAPGKGLEWVAR**RIRSKYDYKDDDDKADSVKDRFT**ISRDDSKNTAYLQMNNLKTEDTAVYY
CVR**HGNFGNSYISYWAY**WGQGLTVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLSCEAS**GFTF**
SKFGMSWVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:528)

Pro694

aB7H3 hF12 (S59A) sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTAYADSVKGR**
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAA**GGVLAHHNIEYDY**WGQGLTVTVSS/**GGGSGGGG**/EVQ
LVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**RIRSKYNNYATYYADQVKDRFT**
ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/**GGGSGGGG**/QTV
VTQEPSLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
AALTSGVQPEDEAEYYCT**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLS
CEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTAYADSVKGR**RFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAA**GGVLAHHNIEYDY**WGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLTC**GSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPE
DEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKY**
AMNWVRQAPGKGLEWVAR**RIRSKYDYKDDDDKADSVKDRFT**ISRDDSKNTAYLQMNNLKTEDTAVYY
CVR**HGNFGNSYISYWAY**WGQGLTVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLSCEAS**GFTF**
SKFGMSWVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:529)

Figure 10E

Pro695

aB7H3 hF12 (N57D) sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGDTSYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFT
ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
VTQEPLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGDTSYADSVKGRFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGT
VTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLCAASGFTF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:530)

Pro766

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– NCL-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFT
ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
VTQEPLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
AALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSGGNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
DTAVYYCAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGGSGGGGGG/QTVVTQEPLTVSPGGT
VTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
AMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCLCAASGFTF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI
GGSLVSSQGLTVTVSS/HHHHHH (SEQ ID NO:531)

Figure 10F

Pro565

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – acEpCAM hVIB664 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGKEREFVAAISWSGGSTDYAYSVKGR
FTISRDN SKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPLSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGKEREFVAAISWSGGSTDYAYSVKGRFTISRDN SKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLS
TVSPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASG
FTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLRSC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDT
AVYYCTGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:288)

Pro566

acEpCAM hVIB665 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – acEpCAM hVIB665 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTFSDYDMGWFRQGPGKEREFVAAISWSGGHTNYADSVKG
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPLSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTFSDYDMGWFRQGPGKEREFVAAISWSGGHTNYADSVKGRFTISRDN SKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLS
TVSPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCTVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGF
TFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLRSCA
ASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAV
YYCTGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:289)

Figure 10G

Pro567

acEpCAM hVIB666 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB666 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGRSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAIWSGGSTDYAYSVTGR
FTISRDNKNSLYLQMNSLRAEDTALYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGRSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAIWSGGSTDYAYSVTGRFTISRDNKNSLYLQMNS
LRAEDTALYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPST
TVSPGGTVTLTGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASG
FTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
DTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDT
AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:290)

Pro568

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB664 sdAb

– NCL-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAIWSGGSTDYAYSVKGR
FTISRDNKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAIWSGGSTDYAYSVKGRFTISRDNKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGGSGGGGS/QTVVTQEPS
LTVSPGGTVTLTGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAAS
GFTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDT
AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:291)

Figure 10H

Pro727

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – acEpCAM hVIB664 sdAb
– Meprin-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSTLVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGRFTISRDNSKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/SGGGKKLADEPEGGS/QTVVTQEPSTL
VSPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLS
GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGF
TFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDNSKNTAYLQMNNLKTED
TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAA
SGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAV
YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:292)

Pro728

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – acEpCAM hVIB664 sdAb
– MMP9v - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSTLVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGRFTISRDNSKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/SGGGPGPAGMHGLPGGS/QTVVTQE
PSLTVSPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAA
LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSA
ASGFTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDNSKNTAYLQMNNL
KTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRL
SCAASSGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPE
DTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:293)

Figure 10I

Pro729

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB664 sdAb
– CathS - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGRFTISRDNSKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSARLQSAAPGGGS/QTVVTQEPS
LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS
GFTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDT
AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:294)

Pro730

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB664 sdAb
– S9 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
RLSCAASGRTLDNYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGRFTISRDNSKNTLYLQMNS
LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/GARLQSAAPAGLKGAG/QTVVTQEPS
LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS
GFTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDT
AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:295)

Figure 10J

Pro731

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – acEpCAM hVIB664 sdAb
– ST14-MS - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLRSCAAS GRTLDNYDMGWFRQGP GKERE FVA AISW SGGSTDYAYS VKGR
FTISRDN SKNTLYLQMN SLRAEDTAVYYCAA DLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSGGGG
/EVQLVES GGGGLVQP GGSRLRSCAAS GFTFNKYAINWVRQAPGK GLEWVAR IRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
QTVVTQE PSLTVSPGGTVTLTC ASSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGSL
GGKAALT LSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES GGGGLVQP GGSRL
RLSCAAS GRTLDNYDMGWFRQGP GKERE FVA AISW SGGSTDYAYS VKGRRFTISRDN SKNTLYLQMN S
LRAEDTAVYYCAA DLRFTGGDTMTPETYDYWGQGLTVTVSS/GGGSLSGRSDNHGGG/QTVVTQE P
LTVSPGGTVTLTC GSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLGGKAALT
LSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVES GGGGLVQP GGSRLRSCAAS
GFTFNKYAMNWVRQAPGK GLEWVAR IRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMN NLKT
EDTAVYYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVES GGGGLVQP GNSRLRSC
AAS GFTFSKFGMSWVRQAPGK GLEWVSS SISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQMN SLRPEDT
AVYYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:296)

Pro676

aTrop2 hVIB565 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aTrop2 hVIB565 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLRSCAAS GFTFDYYAIGWFRQAPGK EREGVS CISSSHGSTYYADSVKGRRFTI
SRDN SKNTVYLQMN SLRAEDTAVYYCAT AGDGGDYHCSGLVDYGM DYWGKGLTVTVSS/GGGSGGGG
S/EVQLVESGGGLVQP GGSRLRSCAAS GFTFNKYAINWVRQAPGK GLEWVAR IRISKYNNYATYYADQV
KDRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG
S/QTVVTQEPSLTVSPGGTVTLTC ASSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGS
LLGGKAALT LSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES GGGGLVQP GGS
SLRSCAAS GFTFDYYAIGWFRQAPGK EREGVS CISSSHGSTYYADSVKGRRFTISRDN SKNTVYLQMN SL
RAEDTAVYYCAT AGDGGDYHCSGLVDYGM DYWGKGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQE
PSLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLGGKAA
LTL SGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVES GGGGLVQP GGSRLRSCA
AS GFTFNKYAMNWVRQAPGK GLEWVAR IRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMN NL
KTEDTAVYYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVES GGGGLVQP GNSRLR
SCAAS GFTFSKFGMSWVRQAPGK GLEWVSS SISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQMN SLRPE
DTAVYYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:297)

Figure 10K

Pro677

aTrop2 hVIB557 sdAb sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aTrop2 hVIB557 sdAb sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES^{GGGLVQPGGSLRL}SCAASGRTFSSQSMGWFRQAPGKEREFVSAISWTGANPTYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAADTSGGSYYYERATAETSYDYWGQGLTVTVSS/GGGSGG
GS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ
VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGG
GS/QTVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFS
GSLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES^{GGGLVQPGGSLRL}SCAASGRTFSSQSMGWFRQAPGKEREFVSAISWTGANPTYADSVKGRFTISRDNKNTLYLQ
MNSLRAEDTAVYYCAADTSGGSYYYERATAETSYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTV
VTQEPSTVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLK
LSAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQ
MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGGSLK
GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQM
NSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:298)

Pro678

aTrop2 hVIB575 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aTrop2 hVIB575 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES^{GGGLVQPGGSLRL}SCLASGRTVGRTAMGWFRQPPGKEREFVATISWAGGTTYAD^{DFVKGR}
FTISRDNKNTLYLQMNSLRAEDTAVYYCAASEPYSDYDPSGMVYWGKGLTVTVSS/GGGSGGGS/EV
QLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR
FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QT
VVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG
KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES^{GGGLVQPGGSLRL}
SCLASGRTVGRTAMGWFRQPPGKEREFVATISWAGGTTYAD^{DFVKGR}FTISRDNKNTLYLQMNSLRA
EDTAVYYCAASEPYSDYDPSGMVYWGKGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGG
TVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPE
DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSCAASGFTF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTI
GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:299)

Figure 10L

Pro679

aTrop2 hVIB578 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aTrop2 hVIB578 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLSCAAS GRTFGRAAMGWFRQPPGKEREF AATISWSGSNTYYAD FVKGR
FTISRDN SKNTVYLQMN SLRAEDTAVYYCAA SEPYSDYDPSGMVYWGKGLTVTVSS/GGGSGGGS/EV
QLVESGGGLVQP GGSRLSCAAS GFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR
FTISRDDS KNTAYLQMN NLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QT
VVTQEPSLTVSPGGTVTLTCA SSSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGG
KAALTLSGVQPEDEAEYYCT TLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES GGGGLVQP GGSRL
SCAAS GRTFGRAAMGWFRQPPGKEREF AATISWSGSNTYYAD FVKGRFTISRDN SKNTVYLQMN SLR
AEDTAVYYCAA SEPYSDYDPSGMVYWGKGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPG
GTVTLTCA SSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGGKAALTLSGVQ
PEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQP GGSRLSCAAS GFTFN
KYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDS KNTAYLQMN NLKTEDTAV
YYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GNSRLSCAAS GF
TFSKFGMSWVRQAPGKGLEWVSS SISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMN SLRPEDTAVYYC
T IGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:300)

Pro808

aTROP2 hVIB609 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aTROP2 hVIB609 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLSCALS GLTFNTYPMAWFRQPPGQEREFVADMSWSGTNTYYADSVKG
RFTISRDN SKNTLYLQMN SLRAEDTAVYYCAA GWPYSGTGRSTTDYTYWGQGLTVTVSS/GGGSGGGS
/EVQLVESGGGLVQP GGSRLSCAAS GFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
DRFTISRDDS KNTAYLQMN NLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSLTVSPGGTVTLTCA SSSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCT TLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES GGGGLVQP GGSRL
RLSCALS GLTFNTYPMAWFRQPPGQEREFVADMSWSGTNTYYADSVKGRFTISRDN SKNTLYLQMN S
LRAEDTAVYYCAA GWPYSGTGRSTTDYTYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLT
VSPGGTVTLTCA SSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGGKAALTLS
GVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQP GGSRLSCAAS GF
TFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDS KNTAYLQMN NLKTED
TAVYYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GNSRLSCAA
SGFTFSKFGMSWVRQAPGKGLEWVSS SISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMN SLRPEDTAV
YYCT IGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:301)

Figure 10M

Pro819

aTROP2 hVIB619 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aTROP2 hVIB619 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLS CAAS GRSFSRYGMGWLRQAPGKERELVA SISWSGHSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA ESLPYESGSPRLTDFASWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAINWVRQAPGKLEWVAR RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSTLVSPGGTVTLTCA ASSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCT TLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES GGGGLVQP GGSRLS CAAS GRSFSRYGMGWLRQAPGKERELVA SISWSGHSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA ESLPYESGSPRLTDFASWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTLVSPGGTVTLTCA GSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCT VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAMNWVRQAPGKLEWVAR RIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GNSRLS CAAS GFTFSKFGMSWVRQAPGKLEWVSS SISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:302)

Pro681

aTrop2 hVIB557 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aTrop2 hVIB557 sdAb
– NCL-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLS CAAS GRTFSSQSMGWFRQAPGKEREFVSA ISWTGANPTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA DTSGGSYYYERATAETSYDYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAINWVRQAPGKLEWVAR RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSTLVSPGGTVTLTCA ASSTGAVTSGNYPNWVQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCT TLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES GGGGLVQP GGSRLS CAAS GRTFSSQSMGWFRQAPGKEREFVSA ISWTGANPTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA DTSGGSYYYERATAETSYDYWGQGLTVTVSS/GGGSGGGGGSGGGGS/QTVVTQEPSTLVSPGGTVTLTCA GSSTGAVTSGNYPNWVQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGKAAALTLSGVQPEDEAEYYCT VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAMNWVRQAPGKLEWVAR RIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQP GNSRLS CAAS GFTFSKFGMSWVRQAPGKLEWVSS SISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNSLRPEDTAVYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:303)

Figure 10N

Pro621

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– CathS-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKG
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGG SARLQSAAPGGG/QTVVTQEPSLT
 VSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLS
 GVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGF
 TFNKYAMN WVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAA
 SGGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAV
 YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:304)

Pro622

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– CathS-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGR
 FTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT
 ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSLTVSPGGTVTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAE
 DTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GGG SARLQSAAPGGG/QTVVTQEPSLTVSPGGT
 VTLTCASTGAVTSGNYPNWWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPE
 DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKY
 AMN WVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY
 CVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTF
 SKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTI
 GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:305)

Figure 100

Pro640

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– MMP9v - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGR
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPS
 LTVSPGGTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALT
 LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAAS
 GFTFNKYAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKT
 EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLRSC
 AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDT
 AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:306)

Pro641

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9v - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGR
 FTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT
 ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAE
 DTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPSTVSPG
 GTVTLTCSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQ
 PEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFN
 KYAMNWWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV
 YYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLRSCAASGF
 TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYC
 TIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:307)

Figure 10P

Pro642

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– MMP9v - aCD3Vli2 – NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGR
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPS
 LTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALT
 SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASG
 FTFNKHAMNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAA
 SGGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAV
 YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:308)

Pro643

aB7H3 hF12 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF12 sdAb

– MMP9v - aCD3Vli2 – NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGR
 FTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GGGSGGGG/EVQ
 LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT
 ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTV
 VTQEPSTVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLS
 CEASPRTFSTYSMAWFRQAPGKERSFVAAINWSSGGNTSYADSVKGRFTISRDN SKNTLYLQMNSLRAE
 DTAVYYCAAAGGVLAHHNYEYDYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPSTVSPG
 GTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGVQPE
 DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKH
 AMNWVRQAPGKGLEWVARIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC
 VRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGGFTFS
 KFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIG
 GSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:309)

Figure 10Q

Pro744

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– MMP9-15 (K->E) - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/ EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/ QTVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVP GTPARFSGSLL GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS LRLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMEGLPGS/QTVVTQEPSLTV SPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFT FNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLS CAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDN AKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:310)

Pro746

haB7H3 F7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - haB7H3 F7 sdAb

– MMP9-15 (M->P) - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/ EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/ QTVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLVP GTPARFSGSLL GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS LRLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGPKGLPGS/QTVVTQEPSLTVS PGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFT FNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLS CAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDN AKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:311)

Figure 10R

Pro 108

aFOLR1 h77-2 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aFOLR1 h77-2 sdAb

– MMP9v - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAVYVCNRNFDRIYWGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLVQ
PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTA
YLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ QTVVTQEPSLTVSP
GGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP
EDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ QVQLVESGGGLVQPGGSLRLSCAASGFTVSN
SVMAWYRQTPGNEREFVAIINSIGITNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYVCNRNFD
RIYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/ QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYP
NWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVF
GGGTKLTVL/GGGSGGGGS/ EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWV
ARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAY
WGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAPGKGL
EWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVTVSS/
HHHHHH (SEQ ID NO:312)

Pro 109

aFOLR1 h59.3 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aFOLR1 h59.3 sdAb

– MMP9v - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGR
FTISRDNKNTLYLQMNSLRAEDTAVYYCKHYGIDYWGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLV
QPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT
AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ QTVVTQEPSLTV
SPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV
QPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ QVQLVESGGGLVQPGGSLRLSCAAPGNTF
SISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCK
HYGIDYWGQGLTVTVSS/GSGGPGPAGMHGLPGGS/ QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSG
NYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR
WVFGGGTKLTVL/GGGSGGGGS/ EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGL
EWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
GKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVT
VSS/HHHHHH (SEQ ID NO:313)

Figure 10S

Pro396

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

– MMP9v-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/Q
TVVTQEPLSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSGVQTGGSLR
LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GSGGPGPAGMHGLPGGS/QTVVTQEPLS
TVSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASG
FTFNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTE
DTAVYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLSC
AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDT
AVYYCTGGSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:314)

Pro476

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

– MMP9-15 - aCD3Vli2 – NCL-8 - aCD3Vhi2 – aHSA (10GE) - His6

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/E
VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/Q
TVVTQEPLSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSGVQTGGSLR
LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLSLTVS
PGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKDDAPGTPARFSGSLLGGKAALTLSGV
QPEDEAEYYCTVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTF
NKHAMNWVRQAPGKGLEWVARRIRSKYNNYATAYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV
YYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRSLSCAASGF
TFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVYYC
TGGSLSVSSQGTQVTVSS/HHHHHH (SEQ ID NO:315)

Figure 10T

Pro706**aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb****– uPA - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) – His6**

QVKLEESGGGVSQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGVSQTGGSLR
 LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLIEYDYWGQGTQTVSS/GGGSHTRGSAYFGGGS/QTVVTQEPSLTV
 SPGGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGTQTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGTQTVSS/HHHHHH (SEQ ID NO:316)

Pro709**aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb****– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6**

EVQLVESGGGVVRPGGSLRLSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNAKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLIEYDYWGQGTQTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGVVRPGGSLR
 LSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNAKNSLYLQMNSLR
 AEDTALYYCAAAAGSAWYGTLIEYDYWGQGTQTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSP
 GGTVTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGV
 QPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTF
NKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTEDTA
 VYYCVRHGNFGNSYISYWAYWGQGTQTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGTQTVSS/HHHHHH (SEQ ID NO:317)

Figure 10U

Pro470

aFOLR1 h77.2 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAVYYCNRNFDRIYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQ
 PGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKNTA
 YLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEPSLTVSP
 GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP
 EDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGVVRPGGSLTSCAASGRTSRSY
GMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNKNSLYLQMNSLRAEDTALYYCAAA
AGSAWYGTLYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCSSST
GAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL
WYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ
 APGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG
NSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSW
 VRQAPGKGLEWVSSSISGGRDTLAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTGGSLSVSS
 QGTLTVTVSS/HHHHHH (SEQ ID NO:318)

Pro471

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aFOLR1 h77.2 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLR
 LSCAASGFTVSNSVMAWYRQTPGNREFVAIINSIGITNYADSVKGRRFTISRDNKNTLYLQMNSLRAED
 TAVYYCNRNFDRIYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCSSSTG
AVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLW
YSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP
 GKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS
YISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVR
 QAPGKGLEWVSSSISGGRDTLAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTGGSLSVSSQG
 TLTVTVSS/HHHHHH (SEQ ID NO:319)

Figure 10V

Pro551

EGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aFOLR1 h59.3 sdAb

– MMP9-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVKLEESGGGVSQTTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGG/E
 VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/Q
 TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGLVQPGGSLR
 LSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGRRFTISRDNKNTLYLQMNSLR
 AEDTAVYYCKHYYGIDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCAGSS
TGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCV
LWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVR
 QAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF
GNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSAASGFTFSKFGMS
 WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVS
 SQGTQVTVSS/HHHHHH (SEQ ID NO:320)

Pro552

aFOLR1 h59.3 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – EGFR sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAAPGNTFSISAMGWYRQAPGKQREWVAVTHSDYSTNYADSVKGR
 FTISRDNKNTLYLQMNSLRAEDTAVYYCKHYYGIDYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLV
 QPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKNT
 AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/QTVVTQEPSLTV
 SPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAALTLSGV
 QPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGVSQTTGGSLRLTCAASGRTS
RSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNKNTVDLQMNSLKPEDTAIYYC
 AAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCA
GSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEY
 YCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMN
 WVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH
GNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSAASGFTFSKFG
MSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSL
 SVSSQGTQVTVSS/HHHHHH (SEQ ID NO:321)

Figure 10W

Pro623**aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB664 sdAb****– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6**

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSLR
 LSCAASGRTLNDYDMGWFRQGPGRKREFVAAISWSGGSTDYAYSVKGRRFTISRDNKNTLYLQMNSL
 RAEDTAVYYCAADLRFTGGDTMTPEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLT
 VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLS
 GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGF
TFNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAA
SGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAV
 YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:322)

Pro624**aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB665 sdAb****– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6**

QVKLVESGGGVVRPGGSLTSCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNSLYLQMNSLRAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSLR
 LSCAASGRTFSDYDMGWFRQGPGRKREFVAAISWSGGHTNYADSVKGRRFTISRDNKNTLYLQMNSL
 RAEDTAVYYCAADLRFTGGDTTTPETDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLT
 VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLS
 GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGF
TFNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAA
SGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAV
 YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:323)

Figure 10X

Pro698

acEpCAM hVIB665 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aEGFR sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTFSDYDMGWFRQGPGRKEREFAAAISWSGGHTNYADSVKG
 RFTISRDNKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/GGGSGGGS/
 /EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
 QTVVTQEPSTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGT PARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLVESGGGVVRPGGSL
 TLSCAASGRTSRSYGMGWFRQAPGKEREFAAGISWRGDSTGYADSVKGRFTISRDNKNTLYLQMNSL
 RAEDTALYYCAAAAGSAWYGTLYEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTV
 PGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFT
FNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNSLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:324)

Pro655

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB664 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFAAVINWSGGSTVYADSVKG
 RFTISRDNKNTLYLQMNSLRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGS/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
 QTVVTQEPSTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGT PARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLESGGGLVQPGGSL
 RLSCAASGRTLDNYDMGWFRQGPGRKEREFAAAISWSGGSTDYAYSVKGRRFTISRDNKNTLYLQMNS
 LRAEDTAVYYCAADLRFTGGDTMTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTV
 TVSPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALT
 SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASG
FTFNKYAMNWVRQAPGKGLEWVARIRISKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQMNSLKT
 EDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSC
 AASGFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDT
 AVYYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:325)

Figure 10Y

Pro656

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB665 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGR
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAA GGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSCAASSGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLESGGGLVQPGGSL
 RLSCAASGRTFSDYDMGWFRQGPGRKEREFAAISWSSGGHTNYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLT
 VSPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLS
 GVPQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGF
TFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAA
SGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAV
 YYCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:326)

Pro657

acEpCAM hVIB664 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - haB7H3 F7 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLSCAASGRTLNDYDMGWFRQGPGRKEREFAAISWSSGGSTDYAYSVKGR
 FTISRDN SKNTLYLQMNSLRAEDTAVYYCAADLRFTGGDTMTPEYDYWGQGLTVTVSS/GGGSGGGG/
 /EVQLVESGGGLVQPGGSLKLSCAASSGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 RLSCAPSRRTFHTYHMGWFRQAPGKEREFAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTV
 SPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDN AKTTLYLQMNSLRPEDTAV
 YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:327)

Figure 10Z

Pro658**acEpCAM hVIB665 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) - haB7H3 F7 sdAb****– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6**

QVQLLES~~GGGLVQPGGSLRL~~SCAASGRTFSDYDMGWFRQGP~~GKERE~~FVAAISWSSGGHTNYADSVKG
 RFTISRDN~~SKNTLYLQMNS~~LR~~AEDTAVYYCAA~~DLRFTGGDTTTPETYDYWGQGLTVTVSS/GGGSGGGG
 /EVQLVES~~GGGLVQPGGSLKL~~SCAASGFTFNKYAINWVRQAP~~GKLEW~~VARIRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEP~~SLTVSPGGTVTLT~~CASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSL
 LGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAP~~GKERE~~FVAVINWSSGGSTVYADSVKGRFTISRDN~~SKNTLYLQMNS~~
 LRAEDTAVYYCAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEP~~SLTV~~
 SPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAP~~GKLEW~~VARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAAS
GFTFSKFGMSWVRQAP~~GKLEW~~VSSSISGSGRDTLYAESVKGRFTISRDN~~AKTTLYLQMNS~~LRPEDTAVY
 YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:328)

Pro516**aCA9 hVIB456 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aCA9 hVIB456 sdAb****– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6**

QVQLVESGGGLVQPGGSLRLSCAASGSALIINAMGWYRQAP~~GKQREL~~VATTVTRSGRTNYADSVKGRF
 TISRDN~~SKNTLYLQMNS~~LR~~AEDTAVYYCNV~~ALWIADGEYDYWGQGLTVTVSS/GGGSGGGG/EVQLVE
 SGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP~~GKLEW~~VARIRISKYNNYATYYADQVKDRFTISR
 DDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVTQ
 EP~~SLTVSPGGTVTLT~~CASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLGGKAAL
 TLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGLVQPGGSLRLSCAA
SGSALIINAMGWYRQAP~~GKQREL~~VATTVTRSGRTNYADSVKGRRFTISRDN~~SKNTLYLQMNS~~LR~~AEDTAV~~
 YYCNVALWIADGEYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEP~~SLTVSPGGTVTLT~~CGS
STGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLGGKAALTLSGVQPEDEAEYYC
VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV
 RQAP~~GKLEW~~VARIRISKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN
FGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS
 WVRQAP~~GKLEW~~VSSSISGSGRDTLYAESVKGRFTISRDN~~AKTTLYLQMNS~~LRPEDTAVYYCTIGGSLSVS
 SQGLTVTVSS/HHHHHH (SEQ ID NO:329)

Figure 10AA

Pro517

aCA9 hVIB476 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aCA9 hVIB476 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAASGNIFIINVMGWYRQAPGKQRELVATITNGGRTHYADSVKGRRFT
 ISRDNSKNTLYLQMNSLRAEDTAVYYCNANHIELGDYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGL
 VQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKN
 TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVTQEPSLT
 VSPGGTVTLTASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV
 QPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGLVQPGGSLRLSCAASGNIFI
INVMGWYRQAPGKQRELVATITNGGRTHYADSVKGRRFTISRDNKNTLYLQMNSLRAEDTAVYYCNA
NHIELGDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTGSSTGAVTSG
NYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR
WVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL
 EWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
 GKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVT
 VSS/HHHHHH (SEQ ID NO:330)

Pro518

aCA9 hVIB407 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aCA9 hVIB407 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCTASGIIFSVYDMGWYRQTPGKQREFVARITAGGGTYLTDSVKGRRFTI
 SRDNKNTLYLQMNSLRAEDTGYYCNAAWIGDDYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGL
 VQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKN
 TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVTQEPSLT
 VSPGGTVTLTASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV
 QPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGLVQPGGSLRLSCTASGIIFS
VYDMGWYRQTPGKQREFVARITAGGGTYLTDSVKGRRFTISRDNKNTLYLQMNSLRAEDTGYYCNA
AWIGDDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTGSSTGAVTSG
NYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNR
WVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL
 EWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
 GKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTVT
 VSS/HHHHHH (SEQ ID NO:331)

Figure 10BB

Pro519

aCA9 hVIB445 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aCA9 hVIB445 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVKPGGSLRLSCAASGITFNLHAMRWYRRAPGKQRELVAYISARDWTNYADSVKGRFT
TISRDNAKNSLYLQMNSLRAEDTAVYYCNTDLVGEDYWGRGTLTVSS/GGGSGGGS/EVQLVESGGGL
VQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKN
TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLT
VSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTSGV
QPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVKPGGSLRLSCAASGITF
NLHAMRWYRRAPGKQRELVAYISARDWTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCN
TDLVGEDYWGRGTLTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTSPGGTVTLTCGSSTGAVTSG
NYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLWYSNR
WVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL
EWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGTTLTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
GKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSQGT
VSS/HHHHHH (SEQ ID NO:332)

Pro513

aCA9 hVIB476 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aCA9 hVIB476 sdAb

– NCL-16 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGLVQPGGSLRLSCAASGNIFIINVMGWYRQAPGKQRELVATITNGGRTHYADSVKGRFT
ISRDNKNTLYLQMNSLRAEDTAVYYCNANHIELGDYWGQGTTLTVSS/GGGSGGGS/EVQLVESGGGL
VQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRFTISRDDSKN
TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTTLTVSS/GGGSGGGS/QTVVTQEPSLT
VSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTSGV
QPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVESGGGLVQPGGSLRLSCAASGNIFI
INVMGWYRQAPGKQRELVATITNGGRTHYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCNA
NHIELGDYWGQGTTLTVSS/GGGSGGGSGGGSGGGS/QTVVTQEPSLTSPGGTVTLTCGSSTGAVTS
GNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLWYSNR
WVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAPGKGL
EWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY
WAYWGQGTTLTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMSWVRQAP
GKGLEWVSSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSQGT
VSS/HHHHHH (SEQ ID NO:333)

Figure 10CC

Pro186

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/GGGSGGGG/E
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQTVSS/GGGSGGGG/Q
 TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSGVQTGGSLR
 LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNKNTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVS
 PGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGTQTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGTQTVSS/HHHHHH (SEQ ID NO:334)

Pro214

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

– NCL-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/GGGSGGGG/E
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQTVSS/GGGSGGGG/Q
 TVVTQEPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVKLEESGGGSGVQTGGSLR
 LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNKNTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQTVSS/GGGSGGGGSGGGG/QTVVTQEPSLTV
 SPGGTVTLTCAGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGTQTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKNTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGTQTVSS/HHHHHH (SEQ ID NO:335)

Figure 10DD

Pro225

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKG
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSTLVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTLV
 SPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFT
 FNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAAS
 GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDN AKTTLYLQMNSLRPEDTAVY
 YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:336)

Pro295

aB7H3 hF7 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aB7H3 hF7 sdAb

– NCL-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKG
 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGG/
 EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
 DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
 QTVVTQEPSTLVSPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
 GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGS
 LRLSCAPSRRTFHTYHMGWFRQAPGKEREFVAVINWSSGGSTVYADSVKGRFTISRDN SKNTLYLQMNS
 LRAEDTAVYYCAAAGGATTQRATEASYDYWGQGLTVTVSS/GGGSGGGGSGGGG/QTVVTQEPSTLV
 SPGGTVTLTCASTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLS
 GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGF
 TFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTED
 TAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAA
 SGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRTISRDN AKTTLYLQMNSLRPEDTAV
 YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:337)

Figure 10EE

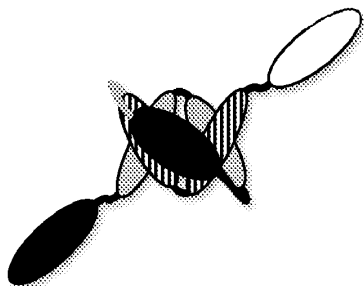
Pro 817

aEGFR sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - aEGFR sdAb

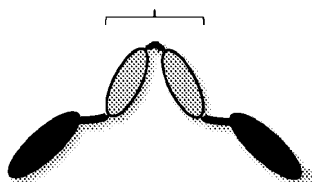
– MMP9-15 - aCD3Vli –NCL-8 - aCD3Vhi – HSA

QVKLEESGGGSGVQTGGSLRLTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGR
 FTISRDNKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKD
 RFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTTLTCAASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVKLEESGGGSGVQTGGSLR
 LTCAASGRTSRSYGMGWFRQAPGKEREFVSGISWRGDSTGYADSVKGRRFTISRDNKNTVDLQMNSL
 KPEDTAIYYCAAAAGSAWYGTLYEYDYWGQGTQVTVSS/SGGPAGMKGLPGS/QTVVTQEPSLTVS
 PGGTTLTCAGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLSG
 VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFT
FNKYAMNWVRQAPGKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVRHGNFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/DAHKSEVAHFRKDLGEENFKALVLI
 AFAQYLQQCPFEDHVKLNVETFAKTCVADESAENCDSLHTLFGDKLCTVATLRETYGEMADCCAKQ
 EPERNECFLQHKDDNPRLPRLVRPEVDVMCTAFHDNEETFLKKYLYEARRHPYFYAPELLFFAKRYKAAF
 TECCQAADKAACLLPKLDELDEGKASSAQRLKCASLQKFGERAFAKAWAVARLSQRFPKAFAEVSCLV
 TDLTKVHTECCHGDLLECADRADLAKYICENQDSISSKLKECCEKPLEKSHCIAEVENDEMPADLPSLAA
 DFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYKTTLEKCCAAADPHECYAKVDFEFK
 PLVEEPQNLKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPC
 AEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKE
 RQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKADDKETCFAEEGKKLVAASRAALGL (SEQ
 ID NO:338)

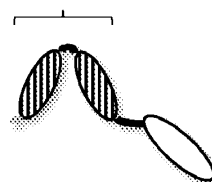
Figure 11

Pro186 Pre-Cleavage

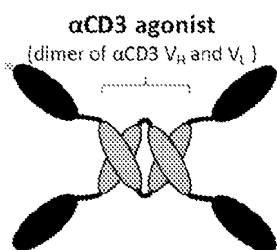
Binds EGFR
Impaired CD3 Binding
Binds serum albumin

Predicted Pro186 Cleavage Products α CD3 V_H and V_L

Binds EGFR
Impaired CD3 Binding

inactive V_H and V_L

Binds serum albumin



Binds EGFR
Binds CD3

Figure 12A

 α LyPD3 h787 COBRA

QVQLLES GGGGLVQP GGSRLRLSCAAS GFTLDYYAIGWFRQAPGKEHEAVS CISSSDGSTYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAVYYCAT VKSCYSDGYALWGSWGQGLTVTVSS/GGGSGGGGS/ EVQL
VESGGGLVQP GGSRLKLSAAS GFTFNKYAINWVRQAPGKGLEWVAR RIRSKYNNYATYYADQVKDRFTI
SRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ QTVV
TQEPSTVSPGGTVTLTCA ASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ QVQLLES GGGGLVQP GGSRLRLSC
AAS GFTLDYYAIGWFRQAPGKEHEAVS CISSSDGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA
VYYCAT VKSCYSDGYALWGSWGQGLTVTVSS/SGGPGPAGMKGLPGS/ QTVVTQEPSTVSPGGTVTL
TC GSSTGAVTSGNYPNWVQQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEA
EYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ EVQLVESGGGLVQP GGSRLKLSAAS GFTFNKYAM
NWVRQAPGKGLEWVAR IRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR
HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLVQP GNSRLRLSCAAS GFTFSKF
GMSWVRQAPGKGLEWVS SISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTI GGG
LSVSSQGLTVTVSSHHHHHH (SEQ ID NO:453)

 α LyPD3 h790 COBRA

QVQLLES GGGGLVQP GGSRLRLSCAAS GFTLDYYSIGWFRQAPGKEREGVS CISSSDGSTYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAVYYCAT VKSCYVDGYILWGSWGQGLTVTVSS/GGGSGGGGS/ EVQLV
ESGGGLVQP GGSRLKLSAAS GFTFNKYAINWVRQAPGKGLEWVAR RIRSKYNNYATYYADQVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ QTVVT
QEPSTVSPGGTVTLTCA ASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ QVQLLES GGGGLVQP GGSRLRLSC
AAS GFTLDYYSIGWFRQAPGKEREGVS CISSSDGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTA
VYYCAT VKSCYVDGYILWGSWGQGLTVTVSS/SGGPGPAGMKGLPGS/ QTVVTQEPSTVSPGGTVTL
TC GSSTGAVTSGNYPNWVQQKPGQAPRGLIG DYKDDDDKGTPARFSGSLLGGKAALTLSGVQPEDEA
EYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGGS/ EVQLVESGGGLVQP GGSRLKLSAAS GFTFNKYAM
NWVRQAPGKGLEWVAR IRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR
HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGGS/ EVQLVESGGGLVQP GNSRLRLSCAAS GFTFSKF
GMSWVRQAPGKGLEWVS SISGSGRDTLYAESVKGRFTISRDNKNTLYLQMNSLRPEDTAVYYCTI GGG
LSVSSQGLTVTVSSHHHHHH (SEQ ID NO:454)

Figure 12B

 α LyPD3 H804 COBRA

QVQLLES~~GGGLVQPGGSLRL~~SCAASGFTLDYYAIGWFRQAPGKEHEGVSCISSDGSTYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAVYYCATVRSCASPYELGSWGQGLTVTVSS/GGGSGGGS/EVQLVESG
GGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQEP
SLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES~~GGGLVQPGGSLRL~~SCAASG
FTLDYYAIGWFRQAPGKEHEGVSCISSDGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC
ATVRSCASPYELGSWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCGSSTG
AVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLW
YSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVES~~GGGLVQPGGSLKLSAAS~~GFTFNKYAMNWVRQAP
GKLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS
YISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVES~~GGGLVQPGNSLRL~~SCAASGFTFSKFGMSWVR
QAPGKLEWVSSISGSGRDTLYAESVKGRFTISRDNATTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQG
TLTVSSHHHHHH (SEQ ID NO:455)

 α LyPD3 h773 COBRA

QVQLVES~~GGGLVQPGGSLRL~~SCAASGRSFSSYGMGWFRQAPGKEREIVAAISWGGSAVYYANSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAANNRQGRALVRKEFYDYWGQGLTVTVSS/GGGSGGGS/E
VQLVES~~GGGLVQPGGSLKLSAAS~~GFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADQVKD
RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/Q
TVVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG
GKAALTSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLVES~~GGGLVQPGGSLR~~
LSAASGRSFSSYGMGWFRQAPGKEREIVAAISWGGSAVYYANSVKGRFTISRDNSKNTLYLQMNSLR
AEDTAVYYCAANNRQGRALVRKEFYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSP
GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGV
QPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVES~~GGGLVQPGGSLKLSAAS~~GFTF
NKYAMNWVRQAPGKLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA
VYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVES~~GGGLVQPGNSLRL~~SCAAS
GFTFSKFGMSWVRQAPGKLEWVSSISGSGRDTLYAESVKGRFTISRDNATTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGTLTVSSHHHHHH (SEQ ID NO:456)

Figure 12C

 α LyPD3 h840 COBRA

QVQLLES~~GGG~~KVQPGGSLRLSCVVS**GDTSSIYLMG**WYRQTPGKQRELVA**HIRGN****GR****TNYADSVKGR**F
TISRDN**SKNTLYLQMN**SLRAEDTAVYYCN**VRNFWGSAEY**WGQGLTVTVSS/~~GGGSGGGG~~/EVQLVESG
GGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**DRFTISRDD
SKNTAYLQMN**NLKTEDTAVYYCVRHANFGNSYISYWAY**WGQGLTVTVSS/~~GGGSGGGG~~/QTVVTQEP
SLTVSPGGTVTLTC**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALTL
SGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/~~GGGSGGGG~~/QVQLLES~~GGG~~KVQPGGSLRLSCVVS**G**
DTSSIYLMGWYRQTPGKQRELVA**HIRGN****GR****TNYADSVKGR**FRTISRDN**SKNTLYLQMN**SLRAEDTAVYY
CN**VRNFWGSAEY**WGQGLTVTVSS/~~SGGPGPAGMKGLPGS~~/QTVVTQEP**SLTVSPGGTVTLTCGSSTG**
AVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTL**SGVQPEDEAEYYCVLW**
YSNRWVFGGGTKLTVL/~~GGGSGGGG~~/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAMN**WVRQAP
GKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMN**NLKTEDTAVYYCVRHGNFGNS**
YISYWAYWGQGLTVTVSS/~~GGGSGGGG~~/EVQLVESGGGLVQPGNSRLS**CAASGFTFSKFGMS**WVR
QAPGKGLEWVS**SISGSGRDTLYAESVKGR**FRTISRDN**AKTTLYLQMN**SLRPEDTAVYYCTIG**GSLSV**SSQG
TLTVSSHHHHHHH (SEQ ID NO:457)

 α LyPD3 h885 COBRA

QVQLLESGGGLVQPGGSLRLSCVAS**RGTF****SRYS****MG**WFRQAPGKEREFV**GRISW****SGDM****TYADSVKGR**
FTISRDN**SKNTLYLQMN**SLRAEDTAVYYCAA**STLGYVWNHPNMYGY**WGHGTLTVTVSS/~~GGGSGGGG~~/
EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**
DRFTISRDDSKNTAYLQMN**NLKTEDTAVYYCVRHANFGNSYISYWAY**WGQGLTVTVSS/~~GGGSGGGG~~/
QTVVTQEP**SLTVSPGGTVTLTCASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLL
GGKAALTL**SGVQPEDEAEYYCTLWYSNRWV**FGGGTKLTVL/~~GGGSGGGG~~/QVQLLESGGGLVQPGGSL
RLSCVAS**RGTF****SRYS****MG**WFRQAPGKEREFV**GRISW****SGDM****TYADSVKGR**FRTISRDN**SKNTLYLQMN**SL
RAEDTAVYYCAA**STLGYVWNHPNMYGY**WGHGTLTVTVSS/~~SGGPGPAGMKGLPGS~~/QTVVTQEP**SLTV**
SPGGTVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTL**SG**
VQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/~~GGGSGGGG~~/EVQLVESGGGLVQPGGSLKLSAAS**GFT**
FNKYAMNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMN**NLKTEDT**
AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/~~GGGSGGGG~~/EVQLVESGGGLVQPGNSRLS**CAAS**
GFTFSKFGMSWVRQAPGKGLEWVS**SISGSGRDTLYAESVKGR**FRTISRDN**AKTTLYLQMN**SLRPEDTAVY
YCTIG**GSLSV**SSQGTLTVSSHHHHHHH (SEQ ID NO:458)

Figure 12D

 α HER2 1054 COBRA

QVQLQESGGGLVQAGGSLILSCAASGRTFSNYAMGWFRQAPGKEREFVAAINWSGTHTDYADSVKG
RFTISRDNVKRTVYLQMNSLKPEDTATYFCSRGWSVFDPDYRGQGTQVTVSS/GGGSGGGS/EVQLVES
GGGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRD
DSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQE
PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAALT
LSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQAGGSLILSCAAS
GRTFSNYAMGWFRQAPGKEREFVAAINWSGTHTDYADSVKGRFTISRDNVKRTVYLQMNSLKPEDTA
TYFCSRGWSVFDPDYRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCGSST
GAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL
WYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQ
APGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFG
NSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRILSCAASGFTFSKFGMSW
VRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSS
QGLTVTVSSHHHHHH (SEQ ID NO:459)

 α HER21055 COBRA

QVQLQESGGGLVQPGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKNVTYVLQMNSLKPEDTATYFCSRGWSVFDPDYRGQGTQVTVSS/GGGSGGGS/EVQLVESG
GGLVQPGGSLKLSAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/QTVVTQE
SLTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLTCEVSG
RAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRRFTISRDNVKNVTYVLQMNSLKPEDTATYF
CSRGWSVFDPDYRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCGSSTGA
VTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWY
SNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAASGFTFNKYAMNWVRQAP
GKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS
YISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRILSCAASGFTFSKFGMSWVR
QAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ
GLTVTVSSHHHHHH (SEQ ID NO:460)

Figure 12E

 α HER2 1058 COBRA

QVQLQESGGGLVQPGGSLRLTCAAS**GRAISSYAI**SWFRQAPGEEREFVA**AINWSGTH**TNYADSVKGRF
TISRDNVKNVTYVYLMNSLKPEDTATYFC**SRGWSVFD**PDYRGQGTQVTVSS/**GGGSGGGG**/EVQLVESG
GGLVQPGGSLKLSCAAS**GFTFNKYAI**NWVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**DRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/QTVVTQEP
SLTVSPGGTTLTCA**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALT
SGVQPEDEAEYYCT**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLTCAAS
GRAISSYAISWFRQAPGEEREFVA**AINWSGTH**TNYADSVKGRFTISRDNVKNVTYVYLMNSLKPEDTATY
FC**SRGWSVFD**PDYRGQGTQVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGTTLTCA**GSSTG**
AVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPEDEAEYYC**VLW**
YSNRWVFGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAP
GKGLEWVAR**IRSKYDYKDDDDKADSVK**DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNS**
YISYWAYWGQGTQVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSRLS**CAASGFTFSKFGMS**WVR
QAPGKGLEWVSS**SISGSGRDTLYAESVK**GRFTISRDNKTTLYLQMNSLRPEDTAVYYCT**IGGSLSV**SSQG
TLTVSSHSHHHHH (SEQ ID NO:461)

 α HER2 1059 COBRA

QVQLQESGGGLVQPGGSLRLTCAAS**GRAISSYAI**SWFRQAPGEEREFVA**AINWSGTH**TDYADSVKGRF
TISRDNKNTYVYLMNSLKPEDTAVYFC**SRGWSVFD**PDYRGQGTQVTVSS/**GGGSGGGG**/EVQLVESG
GGLVQPGGSLKLSCAAS**GFTFNKYAI**NWVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**DRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/QTVVTQEP
SLTVSPGGTTLTCA**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALT
SGVQPEDEAEYYCT**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLTCAAS
GRAISSYAISWFRQAPGEEREFVA**AINWSGTH**TDYADSVKGRFTISRDNKNTYVYLMNSLKPEDTAV
YFC**SRGWSVFD**PDYRGQGTQVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSTVSPGGTTLTCA**GSST**
GAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPEDEAEYYC**VL**
WYSNRWVFGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQ
APGKGLEWVAR**IRSKYDYKDDDDKADSVK**DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFG**
NSYISYWAYWGQGTQVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSRLS**CAASGFTFSKFGMS**W
VRQAPGKGLEWVSS**SISGSGRDTLYAESVK**GRFTISRDNKTTLYLQMNSLRPEDTAVYYCT**IGGSLSV**SS
QGTTLTVSSHSHHHHH (SEQ ID NO:462)

Figure 12F

 α HER2 1065 COBRA

QVQLQESGGGLVQPGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVVKRTVYLQMNLSKPEDTATYFCSRGWSVFDPDYRGQGTQVTVSS/GGGSGGGG/EVQLVESG
GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/QTVVTQEP
SLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRLTCEVSG
RAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRFTISRDNVVKRTVYLQMNLSKPEDTATYF
CSRGWSVFDPDYRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCSSTGA
VTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTARFSGSLLGGKAALTSGVQPEDEAEYYCVLWY
SNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAP
GKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS
YISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVR
QAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNLSRPEDTAVYYCTIGGSLSVSSQG
TLTVSSHSHHHH (SEQ ID NO:463)

 α HER2 1090 COBRA

QVQLQESGGGLVQTGGSLRLTCEVSGRAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRF
TISRDNVKNVTYVLQMNLSKPEDTATYFCSRGWSLFDPDYRGQGTQVTVSS/GGGSGGGG/EVQLVESG
GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/QTVVTQEP
SLTVSPGGTVTLTCASTGAVTSGNYPNWWQKPGQAPRGLIGGTFKFLVPGTPARFSGSLLGGKAALT
SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQTGGSLRLTCEVSG
RAISSYAIWFRQAPGEEREFVAAINWSGTHTNYADSVKGRFTISRDNVKNVTYVLQMNLSKPEDTATYF
CSRGWSLFDPDYRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCSSTGA
VTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTARFSGSLLGGKAALTSGVQPEDEAEYYCVLWY
SNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWWVRQAP
GKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNS
YISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSLCAASGFTFSKFGMSWVR
QAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNKTTLYLQMNLSRPEDTAVYYCTIGGSLSVSSQG
TLTVSSHSHHHH (SEQ ID NO:464)

Figure 12G

 α HER2 1091 COBRA

QVQLQESGGGLVQPGGSLRLSCAAS**GFTFDDYAMS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**
RFTISRDNANTLYLQMNSLKSEDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTVSS/**GGGSGGGG**/EVQ
LVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKDRFT**
ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/QTV
VTQEPSLTVSPGGTVTLT**CASTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
AALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGSLRLS
CAAS**GFTFDDYAMS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**RFTISRDNANTLYLQMNSLK
EDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLT**CGSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGVQPE
DEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKY**
AMNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDRFT**ISRDDSKNTAYLQMNNLKTEDTAVYY
CVR**HGNFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSRLS**CAASGFTF**
SKFGMSWVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNANTLYLQMNSLRPEDTAVYYCTI
GGSLSVSSQGTQVTVSSHHHHHH (SEQ ID NO:465)

 α HER2 1092 COBRA

QVQLQESGGGLVQAGASRLS**CAASGFTFDDYALS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**
RFTISRDNANTLYLQMNSLKSEDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTVSS/**GGGSGGGG**/EVQ
LVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKDRFT**
ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/QTV
VTQEPSLTVSPGGTVTLT**CASTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
AALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQAGASRLS
CAAS**GFTFDDYALS**WVRQAPGKGLEWVSS**SINWSGTHTDYADSVKG**RFTISRDNANTLYLQMNSLK
EDSAVYYCVK**GWRLTGGYYDSV**QGQGTQVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSPGGT
VTLT**CGSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGVQPE
DEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKY**
AMNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDRFT**ISRDDSKNTAYLQMNNLKTEDTAVYY
CVR**HGNFGNSYISYWAY**WGQGTQVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSRLS**CAASGFTF**
SKFGMSWVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNANTLYLQMNSLRPEDTAVYYCTI
GGSLSVSSQGTQVTVSSHHHHHH (SEQ ID NO:466)

Figure 12H

αHER2 1097 COBRA

QVQLQESGGGLVQPGGSLRLSCAASGFIFDDYAMTWVRQAPGKGLEWVSSSINWSGTHTDYADSVKG
 RFTISRDNAKNTLYLQMNSLKSEDSAVYYCVKGWRHTDNYYAGVQGGGTQVTVSS/GGGSGGGG/EV
 QLVEGGGLVQPGGSLKLSAASGFIFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR
 FTISRDDSNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/QT
 VVTQEPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGG
 KAALTLGVPEDAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQPGGSLRL
 SCAASGFIFDDYAMTWVRQAPGKGLEWVSSSINWSGTHTDYADSVKGRFTISRDNAKNTLYLQMNSLK
 SEDSAVYYCVKGWRHTDNYYAGVQGGGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGG
 TVTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLGVPQPE
 DEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFIFNKY
AMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSNTAYLQMNNLKTEDTAVYY
 CVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAASGFIF
SKFGMSWVRQAPGKGLEWVSSSISGSGRDTLYAESVKGRRFTISRDNAKNTLYLQMNSLRPEDTAVYYCTI
GGSLSVSSQGTQVTVSSHHHHHH (SEQ ID NO:467)

αHER2 1118 COBRA

QVQLQESGGGLVQAGGSLRLSCAASGFIFDDYAMSWVRQTPGKGLEWVSSSINWSGTHTNYADSVKG
 RFTISRDNAKNTLYLQMNSLKSEDTAVYYCARGGWMMVVPDSTRGQGTQVTVSS/GGGSGGGG/EVQLVE
 SGGGLVQPGGSLKLSAASGFIFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR
 DDSNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/QTVVTQ
 EPSTVSPGGTVTLTCASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGTTPARFSGSLLGGKAAL
 TLGVPQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCAA
SGFIFDDYAMSWVRQTPGKGLEWVSSSINWSGTHTNYADSVKGRFTISRDNAKNTLYLQMNSLKSEDT
 AVYYCARGGWMMVVPDSTRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCG
SSTGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTLGVPQPEDEAEYY
 CVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAASGFIFNKYAMNW
 VRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSNTAYLQMNNLKTEDTAVYYCVRHG
NFGNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLSCAASGFIFSKFGM
SWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRRFTISRDNAKNTLYLQMNSLRPEDTAVYYCTIGGSLSV
 SSQGTQVTVSSHHHHHH (SEQ ID NO:468)

Figure 12I

 α HER2 1121 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GFIFSDYAMT**WVRQAPGKGLEWVSS**SINWSGTH**TNYADSVKG
 RFTISRDNAKKTLTLQMNLSKSEDTAVYYCARG**WMVVPDSTR**RGQGTQVTVSS/GGGSGGGG/EVQLVE
 SGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR
 DDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTTLTVSS/GGGSGGGG/QTVVTQ
 EPSLTVSPGGTVTLT**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GT PARFSGSLLGGKAAL
 TLGSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCAA
SGFIFSDYAMTWVRQAPGKGLEWVSS**SINWSGTH**TNYADSVKG**RFTISRDNAKKTLTLQMNLSKSEDTA**
 VYYCARG**WMVVPDSTR**RGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLT**CGS**
STGAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GT PARFSGSLLGGKAALTLGSGVQPEDEAEYYC
VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WV
 RQAPGKGLEWVARIRSKY**DYKDDDDKADSVKDR**FTISRDDSNTAYLQMNNLKTEDTAVYYCVR**HGN**
FGNSYISYWAYWGQGTTLTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**
 WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKG**RFTISRDNAKKTLTLQMNLRPEDTAVYYCT**IGGSLSV**S
 SQGTTLTVSSHHHHHH (SEQ ID NO:469)

 α HER2 1134 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFSAAVMA**WYRQPPGEQRELVA**SITHRGFTRYADSVKDR**FT
 ISRDNVNNTMYLQMNRLSPEDTAIYYCRL**LNGDY**WGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLV
 QPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSNT
 AYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTTLTVSS/GGGSGGGG/QTVVTQEPSLTV
 SPGGTVTLT**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GT PARFSGSLLGGKAALTLGSGV
 QPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCAAS**GRIF**
SAAVMAWYRQPPGEQRELVA**SITHRGFTRYADSVKDR**FTISRDNVNNTMYLQMNRLSPEDTAIYYCRL
LNGDYWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLT**CGSSTGAVTSGNY**
PNWVQKPGQAPRGLIG**DYKDDDDK**GT PARFSGSLLGGKAALTLGSGVQPEDEAEYYC**VLWYSNRWV**
 FGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQAPGKGLEW
 VARIRSKY**DYKDDDDKADSVKDR**FTISRDDSNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**
 WGQGTTLTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSKFGMS**WVRQAPGKGL
 EWVSS**SISGSGRDTLYAESVKG**RFTISRDNAKKTLTLQMNLRPEDTAVYYCT**IGGSLSV**SSQGTTLTVSSH
 HHHHH (SEQ ID NO:470)

Figure 12J

 α HER2 1138 COBRA

QVQLQESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKEMEWVSGINWSGTHTRYADSVK
GRFTISRDNAKNTLDLQMNSLISEDTAVYYCARGGFAADSRSTRRGQGTQVTVSS/GGGSGGGS/EVQLVE
SGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR
DDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTVVTQ
EPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGT PARFSGSLLGGKAAL
TLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLSCAA
SGFTFDDYAMSWVRQAPGKEMEWVSGINWSGTHTRYADSVKGRFTISRDNAKNTLDLQMNSLISED
TAVYYCARGGFAADSRSTRRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCAS
STGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYYC
VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV
RQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGN
FGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMS
WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIIGGSLSVS
SQGTQVTVSSHHHHHH (SEQ ID NO:471)

 α HER2 1139 COBRA

QVQLQESGGGLVQPGGSLRLSCAASGFTFDDYAMSWVRQAPGKEMEWVSGINWSGTHTRYADSVK
GRFTISRDNAKNTLDLQMNSLISEDTAVYYCARGGFAADSRSTRRGQGTQVTVSS/GGGSGGGS/EVQLVE
SGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR
DDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTQVTVSS/GGGSGGGS/QTVVTQ
EPSLTVSPGGTVTLTCAASSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLVPGT PARFSGSLLGGKAAL
TLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLSCAA
SGFTFDDYAMSWVRQAPGKEMEWVSGINWSGTHTRYADSVKGRFTISRDNAKNTLDLQMNSLISED
TAVYYCARGGFAADSRSTRRGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLTCAS
TGAVTSGNYPNWVQKPGQAPRGLIGDYKDDDDKGT PARFSGSLLGGKAALTLSGVQPEDEAEYYC
LWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR
QAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF
GNSYISYWAYWGQGTQVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLSCAASGFTFSKFGMS
WVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIIGGSLSVS
SQGTQVTVSSHHHHHH (SEQ ID NO:472)

Figure 12K

 α HER2 1140 COBRA

QVQLQESGGGLVQPGGSLRLSCVAS**GFTFDDYAMS**WVRQAPGKEMEWVS**GINWSGTHTRYADSVK**
GRFTISRDNAKNTLDLQMNLSIEDTAVYYCARGFAADSRSTRGQGTQVTVSS/GGGSGGGS/EVQLVE
SGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKLEWVAR**IRSKYNNYATYYADQVK**RFTISR
DDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/GGGSGGGS/QTVVTQ
EPSLTVSPGGTVTLT**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAAL
TLSGVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQPGGSLRLSCVA
SGFTFDDYAMSWVRQAPGKEMEWVS**GINWSGTHTRYADSVKGR**RFTISRDNAKNTLDLQMNLSIED
TAVYYCARG**GFAADSRSTR**GQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTVTLT**CGS**
STGAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGVQPEDEAEYYC
VLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAMN**WV
RQAPGKLEWVAR**IRSKYDYKDDDDKADSVKDR**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGN**
FGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSAAS**GFTFSKFGMS**
WVRQAPGKLEWVS**SISGSGRDTLYAESVKGR**RFTISRDNAKNTLYLQMNSLRPEDTAVYYCTI**GGSLSVS**
SQGLTVTVSSHHHHHH (SEQ ID NO:473)

 α HER2 1145 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFKNYPMG**WFRQPPGKDFEVA**AITSSGGTTHYRDSVKGR**
FTISRDNAKNTVYLQMNSLKPDDETAVYYCAG**SSTPWDIPLGPNEVG**YWGQGTQVTVSS/GGGSGGGS
/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKLEWVAR**IRSKYNNYATYYADQVK**
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSLTVSPGGTVTLT**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLL
GGKAALTLSGVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQAGGS
LRLSCAAS**GRIFKNYPMG**WFRQPPGKDFEVA**AITSSGGTTHYRDSVKGR**RFTISRDNAKNTVYLQMNS
LKPDDETAVYYCAG**SSTPWDIPLGPNEVG**YWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSLT
VSPGGTVTLT**GSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTS
GVQPEDEAEYY**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAAS**GF**
TFNKYAMNWVRQAPGKLEWVAR**IRSKYDYKDDDDKADSVKDR**RFTISRDDSKNTAYLQMNNLKTED
TAVYYCVR**HGNFGNSYISYWAY**WGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLSAA
SGFTFSKFGMSWVRQAPGKLEWVS**SISGSGRDTLYAESVKGR**RFTISRDNAKNTLYLQMNSLRPEDTAV
YYCTI**GGSLSVS**SQGLTVTVSSHHHHHH (SEQ ID NO:474)

Figure 12L

 α HER2 1146 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GRIFKNYPMG**WFRQPPGKDFEVA**AITSSGGTTPYRDSVKGR**FTISRDNANTVYLQMNSLKPEDTAVYYCAG**SSTPW****DIPLGPNEVG**FWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCAAS**GRIFKNYPMG**WFRQPPGKDFEVA**AITSSGGTTPYRDSVKGR**FTISRDNANTVYLQMNSLKPEDTAVYYCAG**SSTPW****DIPLGPNEVG**FWGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAMN**WVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSCAAS**GFTFSKFGMS**WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNANTLYLQMNSLRPEDTAVYCTI**GGSLSV**SSQGTQVTVSSHHHHHH (SEQ ID NO:475)

 α HER2 1149 COBRA

QVQLQESGGGLVQAGGSLRLSCVAS**GNIFGFNV**MGWYRQVPGKQRELVA**ISTGGRSTDYADSAKGR**FTISRNNAKDTVYLQMNSLKPEDTAVYYCKM**TMASSDY**WGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKD**RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/QTVVTQEPSTVSPGGTTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCVAS**GNIFGFNV**MGWYRQVPGKQRELVA**ISTGGRSTDYADSAKGR**FTISRNNAKDTVYLQMNSLKPEDTAVYYCKM**TMASSDY**WGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGKAALTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAMN**WVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRSCAAS**GFTFSKFGMS**WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNANTLYLQMNSLRPEDTAVYYCTI**GGSLSV**SSQGTQVTVSSHHHHHH (SEQ ID NO:476)

Figure 12M

 α HER2 1150 COBRA

QVQLQESGGGLVQAGGSLRLSCVAS**GNIFGFNV**MGWYRQVPGKQRELVA**ISTGGGSTNYADSAKGRF**
TVSRNNAKDTVYLQMNSLKPEDTAVYYCKM**TMASVDY**WGQGTQVTVSS/GGGSGGGG/EVQLVESG
GGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD
SKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/QTVVTQEP
SLTVSPGGTTLTLC**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALT
SGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLRLSCVAS
GNIFGFNVMGWYRQVPGKQRELVA**ISTGGGSTNYADSAKGRF**TVSRNNAKDTVYLQMNSLKPEDTA
VYYCKM**TMASVDY**WGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGTTLTLC**GSST**
GAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPEDEAEYYC**VL**
WYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVRQ
APGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNFG**
NSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLRSCAAS**GFTFSKFGMSW**
VRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLSV**SS
QGTQTLTVSSHHHHHHH (SEQ ID NO:477)

 α HER2 1156 COBRA

QVQLQESGGGLVQAGGSLKVSAA**SRNIGSNYAVG**WFRQAPGKEREPVA**ALRWTSIIGYDDSLRGR**
FTISKDDAKNTVYLQMNSLKPEDTGYYCA**RILDRSSYDY**WGQGTQVTVSS/GGGSGGGG/EVQLVES
GGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR
DSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTVSS/GGGSGGGG/QTVVTQE
PSLTVSPGGTTLTLC**ASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGKAALT
LSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGG/QVQLQESGGGLVQAGGSLKVSAA
SRNIGSNYAVGWFRQAPGKEREPVA**ALRWTSIIGYDDSLRGR**FTISKDDAKNTVYLQMNSLKPEDTG
VYYCA**RILDRSSYDY**WGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPLTVSPGGTTLTLC**GS**
TGAVTSGNYPNWVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTSGVQPEDEAEYYC**CV**
LWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAMN**WVR
QAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HGNF**
GNSYISYWAYWGQGTQVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSRLRSCAAS**GFTFSKFGMS**
WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNAKTTLYLQMNSLRPEDTAVYYCTI**GGSLSV**S
SQGTQTLTVSSHHHHHHH (SEQ ID NO:478)

Figure 12N

 α HER2 1158 COBRA

QVQLQESGGGLVQAGGSLRLSCTAS**GRTFSSYAMG**WFRQAPEKEREFVA**AITWSGGTTHYAESVKGR**
 FTISRDNANTVYLQMNLTPEDTAVYYCAAR**INYSTISSNEKMYHY**WGQGTQVTSS/GGGSGGGS/E
 VQLVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKD**
 RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTSS/GGGSGGGS/Q
 TVVTQEPSLTVSPGGTVTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLG
 GKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQAGGSL
 RLSTAS**GRTFSSYAMG**WFRQAPEKEREFVA**AITWSGGTTHYAESVKGR**RFTISRDNANTVYLQMNLT
 EPEDTAVYYCAAR**INYSTISSNEKMYHY**WGQGTQVTSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVS
 PGGTVTLT**CGSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGKAALTLSG
 VQPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAAS**GFT**
FNKYAMNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**RFTISRDDSKNTAYLQMNNLKTEDT
 AVYYCVR**HGNFGNSYISYWAY**WGQGTQVTSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLS
 CAAS**GFTFSKFGMS**WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNANTLYLQMN
 SLRPEDTAVYCT**IGSLSV**SSQGTQVTSSHHHHHH (SEQ ID NO:479)

 α HER2 1159 COBRA

QVQLQESGGGLVQAGGSLRLSCATS**GRTFSSLAMG**WFRQAPGKERELV**AGISWSGSTTYYADSVKGR**
 FAISRDNANTVYLQMNLSKPEDTAVYYCAAR**RTSSIATIGREYDY**WGQGTQVTSS/GGGSGGGS/EVQ
 LVESGGGLVQPGGSLKLSAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKDR**FT
 ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGTQVTSS/GGGSGGGS/QTV
 VTQEPSLTVSPGGTVTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
 AALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQAGGSLRLS
 CATS**GRTFSSLAMG**WFRQAPGKERELV**AGISWSGSTTYYADSVKGR**FAISRDNANTVYLQMNLSKPE
 DTAVYYCAAR**RTSSIATIGREYDY**WGQGTQVTSS/SGGPGPAGMKGLPGS/QTVVTQEPSLTVSPGGTV
 TLT**CGSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGVQPEDE
 AEYYC**VLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSAAS**GFTFNKYA**
MNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**RFTISRDDSKNTAYLQMNNLKTEDTAVYYC
 VR**HGNFGNSYISYWAY**WGQGTQVTSS/GGGSGGGS/EVQLVESGGGLVQPGNSRLS
 CAAS**GFTFS**
KFGMSWVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**RFTISRDNANTLYLQMN
 SLRPEDTAVYCT**IG**
SLSVSSQGTQVTSSHHHHHH (SEQ ID NO:480)

Figure 120

 α HER2 1160 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GR****TF****S****NER****L****GW****FRQAPGKERELVA****AIRWSGVIIGYADSVRGRF**
TISRDNASTVYLQ**M**NSLRPEDTAVYFCAA**DR****GVYGTWDY****WGQGTQVT****VSS/****GGGSGGGG****/EVQLVE**
SGGGLVQPGGSLKLSCAAS**G****FT****F****NKYAIN****WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR**
DDSKNTAYLQMN**N**LKTEDTAVYYCVR**HANFGNSYISYWAY****WGQGLTVTVSS/****GGGSGGGG****/QTVVTQ**
EPSTVSPGGTVTLT**CAS****STGAVTSGNYPN****WVQKPGQAPRGLIG****G****TKFLVP****GTPARFSGSLLGGKAAL**
TLSGVQPEDEAEYYC**TLWYSNRWV****FGGGTKLTVL/****GGGSGGGG****/QVQLQESGGGLVQAGGSLRLSCAA**
S**GR****TF****S****NER****L****GW****FRQAPGKERELVA****AIRWSGVIIGYADSVRGRF****TISRDNASTVYLQ****M**NSLRPEDTAV
YFCAA**DR****GVYGTWDY****WGQGTQVT****VSS/****SGGPGPAGMKGLPGS****/QTVVTQEPSTVSPGGTVTLT****C****G**
S**TGAVTSGNYPN****WVQKPGQAPRGLIG****DYKDDDDK****GTPARFSGSLLGGKAAL****TLSGVQPEDEAEYYC**
VLWYSNRWV**FGGGTKLTVL/****GGGSGGGG****/EVQLVESGGGLVQPGGSLKLSCAAS****G****FT****F****NKYAMN****WV**
RQAPGKGLEWVARIRSKYD**YKDDDDKADSVKDR****FTISR****DD****SKNTAYLQMN****N**LKTEDTAVYYCVR**HGN**
FGNSYISYWAY**WGQGLTVTVSS/****GGGSGGGG****/EVQLVESGGGLVQPGNSLR****LSCAAS****G****FT****F****S****K****F****G****M****S**
WVRQAPGKGLEWVSSISGSGRDTLYAESVKGR**FTISR****DN****AKT****TLYLQMN****SLR****PEDTAVYYCT****I****G****G****S****L****S****V**
SQGLTVTVSSHHHHHH (SEQ ID NO:481)

 α HER2 1161 COBRA

QVQLQESGGGLVQPGKSLRLSCAVS**G****D****I****F****G****T****Y****G****M****A****WYRQAPGKQREPVA****SISIGGIINYADSVKGRFTI**
SRDN**V****K****N****T****V****Y****L****Q****M****N****S****L****K****P****E****D****T****A****V****Y****C****K****L****L****D****W****N****Y****W****G****R****G****T****Q****V****T****V****S****S/****GGGSGGGG****/EVQLVESGGGLVQ**
P**G****G****S****L****K****L****S****C****A****A****S****G****FT****F****NKYAIN****WVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR****DD****SKNTA**
Y**L****Q****M****N****N****L****K****T****E****D****T****A****V****Y****C****V****R****HANFGNSYISYWAY****WGQGLTVTVSS/****GGGSGGGG****/QTVVTQEPSTVSP**
G**G****T****V****T****L****T****C****AS****STGAVTSGNYPN****WVQKPGQAPRGLIG****G****TKFLVP****GTPARFSGSLLGGKAAL****TLSGVQ**
E**D****E****A****E****Y****C****TLWYSNRWV****FGGGTKLTVL/****GGGSGGGG****/QVQLQESGGGLVQPGKSLRLSCAVS****G****D****I****F****G****T**
Y**G****M****A****WYRQAPGKQREPVA****SISIGGIINYADSVKGRFTISR****DN****V****K****N****T****V****Y****L****Q****M****N****S****L****K****P****E****D****T****A****V****Y****C****K****L****D**
W**N****Y****W****G****R****G****T****Q****V****T****V****S****S/****SGGPGPAGMKGLPGS****/QTVVTQEPSTVSPGGTVTLT****C****S****S****T****G****A****V****T****S****G****N****Y****P****N**
WVQKPGQAPRGLIG**DYKDDDDK****GTPARFSGSLLGGKAAL****TLSGVQPEDEAEYYC****V****L****W****Y****S****N****R****W****V****F**
G**G****T****K****L****T****V****L/****GGGSGGGG****/EVQLVESGGGLVQPGGSLKLSCAAS****G****FT****F****NKYAMN****WVRQAPGKGLEWVA**
RIRSKYD**YKDDDDKADSVKDR****FTISR****DD****SKNTAYLQMN****N**LKTEDTAVYYCVR**HGNFGNSYISYWAY**
WGQGLTVTVSS/**GGGSGGGG****/EVQLVESGGGLVQPGNSLR****LSCAAS****G****FT****F****S****K****F****G****M****S****WVRQAPGKGLE**
WVSSISGSGRDTLYAESVKGR**FTISR****DN****AKT****TLYLQMN****SLR****PEDTAVYYCT****I****G****G****S****L****S****V**
SSQGLTVTVSSHH
HHHH (SEQ ID NO:482)

Figure 12P

 α HER2 1162 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GRPFSGNAMG**WFRQAPGKEREFVA**AISWSGDSTYYADSVKG**
RFTISRDNENTAYLQMNSLKPEDTAVYYCAAT**TRSFYSRTYYTRPSDYN**YWGPGTQVTVSS/GGGSGG
GS/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQ**
VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/GGGSGG
GS/QTVVTQEPSTLVSPGGTVTLT**CSSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFS
GSLGGAALTLSGVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQA
GGSRLS**CAASGRPFSGNAMG**WFRQAPGKEREFVA**AISWSGDSTYYADSVKG**RFTISRDNENTAYL
QMNSLKPEDTAVYYCAAT**TRSFYSRTYYTRPSDYN**YWGPGTQVTVSS/SGGPGPAGMKGLPGS/QTVVT
QEPSTLVSPGGTVTLT**CSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLGGA
AALTLSGVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLS
CAAS**GFTFNKYAMN**WVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMN
NLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNS
LRLS**CAASGFTFSKFGMS**WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNAKTTLYLQMN
SLRPEDTAVYYCTI**GGSLSV**SSQGLTVTVSSHHHHHH (SEQ ID NO:483)

 α HER2 1163 COBRA

QVQLQESGGGLVQAGGSLRLSCAAS**GRRFN**NYFMG**WFRQAPGKEREFVALLRESGDNTYYTNSVKGR**
FTISRDNARNTVYLQMNSLKPEDTAVYYCAAR**LDTGFLYSANSYAY**WGQGTQVTVSS/GGGSGGGS/
EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/GGGSGGGS/
QTVVTQEPSTLVSPGGTVTLT**CSSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSL
GGKAALTLSGVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/QVQLQESGGGLVQAGGS
LRLS**CAASGRRFN**NYFMG**WFRQAPGKEREFVALLRESGDNTYYTNSVKGR**FTISRDNARNTVYLQMN
SLRPEDTAVYYCAAR**LDTGFLYSANSYAY**WGQGTQVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPST
LVSPGGTVTLT**CSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLGGAALTLS
GVQPEDEAEYY**CTLWYSNRWV**FGGGTKLTVL/GGGSGGGS/EVQLVESGGGLVQPGGSLKLSCAAS**GF**
TFNKYAMNWVRQAPGKGLEWVAR**IRSKYDYKDDDDKADSVKDR**FTISRDDSKNTAYLQMN
NLKTEDTAVYYCVR**HGNFGNSYISYWAY**WGQGLTVTVSS/GGGSGGGS/EVQLVESGGGLVQPGNSLRLS
CAAS**GFTFSKFGMS**WVRQAPGKGLEWVSS**SISGSGRDTLYAESVKGR**FTISRDNAKTTLYLQMN
SLRPEDTAVYYCTI**GGSLSV**SSQGLTVTVSSHHHHHH (SEQ ID NO:484)

Figure 12Q

Trop-2/EpCAM Hetero-COBRAsPro824 (aEpCAM h665/aTrop-2 h557)

QVQLLES~~GGGLVQPGGSLRL~~SCAASGRTFSDYDMGWFRQGP~~GKERE~~FVAAISWSGGHTNYADSVKG
RFTISR~~DNSKNTLYLQMN~~SLRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/GGGSGGGS
/EVQLVES~~GGGLVQPGGSLKL~~SCAASGFTFNKYAINWVRQAP~~GKLEWVARIR~~SKYNNYATYYADQVK
DRFTISR~~DDSKNTAYLQMN~~NLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/
QTVVTQEP~~SLTVSPGGTVTLT~~CASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES~~GGGLVQPGGSL~~
RLSCAASGRTFSSQSMGWFRQAP~~GKERE~~FVSAISWTGANPTYADSVKGRRFTISR~~DNSKNTLYLQMN~~SL
RAEDTAVYYCAADTSGGSYYYERATAETSYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEP
SLTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAAL
TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVES~~GGGLVQPGGSLKL~~SCAA
SGFTFNKYAMNWVRQAP~~GKLEWVARIR~~SKYDYKDDDDKADSVKDRFTISR~~DDSKNTAYLQMN~~NL
TETAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVES~~GGGLVQPGNSLR~~LS
CAASGFTFSKFGMSWVRQAP~~GKLEWVSSISG~~SGRDTLYAESVKGRFTISR~~DNATTLYLQMN~~SLRPED
TAVYYCTIGGSLSVSSQGLTVTVSSHHHHHHH (SEQ ID NO:485)

Pro826 (aTrop-2 h557/aEpCAM h665)

QVQLLES~~GGGLVQPGGSLRL~~SCAASGRTFSSQSMGWFRQAP~~GKERE~~FVSAISWTGANPTYADSVKGR
FTISR~~DNSKNTLYLQMN~~SLRAEDTAVYYCAADTSGGSYYYERATAETSYDYWGQGLTVTVSS/GGGSGG
GS/EVQLVES~~GGGLVQPGGSLKL~~SCAASGFTFNKYAINWVRQAP~~GKLEWVARIR~~SKYNNYATYYADQ
VKDRFTISR~~DDSKNTAYLQMN~~NLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGG
GS/QTVVTQEP~~SLTVSPGGTVTLT~~CASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFS
GSLLGGKAALTLSGVQPEDEAEYYCTTLWYSNRWVFGGGTKLTVL/GGGSGGGS/QVQLLES~~GGGLVQPG~~
GSLRLSCAASGRTFSDYDMGWFRQGP~~GKERE~~FVAAISWSGGHTNYADSVKGRRFTISR~~DNSKNTLYLQ~~
MNSLRAEDTAVYYCAADLRFTGGDTTTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQ
EP~~SLTVSPGGTVTLT~~CGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKA
ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGS/EVQLVES~~GGGLVQPGGSLKL~~SC
AASGFTFNKYAMNWVRQAP~~GKLEWVARIR~~SKYDYKDDDDKADSVKDRFTISR~~DDSKNTAYLQMN~~N
LKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGS/EVQLVES~~GGGLVQPGNSLR~~
LSCAASGFTFSKFGMSWVRQAP~~GKLEWVSSISG~~SGRDTLYAESVKGRFTISR~~DNATTLYLQMN~~SLRP
EDTAVYYCTIGGSLSVSSQGLTVTVSSHHHHHHH (SEQ ID NO:486)

Figure 13

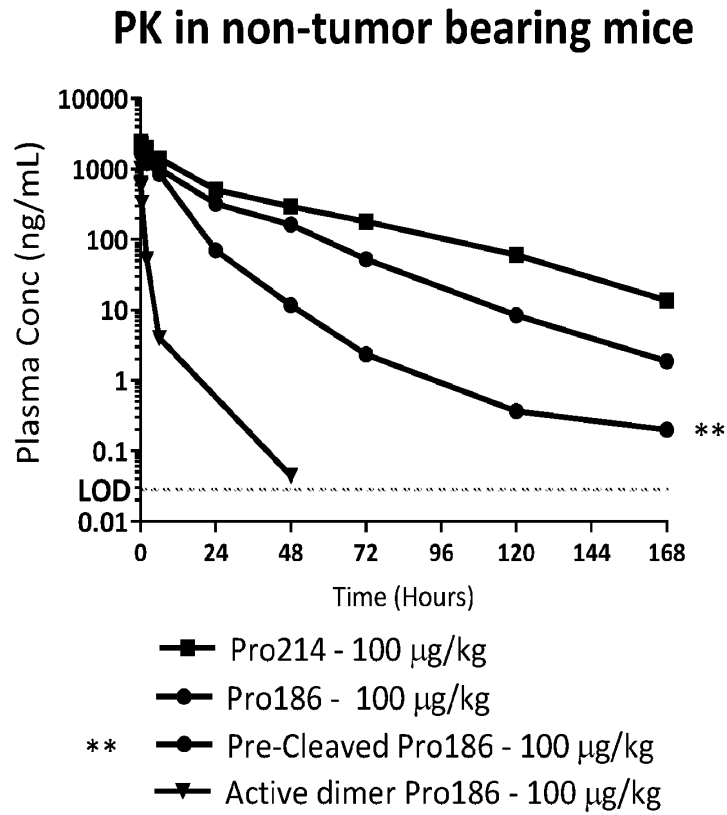
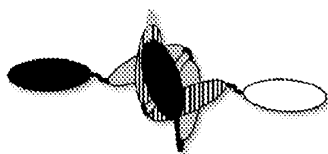


Figure 14

Pro225



Equivalent B7H3 Binding

Species	α B7H3 K_D (nM)	α CD3 K_D (nM)	α HSA K_D (nM)
Human	0.3 (4lg) 0.6 (2lg)	ND*	11.3
Cyno	0.1 (4lg) 0.2 (2lg)	ND	10.8
Mouse	0.1 (2lg)	ND	106.3

*ND = Not Detectable

Figure 15A

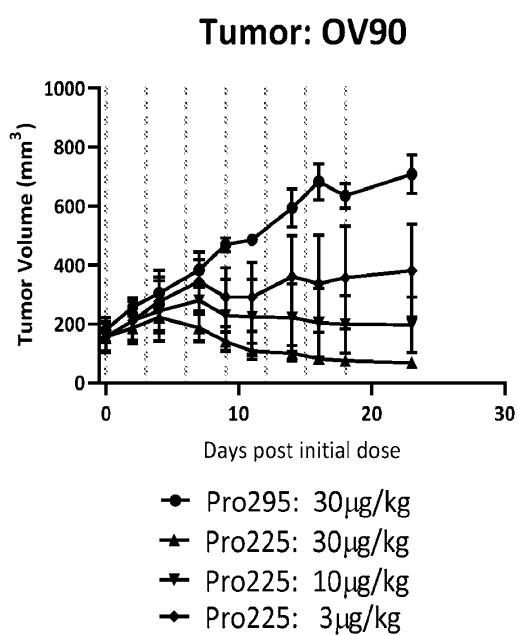
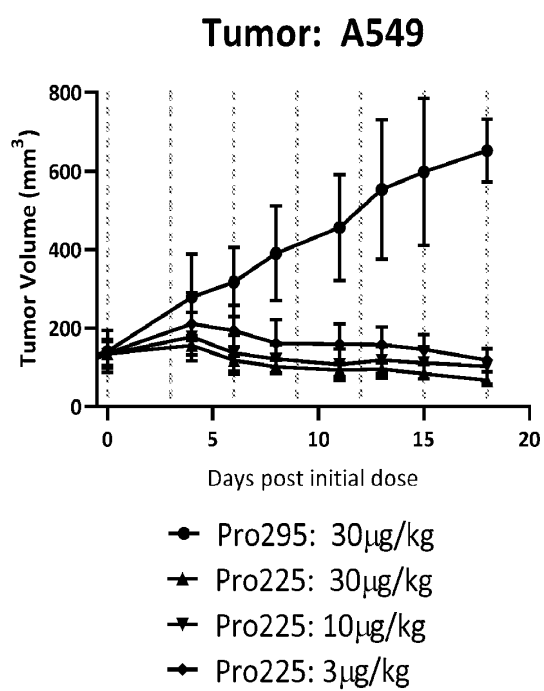
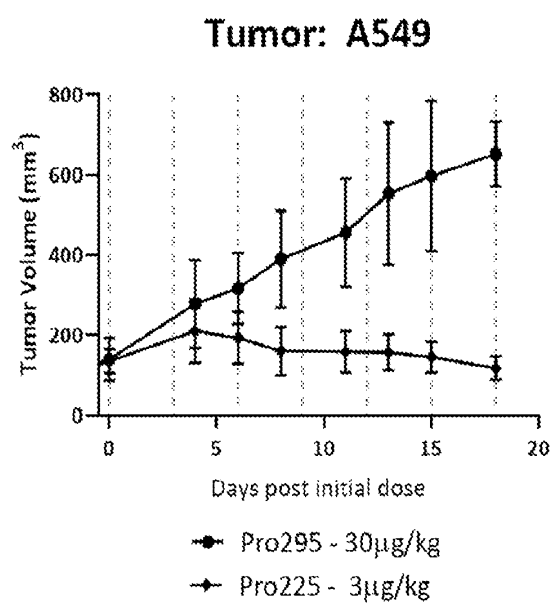
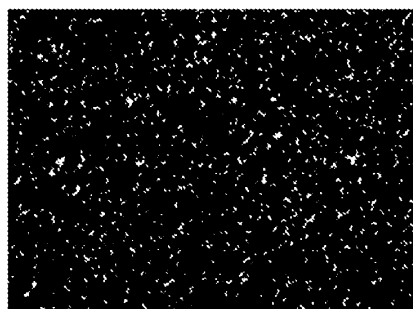
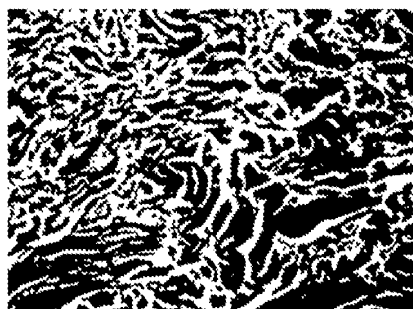


Figure 15B

**H&E: Day 18 Xenograft**

untreated



10 µg/kg

Figure 16A

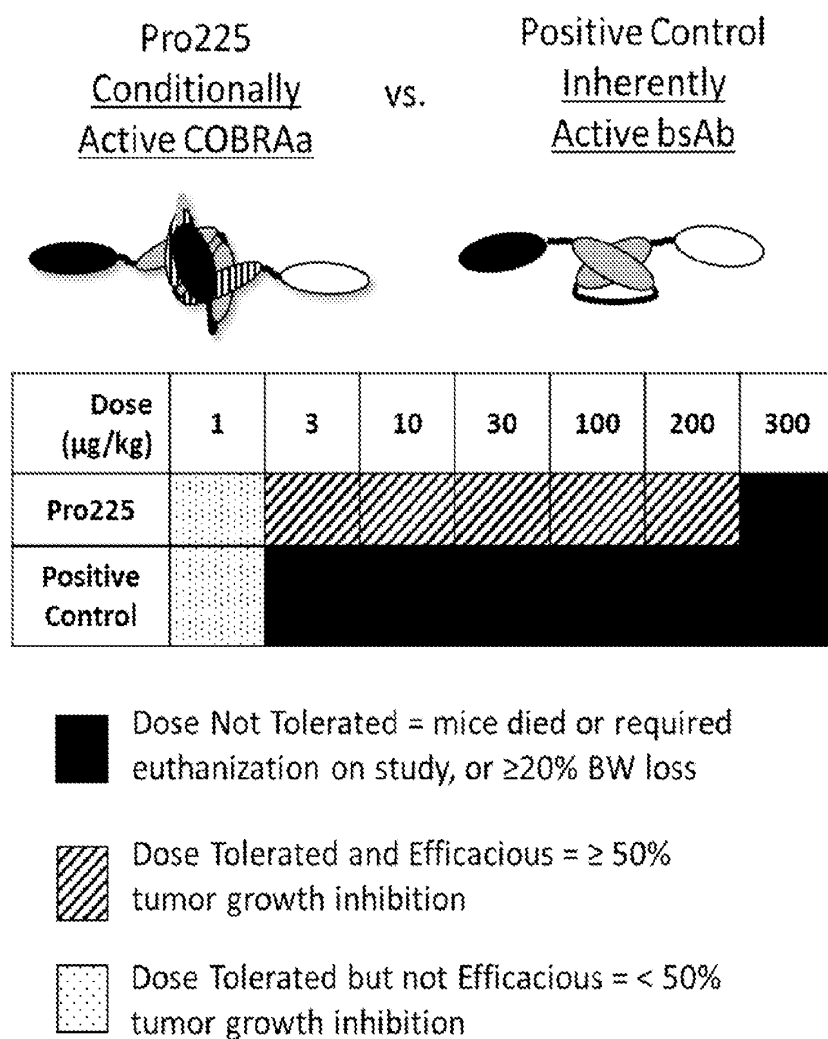
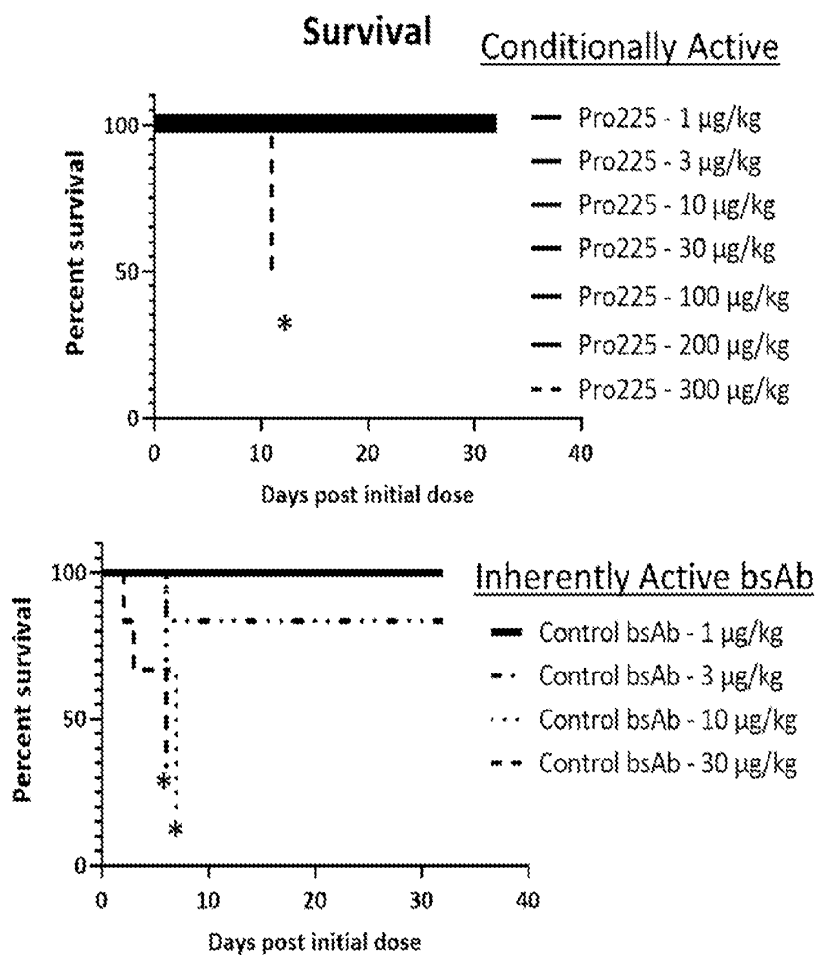


Figure 16B



*Remaining mice euthanized

Figure 16C

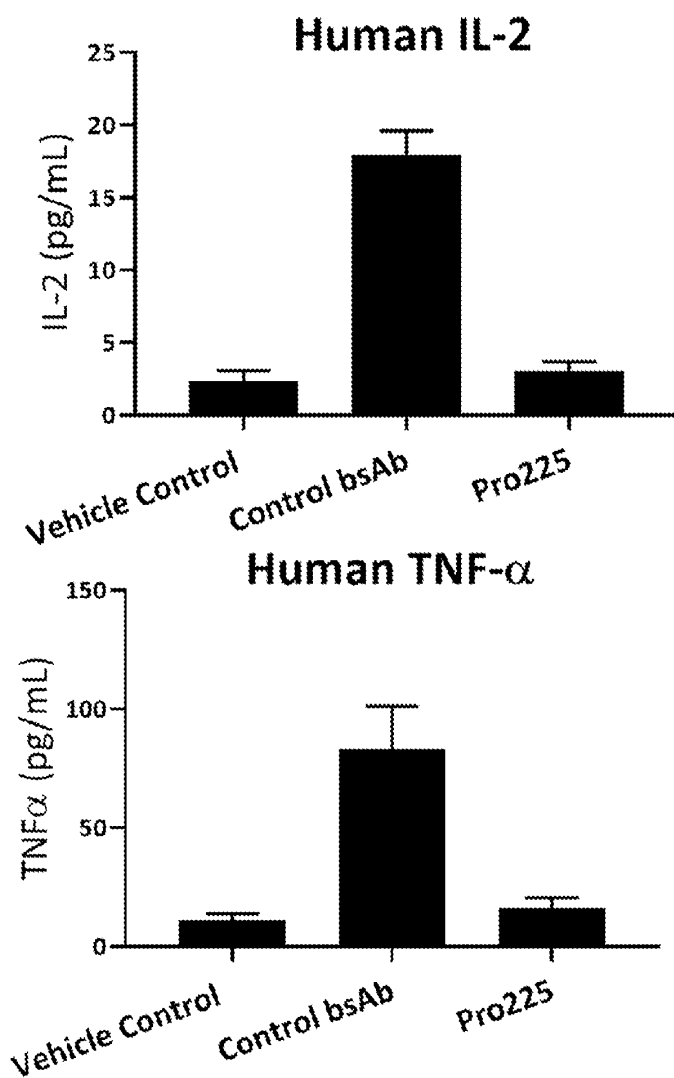


Figure 16D

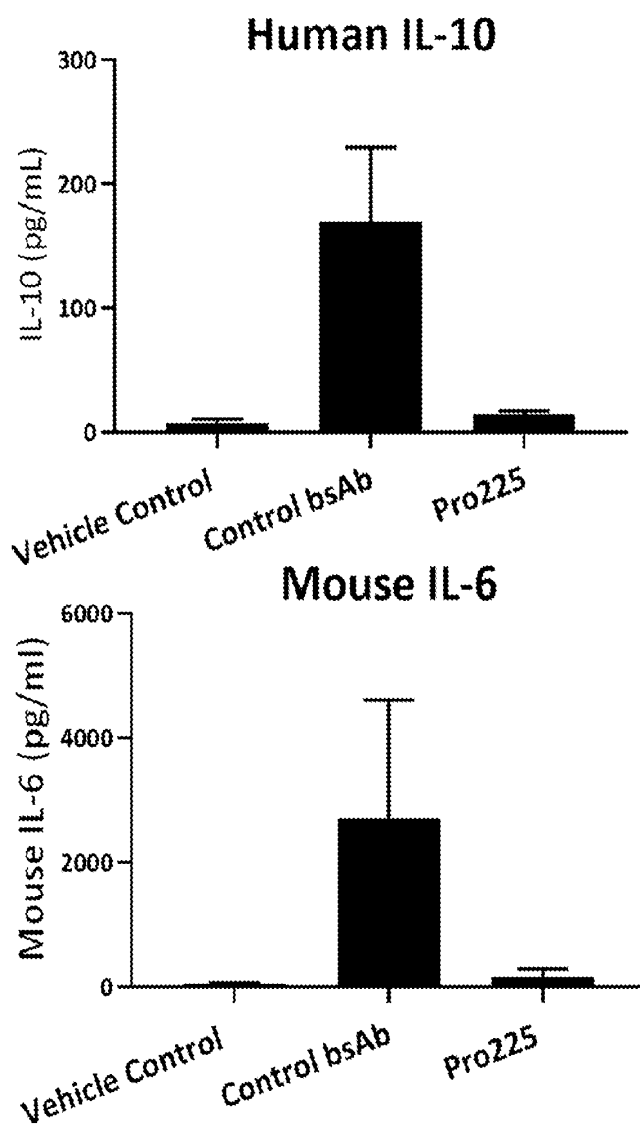


Figure 17

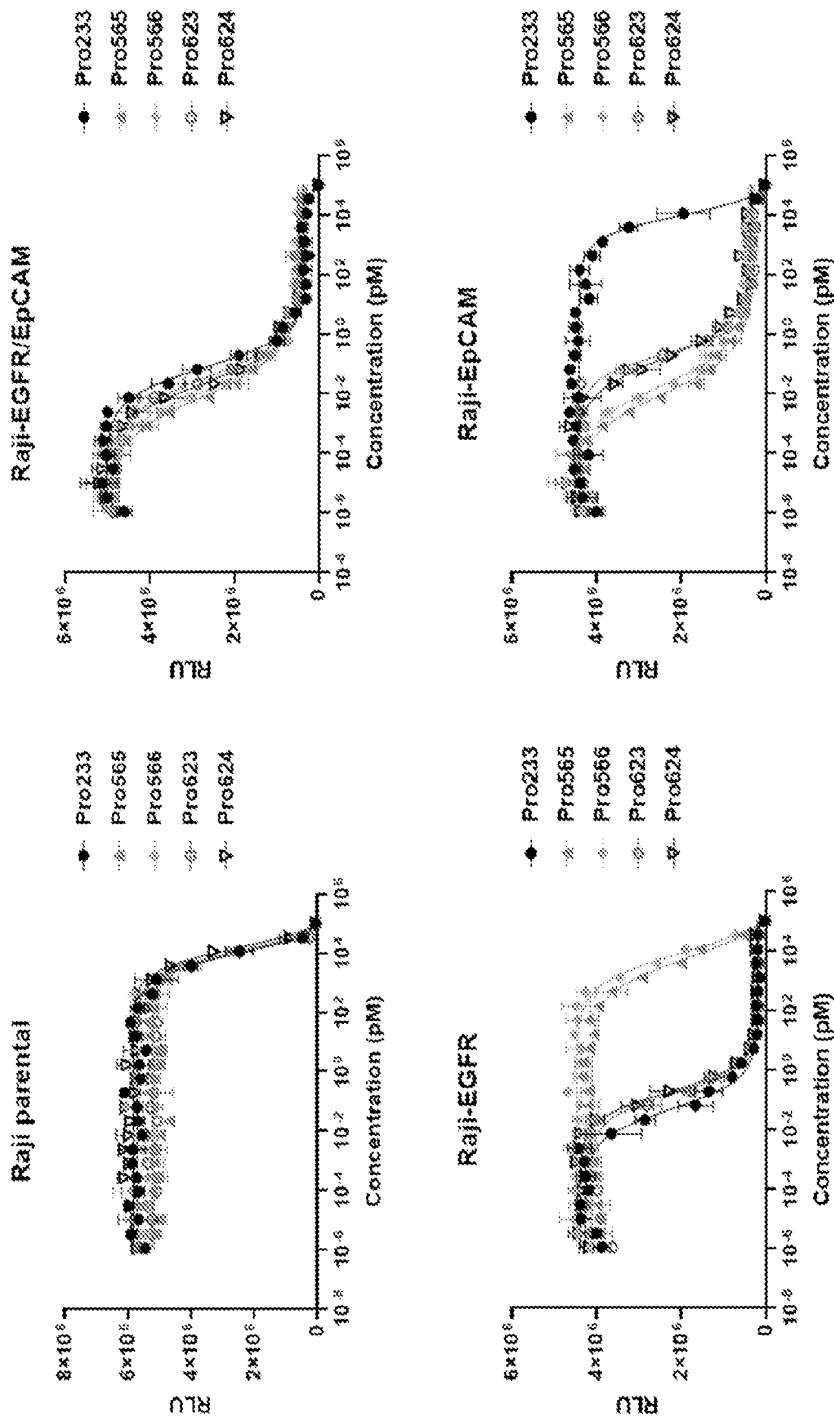


Figure 18

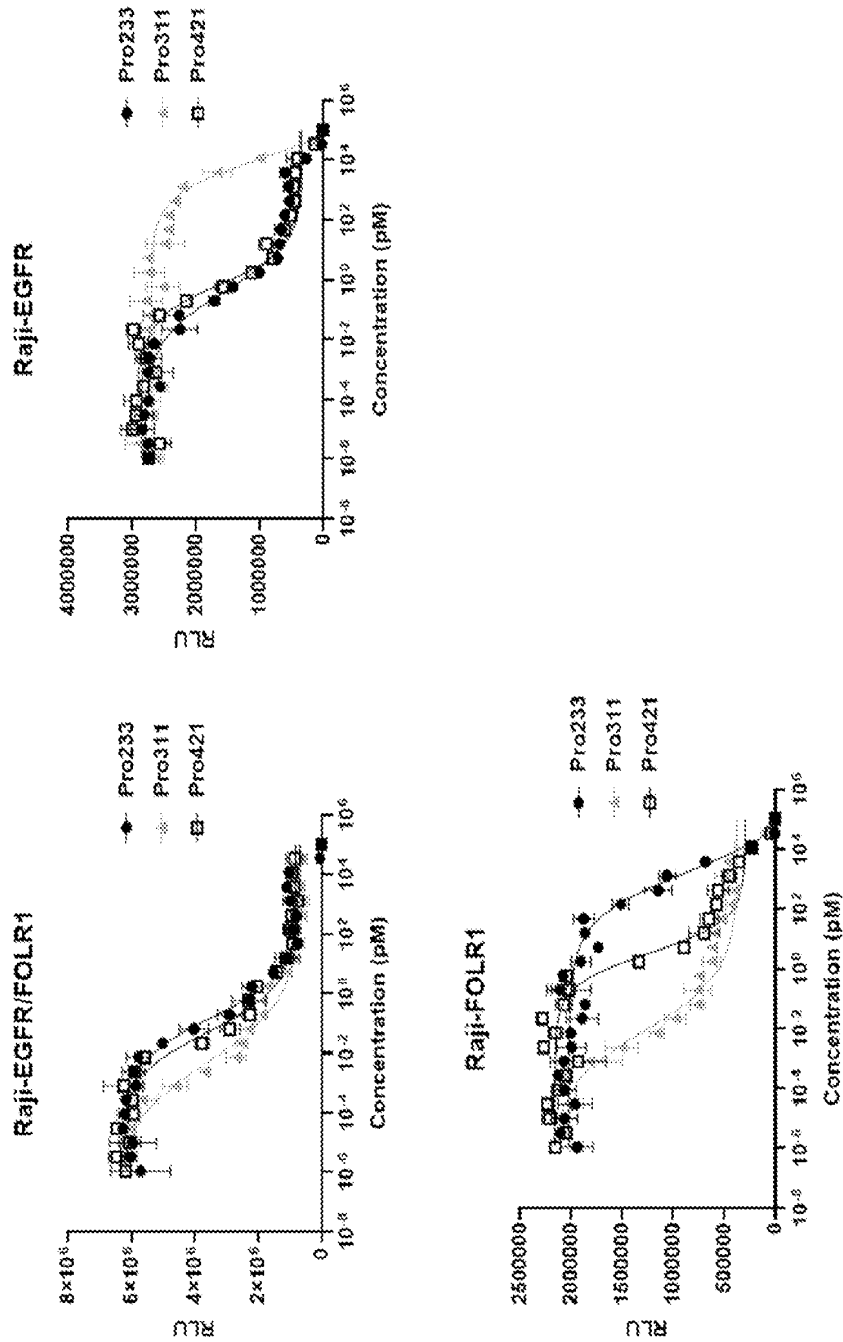


Figure 19

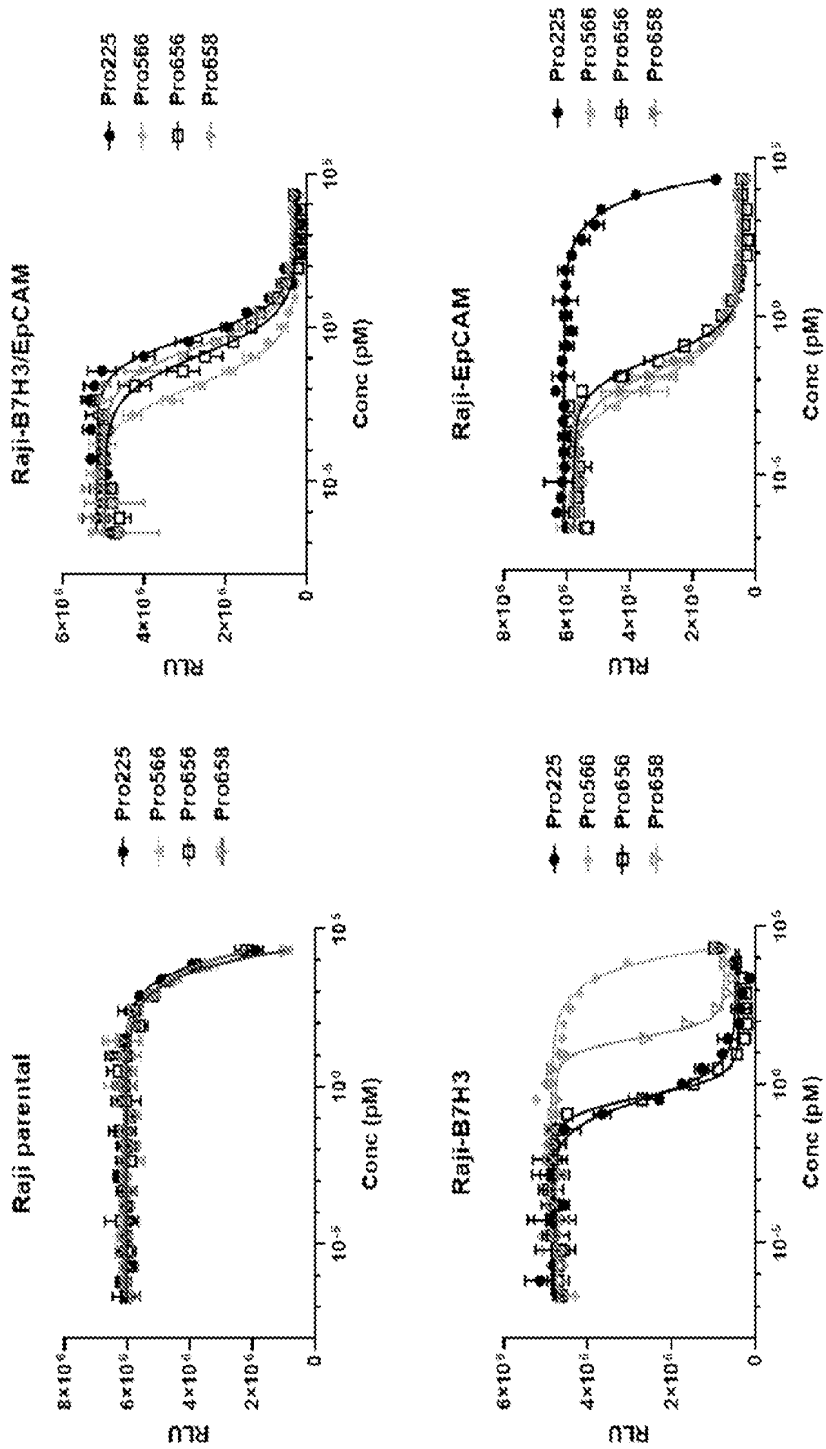


Figure 20

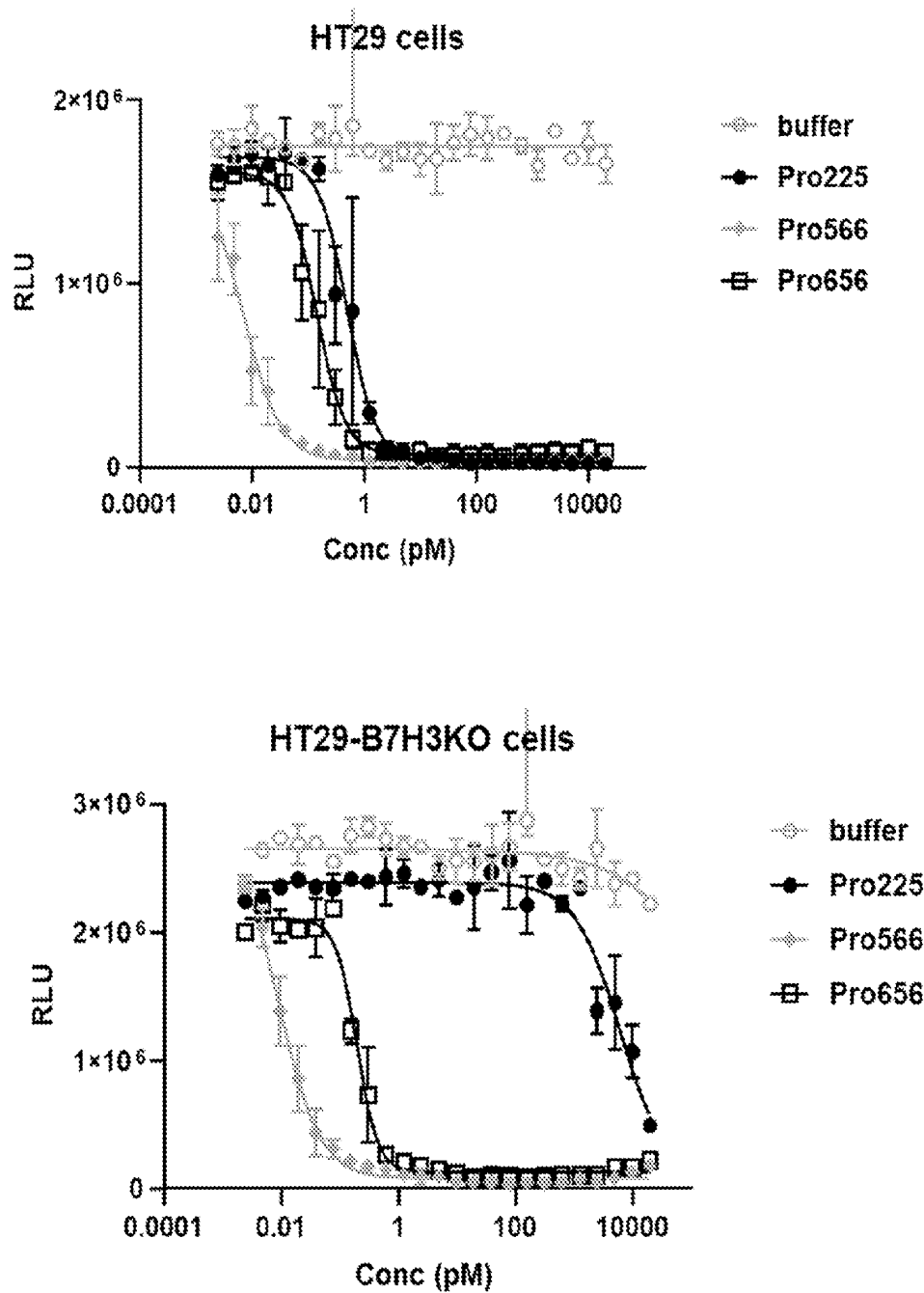


Figure 21

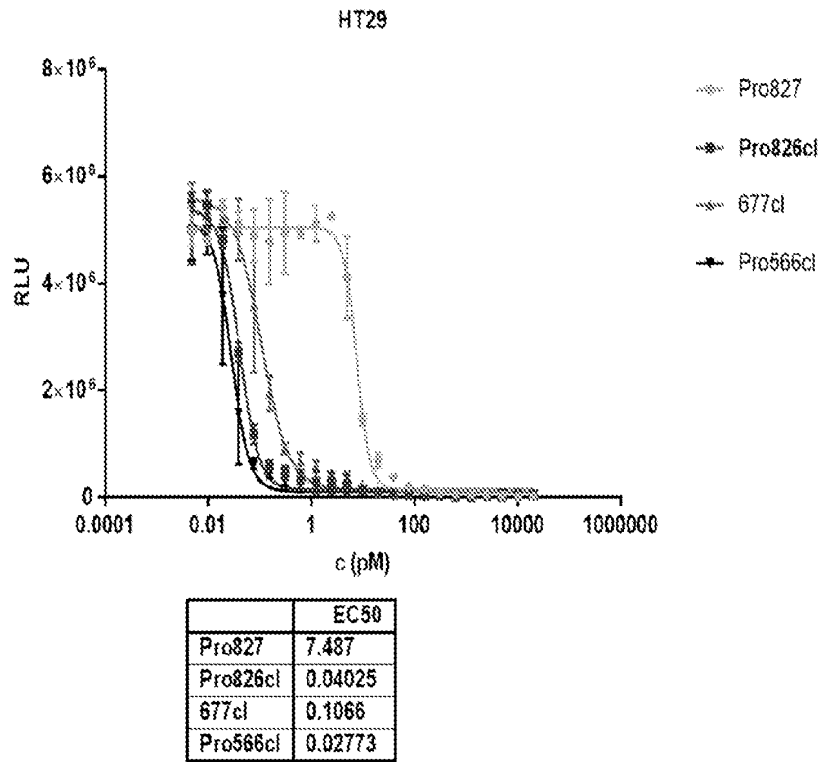
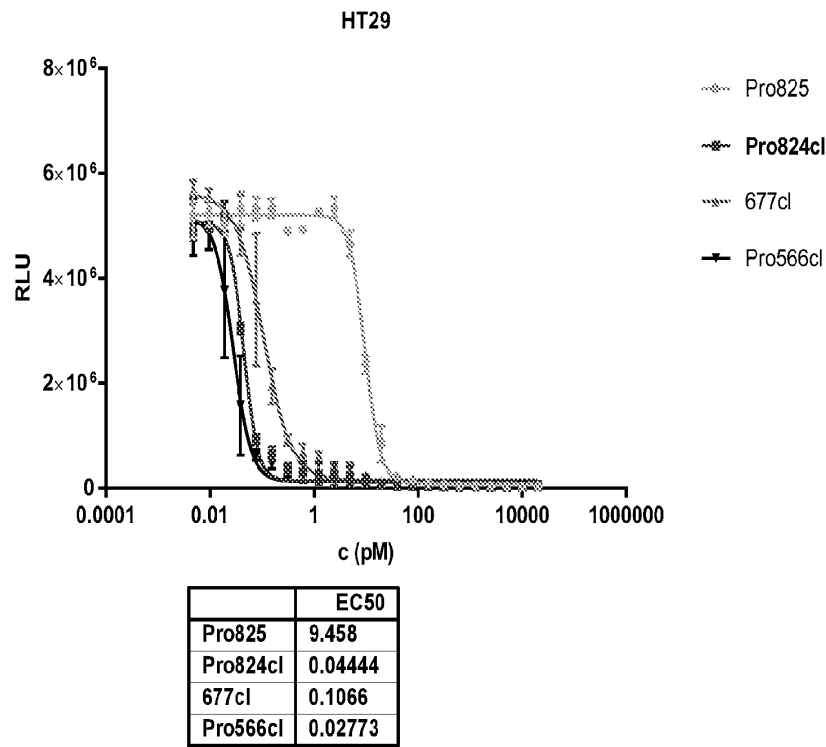


Figure 22

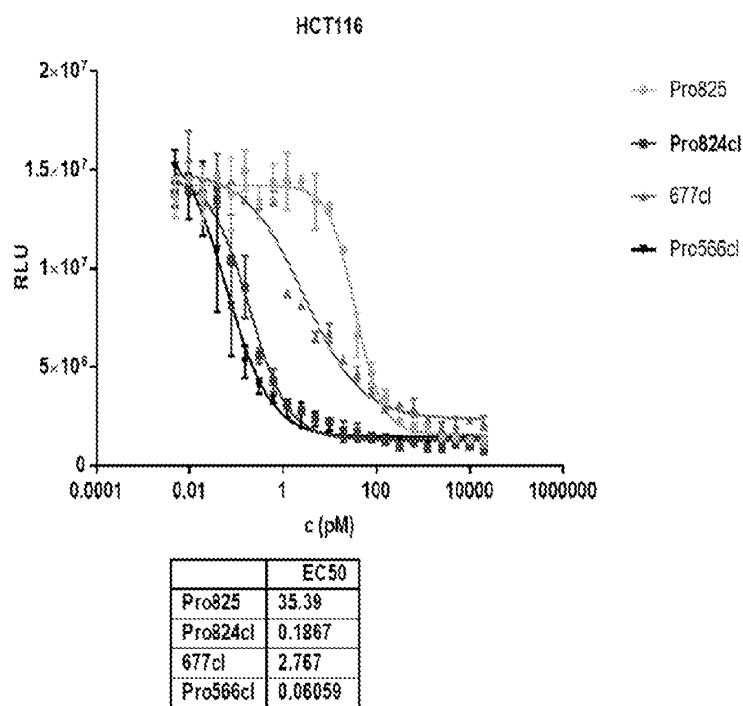
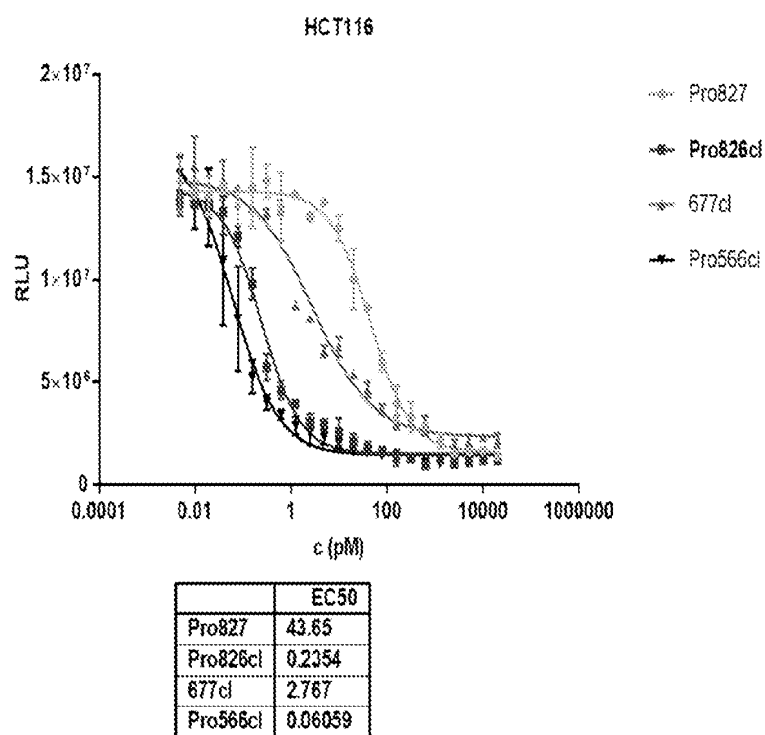


Figure 23

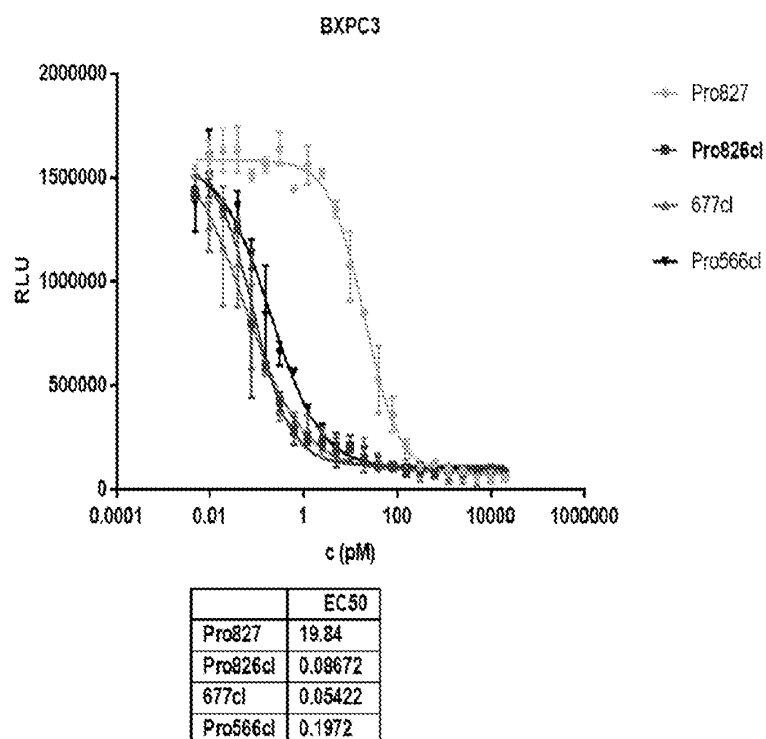
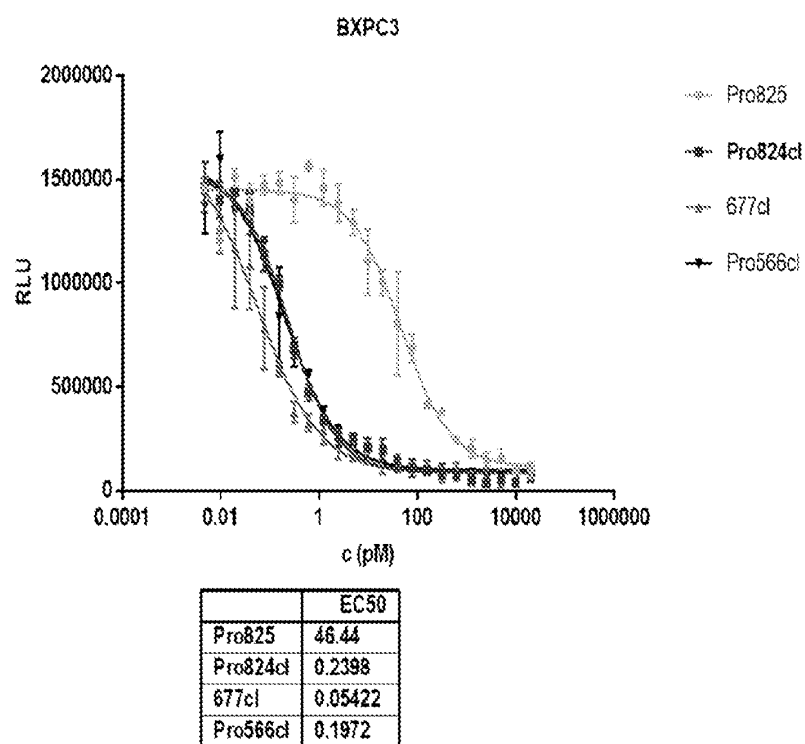


Figure 24

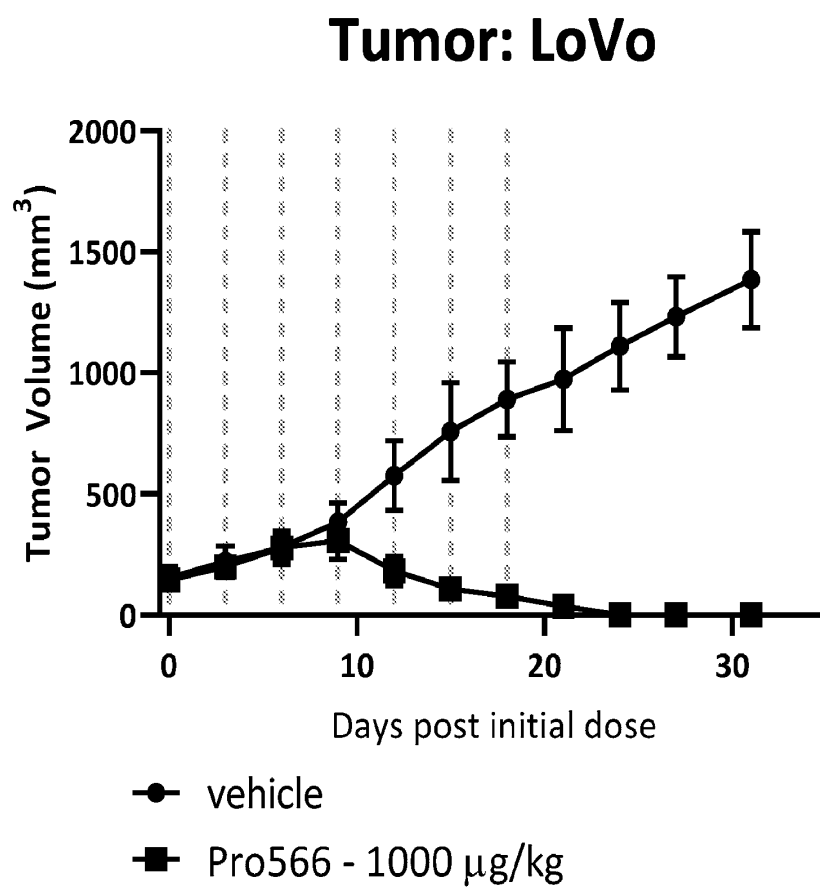


Figure 25

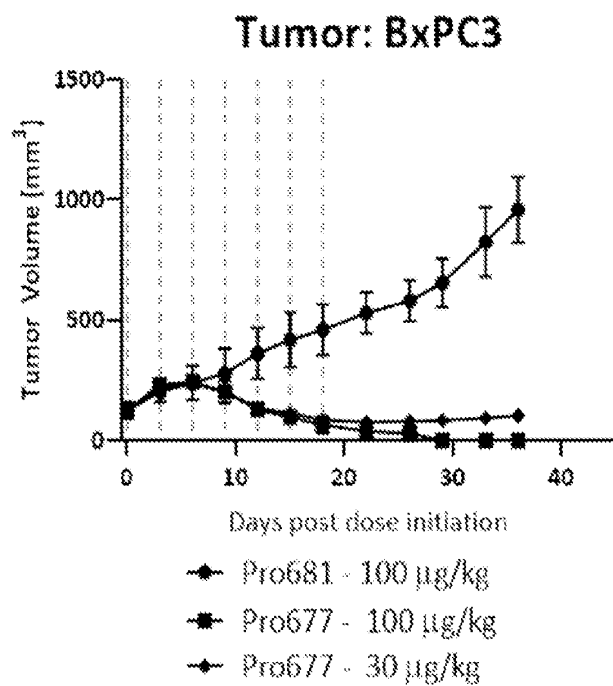


Figure 26

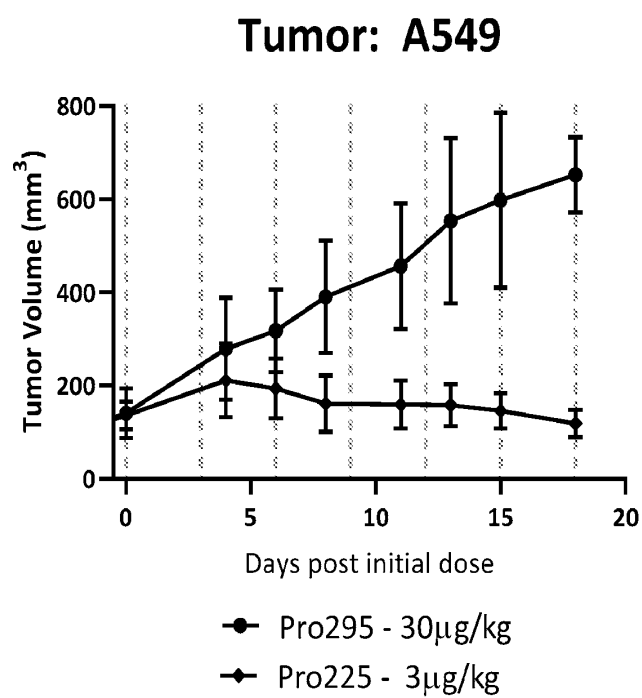


Figure 27A

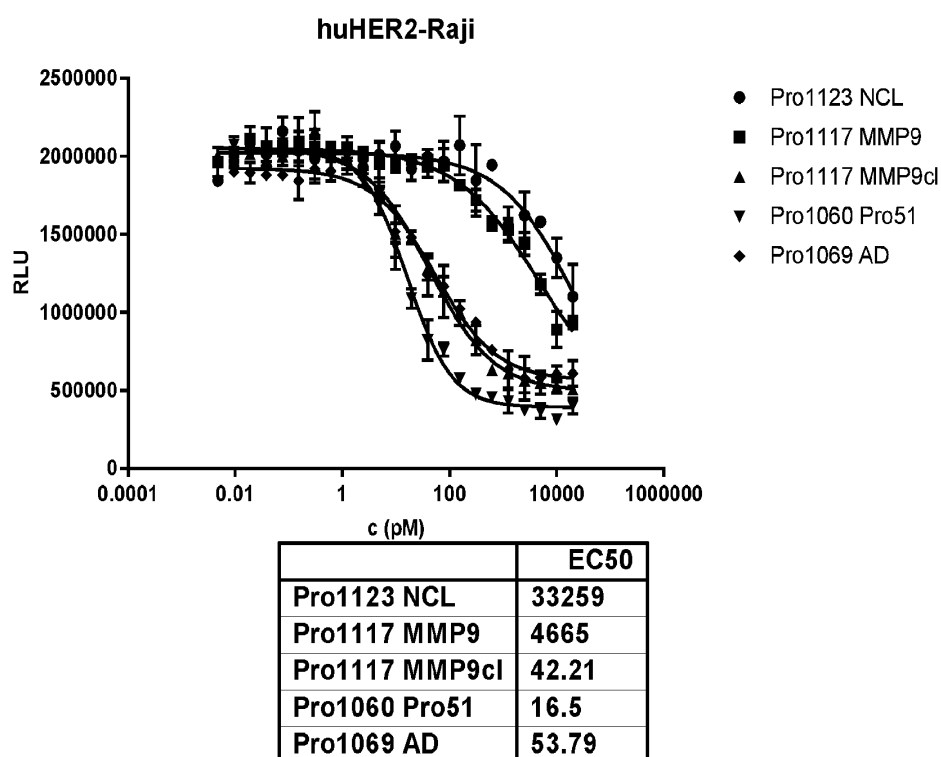
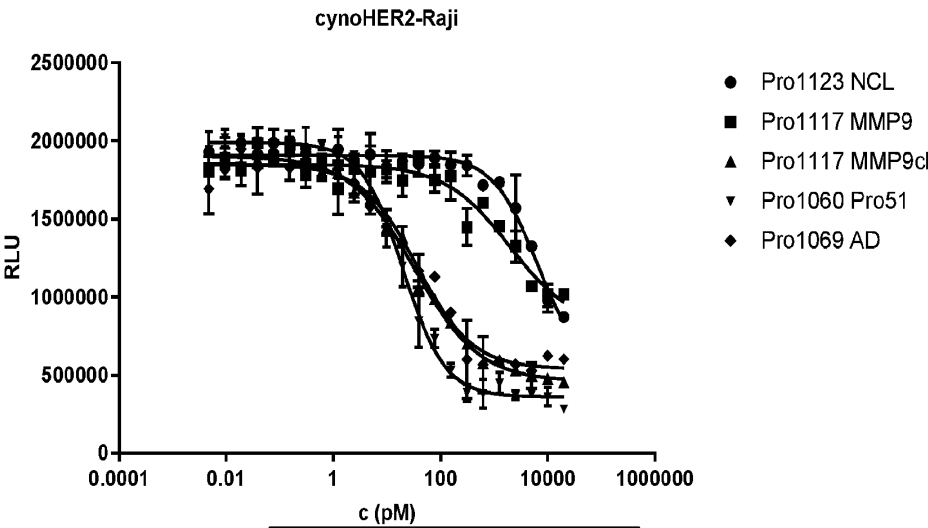
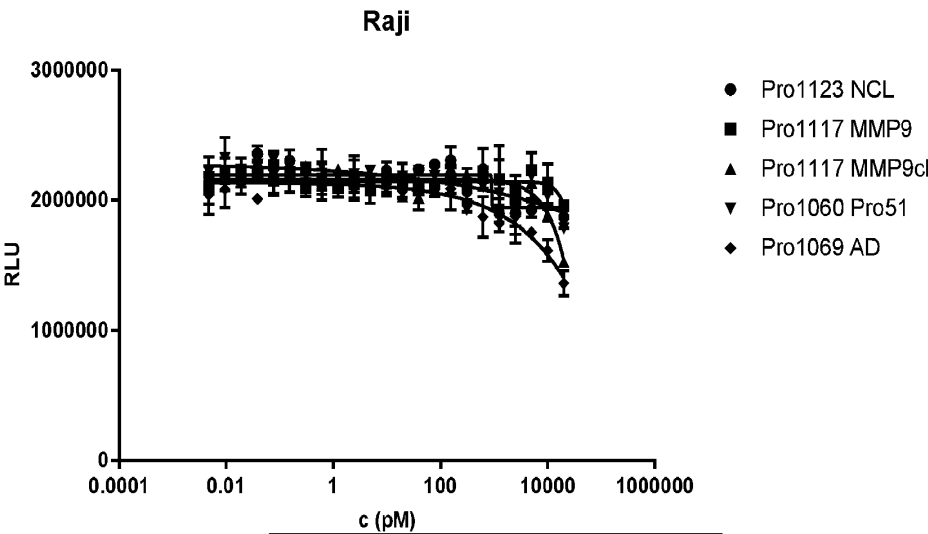


Figure 27B



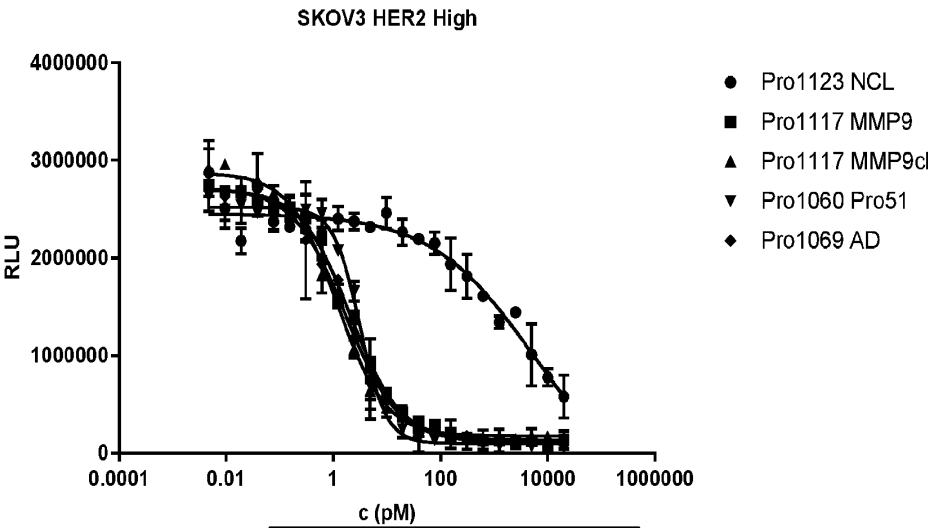
	EC50
Pro1123 NCL	6671
Pro1117 MMP9	1972
Pro1117 MMP9cl	33.02
Pro1060 Pro51	20.15
Pro1069 AD	37.22

Figure 27C



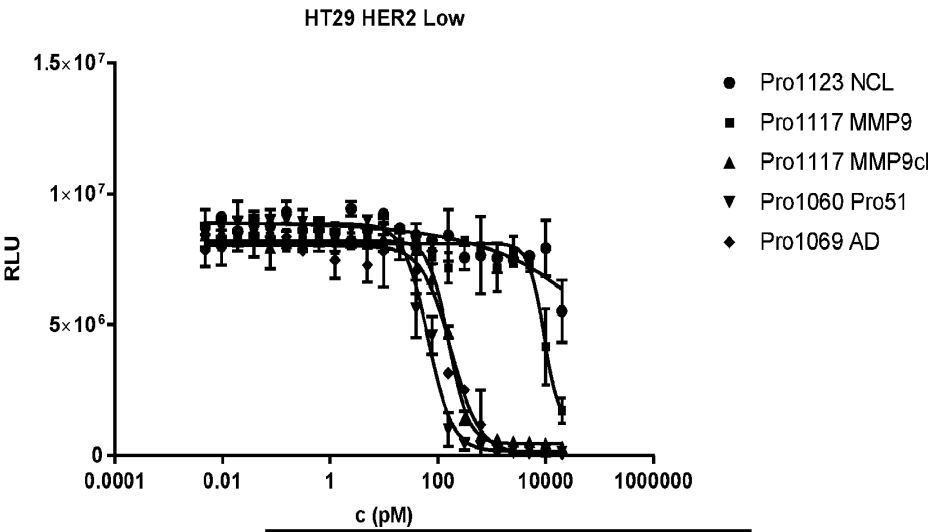
	EC50
Pro1123 NCL	~ 907.3
Pro1117 MMP9	~ 141011
Pro1117 MMP9cl	~ 730276
Pro1060 Pro51	~ 3.624e+015
Pro1069 AD	~ 13427528938

Figure 27D



	EC50
Pro1123 NCL	5329
Pro1117 MMP9	2.066
Pro1117 MMP9cl	1.194
Pro1060 Pro51	3.124
Pro1069 AD	1.695

Figure 27E



	EC50
Pro1123 NCL	~ 4377161900916
Pro1117 MMP9	9277
Pro1117 MMP9cl	158.5
Pro1060 Pro51	65.01
Pro1069 AD	174.7

Figure 28A

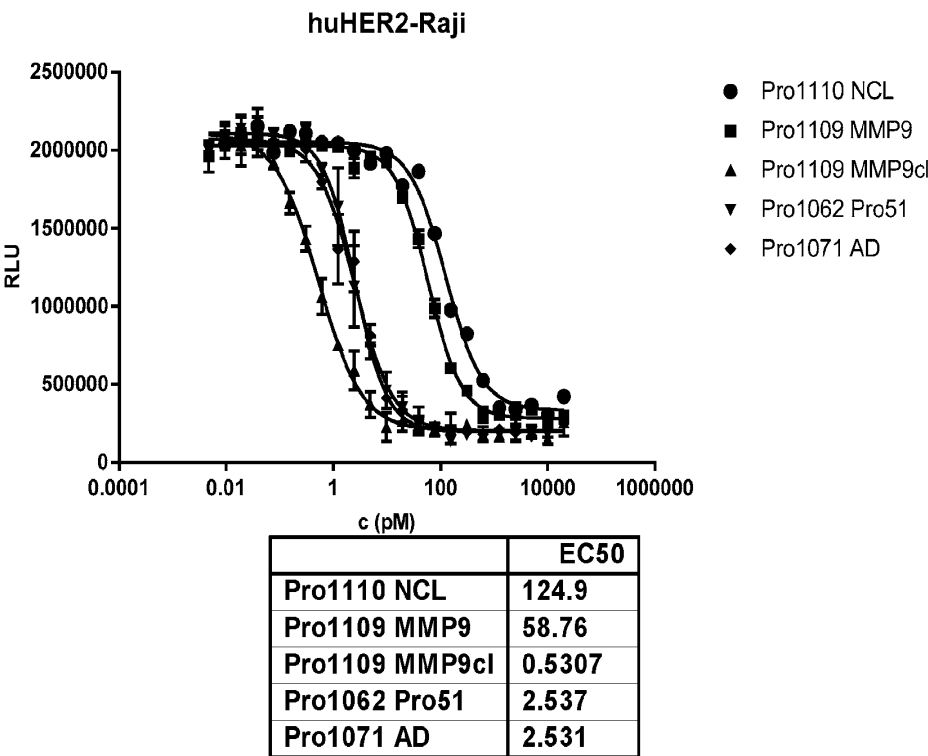
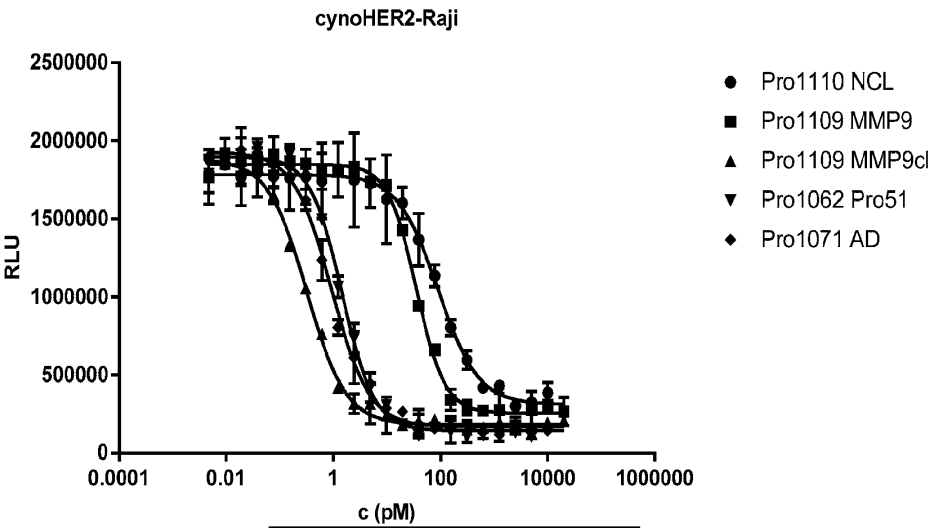
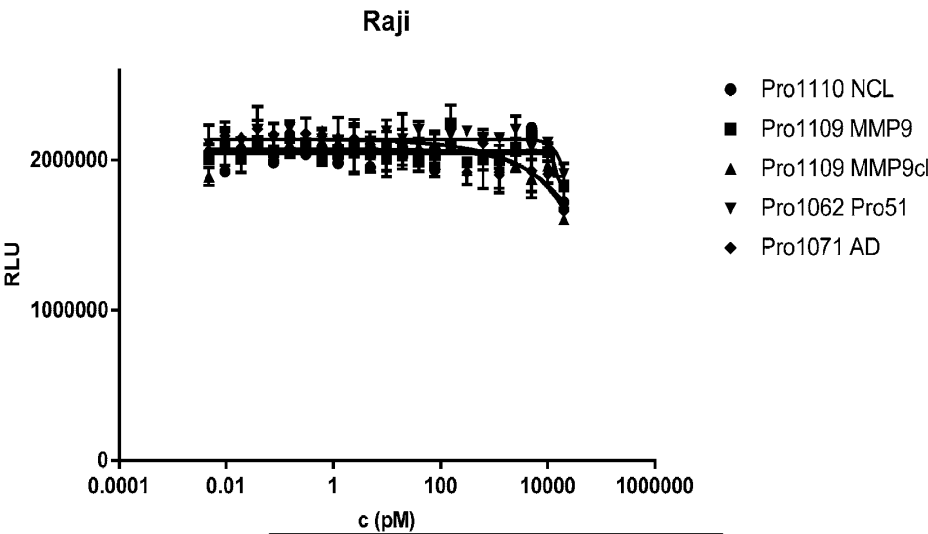


Figure 28B



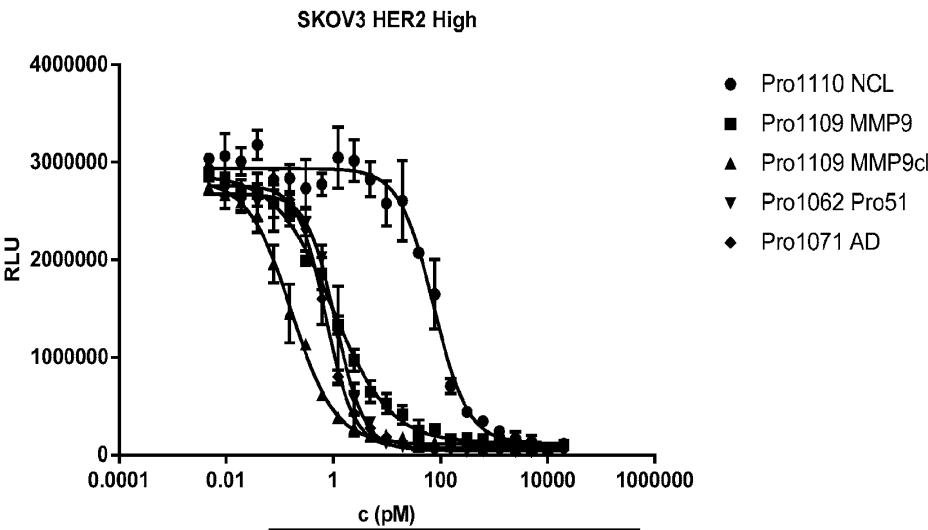
	EC50
Pro1110 NCL	89.88
Pro1109 MMP9	35.42
Pro1109 MMP9cl	0.3203
Pro1062 Pro51	1.464
Pro1071 AD	0.9275

Figure 28C



	EC50
Pro1110 NCL	12914
Pro1109 MMP9	~ 13960
Pro1109 MMP9cl	~ 329519827
Pro1062 Pro51	~ 73414
Pro1071 AD	~ 12279495900

Figure 28D



	EC50
Pro1110 NCL	74.53
Pro1109 MMP9	0.9748
Pro1109 MMP9cl	0.1659
Pro1062 Pro51	1.108
Pro1071 AD	0.727

Figure 28E

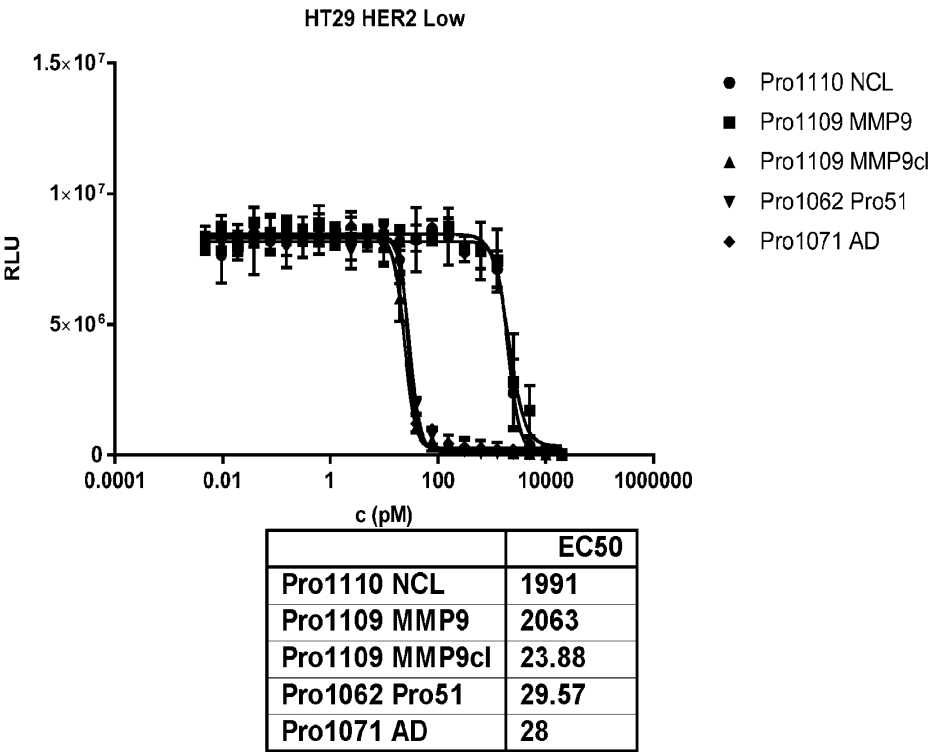


Figure 29A

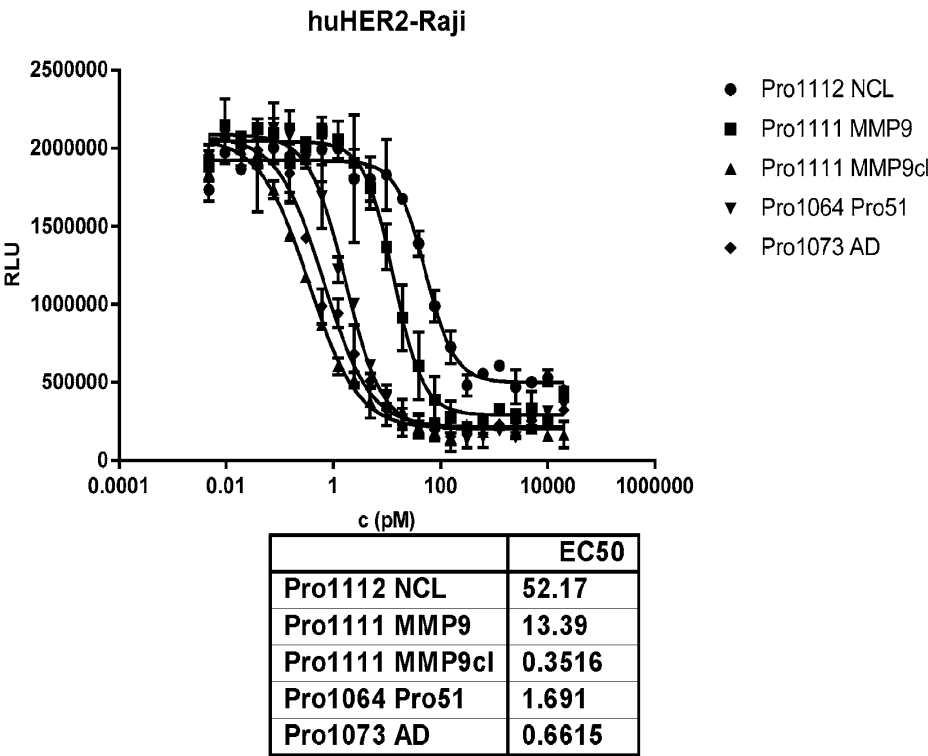
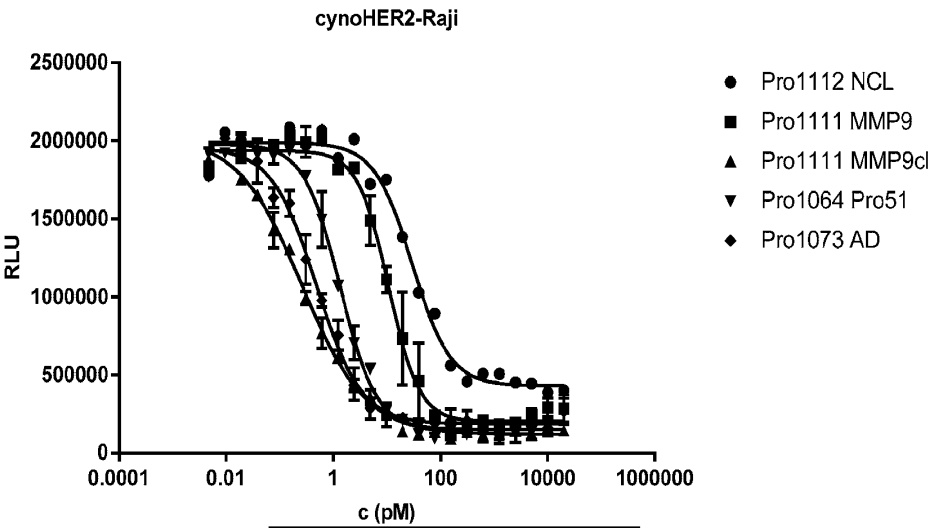
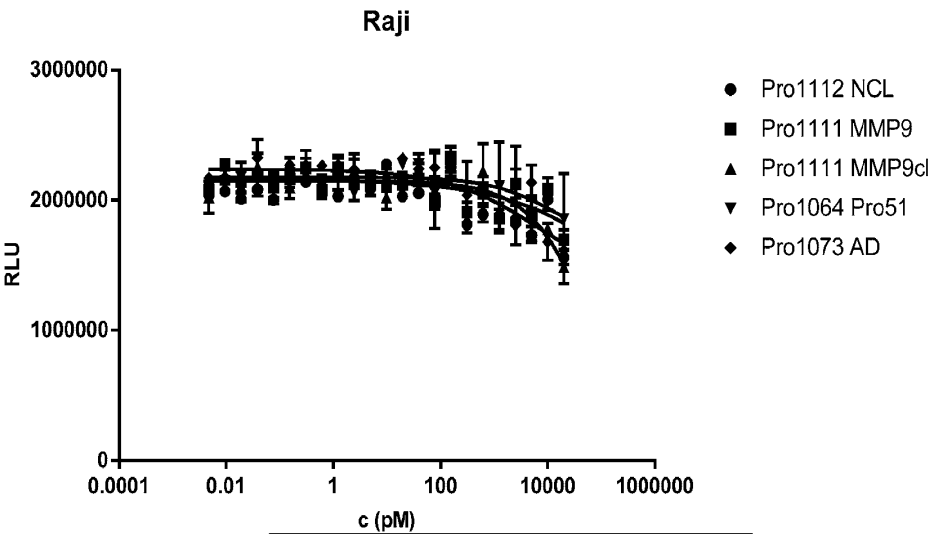


Figure 29B



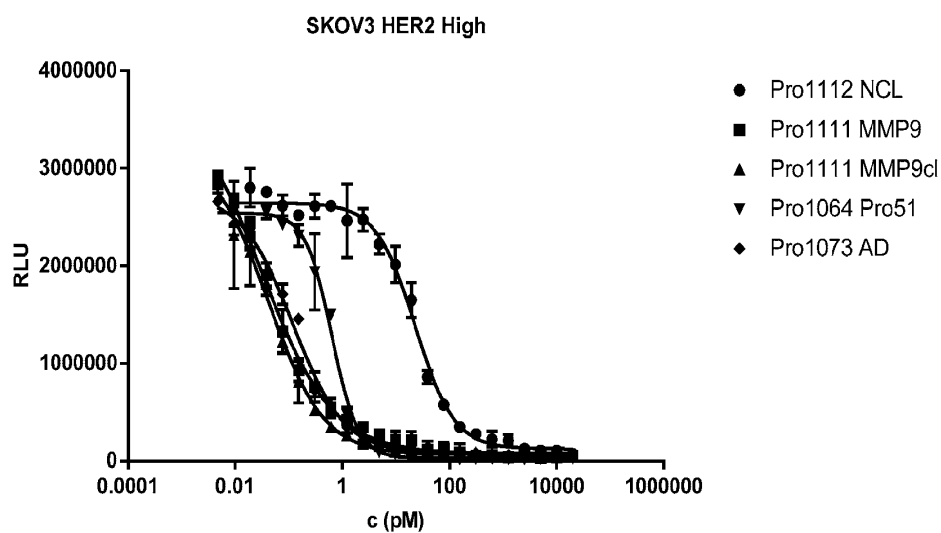
	EC50
Pro1112 NCL	29.72
Pro1111 MMP9	10.7
Pro1111 MMP9cl	0.2613
Pro1064 Pro51	1.341
Pro1073 AD	0.4876

Figure 29C



	EC50
Pro1112 NCL	
Pro1111 MMP9	~ 2345311666901
Pro1111 MMP9cl	182533
Pro1064 Pro51	15762
Pro1073 AD	6477

Figure 29D



	EC50
Pro1112 NCL	22.88
Pro1111 MMP9	0.03226
Pro1111 MMP9cl	0.04267
Pro1064 Pro51	0.6359
Pro1073 AD	0.1188

Figure 29E

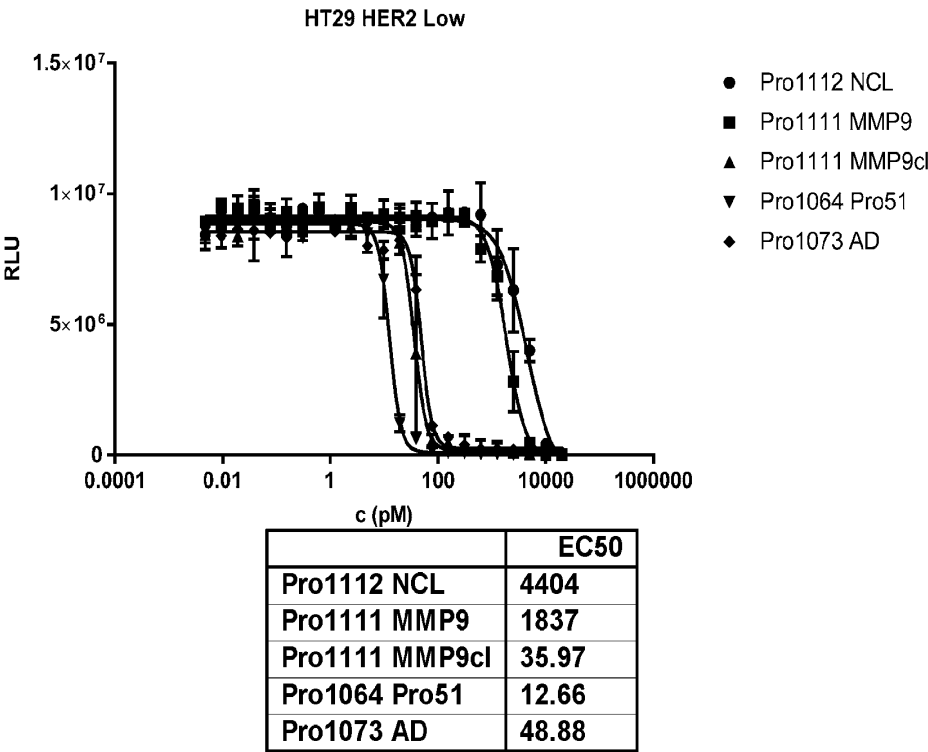


Figure 30A

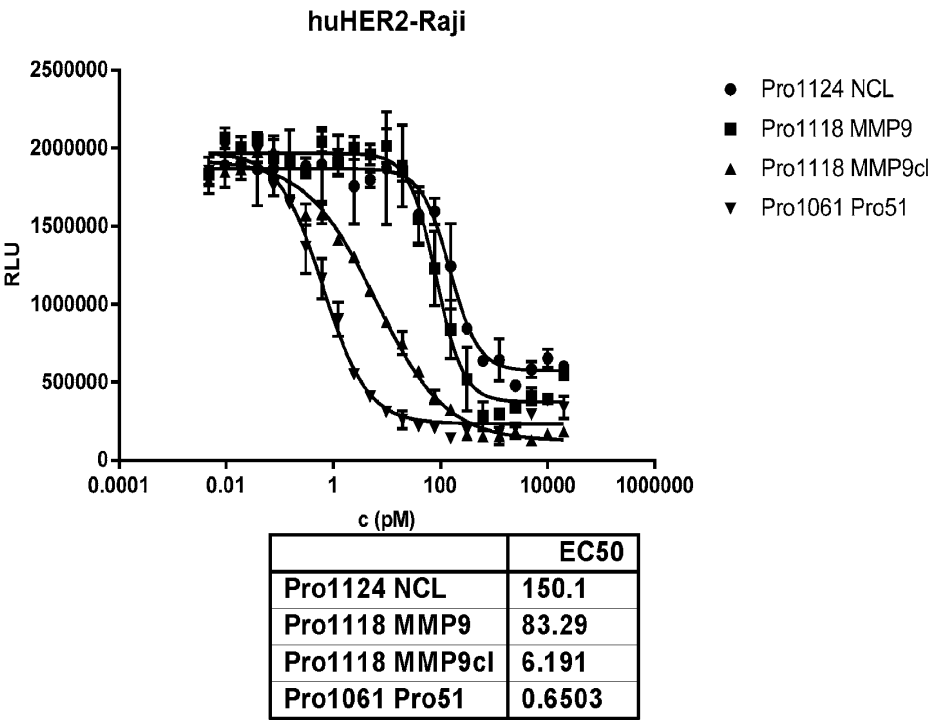


Figure 30B

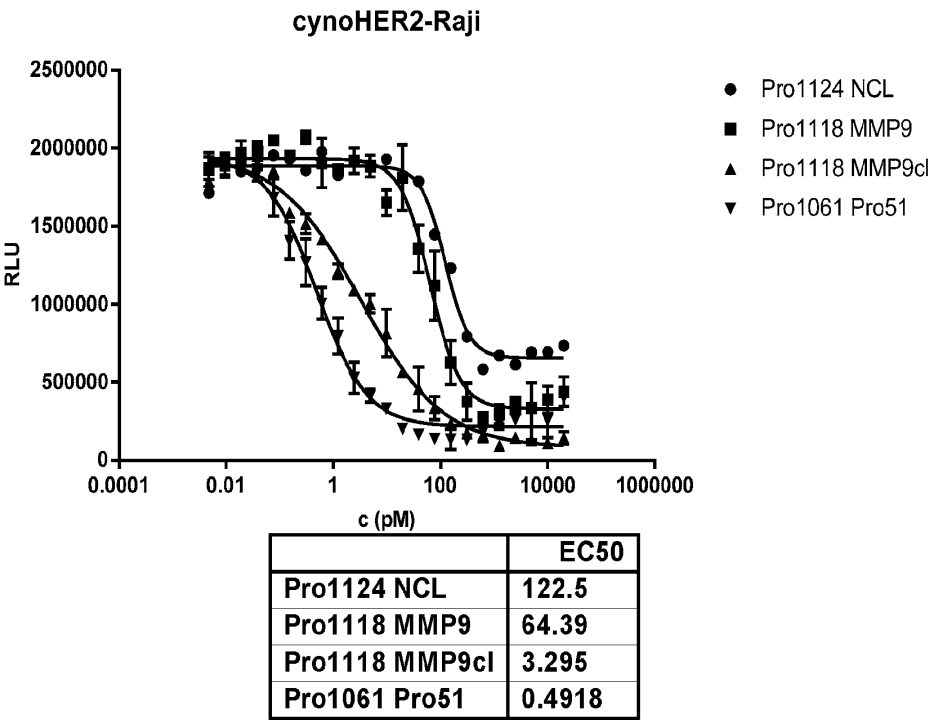
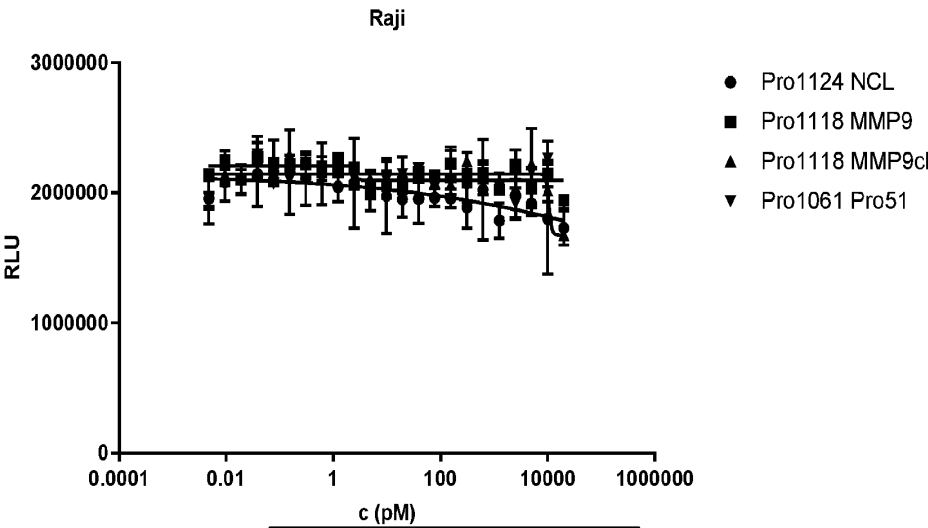
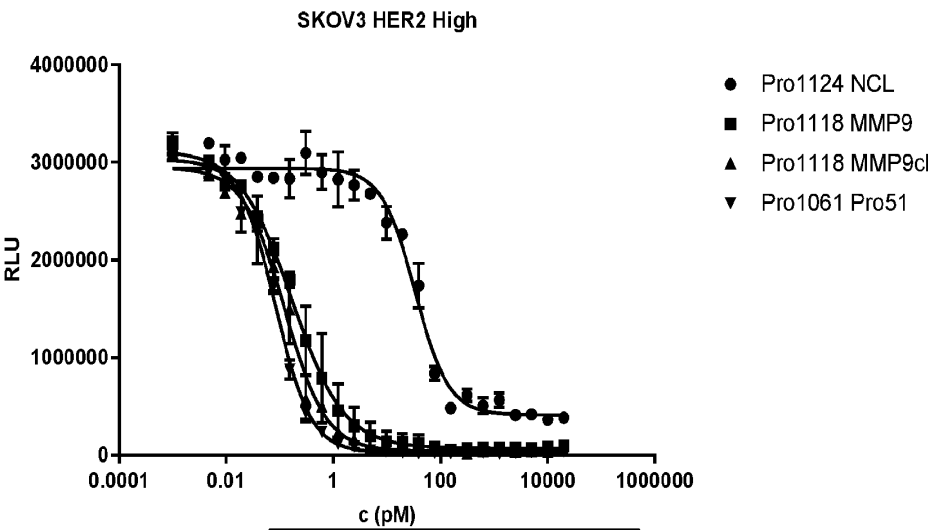


Figure 30C



	EC50
Pro1124 NCL	279359
Pro1118 MMP9	~ 2.605
Pro1118 MMP9cl	~ 10630
Pro1061 Pro51	

Figure 30D



	EC50
Pro1124 NCL	33.66
Pro1118 MMP9	0.1668
Pro1118 MMP9cl	0.124
Pro1061 Pro51	0.08374

Figure 30E

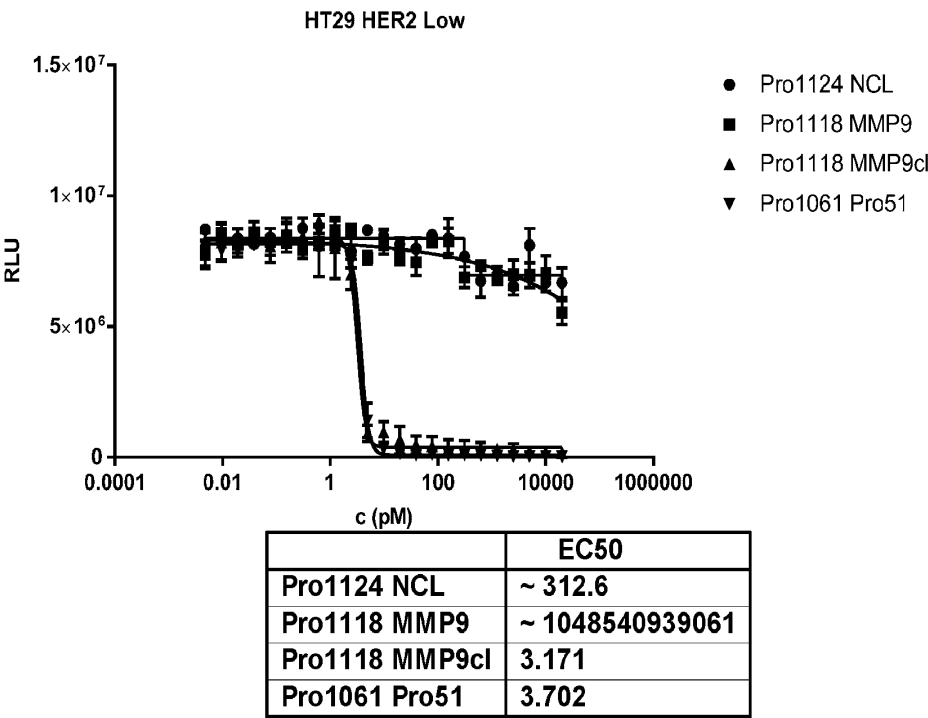
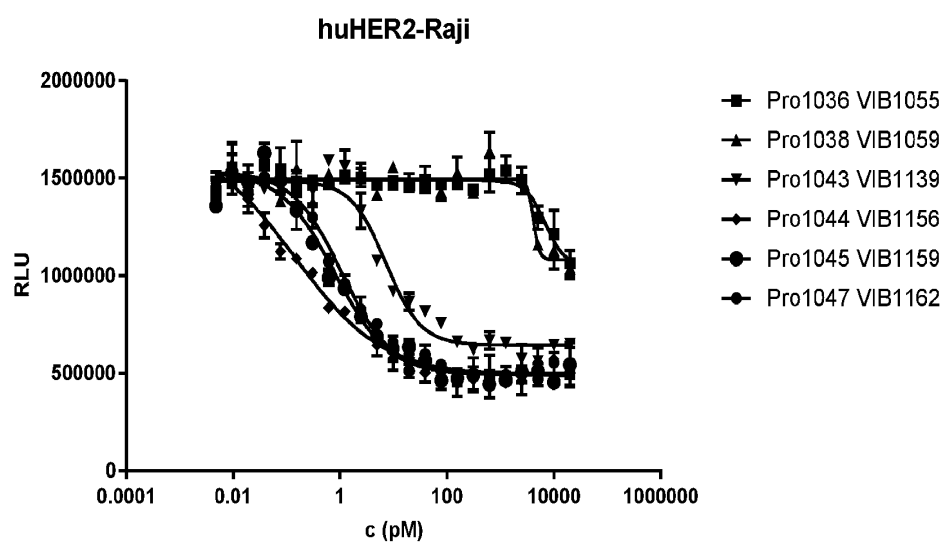
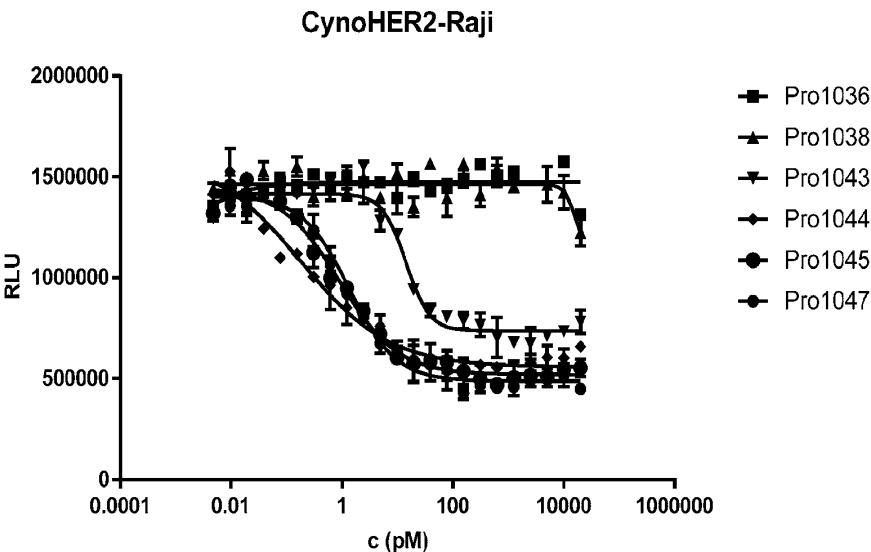


Figure 31A



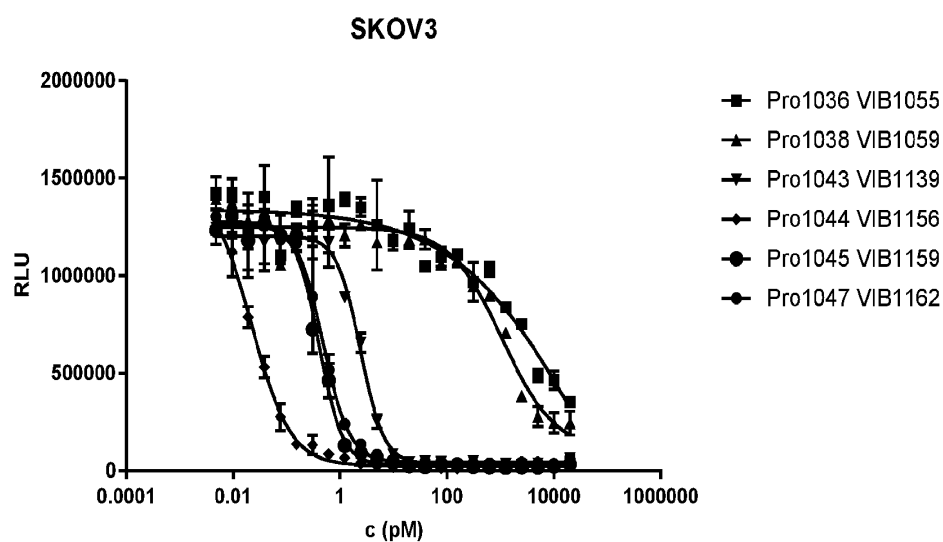
	EC50
Pro1036 VIB1055	6901
Pro1038 VIB1059	4123
Pro1043 VIB1139	7.189
Pro1044 VIB1156	0.1431
Pro1045 VIB1159	0.7976
Pro1047 VIB1162	1.069

Figure 31B



	EC50
Pro1036	~ 8.307e-005
Pro1038	16608
Pro1043	14.21
Pro1044	0.1837
Pro1045	0.8972
Pro1047	1.348

Figure 31C



	EC50
Pro1036 VIB1055	29821
Pro1038 VIB1059	1084
Pro1043 VIB1139	2.401
Pro1044 VIB1156	0.02212
Pro1045 VIB1159	0.4071
Pro1047 VIB1162	0.4788

Figure 32

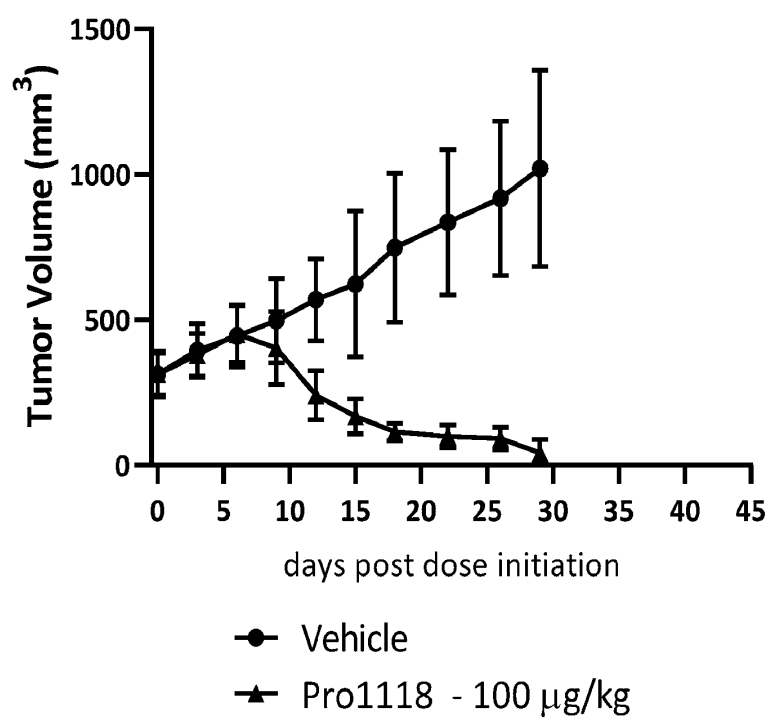


Figure 33

Mouse PK: Pro1111 30 $\mu\text{g/kg}$

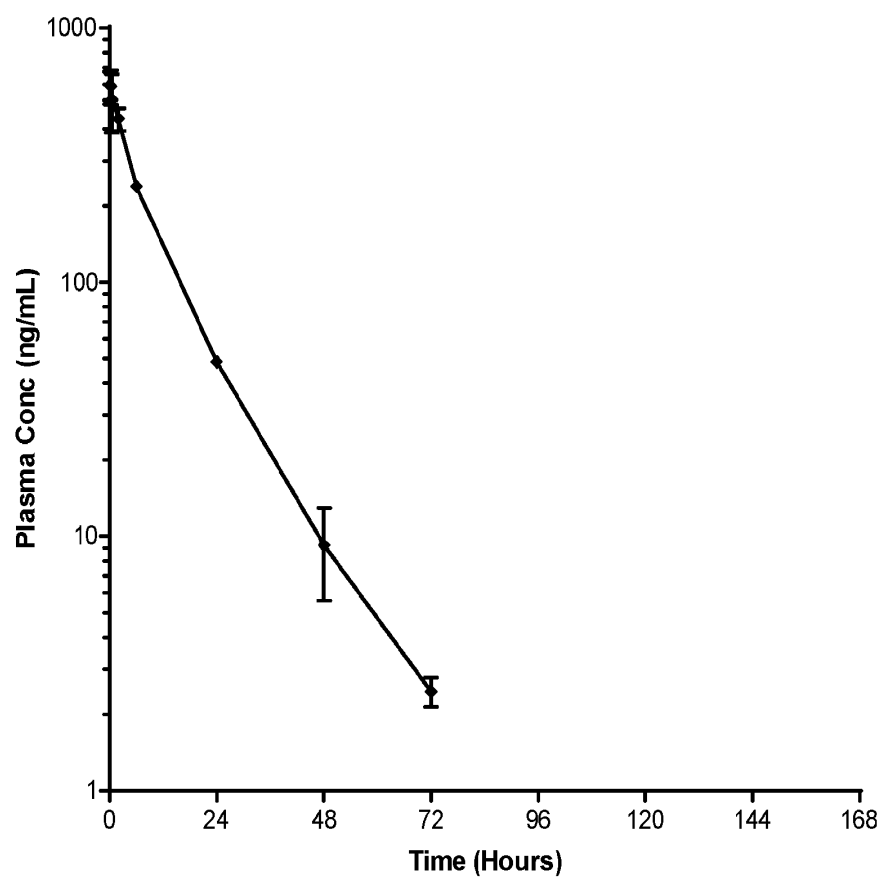


Figure 34

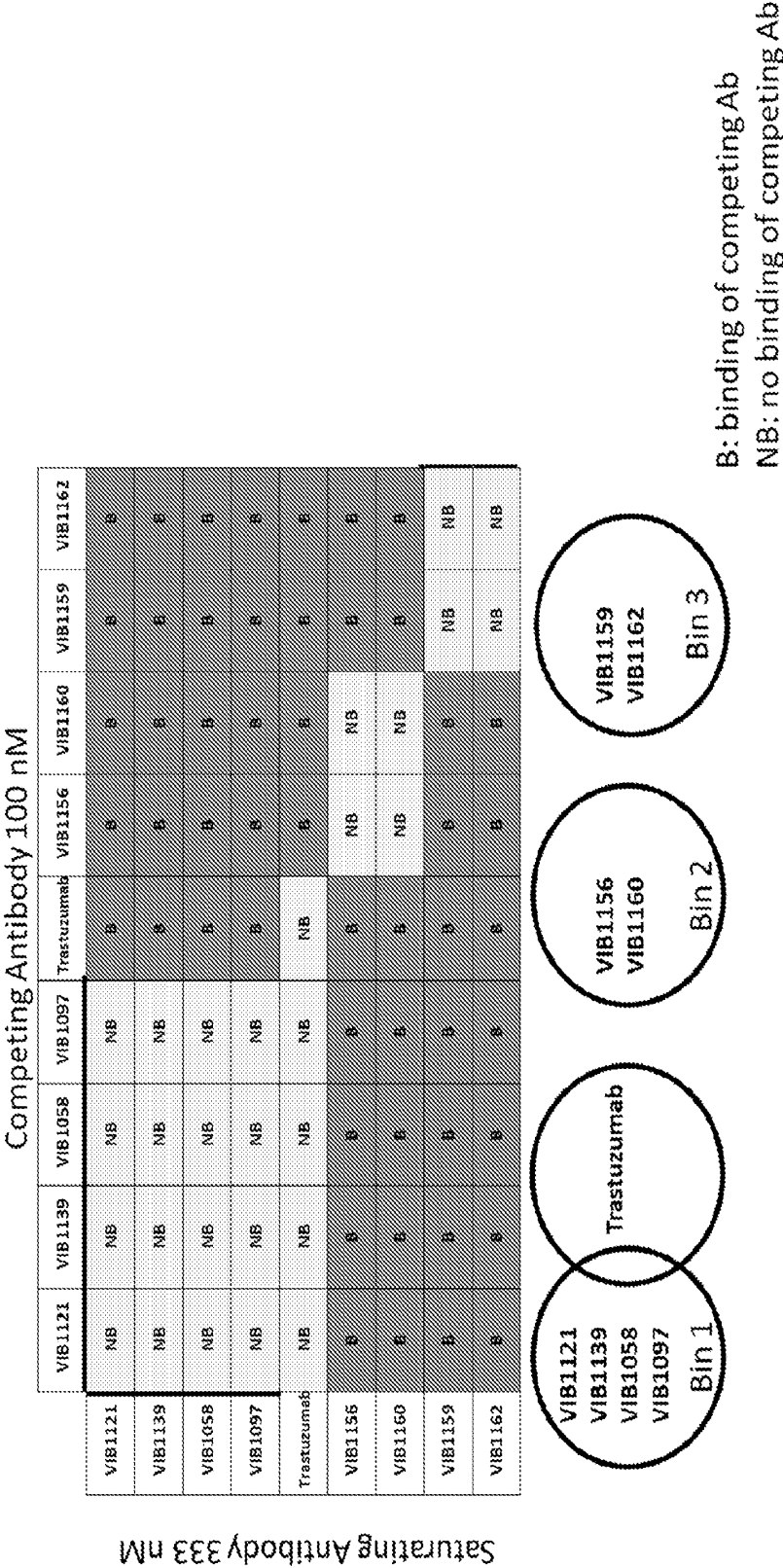


Figure 35

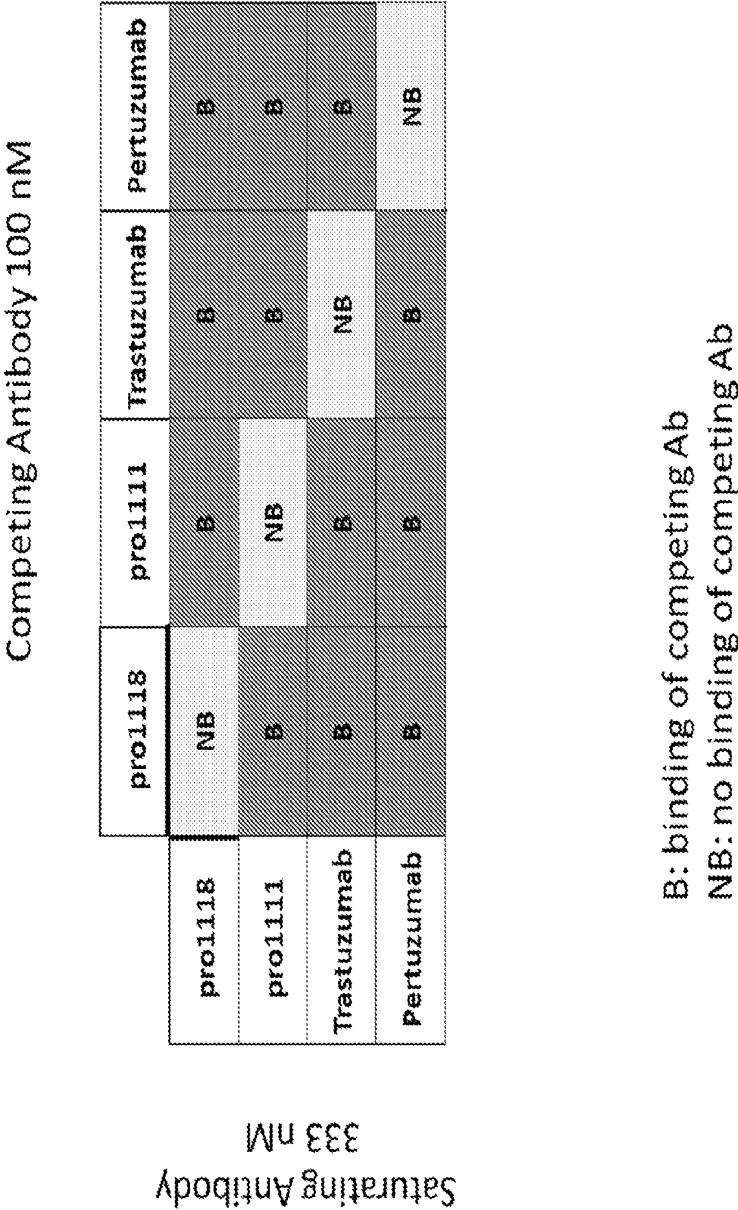


Figure 36

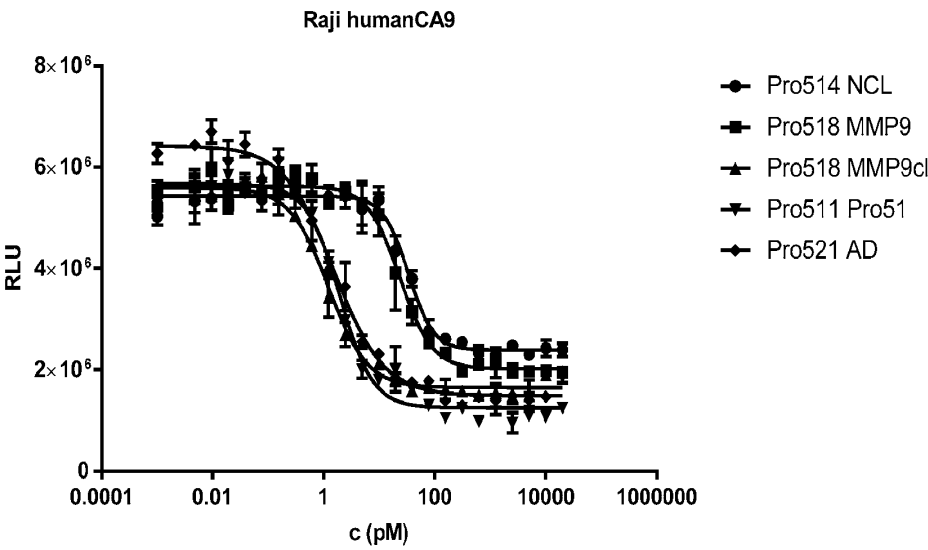
Epitope Mapping of HER2 sdAb h1156 (Pro1061)			
Amino Acid (AA) location	AA sequence	SEQ ID NOs	
AA147-148	WK		
AA157-161	LALTL (main)	515	
AA194-198	TRTVC	516	

Epitope Mapping of HER2 sdAb h1162 (Pro1064)			
Amino Acid (AA) location	AA sequence	SEQ ID NOs	
AA462-472	QLTFRNP HQALL	517	

Figure 37

sdAb	ProIdent	human HER2			cyno HER2			mouse HER2		
		k_{on} (1/Ms)	k_{off} (1/s)	K_D (nM)	k_{on} (1/Ms)	k_{off} (1/s)	K_D (nM)	k_{on} (1/Ms)	k_{off} (1/s)	K_D (nM)
1055	Pro1036	3.20E+05	1.70E-02	53.1	3.49E+05	2.44E-02	69.9	nb		
1058	Pro1037	2.15E+05	1.85E-03	8.6	3.15E+05	3.06E-03	9.7	nb		
1059	Pro1038	3.86E+05	8.86E-03	23.0	2.40E+05	2.04E-02	85.0	nb		
1091	Pro1039	1.19E+05	7.12E-04	6.0	1.36E+05	1.15E-03	8.5	nb		
1092	Pro1040	1.13E+05	3.49E-04	3.1	1.19E+05	5.39E-04	4.5	nb		
1097	Pro1041	1.20E+05	3.04E-04	2.5	1.46E+05	6.30E-04	4.3	nb		
1121	Pro1042	2.26E+05	8.53E-04	3.8	1.77E+05	8.09E-04	4.6	nb		
1139	Pro1043	3.08E+05	1.71E-03	5.6	3.91E+05	2.61E-03	6.7	nb		
1156	Pro1044	9.44E+03	6.24E-05	6.6	1.07E+04	9.58E-05	9.0	nb		
1159	Pro1045	2.57E+04	4.63E-04	18.0	2.68E+04	4.55E-04	17.0	4.20E+04	3.36E-03	80.0
1160	Pro1046	3.00E+03	1.70E-04	56.7	1.57E+04	1.69E-04	10.8	nb		
1162	Pro1047	1.52E+05	3.26E-03	21.4	1.72E+05	3.64E-03	21.2	1.36E+06	7.35E-02	54.0
h1058	Pro1056	2.28E+05	4.82E-03	21.1	2.83E+05	8.27E-03	29.2	nb		
h1092	Pro1057	1.11E+05	4.71E-04	4.2	1.68E+05	8.52E-04	5.1	nb		
h1097	Pro1058	1.05E+05	5.42E-04	5.2	2.05E+05	1.25E-03	6.1	nb		
h1121	Pro1059	3.09E+05	2.99E-03	9.7	3.02E+05	2.79E-03	9.2	nb		
h1139	Pro1060	3.12E+05	2.29E-03	7.3	5.16E+05	3.84E-03	7.4	nb		
h1156	Pro1061	1.66E+05	<1.0e-7	<0.01	1.88E+05	<1.0e-7	<0.01	nb		
h1159	Pro1062	8.41E+03	8.93E-04	106.2	2.36E+04	8.74E-04	37.0	2.71E+02	5.18E-03	19114.4
h1160	Pro1063	9.90E+03	4.22E-04	42.6	1.14E+04	5.10E-04	44.7	nb		
h1162	Pro1064	1.74E+05	3.99E-03	22.9	2.14E+05	4.67E-03	21.8	9.66E+05	1.18E-01	122.2

Figure 38A



	EC50
Pro514 NCL	33.39
Pro518 MMP9	23.42
Pro518 MMP9cl	1.227
Pro511 Pro51	1.951
Pro521 AD	1.525

Figure 38B

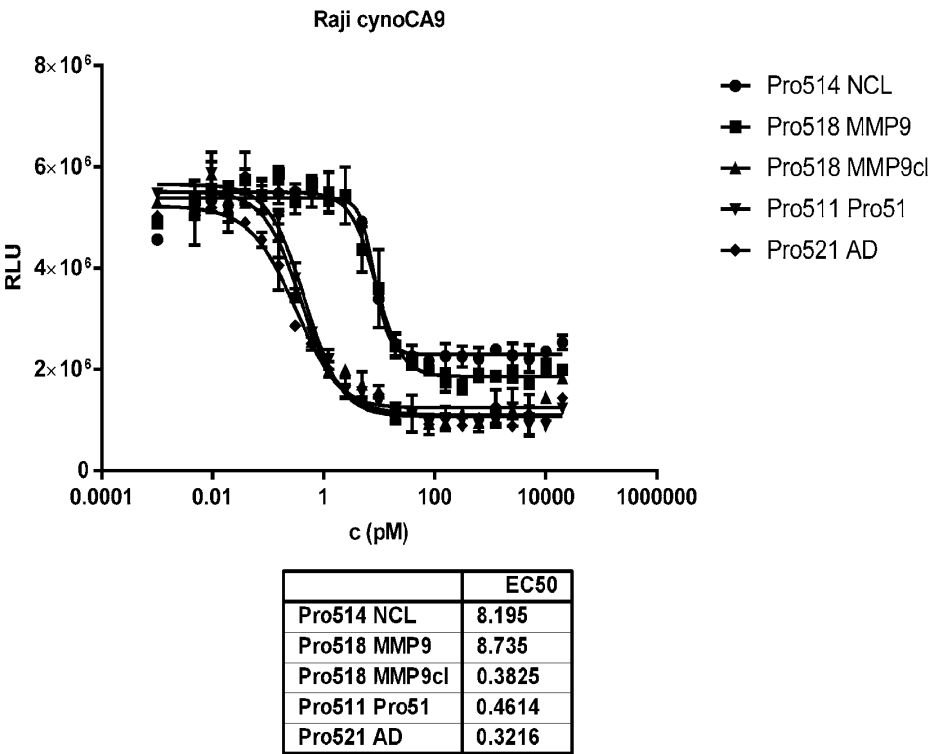


Figure 38C

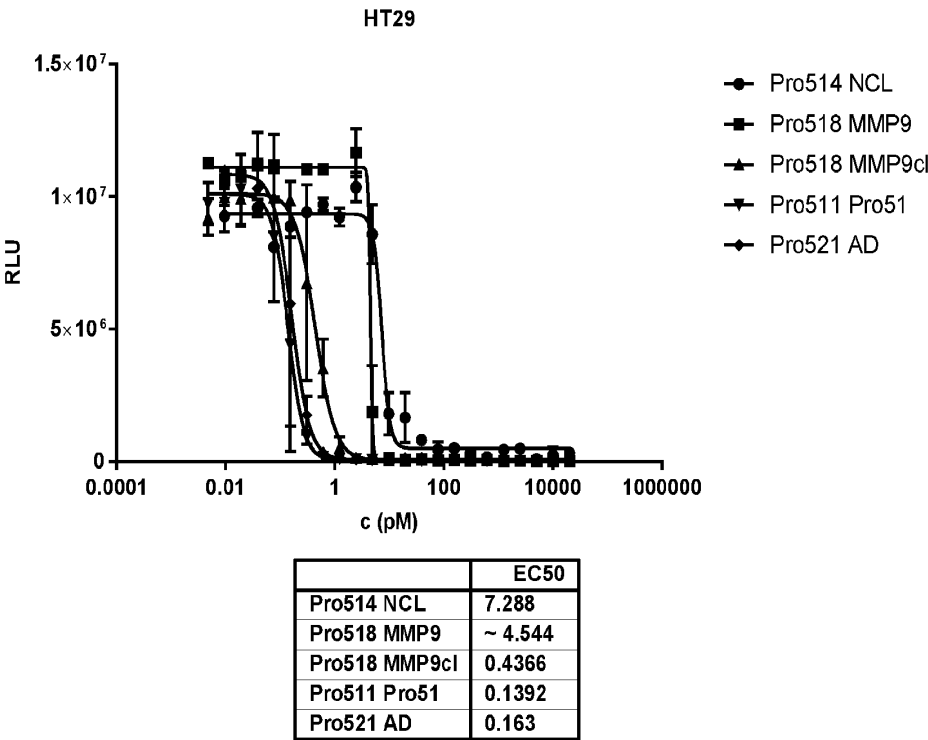


Figure 39A

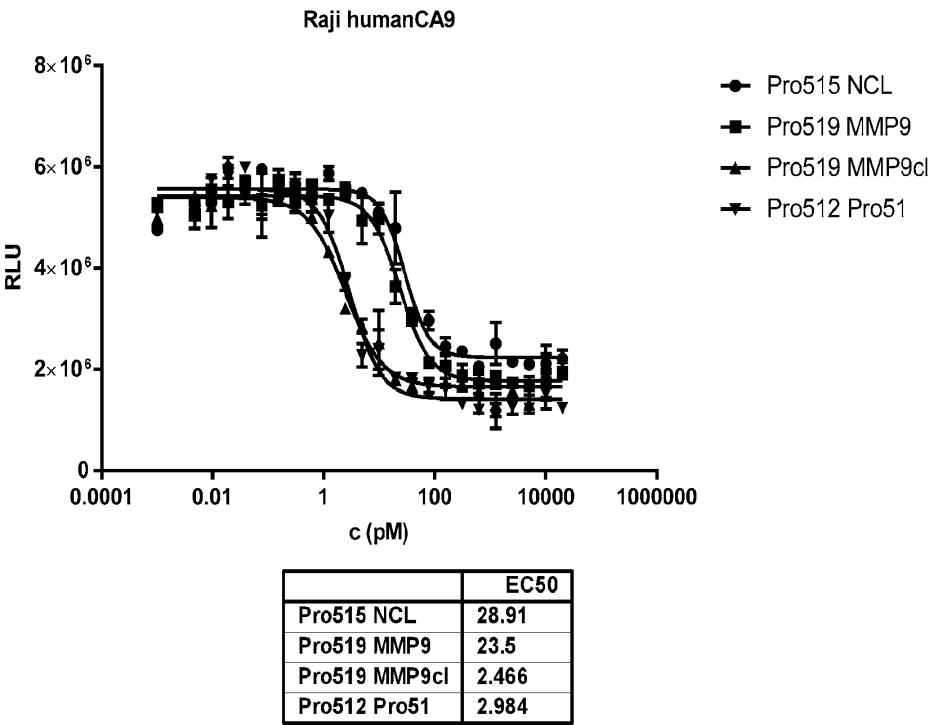


Figure 39B

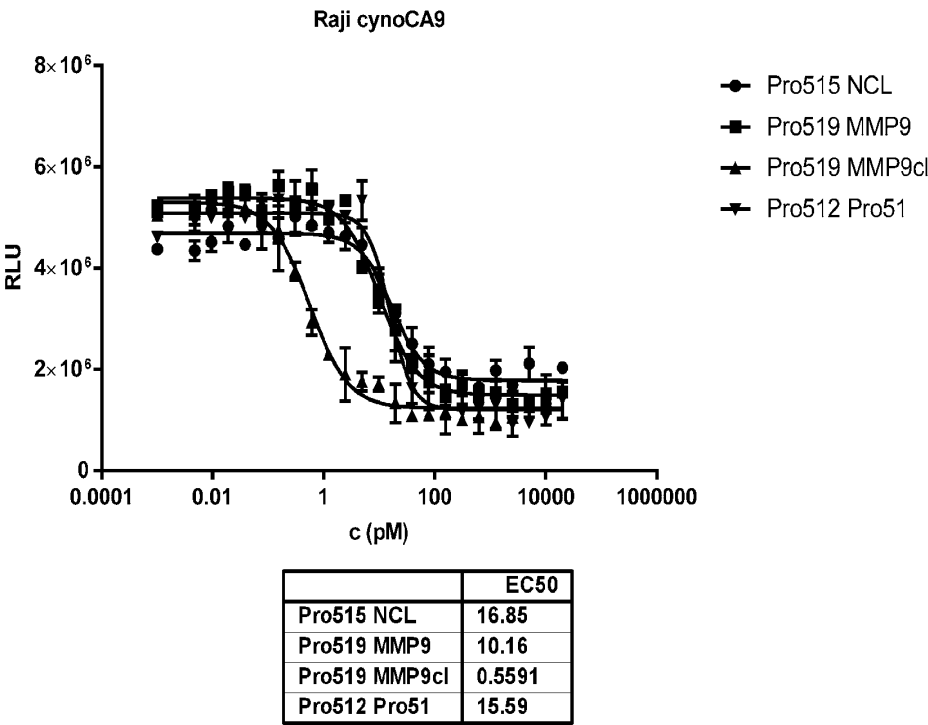


Figure 39C

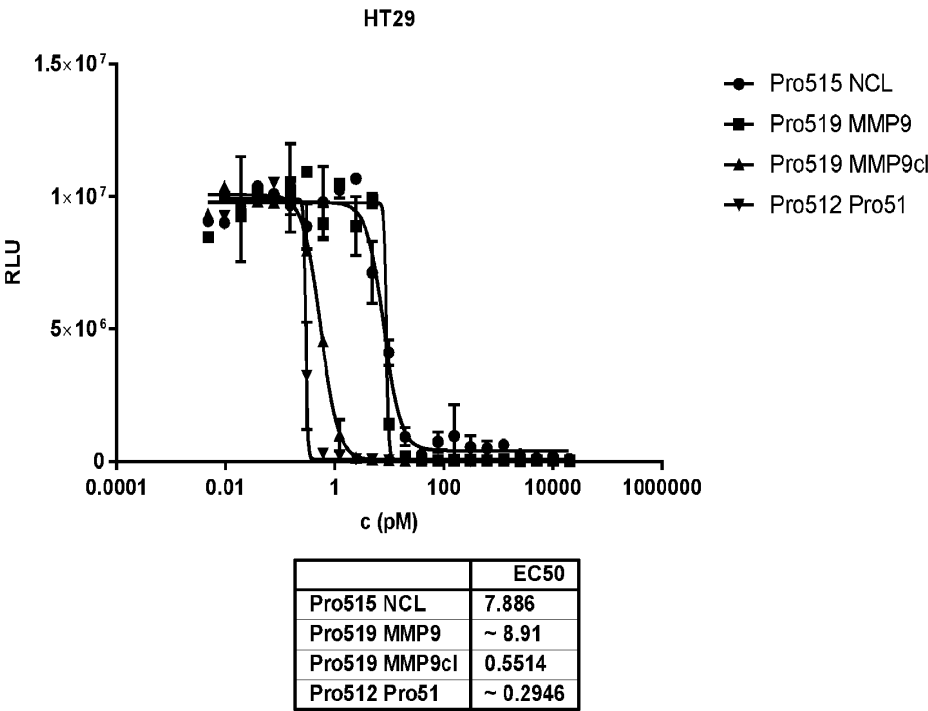
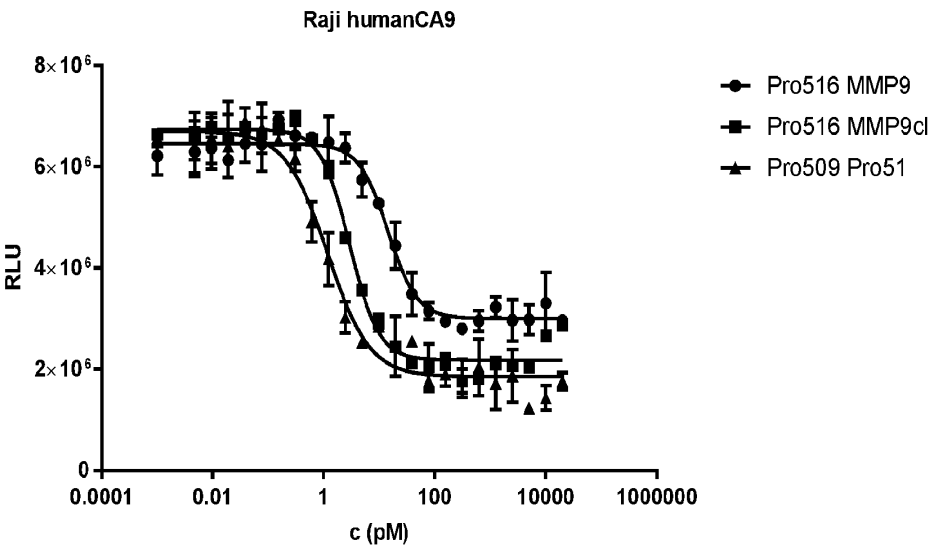


Figure 40A



	EC50
Pro516 MMP9	14.4
Pro516 MMP9cl	2.941
Pro509 Pro51	1.183

Figure 40B

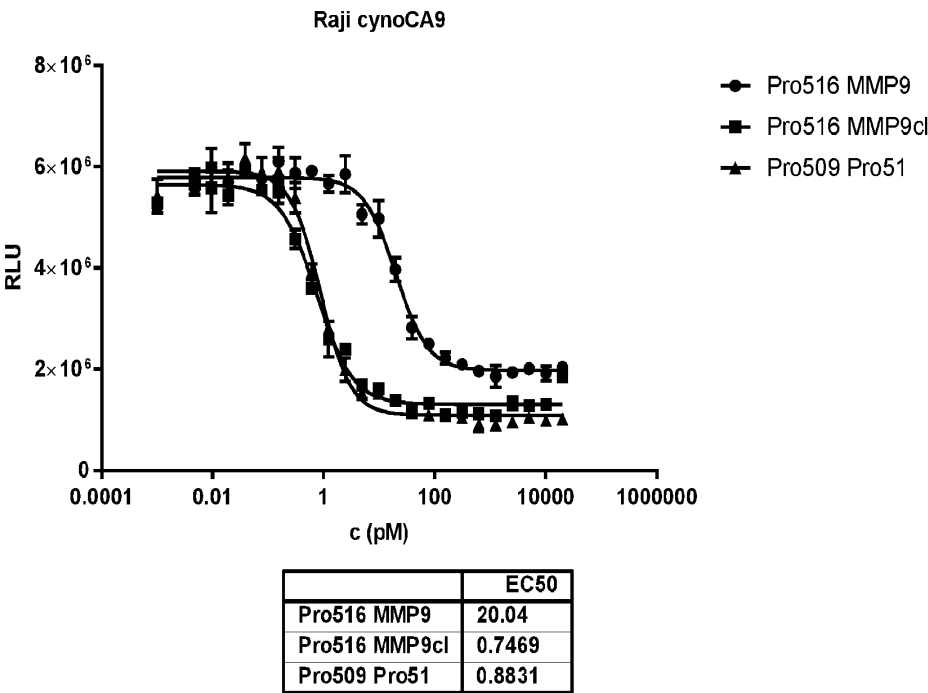


Figure 40C

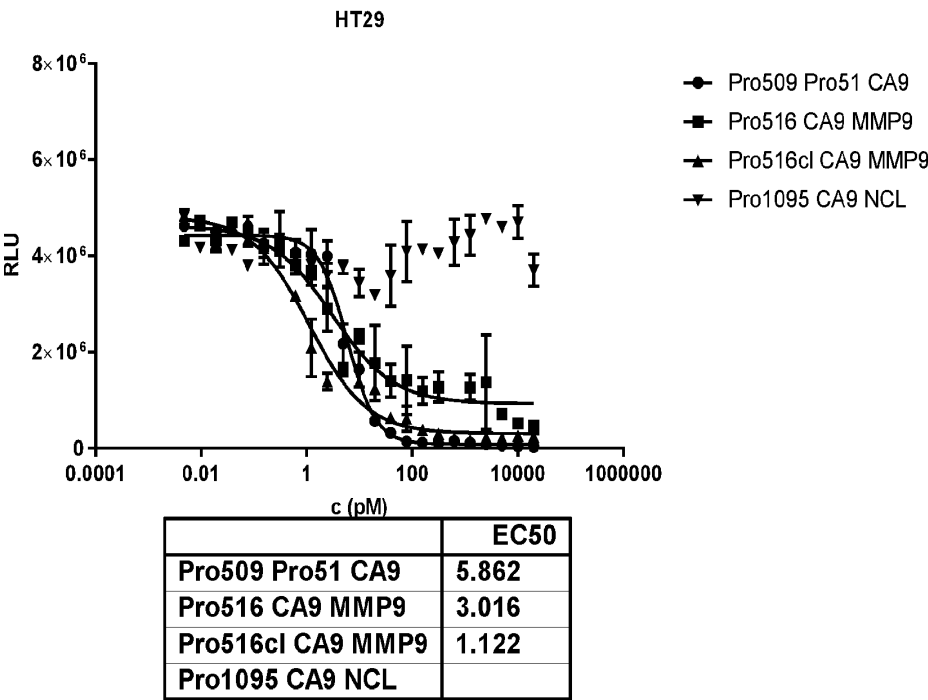
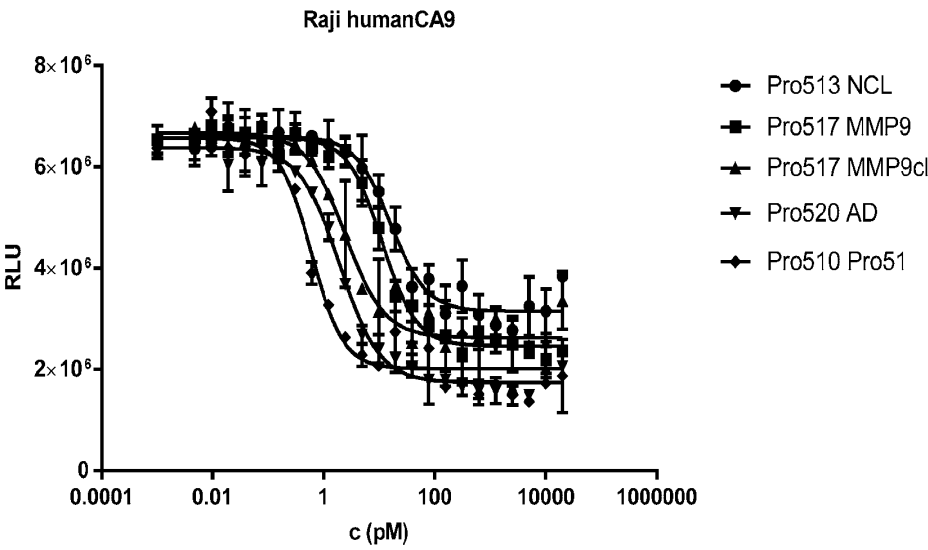


Figure 41A



	EC50
Pro513 NCL	16.09
Pro517 MMP9	11.28
Pro517 MMP9cl	2.455
Pro520 AD	1.946
Pro510 Pro51	0.6043

Figure 41B

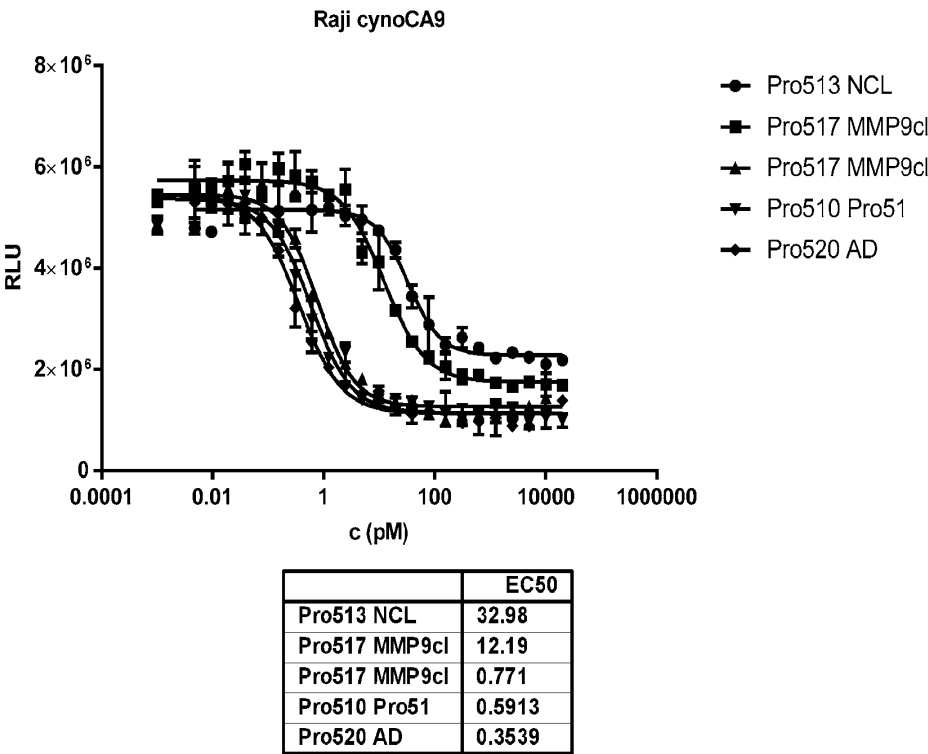
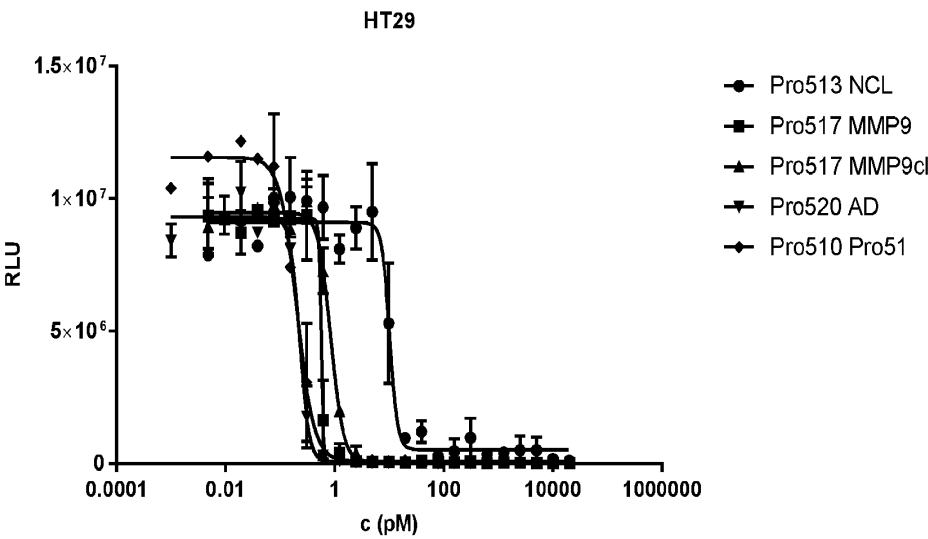


Figure 41C



	EC50
Pro513 NCL	10.17
Pro517 MMP9	~ 0.5645
Pro517 MMP9cl	0.8497
Pro520 AD	0.2265
Pro510 Pro51	0.2015

Figure 42

		K_D (nM)		
sdAb	Prodent	human CA9	cyno CA9	mouse CA9
407		1.0	<0.001	nb
445		2.6	3.4	nb
456		2.1	7.2	8.2
472		3.5	4.0	nb
476		1.7	2.1	nb
h445	Pro512	3.1	4.9	nb
h456	Pro509	0.7	1.1	1.4
h476	Pro510	1.6	1.2	nb

Figure 43A

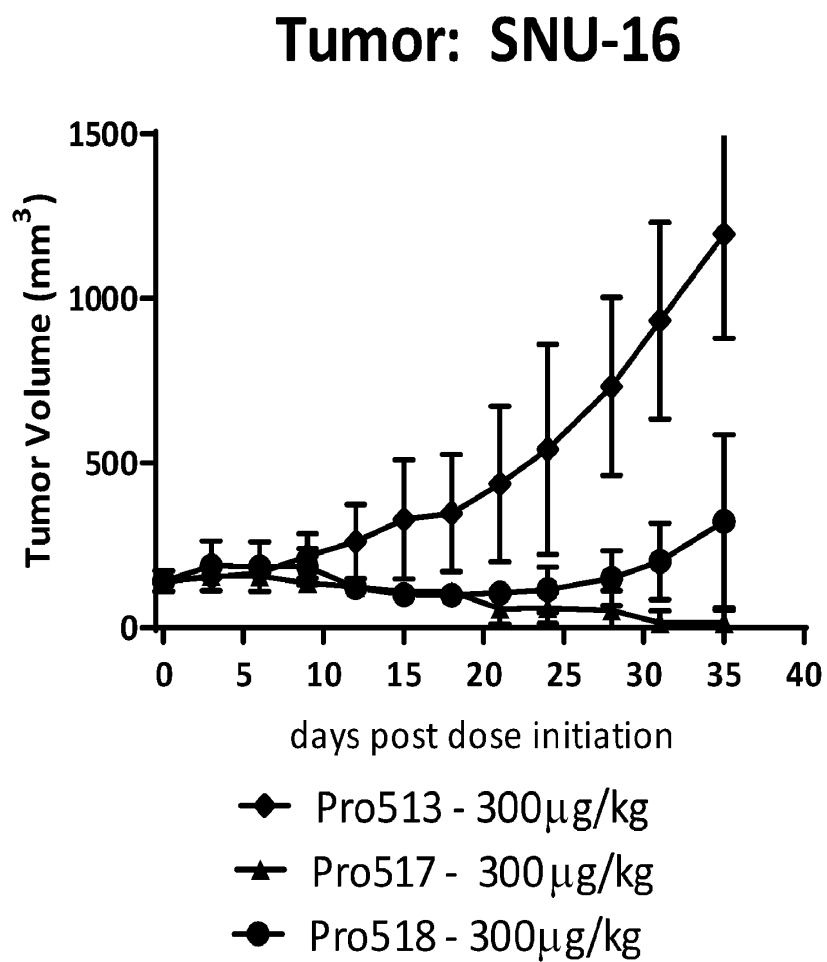


Figure 43B

Tumor: 786-O

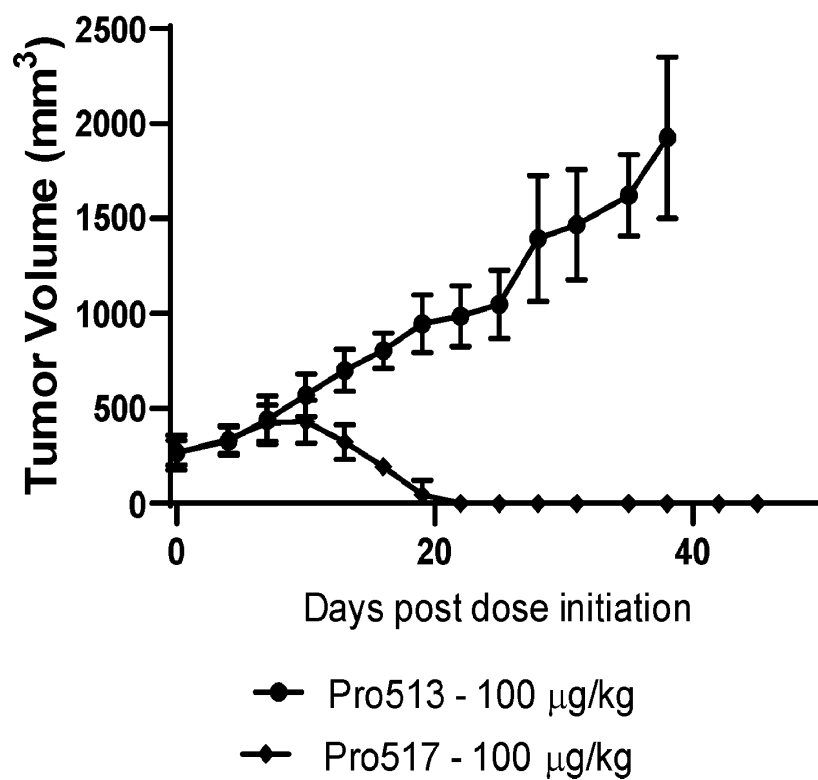


Figure 44

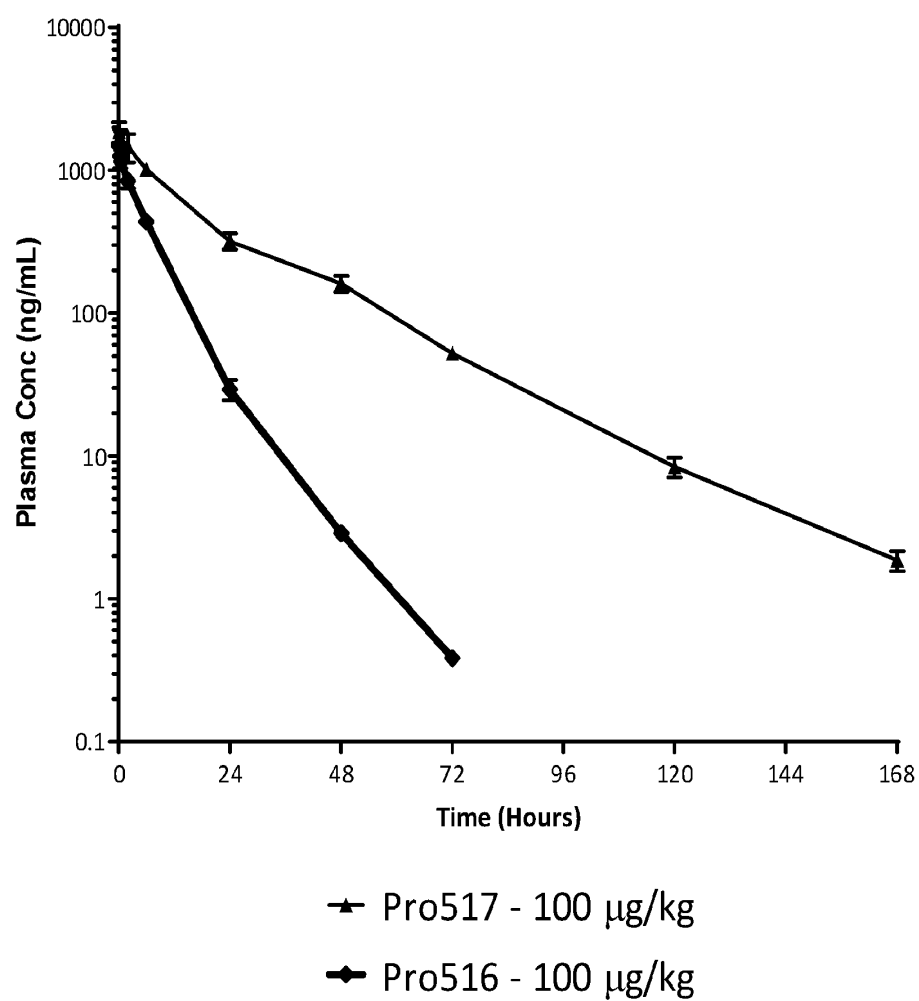
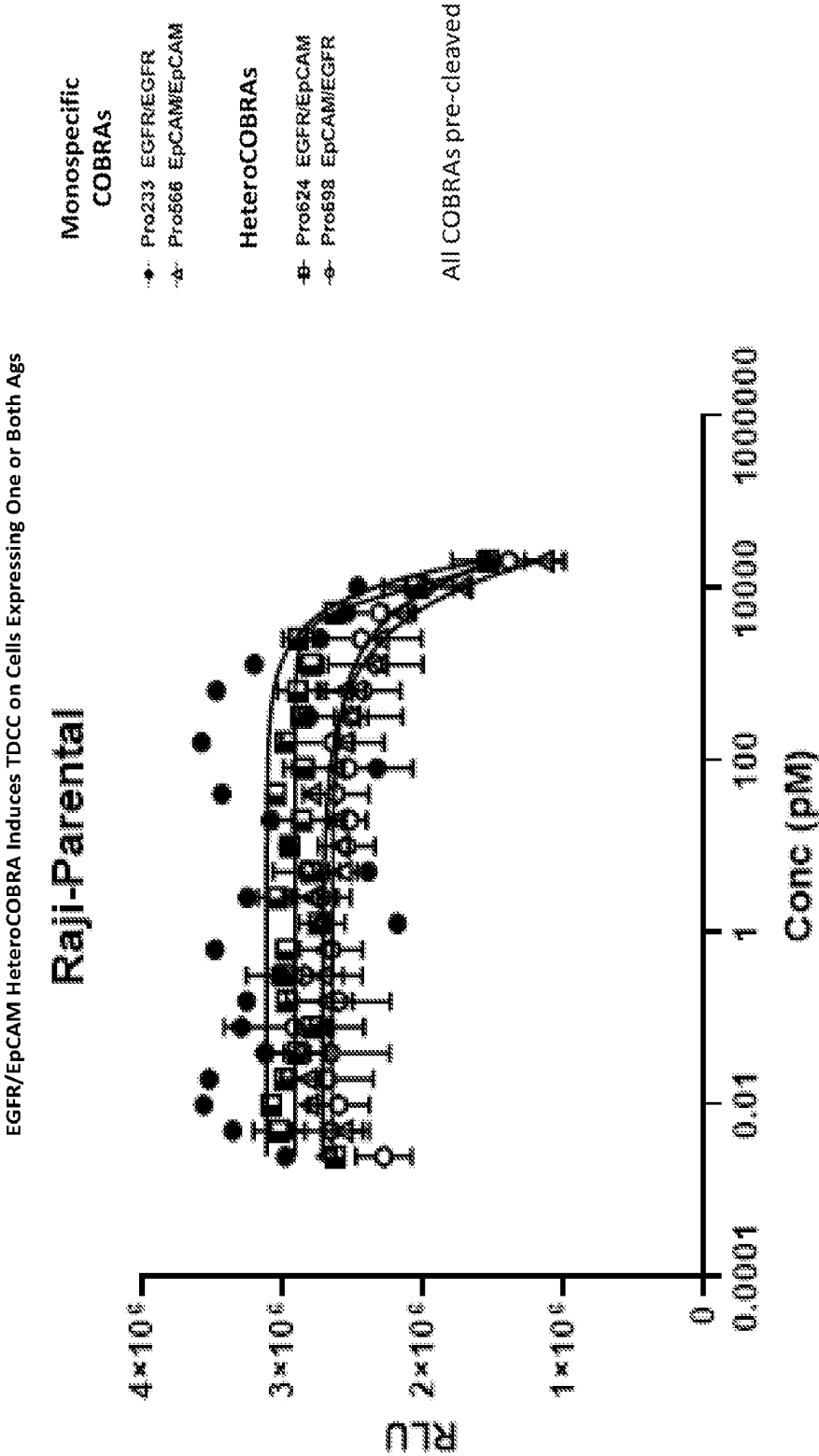


Figure 45A



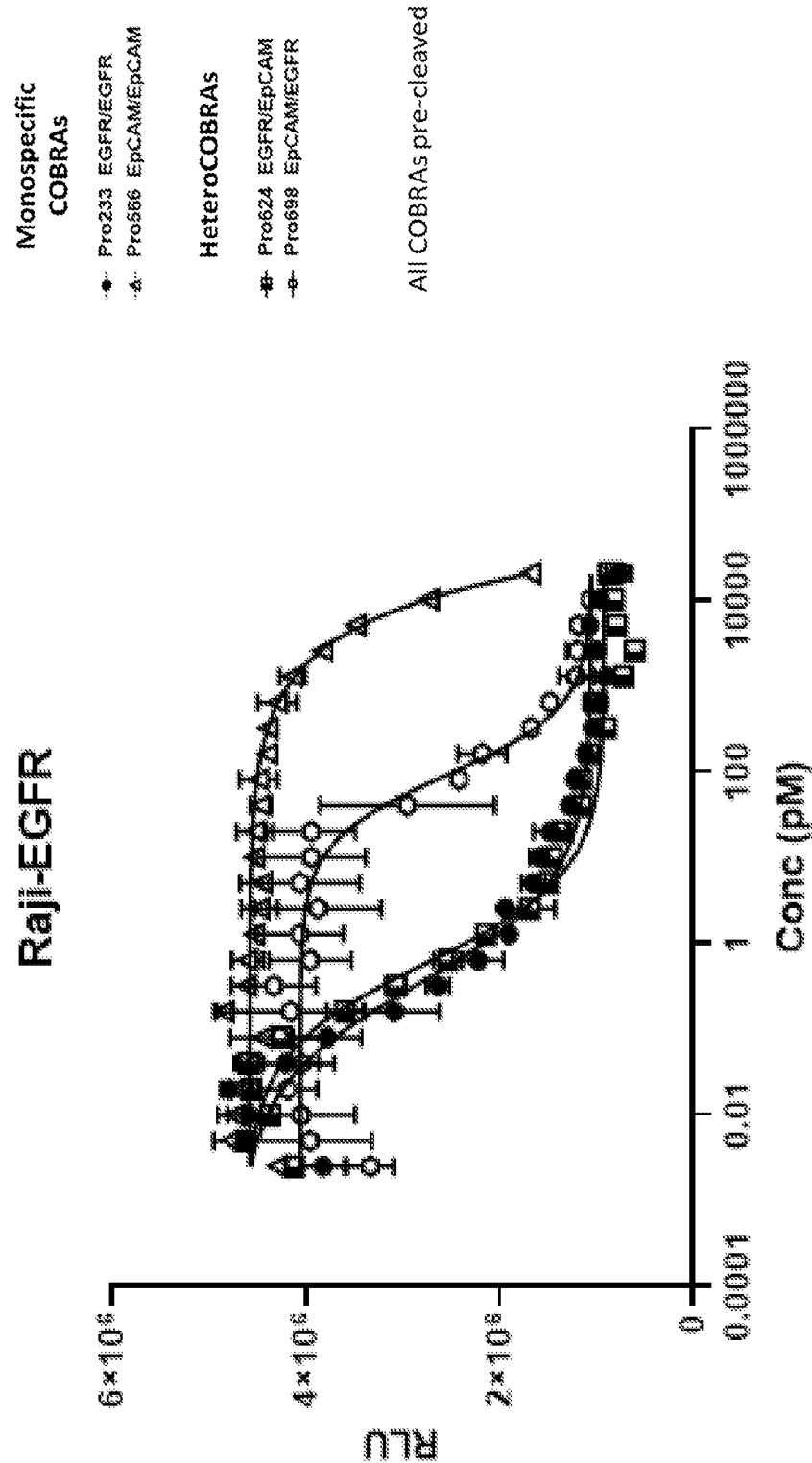


Figure 45B

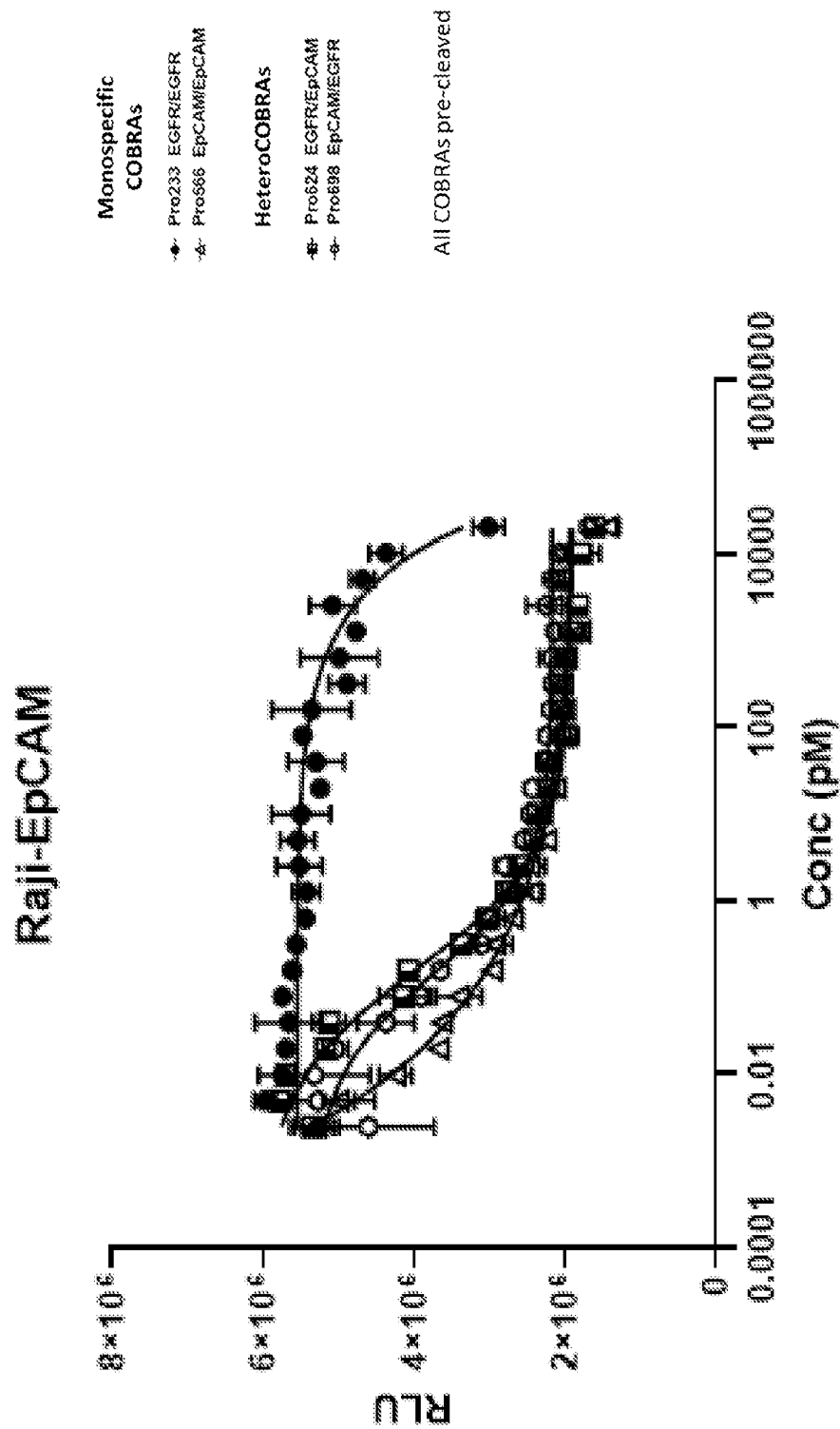


Figure 45C

Figure 45D

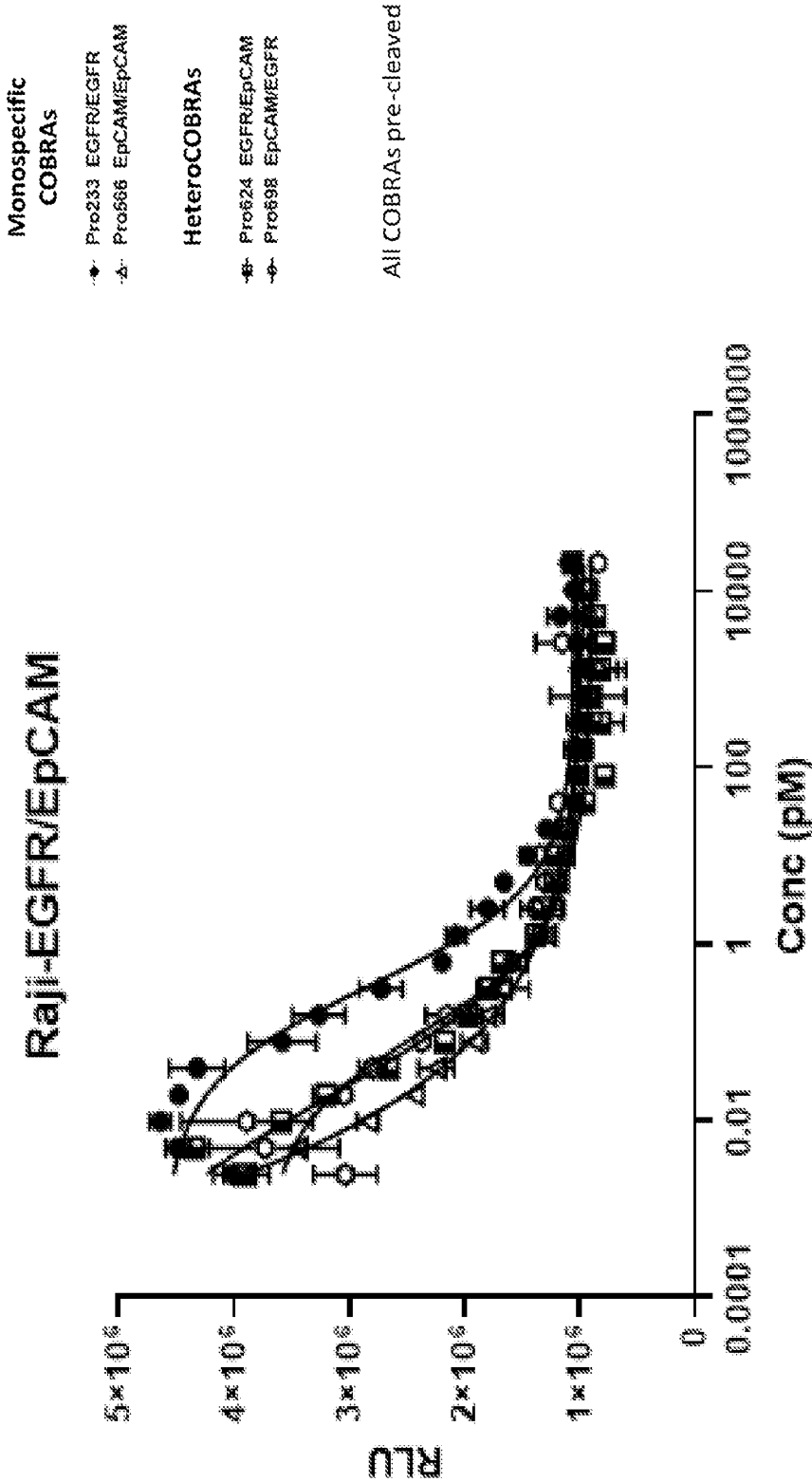
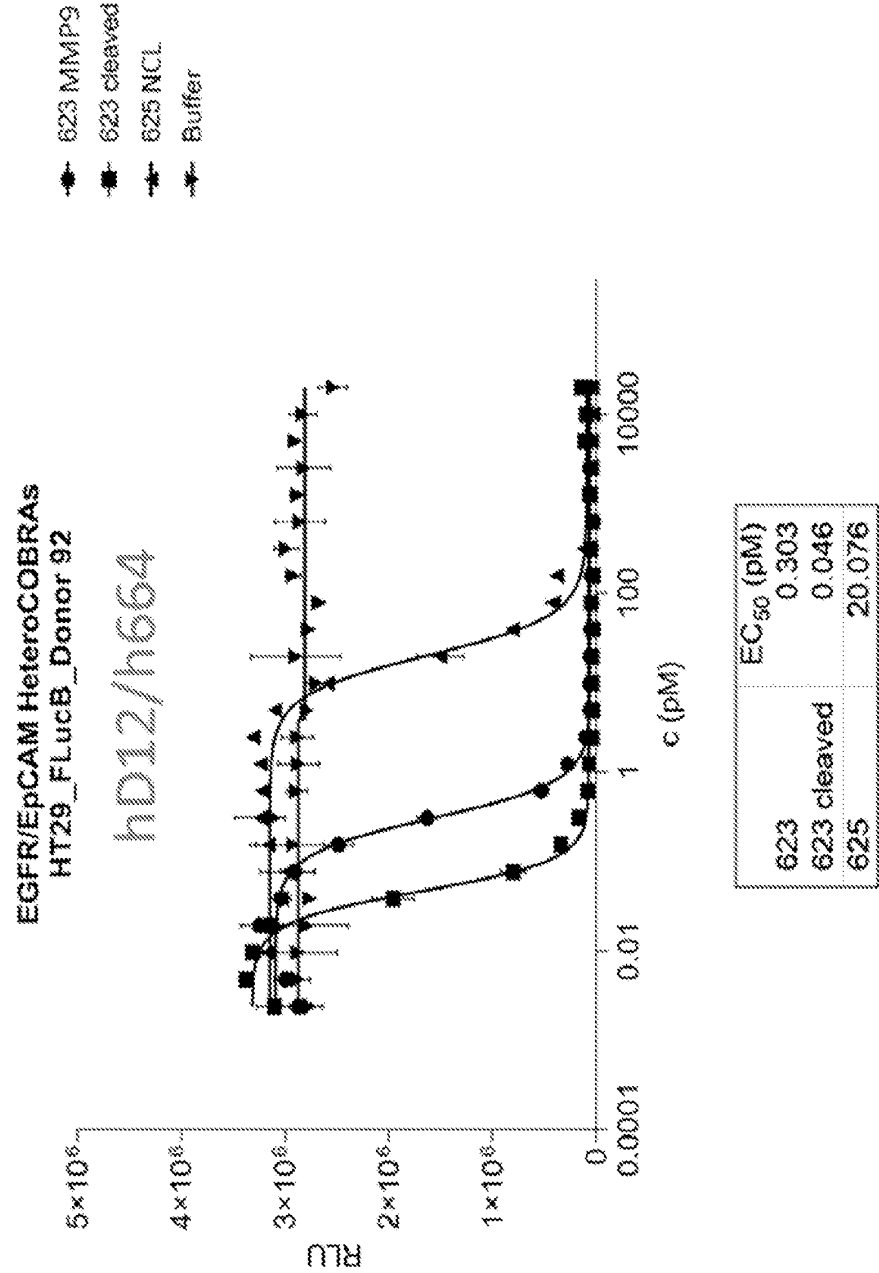


Figure 46A



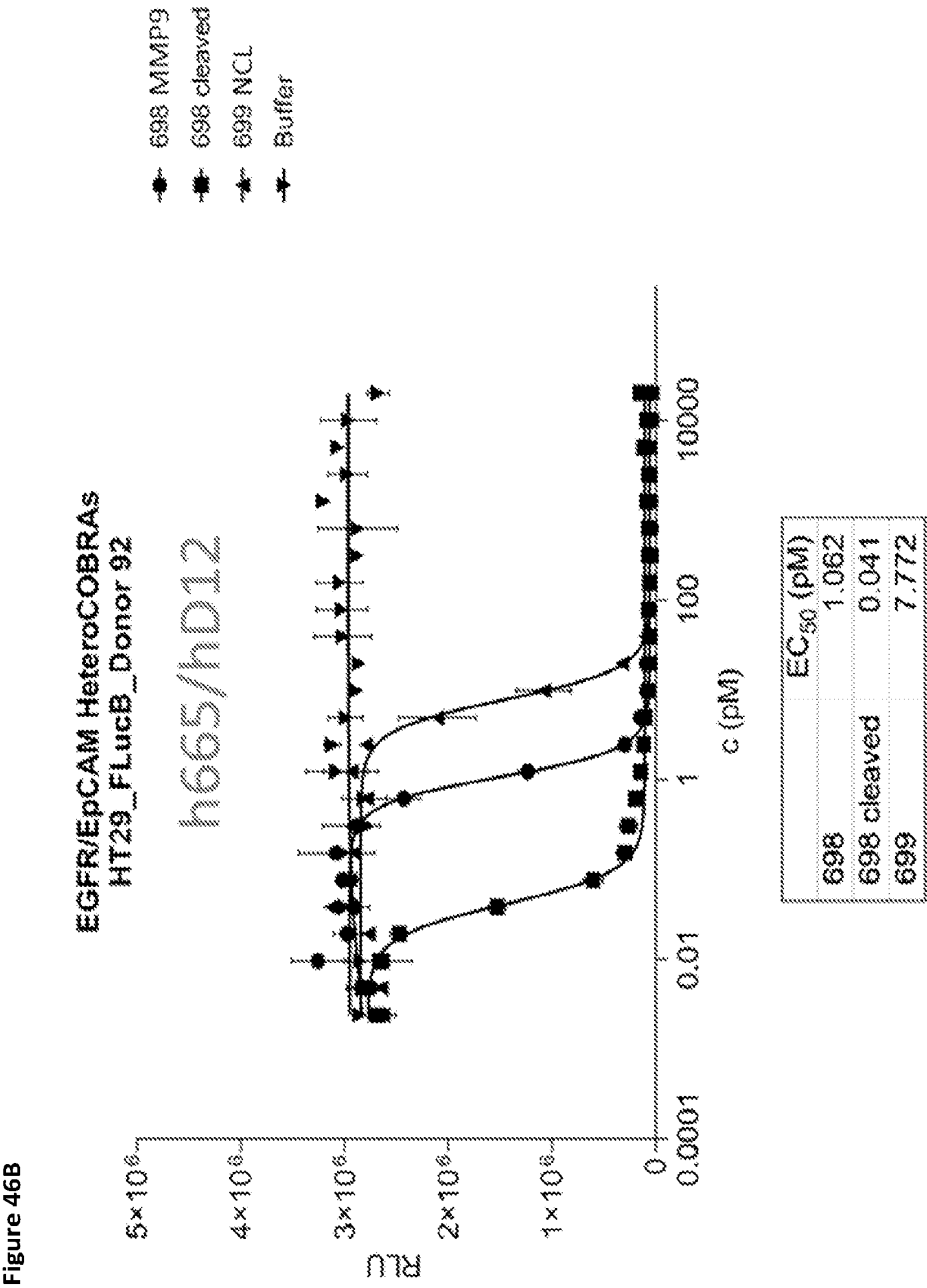
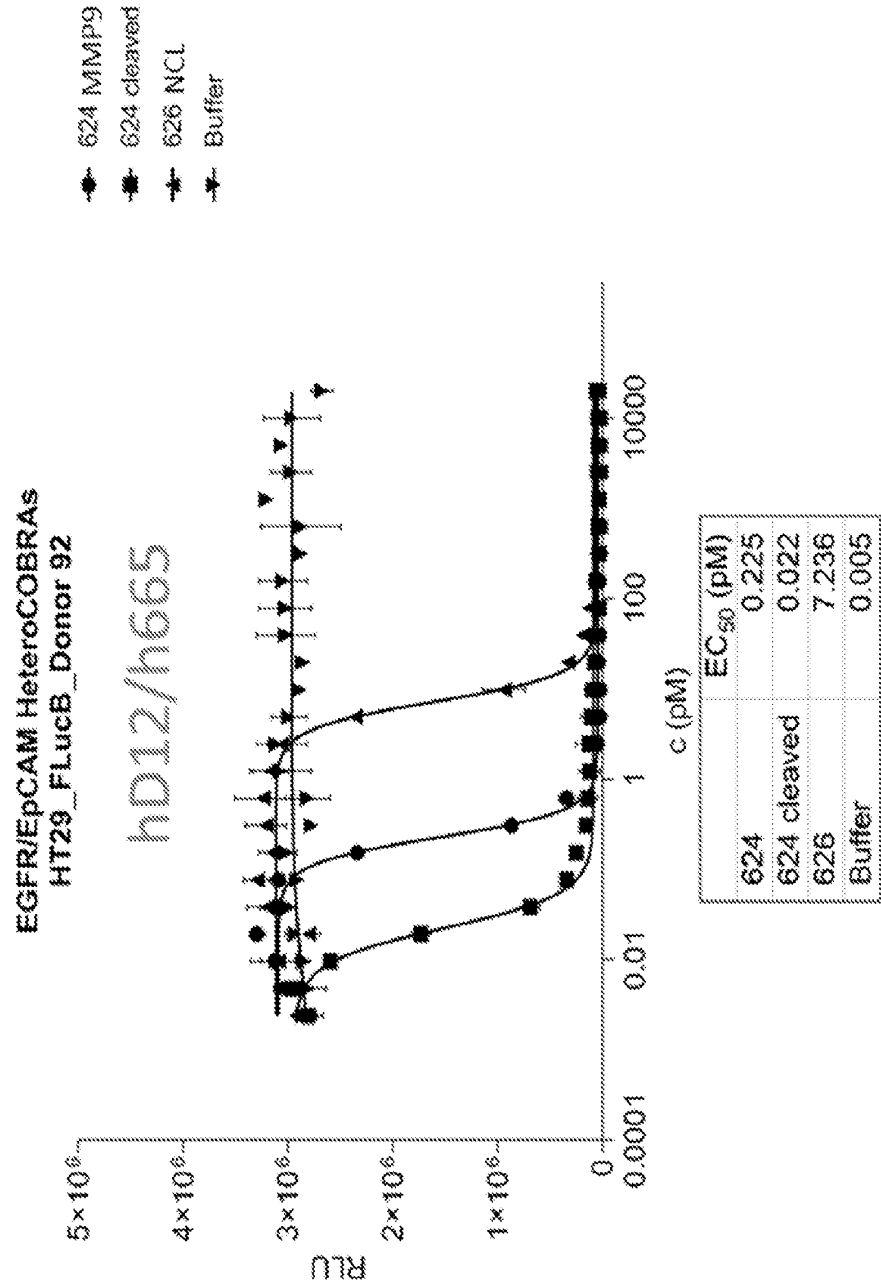


Figure 46C



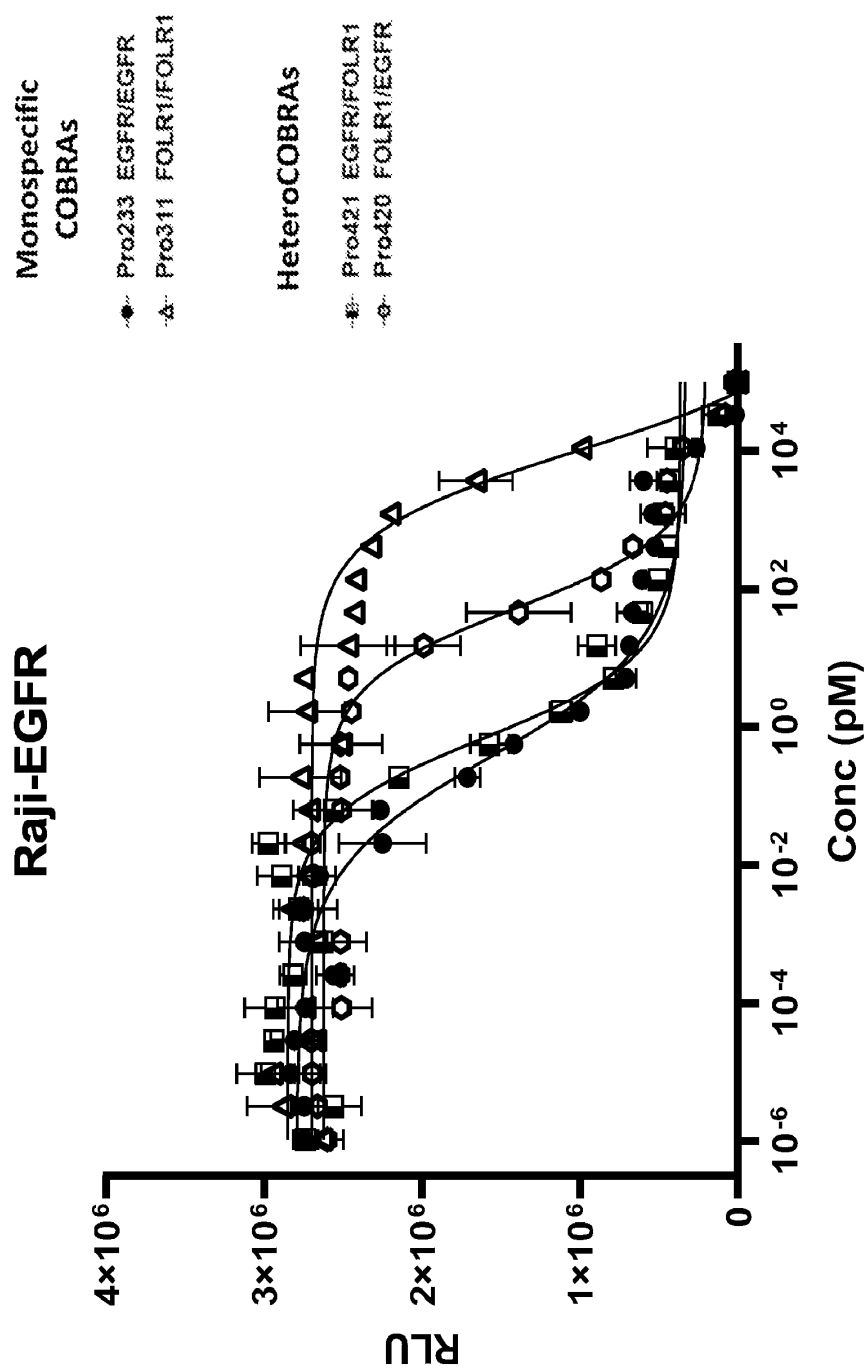


Figure 47A

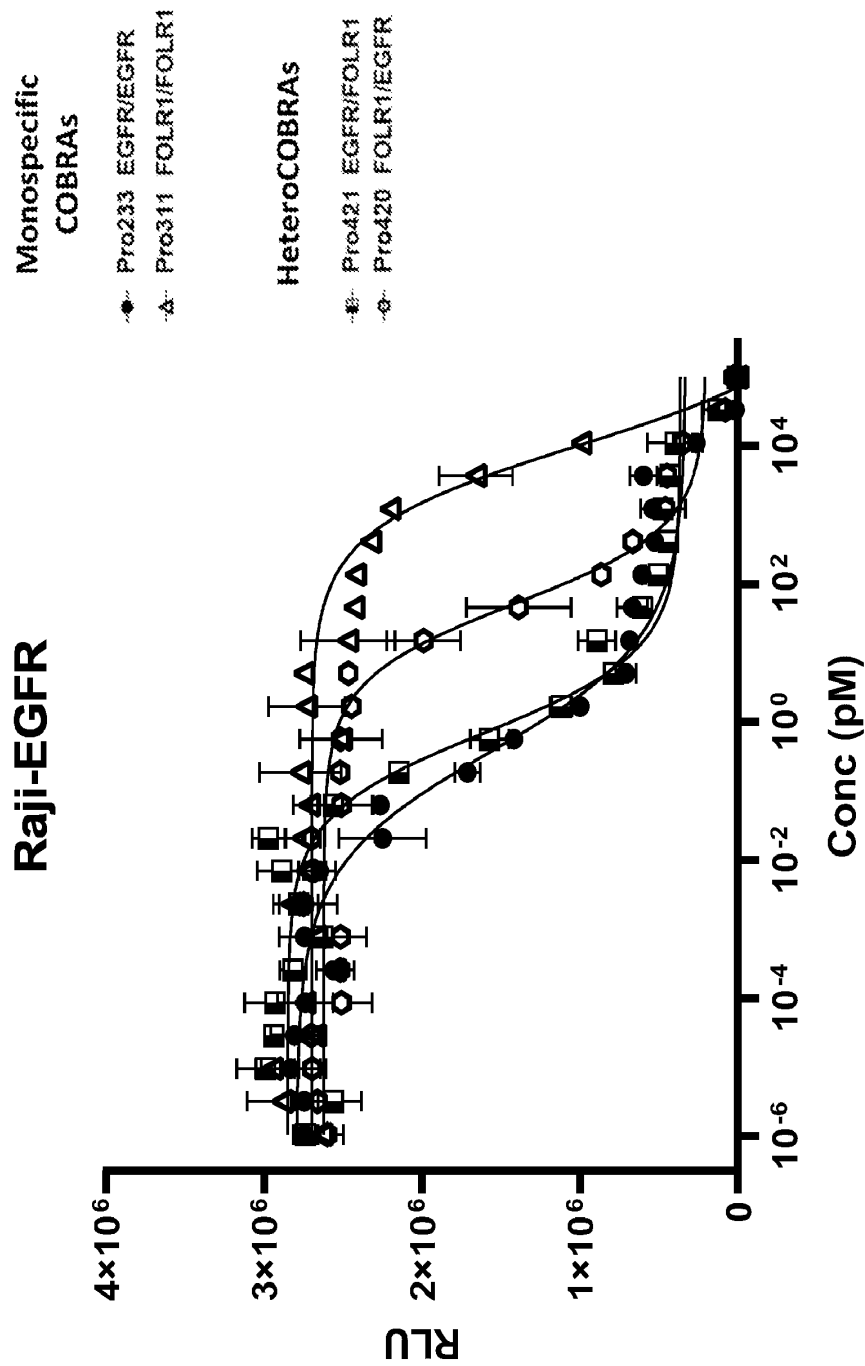


Figure 47A

Figure 47C

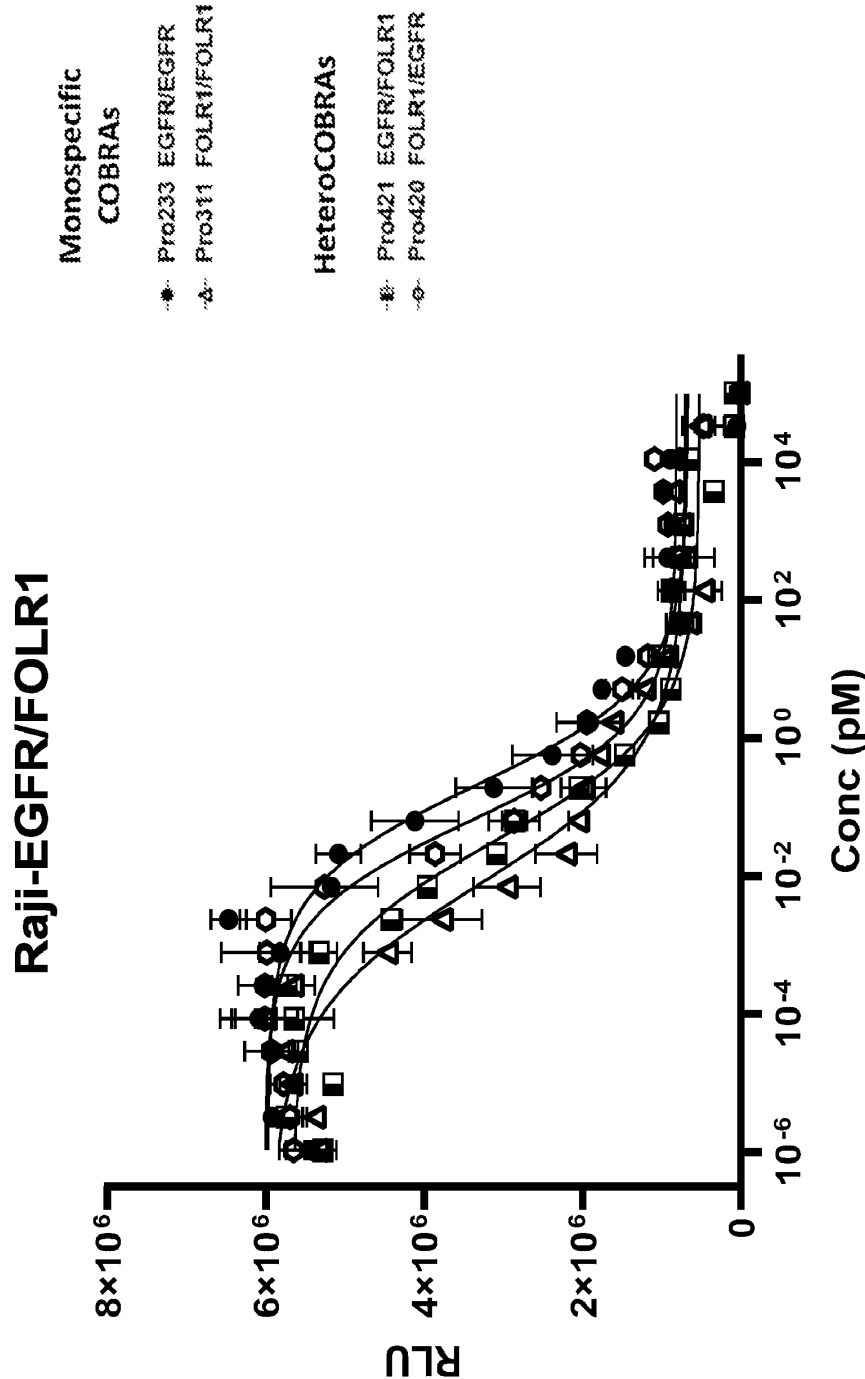


Figure 48A

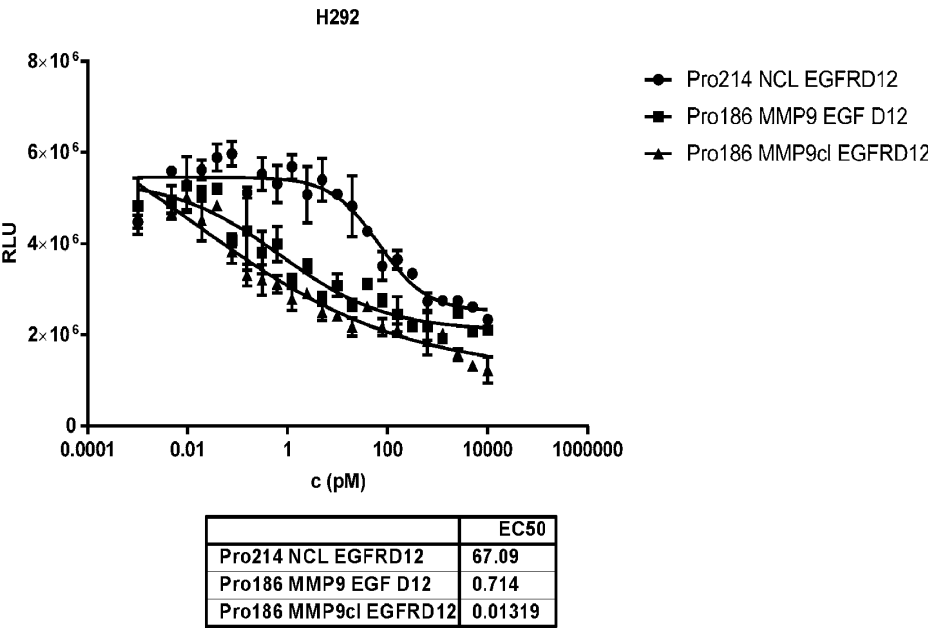
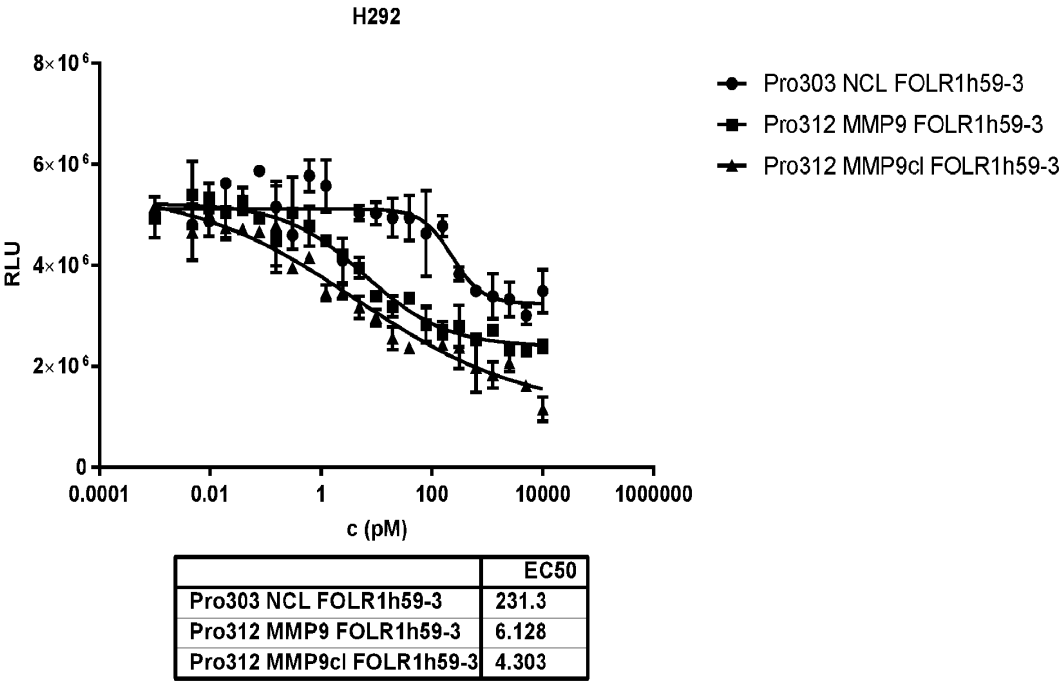
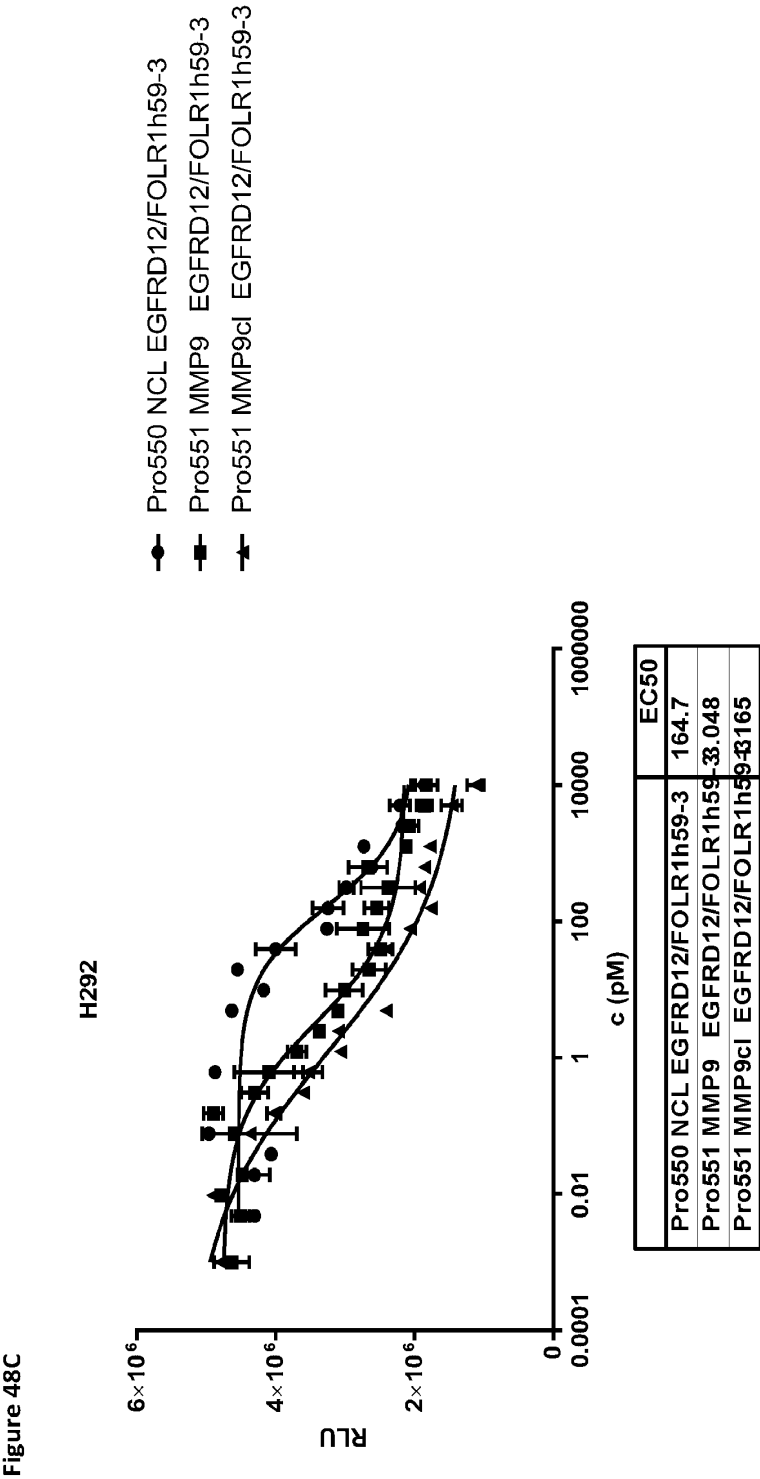
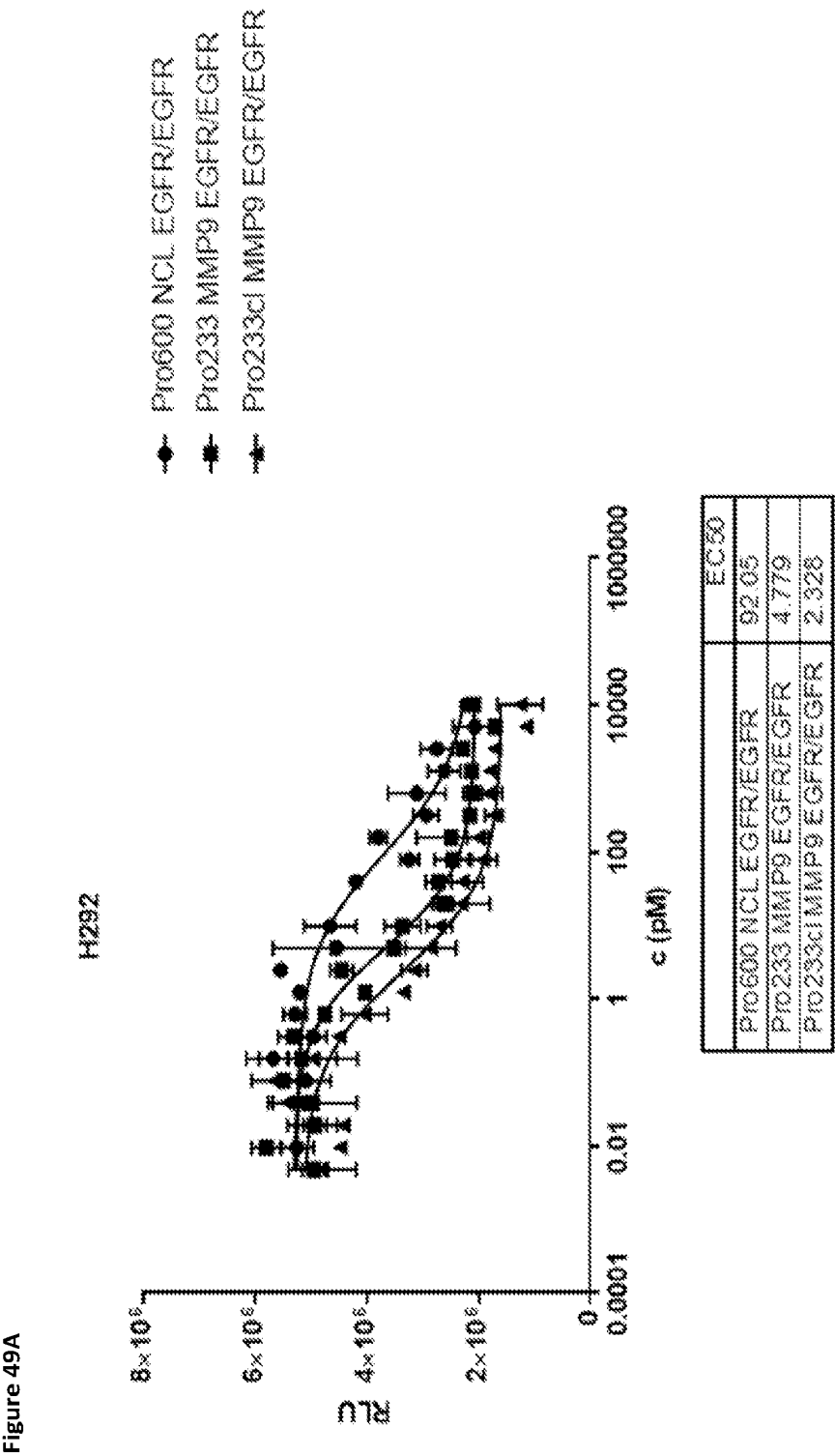


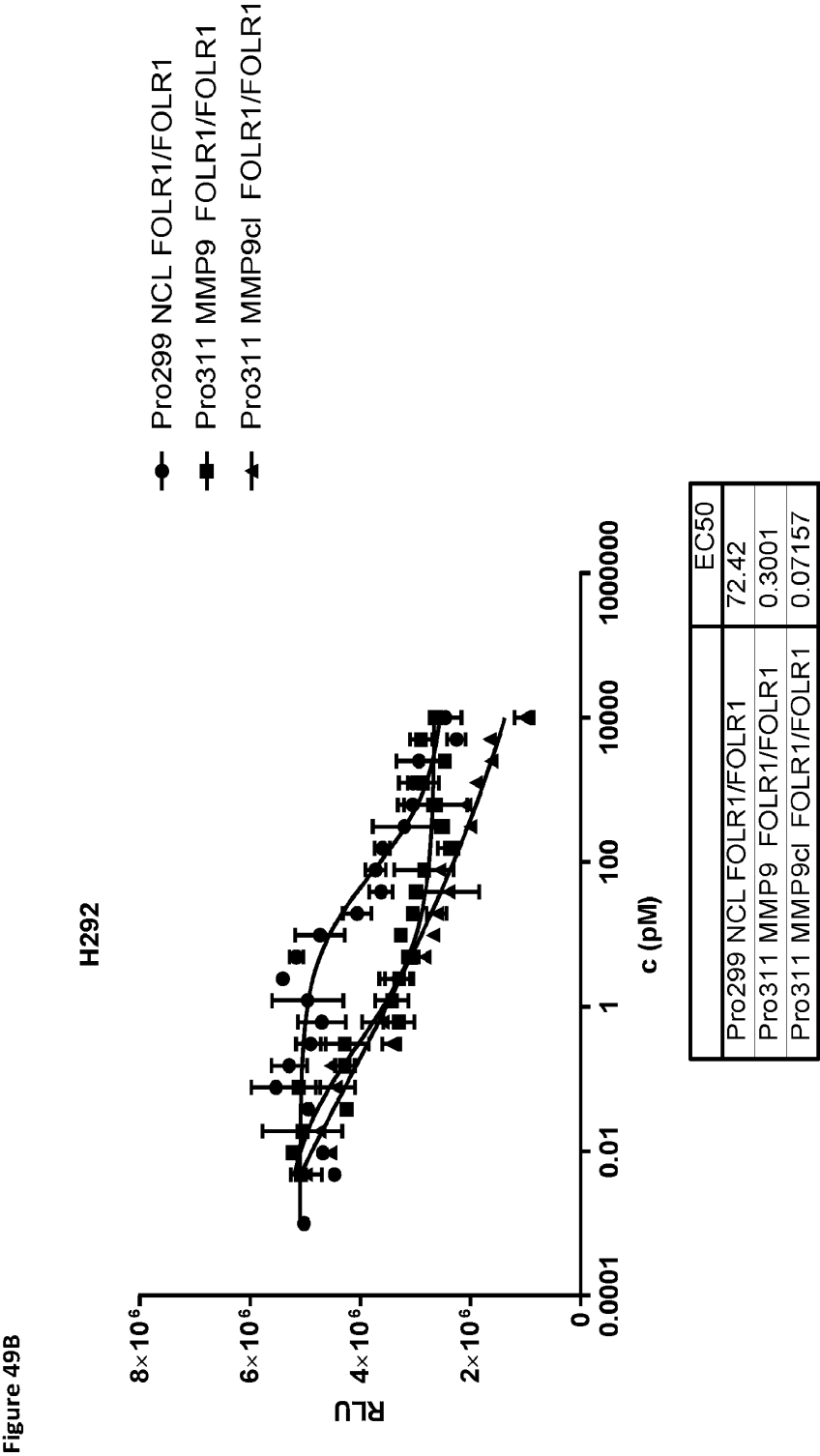
Figure 48B

aFOLR1(h59-3)/aEGFR (D12) kills tumor cell lines expressing both FOLR1 and EGFR conditionally









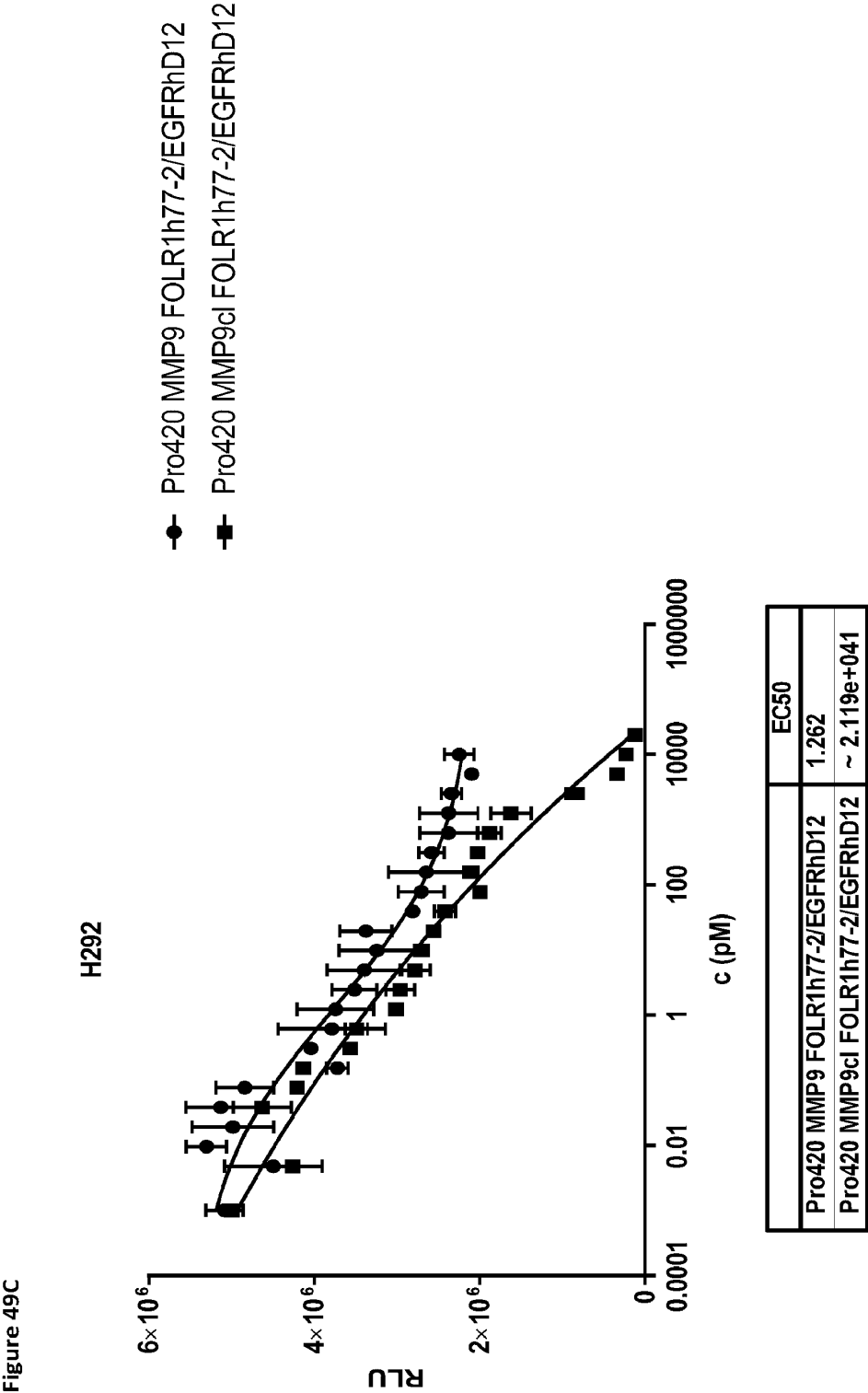


Figure 49D

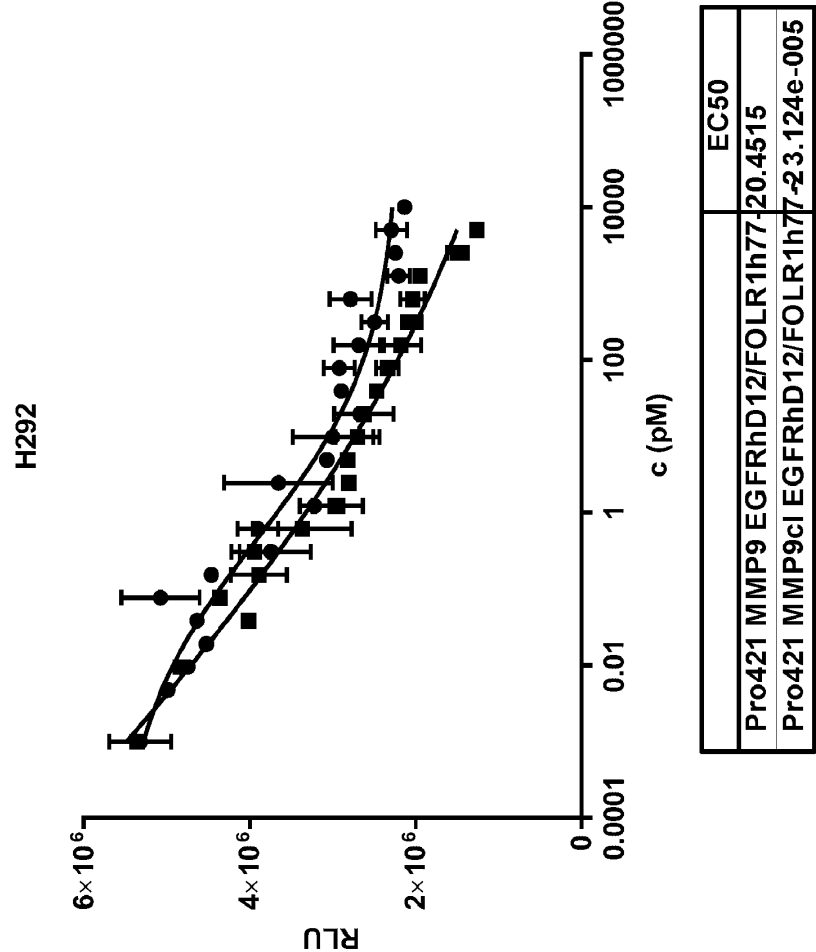


Figure 50

Prodent	Molecule type	1st / 2nd position	K _D (nM)		
			huEGFR	huFOLR1	huEGFR + huFOLR1
Pro473	NCL	EGFR/FOLR1	5.1	3	0.15
Pro51	Pro51	EGFR/-	2.5		
Pro300	Pro51	FOLR1/-		2.1	

Figure 51A

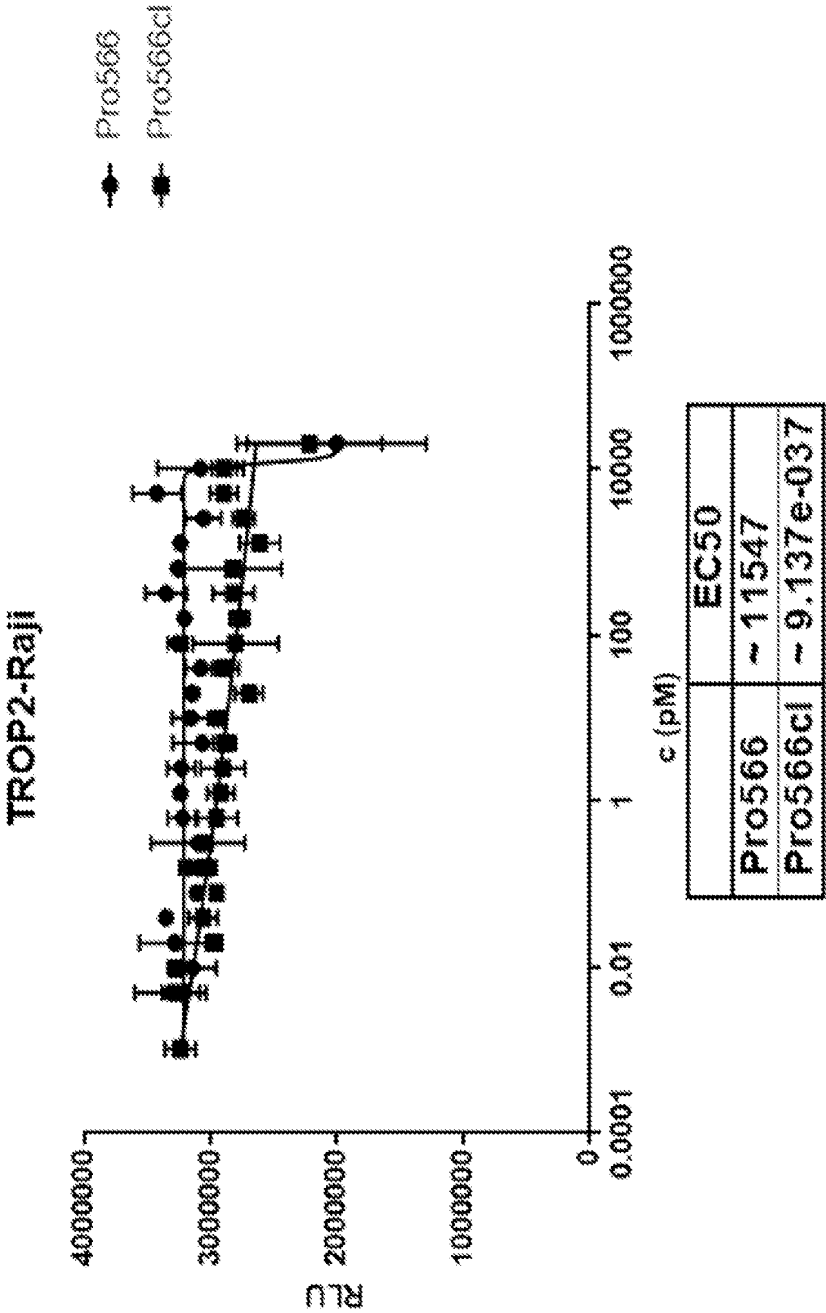
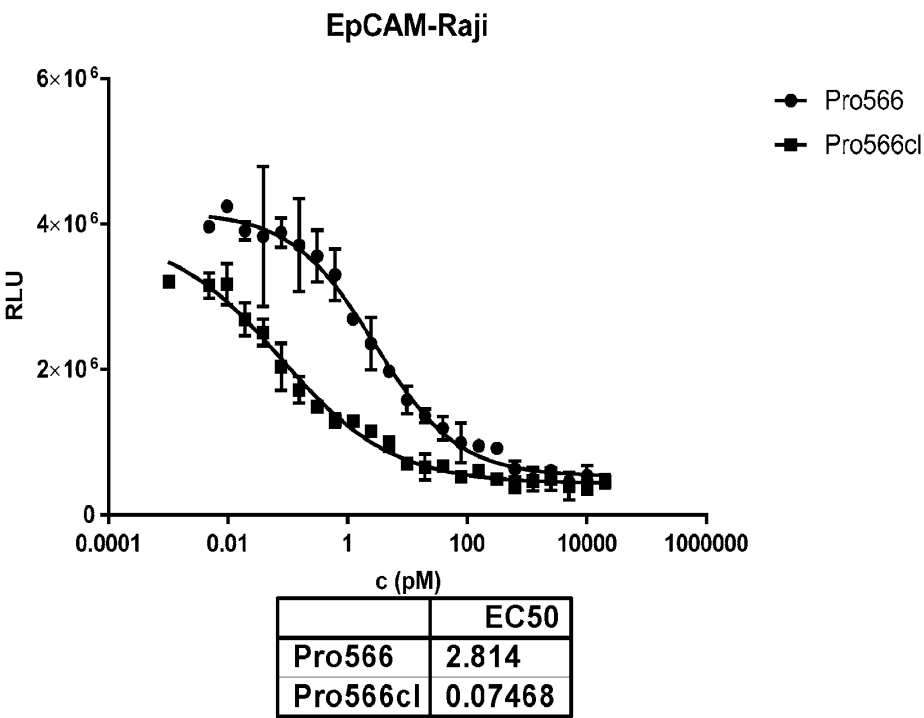
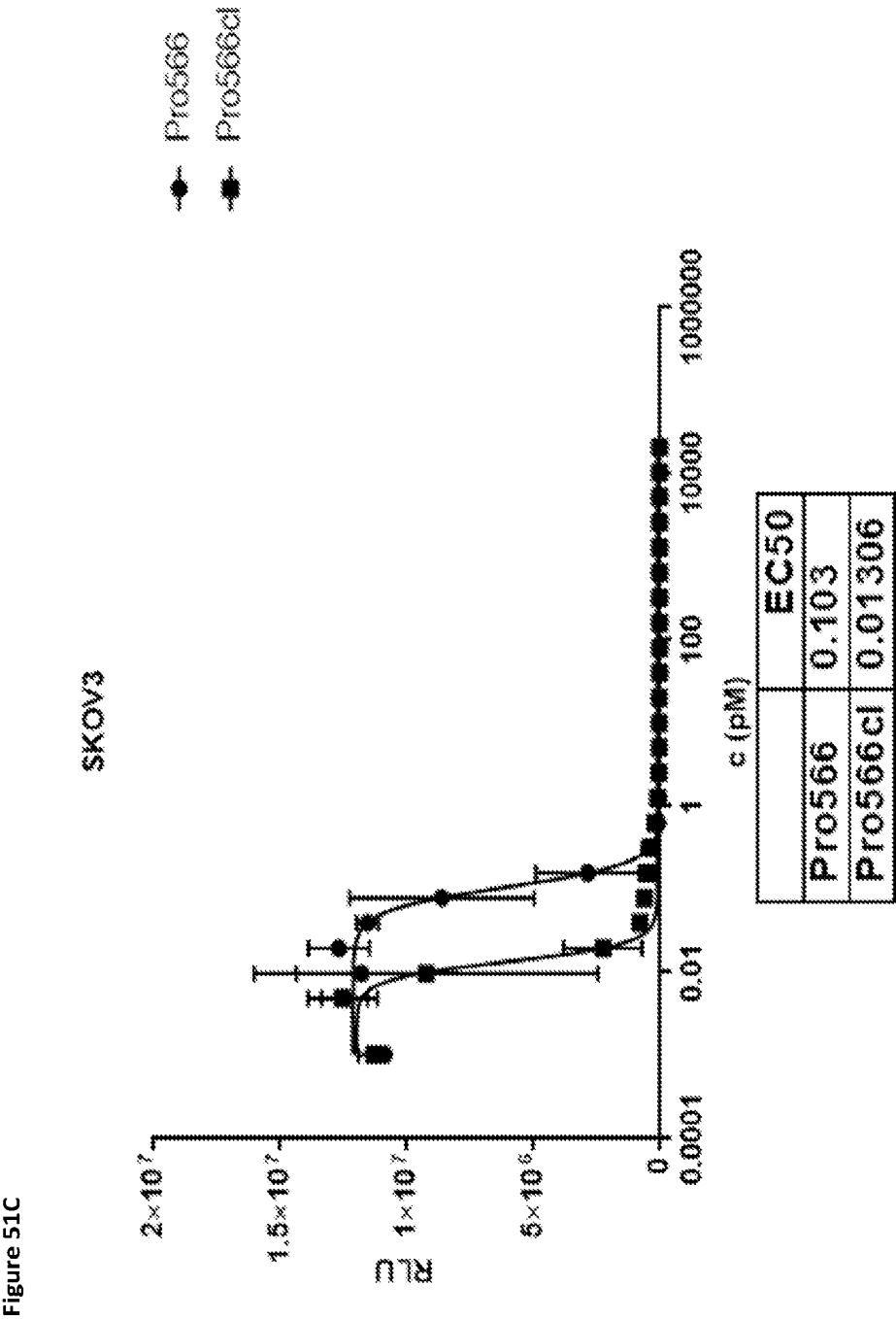
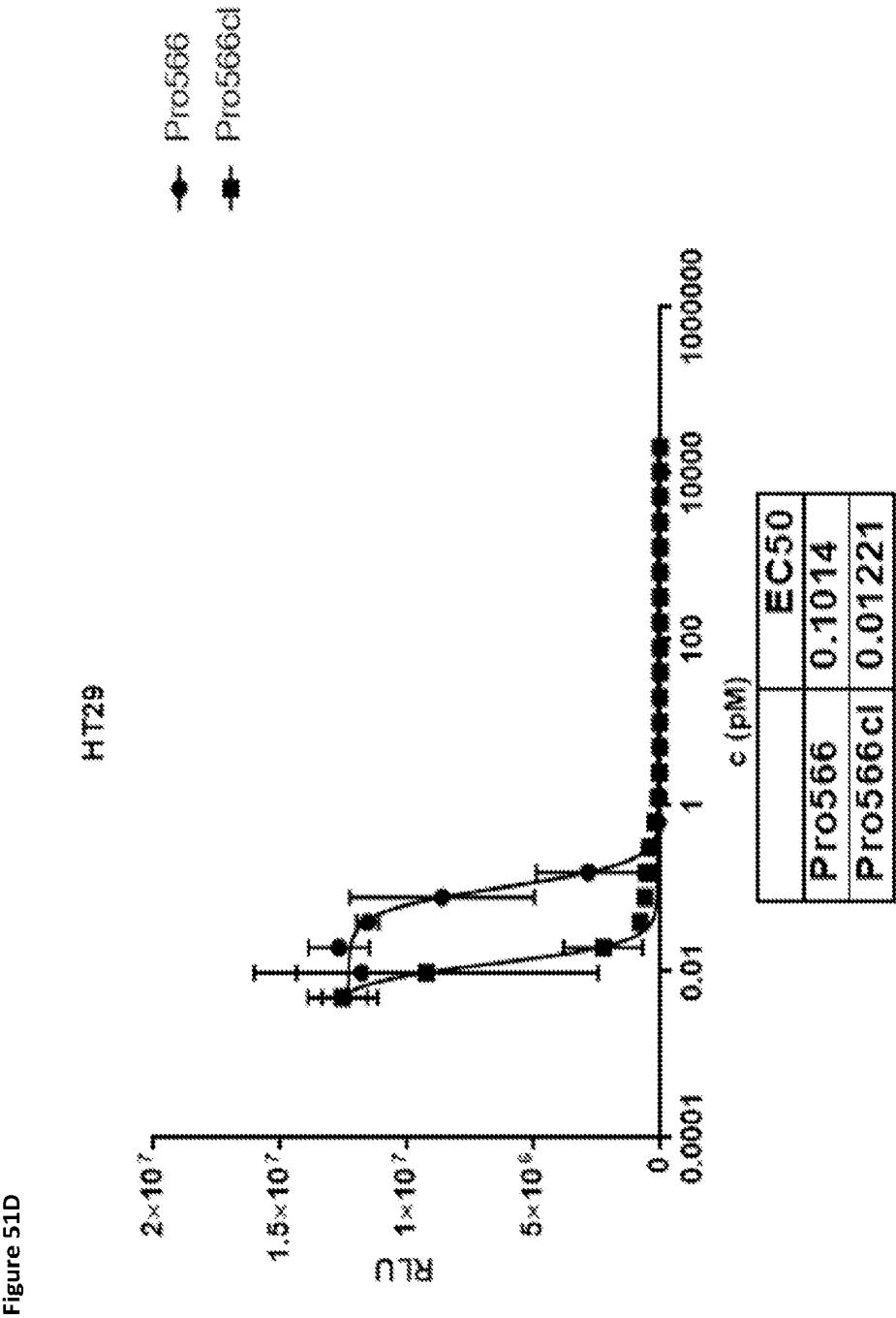


Figure 51B







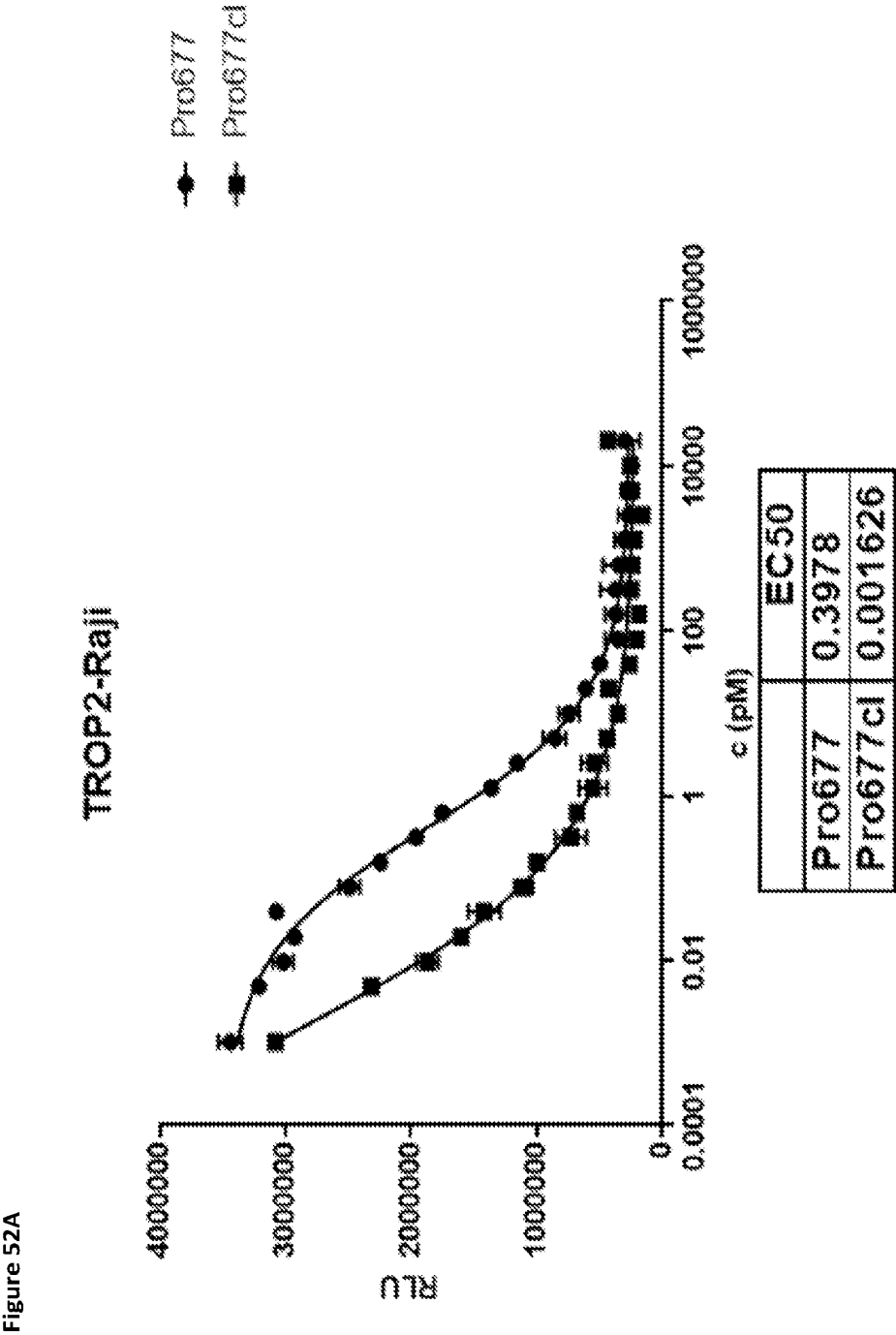


Figure 52B

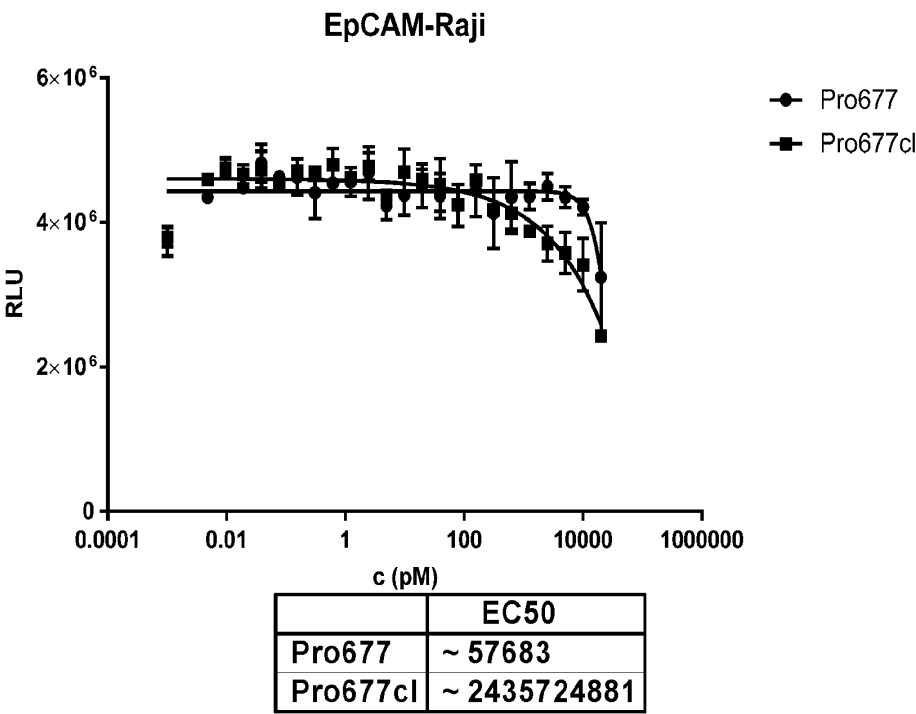


Figure 52C

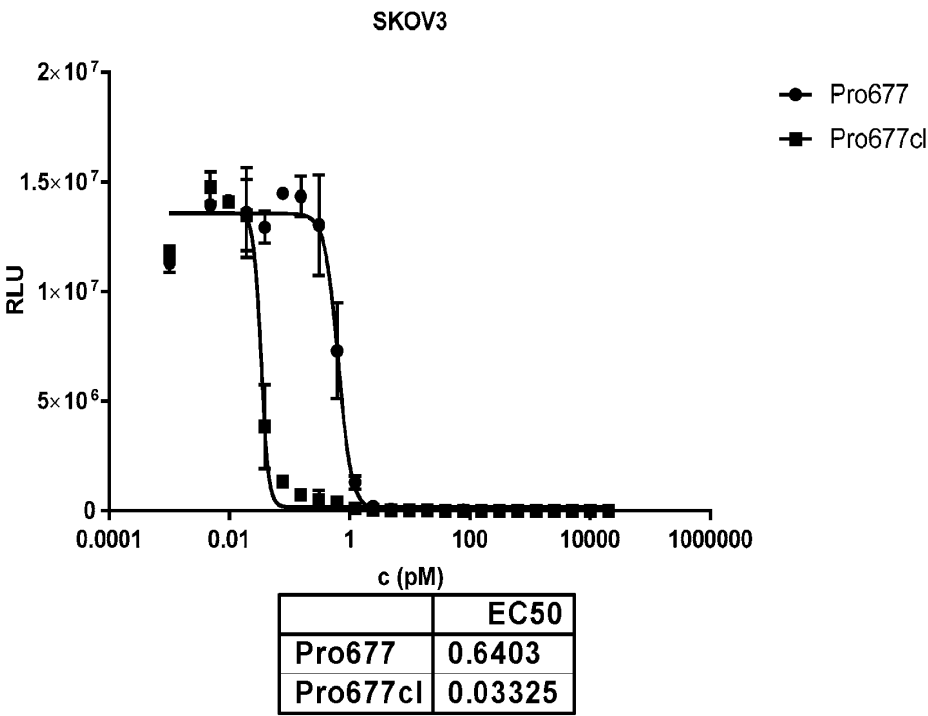


Figure 52D

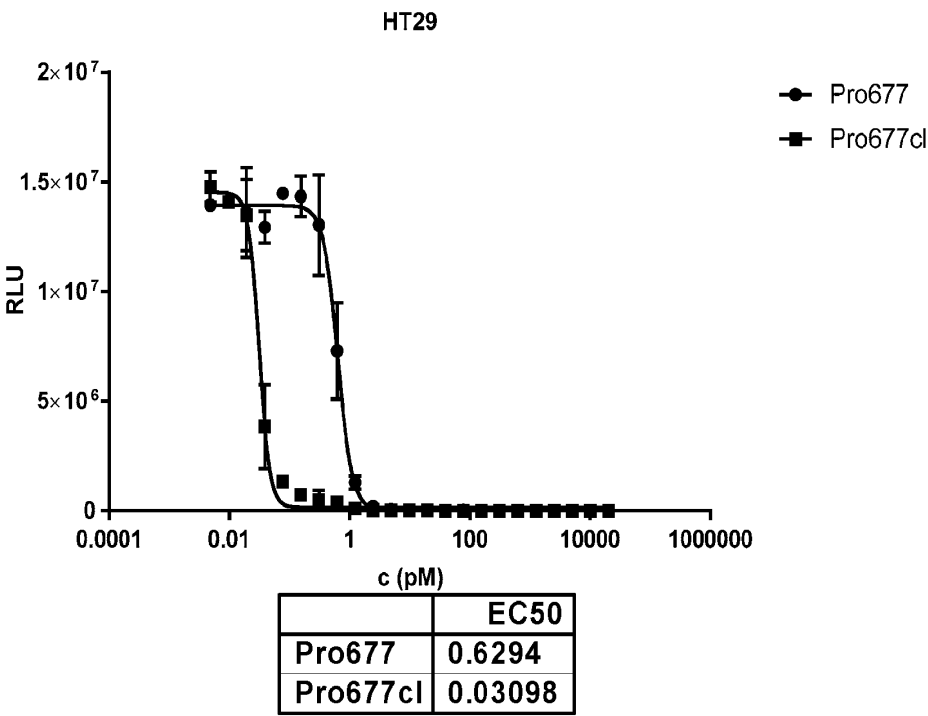


Figure 53A

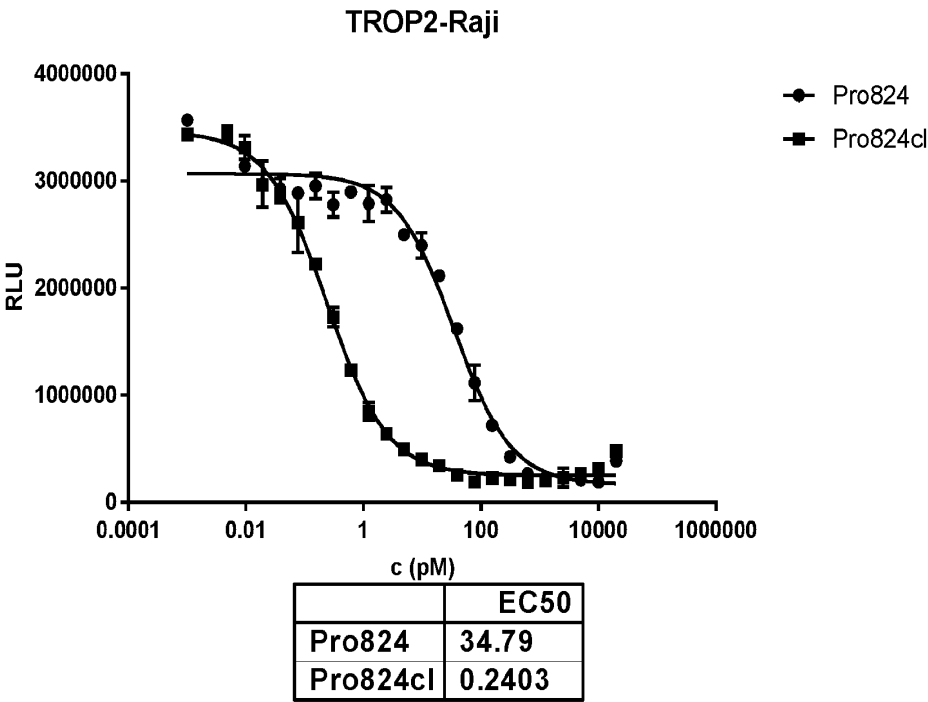


Figure 53B

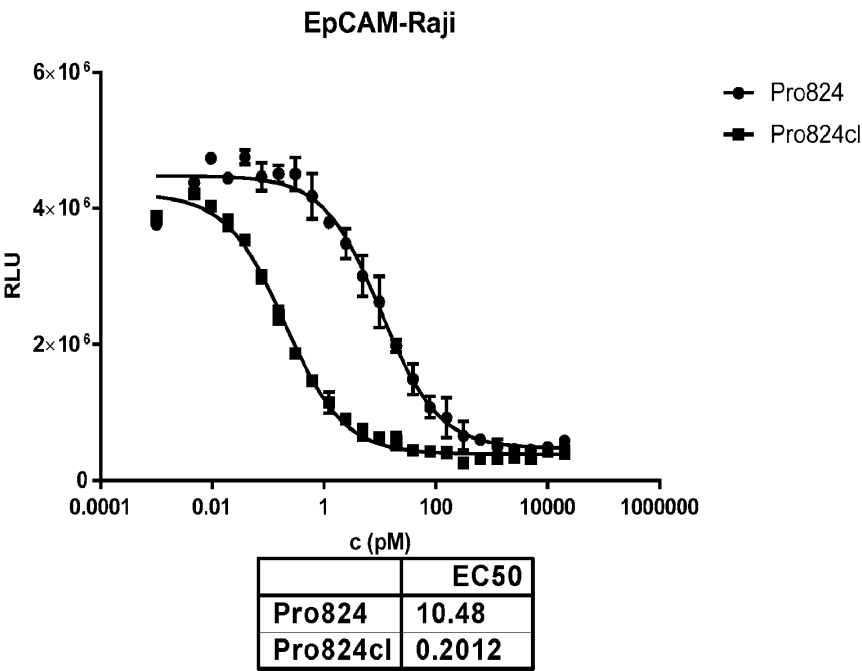


Figure 53C

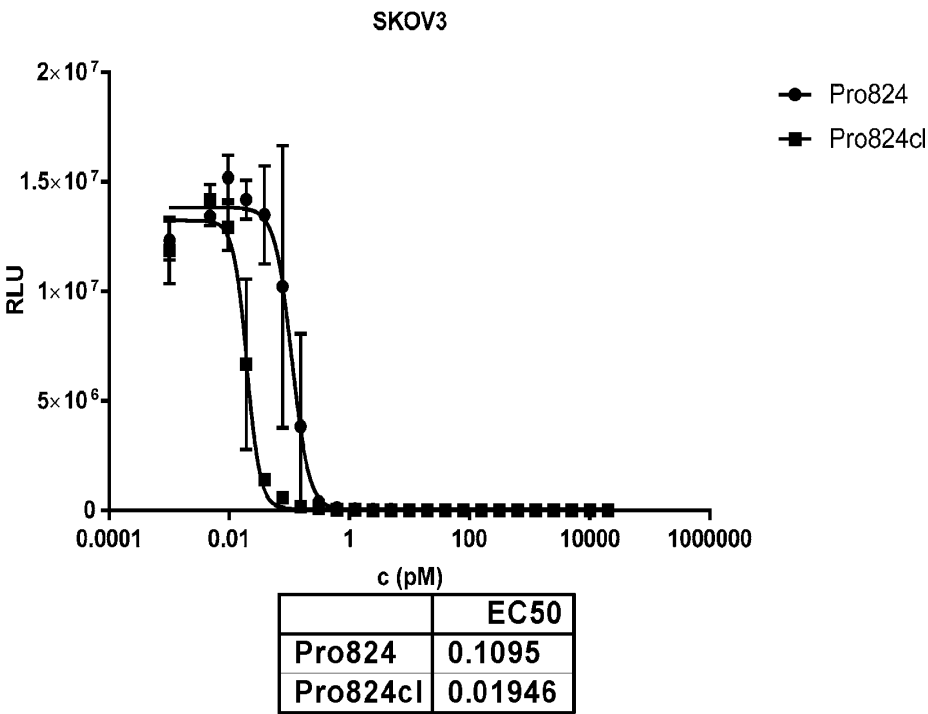


Figure 53D

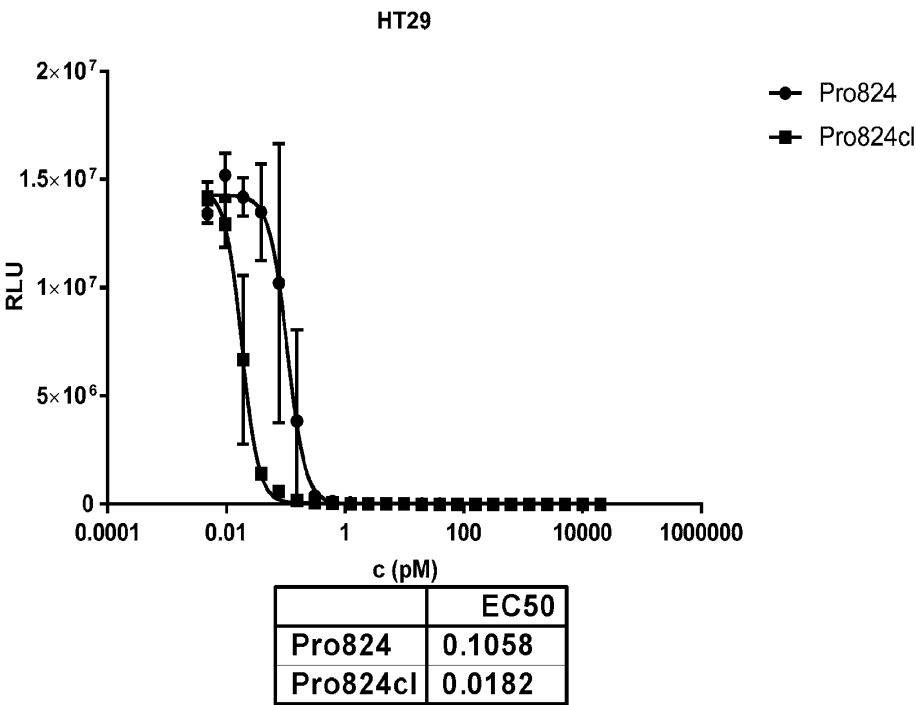


Figure 54A

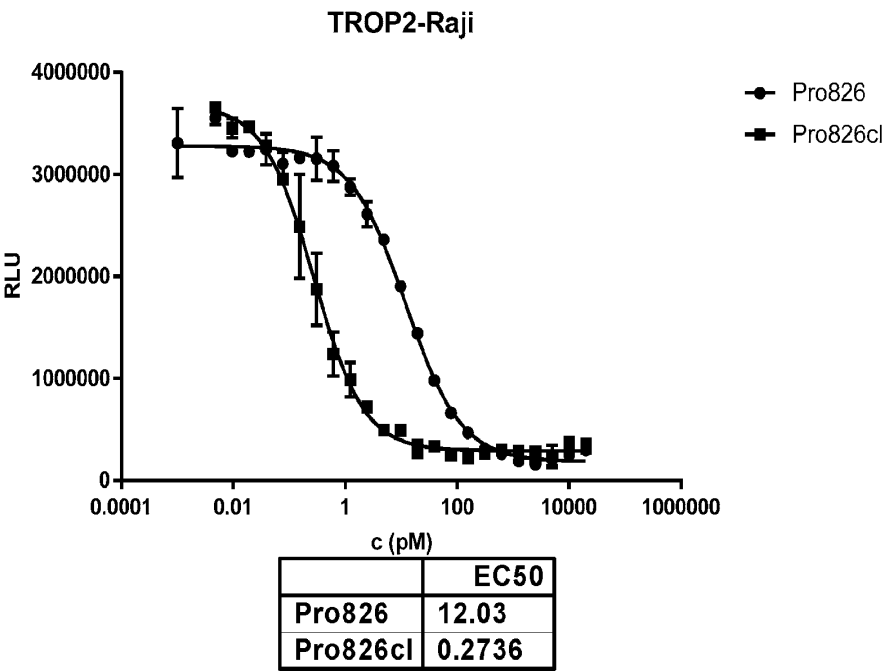


Figure 54B

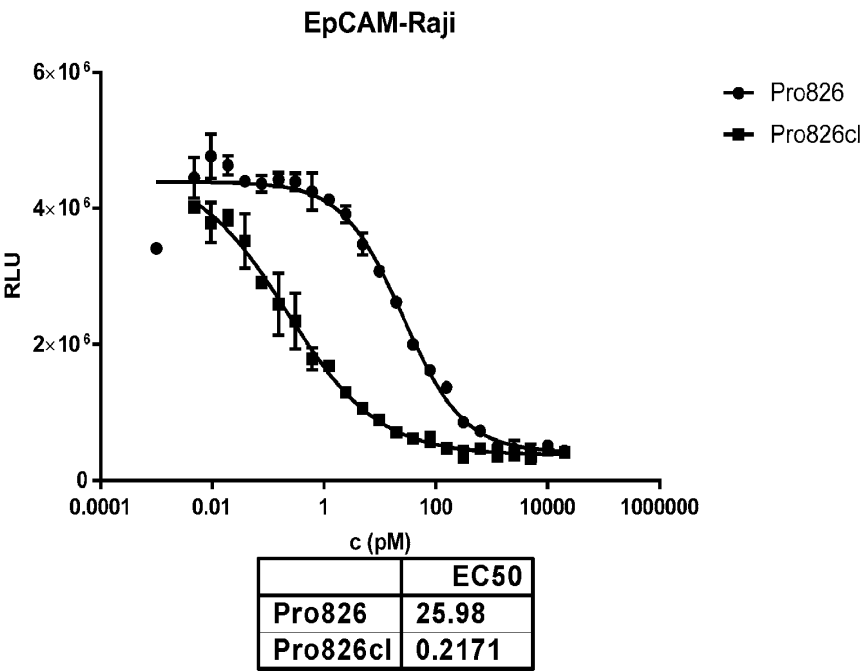


Figure 54C

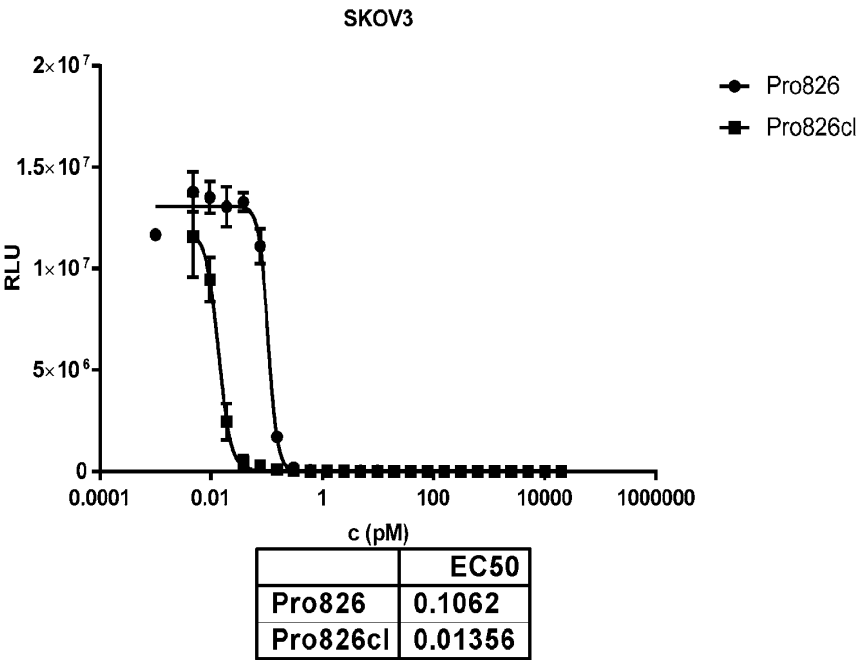


Figure 54D

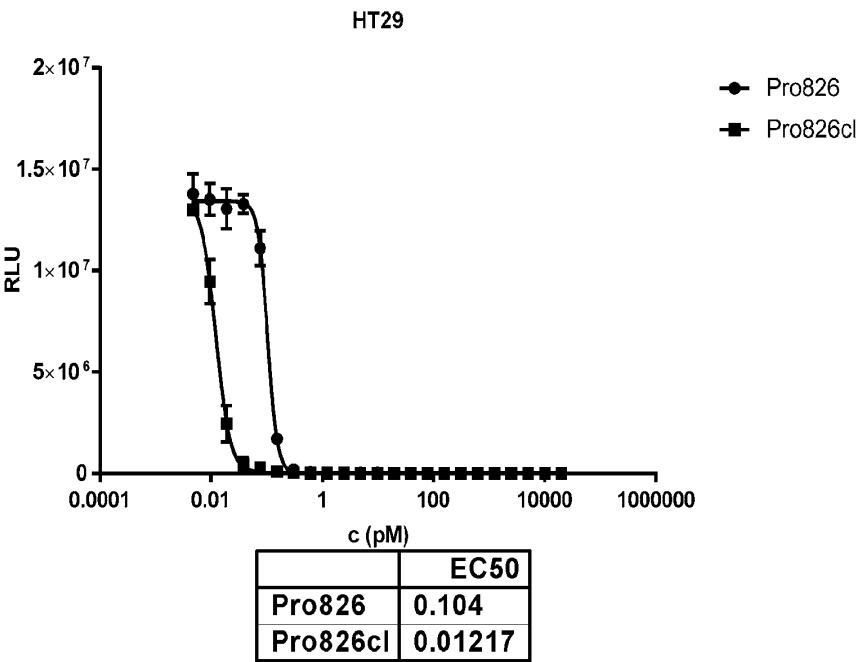


Figure 55A

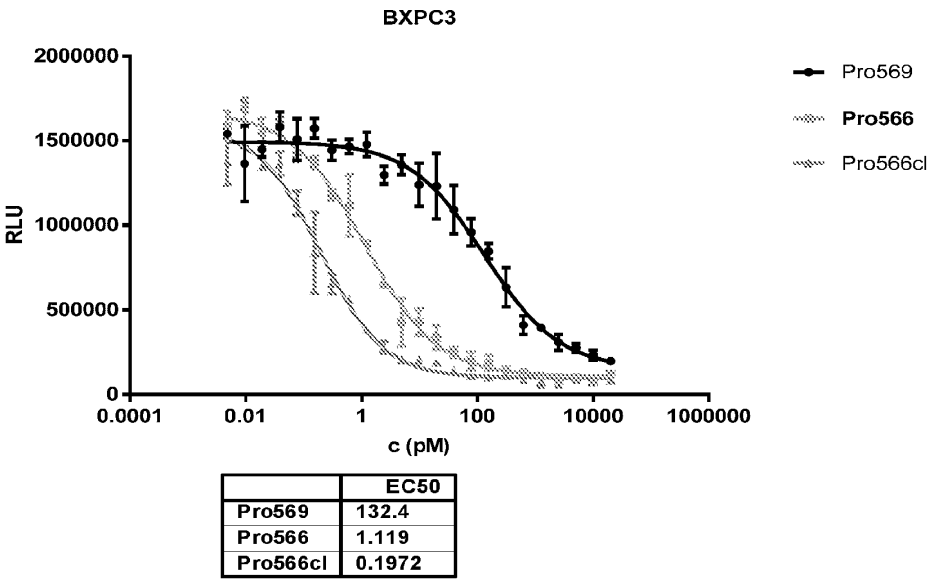


Figure 55B

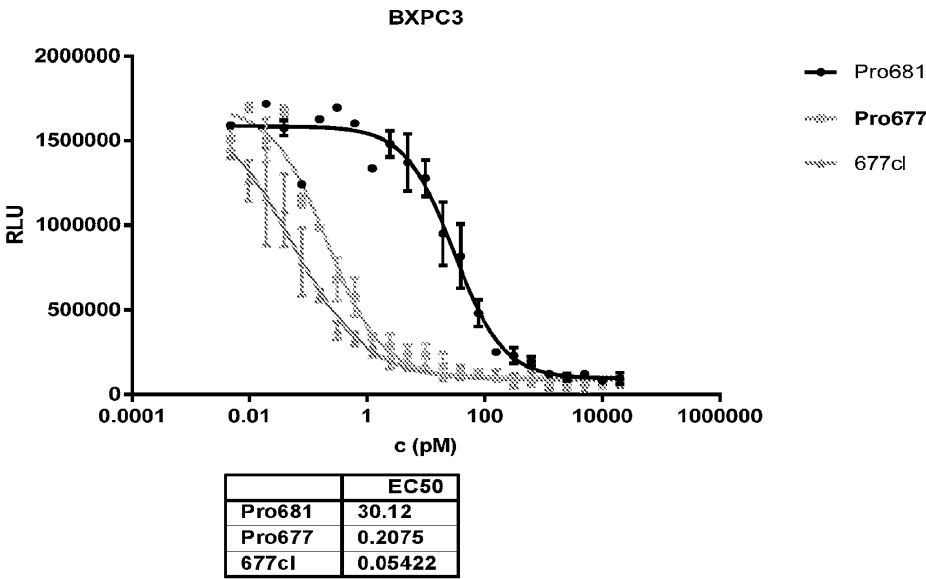


Figure 55C

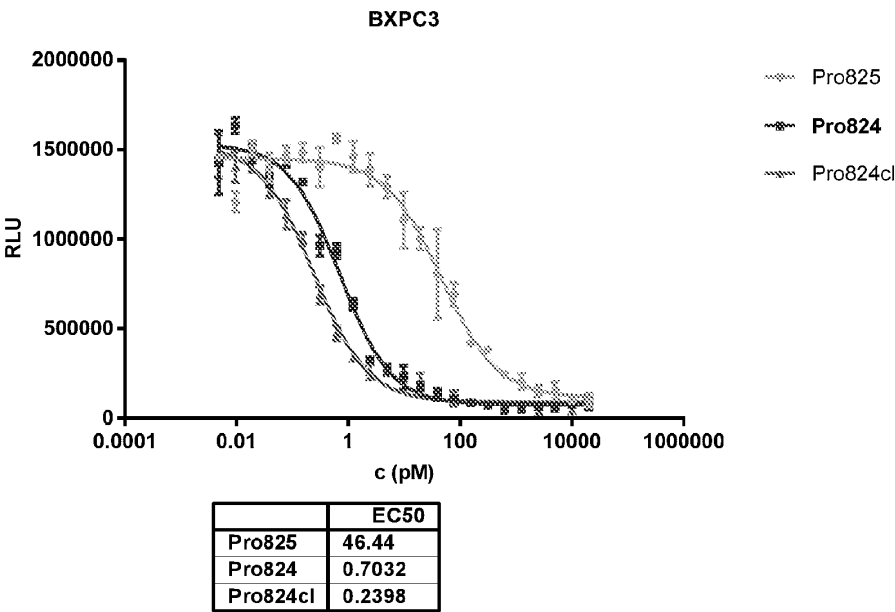


Figure 55D

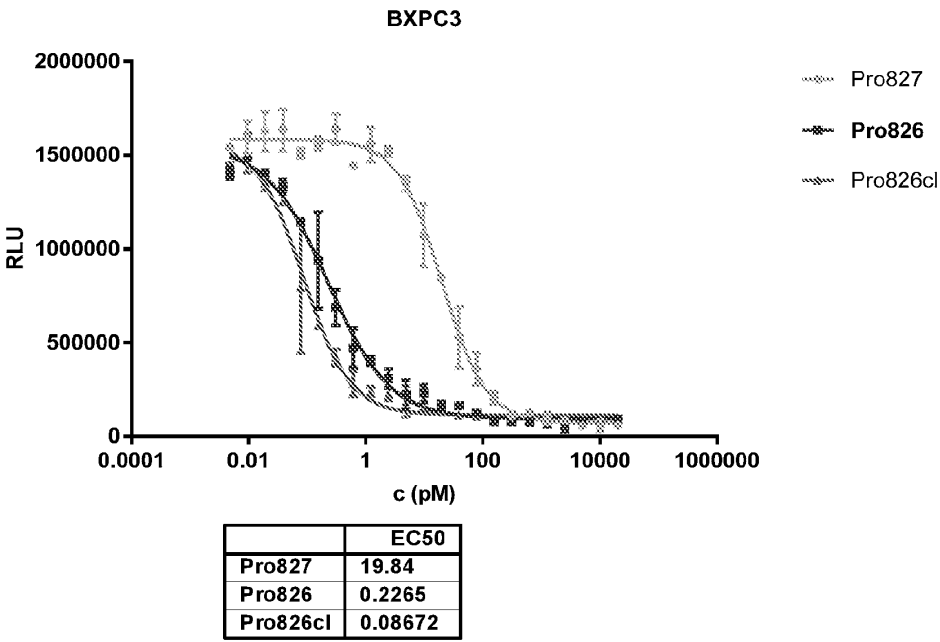


Figure 56A

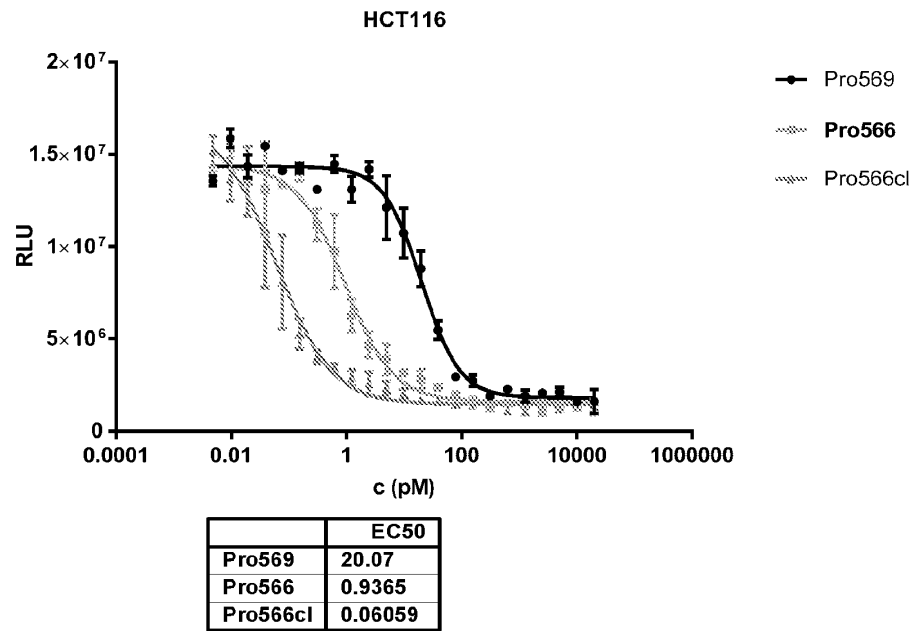


Figure 56B

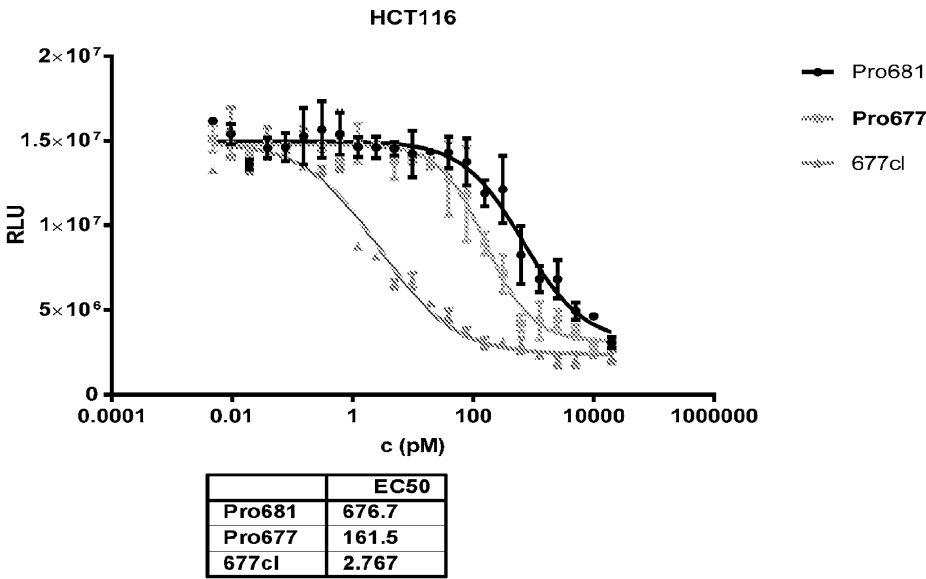


Figure 56C

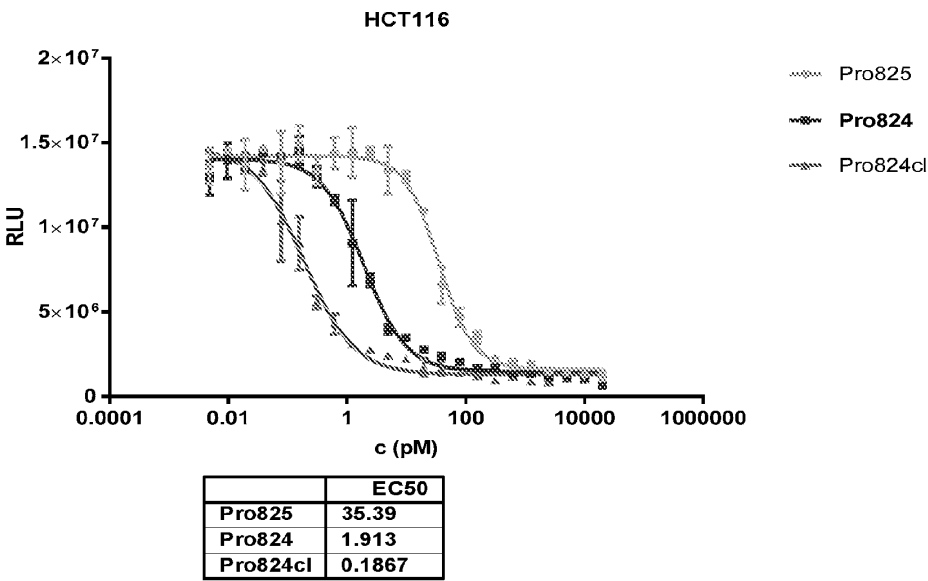


Figure 56D

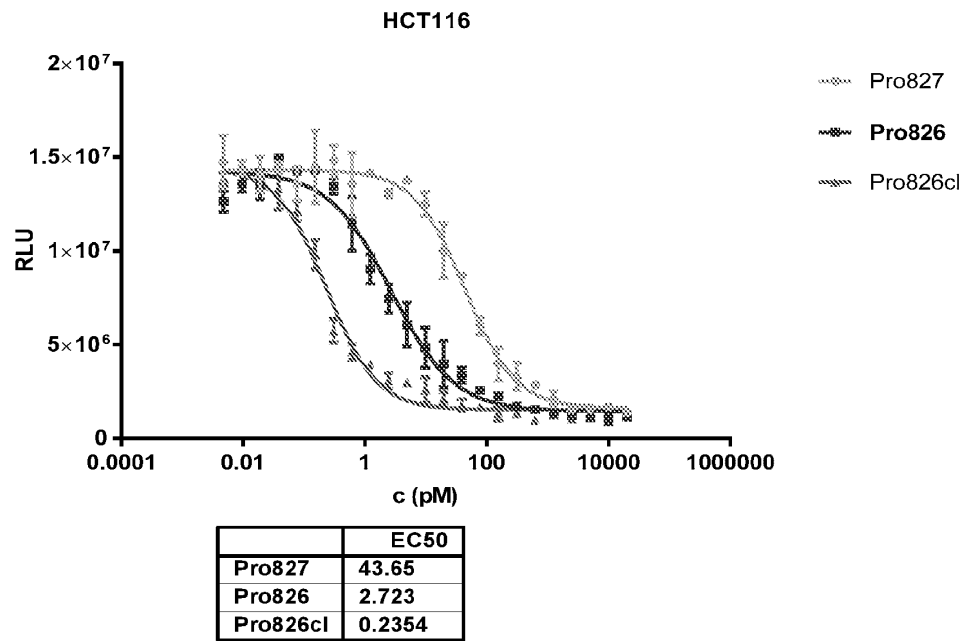


Figure 57A

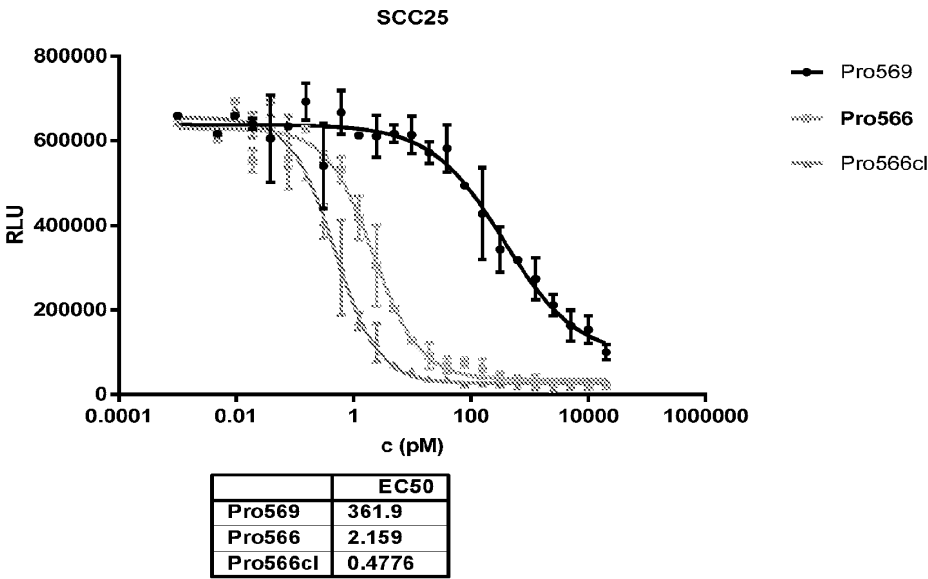


Figure 57B

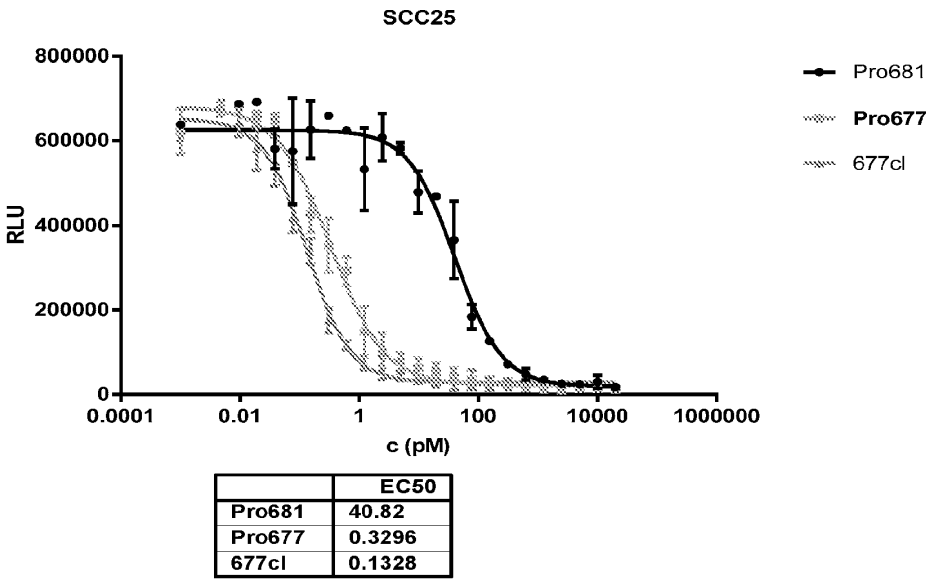


Figure 57C

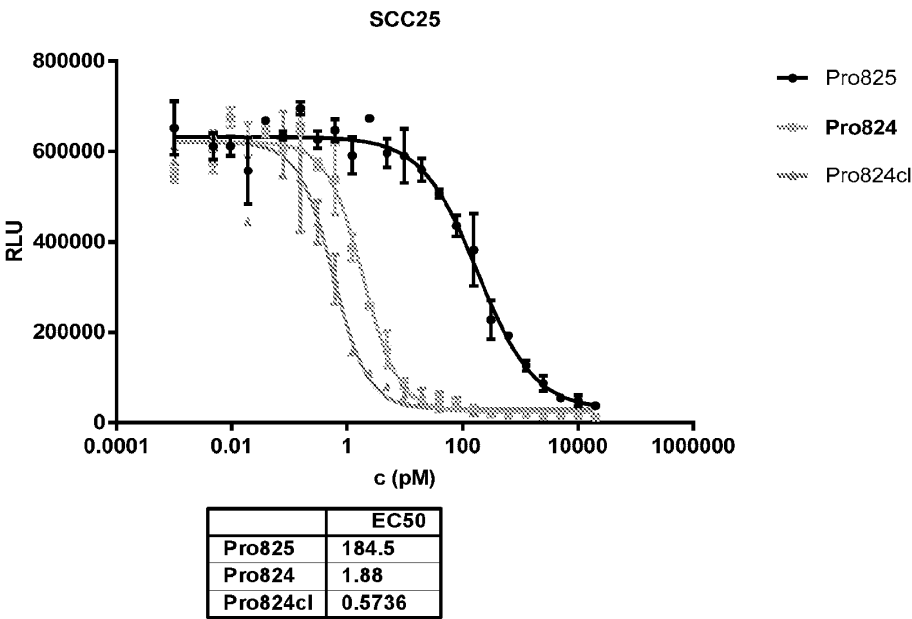
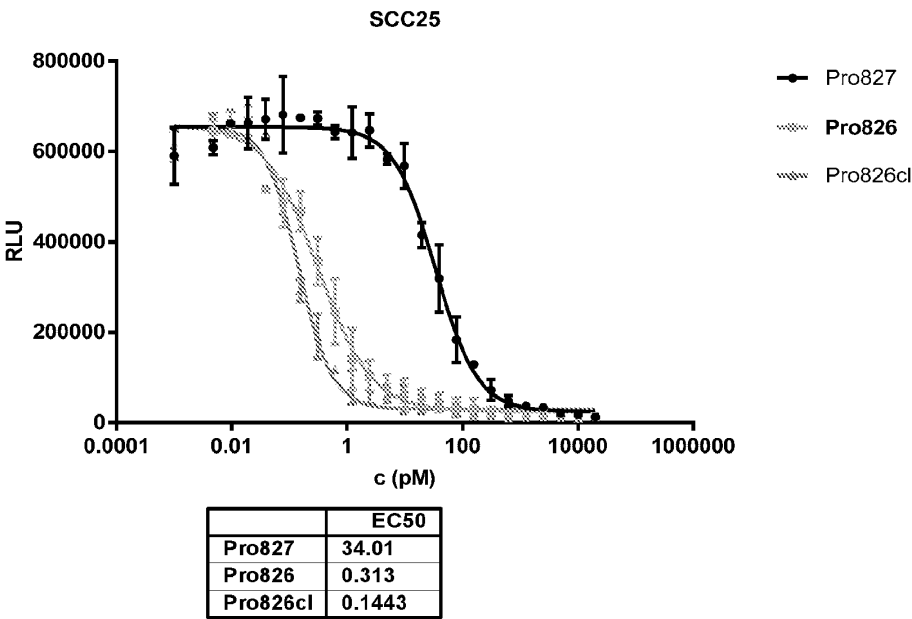


Figure 57D



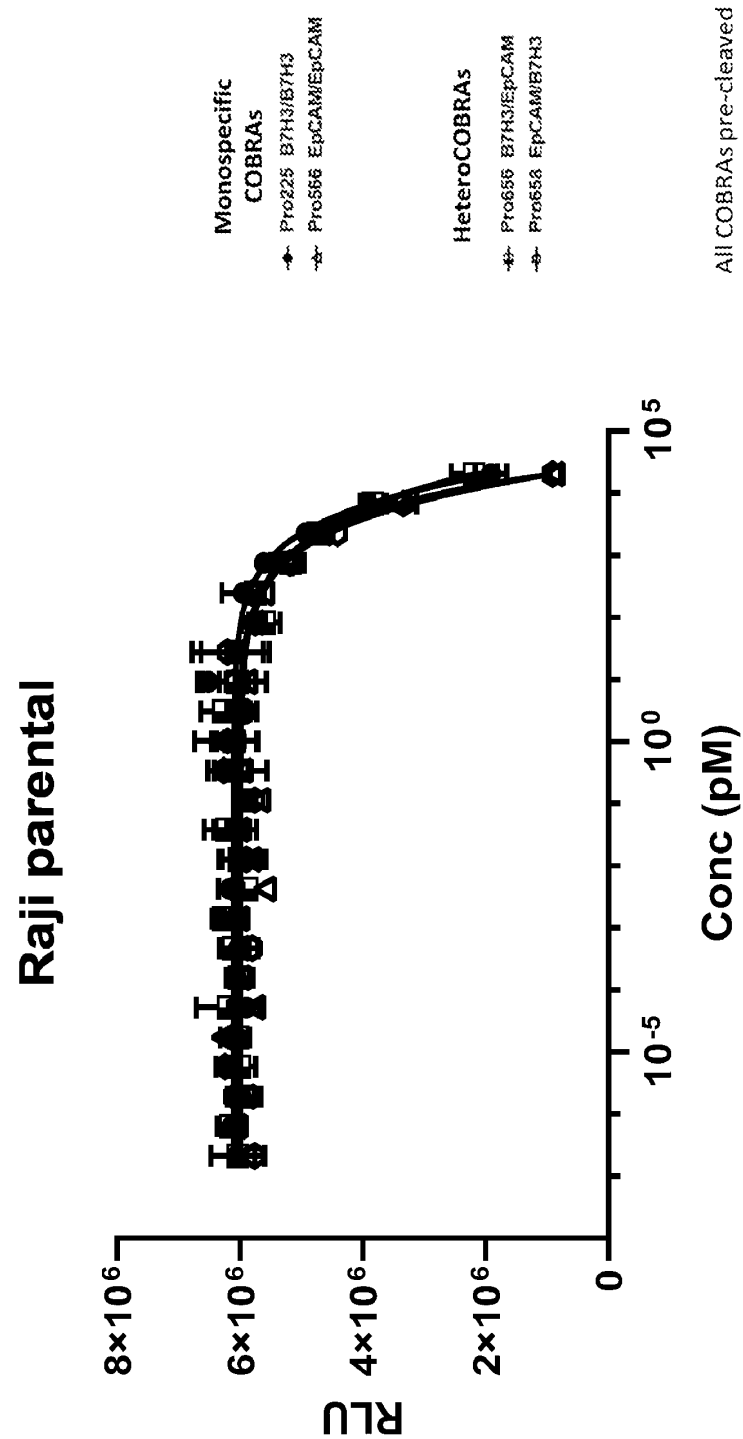


Figure 58A

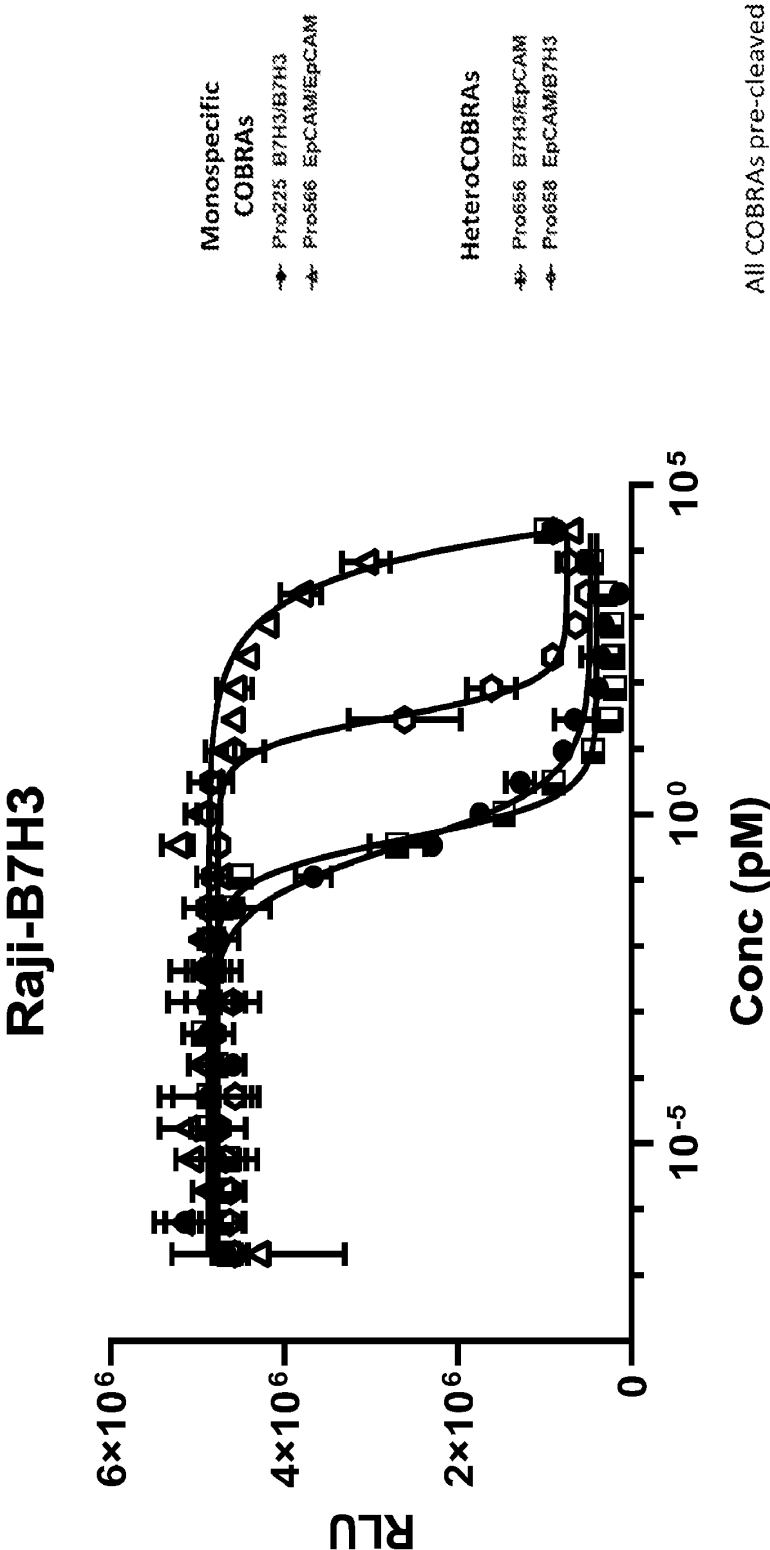


Figure 58B

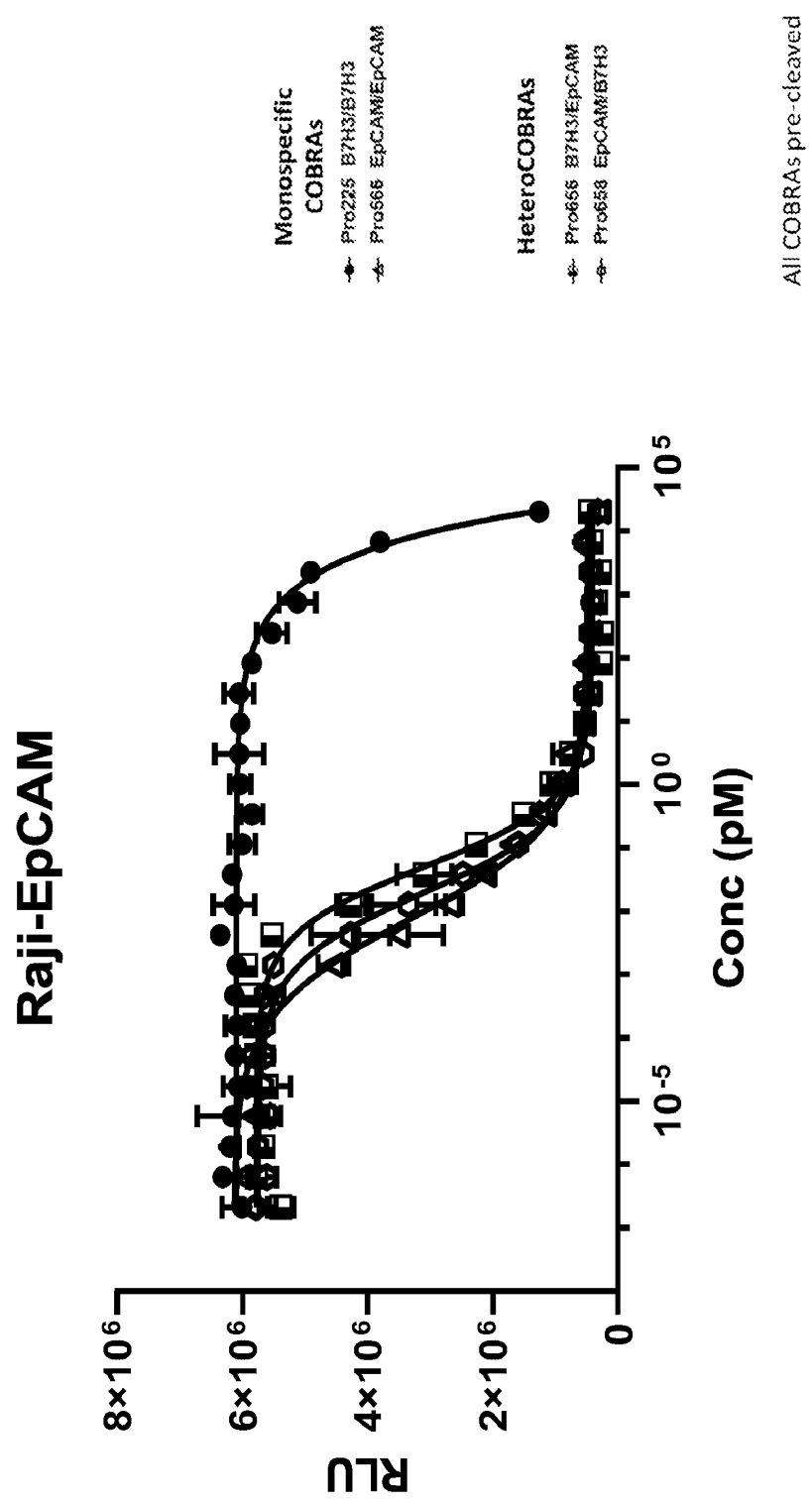
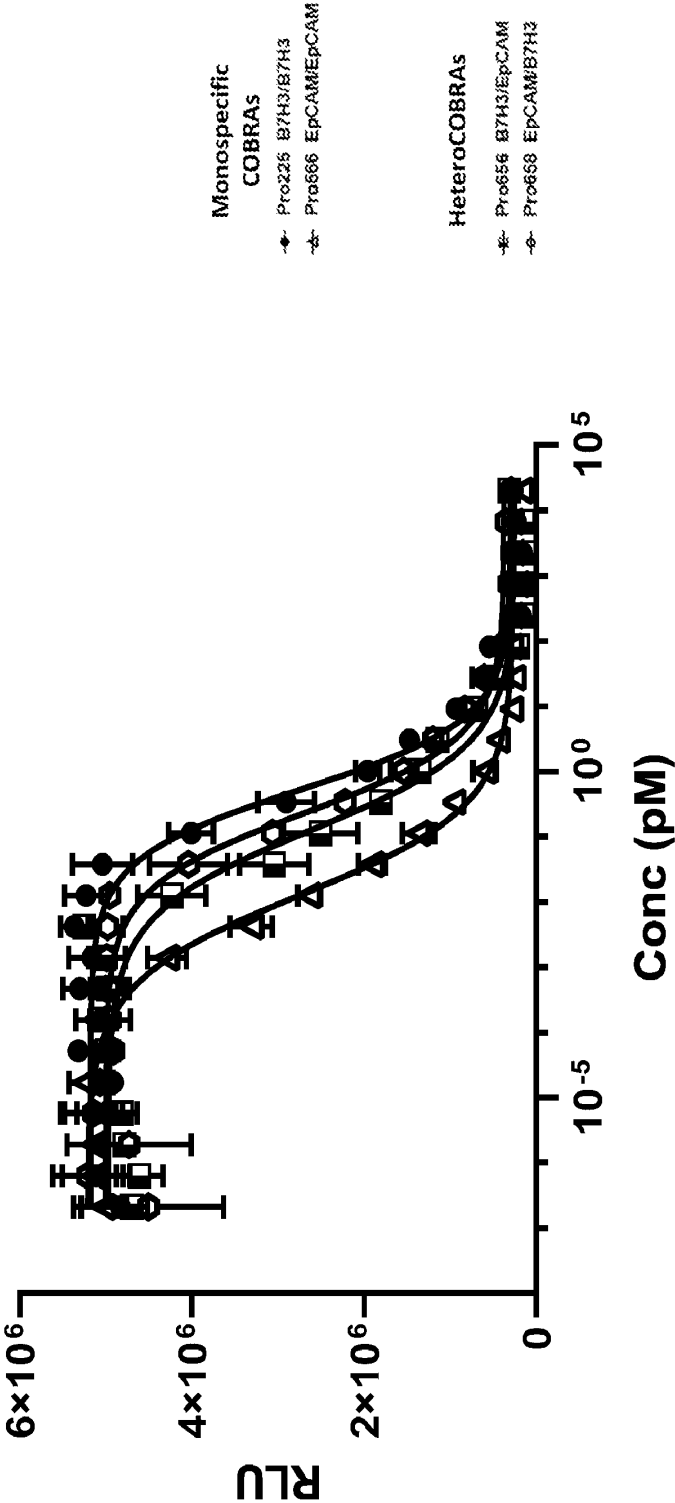


Figure 58C

Figure 58D

Raji-B7H3/EpCAM



All COBRAs pre-cleaved

HT29

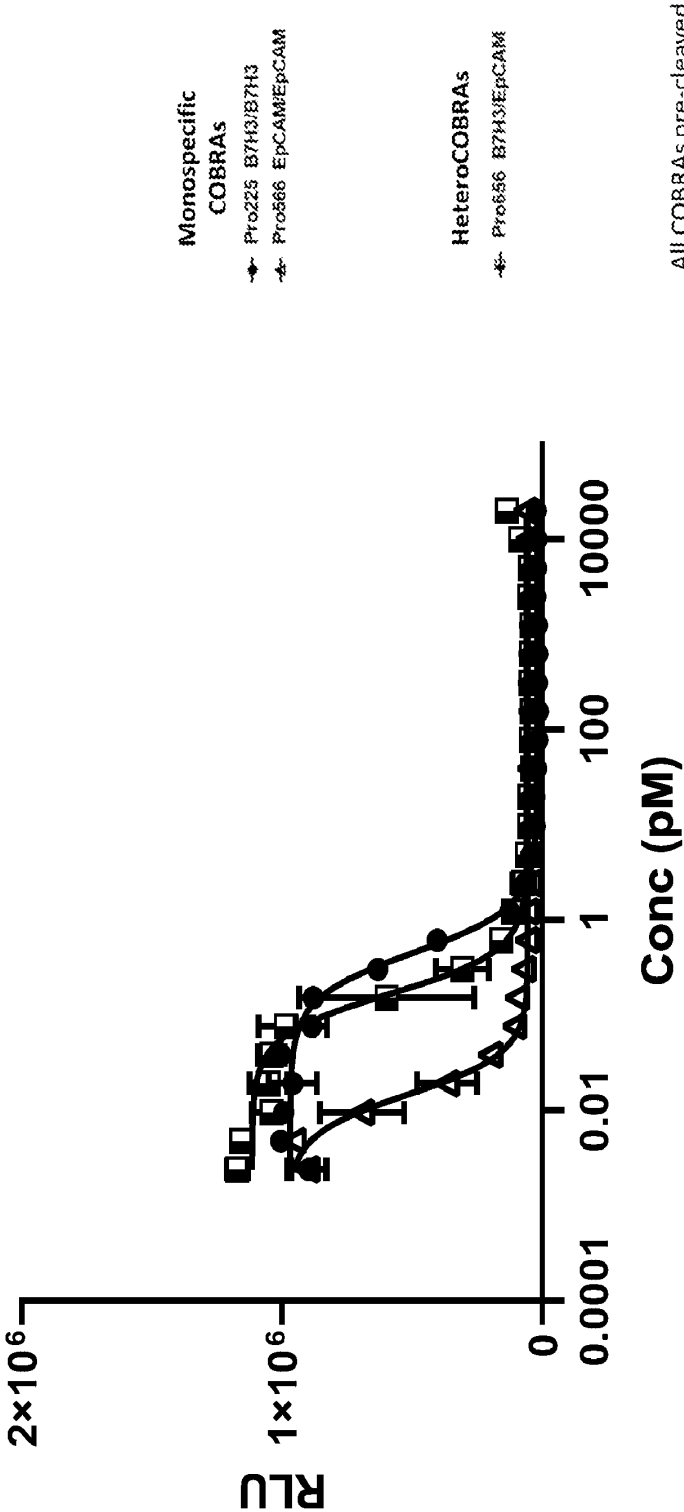


Figure 59A

Figure 59B

HT29-B7H3 KO cells

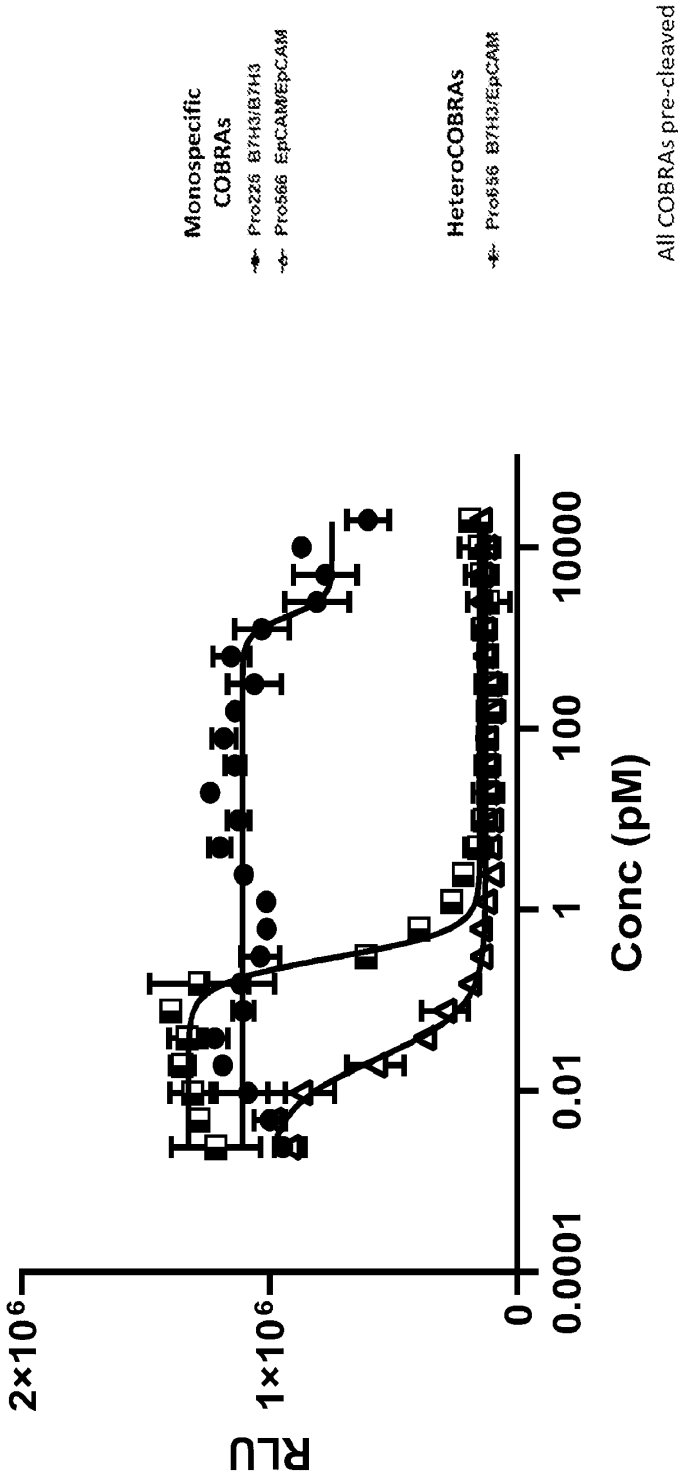
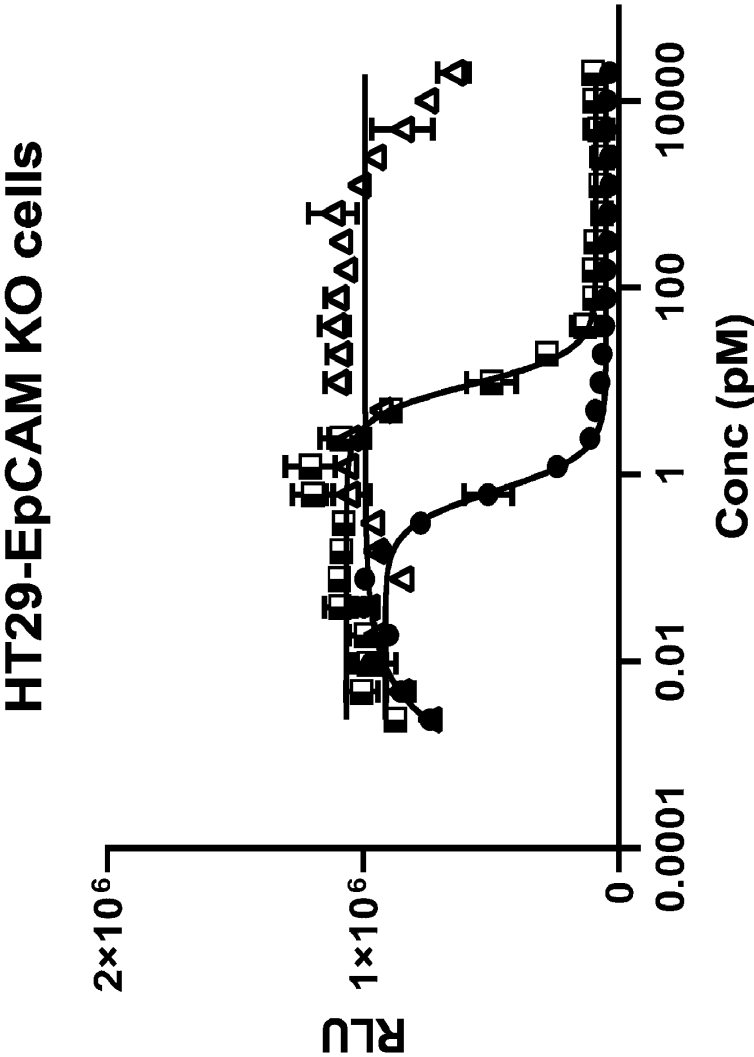


Figure 59C



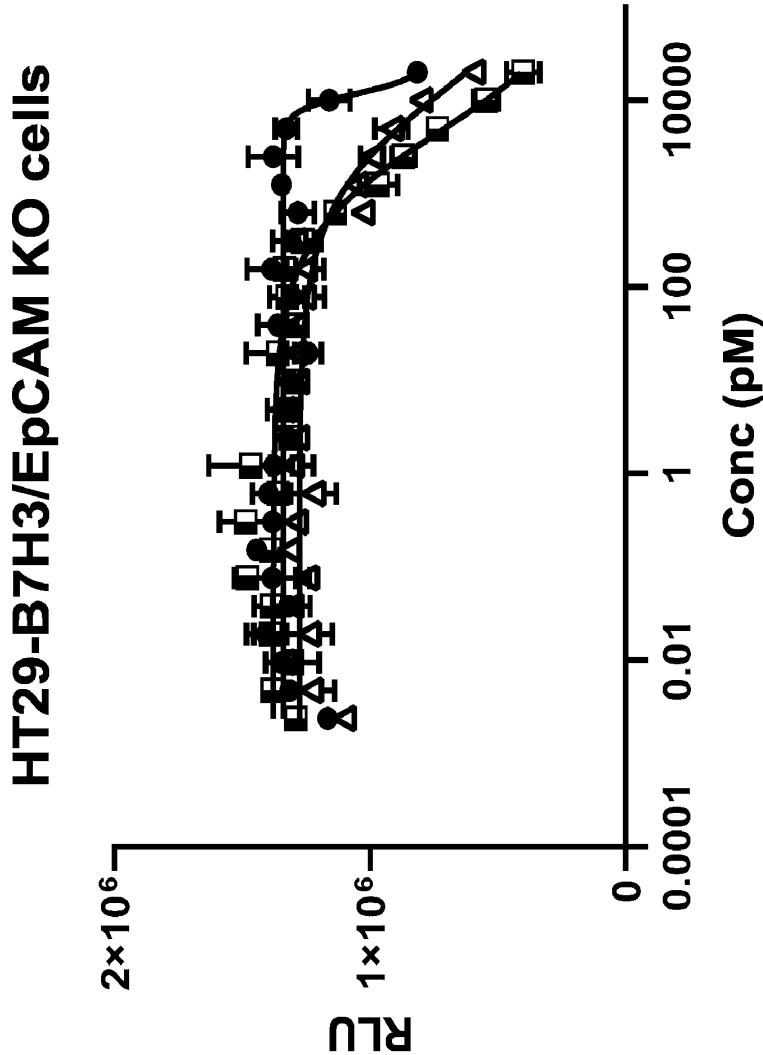


Figure 59D

Figure 60A

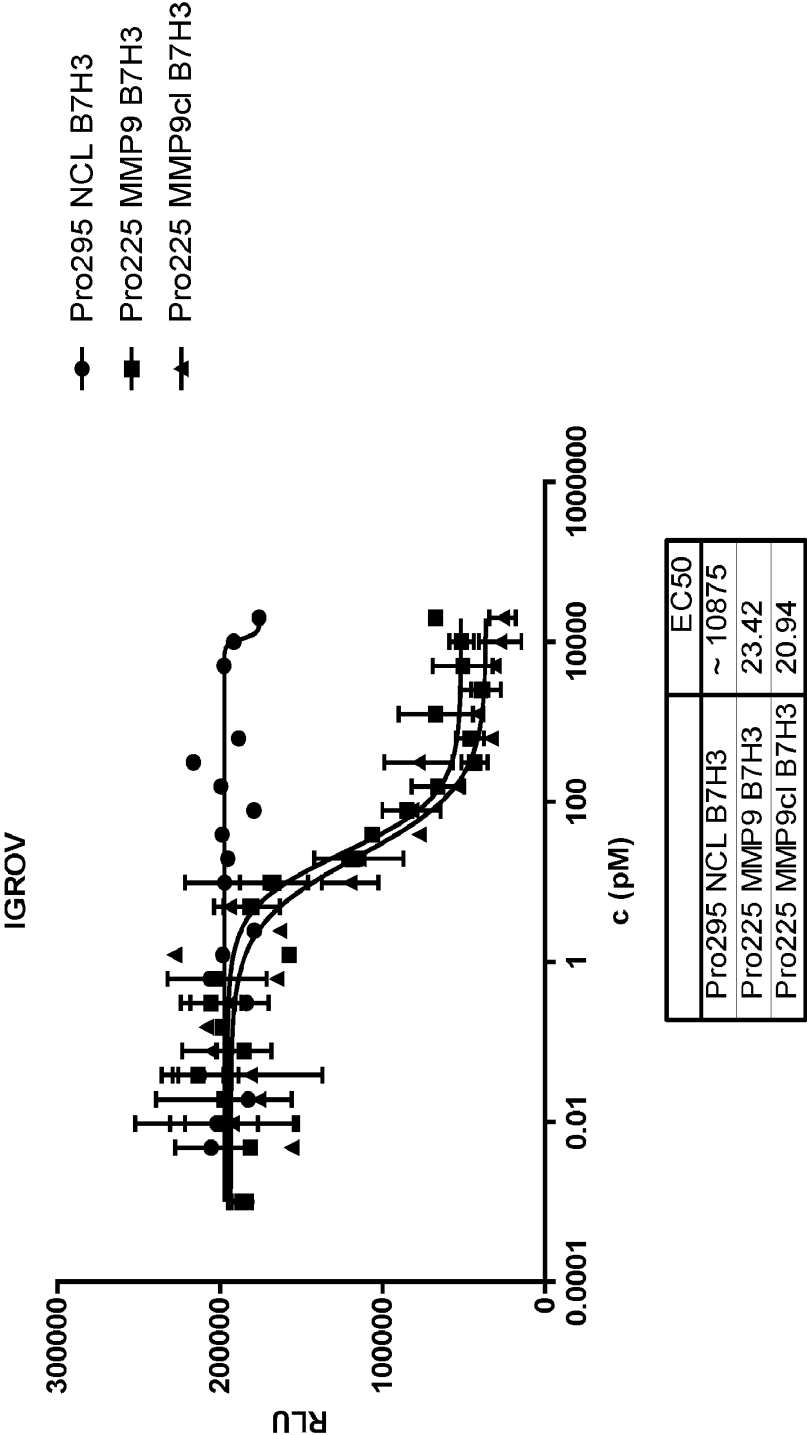


Figure 60B

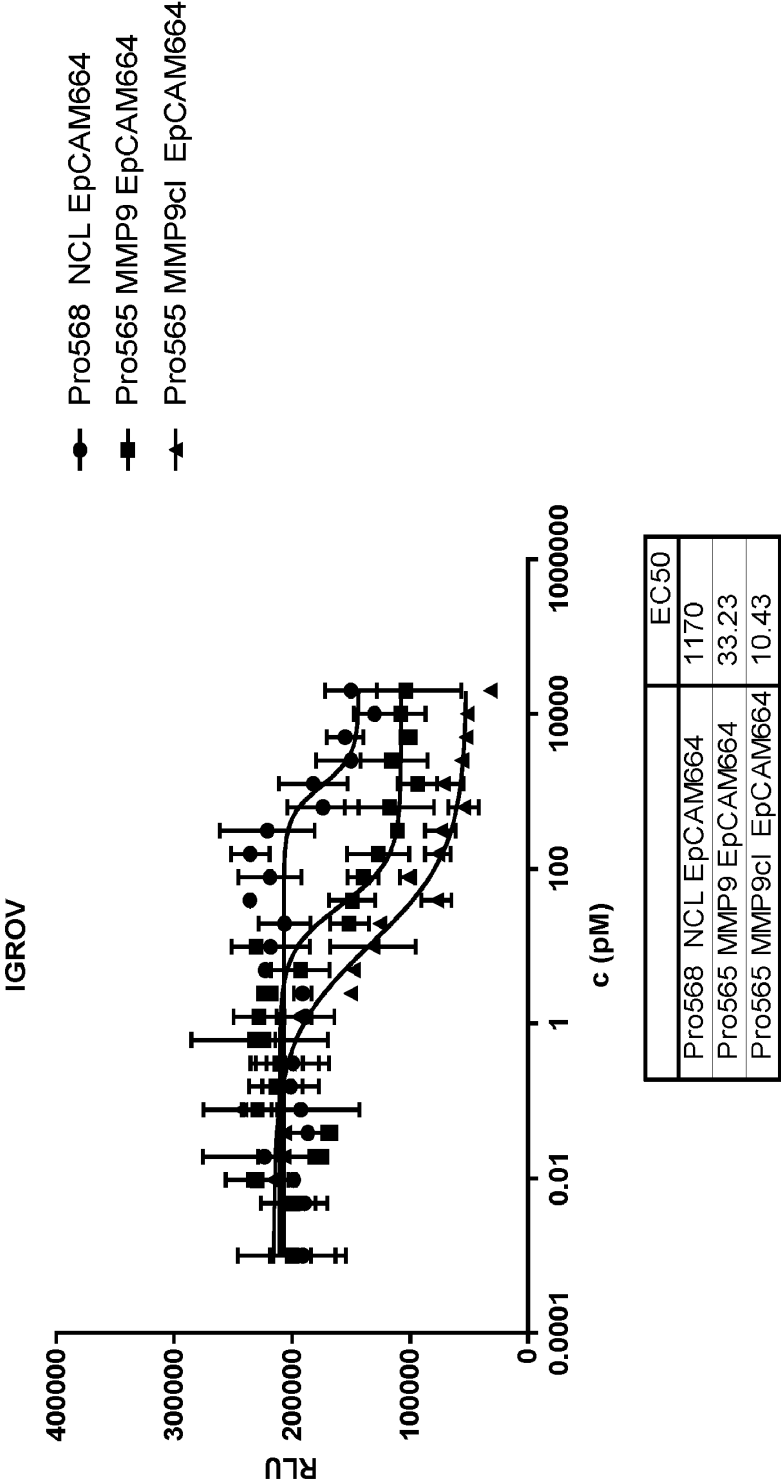


Figure 60C

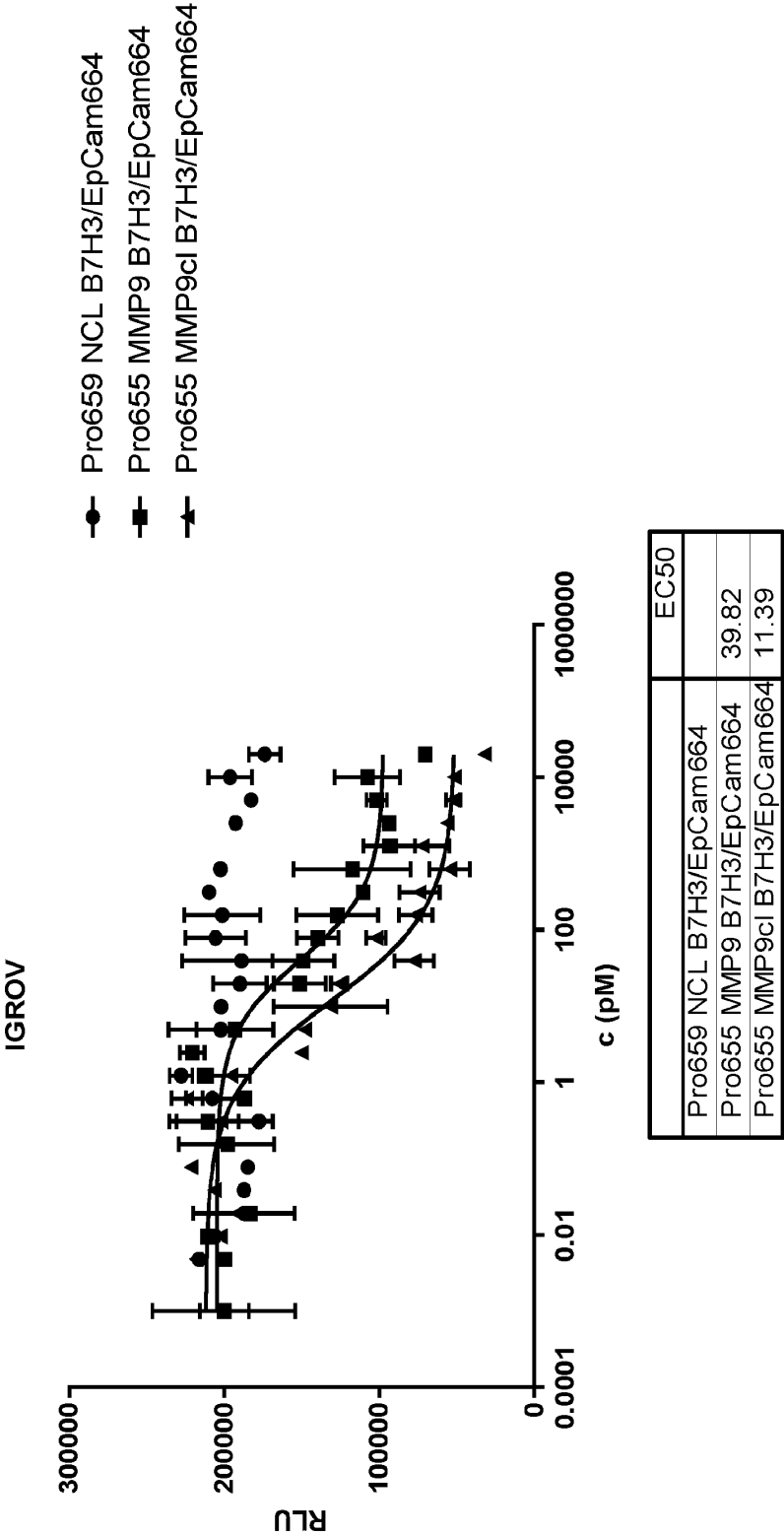


Figure 60D

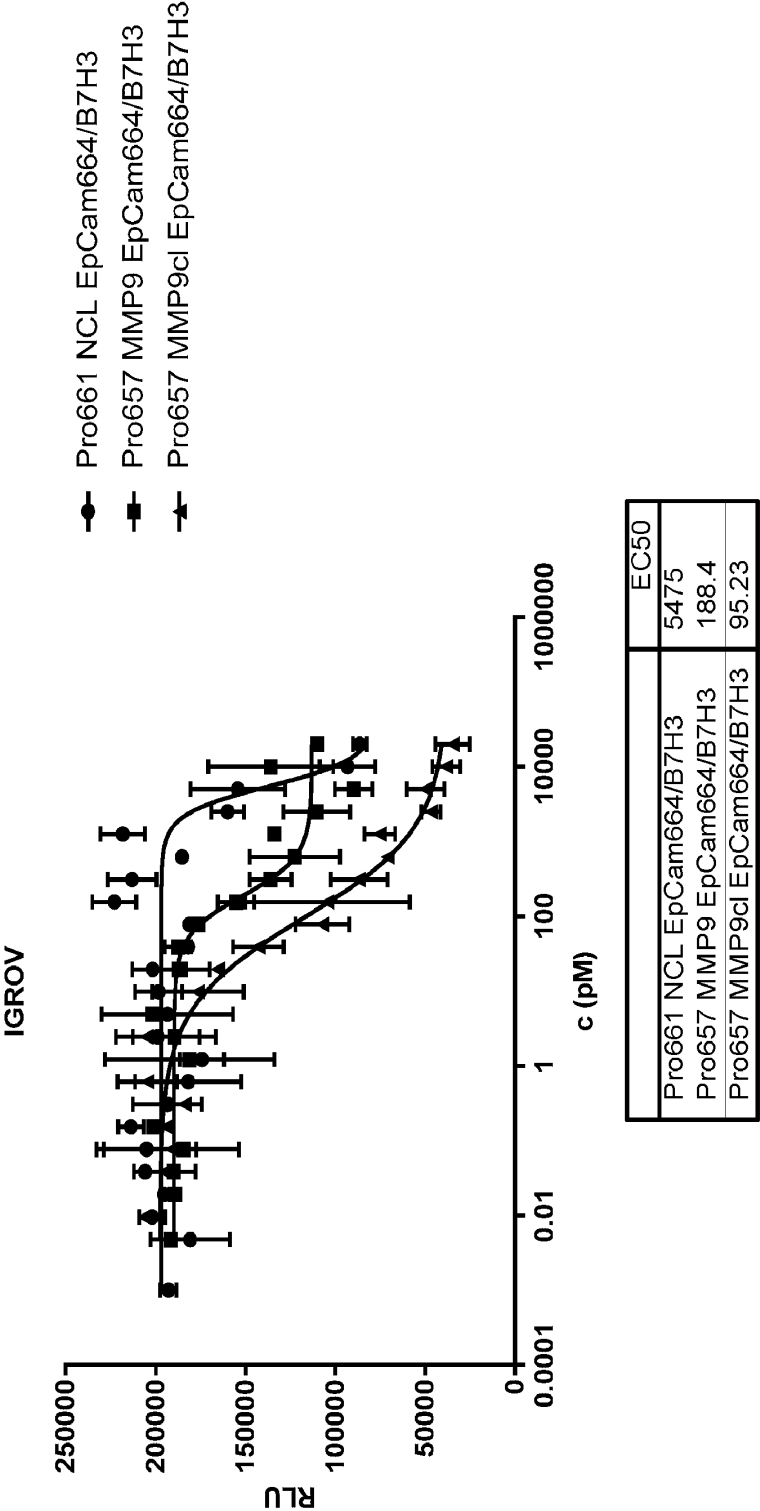


Figure 61A

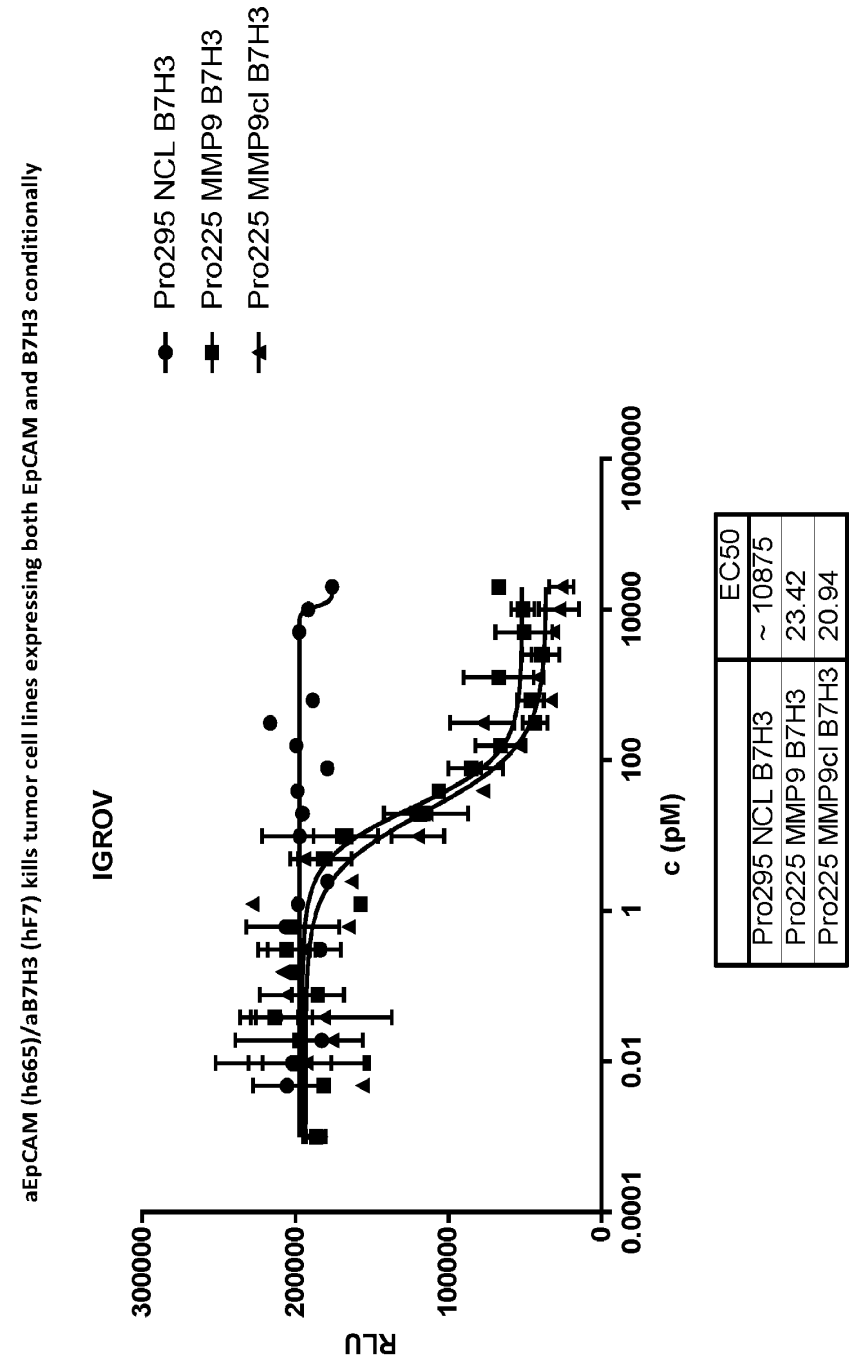


Figure 61B

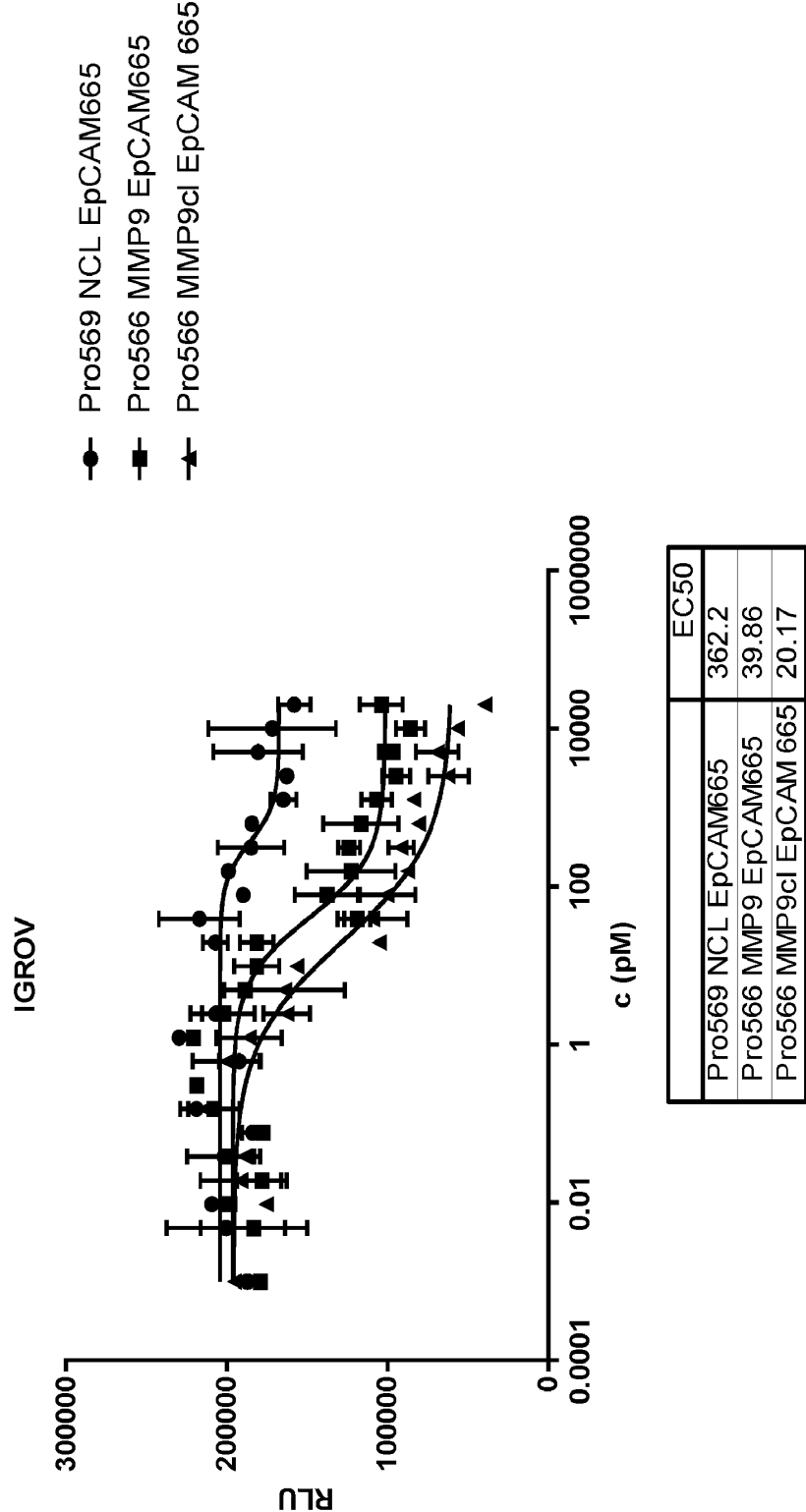


Figure 61C

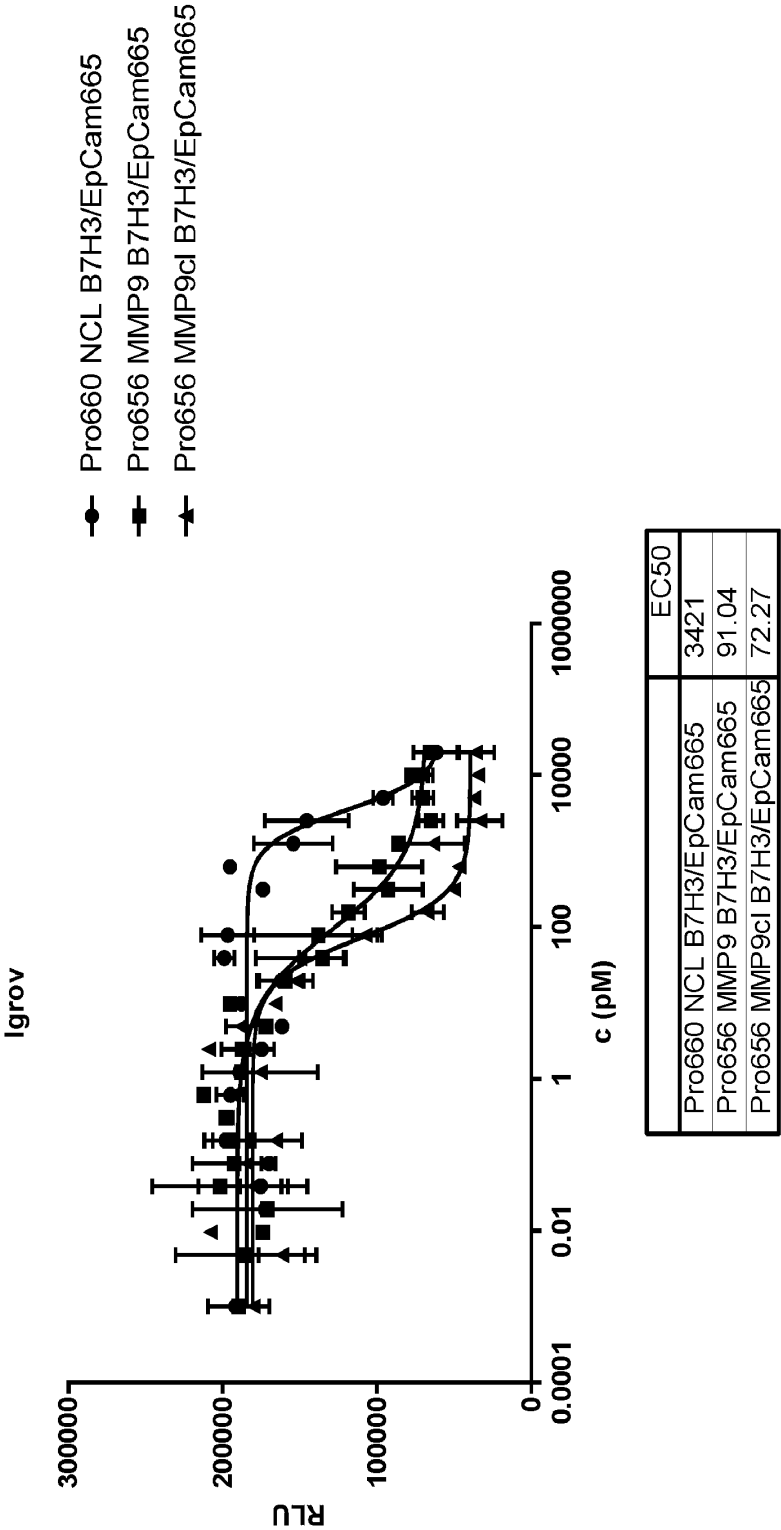


Figure 61D

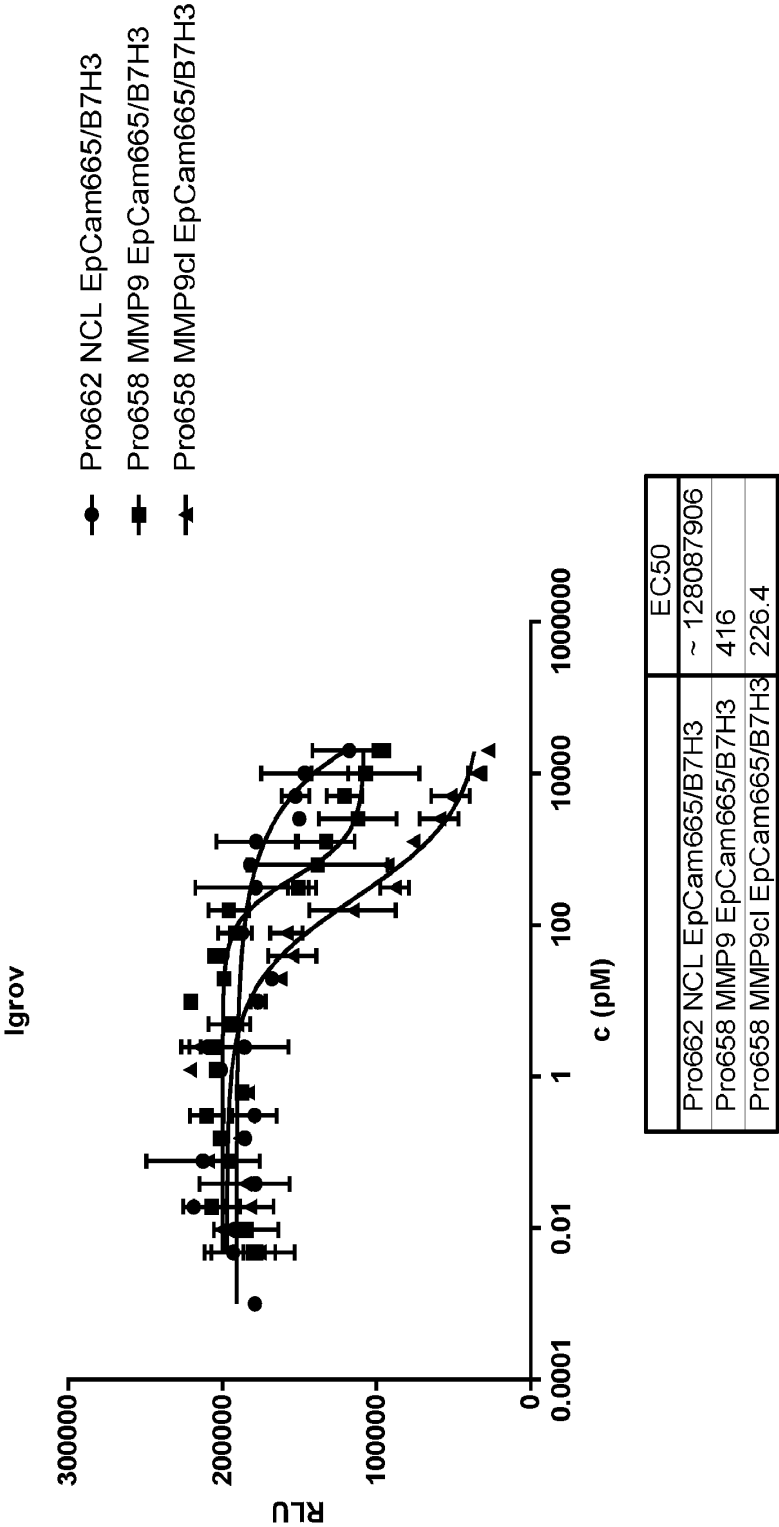


Figure 62A

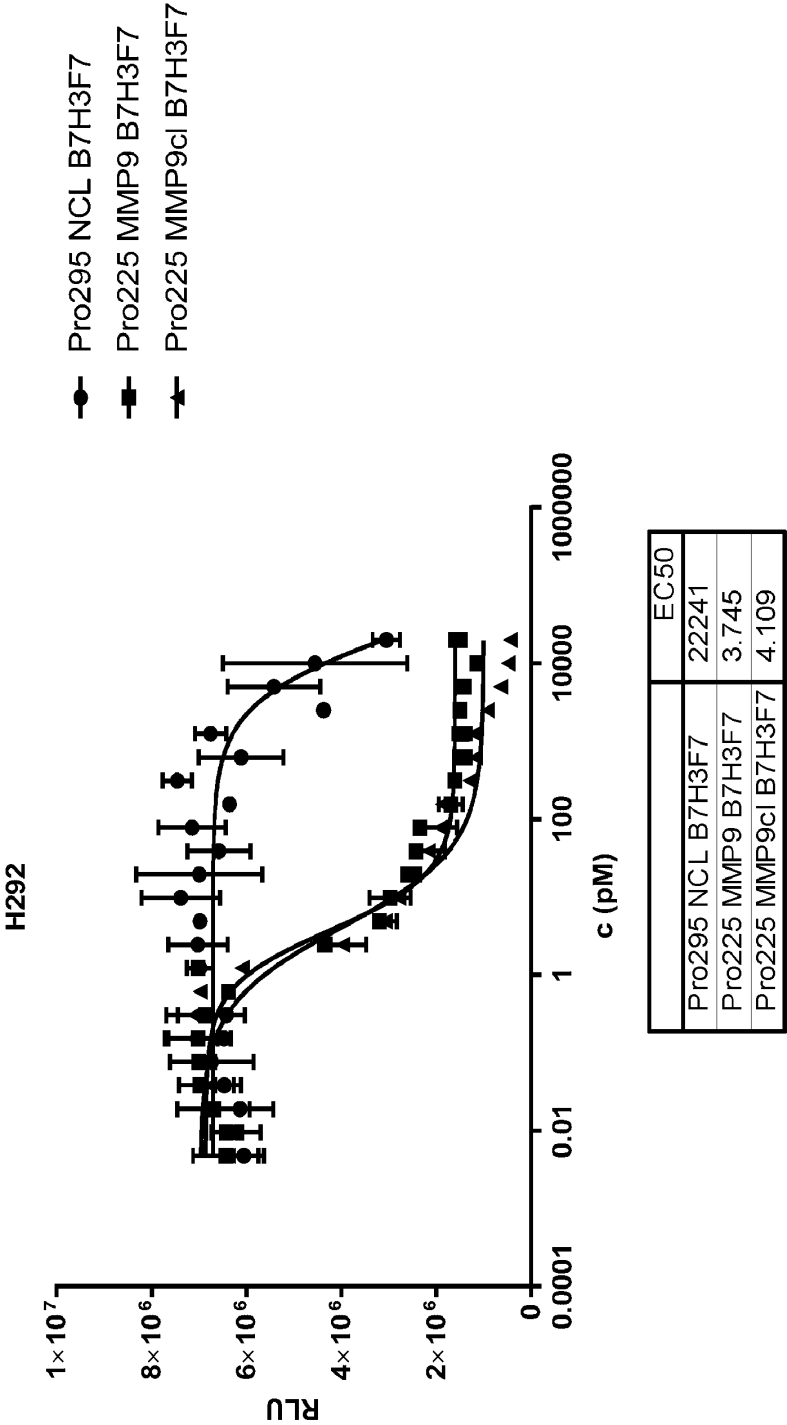


Figure 62B

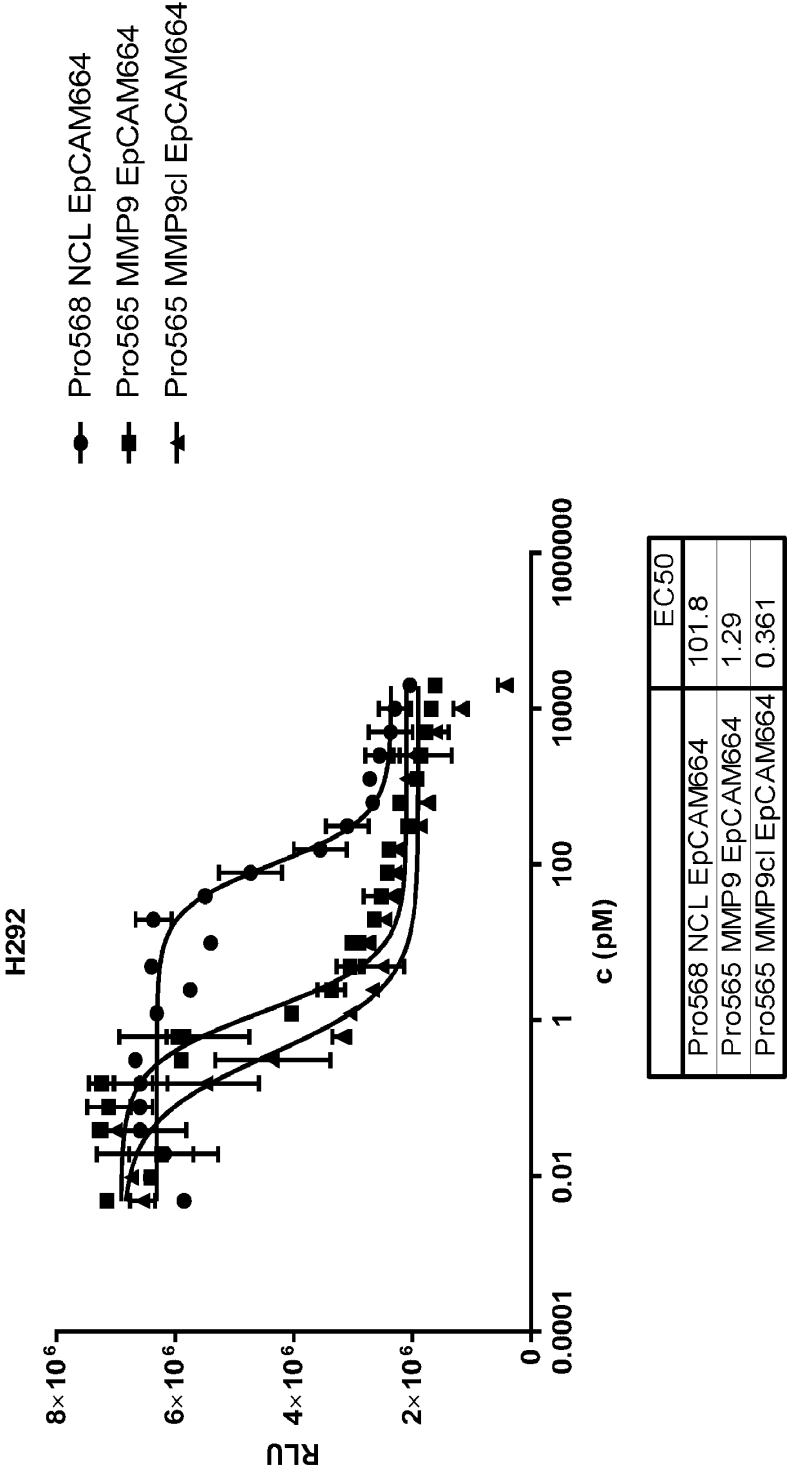


Figure 62C

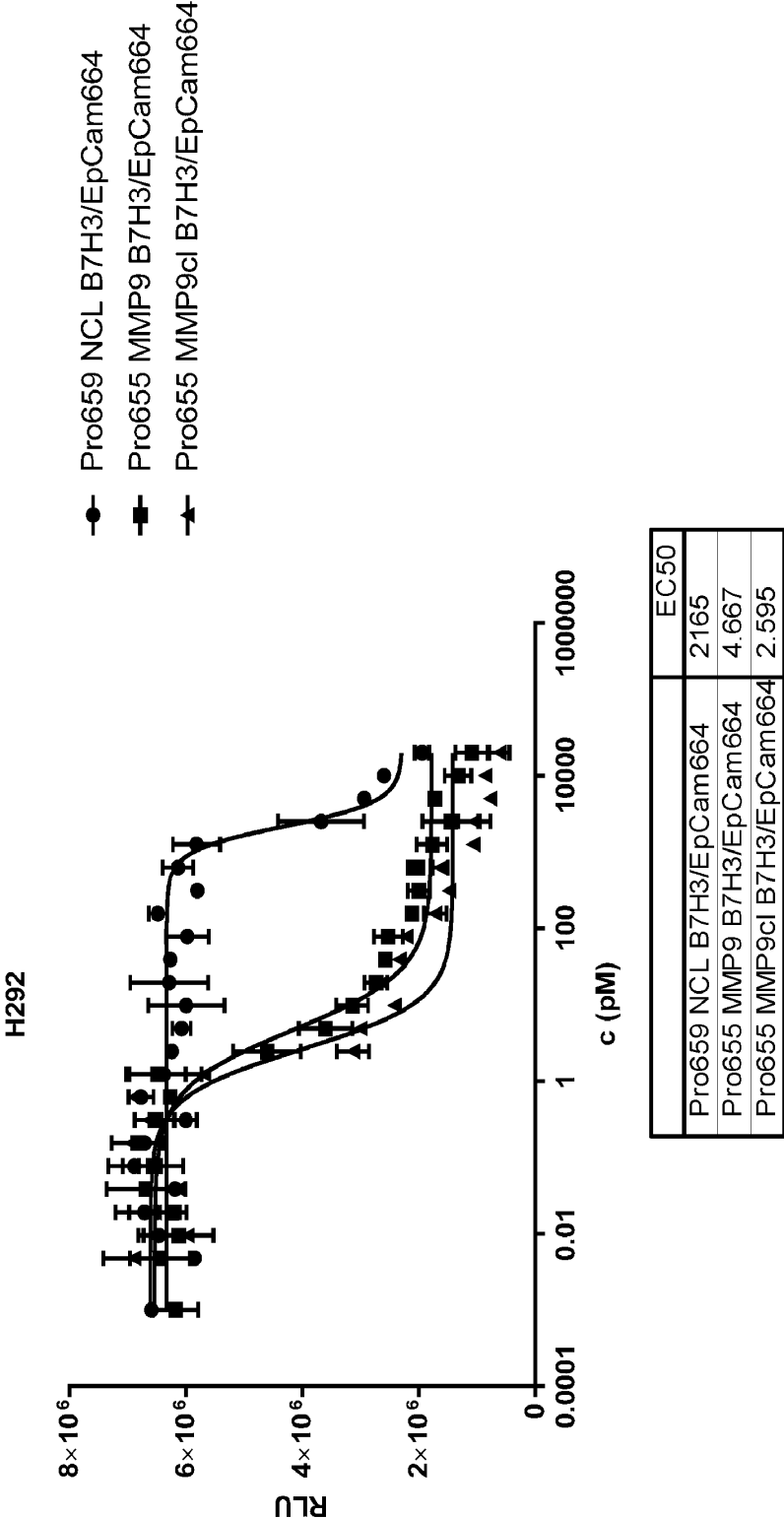


Figure 62D

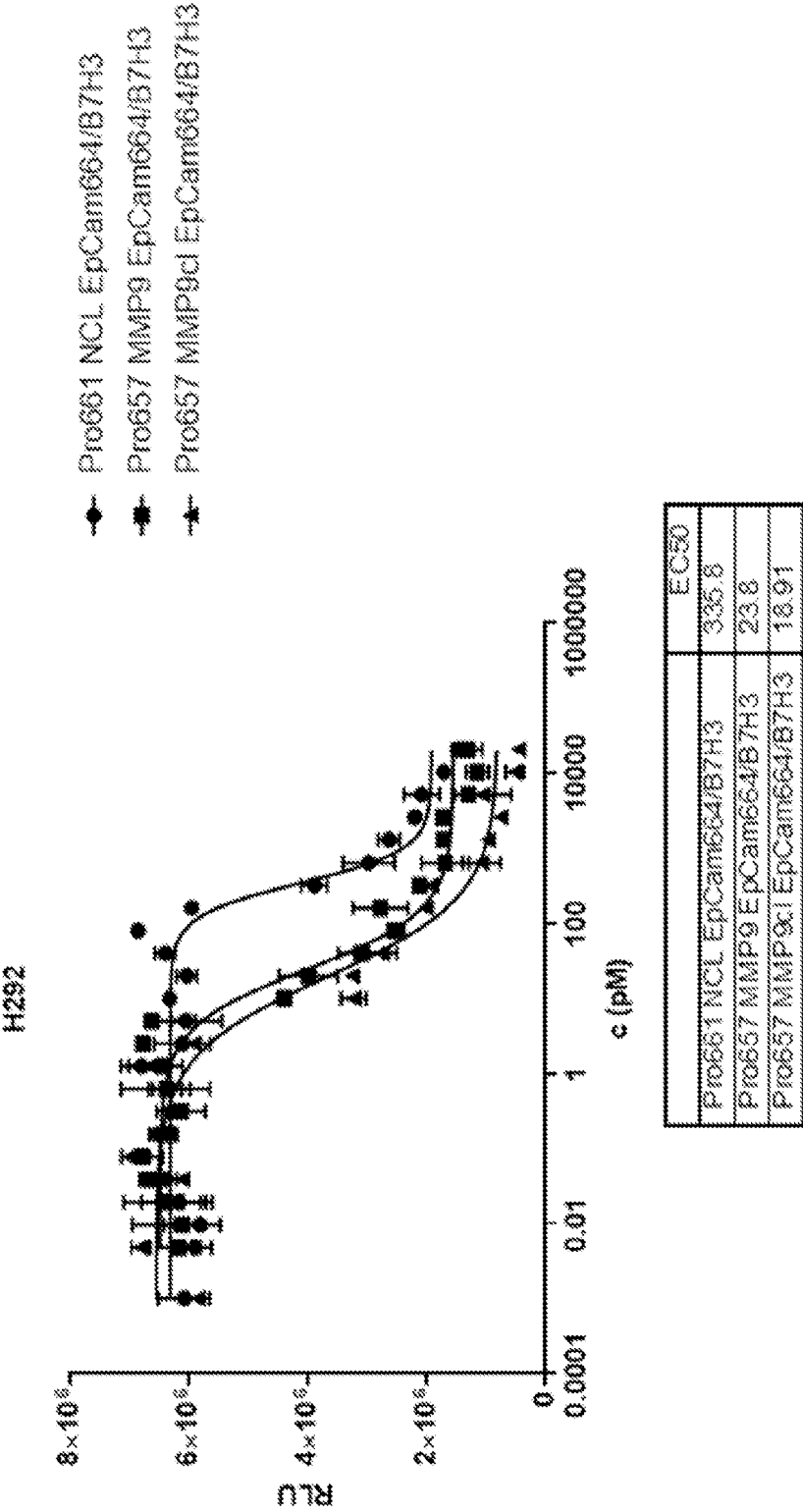


Figure 63A

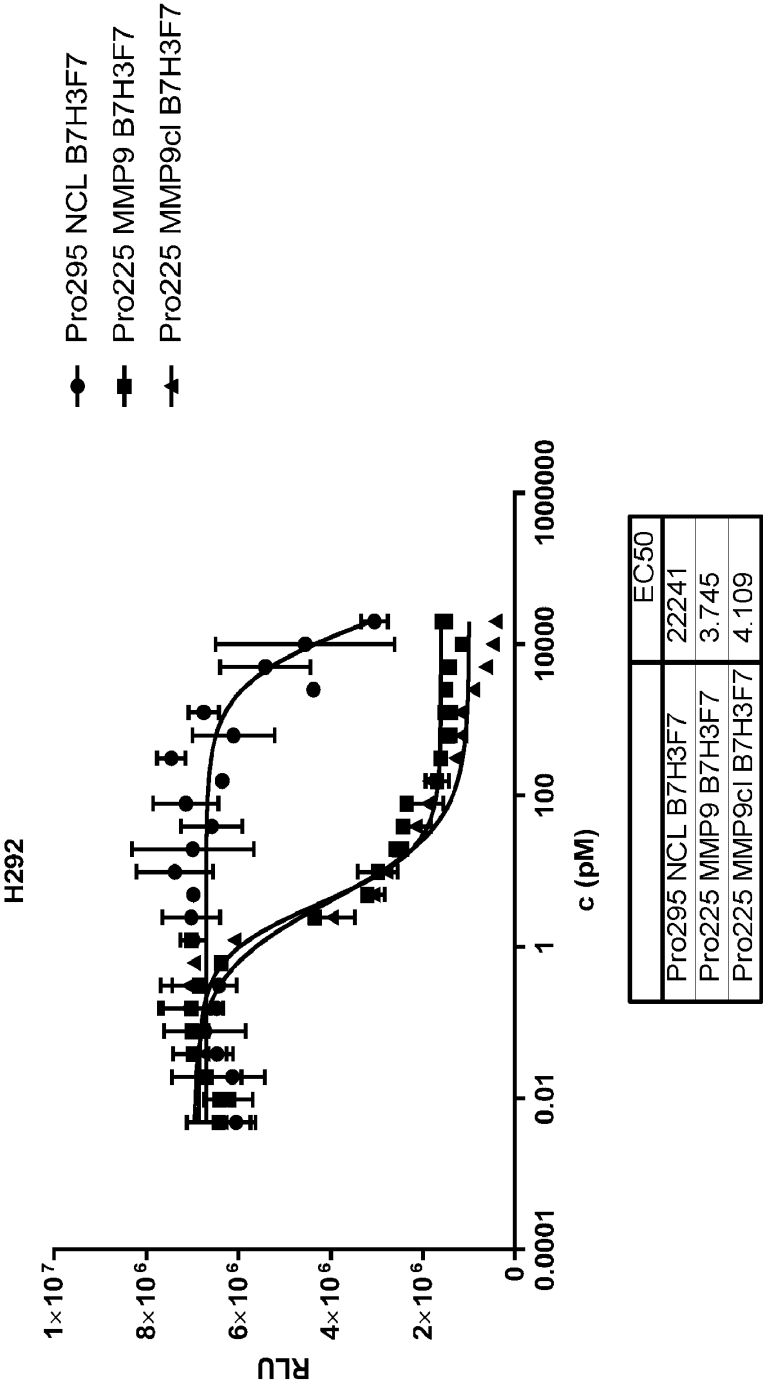


Figure 63B

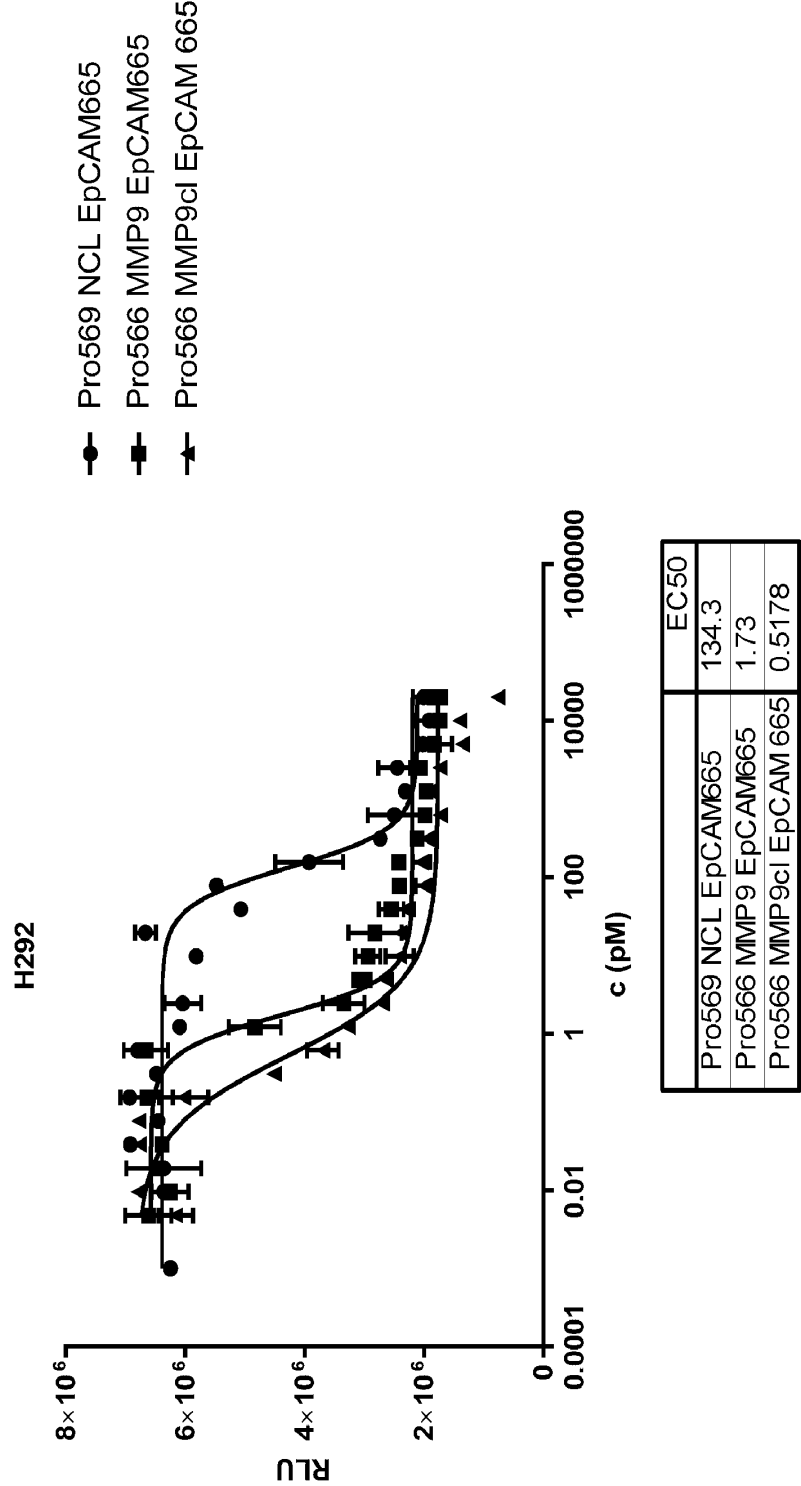


Figure 63C

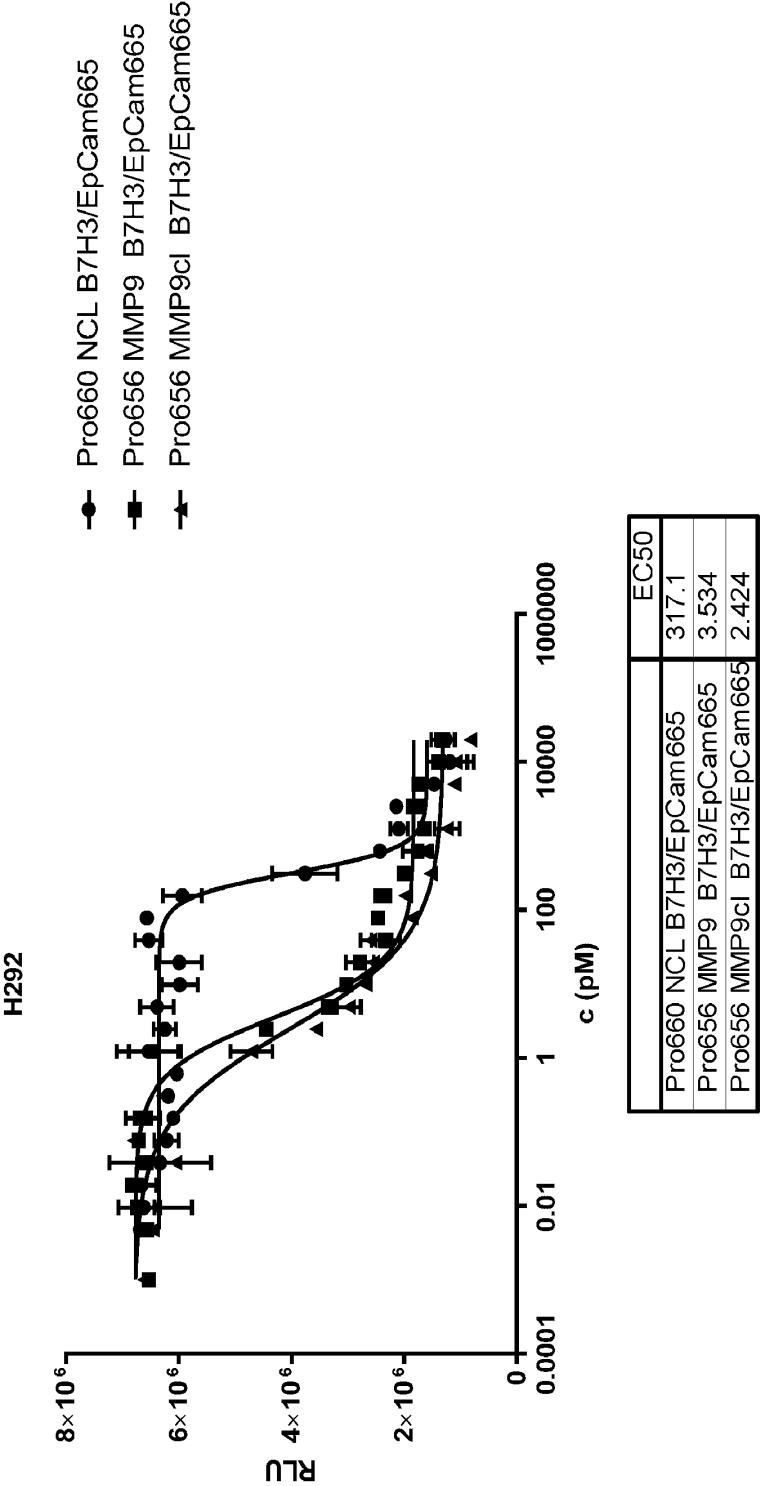


Figure 63D

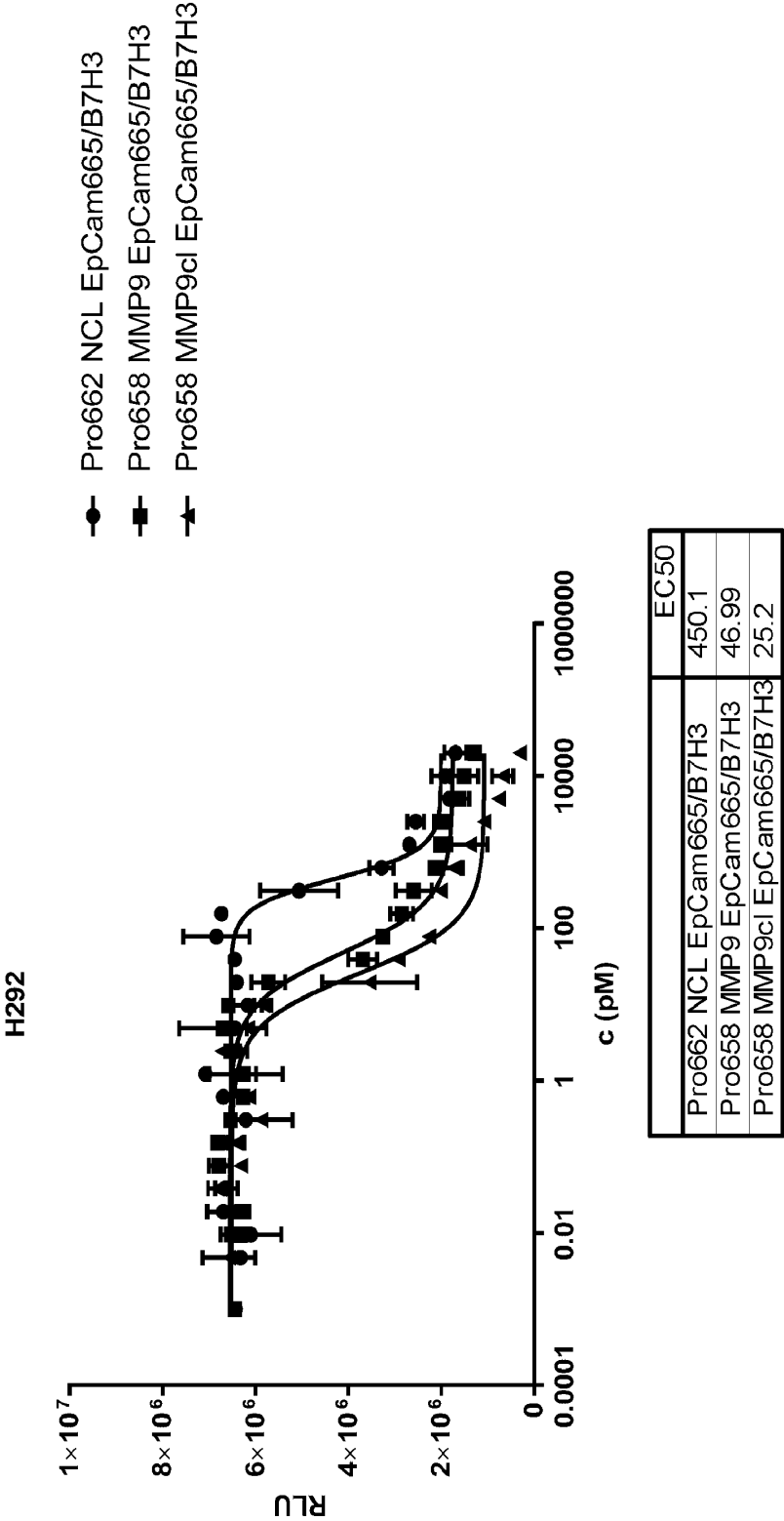


Figure 64A

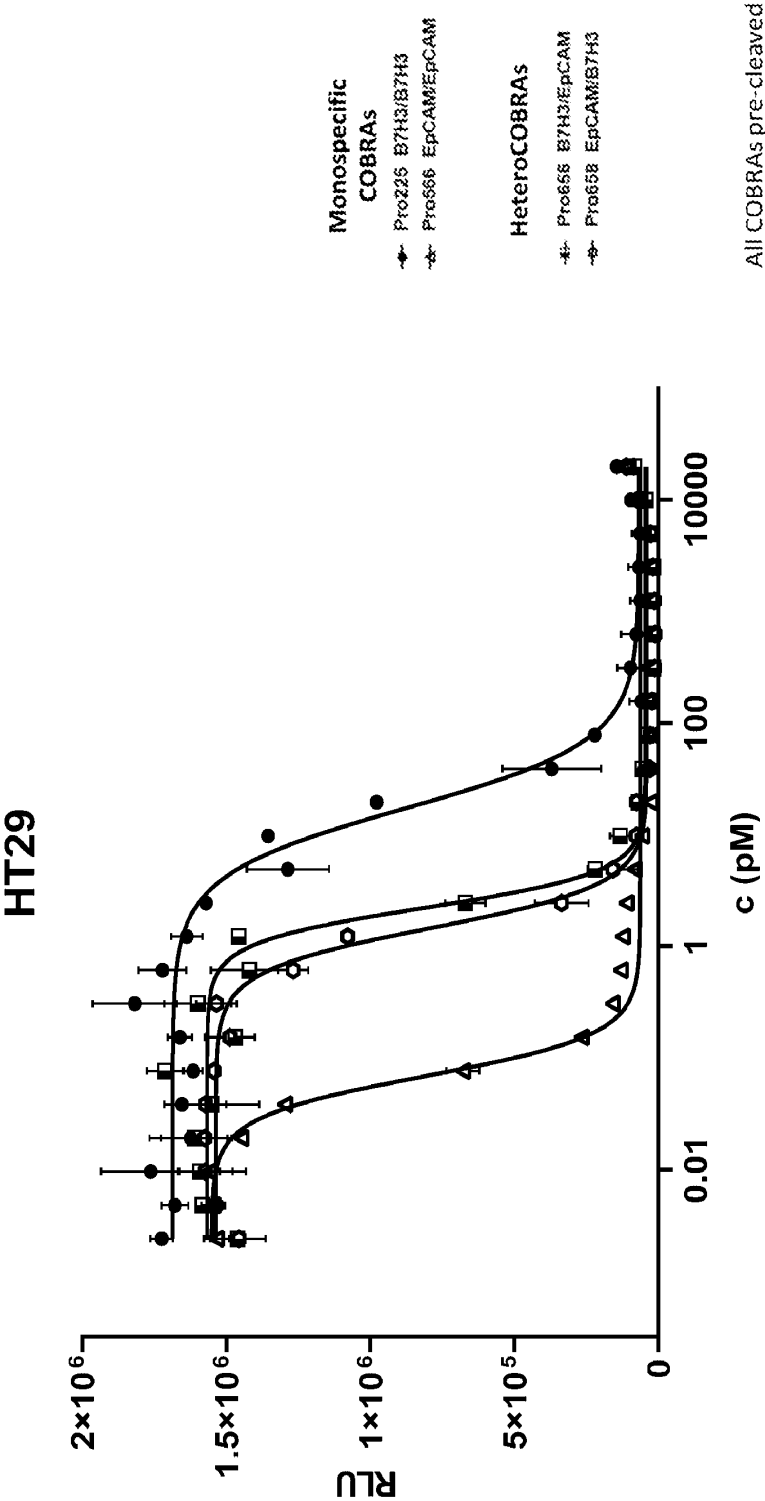
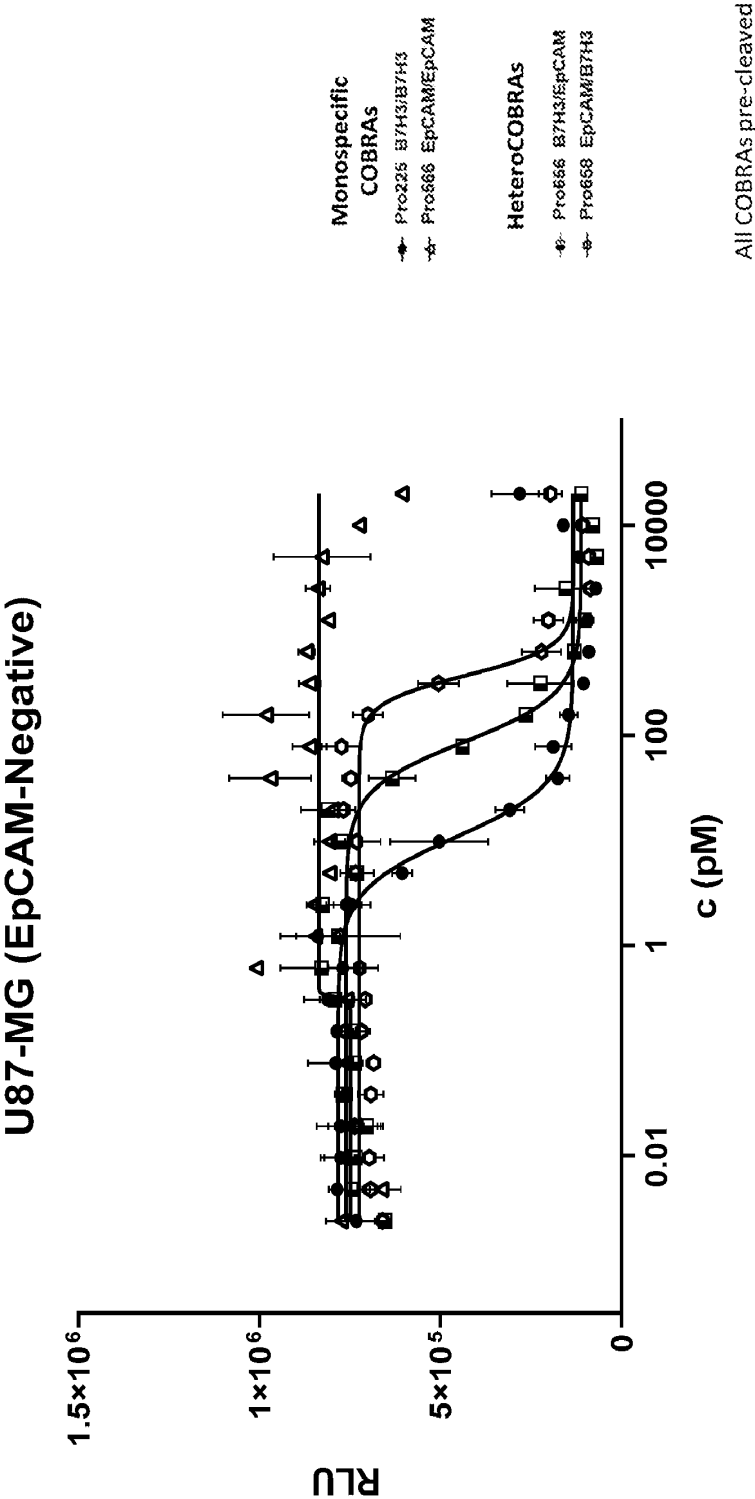


Figure 64B



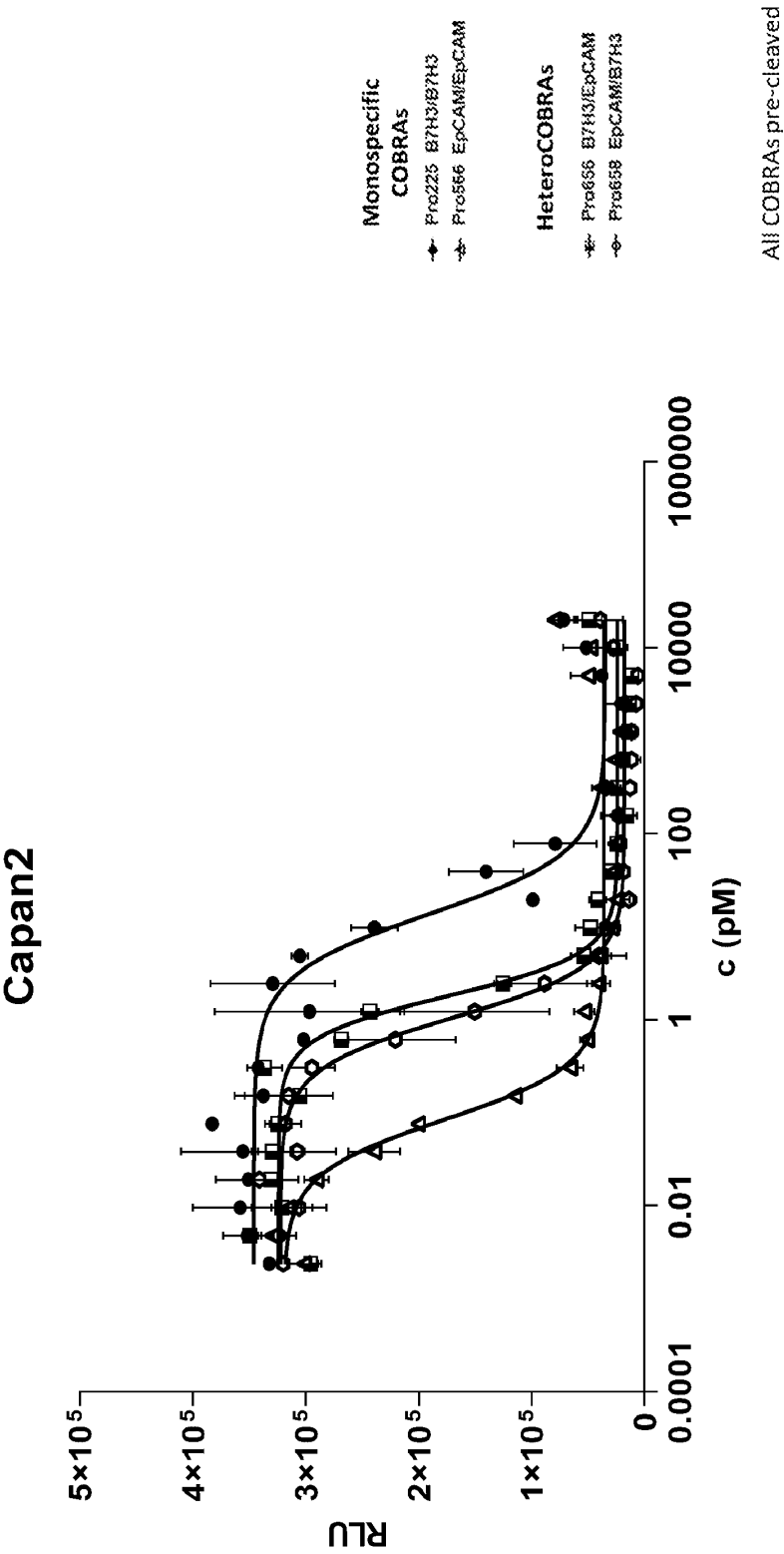


Figure 64C

Figure 64D

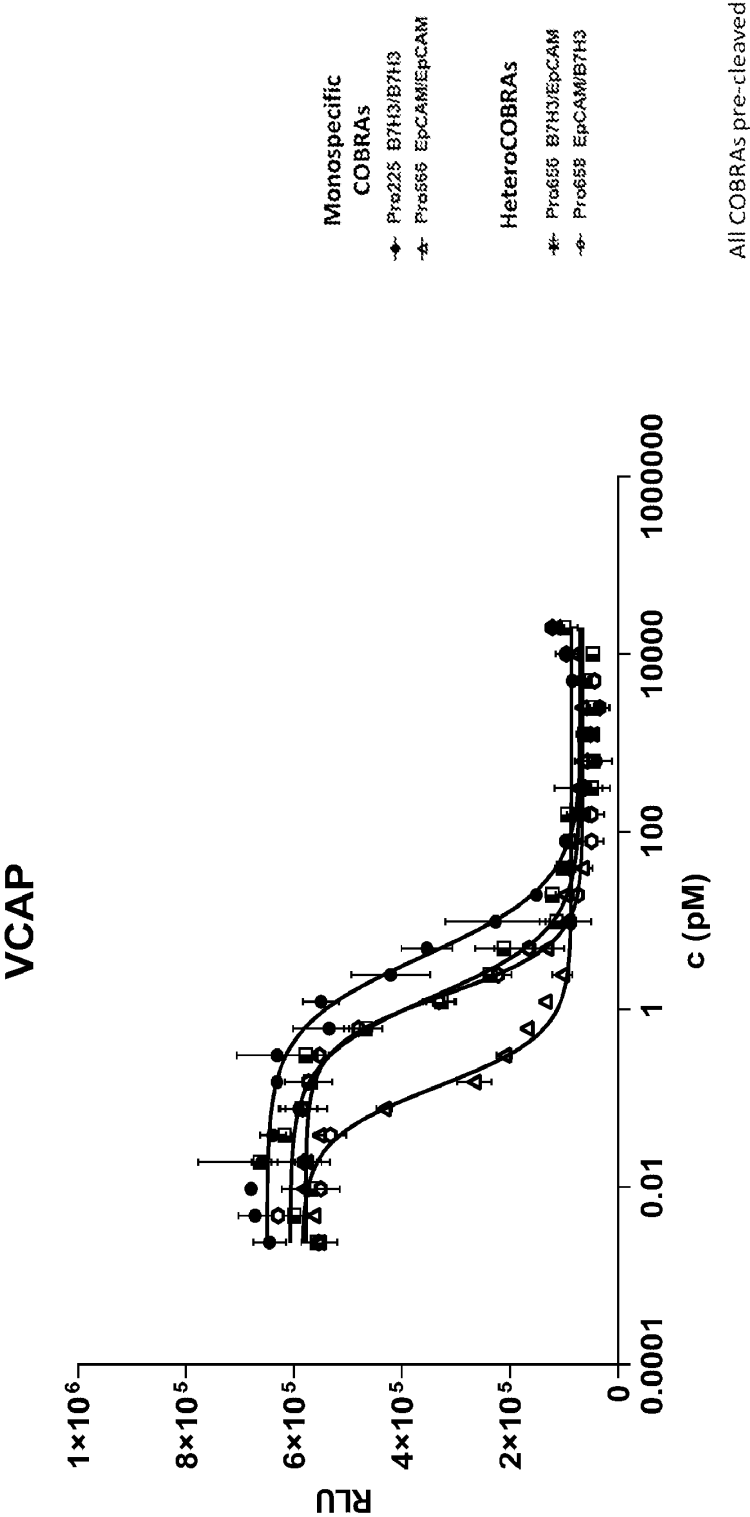
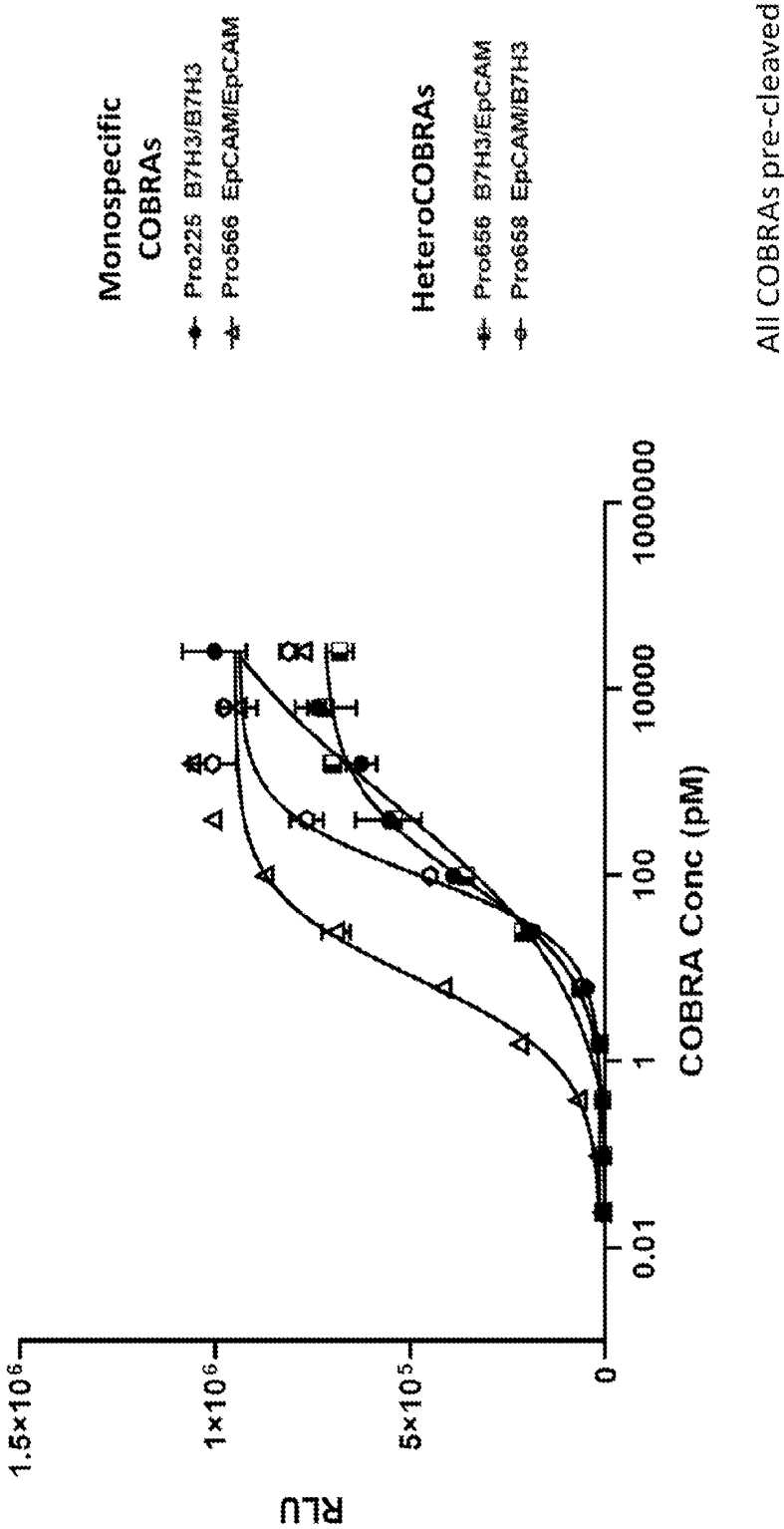


Figure 65



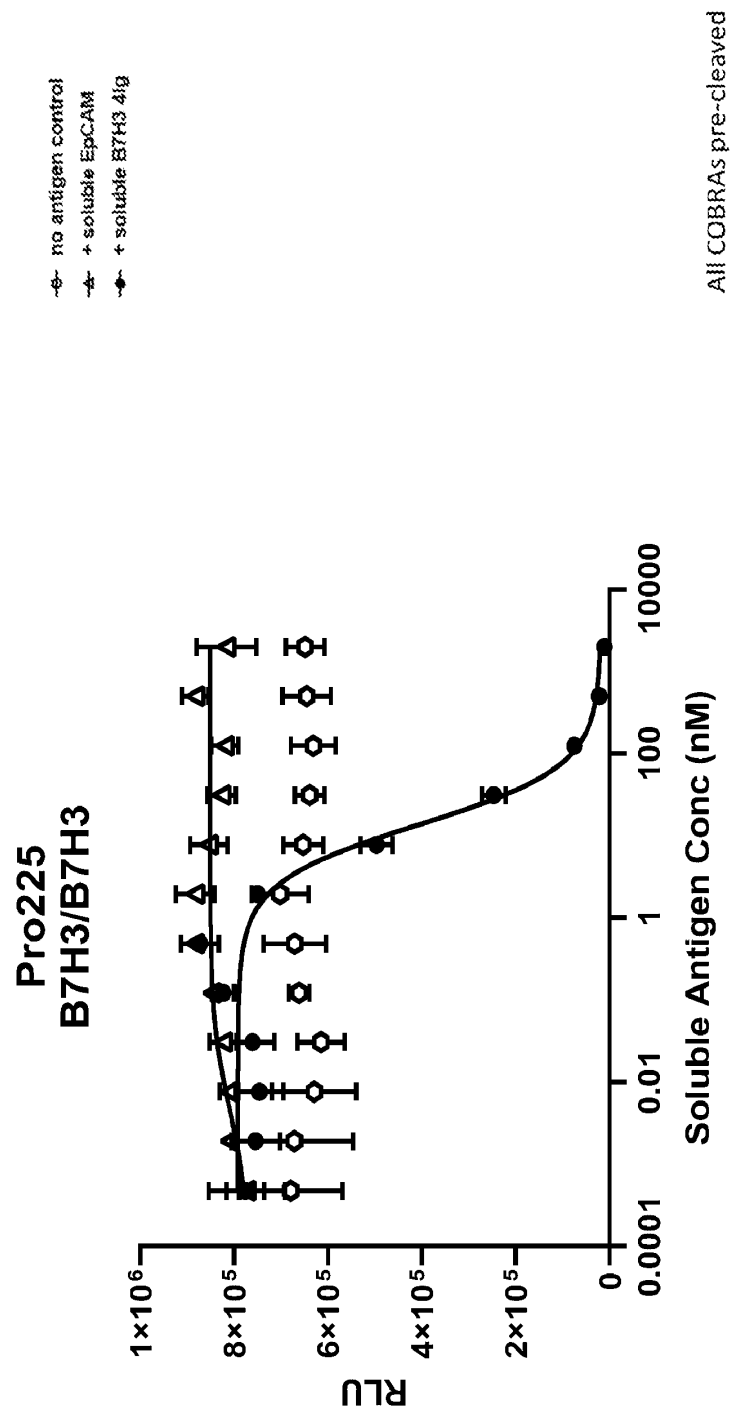


Figure 66A

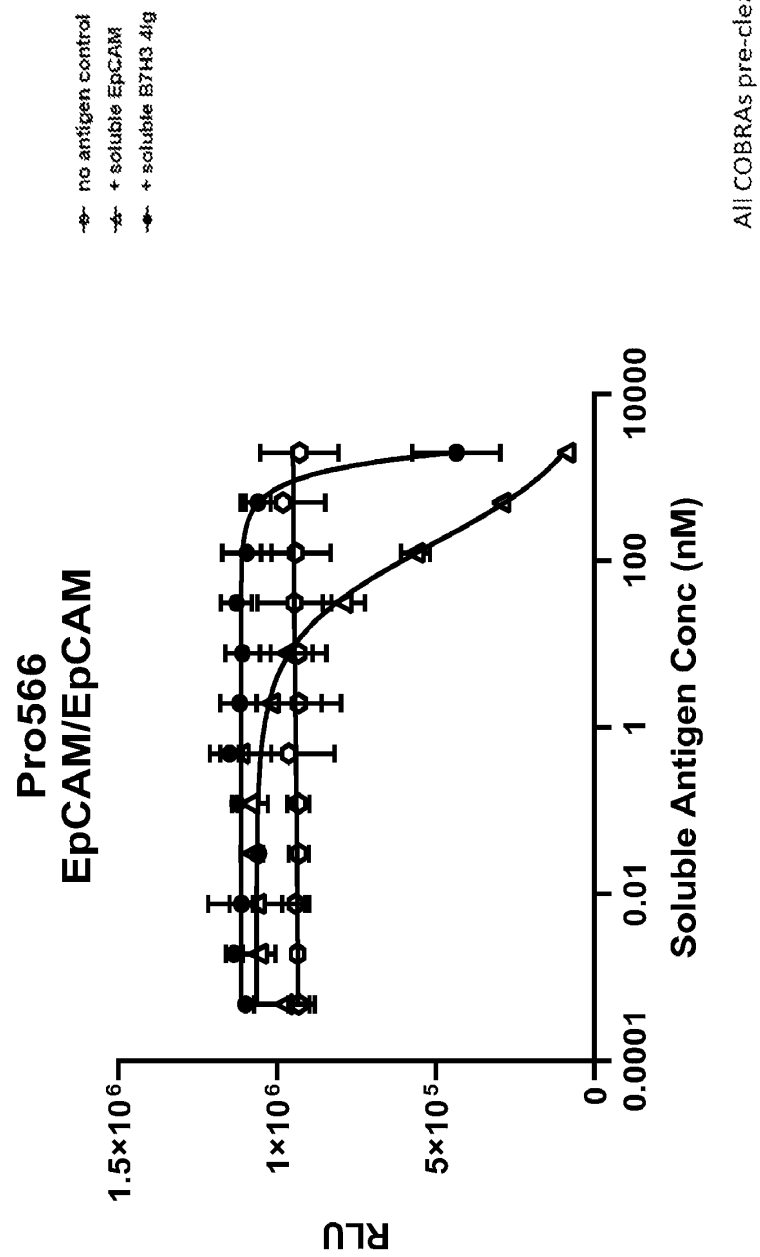
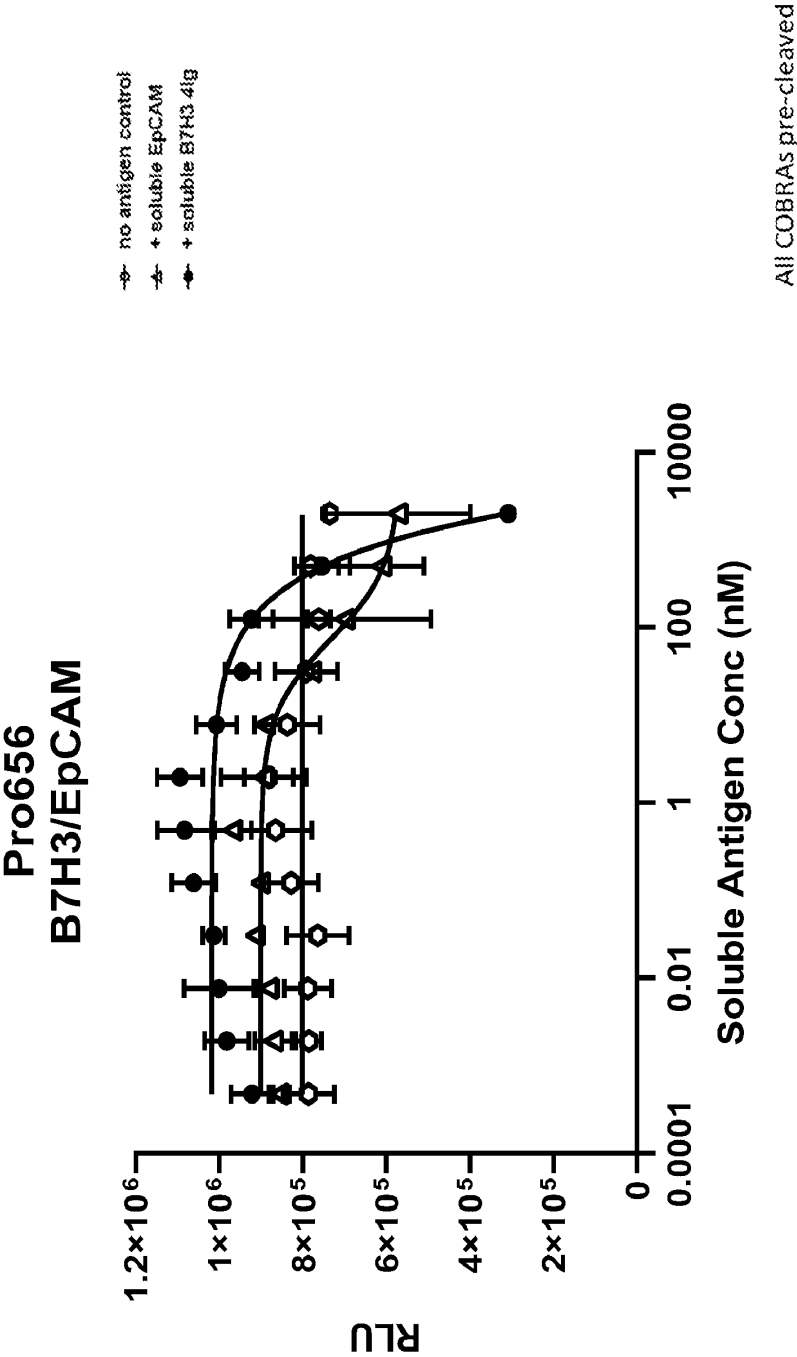


Figure 66B

Figure 66C



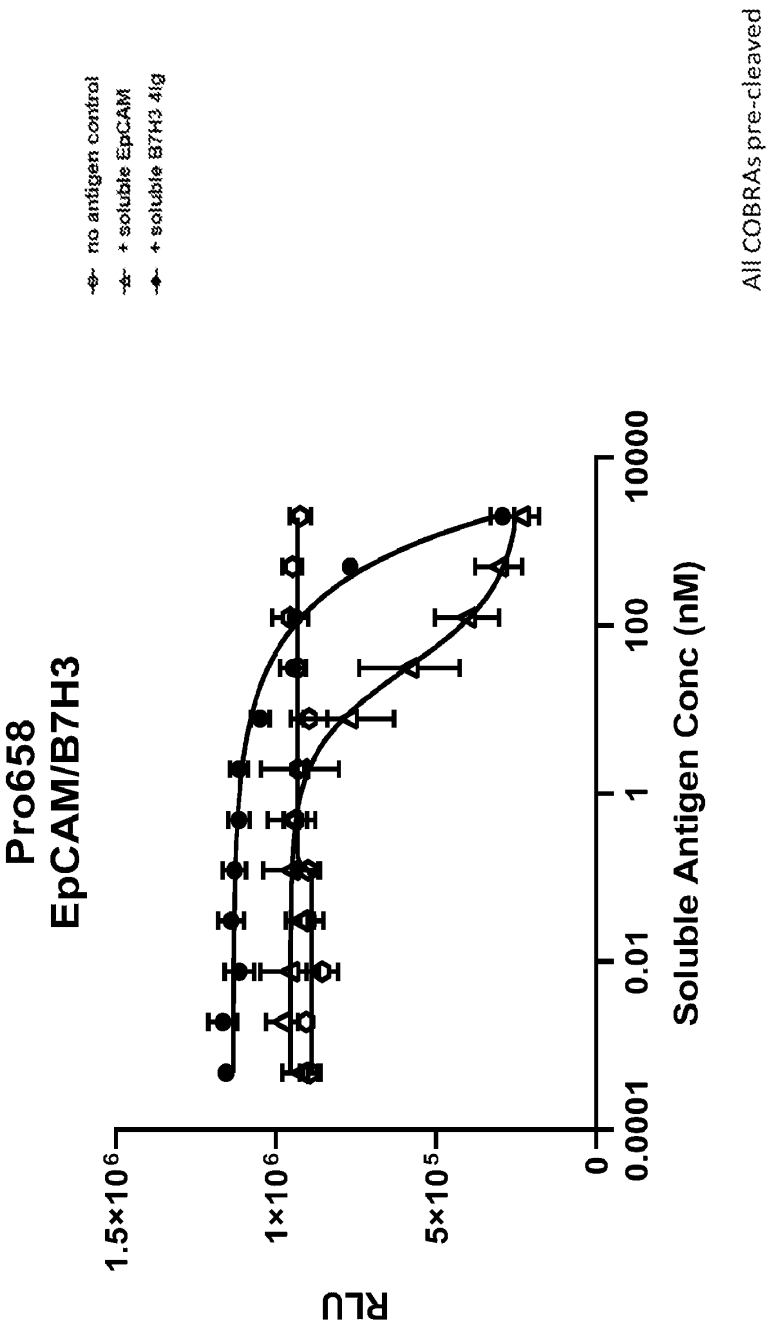


Figure 66D

Figure 67

Affinities of B7H3/EpCAM HeteroCOBRAS				
		K _D (nM)		
Prodent	1st / 2nd position	huB7H3-4Ig	huEpCAM	huB7H3-4Ig + huEpCAM
Pro656	B7H3/EpCAM	6.9	13.6	0.13
Pro658	EpCAM/B7H3	7.8	7.7	0.061

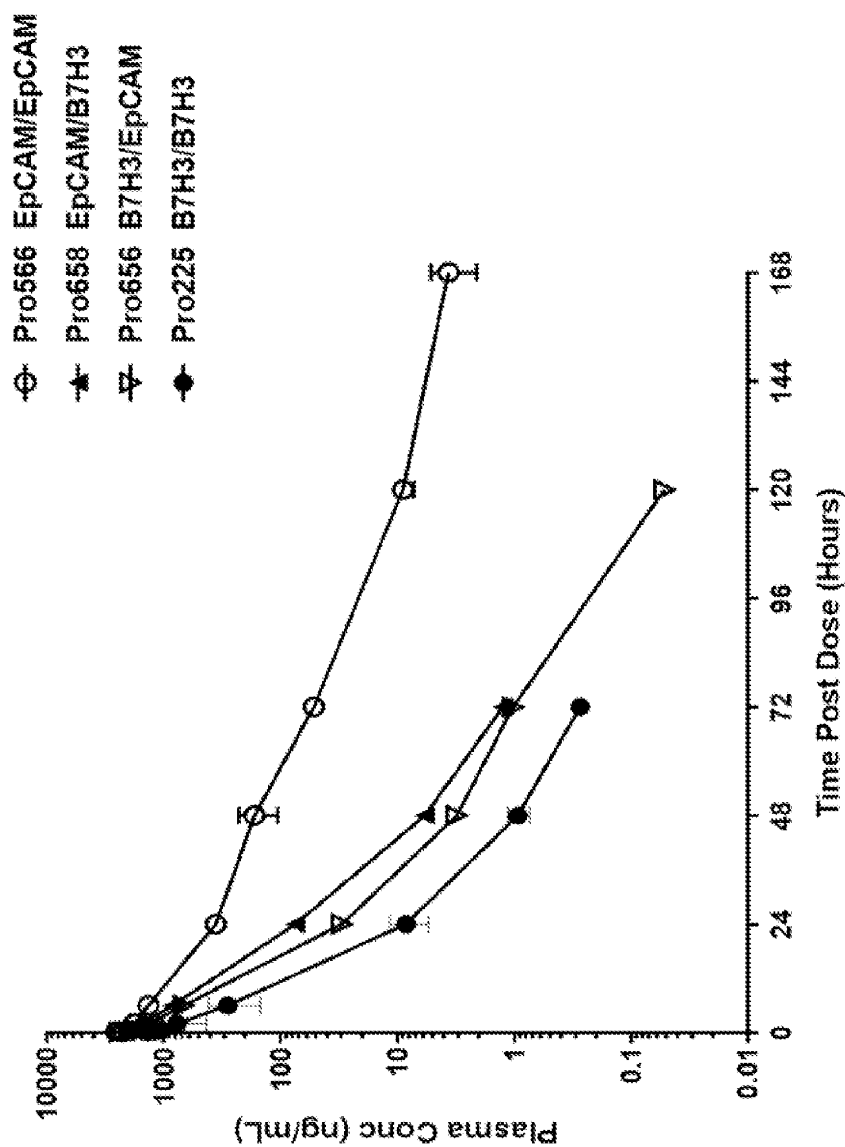
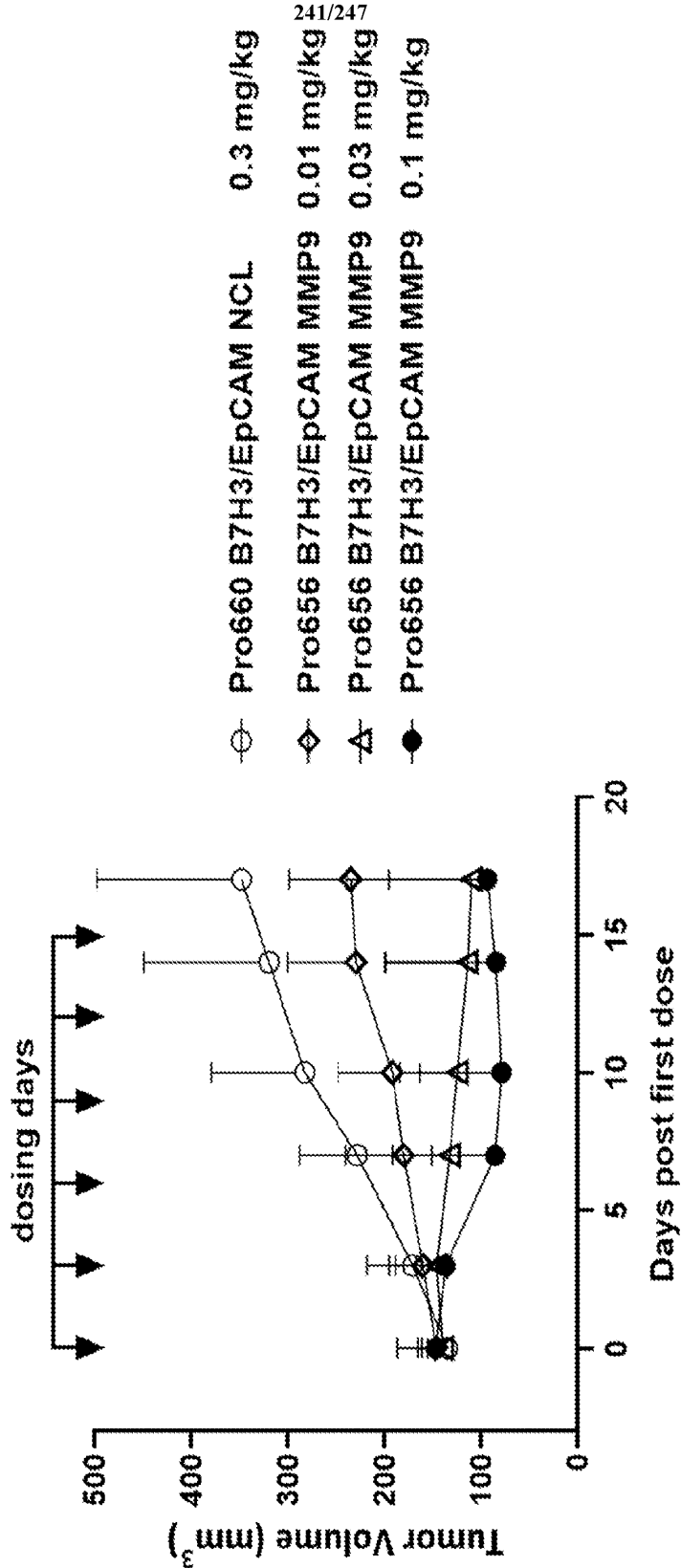


Figure 68

Figure 69



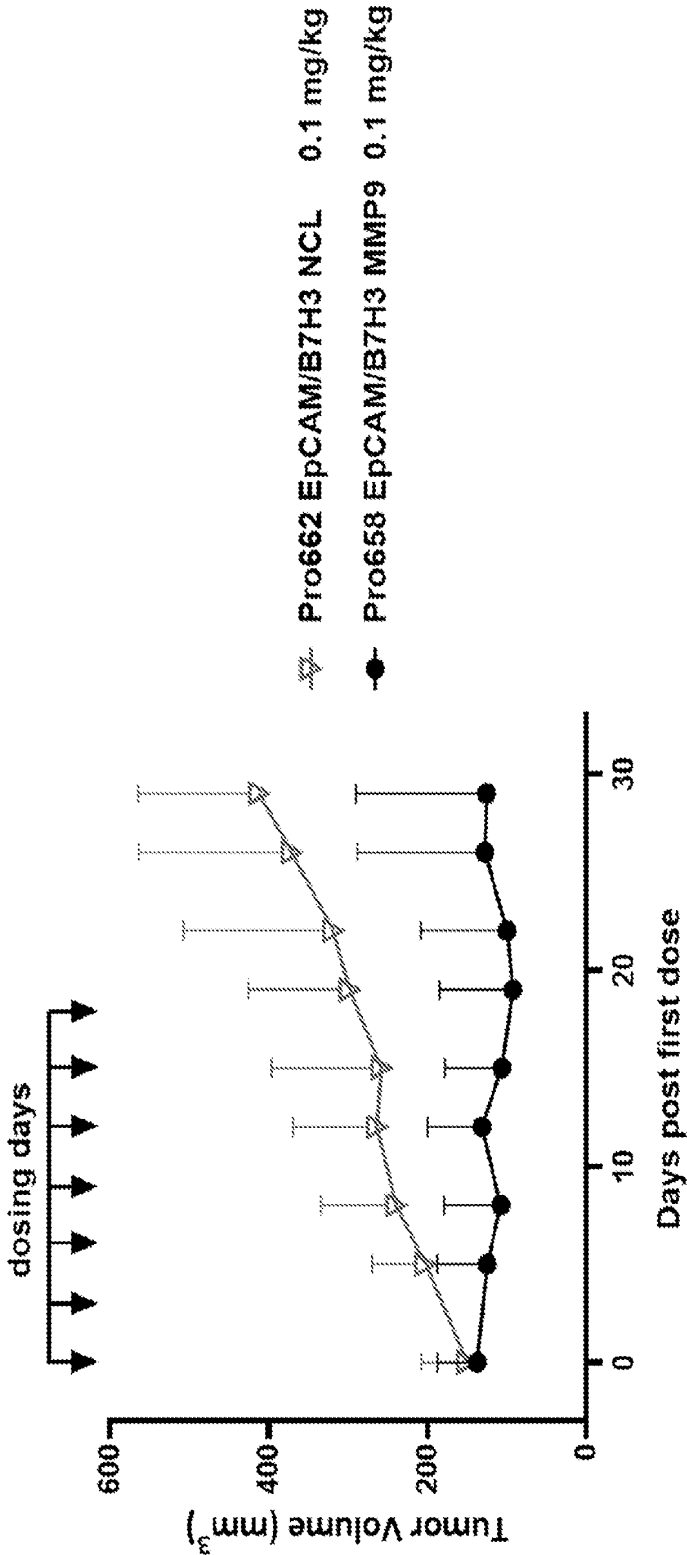


Figure 70

Figure 71

B7H3/EpCAM hetero-COBRAs**Pro751**

aB7H3 hF12 sdAb (S59Y) – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB665 sdAb – MMP9-15 - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLQESGGGLVQPGGSLRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTYYADSVKGR**
FTISRDN SKNTLYLQMNSLRAEDTAVYYCA**AGGVLAHHNYEYDY**WGQGLTVTVSS/**GGGSGGGG**/EVQ
LVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVKDRFT**
ISRDDSKNTAYLQMNNLKTEDTAVYYCVR**HANFGNSYISYWAY**WGQGLTVTVSS/**GGGSGGGG**/QTV
VTQEPSLTVSPGGTVTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLLGGK
AALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLLESGGGLVQPGGSLRLS
CAAS**GRTFSDYDMG**WFRQGP GKERE FVA**AIWSGGHTNYADSVKGR**RFTISRDN SKNTLYLQMNSLRA
EDTAVYYCA**DLRFTGGDTTTTPETYDY**WGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSP
GGTVTLT**GSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGV
QPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAAS**GFTF**
NKYAMNWVRQAPGKGLEWVAR**IR**SKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA
VYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLS**CAASG**
FTFSKFGMSWVRQAPGKGLEWV**SISGSGRDTLYAESVKGR**RFTISRDN AKTTLYLQMNSLRPEDTAVYY
CT**IGGSLSV**SSQGLTVTVSS/HHHHHH (SEQ ID NO:487)

Pro752

acEpCAM hVIB665 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) - haB7H3 F12 sdAb (S59Y) – MMP9-15 - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLESGGGLVQPGGSLRLS**CAASGRTFSDYDMG**WFRQGP GKERE FVA**AIWSGGHTNYADSVKG**
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCA**DLRFTGGDTTTTPETYDY**WGQGLTVTVSS/**GGGSGGGG**
/EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNKYAIN**WVRQAPGKGLEWVAR**IRSKYNNYATYYADQVK**
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGG**/
QTVVTQEPSLTVSPGGTVTLT**CASSTGAVTSGNYPN**WVQKPGQAPRGLIG**GTKFLVP**GTPARFSGSLL
GGKAALTLSGVQPEDEAEYYC**TLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/QVQLQESGGGLVQPGGS
LRLSCEAS**PRTFSTYSMA**WFRQAPGKERSFVA**AINWSGGNTYYADSVKGR**RFTISRDN SKNTLYLQMNS
LRAEDTAVYYCA**AGGVLAHHNYEYDY**WGQGLTVTVSS/**SGGPGPAGMKGLPGS**/QTVVTQEPSLTVSP
GGTVTLT**GSSTGAVTSGNYPN**WVQKPGQAPRGLIG**DYKDDDDK**GTPARFSGSLLGGKAALTLSGV
QPEDEAEYYC**VLWYSNRWV**FGGGTKLTVL/**GGGSGGGG**/EVQLVESGGGLVQPGGSLKLSCAAS**GFTF**
NKYAMNWVRQAPGKGLEWVAR**IR**SKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTA
VYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/**GGGSGGGG**/EVQLVESGGGLVQPGNSLRLS**CAASG**
FTFSKFGMSWVRQAPGKGLEWV**SISGSGRDTLYAESVKGR**RFTISRDN AKTTLYLQMNSLRPEDTAVYY
CT**IGGSLSV**SSQGLTVTVSS/HHHHHH (SEQ ID NO:488)

Figure 72

Trop2/hEpCAM Hetero-COBRAsPro824

acEpCAM hVIB665 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aTrop2 hVIB557 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLS CAAS GRTFSDYDMGWFRQPGKERE FVA AISWSGGHTNYADSVKG
RFTISRDN SKNTLYLQ MNSLRAEDTAVYYCAA DLRFTGGDTTTPETYDYWGQGLTVTVSS/GGGSGGGG
/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAINWVRQAPGKGLEWVAR IRISKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMN NLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
QTVVTQEP SLTVSPGGTVTLTC ASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGT PARFSGSLL
GGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES GGGGLVQP GGSRLS
CAAS GRTFSSQSMGWFRQAPGKERE FVS AISWTGANPTYADSVKGRRFTISRDN SKNTLYLQ MNSL
RAEDTAVYYCAA DTSGGSYYYERATAETSYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEP
SLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIG DYKDDDDKGT PARFSGSLLGGKAAL
TLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQP GGSRLS CAAS
SGFTFNKYAMNWVRQAPGKGLEWVAR IRISKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQ MNSL
KTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQP GNSRLSC
AAS GFTFSKFGMSWVRQAPGKGLEWVSS SISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQ MNSLRPEDT
AVYYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:489)

Pro826

aTrop2 hVIB557 sdAb sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – acEpCAM hVIB665
sdAb

– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES GGGGLVQP GGSRLS CAAS GRTFSSQSMGWFRQAPGKERE FVS AISWTGANPTYADSVKGR
FTISRDN SKNTLYLQ MNSLRAEDTAVYYCAA DTSGGSYYYERATAETSYDYWGQGLTVTVSS/GGGSGG
GS/EVQLVESGGGLVQP GGSRLS CAAS GFTFNKYAINWVRQAPGKGLEWVAR IRISKYNNYATYYADQ
VKDRRFTISRDDSKNTAYLQ MNSLRAEDTAVYYCVR HANFGNSYISYWAYWGQGLTVTVSS/GGGSGG
GS/QTVVTQEP SLTVSPGGTVTLTC ASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGT PARF
SLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES GGGGLVQP
GGSRLS CAAS GRTFSDYDMGWFRQPGKERE FVA AISWSGGHTNYADSVKGRRFTISRDN SKNTLYLQ
MNSLRAEDTAVYYCAA DLRFTGGDTTTPETYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQ
EP SLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIG DYKDDDDKGT PARFSGSLLGGKA
ALTLSGVQPEDEAEYYC VLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQP GGSRLS
CAAS GFTFNKYAMNWVRQAPGKGLEWVAR IRISKYDYKDDDDKADSVKDRRFTISRDDSKNTAYLQ MNSL
KTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQP GNSLR
LSCAAS GFTFSKFGMSWVRQAPGKGLEWVSS SISGSGRDTLYAESVKGRRFTISRDN AKTTLYLQ MNSLRP
EDTAVYYCTI GGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:490)

Figure 73

Humanized Her2 COBRAsPro1109

aHER2 hVIB1159 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aHER2 hVIB1159 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES^{GGGLVQPGGSLRL}SCATSSGRTFSSLAMGWFRQAPGKERELVAGISWSGSTTYYADSVKGRF
AISRDNSKNTLYLQMNSLRAEDTAVYYCAARTSSIIATIGREYDYWGQGLTVTVSS/GGGSGGGG/EVQLV
ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS
RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVT
QEPSTLVSPGGTVTLTCASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKA
ALTSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES^{GGGLVQPGGSLRL}SC
ATSSGRTFSSLAMGWFRQAPGKERELVAGISWSGSTTYYADSVKGRFAISRDNSKNTLYLQMNSLRAED
TAVYYCAARTSSIIATIGREYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTLVSPGGTVTL
TCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALTSGVQPEDEA
EYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVES^{GGGLVQPGGSLKLS}CAASGFTFNKYAM
NWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR
HGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVES^{GGGLVQPGNSLR}LSCAASGFTFSKF
GMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGS
LSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:491)

Pro1111

aHER2 hVIB1162 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3VI (2B2) – aHER2 hVIB1162 sdAb
– MMP9-15 - aCD3Vli – NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLLES^{GGGLVQPGGSLRL}SCAASGRPFSGNAMGWFRQAPGKEREFVAAISWSGSDSTYYADSVKGR
FTISRDNKNTLYLQMNSLRAEDTAVYYCAARTSFYSRTYYTRPSDYNWGPGLTVTVSS/GGGSGGGG/
EVQLVES^{GGGLVQPGGSLKLS}CAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK
DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/
QTVVTQEPSTLVSPGGTVTLTCASSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLVPGTPARFSGSLL
GGKAALTSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLES^{GGGLVQPGGSL}
RLSCAASGRPFSGNAMGWFRQAPGKEREFVAAISWSGSDSTYYADSVKGRFTISRDNKNTLYLQMNSL
RAEDTAVYYCAARTSFYSRTYYTRPSDYNWGPGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTL
VSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGDYKDDDDKGTTPARFSGSLLGGKAALT
SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVES^{GGGLVQPGGSLKLS}CAASGF
TFNKYAMNWVRQAPGKGLEWVARIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDT
AVYYCVRHGNFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVES^{GGGLVQPGNSLR}LSCAAS
GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY
YCTIGGSLSVSSQGLTVTVSS/HHHHHH (SEQ ID NO:492)

Figure 74

Pro1117

aHER2 hVIB1139 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aHER2 hVIB1139 sdAb
 – MMP9-15 - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) - His6

QVQLVESGGGVVRPGGSLRLSCAASGFTFDDYAMSWIRQAPGKEMEWVSGINWSGTHTRYADSVKG
 RFTISRDNAKNSLYLQMNSLRAEDTALYYCARGGFAADSRSTRRGQGLTVTVSS/GGGSGGGG/EVQLVESG
 GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRRFTISRDD
 SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVTQEP
 SLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT
 SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLVESGGGVVRPGGSLRLSCAASG
FTFDDYAMSWIRQAPGKEMEWVSGINWSGTHTRYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAL
 YYCARGGFAADSRSTRRGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCGSSTG
AVTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLW
YSNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP
 GKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI
 SYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQA
 PGKLEWVSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTV
 TVSS/HHHHHH (SEQ ID NO:493)

Pro1118

aHER2 hVIB1156 sdAb – aCD3 Vh (2B2) – NCL-8 – aCD3Vl (2B2) – aHER2 hVIB1156 sdAb
 – MMP9-15 - aCD3Vli –NCL-8 - aCD3Vhi – aHSA (10GE) – His6

QVQLLESGGGLVQPGGSLRLSCAASRNIGSNYAVGWFRQAPGKEREPVAALRWGTSGIIGYDDSLRGRRF
 TISKDNSKNTLYLQMNSLKPEDTAVYYCAARRILDRSSYDYWGQGLTVTVSS/GGGSGGGG/EVQLVESG
 GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARRIRSKYNNYATYYADQVKDRRFTISRDD
 SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGLTVTVSS/GGGSGGGG/QTVVTQEP
 SLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT
 SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL/GGGSGGGG/QVQLLESGGGLVQPGGSLRLSCAASR
NIGSNYAVGWFRQAPGKEREPVAALRWGTSGIIGYDDSLRGRRFTISKDNSKNTLYLQMNSLKPEDTAVYY
 CAARRILDRSSYDYWGQGLTVTVSS/SGGPGPAGMKGLPGS/QTVVTQEPSTVSPGGTVTLTCGSSTGA
VTSGNYPNWVQQKPGQAPRGLIGDYKDDDDKGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLWY
SNRWVFGGGTKLTVL/GGGSGGGG/EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP
 GKGLEWVARRIRSKYDYKDDDDKADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI
 SYWAYWGQGLTVTVSS/GGGSGGGG/EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQA
 PGKLEWVSSISGSGRDTLYAESVKGRRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGLTV
 TVSS/HHHHHH (SEQ ID NO:494)

Figure 75

Humanized aEpCAM sdAb**h664**

QVQLLES GGGVLVQPGGSLRLSCAAS GRTL DNYDMGWFRQGP GKERE FVA AI SWSGGSTDYAYS VKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAA DLRFTGGDTMTPE TYDYWGQGLTVTVSS (SEQ ID
NO:495)

sdCDR1 GRTL DNYDMG (SEQ ID NO:496)

sdCDR2 AI SWSGGSTDYAYS VKG (SEQ ID NO:497)

sdCDR3 DLRFTGGDTMTPE TYDY (SEQ ID NO:498)

Humanized aHer2 sdAbs**h1139**

QVQLVES GGGVVRPGGSLRLSCAAS GFTFDDYAMSWIRQAPGKEME WVSG GINWSGTHTRYADSVKG
RFTISRDNAKNSLYLQMNSLRAEDTALYYCAR GFAADSRSTRQGGLTVTVSS (SEQ ID NO:499)

sdCDR1 GFTFDDYAMS (SEQ ID NO:500)

sdCDR2 GINWSGTHTRYADSVKG (SEQ ID NO:501)

sdCDR3 GFAADSRST (SEQ ID NO:502)

h1156

QVQLLES GGGVLVQPGGSLRLSCAAS RNIGSNYAVGWFRQAPGKEREPVA ALRW TGSIIGYDDSLRGRF
TISKDNSKNTLYLQMNSLPEDTAVYYCAA RILDRSSYDYWGQGLTVTVSS (SEQ ID NO:503)

sdCDR1 RNIGSNYAVG (SEQ ID NO:504)

sdCDR2 ALRW TGSIIGYDDSLRG (SEQ ID NO:505)

sdCDR3 RILDRSSYDY (SEQ ID NO:506)

h1159

QVQLLES GGGVLVQPGGSLRLSCATS GRTFSSLAMGWFRQAPGKERELVA GISWSGSTTYADSVKGRF
AISRDNSKNTLYLQMNSLRAEDTAVYYCAART SSIATIGREYDYWGQGLTVTVSS (SEQ ID NO:507)

sdCDR1 GRTFSSLAMG (SEQ ID NO:508)

sdCDR2 GISWSGSTTYADSVKG (SEQ ID NO:509)

sdCDR3 RTSSIATIGREYDY (SEQ ID NO:510)

h1162

QVQLLES GGGVLVQPGGSLRLSCAAS GRPFSGNAMGWFRQAPGKEREFVA AI SWSGDSTYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDTAVYYCAA TRSFYSRTYYTRPSDYNYWGPGTLTVTVSS (SEQ ID
NO:511)

sdCDR1 GRPFSGNAMG (SEQ ID NO:512)

sdCDR2 AI SWSGDSTYYADSVKG (SEQ ID NO:513)

sdCDR3 TRSFYSRTYYTRPSDYN (SEQ ID NO:514)