

Figura 36H

>XENP39968 CD20-C H1L1 Fab-CD20-C H1L1 Fab-IgG1 pl(-) Isostérico A /PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Cadena 1 - CD20-C_H1_IgG1_pl(-)_Isostérico_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 436)

EVQLVESGGGLVQPGRSRLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADS VKGRFTISRDN
KKSLEYQMNSLRAEDTALYYCAKDIQYGNYYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKS
CDKTHCTCPCPAPFPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEE
YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVS
GFYPDSIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSP
GK

Cadena 2 - CD20-C_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del (G4S)3_1A7[CD28]_H1.14_scFv(GKPGS)4 (SEQ ID NO: 512)

EVQLVESGGGLVQPGRSRLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADS VKGRFTISRDN
KKSLEYQMNSLRAEDTALYYCAKDIQYGNYYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHCTCPCPAPFPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSP
GGGGSGGGSGGGGS/ EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSDST
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKSGEGLRQVGFYWGQGTITVTVSS/GKPGSGKPGSG
KPGSGKPGS/DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS
GSGTDFTLTISSLPEDFATYYCQQSYSTPPTFGQGTKLEIK

Cadena 3 - CD20-C_L1 (SEQ ID NO: 366)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAITGIPARFSGSGSGTDFTLTI
SSLEPEDFAVYYCQQRSNWEIFTGQGTLEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRRGEC

>XENP39969 CD20-C H1L1 Fab-CD20-C H1L1 Fab-IgG1 pl(-) Isostérico A /PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q/K447del (G4S)3 1A7[CD28] H1 L1.71 scFv(GKPGS)4

Cadena 1 - CD20-C_H1_IgG1_pl(-)_Isostérico_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 436)

EVQLVESGGGLVQPGRSRLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADS VKGRFTISRDN
KKSLEYQMNSLRAEDTALYYCAKDIQYGNYYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKS
CDKTHCTCPCPAPFPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEE
YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVS
GFYPDSIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSP
GK

Cadena 2 - CD20-

C_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del (G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 513)

EVQLVESGGGLVQPGRSRLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADS VKGRFTISRDN
KKSLEYQMNSLRAEDTALYYCAKDIQYGNYYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHCTCPCPAPFPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPDSIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHEALHNHYTQKSLSLSP
GGGGSGGGSGGGGS/ EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSDST
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKSGEGLRQVGFYWGQGTITVTVSS/GKPGSGKPGSG
KPGSGKPGS/DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGS
GSGTDFTLTISSLPEDFATYYCQQVYSTPPTFGQGTKLEIK

Cadena 3 - CD20-C_L1 (SEQ ID NO: 366)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAITGIPARFSGSGSGTDFTLTI
SSLEPEDFAVYYCQQRSNWEIFTGQGTLEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRRGEC