

Figura 36I

>XENP39970 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] H1.1 L1.71 scFv(GKPGS)4

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

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADSVKGRFTISRDN
KKSLEYLQMNSLRAEDTALYYCAKDIQYGNYYYGMEVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKS
CDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEE
YNSTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVS
GFYPSPDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGVFSCSVMHEALHNHYTQKSLSLSP
GK

Cadena 2 - CD20-

C_H1_IgG1_PVA /S267K/S364K/E357Q/K447del (G4S)3 1A7[CD28] H1.1 L1.71 scFv(GKPGS)4 (SEQ ID NO: 514)

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADSVKGRFTISRDN
KKSLEYLQMNSLRAEDTALYYCAKDIQYGNYYYGMEVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP
GGGGSGGGSGGGGS /EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYMSWVRQAPGKGLEWVSTISGSGDST
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKSGEGLRQVGFYWGQGTITVTVSS /GKPGSGKPGSG
KPGSGKPGS /DIQMTQSPSSLSASVGRVITITCRASQSISSYLNWYQQKPKGAPKLLIYAASLQSGVPSRFSGS
SGSDFTLTITISLQPEDFATYYCQQVYSTPFTFGQGTKLEIK

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

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIT
SSLEPEDFAVYYCQQRSNWEIFFGQGTREIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYLSLSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP39971 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 L1.71 scFv(GKPGS)4

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

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADSVKGRFTISRDN
KKSLEYLQMNSLRAEDTALYYCAKDIQYGNYYYGMEVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKS
CDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEE
YNSTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVS
GFYPSPDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGVFSCSVMHEALHNHYTQKSLSLSP
GK

Cadena 2 - CD20-

C_H1_IgG1_PVA /S267K/S364K/E357Q/K447del (G4S)3 1A7[CD28] H1.14 L1.71 scFv(GKPGS)4 (SEQ ID NO: 515)

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSTISWNSGSIQYADSVKGRFTISRDN
KKSLEYLQMNSLRAEDTALYYCAKDIQYGNYYYGMEVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP
GGGGSGGGSGGGGS /EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYMSWVRQAPGKGLEWVSTISGSGDST
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKSGEGLRQVGFYWGQGTITVTVSS /GKPGSGKPGSG
KPGSGKPGS /DIQMTQSPSSLSASVGRVITITCRASQSISSYLNWYQQKPKGAPKLLIYAASLQSGVPSRFSGS
SGSDFTLTITISLQPEDFATYYCQQVYSTPFTFGQGTKLEIK

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

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIT
SSLEPEDFAVYYCQQRSNWEIFFGQGTREIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYLSLSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC