Figure 1A

Human CD28 sequence SEQ ID NO: 1

>sp|P10747|CD28_HUMAN T-cell-specific surface glycoprotein CD28 OS=Homo sapiens OX=9606 GN=CD28 PE=1 SV=1

MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQ
LQVYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPS
KPFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS

Human CD28, extracellular domain SEQ ID NO: 2

>sp|P10747|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNE
SVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP

Mouse CD28 sequence SEQ ID NO: 3

>sp|P31041|CD28_MOUSE T-cell-specific surface glycoprotein CD28 OS=Mus musculus OX=10090 GN=Cd28 PE=1 SV=2

MTLRLLFLALNFFSVQVTENKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNGNFTY
QPQFRSNAEFNCDGDFDNETVTFRLWNLHVNHTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHLCHTQSSPKL
FWALVVVAGVLFCYGLLVTVALCVIWTNSRRNRLLQSDYMNMTPRRPGLTRKPYQPYAPARDFAAYRP

Mouse CD28, extracellular domain SEQ ID NO: 4

>sp|P31041|20-150

NKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNGNFTYQPQFRSNAEFNCDGDFDNE
TVTFRLWNLHVNHTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHLCHTQSSPKL

Cynomolgus CD28 sequence SEQ ID NO: 5

>tr|Q0PDN3|Q0PDN3_MACFA CD28 OS=Macaca fascicularis OX=9541 GN=CD28 PE=2 SV=1

MLRLLLALNLLPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQ
LQVYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPS
KPFWALVVVGGVLACYSLLVTVAFCIFWMRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS

Cynomolgus CD28, extracellular domain SEQ ID NO: 6

>tr|Q0PDN3|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNE
SVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP

Cynomolgus CD28 sequence (predicted) SEQ ID NO: 7

>XP_015308533.1 PREDICTED: CD276 antigen isoform X1 [Macaca fascicularis]

MKLSSDHVFPLFRKLQWLPAAFRIQFTPVSPSAGAAFHHGEPSCQLPHSKMLHRRGSPGMGVHVGAALGALWFCL
TGALEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLL
AQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAE
VFWQDGQGAPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQ
VPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASL
RLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQ
GAPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEALWVTVGLSV
CLVALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKEDDGQELA

Figure 1B

Cynomolgus CD28, extracellular domain SEQ ID NO: 8

>XP_015308533.1|79-516

LEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQG
NASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFW
QDGQGAPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQVPE
DPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASLRLQ
RVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGAP
LTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEA

Figure 2

Human TROP2 sequence SEQ ID NO: 9

>sp|P09758|TACD2_HUMAN Tumor-associated calcium signal transducer 2 OS=Homo sapiens OX=9606 GN=TACSTD2 PE=1 SV=3
MARGPGLAPPPLRLPLLLLVLAAVTGHTAAQDNCTCPTNKMTVCSPDGPGGRCQCRALGSGMAVDCSTLTSKCLL
LKARMSAPKNARTLVRPSEHALVDNDGLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVR
THHILIDLRHRPTAGAFNHSDLDAELRRLFRERYRLHPKFVAAVHYEQPTIQIELRQNTSQKAAGDVDIGDAAYY
FERDIKGESLFQGRGGLDLRVRGEPLQVERTLIYYLDEIPPKFSMKRLTAGLIAVIVVVVVALVAGMAVLVITNR
RKSGKYKKVEIKELGELRKEPSL

Human TROP2 sequence, extracellular domain SEQ ID NO: 10

>sp|P09758|27-274
HTAAQDNCTCPTNKMTVCSPDGPGGRCQCRALGSGMAVDCSTLTSKCLLLKARMSAPKNARTLVRPSEHALVDND
GLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVRTHHILIDLRHRPTAGAFNHSDLDAEL
RRLFRERYRLHPKFVAAVHYEQPTIQIELRQNTSQKAAGDVDIGDAAYYFERDIKGESLFQGRGGLDLRVRGEPL
QVERTLIYYLDEIPPKFSMKRLT

Mouse TROP2 sequence SEQ ID NO: 11

>sp|Q8BGV3|TACD2_MOUSE Tumor-associated calcium signal transducer 2 OS=Mus musculus OX=10090 GN=Tacstd2 PE=1 SV=1
MARGLDLAPLLLLLLAMATRFCTAQSNCTCPTNKMTVCDTNGPGGVCQCRAMGSQVLVDCSTLTSKCLLLKARMS
ARKSGRSLVMPSEHAILDNDGLYDPECDDKGRFKARQCNQTSVCWCVNSVGVRRTDKGDQSLRCDEVVRTHHILI
ELRHRPTDRAFNHSDLDSELRRLFQERYKLHPSFLSAVHYEEPTIQIELRQNASQKGLRDVDIADAAYYFERDIK
GESLFMGRRGLDVQVRGEPLHVERTLIYYLDEKPPQFSMKRLTAGVIAVIAVVSVAVVAGVVVLVVTKRRKSGKY
KKVELKELGEMRSEPSL

Mouse TROP2 sequence, extracellular domain SEQ ID NO: 12

>sp|Q8BGV3|25-270
QSNCTCPTNKMTVCDTNGPGGVCQCRAMGSQVLVDCSTLTSKCLLLKARMSARKSGRSLVMPSEHAILDNDGLYD
PECDDKGRFKARQCNQTSVCWCVNSVGVRRTDKGDQSLRCDEVVRTHHILIELRHRPTDRAFNHSDLDSELRRLF
QERYKLHPSFLSAVHYEEPTIQIELRQNASQKGLRDVDIADAAYYFERDIKGESLFMGRRGLDVQVRGEPLHVER
TLIYYLDEKPPQFSMKRLTAG

Macaca fascicularis TROP2 sequence SEQ ID NO: 13

>XP_005543292.2 tumor-associated calcium signal transducer 2 [Macaca fascicularis]
MARGPGLAPPPLRLPLLLLLLAAVTGHTAAQDNCTCPTNKMTVCSPDGPGGRCQCRALGSGVAVDCSTLTSKCLL
LKARMSAPKNARTLVRPNEHALVDNDGLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVR
THHILIDLRHRPTASAFNHSDLDAELRRLFRERYRLHPKFVAAVHYEQPTIQIELRQNTSQKAAGDVDIGDAAYY
FERDVKGESLFQGRGGLDLRVRGEPLQVERTLIYYLDEIPPKFSMKRLTAGLIAVIVVVVVALVAGVAVLVISNR
RKSGKYKKVEIKELGELRKEPSL

Macaca fascicularis TROP2 sequence, extracellular domain (predicted) SEQ ID NO: 14

>XP_005543292.2|27-274
HTAAQDNCTCPTNKMTVCSPDGPGGRCQCRALGSGVAVDCSTLTSKCLLLKARMSAPKNARTLVRPNEHALVDND
GLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVRTHHILIDLRHRPTASAFNHSDLDAEL
RRLFRERYRLHPKFVAAVHYEQPTIQIELRQNTSQKAAGDVDIGDAAYYFERDVKGESLFQGRGGLDLRVRGEPL
QVERTLIYYLDEIPPKFSMKRLT

Figure 3A

Monomer 1	Monomer 2
F405A	T394F
S364D	Y349K
S364E	L368K
S364E	Y349K
S364F	K370G
S364H	Y349K
S364H	Y349T
S364Y	K370G
T411K	K370E
V397S/F405A	T394F
K370R/T411K	K370E/T411E
L351E/S364D	Y349K/L351K
L351E/S364E	Y349K/L351K
L351E/T366D	L351K/T366K
P395T/V397S/F405A	T394F
S364D/K370G	S364Y/K370R
S364D/T394F	Y349K/F405A
S364E/F405A	Y349K/T394F
S364E/F405S	Y349K/T394Y
S364E/T411E	Y349K/D401K
S364H/D401K	Y349T/T411E
S364H/F405A	Y349T/T394F
S364H/T394F	Y349T/F405A
Y349C/S364E	Y349K/S354C
L351E/S364D/F405A	Y349K/L351K/T394F
L351K/S364H/D401K	Y349T/L351E/T411E
S364E/T411E/F405A	Y349K/T394F/D401K
S364H/D401K/F405A	Y349T/T394F/T411E
S364H/F405A/T411E	Y349T/T394F/D401K

Figure 3B

Monomer 1	Monomer 2
K370E/T411D	T411K
L368E/K409E	L368K
Y349T/T394F/S354C	S364H/F405A/Y349C
T411E	D401K
T411E	D401R/T411R
Q347E/K360E	Q347R
L368E	S364K
L368E/K370S	S364K
L368E/K370T	S364K
L368E/D401R	S364K
L368E/D401N	S364K
L368E	E357S/S364K
L368E	S364K/K409E
L368E	S364K/K409V
L368D	S364K
L368D/K370S	S364K
L368D/K370S	S364K/E357L
L368D/K370S	S364K/E357Q
T411E/K360E/Q362E	D401K
K370S	S364K
L368E/K370S	S364K/E357Q
K370S	S364K/E357Q
T411E/K360D	D401K
T411E/K360E	D401K
T411E/Q362E	D401K
T411E/N390D	D401K
T411E	D401K/Q347K
T411E	D401K/Q347R
T411E/K360D/Q362E	D401K

Figure 3C

Monomer 1	Monomer 2
T411E/K360E/N390D	D401K
T411E/Q362E/N390D	D401K
T411E/Q347R	D401K/K360D
T411E/Q347R	D401K/K360E
T411E/K360	D401K/Q347K
T411E/K360D	D401K/Q347R
T411E/K360E	D401K/Q347K
T411E/K360E	D401K/Q347R
T411E/S364K	D401K/K370S
T411E/K370S	D401K/S364K
Q347E	E357Q
Q347E	E357Q/Q362K
K360D/Q362E	Q347R
K360D/Q362E	D401K
K360D/Q362E	Q347R/D401K
K360E/Q362E	Q347R
K360E/Q362E	D401K
K360E/Q362E	Q347R/D401K
Q362E/N390D	D401K
Q347E/K360D	D401N
K360D	Q347R/N390K
K360D	N390K/D401N
K360E	Y349H
K370S/Q347E	S364K
K370S/E357L	S364K
K370S/E357Q	S364K
K370S/Q347E/E357L	S364K
K370S/Q347E/E357Q	S364K

Figure 3D

Monomer 1	Monomer 2
L368D/K370S/Q347E	S364K
L368D/K370S/E357L	S364K
L368D/K370S/E357Q	S364K
L368D/K370S/Q347E/E357L	S364K
L368D/K370S/Q347E/E357Q	S364K
L368E/K370S/Q347E	S364K
L368E/K370S/E357L	S364K
L368E/K370S/E357Q	S364K
L368E/K370S/Q347E/E357L	S364K
L368E/K370S/Q347E/E357Q	S364K
L368D/K370T/Q347E	S364K
L368D/K370T/E357L	S364K
L368D/K370T/E357Q	S364K
L368D/K370T/Q347E/E357L	S364K
L368D/K370T/Q347E/E357Q	S364K
L368E/K370T/Q347E	S364K
L368E/K370T/E357L	S364K
L368E/K370T/E357Q	S364K
L368E/K370T/Q347E/E357L	S364K
L368E/K370T/Q347E/E357Q	S364K
T411E/Q362E	D401K/T411K
T411E/N390D	D401K/T411K
T411E/Q362E	D401R/T411R
T411E/N390D	D401R/T411R
Y407T	T366Y
F405A	T394W
T366Y/F405A	T394W/Y407T
Y407A	T366W
T366S/L368A/Y407V	T366W
T366S/L368A/Y407V/Y349C	T366W/S354C

Figure 3E

Monomer 1	**Monomer 2**
T366S/L368A/Y407V/S354C	T366W/Y349C
S354C	Y349C
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	P217R/P228R/N276K
K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	N276K
N384S/K392N/V397M/Q419E	N276K
D221E/P228E/L368E	D221R/P228R/K409R
C220E/P228E/L368E	C220R/E224R/P228R/K409R
F405L	K409R
T366I/K392M/T394W	F405A/Y407V
T366V/K409F	L351Y/Y407A
T366A/K392E/K409F/T411E	D399R/S400R/Y407A
L351K	L351E
K274Q/R355Q/Q419E/K447_	P217R/P228R/N276K
K274Q/R355Q/Q419E/K447_	N276K
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/N276K
I199T/N203D/K274Q/R355Q/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K274Q/R355Q/Q419E/K447_	Q196K/I199T/N276K

Figure 3F

Monomer 1	Monomer 2
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	
N208D/Q295E/N384D/Q418E/N421D	
N208D/Q295E/Q418E/N421D	
Q196K/I199T/P217R/P228R/N276K	
Q196K/I199T/N276K	
K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	
Q295E/N384D/Q418E/N421D	
Q295E/Q418E/N421D	
P217R/P228R/N276K	
N276K	
E269Q/E272Q/E283Q/E357Q	
E269Q/E272Q/E283Q	
E269Q/E272Q	
E269Q/E283Q	
E272Q/E283Q	
E269Q	

Figure 4

Variant constant region	Substitutions
pI-ISO(-)	I199T/N203D/K274Q/R355Q/N384S/K392N/N397M/Q418E/K447_
pI_ISO(-)-Fc only	K274Q/R355Q/N384S/K392N/V397M/Q418E/K447_
pI_(-)_isosteric_A	N208D/Q295E/N384D/Q418E/N421D
pI_(-)_isosteric A-Fc only	Q295E/N384D/Q418E/N421D
pI_(-)_isosteric_B	N208D/Q295E/Q418E/N421D
pI_(-)_isosteric_B-Fc only	Q295E/Q418E/N421D
pI_ISO(+RR)	Q196K/I199T/P217R/P228R/N276K
pI_ISO(+RR)-Fc only	P217R/P228R/N276K
pI_ISO(+)	Q196K/I199T/N276K
pI_ISO(+)-Fc only	N276K
pI_(+)_isosteric_A	E269Q/E272Q/E283Q/E357Q
pI_(+)_isosteric_B	E269Q/E272Q/E283Q
pI_(+)_isosteric_E269Q/E272Q	E269Q/E272Q
pI_(+)_isosteric_E269Q/E283Q	E269Q/E283Q
pI_(+)_isosteric_E272Q/E283Q	E272Q/E283Q
pI_(+)_isosteric_E269Q	E269Q

Figure 5

Ablation Variants

G236R
S239G
S239K
S239Q
S239R
V266D
S267K
S267R
H268K
E269R
T299R
T299K
K322A
A327G
A327L
A327N
A327Q
L328E
L328R
P329A
P329H
P329K
A330L
A330S/P331S
I332K
I332R
V266D/A327Q
V266D/P329K
S267R/A327Q
S267R/P329K
G236R/L328R
E233P/L234V/L235A/G236_/S239K
E233P/L234V/L235A/G236_/S267K
E233P/L234V/L235A/G236_/S239K/A327G
E233P/L234V/L235A/G236_/S267K/A327G
E233P/L234V/L235A/G236_
S239K/S267K
S267K/P329K
L234A/L235A/D265S

Figure 6A

Positive Charged scFv Linkers

Name	Sequence	Length	Charge	
Gly-Ser 15	GGGGSGGGGSGGGGS	15	0	SEQ ID NO: 15
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	SEQ ID NO: 16
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	SEQ ID NO: 17
+B	GKGGSGKGGSGKGGS	15	+3	SEQ ID NO: 18
+C	GGKGSGGKGSGGKGS	15	+3	SEQ ID NO: 19
+D	GGGKSGGGKSGGGKS	15	+3	SEQ ID NO: 20
+E	GKGKSGKGKSGKGKS	15	+6	SEQ ID NO: 21
+F	GGGKSGGKGSGKGGS	15	+3	SEQ ID NO: 22
+G	GKPGSGKPGSGKPGS	15	+3	SEQ ID NO: 23
+H	/GKPGSGKPGSGKPGSGKPGS/	20	+4	SEQ ID NO: 24
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	SEQ ID NO: 25

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	
Gly-Ser 20	GGGGSGGGGSGGGGSGGGGS	20	0	SEQ ID NO: 26
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	SEQ ID NO: 27
-B	GEGGSGEGGSGEGGS	15	-3	SEQ ID NO: 28
-C	GGEGSGGEGSGGEGS	15	-3	SEQ ID NO: 29
-D	GGGESGGGESGGGES	15	-3	SEQ ID NO: 30
-E	GEGESGEGESGEGES	15	-6	SEQ ID NO: 31
-F	GGGESGGEGSGEGGS	15	-3	SEQ ID NO: 32
-G	GEGESGEGESGEGESGEGES	20	-8	SEQ ID NO: 33

Figure 6B

Additional scFv Linkers

GGGGSGGGGSGGGGS	SEQ ID NO: 15
GGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 26
GSTSGSGKPGSGEGSTKG	SEQ ID NO: 16
PRGASKSGSASQTGSAPGS	SEQ ID NO: 34
GTAAAGAGAAGGAAAGAAG	SEQ ID NO: 35
GTSGSSGSGSGGSGSGGGG	SEQ ID NO: 36
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 24

Figure 7

Useful domain linkers

Name	Sequence	SEQ ID NO:
$(GGGGS)_1$ or GGGGS	GGGGS	SEQ ID NO: 37
$(GGGGS)_2$	GGGGSGGGGS	SEQ ID NO: 38
$(GGGGS)_3$	GGGGSGGGGSGGGGS	SEQ ID NO: 15
$(GGGGS)_4$	GGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 26
$(GGGGS)_5$	GGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 39
$(GGGGS)_6$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 40
$(GGGGS)_7$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 41
$(GGGGA)_1$ or GGGGA	GGGGA	SEQ ID NO: 42
$(GGGGA)_2$	GGGGAGGGGA	SEQ ID NO: 43
$(GGGGA)_3$	GGGGAGGGGAGGGGA	SEQ ID NO: 44
$(GGGGA)_4$	GGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 45
$(GGGGA)_5$	GGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 46
$(GGGGA)_6$	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 47
$(GGGGA)_7$	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 48
30AA-linker	DPALVHQRPAPPGGGGSGGGGSGGGGSGGG	SEQ ID NO: 49
$(GKPGS)_1$ or GKPGS	GKPGS	SEQ ID NO: 50
$(GKPGS)_5$	/GKPGSGKPGSGKPGSGKPGS/GKPGS	SEQ ID NO: 51
$(GKPGS)_6$	/GKPGSGKPGSGKPGSGKPGS/GKPGSGKPGS	SEQ ID NO: 52
$(GGGES)_1$ or GGGES	GGGES	SEQ ID NO: 53
“full hinge”	EPKSCDKTHTCPPCP	SEQ ID NO: 54
“lower half hinge”	KTHTCPPCP	SEQ ID NO: 55
“full hinge C220S variant”	EPKSSDKTHTCPPCP	SEQ ID NO: 56
“flex lower half hinge”	GGGGSGGGGSKTHTCPPCP	SEQ ID NO: 57
“charged lower half hinge1”	GKPGSGKPGSKTHTCPPCP	SEQ ID NO: 58
“charged lower half hinge2”	GKPGSKTHTCPPCP	SEQ ID NO: 59
“upper half hinge”	EPKSC	SEQ ID NO: 60
“flex upper half hinge”	EPKSCGGGGSGGGGS	SEQ ID NO: 61
“charged upper half hinge1”	EPKSCGKPGSGKPGS	SEQ ID NO: 62
“charged upper half hinge2”	EPKSCGKPGS	SEQ ID NO: 63

Figure 8

Monomer 1 (scFv-Fc)	**Monomer 2 (HC)**
Heterodimer skew variants S364K/E357Q	Heterodimer skew variants L368D/K370S
	Isosteric pI variant N208D/Q295E/N384D/Q418E/N421D
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S for FcRn	±M428L/N434S for FcRn

Figure 9

XENP	Heterodimer-skew variant, Chain 1	Heterodimer-skew variant, Chain 2	Heterodimer Yield (%)	CH3 Tm (°C)
12757	none	none	52.7	83.1
12758	L368D/K370S	S364K	94.4	76.6
12759	L368D/K370S	S364K/E357L	90.2	77.2
12760	L368D/K370S	S364K/E357Q	95.2	77.5
12761	T411E/K360E/Q362E	D401K	85.6	80.6
12496	L368E/K370S	S364K	91.5	n.d.
12511	K370S	S364K	59.9	n.d.
12840	L368E/K370S	S364K/E357Q	59.5	n.d.
12841	K370S	S364K/E357Q	90.4	n.d.
12894	L368E/K370S	S364K	41.0	n.d.
12895	K370S	S364K	49.3	n.d.
12896	L368E/K370S	S364K/E357Q	73.9	n.d.
12901	K370S	S364K/E357Q	87.9	n.d.

Figure 10A

Heterodimeric Fc Backbone 1

>Heterodimeric Fc Backbone 1 monomer 1 (-) (SEQ ID NO: 64)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 1 monomer 2 (+) (SEQ ID NO: 65)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 2

>Heterodimeric Fc Backbone 2 monomer 1 (-) (SEQ ID NO: 66)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone monomer 2 (+) (SEQ ID NO: 67)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 3

>Heterodimeric Fc Backbone 3 monomer 1 (-) (SEQ ID NO: 68)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 3 monomer 2 (+) (SEQ ID NO: 69)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 4

>Heterodimeric Fc Backbone 4 monomer 1 (-) (SEQ ID NO: 70)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLEVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 4 monomer 2 (+) (SEQ ID NO: 71)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSKGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 10B

Heterodimeric Fc Backbone 5

>Heterodimeric Fc Backbone 5 monomer 1 (-) (SEQ ID NO: 72)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 5 monomer 2 (+) (SEQ ID NO: 73)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 6

>Heterodimeric Fc Backbone 6 monomer 1 (-) (SEQ ID NO: 74)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 6 monomer 2 (+) (SEQ ID NO: 75)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 7

>Heterodimeric Fc Backbone 7 monomer 1 (-) (SEQ ID NO: 76)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 7 monomer 2 (+) (SEQ ID NO: 77)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 8

>Heterodimeric Fc Backbone 8 monomer 1 (-) (SEQ ID NO: 78)
APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWEEGDVFSCSVMHEALHNHYTQKSLSLSLGK

>Heterodimeric Fc Backbone 8 monomer 2 (+) (SEQ ID NO: 79)
APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVKLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Figure 10C

Heterodimeric Fc Backbone 9

>Heterodimeric Fc Backbone 9 monomer 1 (-) (SEQ ID NO: 80)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 9 monomer 2 (+) (SEQ ID NO: 81)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 10

>Heterodimeric Fc Backbone 10 monomer 1 (-) (SEQ ID NO: 82)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 10 monomer 2 (+) (SEQ ID NO: 83)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 11

>Heterodimeric Fc Backbone 11 monomer 1 (-) (SEQ ID NO: 84)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 11 monomer 2 (+) (SEQ ID NO: 85)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Heterodimeric Fc Backbone 12

>Heterodimeric Fc Backbone 12 monomer 1 (-) (SEQ ID NO: 86)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 12 monomer 2 (+) (SEQ ID NO: 87)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 10D

Heterodimeric Fc Backbone 13

>Heterodimeric Fc Backbone 13 monomer 1 (SEQ ID NO: 88)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 13 monomer 2 (SEQ ID NO: 89)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Heterodimeric Fc Backbone 14

>Heterodimeric Fc Backbone 14 monomer 1 (SEQ ID NO: 90)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHAHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 14 monomer 2 (SEQ ID NO: 91)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAHYTQKSLSLSPGK

Heterodimeric Fc Backbone 15

>Heterodimeric Fc Backbone 15 monomer 1 (SEQ ID NO: 92)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHAHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 15 monomer 2 (SEQ ID NO: 93)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAHYTQKSLSLSPGK

Figure 11

2 + 1 mAb-scFv Heterodimeric Fc Backbone

>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 1 (SEQ ID NO: 94)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 2 (SEQ ID NO: 95)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Figure 12

IgG1 CH1(+) (SEQ ID NO: 96)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKV

IgG1 CH1(-) (SEQ ID NO: 97)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKV

IgG2 CH1(+) (SEQ ID NO: 98)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTV

IgG2 CH1(-) (SEQ ID NO: 99)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTV

IgG4 CH1(+) (SEQ ID NO: 100)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSNTKVDKRV

IgG4 CH1(-) (SEQ ID NO: 101)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRV

Figure 13

IgG1 hinge (SEQ ID NO: 102)
EPKSCDKTHTCPPCP

IgG2 hinge (SEQ ID NO: 103)
ERKCCVECPPCP

IgG4 hinge (SEQ ID NO: 104)
ESKYGPPCPSCP

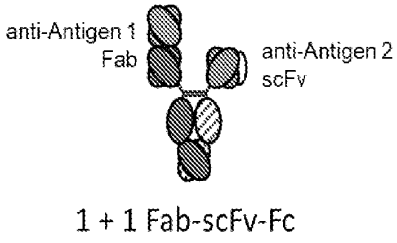
Figure 14

Light Chain Constant Domain – Kappa (SEQ ID NO: 105)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Light Chain Constant Domain – Lambda (SEQ ID NO: 106)
GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

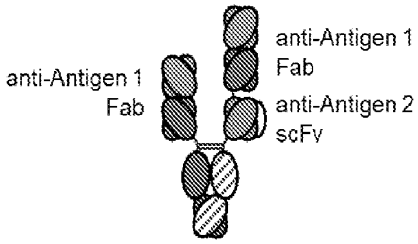
Figures 15A-15F

Figure 15A



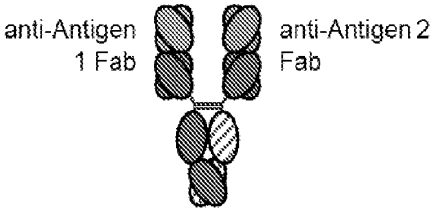
1 + 1 Fab-scFv-Fc

Figure 15B



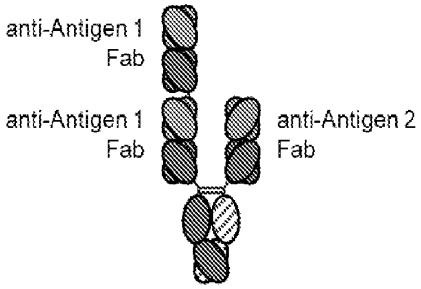
2 + 1 Fab_2-scFv-Fc

Figure 15C



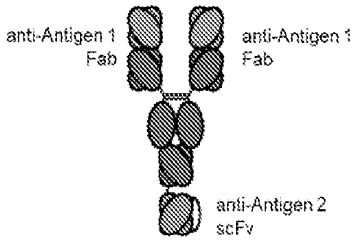
1 + 1 Common Light Chain

Figure 15D



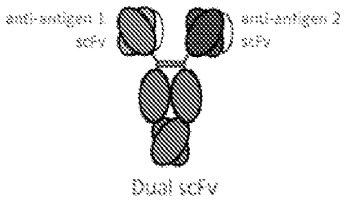
2 + 1 Common Light Chain

Figure 15E



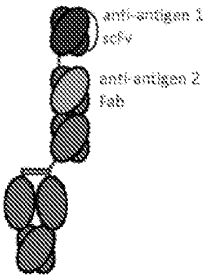
2+1 mAb-scFv

Figure 15F



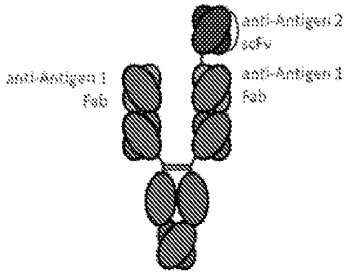
Figures 15G-15L

Figure 15G



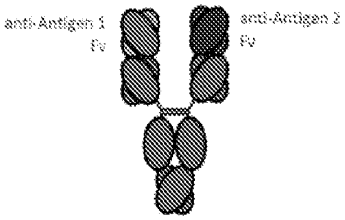
One-arm scFv-mAb

Figure 15H



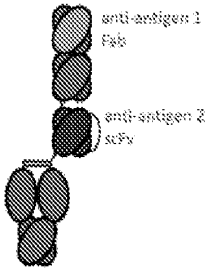
scFv-mAb

Figure 15I



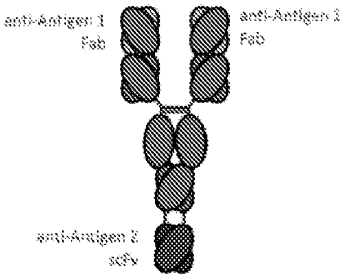
Bispecific mAb

Figure 15J



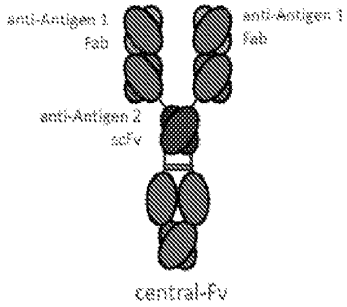
One-arm central-scFv

Figure 15K



mAb-Fv

Figure 15L



central-Fv

Figures 15M-15N

Figure 15M

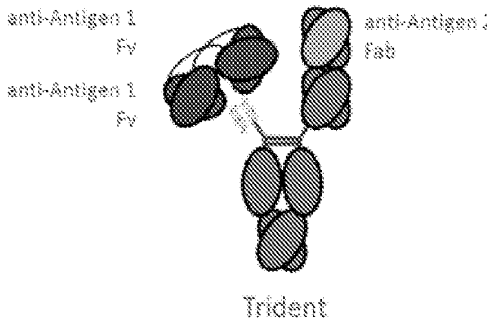


Figure 15N

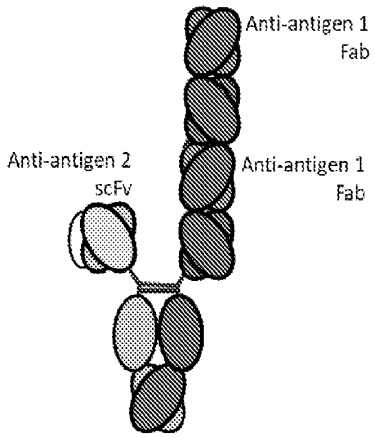


Figure 16

1A7[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLVTVSS	107
vhCDR1	SYAMS	108
vhCDR2	TISGSGDSTYYADSVKG	109
vhCDR3	SGPGLRQVGFDY	110
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PFTFGQGTKLEIK	111
vlCDR1	RASQSISSYLN	112
vlCDR2	AASSLQS	113
vlCDR3	QQSYSTPFT	114

>XENP28428 1A7[CD28]_H1L1_IgG1_PVA_/S267K

Heavy Chain (SEQ ID NO: 115)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Light Chain (SEQ ID NO: 116)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17A

>**1A7[CD28]_H1.1** SEQ ID NO: 117
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.2** SEQ ID NO: 118
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.3** SEQ ID NO: 119
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.4** SEQ ID NO: 120
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.5** SEQ ID NO: 121
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.6** SEQ ID NO: 122
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.7** SEQ ID NO: 123
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.8** SEQ ID NO: 124
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.9** SEQ ID NO: 125
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.10** SEQ ID NO: 126
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIDGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.11** SEQ ID NO: 127
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIEGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.12** SEQ ID NO: 128
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIYGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.13** SEQ ID NO: 129
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17B

>**1A7[CD28]_H1.14** SEQ ID NO: 130
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.15** SEQ ID NO: 131
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.16** SEQ ID NO: 132
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.17** SEQ ID NO: 133
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.18** SEQ ID NO: 134
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.19** SEQ ID NO: 135
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.20** SEQ ID NO: 136
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.21** SEQ ID NO: 137
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.22** SEQ ID NO: 138
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.23** SEQ ID NO: 139
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.24** SEQ ID NO: 140
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.25** SEQ ID NO: 141
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.26** SEQ ID NO: 142
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17C

>**1A7[CD28]_H1.27** SEQ ID NO: 143
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.28** SEQ ID NO: 144
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.29** SEQ ID NO: 145
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.30** SEQ ID NO: 146
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.31** SEQ ID NO: 147
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.32** SEQ ID NO: 148
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.33** SEQ ID NO: 149
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.34** SEQ ID NO: 150
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.35** SEQ ID NO: 151
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.36** SEQ ID NO: 152
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.37** SEQ ID NO: 153
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.38** SEQ ID NO: 154
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.39** SEQ ID NO: 155
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17D

>**1A7[CD28]_H1.40** SEQ ID NO: 156
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.41** SEQ ID NO: 157
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIEGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.42** SEQ ID NO: 158
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.43** SEQ ID NO: 159
EVQLLESGGGLVQPGGSLRLSCAASGFSFSGNYMTWVRQAPGKGLEWVATITADSDATYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.44** SEQ ID NO: 160
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYSMNWVRQAPGKGLEWVATIYANGSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.45** SEQ ID NO: 161
EVQLLESGGGLVQPGGSLRLSCAASGFNFEEYSMNWVRQAPGKGLEWVATITYNGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.46** SEQ ID NO: 162
EVQLLESGGGLVQPGGSLRLSCAASGFSFRTYYMTWVRQAPGKGLEWVATITSDGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.47** SEQ ID NO: 163
EVQLLESGGGLVQPGGSLRLSCAASGFSFKGYSMNWVRQAPGKGLEWVATIYASSDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.48** SEQ ID NO: 164
EVQLLESGGGLVQPGGSLRLSCAASGFSFGEYSMNWVRQAPGKGLEWVSTIYADGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.49** SEQ ID NO: 165
EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYSMNWVRQAPGKGLEWVATIYADSSSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.50** SEQ ID NO: 166
EVQLLESGGGLVQPGGSLRLSCAASGFTFGGYSMNWVRQAPGKGLEWVATIYYDSTTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.51** SEQ ID NO: 167
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYSMNWVRQAPGKGLEWVSTIYNDGATTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.52** SEQ ID NO: 168
EVQLLESGGGLVQPGGSLRLSCAASGFSFEAYSMNWVRQAPGKGLEWVATIYYDSSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17E

>**1A7[CD28]_H1.53** SEQ ID NO: 169
EVQLLESGGGLVQPGGSLRLSCAASGFSFGSYYMSWVRQAPGKGLEWVASIYYGGYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.54** SEQ ID NO: 170
EVQLLESGGGLVQPGGSLRLSCAASGFNFAEYSMSWVRQAPGKGLEWVATIYAGSDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.55** SEQ ID NO: 171
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYSINWVRQAPGKGLEWVATIYYDGSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.56** SEQ ID NO: 172
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYYINWVRQAPGKGLEWVASIYDGGADTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.57** SEQ ID NO: 173
EVQLLESGGGLVQPGGSLRLSCAASGFSFGTYSINWVRQAPGKGLEWVSTIYYDGASTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.58** SEQ ID NO: 174
EVQLLESGGGLVQPGGSLRLSCAASGFTFGKYSISWVRQAPGKGLEWVATIYNDGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.59** SEQ ID NO: 175
EVQLLESGGGLVQPGGSLRLSCAASGFSFEKYYISWVRQAPGKGLEWVASIYDGSYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.60** SEQ ID NO: 176
EVQLLESGGGLVQPGGSLRLSCAASGFSFGTYSMNWVRQAPGKGLEWVATIDYDGSNTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.61** SEQ ID NO: 177
EVQLLESGGGLVQPGGSLRLSCAASGFSFAAYSMSWVRQAPGKGLEWVATIYAGSDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.62** SEQ ID NO: 178
EVQLLESGGGLVQPGGSLRLSCAASGFTFTTYSMTWVRQAPGKGLEWVATIYNDGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.63** SEQ ID NO: 179
EVQLLESGGGLVQPGGSLRLSCAASGFSFKDYSMNWVRQAPGKGLEWVATIYYDGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.64** SEQ ID NO: 180
EVQLLESGGGLVQPGGSLRLSCAASGFSFAAYSMNWVRQAPGKGLEWVATIYAGGAYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.65** SEQ ID NO: 181
EVQLLESGGGLVQPGGSLRLSCAASGFNFAEYYISWVRQAPGKGLEWVASIYNGGSDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17F

>**1A7[CD28]_H1.66** SEQ ID NO: 182
EVQLLESGGGLVQPGGSLRLSCAASGFSLGEYYMNWVRQAPGKGLEWVSTIDYDGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.67** SEQ ID NO: 183
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYYITWVRQAPGKGLEWVSSIYSSSYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.68** SEQ ID NO: 184
EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYYITWVRQAPGKGLEWVSSIYTSGYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.69** SEQ ID NO: 185
EVQLLESGGGLVQPGGSLRLSCAASGFSFGKYSINWVRQAPGKGLEWVATIYSDGTDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 18A

>**1A7[CD28]_L1.1** SEQ ID NO: 186
DIQMTQSPSSLSASVGDRVTITCRASQSISAYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.2** SEQ ID NO: 187
DIQMTQSPSSLSASVGDRVTITCRASQSISDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.3** SEQ ID NO: 188
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.4** SEQ ID NO: 189
DIQMTQSPSSLSASVGDRVTITCRASQSISHYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.5** SEQ ID NO: 190
DIQMTQSPSSLSASVGDRVTITCRASQSISKYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.6** SEQ ID NO: 191
DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.7** SEQ ID NO: 192
DIQMTQSPSSLSASVGDRVTITCRASQSISQYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.8** SEQ ID NO: 193
DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.9** SEQ ID NO: 194
DIQMTQSPSSLSASVGDRVTITCRASQSISVYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.10** SEQ ID NO: 195
DIQMTQSPSSLSASVGDRVTITCRASQSISYYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.11** SEQ ID NO: 196
DIQMTQSPSSLSASVGDRVTITCRASQSISSALNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.12** SEQ ID NO: 197
DIQMTQSPSSLSASVGDRVTITCRASQSISSDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.13** SEQ ID NO: 198
DIQMTQSPSSLSASVGDRVTITCRASQSISSFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 18B

>**1A7[CD28]_L1.14** SEQ ID NO: 199
DIQMTQSPSSLSASVGDRVTITCRASQSISSHLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.15** SEQ ID NO: 200
DIQMTQSPSSLSASVGDRVTITCRASQSISSKLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.16** SEQ ID NO: 201
DIQMTQSPSSLSASVGDRVTITCRASQSISSLLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.17** SEQ ID NO: 202
DIQMTQSPSSLSASVGDRVTITCRASQSISSNLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.18** SEQ ID NO: 203
DIQMTQSPSSLSASVGDRVTITCRASQSISSQLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.19** SEQ ID NO: 204
DIQMTQSPSSLSASVGDRVTITCRASQSISSSLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.20** SEQ ID NO: 205
DIQMTQSPSSLSASVGDRVTITCRASQSISSWLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.21** SEQ ID NO: 206
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.22** SEQ ID NO: 207
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLDWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.23** SEQ ID NO: 208
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLGWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.24** SEQ ID NO: 209
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLHWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.25** SEQ ID NO: 210
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLQWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.26** SEQ ID NO: 211
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 18C

>**1A7[CD28]_L1.27** SEQ ID NO: 212
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.28** SEQ ID NO: 213
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLYWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.29** SEQ ID NO: 214
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.30** SEQ ID NO: 215
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.31** SEQ ID NO: 216
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.32** SEQ ID NO: 217
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYLASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.33** SEQ ID NO: 218
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.34** SEQ ID NO: 219
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYSASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.35** SEQ ID NO: 220
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.36** SEQ ID NO: 221
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYWASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.37** SEQ ID NO: 222
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYYASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.38** SEQ ID NO: 223
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASALQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.39** SEQ ID NO: 224
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASDLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 18D

>**1A7[CD28]_L1.40** SEQ ID NO: 225
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASKLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.41** SEQ ID NO: 226
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.42** SEQ ID NO: 227
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASQLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.43** SEQ ID NO: 228
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.44** SEQ ID NO: 229
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASYLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.45** SEQ ID NO: 230
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLASGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.46** SEQ ID NO: 231
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLESGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.47** SEQ ID NO: 232
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLFSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.48** SEQ ID NO: 233
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLHSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.49** SEQ ID NO: 234
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLISGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.50** SEQ ID NO: 235
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLKSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.51** SEQ ID NO: 236
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLNSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.52** SEQ ID NO: 237
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLSSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 18E

>**1A7[CD28]_L1.53** SEQ ID NO: 238
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLVSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.54** SEQ ID NO: 239
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLYSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.55** SEQ ID NO: 240
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQAGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.56** SEQ ID NO: 241
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQDGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.57** SEQ ID NO: 242
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQGGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.58** SEQ ID NO: 243
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.59** SEQ ID NO: 244
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQKGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.60** SEQ ID NO: 245
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQQGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.61** SEQ ID NO: 246
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQTGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.62** SEQ ID NO: 247
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQVGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.63** SEQ ID NO: 248
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQYGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.64** SEQ ID NO: 249
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQAYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.65** SEQ ID NO: 250
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQDYSTPFTFGQGTKLEIK

Figure 18F

>**1A7[CD28]_L1.66** SEQ ID NO: 251
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQFYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.67** SEQ ID NO: 252
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQHYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.68** SEQ ID NO: 253
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQKYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.69** SEQ ID NO: 254
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQLYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.70** SEQ ID NO: 255
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQTYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.71** SEQ ID NO: 256
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.72** SEQ ID NO: 257
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQYYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.73** SEQ ID NO: 258
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSASTPFTFGQGTKLEIK

>**1A7[CD28]_L1.74** SEQ ID NO: 259
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSDSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.75** SEQ ID NO: 260
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSFSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.76** SEQ ID NO: 261
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSHSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.77** SEQ ID NO: 262
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSKSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.78** SEQ ID NO: 263
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSLSTPFTFGQGTKLEIK

Figure 18G

>**1A7[CD28]_L1.79** SEQ ID NO: 264
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSQSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.80** SEQ ID NO: 265
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSVSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.81** SEQ ID NO: 266
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSWSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.82** SEQ ID NO: 267
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYATPFTFGQGTKLEIK

>**1A7[CD28]_L1.83** SEQ ID NO: 268
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYDTPFTFGQGTKLEIK

>**1A7[CD28]_L1.84** SEQ ID NO: 269
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYGTPFTFGQGTKLEIK

>**1A7[CD28]_L1.85** SEQ ID NO: 270
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYHTPFTFGQGTKLEIK

>**1A7[CD28]_L1.86** SEQ ID NO: 271
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYKTPFTFGQGTKLEIK

>**1A7[CD28]_L1.87** SEQ ID NO: 272
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYNTPFTFGQGTKLEIK

>**1A7[CD28]_L1.88** SEQ ID NO: 273
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYQTPFTFGQGTKLEIK

>**1A7[CD28]_L1.89** SEQ ID NO: 274
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYTTPFTFGQGTKLEIK

>**1A7[CD28]_L1.90** SEQ ID NO: 275
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYVTPFTFGQGTKLEIK

>**1A7[CD28]_L1.91** SEQ ID NO: 276
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYYTPFTFGQGTKLEIK

Figure 18H

>**1A7[CD28]_L1.92** SEQ ID NO: 277
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSAPFTFGQGTKLEIK

>**1A7[CD28]_L1.93** SEQ ID NO: 278
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSDPFTFGQGTKLEIK

>**1A7[CD28]_L1.94** SEQ ID NO: 279
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSFPFTFGQGTKLEIK

>**1A7[CD28]_L1.95** SEQ ID NO: 280
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSIPFTFGQGTKLEIK

>**1A7[CD28]_L1.96** SEQ ID NO: 281
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSKPFTFGQGTKLEIK

>**1A7[CD28]_L1.97** SEQ ID NO: 282
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSLPFTFGQGTKLEIK

>**1A7[CD28]_L1.98** SEQ ID NO: 283
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSQPFTFGQGTKLEIK

>**1A7[CD28]_L1.99** SEQ ID NO: 284
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSSPFTFGQGTKLEIK

>**1A7[CD28]_L1.100** SEQ ID NO: 285
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSVPFTFGQGTKLEIK

>**1A7[CD28]_L1.101** SEQ ID NO: 286
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSYPFTFGQGTKLEIK

>**1A7[CD28]_L1.102** SEQ ID NO: 287
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPITFGQGTKLEIK

>**1A7[CD28]_L1.103** SEQ ID NO: 288
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPLTFGQGTKLEIK

>**1A7[CD28]_L1.104** SEQ ID NO: 289
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPWTFGQGTKLEIK

Figure 18I

>**1A7[CD28]_L1.105** SEQ ID NO: 290
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.106** SEQ ID NO: 291
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYNTPFTFGQGTKLEIK

Figure 19A

1A7[CD28]_H1.1_L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISG SGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQV GFDYWGQGTLVTVSS	292
vhCDR1	SYYMS	293
vhCDR2	TISGSGDSTYYADSVKG	294
vhCDR3	SGPGLRQVGFDY	295
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGQGTKLEI K	296
vlCDR1	RASQSISSYLN	297
vlCDR2	AASSLQS	298
vlCDR3	QQSYSTPFT	299

1A7[CD28]_H1_L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISG SGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQV GFDYWGQGTLVTVSS	300
vhCDR1	SYAMS	301
vhCDR2	TISGSGDSTYYADSVKG	302
vhCDR3	SGPGLRQVGFDY	303
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEI K	304
vlCDR1	RASQSISSYLN	305
vlCDR2	AASSLQS	306
vlCDR3	QQVYSTPFT	307

Figure 19B

1A7[CD28]_H1.1_L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGS GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	308
vhCDR1	SYYMS	309
vhCDR2	TISGSGDSTYYADSVKG	310
vhCDR3	SGPGLRQVGFDY	311
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEIK	312
vlCDR1	RASQSISSYLN	313
vlCDR2	AASSLQS	314
vlCDR3	QQVYSTPFT	315

1A7[CD28]_H1.14_L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISES GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	316
vhCDR1	SYYMS	317
vhCDR2	TISESGDSTYYADSVKG	318
vhCDR3	SGPGLRQVGFDY	319
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGQGTKLEIK	320
vlCDR1	RASQSISSYLN	321
vlCDR2	AASSLQS	322
vlCDR3	QQSYSTPFT	323

Figure 19C

1A7[CD28] H1.14 L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIS ESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	324
vhCDR1	SYYMS	325
vhCDR2	TISESGDSTYYADSVKG	326
vhCDR3	SGPGLRQVGFDY	327
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKL EIK	328
vlCDR1	RASQSISSYLN	329
vlCDR2	AASSLQS	330
vlCDR3	QQVYSTPFT	331

Figure 20A

1A7 VH	SEQ	SEQ ID	
HFR1	EVQLLESGGGLVQPGGSLRLSCAASGFX$_1$X$_2$X$_3$	332	X$_1$ is selected from T,S,N; X$_2$ is selected from F, L; and X$_3$ is selected from S, E, R, K, G, T, A, N
HCDR1	X$_1$X$_2$X$_3$X$_4$X$_5$		X$_1$ is selected from S, G, E, T, D, A, R, K; X$_2$ is selected from Y, N; X$_3$ is selected from A, Y, S; X$_4$ is selected from M, I; and X$_5$ is selected from S, T, N
HFR2	WVRQAPGKGLEWVX$_1$	333	X$_1$ is selected from S, A
HCDR2	X$_1$IX$_2$X$_3$X$_4$X$_5$X$_6$X$_7$TYYADSVKG	334	X$_1$ is selected from T, S; X$_2$ is selected from S, D, E, Y, T; X$_3$ is selected from G, D, E, A, Y, S, N, T; X$_4$ is selected from S, D, N, G; X$_5$ is selected from D, T, Y, S, A; X$_6$ is selected from D, T, Y, S, A; and X$_7$ is selected from S, Y, A, T, D, N
HFR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	335	
HCDR3	SGPGLRQVGFDY	336	
HFR4	WGQGTLVTVSS	337	

Figure 20B

1A7 VL			
LFR1	DIQMTQSPSSLSASVGDRVTITC	338	
LCDR1	RASQSISX$_1$X$_2$LX$_3$	339	X$_1$ is selected from S, A, D, G, H, K, N, Q, T, V, Y; X$_2$ is selected from Y, A, D, F, H, K, L, N, Q, S, W; and X$_3$ is selected from N, A, D, G, H, Q, S, T, Y
LFR2	WYQQKPGKAPKLLIY	340	
LCDR2	X$_1$ASX$_2$LX$_3$X$_4$		X$_1$ is selected from A, D, G, K, L, Q, S, T, W, Y; X$_2$ is selected from S, A, D, K, N, Q, T, Y; X$_3$ is selected from Q, A, E, F, H, I, K, N, S, V, Y; and X$_4$ is selected from Q, A, E, F, H, I, K, N, S, V, Y
LFR3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	341	
LCDR3	QQX$_1$X$_2$X$_3$X$_4$PX$_5$T	342	X$_1$ is selected from S, A, D, F, H, K, L, T, V, Y; X$_2$ is selected from Y, A, D, F, H, K, L, Q, V, W; X$_3$ is selected from S, A, D, G, H, K, N, Q, T, V, Y; X$_4$ is selected from T, A, D, F, I, K, L, Q, S, V, Y; and X$_5$ is selected from F, I, L, W
LFR4	FGQGTKLEIK	343	

Figure 21

1A7 VH/VL Pair	VH SEQ ID NO:	VL SQ ID NO:	scFv Orientation	K_D for human CD28 (nM)
H1L1			VHVL	1000
H1.1_L1			VHVL	600
H1.14_L1			VHVL	230
H1_L1.71			VHVL	180
H1.1_L1.71			VHVL	96
H1.14_L1.71			VHVL	37
L1.71_H1.14			VLVH	37
L1_H1.14			VLVH	230

Figure 22A

CD28.3[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLQQSGAELVKPGASVRLSCKASGYTFTEYIIHWIKLRSGQGLEW IGWFYPGSNDIQYNAKFKGKATLTADKSSSTVYMELTGLTSEDSAVY FCARRDDFSGYDALPYWGQGTMVTVSS	344
vhCDR1	EYIIH	345
vhCDR2	WFYPGSNDIQYNAKFKG	346
vhCDR3	RDDFSGYDALPY	347
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRTNENIYSNLAWYQQKQGKSPQLL IYAATHLVEGVPSRFSGSGSGTQYSLKITSLQSEDFGNYYCQHFWGT PCTFGGGTKLEIK	348
vlCDR1	RTNENIYSNLA	349
vlCDR2	AATHLVE	350
vlCDR3	QHFWGTPCT	351

hCD28.3[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELKKPGASVKVSCKASGYTFTEYIIHWIKLRSGQGLEW IGWFYPGSNDIQYNAQFKGKATLTADKSSSTVYMELTGLTPEDSAVY FCARRDDFSGYDALPYWGQGTLVTVSA	352
vhCDR1	EYIIH	353
vhCDR2	WFYPGSNDIQYNAQFKG	354
vhCDR3	RDDFSGYDALPY	355
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCKTNENIYSNLAWYQQKDGKSPQLL IYAATHLVEGVPSRFSGSGSGTQYSLTISSLQPEDFGNYYCQHFWGT PCTFGGGTKLEIK	356
vlCDR1	KTNENIYSNLA	357
vlCDR2	AATHLVE	358
vlCDR3	QHFWGTPCT	359

Figure 22B

5.11A1[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVKPGTSVRISCEASGYTFTSYYIHWVKQRPGQGLEW IGCIYPGNVNTNYNEKFKDKATLIVDTSSNTAYMQLSRMTSEDSAVY FCTRSHYGLDWNFDVWGAGTTVTVSS	360
vhCDR1	SYYIH	361
vhCDR2	CIYPGNVNTNYNEKFKD	362
vhCDR3	SHYGLDWNFDV	363
Variable light (vl) domain	DIQMNQSPSSLSASLGDTITITCHASQNIYVWLNWYQQKPGNIPKLL IYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQQGQTY PYTFGGGTKLEIK	364
vlCDR1	HASQNIYVWLN	365
vlCDR2	KASNLHT	366
vlCDR3	QQGQTYPYT	367

TGN1412_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEW IGCIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSDDTAVY FCTRSHYGLDWNFDVWGQGTTVTVSS	368
vhCDR1	SYYIH	369
vhCDR2	CIYPGNVNTNYNEKFKD	370
vhCDR3	SHYGLDWNFDV	371
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQQKPGKAPKLL IYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQTY PYTFGGGTKVEIK	372
vlCDR1	HASQNIYVWLN	373
vlCDR2	KASNLHT	374
vlCDR3	QQGQTYPYT	375

Figure 22C

341VL34[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCGGSGFTFNNAWMNWVRQAPGKGLEW VGRIKGKTDGGTADYAAPVKGRFTISRDYSKNTLYLQMNSLTTEDTA VYYCNTDLPYYYGSGRYSGMDVWGQGTTVTVSS	376
vhCDR1	NAWMN	377
vhCDR2	RIKGKTDGGTADYAAPVKG	378
vhCDR3	DLPYYYGSGRYSGMDV	379
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNT FGPGTKVDIK	380
vlCDR1	RASQSVSSYLA	381
vlCDR2	DASNRAT	382
vlCDR3	QQRSNT	383

>341VL36[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCGGSGFTFNNAWMNWVRQAPGKGLEW VGRIKGKTDGGTADYAAPVKGRFTISRDYSKNTLYLQMNSLKTEDTG VYYCTTYLPYYYGSERWSGMDVWGQGTTVTVSS	384
vhCDR1	NAWMN	385
vhCDR2	RIKGKTDGGTADYAAPVKG	386
vhCDR3	YLPYYYGSERWSGMDV	387
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNT FGPGTKVDIK	388
vlCDR1	RASQSVSSYLA	389
vlCDR2	DASNRAT	390
vlCDR3	QQRSNT	391

Figure 22D

281VL4[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGSELKKPGSSVKVSCKASGGTSRSFAISWVRQAPGQGLEW MGGIIPIFGPANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCARHAIAMGWGVITTNYFDSWGQGTMVTVSS	392
vhCDR1	SFAIS	393
vhCDR2	GIIPIFGPANYAQKFQG	394
vhCDR3	HAIAMGWGVITTNYFDS	395
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPITFGQGTRLEIK	396
vlCDR1	RASQSVSSSYLA	397
vlCDR2	GASSRAT	398
vlCDR3	QQYGSSPIT	399

HuTN228[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSETLSLTCAVSGFSLTSYGVHWIRQPPGKGLEW LGVIWPGGGTNFNSALMSRLTISEDTSKNQVSLKLSSVTAADTAVYY CARDRAYGNYLYAMDYWGQGTLVTVSS	400
vhCDR1	SYGVH	401
vhCDR2	VIWPGGGTNFNSALMS	402
vhCDR3	DRAYGNYLYAMDY	403
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASESVEYYVTSLMQWYQQKPGKA PKLLIYAASNVDSGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQ SRKVPFTFGGGTKVEIK	404
vlCDR1	RASESVEYYVTSLMQ	405
vlCDR2	AASNVDS	406
vlCDR3	QQSRKVPFT	407

Figure 22E

PV1[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGAELVKPGASVKISCKTSGYTFTDGYMNWVEQKPGQGLEW IGRIDPDSGNTRYNQKFQGKATLTRDKSSSTVYMDLRSLTSEDSAVY YCARDGTFYGTYGYWYFDFWGQGTQVTVSS	408
vhCDR1	DGYMN	409
vhCDR2	RIDPDSGNTRYNQKFQG	410
vhCDR3	DGTFYGTYGYWYFDF	411
Variable light (vl) domain	DIVMTQSPYSLAVSAGEKVTMSCRSSQSLYYSGIKKNLLAWYQQKPG QSPKLLIYFTSTRLPGVPDRFTGSGSGTDYTLTITSVQAEDMGHYFC QQGISTPLTFGDGTKLEIR	412
vlCDR1	RSSQSLYYSGIKKNLLA	413
vlCDR2	FTSTRLP	414
vlCDR3	QQGISTPLT	415

m9.3[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLQQSGPGLVTPSQSLSITCTVSGFSLSDYGVHWVRQSPGQGLEW LGVIWAGGGTNYNSALMSRKSISKDNSKSQVFLKMNSLQADDTAVYY CARDKGYSYYYSMDYWGQGTSVTVSS	416
vhCDR1	DYGVH	417
vhCDR2	VIWAGGGTNYNSALMS	418
vhCDR3	DKGYSYYYSMDY	419
Variable light (vl) domain	DIELTQSPASLAVSLGQRATISCRASESVEYYVTSLMQWYQQKPGQP PKLLIFAASNVESGVPARFSGSGSGTNFSLNIHPVDEDDVAMYFCQQ SRKVPYTFGGGTKLEIK	420
vlCDR1	RASESVEYYVTSLMQ	421
vlCDR2	AASNVES	422
vlCDR3	QQSRKVPYT	423

Figure 22F

hu9.3[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSDYGVHWVRQAPGKGLEW VSAIWAGGGTNYASSVMGRFTISRDNAKNSLYLQMNSLRAEDMAVYY CARDKGYSYYYSMDYWGQGTLVTVSS	424
vhCDR1	DYGVH	425
vhCDR2	AIWAGGGTNYASSVMG	426
vhCDR3	DKGYSYYYSMDY	427
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCRASESVEYYVTSLMAWYQQKPGQP PKLLIYAASNVESGVPDRFSGSGSGTNFSLTISSLQAEDVAVYYCQQ SRKVPYTFGQGTKLEIK	428
vlCDR1	RASESVEYYVTSLMA	429
vlCDR2	AASNVES	430
vlCDR3	QQSRKVPYT	431

9G2[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSLKLSCAASGFTFSNYYMAWVRQAPTKGLEW VASITNTGGSTYYRDSVKGRFTISRDNAKSTLYLQMDSLRSEDTATY YCTRGLIYYYDGRNYYDYVMDAWGQGASVTVSS	432
vhCDR1	NYYMA	433
vhCDR2	SITNTGGSTYYRDSVKG	434
vhCDR3	GLIYYYDGRNYYDYVMDA	435
Variable light (vl) domain	DIQMTQSPASLSASLGETVSIECLASEGISNSLAWYQQKPGKSPQLL IYGASSLQDGVPSRFSGSGSGTQYSLKISGMQPEDEGVYYCQQGYKY PLTFGSGTKLEIK	436
vlCDR1	LASEGISNSLA	437
vlCDR2	GASSLQD	438
vlCDR3	QQGYKYPLT	439

Figure 22G

9G2[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSITNTGGSTYYRDSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVY YCTRGLIYYYDGRNYYDYVMDAWGQGTTVTVSS	440
vhCDR1	NYYMA	441
vhCDR2	SITNTGGSTYYRDSVKG	442
vhCDR3	GLIYYYDGRNYYDYVMDA	443
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASEGISNSLAWYQQKPGKSPKLL IYGASSLQDGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGYKY PLTFGSGTKVEIK	444
vlCDR1	RASEGISNSLA	445
vlCDR2	GASSLQD	446
vlCDR3	QQGYKYPLT	447

2F10A3.140[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFSFGGNSMSWVRQAPGKGLEW VATISDNSYSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLVTVSS	448
vhCDR1	GNSMS	449
vhCDR2	TISDNSYSTYYADSVKG	450
vhCDR3	SGPGLRQVGFDY	451
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PFTFGQGTKLEIK	452
vlCDR1	RASQSISSYLN	453
vlCDR2	AASSLQS	454
vlCDR3	QQSYSTPFT	455

Figure 22H

TN228[CD28]_H4L2

	sequence	**SEQ ID NO:**
Variable heavy (vh) domain	QVQLQESGPGLVKPSETLSLTCTVSGFSLTSYGVHWVRQPPGKGLEW IGVIWPGGGTNYNSALKSRVTISEDTSKSQVSLKLSSVTAADTAVYY CARDRAYGNYLYAMDYWGQGTLVTVSS	456
vhCDR1	SYGVH	457
vhCDR2	VIWPGGGTNYNSALKS	458
vhCDR3	DRAYGNYLYAMDY	459
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASESVEYYVTSLMQWYQQKPGQA PRLLIYAASNVDSGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ SRKVPFTFGGGTKVEIK	460
vlCDR1	RASESVEYYVTSLMQ	461
vlCDR2	AASNVDS	462
vlCDR3	QQSRKVPFT	463

Figure 23A

RS7[TROP2]		
Variable Heavy (vh) Domain	VKLQESGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTY TGEPTYTDDFKGRFAFSLETSATTAYLQINNLKSEDMATYFCARGGFGSSYWY FDVWGQGTTVTVSS	SEQ ID NO: 464
Variable Light (vl) Domain	DIQLTQSHKFMSTSVGDRVSITCKASQDVSIAVAWYQQKPGQSPKLLIYSASY RYTGVPDRFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYITPLTFGAGTKLEL K	SEQ ID NO: 465

hRS7[TROP2]		
Variable Heavy (vh) Domain	SVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINT YTGEPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYW YFDVWGQGSLVTVSS	SEQ ID NO: 466
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASY RYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEI K	SEQ ID NO: 467

hRS7v2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINT YTGEPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYW YFDVWGQGSLVTVSS	SEQ ID NO: 468
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASY RYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEI K	SEQ ID NO: 469

AR47A6.4.2[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINT KTGEPTYAEEFKGRFAFSLETSASTAYLQINNLKKEDTATYFCGRGGYGSSYW YFDVWGAGTTVTVSS	SEQ ID NO: 470
Variable Light (vl) Domain	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVYNAKT LAEGVPSRFSGSGSGTQFSLKINSLRPEDFGSYYCQHHYGSPLTFGAGTKLEL R	SEQ ID NO: 471

huAR476A6.4.2 HV2/KV3[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGHEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT KTGEPTYAEEFKGRFVFSLETSASTAYLQISSLKAEDTAMYFCGRGGYGSSYW YFDVWGQGTTVTVSS	SEQ ID NO: 472
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSIAVAWYQQKPGKAPKVLIYSASY RYTGVPDRFSGSGSGTDFTFTISSLQPEDIAVYYCQQHYITPLTFGGGTKVEI K	SEQ ID NO: 473

Figure 23B

huAR476A6.4.2 HV2/KV4[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGHEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT KTGEPTYAEEFKGRFVFSLETSASTAYLQISSLKAEDTAMYFCGRGGYGSSYW YFDVWGQGTTVTVSS	SEQ ID NO: 474
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSIAVAWYQQKPGKAPKVLIYSASY RYTGVPSRFSGSGSGTDFTFTISSLQPEDIAVYYCQQHYITPLTFGGGTKVEI K	SEQ ID NO: 475

huAR476A6.4.2 HV3/KV3[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGHEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT KTGEPTYAEEFKGRFVFSLETSASTAYLQISSLKAEDMAMYFCGRGGYGSSYW YFDVWGQGTTVTVSS	SEQ ID NO: 476
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSIAVAWYQQKPGKAPKVLIYSASY RYTGVPDRFSGSGSGTDFTFTISSLQPEDIAVYYCQQHYITPLTFGGGTKVEI K	SEQ ID NO: 477

huAR476A6.4.2 HV2/KV4[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGHEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQGLEWMGWINT KTGEPTYAEEFKGRFVFSLETSASTAYLQISSLKAEDMAMYFCGRGGYGSSYW YFDVWGQGTTVTVSS	SEQ ID NO: 478
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSIAVAWYQQKPGKAPKVLIYSASY RYTGVPSRFSGSGSGTDFTFTISSLQPEDIAVYYCQQHYITPLTFGGGTKVEI K	SEQ ID NO: 475

4F6[TROP2]		
Variable Heavy (vh) Domain	DVQLEQFGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYP GGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTFEDFAIYYCARGTGGGDYW GQG	SEQ ID NO: 479
Variable Light (vl) Domain	IVITQSPASLSMAIGEKVSIRCITSTDIDDDMNWYQQKPGEPPKLLISEGNTL RPGVPSRFSSSGYGTDFVFTIENMLSEDVADYYCLQSDNL	SEQ ID NO: 480

2G10[TROP2]		
Variable Heavy (vh) Domain	DVQLEQFGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYP GGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTFEDFAIYYCARGTGGGDYW GQG	SEQ ID NO: 481
Variable Light (vl) Domain	IVITQSPASLSMAIGEKVTIRCITSTDIDDDMNWYQQKPGEPPKLLISEGNTL RPGVPSRFSSSGYGTDFVFTIENMLSEDVADYYCLQSDNL	SEQ ID NO: 482

Figure 23C

2EF[TROP2]		
Variable Heavy (vh) Domain	DVQLEQFGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYP GGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTFEDFAIYYCARGTGGGDYW GQG	SEQ ID NO: 483
Variable Light (vl) Domain	DIVMTQSPASLAVSLGQRATISCRASQSVSTSSYSYMHWYQQKPGQPPKLLIK YASNLECGVPARFSGSGCGTDFTLNIHPVEEEDSATYYCQHSREI	SEQ ID NO: 484

K5-70[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGAELVRPGASVKLSCKASGYTFTIYWINWVKQRPGQGLEWIGNIYP SDSYTNYNQKFKDKATLTVDKSSSTAYMQLSSPTSEDSAVYYCTRTSMADYWG QGTTLTVSS	SEQ ID NO: 485
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASE SISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPFTFGSGTKLEI K	SEQ ID NO: 486

K5-107[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGSELVRPGASVKLSCKASGYTFTSYWMHWVKQRHGQGLEWIGNIYP GGGYTNYDEKFKSKGTLTVDTSSSTAYMHLSSLTSEDSAVYYCTRSSVFDYWG QGTTLTVSS	SEQ ID NO: 487
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQNIGTSIHWFQQRTNGSPRLLIKYASE SISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPFTFGSGTKLEI K	SEQ ID NO: 488

K5-116-2-1[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWITWVKQRPGQGLEWIGNIYP SDSYTNYNQKFRDKATLTVDKSSSTAYMQLSSPTSEDSAVYYCSALFDYWGQG TTLTVSS	SEQ ID NO: 489
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQSIGTSIHWYQQRTNGSPRLLIKYASE SISGIPSRFSGSGSGTDFILSINSVESEDIADYYCQQSNSWPFTFGSGTKLEI K	SEQ ID NO: 490

T6-16[TROP2]		
Variable Heavy (vh) Domain	EVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSHGKNLEWIGYIYP YNGGTGYNQRFKSRATMTVDKSSSTAYMELRSLTSDDSAVYYCAREDYGSSPS YAMDYWGQGTSVIVSS	SEQ ID NO: 491
Variable Light (vl) Domain	DVVMTQTPLSLPVSLGDQASISCRSSQSLVHGNGNTYLHWYLQKPGQSPKLLI YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPTFGSGT KLEIK	SEQ ID NO: 492

Figure 23D

KM4097[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPELVRPGTSVRISCKASGYTFTIYWLGWVKQRPGHGLEWIGNIFP GSAYINYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCAREGSNSGYW GQGTTLTVSS	SEQ ID NO: 493
Variable Light (vl) Domain	DIVMTQSPSSLSVSAGEKVTMTCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFTGSGSGTDFTLTINSVQAEDLAVYYCQSDHIYPYTFGG GTKLEIK	SEQ ID NO: 494

HV0LV0[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWLGWVRQAPGQGLEWMGNIFP GSAYINYNEKFKGRVTITADTSTSTAYMELSSLRSEDTAVYYCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 495
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 496

HV3aLV0[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVKKPGASVKVSCKASGYTFTIYWLGWVRQAPGQGLEWMGNIFP GSAYINYNEKFKGKVTITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 497
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 498

HV4LV0[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVKKPGASVKVSCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGRVTITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 499
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 500

HV5LV0[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGKATITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 501
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 502

Figure 23E

HV10LV2[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVVKPGASVKISCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGKATLTADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLLTVSS	SEQ ID NO: 503
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERVTINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 504

HV10LV4[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVVKPGASVKISCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGKATLTADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLLTVSS	SEQ ID NO: 505
Variable Light (vl) Domain	DIVMTQSPDSLAVSAGERVTMNCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 506

7E6[TROP2]		
Variable Heavy (vh) Domain	QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWT GGSTDYNSALMSRLSINKDNSKSQVFLKMNSLQTDDTAMYYCARDGDYDRYTM DYWGQGTSVTVSS	SEQ ID NO: 507
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWYQQKPGQPPKLLIY LASNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGT KLEIK	SEQ ID NO: 508

h7E6[TROP2]		
Variable Heavy (vh) Domain	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYGVHWIRQPPGKGLEWIGVIWT GGSTDYNSALMSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGDYDRYTM DYWGQGTLVTVSS	SEQ ID NO: 509
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSYMHWYQQKPGQPPKLLIY LASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSRELPYTFGQGT KLEIK	SEQ ID NO: 510

h7E6_SVG[TROP2]		
Variable Heavy (vh) Domain	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYGVHWIRQPPGKGLEWIGVIWT SGVTDYNSALMGRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGDYDRYTM DYWGQGTLVTVSS	SEQ ID NO: 511
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSYMHWYQQKPGQPPKLLIY LASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSRELPYTFGQGT KLEIK	SEQ ID NO: 512

Figure 23F

h7E6_SVGL[TROP2]		
Variable Heavy (vh) Domain	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYGVHWIRQPPGKGLEWIGVIWT SGVTDYNSALMGRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGDYDRYTM DYWGQGTLVTVSS	SEQ ID NO: 513
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRASKSVSTSLYSYMHWYQQKPGQPPKLLIY LASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSRELPYTFGQGT KLEIK	SEQ ID NO: 514

h7E6_SVGN[TROP2]		
Variable Heavy (vh) Domain	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYGVHWIRQPPGKGLEWIGVIWT SGVTDYNSALMGRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGDYDRYTM DYWGQGTLVTVSS	SEQ ID NO: 515
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRASKSVSTSNYSYMHWYQQKPGQPPKLLIY LASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSRELPYTFGQGT KLEIK	SEQ ID NO: 516

6G11[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWINWVKQRPGHGLEWIGNIYP SDSYSNYNQKFKDKATLTVDKSSSTAYMQVSSPTSEDSAVYYCTYGSSFDYWG QGTTVTVSS	SEQ ID NO: 517
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQTIGTSIHWYQQRTNGSPRLLIKYASE SISGIPSRFSGSGSGTDFTLSINSVESEDIADYYCQQSNSWPFTFGSGTKLEI K	SEQ ID NO: 518

h6G11[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGLEWMGNIYP SDSYSNYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSSFDYWG QGTLVTVSS	SEQ ID NO: 519
Variable Light (vl) Domain	EIVLTQSPATLSLSPGERATLSCRASQTIGTSIHWYQQKPGQAPRLLIYYASE SISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNSWPFTFGQGTKLEI K	SEQ ID NO: 520

h6G11_FKG_SF[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGLEWMGNIFP SDSYSNYNKKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGSGFDYWG QGTLVTVSS	SEQ ID NO: 521
Variable Light (vl) Domain	EIVLTQSPATLSLSPGERATLSCRASQTIGTSIHWYQQKPGQAPRLLIYYASE SISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCSQSFSWPFTFGQGTKLEI K	SEQ ID NO: 522

Figure 23G

huK5-70[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWINWVRQAPGQRLEWIGNIYP SDSYTNYNQKFKDKATLTVDTSASTAYMELSSLRSEDTAVYYCTRTSMADYWG QGTLVTVSS	SEQ ID NO: 523
Variable Light (vl) Domain	EIVLTQSPATLSLSPGERATLSCRASQSIGTSIHWYQQKPGQAPRLLIKYASE SISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNSWPFTFGQGTKVEI K	SEQ ID NO: 524

huK5-70-2[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWINWVRQAPGQGLEWIGNIYP SDSYTNYNQKFKDKATLTVDTSASTAYMELSSLRSEDTAVYYCTRTSMADYWG QGTLVTVSS	SEQ ID NO: 525
Variable Light (vl) Domain	EIVLTQSPATLSLSPGERATLSCRASQSIGTSIHWYQQKPGQAPRLLIKYASE SISGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNSWPFTFGQGTKVEI K	SEQ ID NO: 526

huT6-16-1[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYP YNGGTGYNQRFKSRATMTVDKSTSTAYMELRSLRSDDTAVYYCAREDYGSSPS YAMDYWGQGTMVTVSS	SEQ ID NO: 527
Variable Light (vl) Domain	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHGNGNTYLHWYLQKPGQSPQLLI YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQTTHVPTFGGGT KVEIK	SEQ ID NO: 528

huT6-16-2[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMHWVRQAPGQGLEWIGYIYP YNGGTGYNQRFKSRATMTVDTSTSTAYMELRSLRSDDTAVYYCAREDYGSSPS YAMDYWGQGTMVTVSS	SEQ ID NO: 529
Variable Light (vl) Domain	DIVMTQSPLSLPVTPGEPASISCRSSQSLVHGNGNTYLHWYLQKPGQSPQLLI YKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQTTHVPTFGGGT KVEIK	SEQ ID NO: 530

TINA[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINT HSGVPKYAEDFKGRFAFSLETSASTAYLQISNLKNEDTTTYFCARSGFGSSYW YFDVWGAGTAVTVSS	SEQ ID NO: 531
Variable Light (vl) Domain	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASY RYTGVPDRFTGSGSGTAFTFTISSVQAEDLAVYYCQQHYITPLTFGAGTKLEL K	SEQ ID NO: 532

Figure 23H

2EF[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKQRPGHGLEWIGDIYP GGGYTNYNEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCARGTGGGDYW GQGTLVTVSA	SEQ ID NO: 533
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATISCRASQSVSTSSYSYMHWYQQKPGQPPKLLIK YASNLESGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGT KLEIK	SEQ ID NO: 534

2G10[TROP2]		
Variable Heavy (vh) Domain	QGQMQQSGAELVKPGASVKLSCKTSGFTFSSSYISWLKQKPRQSLEWIAWIYA GTGGTSYNQKFTGKAQLTVDTSSSTAYMQLSSLTSEDSAIYYCARHNPRYYAM DYWGQGTSVTVSS	SEQ ID NO: 535
Variable Light (vl) Domain	ETTVTQSPASLSMAIGEKVTIRCITSTDIDDDMNWYQQKPGEPPKLLISEGNT LRPGVPSRFSSSGYGTDFVFTIENMLSEDVADYYCLQSDNLPYTFGGGTKLEI K	SEQ ID NO: 536

Hu2EF-7[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVKQAPGQGLEWIGDIYP GGGYTNYNEKFKGRATLTADTSASTAYMELSSLRSEDTAVYYCARGTGGGDYW GQGTLVTVSS	SEQ ID NO: 537
Variable Light (vl) Domain	DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIK YASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSWEIPYTFGGGT KLEIK	SEQ ID NO: 538

Hu2G10-5[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGFTFSSSYISWLRQAPGQRLEWIAWIYA GTGGTSYNQKFTGKATLTVDTSASTAYMELSSLRSEDTAVYYCARHNPRYYAM DYWGQGTTVTVSS	SEQ ID NO: 539
Variable Light (vl) Domain	DTQMTQSPSSLSASVGDRVTITCITSTDIDDDMNWYQQKPGKAPKLLISEGNT LRPGVPSRFSGSGYGTDFTFTISSLQPEDIATYYCLQSDNLPYTFGGGTKVEI K	SEQ ID NO: 540

Hu2G10-6[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGFTFSSSYISWLRQAPGQRLEWIAWIYA GTGGTSYNQKFTGRVTLTVDTSASTAYMELSSLRSEDTAVYYCARHNPRYYAM DYWGQGTTVTVSS	SEQ ID NO: 541
Variable Light (vl) Domain	DTQMTQSPSSLSASVGDRVTITCITSTDIDDDMNWYQQKPGKAPKLLISEGNT LRPGVPSRFSGSGYGTDFTFTISSLQPEDIATYYCLQSDNLPYTFGGGTKVEI K	SEQ ID NO: 542

Figure 23I

BAT-806[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINT YTGEPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYW YFDVWGQGTLVTVSS	SEQ ID NO: 543
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASY RYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEI K	SEQ ID NO: 544

trop2-ab7[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPEVVKPGASVKMSCKASGYRFTDYVINWVKQRSGQGLEWIGQIYP GSDTFHYNKNFKGKATLTADKSSNTAYMQLNSLTSEDSAVYFCARFFEGFAYW GQGTLVTVSA	SEQ ID NO: 545
Variable Light (vl) Domain	DIKMTQSPSSMYAFLGERVTITCKASQGINNYLSWFHLKPGKSPKSLIYRANR LVDGVPSRFSGSGSGQDYSLTISSLDYEDVGIYYCLQYDEFPLTFGGGTKLEL K	SEQ ID NO: 546

Trop2-Ab8TROP2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPEVVKPGASVKMSCKASGYRFTDYVINWVKQRTGQGLEWIGQIYP GSDSFHYNKNFKGKATLTADKSSNTAYMQLNSLTSEDSAVYFCARFFEGLAYW GQGTLVTVSA	SEQ ID NO: 547
Variable Light (vl) Domain	DIKMTQSPSSMYAFLGERVTITCKASQGINNYLSWFQLKPGKSPKSLIYRANR LVDGVPSRFSGSGSGQDYSLTISSLDYEDMGIYYCLQYDEFPLTFGGGTKLEL K	SEQ ID NO: 548

Trop2-Ab22[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPELVKPGASVKMSCKASGYTFTDYVINWVKQRPGQGLEWVGQIYP GSDGTYYNEPFKGEATLTADKSSNTAYMQLSSLTSEDSAVYFCARFFEGFAYW GQGTLVTVSA	SEQ ID NO: 549
Variable Light (vl) Domain	DIKMTQSPSSMFASLGERVTITCKASQDINWYLSWFQQKPGKSPKTLIYRANR LVDGVPSRFSGSGSGQDYSLTISSLDYEDMGVYYCLQYEEFPLTFGAGTKLEL K	SEQ ID NO: 550

Trop2-Ab40TROP2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPEVVKPGASVKMSCKASGYRFTDYVINWVKQRTGQGLEWIGQIYP GSDSFHYNKNFKGKATLTADKSSNTAYMQLNSLTSEDSAVYFCARFFEGLAYW GQGTLVTVSA	SEQ ID NO: 551
Variable Light (vl) Domain	DIKMTQSPSSMYAFLGERVTITCTASQGINNYLSWFQLKPGKSPKSLIYRANR LVDGVPSRFSGSGSGQDYSLTISSLDYEDMGIYYCLQYDEFPLTFGGGTKLEL K	SEQ ID NO: 552

Figure 23J

Trop2-Ab46TROP2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGAELVRPGASVRLSCKSSGYTFTSYWINWVKQRPGQGLEWIGNIFP SHSYTNYNQKFRDKATLTVDKSSSTAYLQLSSPTSDDSAVYYCTRGSGFDYWG QGTALTVSS	SEQ ID NO: 553
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQNIGTSIHWYQQRTNGSPRLLISYASE SISGIPSRFSGSGSGTDFTLLIINSVESEDIADYYCQHSYSWPFTFGSGTKLE VK	SEQ ID NO: 554

Trop2-Ab50TROP2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLDWIKQRPGQGLEWIGNIFP GGDYTNYNEEFRGKATLTADTSSRTAFMQLSSLTSEDSAVYFCARSSYDYWGQ GTLVTVSA	SEQ ID NO: 555
Variable Light (vl) Domain	DILLTQSPAILSVSPGERVSFSCRASQNIGTSIHWYQQRTNGSPRLLIKYSSE SISGIPSRFSGSGSGTDFSLTINSVESEDIGDYYCQHSYTWPFTFGSGTKLEI K	SEQ ID NO: 556

Trop2-Ab51TROP2[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGPEVVKPGASVKMSCRASGYRFTDYVINWVKQRTGQGLEWIGQIYP GSDSFHYNKNFKGKATLTADKSSNTAYMQLNSLTSEDSAVYFCARFFEGFAYW GQGTLVTVSA	SEQ ID NO: 557
Variable Light (vl) Domain	DIKMTQSPSSMYAFLGERVTITCKASQGINNYLSWFQLKPGKSPKSLIYRANR LVDGVPSRFSGSGSGQDYSLTISSLDYEDMGIYYCLQYDEFPLTFGGGTKLEL K	SEQ ID NO: 558

1B3[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGVSVKISCKGSGYTFTDYSINWVKQSHAKSLEWIGVIST YYGDASYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARYGDGYNQF DYWGQGTTLTVSS	SEQ ID NO: 559
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATISCRVSESVDSYGNNFMHWYQQKPGQPPKLLIY RASNLESGVPARFSGSGSGTDFTLTINPMEADDVATYYCQQSYEDPYTFGGGT KLEIK	SEQ ID NO: 560

15D9[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGVSVKISCKGSGYTFTDYSIHWVKQSHAKSLEWIGVISS YYGDATYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCALLGAYNYFD YWGQGTTLTVSS	SEQ ID NO: 561
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLVY RASNLESGIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSYEDPPTFGGGT KLEIK	SEQ ID NO: 562

Figure 23K

15A10[TROP2]		
Variable Heavy (vh) Domain	EVQLEQSGPGLVQPSQSLSITCTVSGFSLTRYGVHWVRQSPGRSLEWLGVIWS GGNTDYNAAFISRLTITKDNSKSQVFFKMNSLQPNDTGVYYCAREDRYVGEFA YWGQGTLVTVSA	SEQ ID NO: 563
Variable Light (vl) Domain	DIVLTQSTASLAVSLGQRATISCRASESVDSYGNSFIHWYQQKPGQPPKLLIY RASNLESGIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPRTFGGGT KLEIK	SEQ ID NO: 564

17B6[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGVSVKISCKGSGYTFTDYGMNWVKQSHAKSLEWIGVIST FYGDANYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARRGNYDSMD YWGQGTSVTVSS	SEQ ID NO: 565
Variable Light (vl) Domain	DIVLTQSPVFLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIY RASNLESGIPARFSGSGSRTDFTLTINPVEADDVETYYCQQSYEDPPTFGGGT KLEIE	SEQ ID NO: 566

17D1[TROP2]		
Variable Heavy (vh) Domain	QVQLQQSGAELVRPGVSVKISCKGSGYTFTDYSIHWVKQSHAKSLEWIGLIST YYGDATYTQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCALLGAYNYFD YWGQGTTLTVSS	SEQ ID NO: 567
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLVY RASNLESGIPARFSGSGSRTDFTLTINPVEADDIATYYCQQSYEDPPTFGGGT KLEIK	SEQ ID NO: 568

M1[TROP2]		
Variable Heavy (vh) Domain	QVQLQQPGAELVRPGASVKLSCRASGYTFTNYWMNWVKQRPEQGLEWIGRIDP NDSETHYNQKFKDRAILTVDKASNTAYMQLSGLTSEDSAVHYCARSGFGSTYW FFDVWGAGTTVTVSS	SEQ ID NO: 569
Variable Light (vl) Domain	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASY RYTGVPDRFAGSGYGTDFTFTISSVQTEDLTVYHCQQHYSTPLTFGPGTRLEL K	SEQ ID NO: 570

HU1[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMNWVRQAPGKGLEWVGRIDP NDSETHYNQKFKDRFTITRDNSKNTLYLQMNSLRAEDTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 571
Variable Light (vl) Domain	AIRMTQSPFSLSASVGDRVTITCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTRIPPRFSGSGYGTDFTLTINNIESEDAAYYFCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 572

Figure 23L

HU2[TROP2]		
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYWMNWVRQAPGKGLEWIGRIDP NDSETHYNQKFKDRVTISVDKSKNQFSLKLSSVTAADTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 573
Variable Light (vl) Domain	ETTLTQSPAFMSATPGDKVNISCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 574

HU3[TROP2]		
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMNWVRQAPGKGLEWMGRIDP NDSETHYNQKFKDRVTISVDKSKNQFSLKLSSVTAADTAVYYCARSGFGSTYW FFDVWGQGTMVTVSS	SEQ ID NO: 575
Variable Light (vl) Domain	DIVMTQTPLSLPVTPGEPASISCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 576

HU4[TROP2]		
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYWMNWVRQAPGKGLEWIGRIDP NDSETHYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGFGSTYW FFDVWGQGTMVTVSS	SEQ ID NO: 577
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQAPRLLIYSASY RYTGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 578

HU5[TROP2]		
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTVSNYWMNWVRQAPGKGLEWIGRIDP NDSETHYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 579
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLFIYSASY RYTGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 580

HU6[TROP2]		
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTVSNYWMNWVRQAPGKGLEWMGRIDP NDSETHYNQKFKDRVTISVDKSKNQFSLKLSSVTAADTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 581
Variable Light (vl) Domain	DVVMTQSPLSLPVTLGQPASISCKASQDVSTAVAWYQQKPGKAPKLFIYSASY RYTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 582

Figure 23M

HU7[TROP2]		
Variable Heavy (vh) Domain	EVQLVESGGGLIQPGGSLKLSCAASGFTVSNYWMNWVRQAPGKGLEWMGRIDP NDSETHYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 583
Variable Light (vl) Domain	AIRMTQSPFSLSASVGDRVTITCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 584

HU8[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWMNWVRQAPGKGLEWMGRIDP NDSETHYNQKFKDRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 585
Variable Light (vl) Domain	AIRMTQSPFSLSASVGDRVTITCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTGVPSRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 586

HU9[TROP2]		
Variable Heavy (vh) Domain	EVQLVESGGGLIQPGGSLRLSCAASGFTVSNYWMNWVRQAPGQGLEWMGRIDP NDSETHYNQKFKDRLTITKDTSKNQVVLTMTNMDPVDTATYYCARSGFGSTYW FFDVWGQGTTVTVSS	SEQ ID NO: 587
Variable Light (vl) Domain	DIVMTQTPLSLPVTPGEPASISCKASQDVSTAVAWYLQKPGQSPQLLIYSASY RYTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQHYSTPLTFGQGTRLEI K	SEQ ID NO: 588

Figure 24

HV0_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWLGWVRQAPGQGLEWMGNIFP GSAYINYNEKFKGRVTITADTSTSTAYMELSSLRSEDTAVYYCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 589

HV3a_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVKKPGASVKVSCKASGYTFTIYWLGWVRQAPGQGLEWMGNIFP GSAYINYNEKFKGKVTITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 590

HV4_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVKKPGASVKVSCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGRVTITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 591

HV5_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGKATITADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLVTVSS	SEQ ID NO: 592

HV10_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGPEVVKPGASVKISCKASGYTFTIYWLGWVKQAPGQGLEWIGNIFP GSAYINYNEKFKGKATLTADTSTSTAYMELSSLRSEDTAVYFCAREGSNSGYW GQGTLLTVSS	SEQ ID NO: 593

LV0_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 594

LV2_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERVTINCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 595

LV4_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPDSLAVSAGERVTMNCKSSQSLLNSGNQQNYLAWYQQKPGQPPKLL IYGASTRESGVPDRFSGSGSGTDFTLTISSVQAEDVAVYYCQSDHIYPYTFGQ GTKLEIK	SEQ ID NO: 596

Figure 25

hTINA1 H1_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTAGMQWVRQAPGQGLEWMGWINT HSGVPKYAEDFKGRVTISADTSTSTAYLQLSSLKSEDTAVYYCARSGFGSSYW YFDVWGQGTLVTVSS	SEQ ID NO: 597

hTINA1 H2_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTAGMQWVRQAPGQGLEWMGWINT HSGVPKYAEDFKGRVTISLDTSTSTAYLQLSSLKSEDTAVYYCARSGFGSSYW YFDVWGQGTLVTVSS	SEQ ID NO: 598

hTINA1 H3_VH[TROP2]		
Variable Heavy (vh) Domain	QIQLVQSGAEVKKPGESVKVSCKASGYTFTTAGMQWVQQMPGKGLEWMGWINT HSGVPKYAEDFKGRVTFSLDTSTSTAYLQLSSLKSEDTAVYYCARSGFGSSYW YFDVWGQGTLVTVSS	SEQ ID NO: 599

hTINA1 L1_VL[TROP2]		
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASY RYTGVPSRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEI K	SEQ ID NO: 600

hTINA1 L2_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASY RYTGVPSRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEI K	SEQ ID NO: 601

hTINA1 L3_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKQPKLLIYSASY RYTGVPSRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEI K	SEQ ID NO: 602

Figure 26

Hu2EF VH4_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYP GGGYTNYNEKFKGRATLTADTSASTAYMELSSLRSEDTAVYYCARGTGGGDYW GQGTLVTVSS	SEQ ID NO: 603

Hu2EF VH5_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVRQAPGQGLEWIGDIYP GGGYTNYNEKFKGRATLTADTSTSTAYMELSSLRSEDTAVYYCARGTGGGDYW GQGTLVTVSS	SEQ ID NO: 604

Hu2EF VH7_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYWIGWVKQAPGQGLEWIGDIYP GGGYTNYNEKFKGRATLTADTSASTAYMELSSLRSEDTAVYYCARGTGGGDYW GQGTLVTVSS	SEQ ID NO: 605

Hu2EF VL1_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIK YASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSWEIPYTFGQGT KLEIK	SEQ ID NO: 606

Hu2EF VL2_VL[TROP2]		
Variable Light (vl) Domain	DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIK YASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQHSWEIPYTFGGGT KLEIK	SEQ ID NO: 607

Figure 27

Hu2G10 VH1_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGFTFSSSYISWLRQAPGQRLEWIAWIYA GTGGTSYNQKFTGKATLTVDTSASTAYMELSSLRSEDTAVYYCARHNPRYYAM DYWGQGTTVTVSS	SEQ ID NO: 608

Hu2G10 VH2_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGFTFSSSYISWLRQAPGQRLEWIAWIYA GTGGTSYNQKFTGRVTLTVDTSASTAYMELSSLRSEDTAVYYCARHNPRYYAM DYWGQGTTVTVSS	SEQ ID NO: 609

Hu2G10 VL1_VL[TROP2]		
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCITSTDIDDDMNWYQQKPGKAPKLLISEGNT LRPGVPSRFSGSGYGTDFTFTISSLQPEDIATYYCLQSDNLPYTFGGGTKVEI K	SEQ ID NO: 610

Hu2G10 VL2_VL[TROP2]		
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCITSTDIDDDMNWYQQKPGKAPKLLISEGNT LRPGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCLQSDNLPYTFGGGTKVEI K	SEQ ID NO: 611

Hu2G10 VL3_VL[TROP2]		
Variable Light (vl) Domain	DTQMTQSPSSLSASVGDRVTITCITSTDIDDDMNWYQQKPGKAPKLLISEGNT LRPGVPSRFSGSGYGTDFTFTISSLQPEDIATYYCLQSDNLPYTFGGGTKVEI K	SEQ ID NO: 612

Figure 28A

DP002 HC1_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYSINWVRQAPGQGLEWMGVIST YYGDASYNQKFKGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARYGDGYNQF DYWGQGTMVTVSS	SEQ ID NO: 613

DP002 HC2_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYSINWVRQAPGQGLEWMGVIST YYGDASYNQKFKGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARYGDGYNQF DYWGQGTLVTVSS	SEQ ID NO: 614

DP002 HC3_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYSINWVRQAPGQRLEWMGVIST YYGDASYNQKFKGRVTITRDTSASTAYMELSSLRSEDTAVYYCARYGDGYNQF DYWGQGTLVTVSS	SEQ ID NO: 615

DP002 HC4_VH[TROP2]		
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYSINWVRQAPGQGLEWMGVIST YYGDASYNQKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYGDGYNQF DYWGQGTLVTVSS	SEQ ID NO: 616

DP002 HC5_VH[TROP2]		
Variable Heavy (vh) Domain	EVQLVQSGAEVKKPGESLKISCKGSGYTFTDYSINWVRQMPGKGLEWMGVIST YYGDASYNQKFKGQVTISADKSISTAYLQWSSLKASDTAMYYCARYGDGYNQF DYWGQGTLVTVSS	SEQ ID NO: 617

DP002 LC1_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCRVSESVDSYGNNFMHWYQQKPGQPPKLLIY RASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSYEDPYTFGQGT KLEIK	SEQ ID NO: 618

DP002 LC2_VL[TROP2]		
Variable Light (vl) Domain	DVVMTQSPLSLPVTLGQPASISCRVSESVDSYGNNFMHWFQQRPGQSPRRLIY RASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSYEDPYTFGGGT KVEIK	SEQ ID NO: 619

DP002 LC3_VL[TROP2]		
Variable Light (vl) Domain	DIVMTQSPLSLPVTPGEPASISCRVSESVDSYGNNFMHWYLQKPGQSPQLLIY RASNLESGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQSYEDPYTFGGGT KVEIK	SEQ ID NO: 620

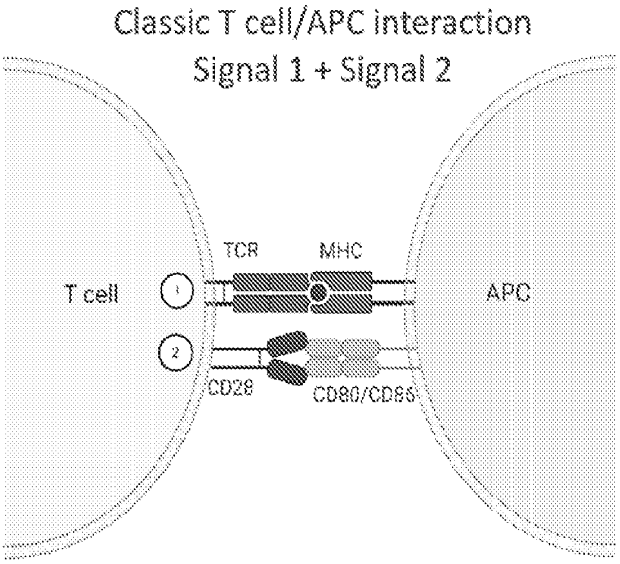
DP002 LC4_VL[TROP2]		
Variable Light (vl) Domain	EIVLTQSPATLSLSPGERATLSCRVSESVDSYGNNFMHWYQQKPGQAPRLLIY RASNLESGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSYEDPYTFGGGT KVEIK	SEQ ID NO: 621

Figure 28B

DP002 LC5_VL[TROP2]		
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRVSESVDSYGNNFMHWYQQKPGKAPKLLIY RASNLESGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQSYEDPYTFGGGT KLEIK	SEQ ID NO: 622

Figures 29A-29B

Figures 29A



Figures 29B

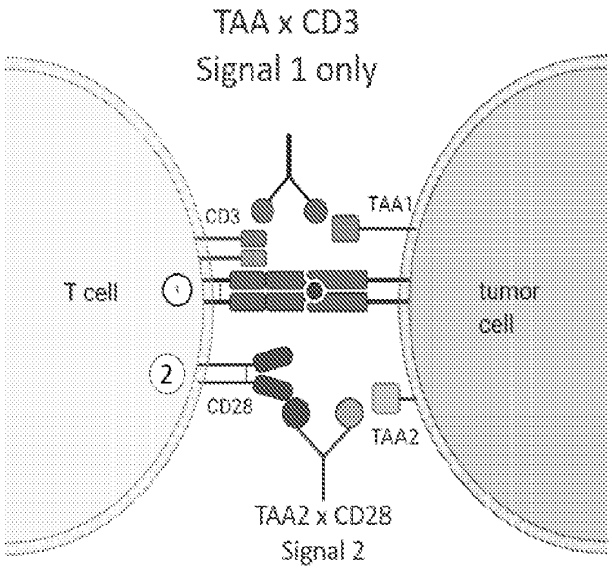


Figure 30A

>XENP41988 sacituzumab[Trop2]_H0L0_Fab-1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - sacituzumab[Trop2]_H0_IgG1_pI(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO:753)

QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVS
TAYLQISSLKADDTAVYFCARGGFGSSYWYFDVWGQGSLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO:754)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIKGKPGSGKPGSGKPGSGKPGSEVQLLESGGGLVQPGGSLRLSCAASGF
TFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR
QVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

Chain 3 - sacituzumab[Trop2]_L0 (SEQ ID NO:755)

DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISS
LQPEDFAVYYCQQHYITPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44424 1F11-1A3.315[Trop2]_H1_L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1F11-1A3.315[Trop2]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 756)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 757)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Figure 30B

Chain 3 - 1F11-1A3.315[Trop2]_L1 (SEQ ID NO: 758)
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44505 1F11-1A3.315[Trop2]_H1_L1_Fab-1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S
Chain 1 - 1F11-1A3.315[Trop2]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 759)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK
Chain 2 - 1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 760)
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIK/GKPGSGKPGSGKPGSGKPGS/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK
Chain 3 - 1F11-1A3.315[Trop2]_L1 (SEQ ID NO: 761)
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 31

>XENP41995 sacituzumab[Trop2]_H0L0_Fab-sacituzumab[Trop2]_H0L0_Fab-IgG1_pI(-)_Isosteric_A_/PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4

Chain 1 - sacituzumab[Trop2]_H0_IgG1_pI(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 626)

QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVS
TAYLQISSLKADDTAVYFCARGGFGSSYWYFDVWGQGSLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Chain 2 - sacituzumab[Trop2]_H0_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_L1.71_H1.14_scFv(GKPGS)4 (SEQ ID NO: 627)

QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVS
TAYLQISSLKADDTAVYFCARGGFGSSYWYFDVWGQGSLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG/GGGGSGGGGSG
GGGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFT
LTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEIK/GKPGSGKPGSGKPGSGKPGS/EVQLLESGGGLVQPGGSLRL
SCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA
KSGPGLRQVGFDYWGQGTLVTVSS

Chain 3 - sacituzumab[Trop2]_L0 (SEQ ID NO: 628)

DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISS
LQPEDFAVYYCQQHYITPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32A

CD3 High – [anti-CD3]_H1.30_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	629
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	630
vhCDR1	TYAMN	631
vhCDR2	RIRSKYNNYATYYADSVKG	632
vhCDR3	HGNFGDSYVSWFAY	633
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	634
vlCDR1	GSSTGAVTTSNYAN	635
vlCDR2	GTNKRAP	636
vlCDR3	ALWYSNHWV	637
Linker	GKPGSGKPGSGKPGSGKPGS	638

CD3 High-Int #1 – [anti-CD3]_H1.32_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	639
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	640
vhCDR1	TYAMN	641
vhCDR2	RIRSKANNYATYYADSVKG	642
vhCDR3	HGNFGDSYVSWFAY	643
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	644
vlCDR1	GSSTGAVTTSNYAN	645
vlCDR2	GTNKRAP	646
vlCDR3	ALWYSNHWV	647
Linker	GKPGSGKPGSGKPGSGKPGS	648

Figure 32B

CD3 High-Int #2 – [anti-CD3]_H1.89_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	649
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	650
vhCDR1	TYAMN	651
vhCDR2	RIRSKYNNYATYYADSVKG	652
vhCDR3	HGNFGDEYVSWFAY	653
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	654
vlCDR1	GSSTGAVTTSNYAN	655
vlCDR2	GTNKRAP	656
vlCDR3	ALWYSNHWV	657
Linker	GKPGSGKPGSGKPGSGKPGS	658

CD3 High-Int – [anti-CD3]_H1.90_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	659
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	660
vhCDR1	TYAMN	661
vhCDR2	RIRSKYNNYATYYADSVKG	662
vhCDR3	HGNFGDPYVSWFAY	663
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	664
vlCDR1	GSSTGAVTTSNYAN	665
vlCDR2	GTNKRAP	666
vlCDR3	ALWYSNHWV	667
Linker	GKPGSGKPGSGKPGSGKPGS	668

Figure 32C

Anti-CD3-Intermediate – [anti-CD3]_H1.33_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	669
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	670
vhCDR1	TYAMN	671
vhCDR2	RIRSKYNNYATYYADSVKG	672
vhCDR3	HGNFGDSYVSWFDY	673
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	674
vlCDR1	GSSTGAVTTSNYAN	675
vlCDR2	GTNKRAP	676
vlCDR3	ALWYSNHWV	677
Linker	GKPGSGKPGSGKPGSGKPGS	678

CD3 High-Int – [anti-CD3]_H1.31_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	679
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	680
vhCDR1	TYAMS	681
vhCDR2	RIRSKYNNYATYYADSVKG	682
vhCDR3	HGNFGDSYVSWFAY	683
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	684
vlCDR1	GSSTGAVTTSNYAN	685
vlCDR2	GTNKRAP	686
vlCDR3	ALWYSNHWV	687
Linker	GKPGSGKPGSGKPGSGKPGS	688

Figure 32D

CD3 High[VL-VH] – [anti-CD3] L1.47 H1.30 scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	689
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	690
vlCDR1	GSSTGAVTTSNYAN	691
vlCDR2	GTNKRAP	692
vlCDR3	ALWYSNHWV	693
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	694
vhCDR1	TYAMN	695
vhCDR2	RIRSKYNNYATYYADSVKG	696
vhCDR3	HGNFGDSYVSWFAY	697
Linker	GKPGSGKPGSGKPGSGKPGS	698

CD3 High-Int #1[VL-VH] – [anti-CD3] L1.47 H1.32 scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	699
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	700
vlCDR1	GSSTGAVTTSNYAN	701
vlCDR2	GTNKRAP	702
vlCDR3	ALWYSNHWV	703
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	704
vhCDR1	TYAMN	705
vhCDR2	RIRSKANNYATYYADSVKG	706
vhCDR3	HGNFGDSYVSWFAY	707
Linker	GKPGSGKPGSGKPGSGKPGS	708

Figure 32E

CD3 High-Int #2[VL-VH] – [anti-CD3]_L1.47_H1.89_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	709
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	710
vlCDR1	GSSTGAVTTSNYAN	711
vlCDR2	GTNKRAP	712
vlCDR3	ALWYSNHWV	713
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	714
vhCDR1	TYAMN	715
vhCDR2	RIRSKYNNYATYYADSVKG	716
vhCDR3	HGNFGDEYVSWFAY	717
Linker	GKPGSGKPGSGKPGSGKPGS	718

CD3 High-Int[VL-VH] – [anti-CD3]_L1.47_H1.90_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	719
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	720
vlCDR1	GSSTGAVTTSNYAN	721
vlCDR2	GTNKRAP	722
vlCDR3	ALWYSNHWV	723
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	724
vhCDR1	TYAMN	725
vhCDR2	RIRSKYNNYATYYADSVKG	726
vhCDR3	HGNFGDPYVSWFAY	727
Linker	GKPGSGKPGSGKPGSGKPGS	728

Figure 32F

Anti-CD3-Intermediate[VL-VH] – [anti-CD3]_L1.47_ H1.33_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	729
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	730
vlCDR1	GSSTGAVTTSNYAN	731
vlCDR2	GTNKRAP	732
vlCDR3	ALWYSNHWV	733
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	734
vhCDR1	TYAMN	735
vhCDR2	RIRSKYNNYATYYADSVKG	736
vhCDR3	HGNFGDSYVSWFDY	737
Linker	GKPGSGKPGSGKPGSGKPGS	738

CD3 High-Int[VL-VH] – [anti-CD3]_L1.47_ H1.31_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	739
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	740
vlCDR1	GSSTGAVTTSNYAN	741
vlCDR2	GTNKRAP	742
vlCDR3	ALWYSNHWV	743
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	744
vhCDR1	TYAMS	745
vhCDR2	RIRSKYNNYATYYADSVKG	746
vhCDR3	HGNFGDSYVSWFAY	747
Linker	GKPGSGKPGSGKPGSGKPGS	748

Figure 33A

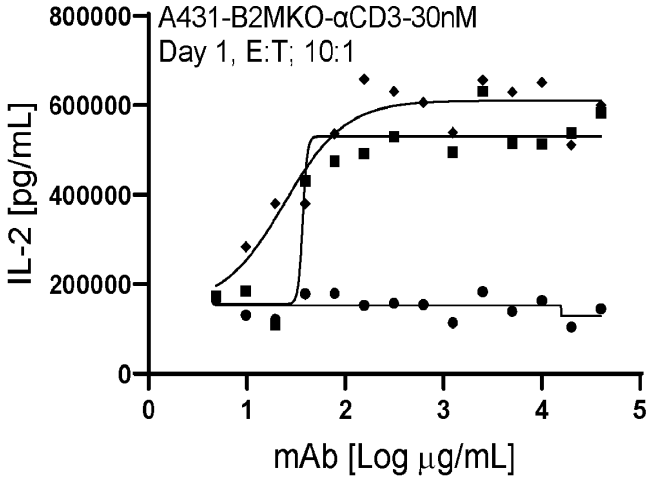
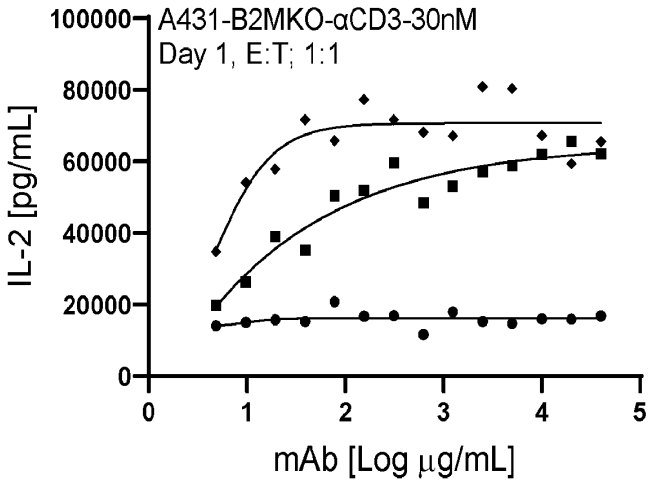


Figure 33B



PBS
XENP41995 Trop2 x CD28; 2 + 1 mAb-scFv
XENP41988 Trop2 x CD28; 1 + 1 Fab-scFv-Fc

Figure 34A

>1A7[CD28]_H1.103 (SEQ ID NO: 762)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERMDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.104 (SEQ ID NO: 763)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.105 (SEQ ID NO: 764)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERLDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.106 (SEQ ID NO: 765)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.107 (SEQ ID NO: 766)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESSDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.108 (SEQ ID NO: 767)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISEPNDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.109 (SEQ ID NO: 768)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERRDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.110 (SEQ ID NO: 769)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVWTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.111 (SEQ ID NO: 770)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERSDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.112 (SEQ ID NO: 771)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERQDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.113 (SEQ ID NO: 772)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERTDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.114 (SEQ ID NO: 773)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.115 (SEQ ID NO: 774)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVMTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.116 (SEQ ID NO: 775)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERKDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.117 (SEQ ID NO: 776)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERHDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 34B

>1A7[CD28]_H1.118 (SEQ ID NO: 777)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.119 (SEQ ID NO: 778)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIVERGDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.120 (SEQ ID NO: 779)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERYDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.121 (SEQ ID NO: 780)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.122 (SEQ ID NO: 781)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVTTISESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.123 (SEQ ID NO: 782)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISENLDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.124 (SEQ ID NO: 783)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESADVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.125 (SEQ ID NO: 784)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISEHGLSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.126 (SEQ ID NO: 785)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERDDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.127 (SEQ ID NO: 786)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISENRDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.128 (SEQ ID NO: 787)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERFDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.129 (SEQ ID NO: 788)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.130 (SEQ ID NO: 789)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.131 (SEQ ID NO: 790)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISEREDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.132 (SEQ ID NO: 791)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESSMSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 34C

>1A7[CD28]_H1.133 (SEQ ID NO: 792)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESVDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.134 (SEQ ID NO: 793)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVMTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.135 (SEQ ID NO: 794)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESWDHTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.136 (SEQ ID NO: 795)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERIDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.137 (SEQ ID NO: 796)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVVTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.138 (SEQ ID NO: 797)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVTTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

1A7 VH	**SEQ**	**SEQ ID**	
HFR1	EVQLLESGGGLVQPGGSLRLSCAASGFTFS	798	
HCDR1	SYYMS	799	
HFR2	WVRQAPGKGLEWVX	800	X is selected from S, W, M, T, V
HCDR2	TIX$_1$EX$_2$X$_3$X$_4$X$_5$TYYADSVKG	801	X$_1$ is selected from A, V, S; X$_2$ is selected from S, N, H, R; X$_3$ is selected from G, L, S, N, R, Q, T, K, H, Y, A, D, F, E, V, W, I, M; X$_4$ is selected from L, M, D; and X$_5$ is selected from S, P, V, Y, H
HFR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	335	
HCDR3	SGPGLRQVGFDY	336	
HFR4	WGQGTLVTVSS	337	

Figure 35

huCD28 KD (nM)	CD28 Mutations
20	1A7_H1.111_IGKV1-39_L1
21	1A7_H1.129_IGKV1-39_L1
28	1A7_H1.125_IGKV1-39_L1
29	1A7_H1.113_IGKV1-39_L1
38	1A7_H1.14_L1.71, 37 nM
43	1A7_H1.106_IGKV1-39_L1
44	1A7_H1.114_IGKV1-39_L1
46	1A7_H1.130_IGKV1-39_L1
57	1A7_H1.107_IGKV1-39_L1
63	1A7_H1.118_IGKV1-39_L1

Figure 36A

1F11-1A3.315[TROP2]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEW MGIINPGGGSTGYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCARDDVVAADVFDYWGQGTLVTVSS	802
vhCDR1	GYTFTRYYMH	803
vhCDR2	IINPGGGSTGYAQKFQG	804
vhCDR3	DDVVAADVFDY	805
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	806
vlCDR1	RASQSISSYLN	807
vlCDR2	AASSLQS	808
vlCDR3	QQSYSTPYT	809

>1F11-1A3.315[Trop2]_H1.1 (SEQ ID NO: 810)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.2 (SEQ ID NO: 811)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.3 (SEQ ID NO: 812)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.4 (SEQ ID NO: 813)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.5 (SEQ ID NO: 814)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.6 (SEQ ID NO: 815)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.7 (SEQ ID NO: 816)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIINPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.8 (SEQ ID NO: 817)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.9 (SEQ ID NO: 818)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.10 (SEQ ID NO: 819)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.11 (SEQ ID NO: 820)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS

Figure 36B

>1F11-1A3.315[Trop2]_H1.12 (SEQ ID NO: 821)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.13 (SEQ ID NO: 822)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.14 (SEQ ID NO: 823)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.15 (SEQ ID NO: 824)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.16 (SEQ ID NO: 825)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.17 (SEQ ID NO: 826)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.18 (SEQ ID NO: 827)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.19 (SEQ ID NO: 828)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.20 (SEQ ID NO: 829)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.21 (SEQ ID NO: 830)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.22 (SEQ ID NO: 831)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTKADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.23 (SEQ ID NO: 832)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYVHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.24 (SEQ ID NO: 833)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTDYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.25 (SEQ ID NO: 834)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTLYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.26 (SEQ ID NO: 835)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVMAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.27 (SEQ ID NO: 836)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTDYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.28 (SEQ ID NO: 837)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTLYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS

Figure 36C

>1F11-1A3.315[Trop2]_H1.29 (SEQ ID NO: 838)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYVHWVRQAPGQGLEWMGIIEPGGGSTDYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.30 (SEQ ID NO: 839)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYVHWVRQAPGQGLEWMGIIEPGGGSTLYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVTAADVFDYWGQGTLVTVSS
>1F11-1A3.315[Trop2]_H1.31 (SEQ ID NO: 840)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYVHWVRQAPGQGLEWMGIIEPGGGSTDYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS

1F11-1A3.315 VH	**SEQ**	**SEQ ID**	
HFR1	QVQLVQSGAEVKKPGASVKVSCKAS	841	
HCDR1	GYTX$_1$TRYYX$_2$H	842	X1 is selected from L, F; X2 is selected from M, V
HFR2	WVRQAPGQGLEWMG	843	
HCDR2	IIX$_1$PGGGSTX$_2$YAQKFQG	844	X1 is selected from N, E; X2 is selected from G, T, S, D, L
HFR3	RVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR	845	
HCDR3	DDVX$_1$X$_2$ADVFDY	846	X1 is selected from V, T, M; X2 is selected from A, K
HFR4	WGQGTLVTVSS	847	

Figure 37

	Human TROP2			Cyno TROP2		
	k_a (M-1 s-1)	k_d (s-1)	K_D	k_a (M-1 s-1)	k_d (s-1)	K_D
1F11-1A3.315[Trop2]_H1_L1	1.90E+05	1.20E-03	6.50E-09	2.10E+05	2.10E-03	9.90E-09
1F11-1A3.315[Trop2]_H1.1_L1	2.40E+05	4.80E-04	2.00E-09	2.70E+05	7.30E-04	2.70E-09
1F11-1A3.315[Trop2]_H1.2_L1	2.50E+05	4.70E-04	2.00E-09	2.70E+05	6.70E-04	2.50E-09
1F11-1A3.315[Trop2]_H1.3_L1	2.00E+05	1.20E-03	6.00E-09	2.30E+05	2.00E-03	8.60E-09
1F11-1A3.315[Trop2]_H1.4_L1	1.80E+05	1.10E-03	6.70E-09	2.20E+05	2.10E-03	9.40E-09
1F11-1A3.315[Trop2]_H1.5_L1	2.40E+05	8.10E-04	3.40E-09	3.20E+05	1.40E-03	4.50E-09
1F11-1A3.315[Trop2]_H1.6_L1	3.20E+05	2.50E-04	7.70E-10	2.90E+05	4.20E-04	1.50E-09
1F11-1A3.315[Trop2]_H1.7_L1	2.80E+05	5.30E-04	1.90E-09	2.80E+05	7.70E-04	2.80E-09
1F11-1A3.315[Trop2]_H1.8_L1	2.30E+05	6.00E-04	2.70E-09	2.50E+05	7.70E-04	3.10E-09
1F11-1A3.315[Trop2]_H1.9_L1	2.40E+05	4.00E-04	1.70E-09	3.20E+05	4.60E-04	1.40E-09
1F11-1A3.315[Trop2]_H1.10_L1	3.30E+05	3.30E-04	9.80E-10	3.40E+05	5.30E-04	1.50E-09
1F11-1A3.315[Trop2]_H1.11_L1	3.40E+05	5.10E-04	1.50E-09	3.00E+05	7.90E-04	2.60E-09
1F11-1A3.315[Trop2]_H1.12_L1	2.70E+05	3.30E-04	1.30E-09	3.60E+05	3.80E-04	1.10E-09
1F11-1A3.315[Trop2]_H1.13_L1	3.30E+05	5.10E-04	1.70E-09	3.00E+05	8.40E-04	2.80E-09
1F11-1A3.315[Trop2]_H1.14_L1	2.90E+05	7.70E-04	2.60E-09	3.60E+05	1.30E-03	3.70E-09
1F11-1A3.315[Trop2]_H1.15_L1	2.30E+05	9.10E-04	4.10E-09	3.10E+05	1.60E-03	5.10E-09
1F11-1A3.315[Trop2]_H1.16_L1	2.70E+05	2.90E-04	1.10E-09	3.10E+05	4.70E-04	1.50E-09
1F11-1A3.315[Trop2]_H1.17_L1	2.70E+05	1.70E-04	6.20E-10	3.50E+05	2.80E-04	8.10E-10
1F11-1A3.315[Trop2]_H1.18_L1	3.20E+05	2.00E-04	6.60E-10	3.70E+05	3.40E-04	9.30E-10
1F11-1A3.315[Trop2]_H1.19_L1	4.10E+05	1.00E-04	2.50E-10	4.50E+05	2.00E-04	4.60E-10
1F11-1A3.315[Trop2]_H1.20_L1	3.20E+05	3.50E-04	1.10E-09	3.40E+05	5.90E-04	1.70E-09
1F11-1A3.315[Trop2]_H1.21_L1	2.10E+05	3.20E-04	1.50E-09	3.90E+05	3.10E-04	8.10E-10
1F11-1A3.315[Trop2]_H1.22_L1	3.80E+05	2.10E-04	5.50E-10	4.00E+05	2.80E-04	7.00E-10
1F11-1A3.315[Trop2]_H1.23_L1	1.70E+05	1.20E-03	7.20E-09	2.30E+05	2.60E-03	1.10E-08
1F11-1A3.315[Trop2]_H1.24_L1	2.40E+05	1.30E-03	5.70E-09	2.50E+05	2.60E-03	1.10E-08
1F11-1A3.315[Trop2]_H1.25_L1	1.70E+05	1.40E-03	8.50E-09	1.90E+05	2.70E-03	1.40E-08
1F11-1A3.315[Trop2]_H1.26_L1	1.90E+05	8.80E-04	4.60E-09	2.50E+05	1.50E-03	6.20E-09
1F11-1A3.315[Trop2]_H1.27_L1	3.30E+05	2.80E-04	9.30E-10	3.90E+05	4.70E-04	1.20E-09
1F11-1A3.315[Trop2]_H1.28_L1	2.10E+05	3.60E-04	1.90E-09	2.70E+05	5.50E-04	2.10E-09
1F11-1A3.315[Trop2]_H1.29_L1	1.50E+05	2.90E-04	2.10E-09	1.90E+05	3.80E-04	2.10E-09
1F11-1A3.315[Trop2]_H1.30_L1	1.70E+05	3.70E-04	2.20E-09	1.50E+05	5.50E-04	3.70E-09
1F11-1A3.315[Trop2]_H1.31_L1	3.00E+05	1.30E-04	4.30E-10	3.00E+05	1.40E-04	4.80E-10

Figure 38A

>XENP44595 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 848)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 849)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 850)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44596 1A7[CD28]_H1.106_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.106_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 851)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 852)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 853)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38B

>XENP44597 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.10_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 854)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.10_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 855)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 856)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44598 1A7[CD28]_H1.106_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.10_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.106_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 857)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.10_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 858)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 859)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38C

>XENP44599 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 860)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.19_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 861)

QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 862)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44600 1A7[CD28]_H1.106_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.106_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 863)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.19_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 864)

QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 865)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38D

>XENP49313 1A7[CD28]_H1.118_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.118_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 866)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 867)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 868)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP49314 1A7[CD28]_H1.118_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.10_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.118_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 869)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.10_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 870)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 871)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38E

>XENP49315 1A7[CD28]_H1.118_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.118_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 872)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.19_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 873)

QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 874)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39A

>XENP44601 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab_(GKPGS)2_1F11-1A3.315[Trop2]_H1_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 875)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_(GKPGS)2_1F11-1A3.315[Trop2]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 876)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRD
TSTSTVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 877)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44602 1A7[CD28]_H1.106_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab_(GKPGS)2_1F11-1A3.315[Trop2]_H1_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.106_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 878)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_(GKPGS)2_1F11-1A3.315[Trop2]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 879)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRD
TSTSTVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 880)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39B

>XENP44869 1F11-1A3.315[Trop2]_H1_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab_(GKPGS)2_1A7[CD28]_H1.129_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1F11-1A3.315[Trop2]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 881)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_(GKPGS)2_1A7[CD28]_H1.129_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 882)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 883)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44870 1F11-1A3.315[Trop2]_H1_L1_Fab-1F11-1A3.315[Trop2]_H1_L1_Fab_(GKPGS)2_1A7[CD28]_H1.106_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1F11-1A3.315[Trop2]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 884)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1_(GKPGS)2_1A7[CD28]_H1.106_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 885)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEWMGIINPGGGSTGYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVAADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 39C

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 886)
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44871 1F11-1A3.315[Trop2]_H1.19_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab_(GKPGS)2_1A7[CD28]_H1.129_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
Chain 1 - 1F11-1A3.315[Trop2]_H1.19_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 887)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK
Chain 2 - 1F11-1A3.315[Trop2]_H1.19_(GKPGS)2_1A7[CD28]_H1.129_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 888)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK
Chain 3 - IGKV1-39_L1 (SEQ ID NO: 889)
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44872 1F11-1A3.315[Trop2]_H1.19_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab_(GKPGS)2_1A7[CD28]_H1.106_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
Chain 1 - 1F11-1A3.315[Trop2]_H1.19_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 890)
QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 39D

Chain 2 - 1F11-1A3.315[Trop2]_H1.19_(GKPGS)2_1A7[CD28]_H1.106_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 891)

QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 892)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figures 40A

>XENP44623 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-Numax[RSV]_H1_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 893)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - Numax[RSV]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 894)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISKDTSK
NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 895)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44624 1A7[CD28]_H1.106_IGKV1-39_L1_Fab-Numax[RSV]_H1_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.106_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 896)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - Numax[RSV]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 897)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISKDTSK
NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 898)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figures 40B

>XENP44880 1A7[CD28]_H1.129_IGKV1-39_L1_Fab-1F11-1A3.315[Trop2]_H1.19_L1_Fab_(GKPGS)2_Numax[RSV]_H1_IGKV1-39_L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - 1A7[CD28]_H1.129_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 899)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1F11-1A3.315[Trop2]_H1.19_(GKPGS)2_Numax[RSV]_H1_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 900)

QVQLVQSGAEVKKPGASVKVSCKASGYTLTRYYMHWVRQAPGQGLEWMGIIEPGGGSTTYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARDDVVKADVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPGSGK
PGS/QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISK
DTSKNQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - IGKV1-39_L1 (SEQ ID NO: 901)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 41

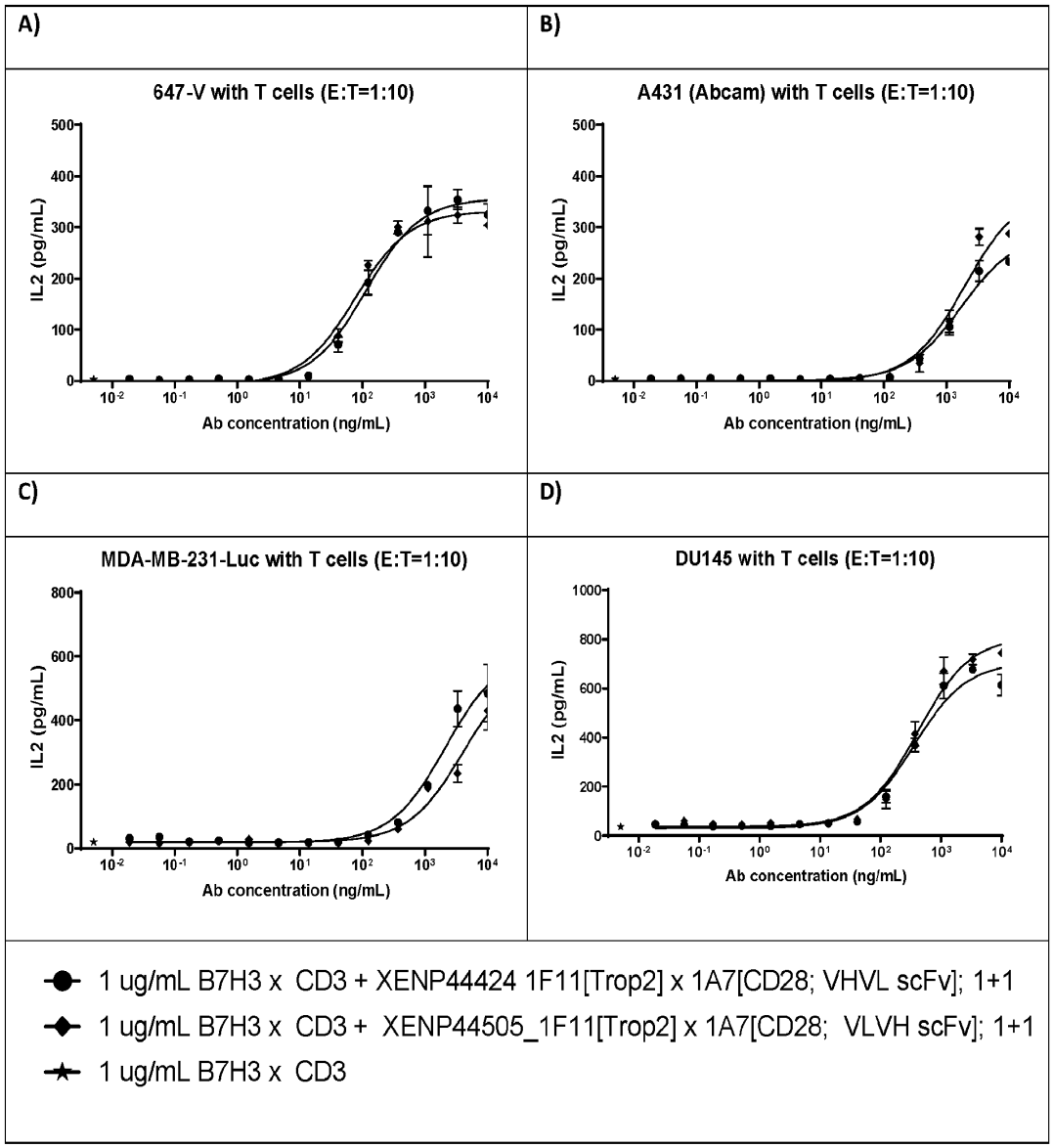

A)
647-V with T cells (E:T=1:10)
IL2 (pg/mL)
Ab concentration (ng/mL)
B)
A431 (Abcam) with T cells (E:T=1:10)
IL2 (pg/mL)
Ab concentration (ng/mL)
C)
MDA-MB-231-Luc with T cells (E:T=1:10)
IL2 (pg/mL)
Ab concentration (ng/mL)
D)
DU145 with T cells (E:T=1:10)
IL2 (pg/mL)
Ab concentration (ng/mL)
1 ug/mL B7H3 x CD3 + XENP44424 1F11[Trop2] x 1A7[CD28; VHVL scFv]; 1+1
1 ug/mL B7H3 x CD3 + XENP44505_1F11[Trop2] x 1A7[CD28; VLVH scFv]; 1+1
1 ug/mL B7H3 x CD3

Figure 42

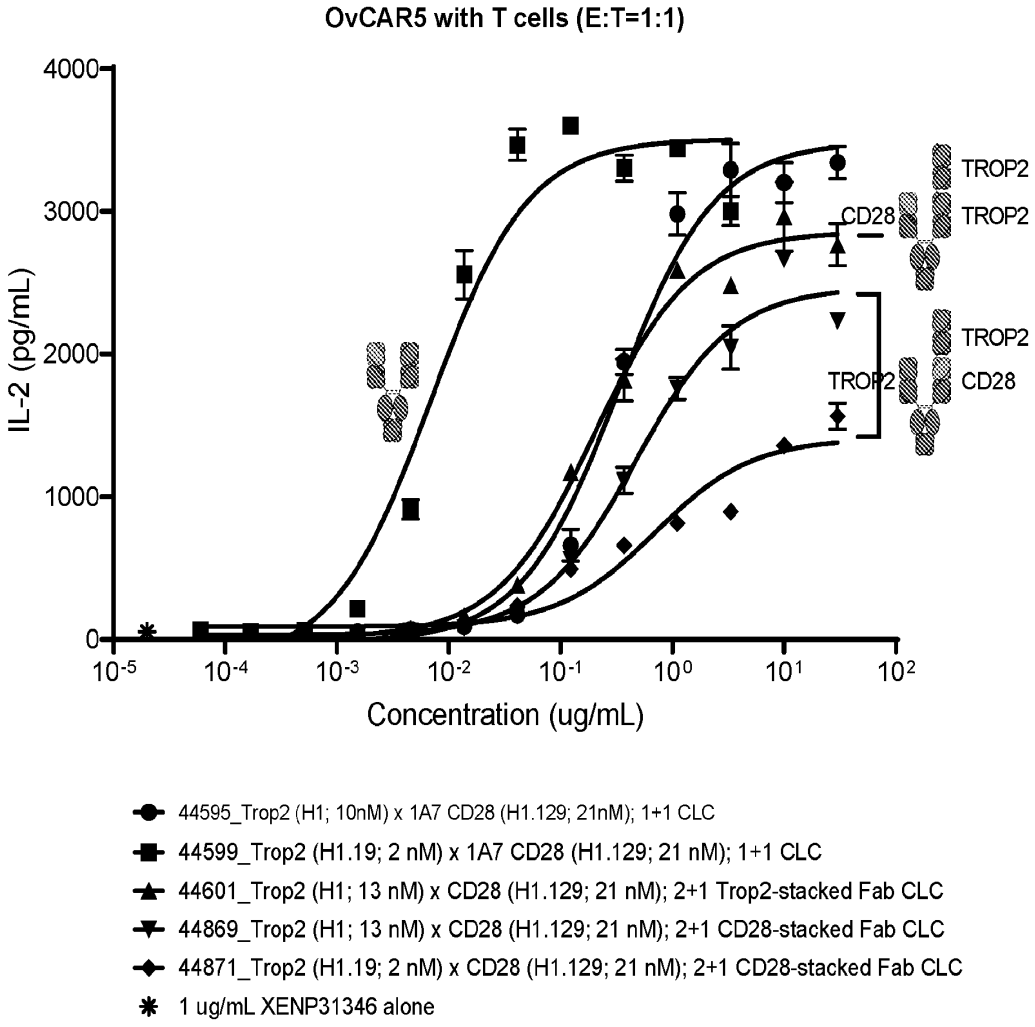

OvCAR5 with T cells (E:T=1:1)
IL-2 (pg/mL)
4000
3000
2000
1000
0
10^{-5}
10^{-4}
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
Concentration (ug/mL)
TROP2
CD28
TROP2
TROP2
TROP2
CD28
44595_Trop2 (H1; 10nM) x 1A7 CD28 (H1.129; 21nM); 1+1 CLC
44599_Trop2 (H1.19; 2 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44601_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 Trop2-stacked Fab CLC
44869_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44871_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
1 ug/mL XENP31346 alone

Figure 43

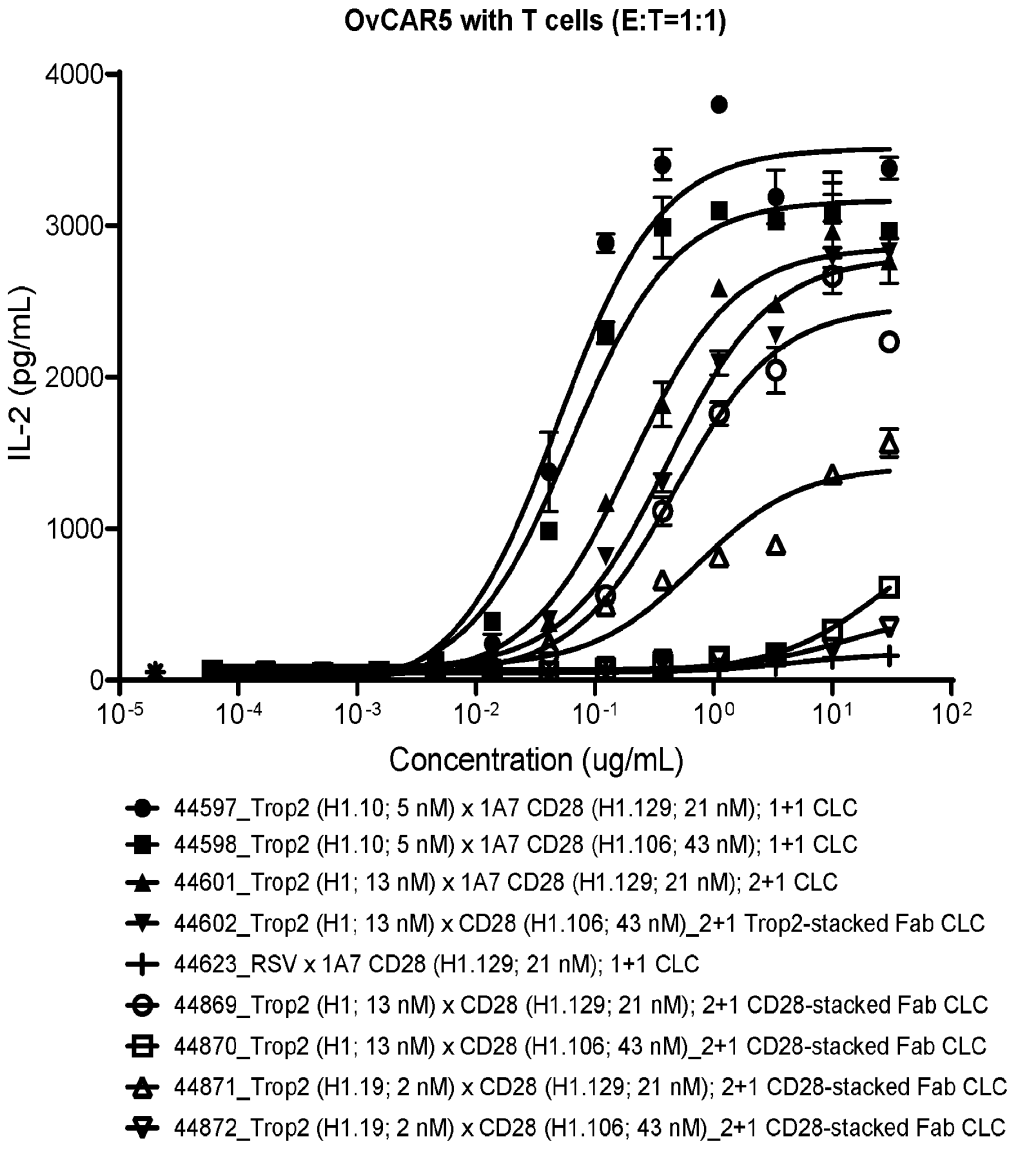

OvCAR5 with T cells (E:T=1:1)
IL-2 (pg/mL)
4000
3000
2000
1000
0
10-5
10-4
10-3
10-2
10-1
100
101
102
Concentration (ug/mL)
44597_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44598_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC
44601_Trop2 (H1; 13 nM) x 1A7 CD28 (H1.129; 21 nM); 2+1 CLC
44602_Trop2 (H1; 13 nM) x CD28 (H1.106; 43 nM)_2+1 Trop2-stacked Fab CLC
44623_RSV x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44869_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44870_Trop2 (H1; 13 nM) x CD28 (H1.106; 43 nM)_2+1 CD28-stacked Fab CLC
44871_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44872_Trop2 (H1.19; 2 nM) x CD28 (H1.106; 43 nM)_2+1 CD28-stacked Fab CLC

Figure 44

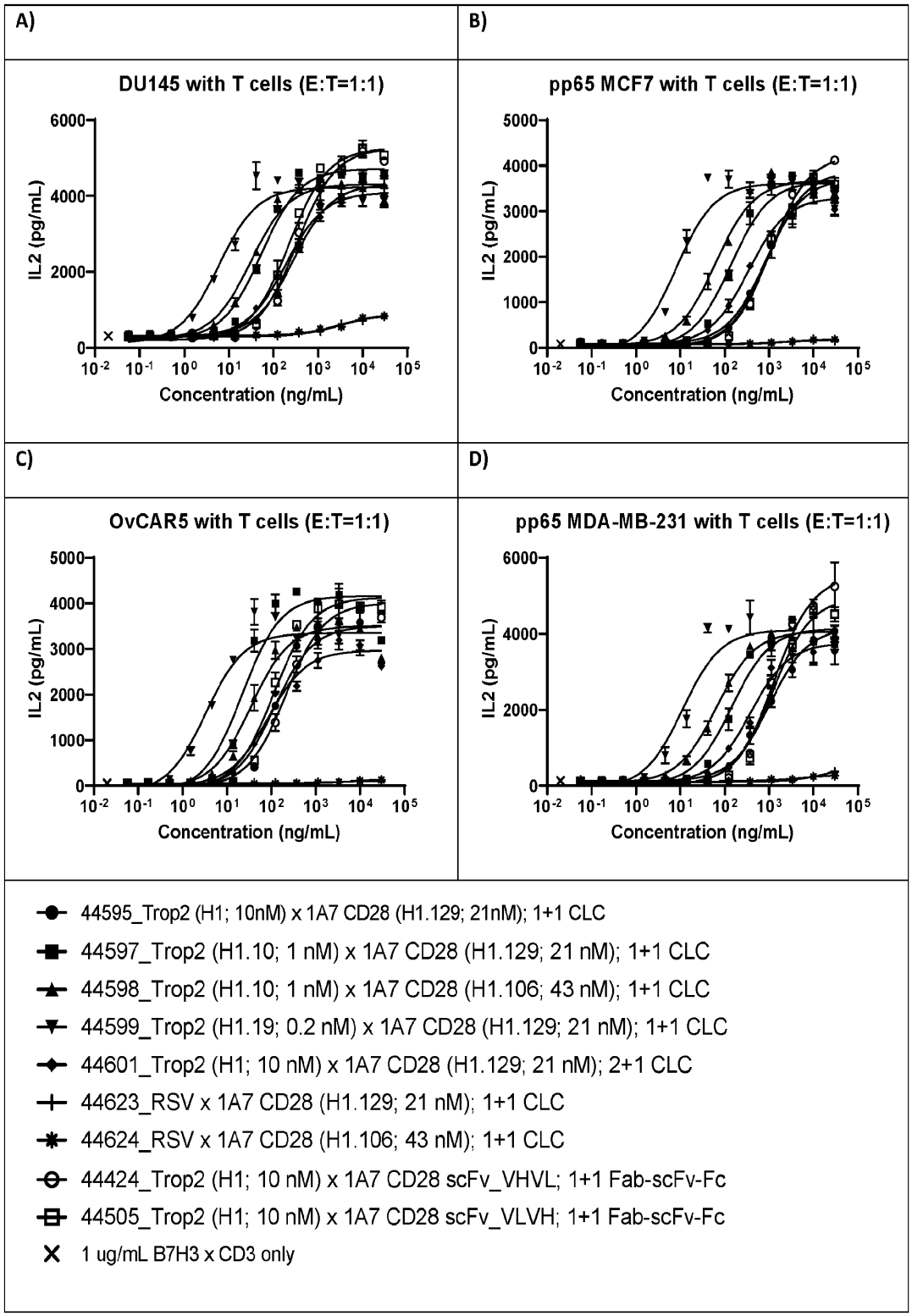

A)
DU145 with T cells (E:T=1:1)
IL2 (pg/mL)
Concentration (ng/mL)
B)
pp65 MCF7 with T cells (E:T=1:1)
IL2 (pg/mL)
Concentration (ng/mL)
C)
OvCAR5 with T cells (E:T=1:1)
IL2 (pg/mL)
Concentration (ng/mL)
D)
pp65 MDA-MB-231 with T cells (E:T=1:1)
IL2 (pg/mL)
Concentration (ng/mL)
44595_Trop2 (H1; 10nM) x 1A7 CD28 (H1.129; 21nM); 1+1 CLC
44597_Trop2 (H1.10; 1 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44598_Trop2 (H1.10; 1 nM) x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC
44599_Trop2 (H1.19; 0.2 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44601_Trop2 (H1; 10 nM) x 1A7 CD28 (H1.129; 21 nM); 2+1 CLC
44623_RSV x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
44624_RSV x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC
44424_Trop2 (H1; 10 nM) x 1A7 CD28 scFv_VHVL; 1+1 Fab-scFv-Fc
44505_Trop2 (H1; 10 nM) x 1A7 CD28 scFv_VLVH; 1+1 Fab-scFv-Fc
1 ug/mL B7H3 x CD3 only

Figure 45

EC50 (ng/mL) by IL2 release	DU145	pp65 MDA-MB-231	OvCAR5	pp65 MCF7
44595_Trop2 (H1; 13 nM) x 1A7 CD28 (H1.129; 21nM); 1+1 CLC	279	1028	117	830
44597_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC	53	144	22	140
44598_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC	31	65	34	62
44599_Trop2 (H1.19; 2 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC	6	11	3	8
44601_Trop2 (H1; 13 nM) x 1A7 CD28 (H1.129; 21 nM); 2+1 CLC	187	379	84	341
44624_RSV x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC	333	1316	210	1086
44505_Trop2 (H1; 13 nM) x 1A7 CD28 scFv_VLVH; 1+1 Fab-scFv-Fc	223	1205	114	931

Figure 46

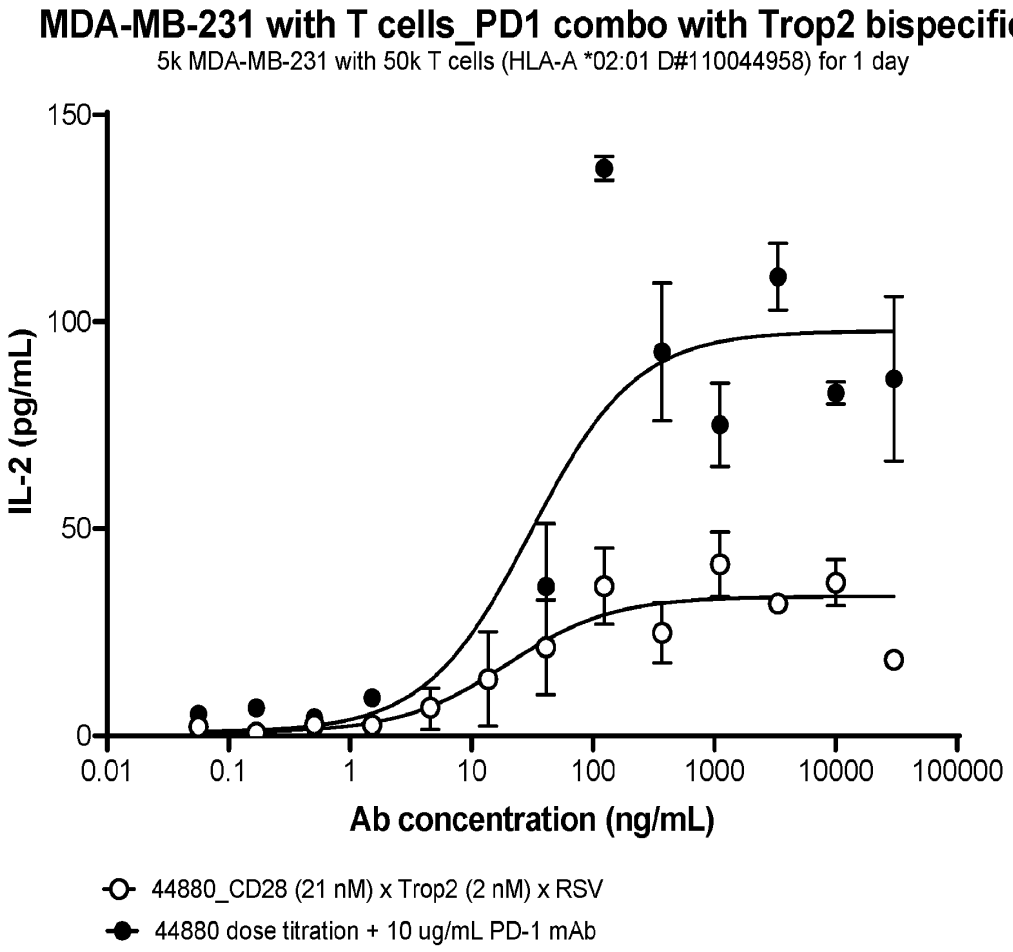

MDA-MB-231 with T cells_PD1 combo with Trop2 bispecific
5k MDA-MB-231 with 50k T cells (HLA-A *02:01 D#110044958) for 1 day
IL-2 (pg/mL)
150
100
50
0
0.01
0.1
1
10
100
1000
10000
100000
Ab concentration (ng/mL)
44880_CD28 (21 nM) x Trop2 (2 nM) x RSV
44880 dose titration + 10 ug/mL PD-1 mAb

Figure 47

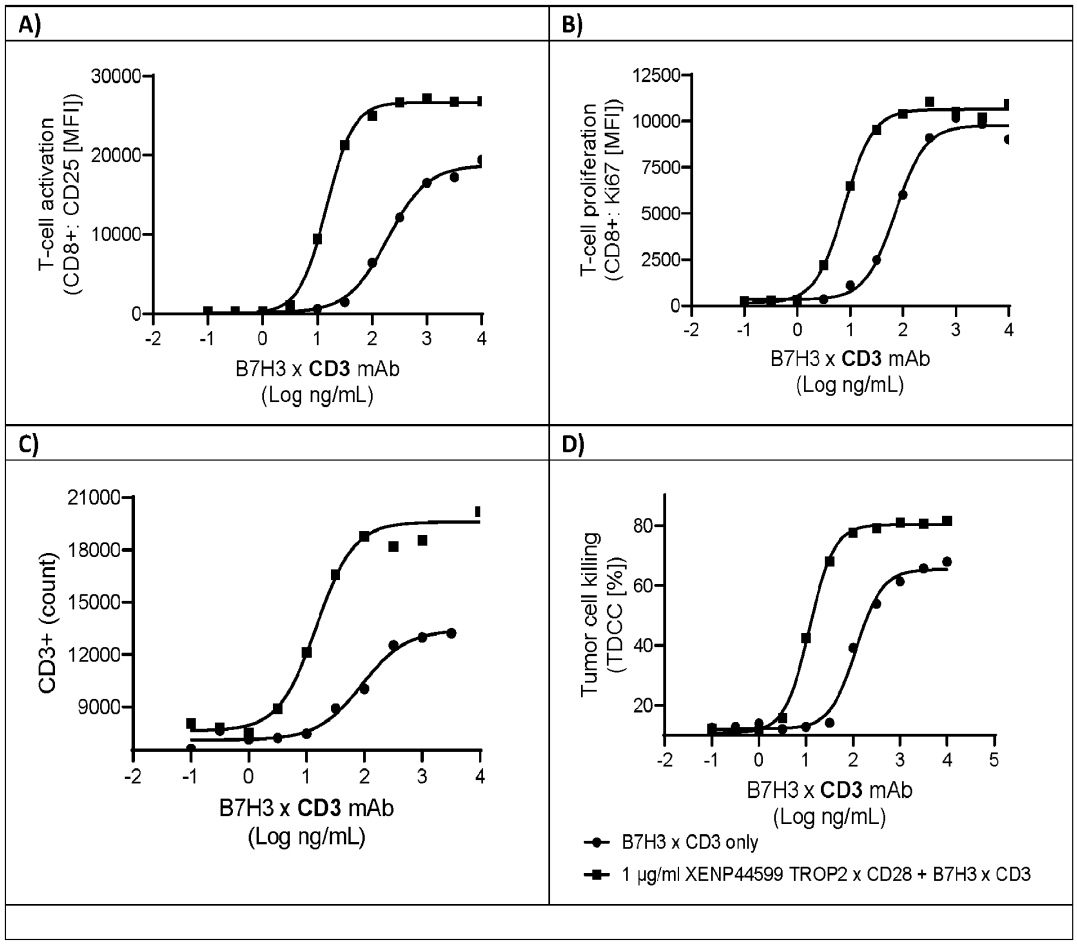
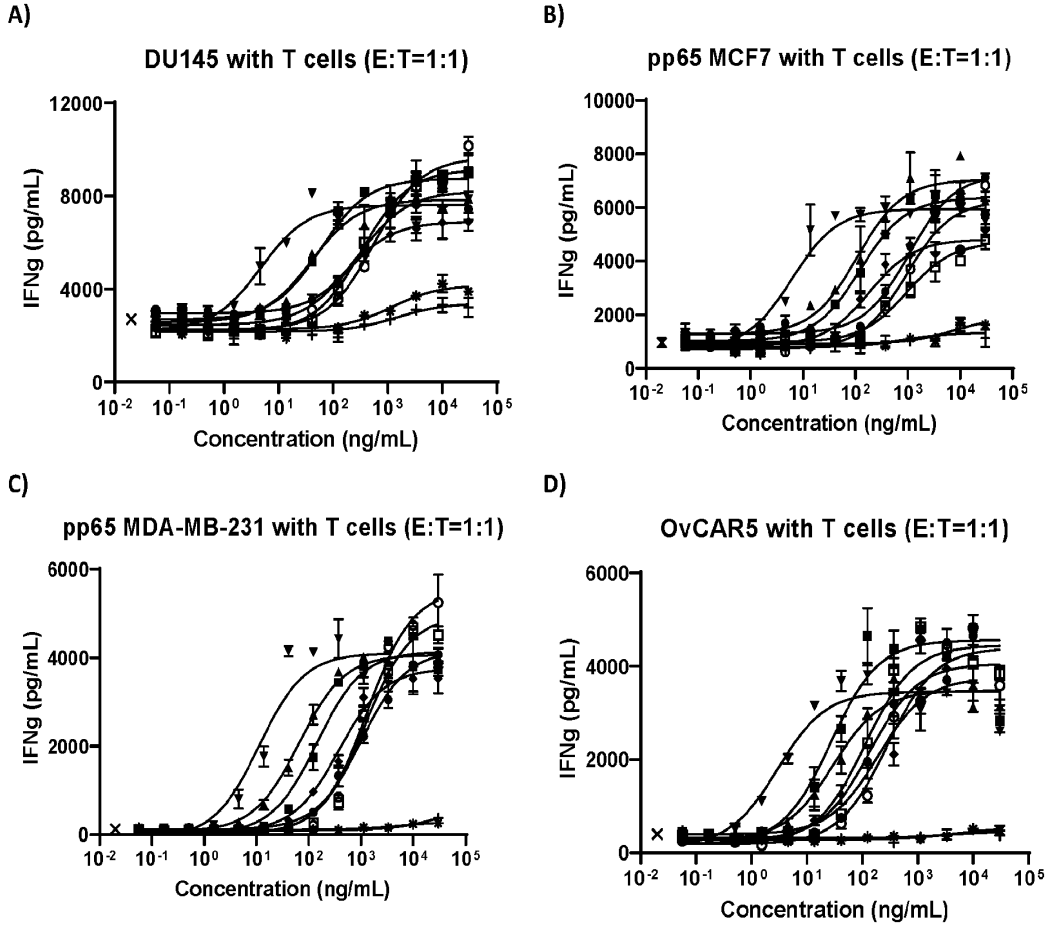

A)
T-cell activation (CD8+: CD25 [MFI])
30000
20000
10000
0
-2 -1 0 1 2 3 4
B7H3 x CD3 mAb (Log ng/mL)
B)
T-cell proliferation (CD8+: Ki67 [MFI])
12500
10000
7500
5000
2500
0
-2 -1 0 1 2 3 4
B7H3 x CD3 mAb (Log ng/mL)
C)
CD3+ (count)
21000
18000
15000
12000
9000
-2 -1 0 1 2 3 4
B7H3 x CD3 mAb (Log ng/mL)
D)
Tumor cell killing (TDCC [%])
80
60
40
20
-2 -1 0 1 2 3 4 5
B7H3 x CD3 mAb (Log ng/mL)
B7H3 x CD3 only
1 µg/ml XENP44599 TROP2 x CD28 + B7H3 x CD3

Figure 48



- 44595_Trop2 (H1; 13nM) x 1A7 CD28 (H1.129; 21nM); 1+1 CLC
- 44597_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
- 44598_Trop2 (H1.10; 5 nM) x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC
- 44599_Trop2 (H1.19; 2 nM) x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
- 44601_Trop2 (H1; 13 nM) x 1A7 CD28 (H1.129; 21 nM); 2+1 CLC
- 44623_RSV x 1A7 CD28 (H1.129; 21 nM); 1+1 CLC
- 44624_RSV x 1A7 CD28 (H1.106; 43 nM); 1+1 CLC
- 44424_Trop2 (H1; 13 nM) x 1A7 CD28 scFv_VHVL; 1+1 Fab-scFv-Fc
- 44505_Trop2 (H1; 13 nM) x 1A7 CD28 scFv_VLVH; 1+1 Fab-scFv-Fc
- 1 ug/mL B7H3 x CD3 only

Figure 49

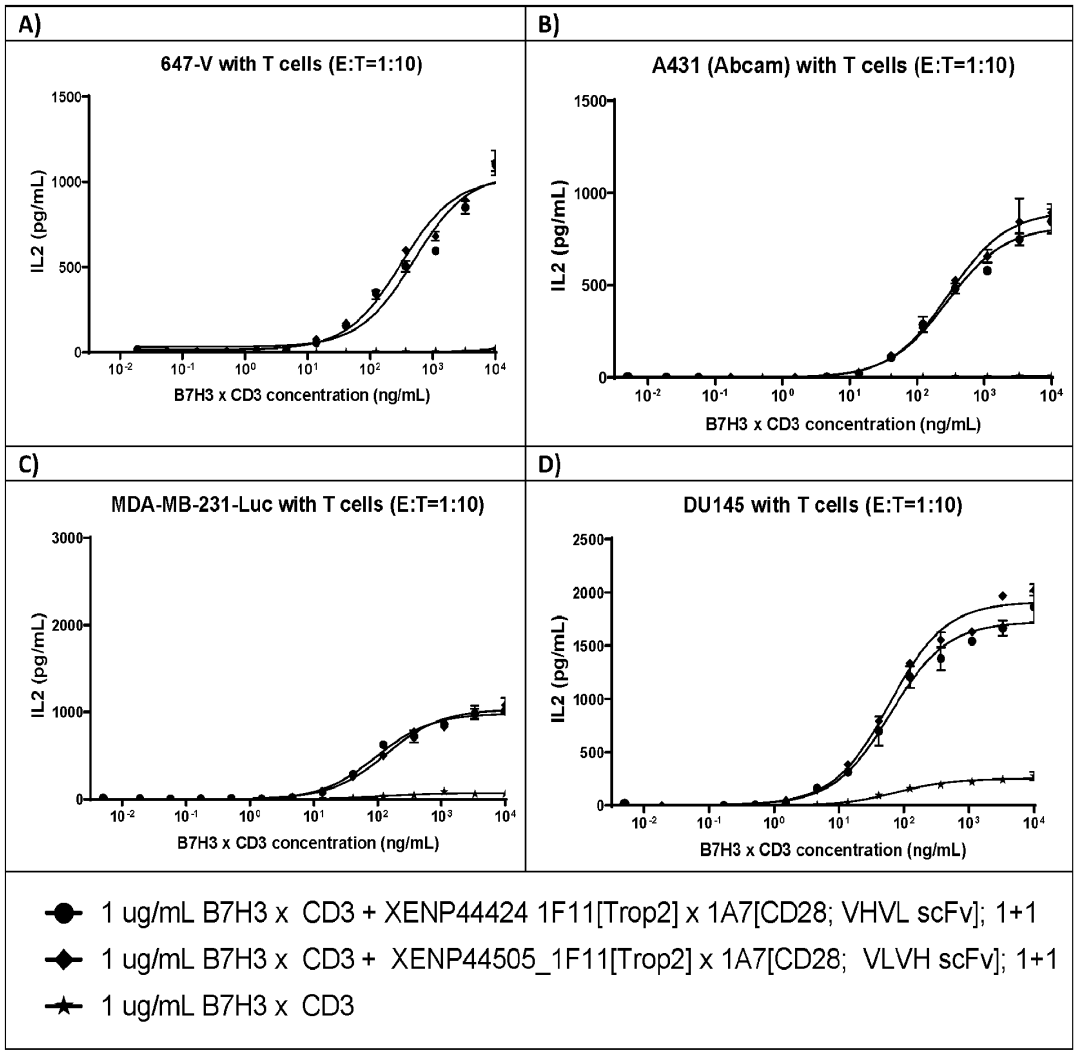

A)
647-V with T cells (E:T=1:10)
IL2 (pg/mL)
B7H3 x CD3 concentration (ng/mL)
B)
A431 (Abcam) with T cells (E:T=1:10)
IL2 (pg/mL)
B7H3 x CD3 concentration (ng/mL)
C)
MDA-MB-231-Luc with T cells (E:T=1:10)
IL2 (pg/mL)
B7H3 x CD3 concentration (ng/mL)
D)
DU145 with T cells (E:T=1:10)
IL2 (pg/mL)
B7H3 x CD3 concentration (ng/mL)
1 ug/mL B7H3 x CD3 + XENP44424 1F11[Trop2] x 1A7[CD28; VHVL scFv]; 1+1
1 ug/mL B7H3 x CD3 + XENP44505_1F11[Trop2] x 1A7[CD28; VLVH scFv]; 1+1
1 ug/mL B7H3 x CD3

Figure 50

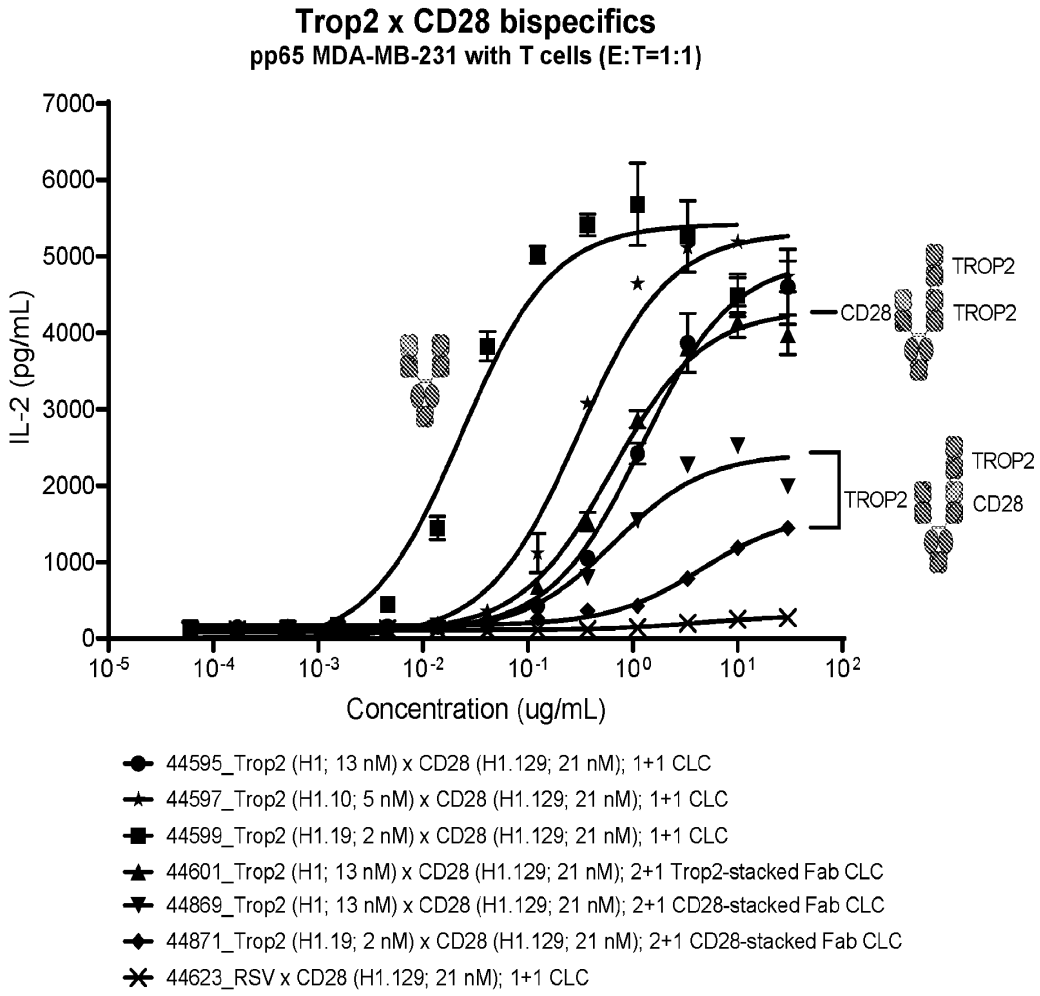

Trop2 x CD28 bispecifics
pp65 MDA-MB-231 with T cells (E:T=1:1)
IL-2 (pg/mL)
7000
6000
5000
4000
3000
2000
1000
0
10-5
10-4
10-3
10-2
10-1
100
101
102
Concentration (ug/mL)
CD28
TROP2
TROP2
TROP2
TROP2
CD28
44595_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 1+1 CLC
44597_Trop2 (H1.10; 5 nM) x CD28 (H1.129; 21 nM); 1+1 CLC
44599_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM); 1+1 CLC
44601_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 Trop2-stacked Fab CLC
44869_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44871_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44623_RSV x CD28 (H1.129; 21 nM); 1+1 CLC

Figure 51

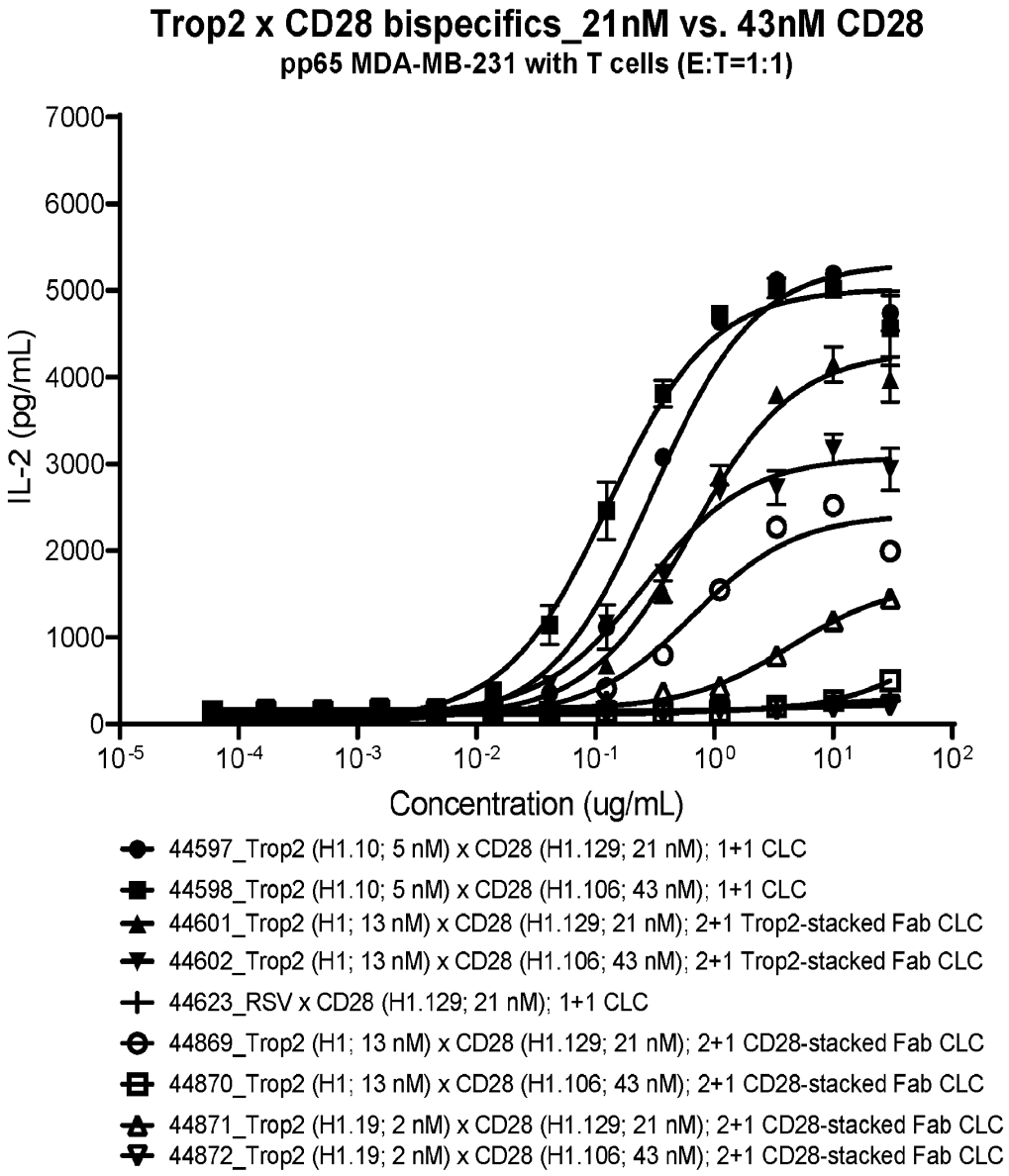

Trop2 x CD28 bispecifics_21nM vs. 43nM CD28
pp65 MDA-MB-231 with T cells (E:T=1:1)
IL-2 (pg/mL)
7000
6000
5000
4000
3000
2000
1000
0
10-5
10-4
10-3
10-2
10-1
100
101
102
Concentration (ug/mL)
44597_Trop2 (H1.10; 5 nM) x CD28 (H1.129; 21 nM); 1+1 CLC
44598_Trop2 (H1.10; 5 nM) x CD28 (H1.106; 43 nM); 1+1 CLC
44601_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 Trop2-stacked Fab CLC
44602_Trop2 (H1; 13 nM) x CD28 (H1.106; 43 nM); 2+1 Trop2-stacked Fab CLC
44623_RSV x CD28 (H1.129; 21 nM); 1+1 CLC
44869_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44870_Trop2 (H1; 13 nM) x CD28 (H1.106; 43 nM); 2+1 CD28-stacked Fab CLC
44871_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM); 2+1 CD28-stacked Fab CLC
44872_Trop2 (H1.19; 2 nM) x CD28 (H1.106; 43 nM); 2+1 CD28-stacked Fab CLC

Figure 52

2C5A3.316[TROP2]_H1L1

	sequence	**SEQ ID NO:**
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTTSGISWVRQAPGQGLEW MGGIVPLLGTVNYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCARSGAATDARYGLDYWGQGTLVTVSS	902
vhCDR1	TSGIS	903
vhCDR2	GIVPLLGTVNYAQKFQG	904
vhCDR3	SGAATDARYGLDY	905
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	906
vlCDR1	RASQSISSYLN	907
vlCDR2	AASSLQS	908
vlCDR3	QQSYSTPYT	909

Figure 53

1A3A4.312[TROP2] H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTRHYMHWVRQAPGQGLEW MGIINPGGGATSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCAREDYAGKWWGMDYWGQGTLVTVSS	910
vhCDR1	RHYMH	911
vhCDR2	IINPGGGATSYAQKFQG	912
vhCDR3	EDYAGKWWGMDY	913
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	914
vlCDR1	RASQSISSYLN	915
vlCDR2	AASSLQS	916
vlCDR3	QQSYSTPYT	917

Figure 54

1B2A4.312[TROP2] H1L1

	sequence	**SEQ ID NO:**
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGSYMHWVRQAPGQGLEW MGIINPSGESTVYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCARDPGGSWPFSYALDYWGQGTLVTVSS	918
vhCDR1	GSYMH	919
vhCDR2	IINPSGESTVYAQKFQG	920
vhCDR3	DPGGSWPFSYALDY	921
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	922
vlCDR1	RASQSISSYLN	923
vlCDR2	AASSLQS	924
vlCDR3	QQSYSTPYT	925

Figure 55

1B11A3.316[TROP2]_H1L1

	sequence	**SEQ ID NO:**
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTRYYMHWVRQAPGQGLEW MGIINPGGGSTIYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVY YCARDDVIVDAFDYWGQGTLVTVSS	926
vhCDR1	RYYMH	927
vhCDR2	IINPGGGSTIYAQKFQG	928
vhCDR3	DDVIVDAFDY	929
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	930
vlCDR1	RASQSISSYLN	931
vlCDR2	AASSLQS	932
vlCDR3	QQSYSTPYT	933

Figure 56

1C9A4.313[TROP2]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNYAIGWVRQAPGQGLEW MGGIVPIFGVADYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCAREGWYLLNYFDYWGQGTLVTVSS	934
vhCDR1	NYAIG	935
vhCDR2	GIVPIFGVADYAQKFQG	936
vhCDR3	EGWYLLNYFDY	937
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	938
vlCDR1	RASQSISSYLN	939
vlCDR2	AASSLQS	940
vlCDR3	QQSYSTPYT	941

Figure 57

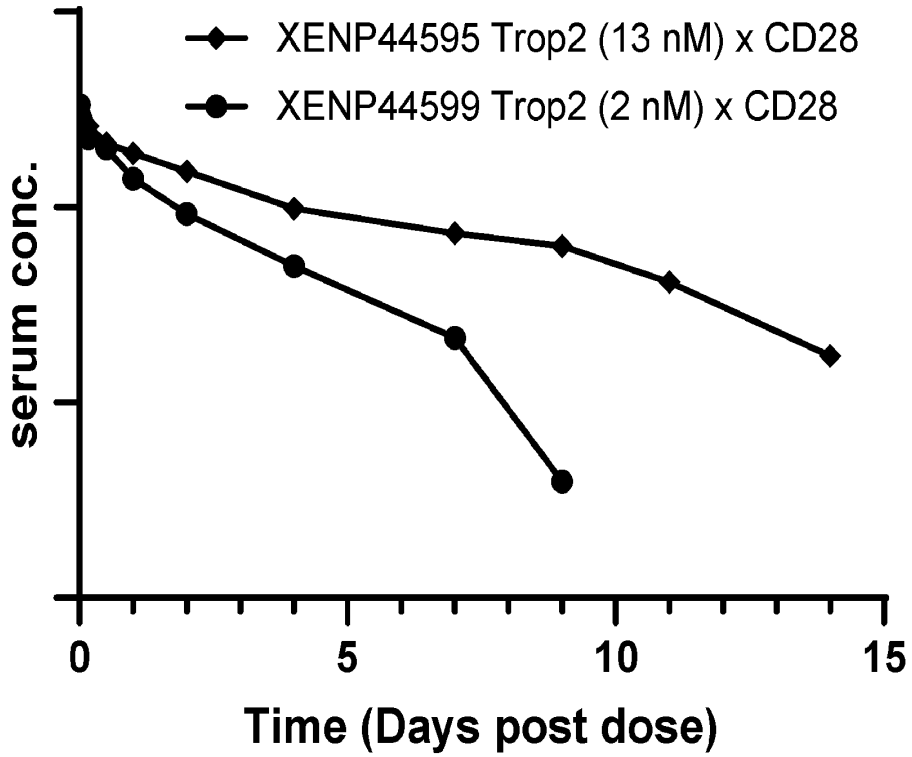
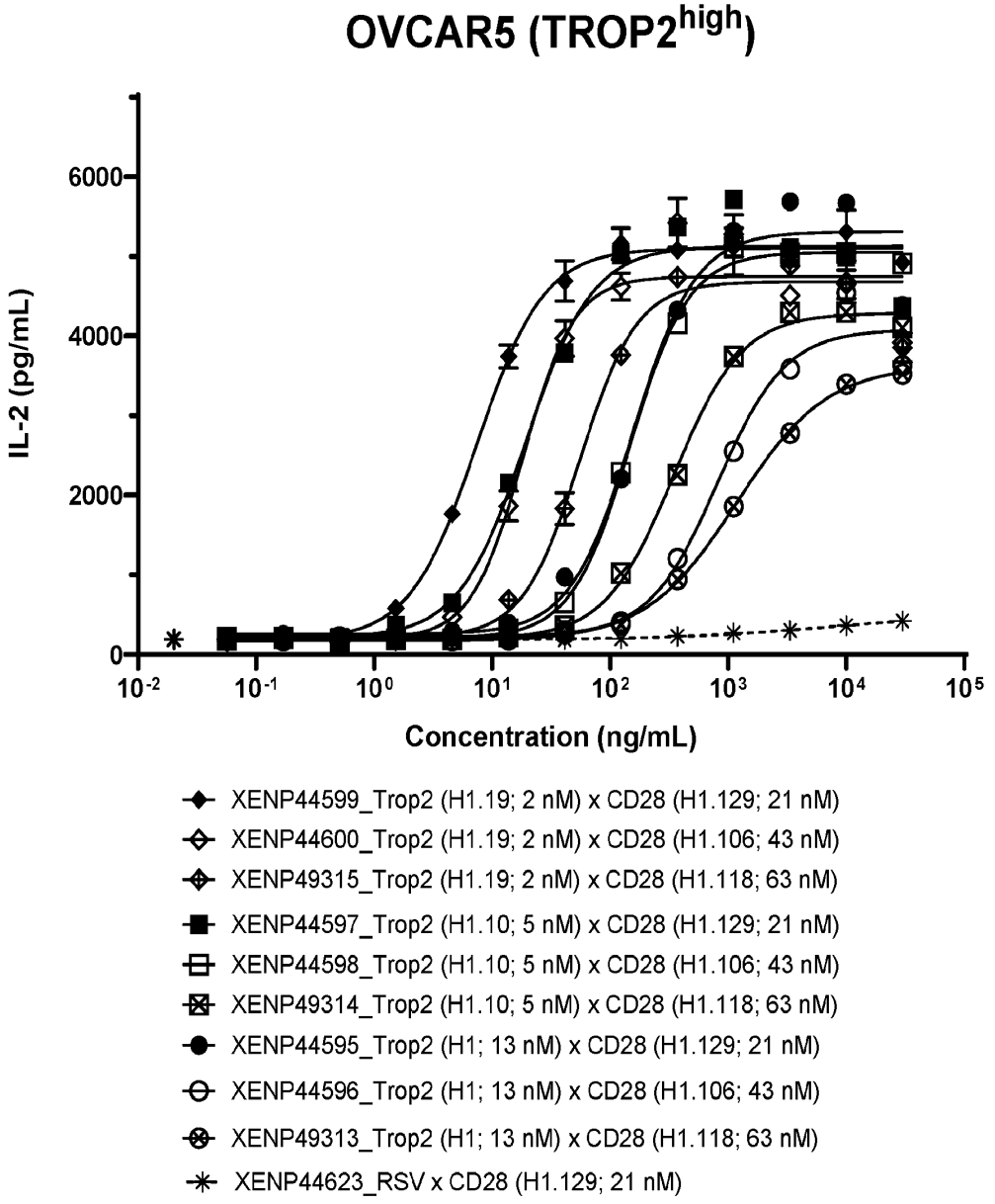
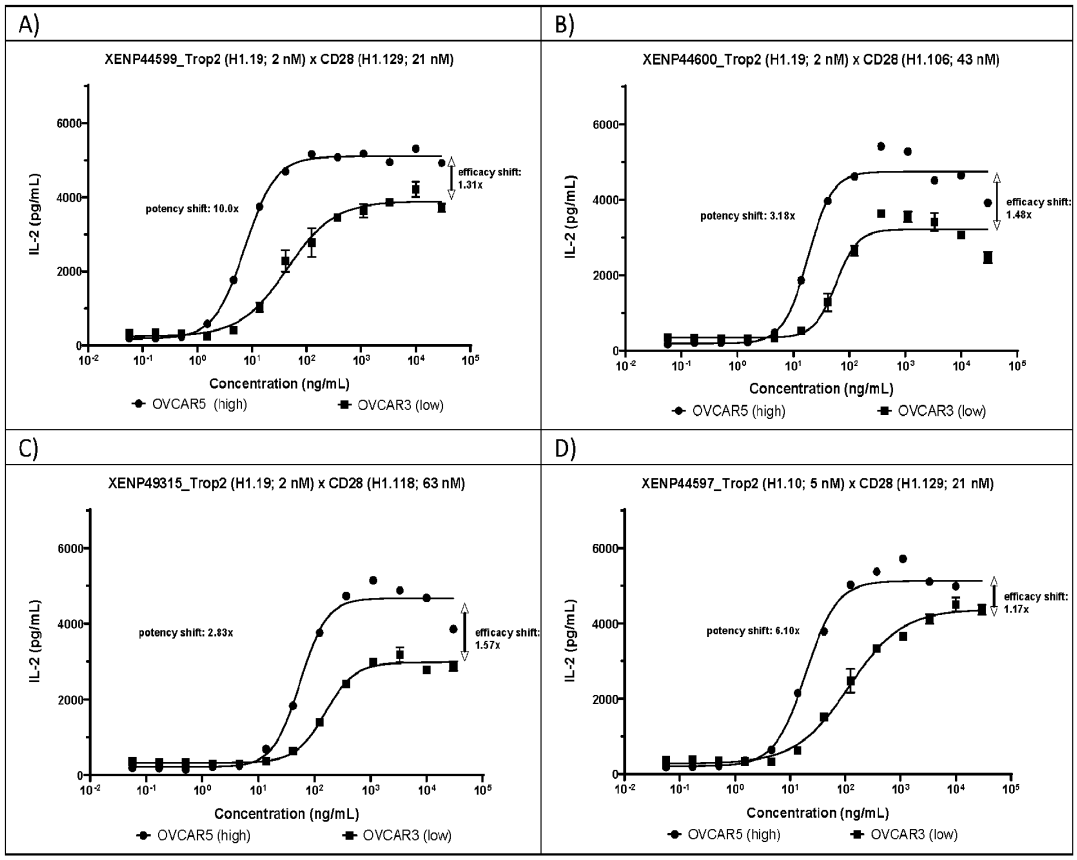

XENP44595 Trop2 (13 nM) x CD28
XENP44599 Trop2 (2 nM) x CD28
serum conc.
0
5
10
15
Time (Days post dose)

Figure 58


OVCAR5 (TROP2high)
IL-2 (pg/mL)
6000
4000
2000
0
10-2
10-1
100
101
102
103
104
105
Concentration (ng/mL)
XENP44599_Trop2 (H1.19; 2 nM) x CD28 (H1.129; 21 nM)
XENP44600_Trop2 (H1.19; 2 nM) x CD28 (H1.106; 43 nM)
XENP49315_Trop2 (H1.19; 2 nM) x CD28 (H1.118; 63 nM)
XENP44597_Trop2 (H1.10; 5 nM) x CD28 (H1.129; 21 nM)
XENP44598_Trop2 (H1.10; 5 nM) x CD28 (H1.106; 43 nM)
XENP49314_Trop2 (H1.10; 5 nM) x CD28 (H1.118; 63 nM)
XENP44595_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM)
XENP44596_Trop2 (H1; 13 nM) x CD28 (H1.106; 43 nM)
XENP49313_Trop2 (H1; 13 nM) x CD28 (H1.118; 63 nM)
XENP44623_RSV x CD28 (H1.129; 21 nM)

Figures 59A-59D



Figures 59E-59H

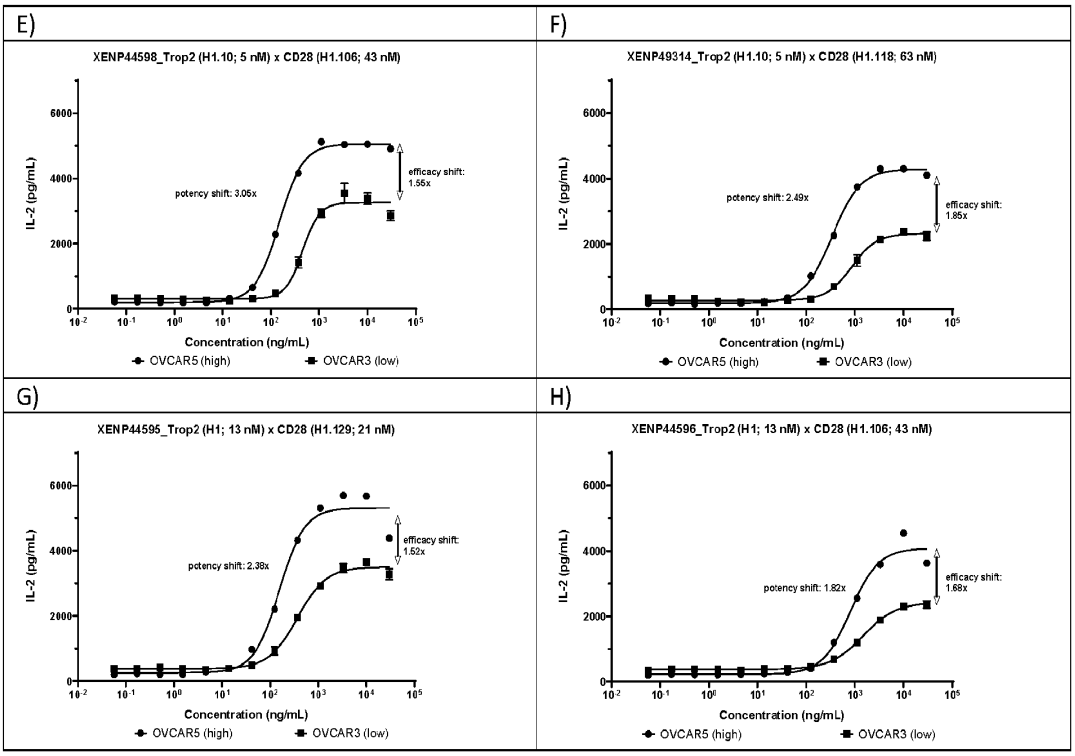


Figure 59I

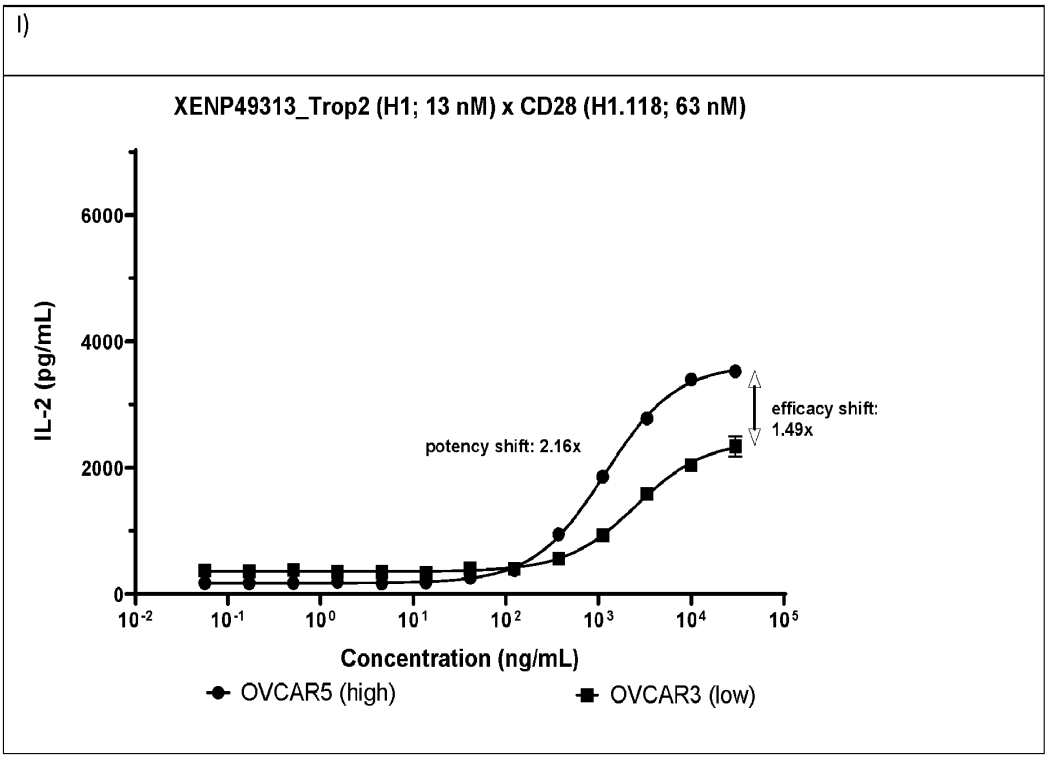
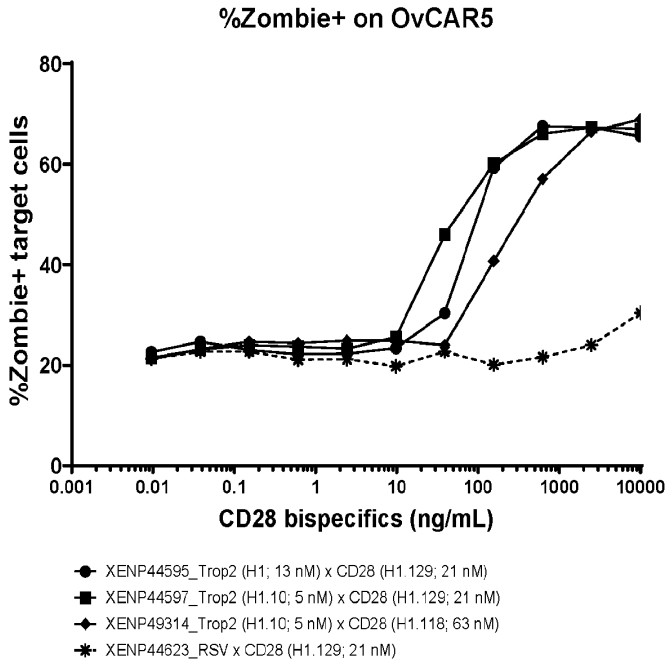
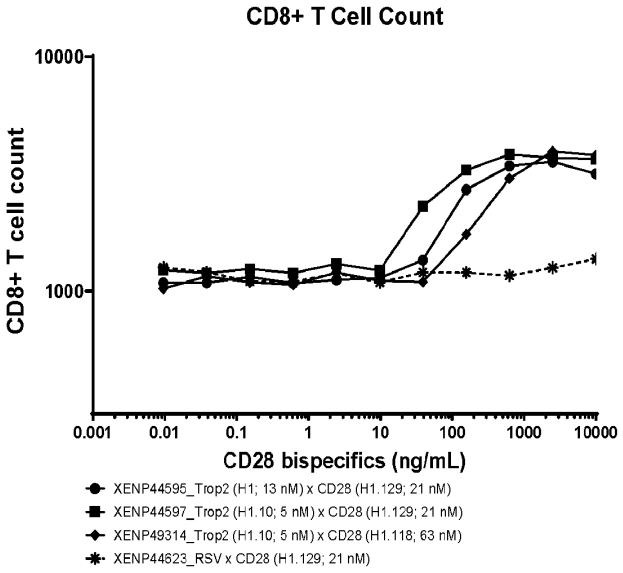

I)
XENP49313_Trop2 (H1; 13 nM) x CD28 (H1.118; 63 nM)
IL-2 (pg/mL)
6000
4000
2000
0
potency shift: 2.16x
efficacy shift:
1.49x
10^{-2} 10^{-1} 10^{0} 10^{1} 10^{2} 10^{3} 10^{4} 10^{5}
Concentration (ng/mL)
OVCAR5 (high)
OVCAR3 (low)

Figure 60

A)


%Zombie+ on OvCAR5
%Zombie+ target cells
80
60
40
20
0
0.001
0.01
0.1
1
10
100
1000
10000
CD28 bispecifics (ng/mL)
XENP44595_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM)
XENP44597_Trop2 (H1.10; 5 nM) x CD28 (H1.129; 21 nM)
XENP49314_Trop2 (H1.10; 5 nM) x CD28 (H1.118; 63 nM)
XENP44623_RSV x CD28 (H1.129; 21 nM)

B)


CD8+ T Cell Count
CD8+ T cell count
10000
1000
0.001
0.01
0.1
1
10
100
1000
10000
CD28 bispecifics (ng/mL)
XENP44595_Trop2 (H1; 13 nM) x CD28 (H1.129; 21 nM)
XENP44597_Trop2 (H1.10; 5 nM) x CD28 (H1.129; 21 nM)
XENP49314_Trop2 (H1.10; 5 nM) x CD28 (H1.118; 63 nM)
XENP44623_RSV x CD28 (H1.129; 21 nM)