

Figure 1

Human CD28 sequence SEQ ID NO:757

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

MLRLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQ
VYSKTGFNC DGKLGNESVT FYLQNLVYNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFW
VLVVVGVLACYSLLVTVAFIIFWVRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

Human CD28, extracellular domain SEQ ID NO:758

>sp|P10747|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNC DGKLGNESV
TFYLQNLVYNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPF

Mouse CD28 sequence SEQ ID NO:759

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

MTLRLFLALNFFSVQVTENKILVKQSPLLVVDSEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGNFTYQP
QFRSNAEFNC DGDFDNETVT FRLWNLHVNHDTIYFCKIEFMYPYPYLDNERSNGTIIHIKEKHLCHTQSSPKLFWAL
VVVAGVLCYGLLVTVLALCVIWTNSRRNRLQSDYMNMTPRRPGPTRKPYQPYAPARDFAAAYRP

Mouse CD28, extracellular domain SEQ ID NO:760

>sp|P31041|20-150

NKILVKQSPLLVVDSEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGNFTYQPQFRSNAEFNC DGDFDNETV
TFRLWNLHVNHDTIYFCKIEFMYPYPYLDNERSNGTIIHIKEKHLCHTQSSPKL

Cynomolgus CD28 sequence SEQ ID NO:761

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

MLRLLALNLLPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQ
VYSKTGFNC DGKLGNESVT FYLQNLVYNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPFW
ALVVVGVLACYSLLVTVAFCIFWMRSKRSRLHSDYMNMTPRRPGPTRKHYPYAPPRDFAAYRS

Cynomolgus CD28, extracellular domain SEQ ID NO:762

>tr|Q0PDN3|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNC DGKLGNESV
TFYLQNLVYNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPFPGPSKPF

Figure 2A

Human B7H3 sequence SEQ ID NO:763**>sp|Q5ZPR3|CD276_HUMAN CD276 antigen OS=Homo sapiens OX=9606 GN=CD276 PE=1 SV=1**

MLRRRGS PGMGVHVGAALGALWFCLTGALVQVPEDPVVALVGTDATLCCSFSPGPGFSLAQLNLIWQLTDTKQLVH
SFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI RDFGSAAVSLQVAAPYSKPSMTLEPNKD
LRPGDTVTITCSSYQGYPEAEVFWQDGGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDA
HSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYA
NRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSS
YRGYPEAEVFWQDGGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTF
PPEALWVTVGLSVCLIALLVALAFVCWRKIKQSC EENAGAEDQDGE GEGSKTALQPLKHS DSKEDD GQEIA

Human B7H3, extracellular domain SEQ ID NO:764**>sp|Q5ZPR3|29-466**

LEVQVPEDPVVALVGTDATSLCCSFSPGPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGN
ASLRLQVRVVADEGSFTCFVSI RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQD
QGVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQQDAHSSVTITPQRSPTGAVEVQVPEDPVVA
LVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFPDLLAQGNASLRLQVRVVADE
GSFTCFVSI RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGGVPLTGNVTTSQ
MANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEA

Human B7H3, V1C1 domain SEQ ID NO:765

LEVQVPEDPVVALVGTDATLCCSFSPGPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNA
SLRLQVRVVADEGSFTCFVSI RDFGSAAVSLQVA

Human B7H3, V2C2 domain SEQ ID NO:766

PTGAVEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFPDLLA
QGNASLRLQVRVVADEGSFTCFVSI RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFW
QDGGVPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTIT

Mouse B7H3 sequence SEQ ID NO:767**>sp|Q8VE98|CD276_MOUSE CD276 antigen OS=Mus musculus OX=10090 GN=Cd276 PE=1 SV=1**

MLRGWGGPSVGVCVRTALGVLCCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVH
SFTEGRDQGSAYSANRTALFPDLLVQGNASLRLQVRVTDEGSYTCFVSIQDFDSAASVSLQVAAPYSKPSMTLEPNKD
LRPGNMVTITCSSYQGYPEAEVFWKDGQGVPLTGNVTTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDA
HGSVTITGQPLTFPPEALWVTVGLSVCLVLLVALAFVCWRKIKQSC EENAGAEDQDGD GEGSKTALRPLKPS ENK
EDDGQEIA

Mouse B7H3, extracellular domain SEQ ID NO:768**>sp|Q8VE98|29-248**

VEVQVSEDPVVALVDTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSANRTALFPDLLVQGNA
SLRLQVRVTDEGSYTCFVSIQDFDSAASVSLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVFWKDGQ
GVPLTGNVTTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPLTFPPEA

Figure 2B

Cynomolgus CD28 sequence (predicted) SEQ ID NO:769**>XP_015308533.1 PREDICTED: CD276 antigen isoform X1 [Macaca fascicularis]**

MKLSSDHVFPLFRKLQWLPAAFRIQFTFVSPSAGAAFHHGEPSCQLPHSKMLHRRGSPGMGVHVGAAALGALWFCLTG
ALEVQVPEDPVVALVGTDLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGN
ASLRLQVRVVADEGSFTCFVSIIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITC SSYRGYPEAEVFWQDG
QGAPLTGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQVPEDPVVA
LVGTDLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASLRLQVRVVADE
GSFTCFVSIIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITC SSYRGYPEAEVFWQDGQGAPLTGNVTTSQ
MANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEALWVTVGLSVCLVALLVALAFVCW
RKIKQSCEENAGAEDQDGE GEGSKTALQPLKHS DSKEDDGQELA

Cynomolgus CD28, extracellular domain SEQ ID NO:770**>XP_015308533.1|79-516**

LEVQVPEDPVVALVGTDLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNA
SLRLQVRVVADEGSFTCFVSIIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITC SSYRGYPEAEVFWQDGQ
GAPLTGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQVPEDPVVAL
VGTDLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASLRLQVRVVADEG
SFTCFVSIIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITC SSYRGYPEAEVFWQDGQGAPLTGNVTTSQ
MANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEA

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
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

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

Figure 6

Positive Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGSGGGGS	15	0	SEQ ID NO:771
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	SEQ ID NO:772
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	SEQ ID NO:773
+B	GKGGSGKGGSGKGGGS	15	+3	SEQ ID NO:774
+C	GGKSGGGKSGGGKGS	15	+3	SEQ ID NO:775
+D	GGGKSGGGKSGGGKS	15	+3	SEQ ID NO:776
+E	GKGKSGKGKSGKGKS	15	+6	SEQ ID NO:777
+F	GGGKSGGGKSGKGGGS	15	+3	SEQ ID NO:778
+G	GKPGSGKPGSGKPGS	15	+3	SEQ ID NO:779
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	SEQ ID NO:780
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	SEQ ID NO:781

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 20	GGGGSGGGSGGGSGGGGS	20	0	SEQ ID NO:782
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	SEQ ID NO:783
-B	GEGSGEGSGEGGS	15	-3	SEQ ID NO:784
-C	GGEGSGEGSGGEGS	15	-3	SEQ ID NO:785
-D	GGGESGGGESGGGES	15	-3	SEQ ID NO:786
-E	GEGESGEGESGEGES	15	-6	SEQ ID NO:787
-F	GGGESGGEGSGEGGS	15	-3	SEQ ID NO:788
-G	GEGESGEGESGEGESGEGES	20	-8	SEQ ID NO:789

Additional scFv Linkers

GGGGSGGGSGGGGS	SEQ ID NO:790
GGGGSGGGSGGGSGGGGS	SEQ ID NO:791
GSTSGSGKPGSGEGSTKG	SEQ ID NO:792
PRGASKSGSASQTGSAPGS	SEQ ID NO:793
GTAAAGAGAAGGAAAGAAG	SEQ ID NO:794
GTSGSSGSGSGSGSGGGG	SEQ ID NO:795
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:796

Figure 7

Useful domain linkers

<u>Name</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
(GGGS) ₁ or GGGS	GGGS	SEQ ID NO:797
(GGGS) ₂	GGGSGGGS	SEQ ID NO:798
(GGGS) ₃	GGGSGGGSGGGS	SEQ ID NO:799
(GGGS) ₄	GGGSGGGSGGGSGGGS	SEQ ID NO:800
(GGGS) ₅	GGGSGGGSGGGSGGGSGGGS	SEQ ID NO:801
(GGGS) ₆	GGGSGGGSGGGSGGGSGGGSGGGS	SEQ ID NO:802
(GGGS) ₇	GGGSGGGSGGGSGGGSGGGSGGGSGGGS	SEQ ID NO:803
(GGGA) ₁ or GGGA	GGGA	SEQ ID NO:804
(GGGA) ₂	GGGAGGGA	SEQ ID NO:805
(GGGA) ₃	GGGAGGGGAGGGA	SEQ ID NO:806
(GGGA) ₄	GGGAGGGGAGGGAGGGA	SEQ ID NO:807
(GGGA) ₅	GGGAGGGGAGGGAGGGAGGGA	SEQ ID NO:808
(GGGA) ₆	GGGAGGGGAGGGAGGGAGGGAGGGA	SEQ ID NO:809
(GGGA) ₇	GGGAGGGGAGGGAGGGAGGGAGGGAGGGA	SEQ ID NO:810
30AA-linker	DPALVHQRPAAPPGGGSGGGSGGGS	SEQ ID NO:811
(GKPGS) ₁ or GKPGS	GKPGS	SEQ ID NO:812
(GKPGS) ₅	GKPGSGKPGSGKPGSGKPGSGKPGS	SEQ ID NO:813
(GKPGS) ₆	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	SEQ ID NO:814
(GGGES) ₁ or GGGES	GGGES	SEQ ID NO:815
“lower half hinge”	KTHTCPPCP	SEQ ID NO:816
“full hinge C220S variant”	EPKSSDKTHTCPPCP	SEQ ID NO:817
“flex lower half hinge”	GGGSGGGSKTHTCPPCP	SEQ ID NO:818
“charged lower half hinge1”	GKPGSGKPGSKTHTCPPCP	SEQ ID NO:819
“charged lower half hinge2”	GKPGSKTHTCPPCP	SEQ ID NO:820
“upper half hinge”	EPKSC	SEQ ID NO:821
“flex upper half hinge”	EPKSCGGGS	SEQ ID NO:822
“charged upper half hinge1”	EPKSCGKPGSGKPGS	SEQ ID NO:1182
“charged upper half hinge2”	EPKSCGKPGS	SEQ ID NO:1183

Figure 8

Monomer 1 (-)	Monomer 2 (+)
Heterodimer skew variants L368D/K370S	Heterodimer skew variants S364K/E357Q
Isosteric pl variant 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:823)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGDVFSQSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 1 monomer 2 (+) (SEQ ID NO:824)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 2**>Heterodimeric Fc Backbone 2 monomer 1 (-) (SEQ ID NO:825)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGDVFSQSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone monomer 2 (+) (SEQ ID NO:826)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 3**>Heterodimeric Fc Backbone 3 monomer 1 (-) (SEQ ID NO:827)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGDVFSQSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 3 monomer 2 (+) (SEQ ID NO:828)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 4**>Heterodimeric Fc Backbone 4 monomer 1 (-) (SEQ ID NO:829)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWQQGDVFSQSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 4 monomer 2 (+) (SEQ ID NO:830)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Figure 10B

Heterodimeric Fc Backbone 5**>Heterodimeric Fc Backbone 5 monomer 1 (-) (SEQ ID NO:831)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 5 monomer 2 (+) (SEQ ID NO:832)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 6**>Heterodimeric Fc Backbone 6 monomer 1 (-) (SEQ ID NO:833)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 6 monomer 2 (+) (SEQ ID NO:834)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 7**>Heterodimeric Fc Backbone 7 monomer 1 (-) (SEQ ID NO:835)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 7 monomer 2 (+) (SEQ ID NO:836)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 8**>Heterodimeric Fc Backbone 8 monomer 1 (-) (SEQ ID NO:837)**

APEFLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWEEGDFVFCFSVMHEALHNHYTQKSLSLSLGK

>Heterodimeric Fc Backbone 8 monomer 2 (+) (SEQ ID NO:838)

APEFLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSLSLGK

Figure 10C

Heterodimeric Fc Backbone 9**>Heterodimeric Fc Backbone 9 monomer 1 (-) (SEQ ID NO:839)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGVDFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 9 monomer 2 (+) (SEQ ID NO:840)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 10**>Heterodimeric Fc Backbone 10 monomer 1 (-) (SEQ ID NO:841)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGVDFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 10 monomer 2 (+) (SEQ ID NO:842)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 11**>Heterodimeric Fc Backbone 11 monomer 1 (-) (SEQ ID NO:843)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGVDFSCSVLHEALHSHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 11 monomer 2 (+) (SEQ ID NO:844)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVLHEALHSHYTQKSLSLSPGK

Heterodimeric Fc Backbone 12**>Heterodimeric Fc Backbone 12 monomer 1 (-) (SEQ ID NO:845)**

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 12 monomer 2 (+) (SEQ ID NO:846)

APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGVDFSCSVMEALHNHYTQKSLSLSPGK

Figure 11

2 + 1 mAb-scFv Heterodimeric Fc Backbone**>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 1 (-) (SEQ ID NO:847)**

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPK

>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 2 (+) (SEQ ID NO:848)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSP

Figure 12

IgG1 CH1(+) + hinge (SEQ ID NO:849)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP

IgG1 CH1(-) + hinge (SEQ ID NO:850)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCP

IgG2 CH1(+) + hinge (SEQ ID NO:851)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCP

IgG2 CH1(-) + hinge (SEQ ID NO:852)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVERKCCVECPPCP

IgG4 CH1(+) + hinge (SEQ ID NO:853)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCP

IgG4 CH1(-) + hinge (SEQ ID NO:854)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRVESKYGPPCPSCP

Figure 13

IgG1 CH1(+) + half hinge (SEQ ID NO:855)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSC

IgG1 CH1(-) + half hinge (SEQ ID NO:856)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSC

Figure 14

IgG1 CH1(+) (SEQ ID NO:857)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKV

IgG1 CH1(-) (SEQ ID NO:858)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKV

IgG2 CH1(+) (SEQ ID NO:859)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTV

IgG2 CH1(-) (SEQ ID NO:860)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTV

IgG4 CH1(+) (SEQ ID NO:861)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSNTKVDKRV

IgG4 CH1(-) (SEQ ID NO:862)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRV

Figure 15

IgG1 hinge (SEQ ID NO:863)

EPKSCDKTHTCPPCP

IgG2 hinge (SEQ ID NO:864)

ERKCCVECPPCP

IgG4 hinge (SEQ ID NO:865)

ESKYGPPCPSCP

Figure 16

Light Chain Constant Domain – Kappa (SEQ ID NO: 866)

RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Light Chain Constant Domain – Lambda (SEQ ID NO:867)

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 17

>XENP16432 Nivolumab H0L0 IgG1 PVA /S267K**Heavy Chain** SEQ ID NO:868

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

Light Chain SEQ ID NO:869

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS S
LEPEDFAVYYCQQSSNWPRTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18

1A7[CD28] H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLES GGG LVQP GGS LRLSCAASGFTFS <u>SYAMS</u> WVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGT LVT VSS	SEQ ID NO:870
vhCDR1	<u>SYAMS</u>	SEQ ID NO:871
vhCDR2	<u>TISGSGDSTYYADSVKG</u>	SEQ ID NO:872
vhCDR3	<u>SGPGLRQVGFDY</u>	SEQ ID NO:873
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYL N WYQQKPGKAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTIS SLQPEDFATYYC <u>QQSYSTPFT</u> FGQGTKLEIK	SEQ ID NO:874
vlCDR1	<u>RAQSISSYLN</u>	SEQ ID NO:875
vlCDR2	<u>AASSLQ</u>	SEQ ID NO:876
vlCDR3	<u>QQSYSTPFT</u>	SEQ ID NO:877

>XENP28428 1A7[CD28] H1L1 IgG1 PVA /S267K**Heavy Chain** SEQ ID NO:878

EVQLLES GGG LVQP GGS LRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGT LVT VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

Light Chain SEQ ID NO:879

DIQMTQSPSSLSASVGDRVTITCRASQSISSYL N WYQQKPGKAPKLLIYAASSLQSGVPSRFS GSGSGTDFTLTIS SLQPEDFATYYC QQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19

	sequence	SEQ ID NO:
Variable heavy (vh) domain 1A7_H1.1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYMSWVRQAPGKGLEW VSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLLTVSS	SEQ ID NO:880
vhCDR1	<u>SYMS</u>	SEQ ID NO:881
vhCDR2	<u>TISGSGDSTYYADSVKG</u>	SEQ ID NO:882
vhCDR3	<u>SGPGLRQVGFDY</u>	SEQ ID NO:883

	sequence	SEQ ID NO:
Variable heavy (vh) domain 1A7_H1.14	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYYMSWVRQAPGKGLEW VSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLLTVSS	SEQ ID NO:884
vhCDR1	<u>SYMS</u>	SEQ ID NO:885
vhCDR2	<u>TISESGDSTYYADSVKG</u>	SEQ ID NO:886
vhCDR3	<u>SGPGLRQVGFDY</u>	SEQ ID NO:887

Figure 20

	sequence	SEQ ID NO:
Variable heavy (vh) domain 1A7_L1.71	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQOKPGKAPKLL IYAASSLQSGVPSRFRSGSGSGTDFTLTISSLQPEDFATYYCQQVYST PFTFGQGTKLEIK	SEQ ID NO:888
vhCDR1	RASQSISSYLN	SEQ ID NO:889
vhCDR2	AASSLQS	SEQ ID NO:890
vhCDR3	QQVYSTPFT	SEQ ID NO:891

Figure 21A

1A7[CD28] H1 L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGT LVTVSS	SEQ ID NO:892
vhCDR1	SYAMS	SEQ ID NO:893
vhCDR2	TISGSGDSTYYADSVKG	SEQ ID NO:894
vhCDR3	SGPGLRQVGFDY	SEQ ID NO:895
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQVYSTPFTFGQGTKLEIK	SEQ ID NO:896
vlCDR1	RASQSISSYLN	SEQ ID NO:897
vlCDR2	AASSLQS	SEQ ID NO:898
vlCDR3	QQVYSTPFT	SEQ ID NO:899

1A7[CD28] H1.1 L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGT LVTVSS	SEQ ID NO:900
vhCDR1	SYMS	SEQ ID NO:901
vhCDR2	TISGSGDSTYYADSVKG	SEQ ID NO:902
vhCDR3	SGPGLRQVGFDY	SEQ ID NO:903
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCQQVYSTPFTFGQGTKLEIK	SEQ ID NO:904
vlCDR1	RASQSISSYLN	SEQ ID NO:905
vlCDR2	AASSLQS	SEQ ID NO:906
vlCDR3	QQVYSTPFT	SEQ ID NO:907

Figure 21B

1A7[CD28] H1.14 L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLES ~~GGGLVQPGGSLRL~~ SCAASGFTFSSYYMSWVRQAPGKGLEWVSTISES GDS ~~TY~~ YADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKSGPGLRQVGF DYWGQGT ~~LVTVSS~~	SEQ ID NO:908
vhCDR1	<u>SYMS</u>	SEQ ID NO:909
vhCDR2	<u>TISESGDSTYYADSVKG</u>	SEQ ID NO:910
vhCDR3	<u>SGPGLRQVGFY</u>	SEQ ID NO:911
Variable Light (vl) Domain	DIQMTQSPSSLSASVGD ~~RVTTITCRASQSISSYL~~ NWYQQKPGKAPKLLIYAASL QSGVPSR ~~FSGSGSDFTLT~~ ISSLPEDFATYYCQ ~~QSYSTPFT~~ FGQGTKLEIK	SEQ ID NO:912
vlCDR1	<u>RASQSISSYL</u>	SEQ ID NO:913
vlCDR2	<u>AASSLQS</u>	SEQ ID NO:914
vlCDR3	<u>QQSYSTPFT</u>	SEQ ID NO:915

1A7[CD28] H1.14 L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLES ~~GGGLVQPGGSLRL~~ SCAASGFTFSSYYMSWVRQAPGKGLEWVSTIS ESGDSTYYADSVKGRFTISRDN ~~SKNTLYLQMN~~ SLRAEDTAVYYCAKSGPGLR QVGFYWGQGT ~~LVTVSS~~	SEQ ID NO:916
vhCDR1	<u>SYMS</u>	SEQ ID NO:917
vhCDR2	<u>TISESGDSTYYADSVKG</u>	SEQ ID NO:918
vhCDR3	<u>SGPGLRQVGFY</u>	SEQ ID NO:919
Variable Light (vl) Domain	DIQMTQSPSSLSASVGD ~~RVTTITCRASQSISSYL~~ NWYQQKPGKAPKLLIYAAS SLQSGVPSR ~~FSGSGSDFTLT~~ ISSLPEDFATYYCQ ~~QVYSTPFT~~ FGQGTKLEIK	SEQ ID NO:920
vlCDR1	<u>RASQSISSYL</u>	SEQ ID NO:921
vlCDR2	<u>AASSLQS</u>	SEQ ID NO:922
vlCDR3	<u>QQVYSTPFT</u>	SEQ ID NO:923

Figure 22

A)

<u>1A7 VH/VL Pair</u>	<u>VH SEQ ID NO:</u>	<u>VL SQ ID NO:</u>	<u>scFv Orientation</u>	<u>K_D for human CD28 (nM)</u>
L1.71_H1.14	SEQ ID NO:598	SEQ ID NO:743	VLVH	36.7 (+/- 4.1)
H1.14_L1.71	SEQ ID NO:598	SEQ ID NO:743	VHVL	35(+/- 1.8)
H1.1_L1.71	SEQ ID NO:585	SEQ ID NO:743	VHVL	91.6 (+/-5.7)
H1_L1.71	SEQ ID NO:870	SEQ ID NO:743	VHVL	180(+/-2)
L1_H1.14	SEQ ID NO:598	SEQ ID NO:874	VLVH	286 (+/- 40)
H1.14_L1	SEQ ID NO:598	SEQ ID NO:874	VHVL	229 (+/- 0.4)

B)

<u>1A7 VH/VL Pair</u>	<u>VH SEQ ID NO:</u>	<u>VL SQ ID NO:</u>		<u>K_D for human CD28 (nM)</u>
H1.1_L1	SEQ ID NO:585	SEQ ID NO:874		232 (XENP37808)
H1.14_L1	SEQ ID NO:598	SEQ ID NO:874		62.8 (XENP31398); 200 (XENP37810)

Figure 23

>XENP27181 HuTN228[CD28] H1L1 IgG1 PVA /S267K**Heavy Chain** SEQ ID NO:924

QVQLQESGPGLVKPSSETLSLTCAVSGFSLTSYGVHWIRQPPGKGLEWLGVIWPGGGTGFNSALMSRLTISEDTSKNQ
 VSLKLSSVTAADTAVYYCARDRAYGNLYAMDNWGQGTLTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
 ESNQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Light Chain SEQ ID NO:925

DIQMTQSPSSLSASVGDRVTITCRASESVEYYVTSLSLQWYQQKPKGKAPKLLIYAASNVDSGVPSRFSGSGSGTDFTL
 TISSLPEDIAATYYCQQSRKVPFTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
 VDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP27656 empty-HuTN228[CD28] H1L1 scFv(GKPGS)4-Fc(216) IgG1 pl(-**) Isosteric A C220S/PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q****Chain 1 - empty-Fc(216) IgG1_pl(-) Isosteric_A_C220S/PVA /S267K/L368D/K370S empty-Fc Heavy Chain**

SEQ ID NO:926

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVS
 GFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - HuTN228[CD28]_H1L1_scFv(GKPGS)4-Fc(216) IgG1_C220S/PVA /S267K/S364K/E357Q scFv-Fc Heavy Chain SEQ ID NO:927

QVQLQESGPGLVKPSSETLSLTCAVSGFSLTSYGVHWIRQPPGKGLEWLGVIWPGGGTGFNSALMSRLTISEDTSKNQ
 VSLKLSSVTAADTAVYYCARDRAYGNLYAMDNWGQGTLTVTSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
 SASVGDRVTITCRASESVEYYVTSLSLQWYQQKPKGKAPKLLIYAASNVDSGVPSRFSGSGSGTDFTLTIISSLPEDIA
 TYYCQQSRKVPFTFGGGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDKHE
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF
 SCSVMHEALHNHYTQKSLSLSPGK

Figure 24

Phage anti-CD28 Clone	K_{Dapp} (M)
Phage Clone A	3.31E-08
Phage Clone B	1.76E-08
Phage Clone C	8.66E-09
Phage Clone D	7.40E-08
Phage Clone E	1.70E-08
Phage Clone F	1.47E-08
Phage Clone G	2.84E-08
Phage Clone 1A7 (XENP28428)	1.45E-08

Figure 25

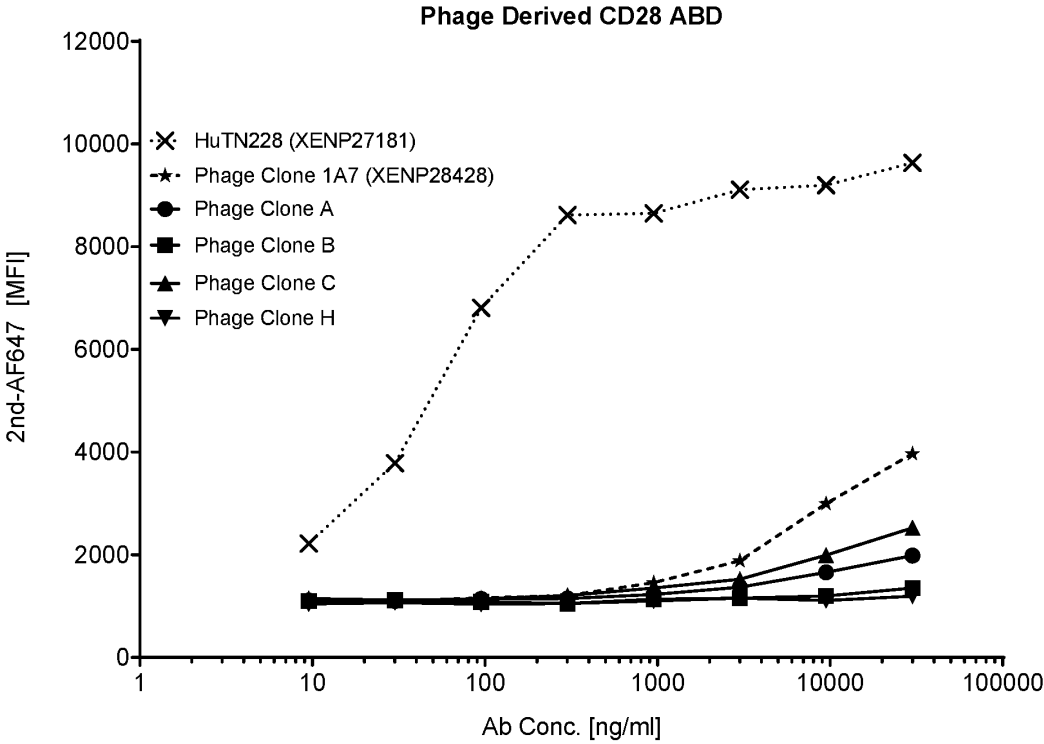


Figure 26

2E4A3.189[B7H3] H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYIFTNYYMHVVRQAPGQGLEWMGIIISPSAGTTSYAQKFQGRVTMTRDTSTSTVYMEISSLRSEDTAVY YCARGGGSSPRLDYWGQGTILVTVSS	SEQ ID NO:928
vhCDR1	<u>NYMH</u>	SEQ ID NO:929
vhCDR2	<u>IISPSAGTTSYAQKFQ</u>	SEQ ID NO:930
vhCDR3	<u>GGGSSPRLDY</u>	SEQ ID NO:931
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKLEIK	SEQ ID NO:932
vlCDR1	<u>RASQSISSYLN</u>	SEQ ID NO:933
vlCDR2	<u>AASSLQ</u>	SEQ ID NO:934
vlCDR3	<u>QQSYSTPYT</u>	SEQ ID NO:935

>XENP32637 2E4A3.189[B7H3] H1L1 IgG1 PVA /S267K**Heavy Chain SEQ ID NO:936**

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNYYMHVVRQAPGQGLEWMGIIISPSAGTTSYAQKFQGRVTMTRDTSTSTVYMEISSLRSEDTAVY YCARGGGSSPRLDYWGQGTILVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

Light Chain SEQ ID NO:937

DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYCQQSYSTPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 27

	sequence	SEQ ID NO:
Variable heavy (vh) domain 2E4A3.189_H1.3	QVQLVQSGAEVKKPGASVKVSCKASGYIFTNHYMHVVRQAPGQGLEWMGIISPSAGSTDYAQKFQGRVTMTRDTSTSTVYMESSLRSEDNAVY YCARGGGSSPRLDYWGQGTILVTVSS	SEQ ID NO:938
vhCDR1	<u>NHYMH</u>	SEQ ID NO:939
vhCDR2	<u>IISPSAGSTDYAQKFQ</u>	SEQ ID NO:940
vhCDR3	<u>GGGSSPRLDY</u>	SEQ ID NO:941

	sequence	SEQ ID NO:
Variable heavy (vh) domain 2E4A3.189_H1.22	QVQLVQSGAEVKKPGASVKVSCKASGYIFTNNYMHVVRQAPGQGLEWMGIISPSVGRITAXAQKFQGRVTMTRDTSTSTVYMESSLRSEDNAVY YCARGGGSSPRLDYWGQGTILVTVSS	SEQ ID NO:942
vhCDR1	<u>NNYMH</u>	SEQ ID NO:943
vhCDR2	<u>IISPSVGRITAXAQKFQ</u>	SEQ ID NO:944
vhCDR3	<u>GGGSSPRLDY</u>	SEQ ID NO:945

Figure 28

6A1[B7H3] H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLES GGG L V Q P G G S L R L S C A A S G F T F S N Y Y M A W V R Q A P G K G L E W V S S I S T G G G S T Y Y R D S V K G R F T I S R D N S K S T L Y L Q M N S L R A E D T A V Y C T T D L S A I A A T P F A Y W G Q G T L V T V S S	SEQ ID NO:946
vhCDR1	<u>NYYMA</u>	SEQ ID NO:947
vhCDR2	<u>SISTGGGSTYYRDSVKG</u>	SEQ ID NO:948
vhCDR3	<u>DLSAIAATPFAY</u>	SEQ ID NO:949
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQNIYTS ~~LA~~ WYQQKPGKAPKLLIYNAHSLQTGIPSRFSGSGSGADFTLTIS ~~SL~~ QPEDFATYFCQQYYSG	SEQ ID NO:950
vlCDR1	<u>RASQNIYTS~~LA~~</u>	SEQ ID NO:951
vlCDR2	<u>NAHSLQT</u>	SEQ ID NO:952
vlCDR3	<u>QQYYSGLT</u>	SEQ ID NO:953

>XENP33383 6A1[B7H3] H1L1 IgG1 PVA /S267K**Heavy Chain** SEQ ID NO:954

EVQLLES GGG L V Q P G G S L R L S C A A S G F T F S N Y Y M A W V R Q A P G K G L E W V S S I S T G G G S T Y Y R D S V K G R F T I S R D N S K S T L Y L Q M N S L R A E D T A V Y C T T D L S A I A A T P F A Y W G Q G T L V T V S S / A S T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S V V T V P S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P C P A P P V A G P S V F L F P P K P K D T L M I S R T P E V T C V V D V K H E D P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

Light Chain SEQ ID NO:955

DIQMTQSPSSLSASVGDRVTITCRASQNIYTS~~LA~~WYQQKPGKAPKLLIYNAHSLQTGIPSRFSGSGSGADFTLTIS~~SL~~QPEDFATYFCQQYYSGLTFFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 29

3C4[B7H3] H1L1.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGFSLTSYHVSWVRQAPGQGLEWMGAISSSGGSSYYNSKRFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYFCTGDLGAALISWFAYWGQGLTVSS	SEQ ID NO:956
vhCDR1	<u>GFSLTSYHVS</u>	SEQ ID NO:957
vhCDR2	<u>AISSSGGSSYYNSKRFQ</u>	SEQ ID NO:958
vhCDR3	<u>DLGAALISWFAY</u>	SEQ ID NO:959
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCRISQSIYKSLAWYQQKPGKAPKLLIYNHSLQGTGIPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQYYSGITFGSGTKLEIK	SEQ ID NO:960
vlCDR1	<u>RTSQSIYKSLA</u>	SEQ ID NO:961
vlCDR2	<u>NAHSLQT</u>	SEQ ID NO:962
vlCDR3	<u>QQYYSGIT</u>	SEQ ID NO:963

Figure 30

4F12[B7H3] H2L1.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFSFSVGYMCWVRQAPGKGLE WVSCIYVSGSGSSGSTYYASVKGRFTISSDTAKTSVYLQMNSLRAEDT AVYFCARTAGSDWRLDLWGQGLTVTVSS	SEQ ID NO:964
vhCDR1	<u>VGYYMC</u>	SEQ ID NO:965
vhCDR2	<u>CIYVSGSGSSGSTYYASVKG</u>	SEQ ID NO:966
vhCDR3	<u>TAGSDWRLDL</u>	SEQ ID NO:967
Variable light (vl) domain	DIVMTQSPSSLSASVGDRTITCRASQSIANELSWYQQKPGKPPKLL IYPASTLTSGVPSRFKSGSGTDFTLTISSLQPEDFATYYCQSTYNG PAIGFGGGKVEIK	SEQ ID NO:968
vlCDR1	<u>RASQSIANELS</u>	SEQ ID NO:969
vlCDR2	<u>RASTLTS</u>	SEQ ID NO:970
vlCDR3	<u>QSTYNGRAIG</u>	SEQ ID NO:971

Figure 31

38E2[B7H3] H2L1.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLES GGGLVQPGGSLRL SCAVSGFSL SYGVIWVRQAPGK GLEY VS WVSSGGSTNYASSVK GRFTISRDT SKNTVYLQMNSLRAEDTAVYF CARGAT NSGTDIWGPGLTV VSS	SEQ ID NO:972
vhCDR1	SYGVI	SEQ ID NO:973
vhCDR2	WVSSGGSTNYASSVK G	SEQ ID NO:974
vhCDR3	GATNSGTDI	SEQ ID NO:975
Variable light (vl) domain	DIVMTQSPSSLSASV GDRVTITCRASQ SIN SWLSWYQQKPGKPPKLL IY GASNLASGVPSRFK SGSGTDFTLT ISSLPEDFATYYCQNNYGI IAAGAT FGGG TKVEIK	SEQ ID NO:976
vlCDR1	RASQ SIN SWLS	SEQ ID NO:977
vlCDR2	GASNLAS	SEQ ID NO:978
vlCDR3	QNNYGI IAAGAT	SEQ ID NO:979

Figure 32

B7H3 Binding Domain	K_D for human B7H3 (V1C1-V2C2) (nM)	K_D for cynomolgus B7H3 (nM)
2E4A3_H1.22_1A7_L1	7.6	4.3
2E4A3_H1.3_1A7_L1	12	7.0
2E4A3_H1.22_L1	6.1	5.3
6A1_H1L1	8.1	4.2
4F12_H2_L1.1	<0.1	<0.1
38E2_H2_L1.1	0.5	1.4
3C4_H1_L1.1	29.7	27.2

Figure 33A

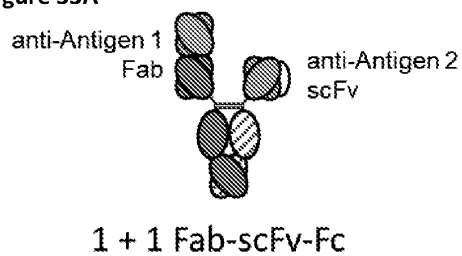


Figure 33B

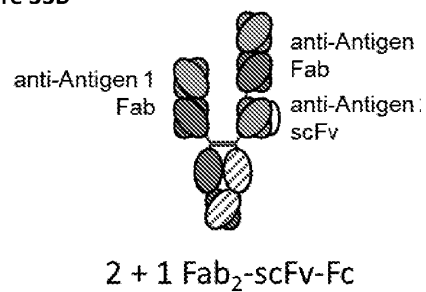


Figure 33C

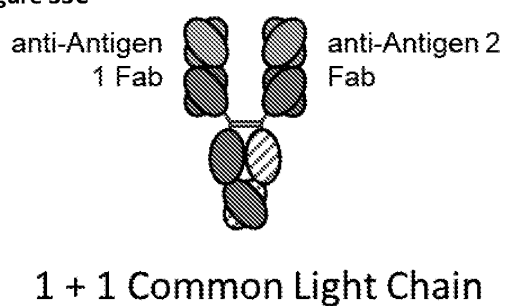


Figure 33D

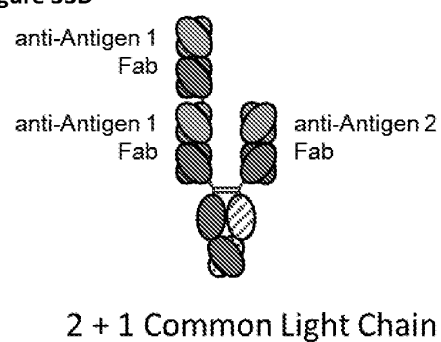


Figure 33E

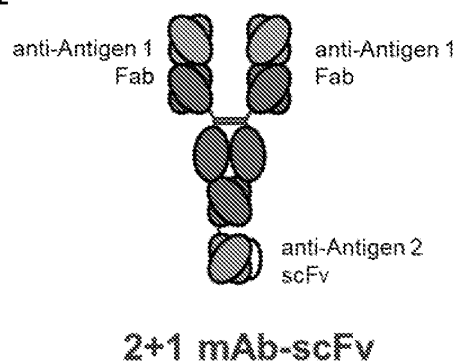
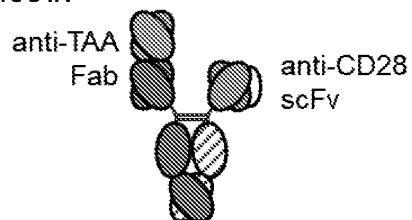
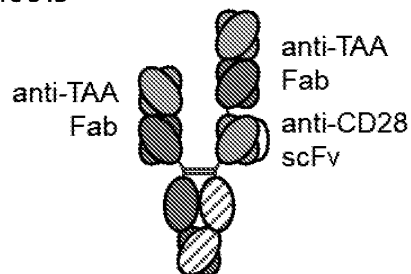


Figure 34A



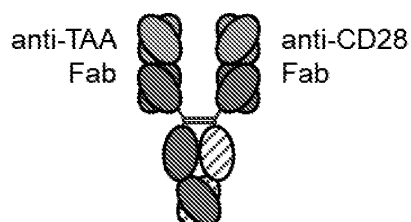
1 + 1 Fab-scFv-Fc

Figure 34B



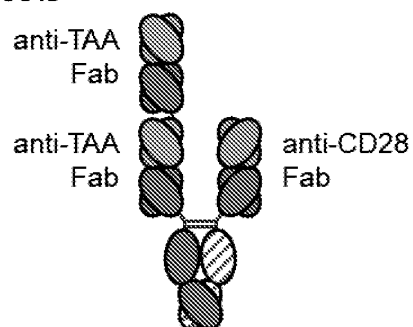
2 + 1 Fab₂-scFv-Fc

Figure 34C



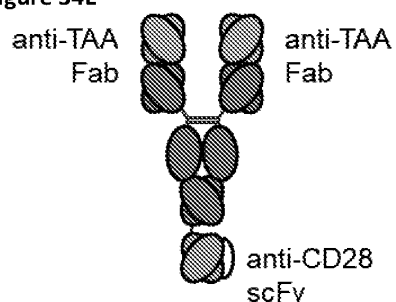
1 + 1 Common Light Chain

Figure 34D



2 + 1 Common Light Chain

Figure 34E



2+1 mAb-scFv

Figure 35A

**>XENP34730 2E4A3.189[B7H3] H1.22 L1 Fab-1A7[CD28] H1.14 L1 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - 2E4A3.189[B7H3]_H1.22_Fab_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S SEQ ID NO:980
QVQLVQSGAEVKKPGASVKVSCKASGYIFTNNYMHVWRQAPGQGLEWMGIISPSVGFTAYAQKFQGRVTMTRDTSTSTVYME
LSSLRSED TAVYYCARGGGSSPRLDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DQGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q SEQ ID NO:981
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSYYMSVWRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSS
LSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC
QQSYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV
MHEALHNHYTQKSLSLSPGK

Chain 3 - 2E4A3.189[B7H3]_L1 Light Chain SEQ ID NO:982
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>XENP34732 6A1[B7H3] H1L1 Fab-1A7[CD28] H1.14 L1 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S**

Chain 1 - 6A1[B7H3]_H1L1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:983
EVQLLES GGGGLVQPGGSLRLSCAASGFTFSNYYMAVWRQAPGKGLEWVSSIISTGGGSTYYRDSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCTDLSAIAATPFANWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S
SEQ ID NO:984

EVQLLES GGGGLVQPGGSLRLSCAASGFTFSYYMSVWRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSS
LSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYC
QQSYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV
LHEALHSHYTQKSLSLSPGK

Chain 3 - 6A1[B7H3]_L1 SEQ ID NO:985

DIQMTQSPSSLSASVGDRVTITCRASQNIYTSLAWYQQKPGKAPKLLIYNAHSLQGTGIPSRFSGSGSGADFTLTIS
LQPEDFATYFCQQYYSGLTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 35B

>XENP35151 4F12[B7H3] H2 L1.1 Fab-1A7[CD28] H1.14 L1 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-

Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - 4F12[B7H3] H2 L1.1 Fab-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S

SEQ ID NO:986

EVQLVESGGGLVQPGGSLRLSCAASGFSFSGVYIMCWVRQAPGKGLEWVSCIYVSGSGSGSTYYASVKGRFTISSDT
AKTSVYLQMNSLRAEDTAVYFCARTAGSDWRDLWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
CPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE
WESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28] H1.14 L1 scFv(GKPGS)4-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S

SEQ ID NO:987

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYCAKSGPGLPQVGFYWGQGTTLTVSS/GKPGSGKPGSGKPGSGKPGS/DI QMTQSPSSL
SASVGDRTVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLT ISSLPEDFATYYC
QQSYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - 4F12[B7H3] L1.1 SEQ ID NO:988

DIVMTQSPSSLSASVGDRTVITCFASQSIANELSWYQQKPGKPPKLLIYFASLTLSGVPSRFRKSGSGTDFTLT ISS
LPEDFATYYCQSTYNGRAIGFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP35153 38E2[B7H3] H2 L1.1 Fab-1A7[CD28] H1.14 L1 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-

Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - 38E2[B7H3] H2 L1.1 Fab-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S

SEQ ID NO:989

EVQLLESGGGLVQPGGSLRLSCAVSGFSLSSYGVIVWRQAPGKGLEWVSVWSSGGSTNYASSVKGRFTISRDT SKNT
VYLQMNSLRAEDTAVYFCARGATNSGTDI WGPGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28] H1.14 L1 scFv(GKPGS)4-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S

SEQ ID NO:990

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYCAKSGPGLPQVGFYWGQGTTLTVSS/GKPGSGKPGSGKPGSGKPGS/DI QMTQSPSSL
SASVGDRTVITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLT ISSLPEDFATYYC
QQSYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - 38E2[B7H3] L1.1 SEQ ID NO:991

DIVMTQSPSSLSASVGDRTVITCFASQSIINSLWYQQKPGKPPKLLIYGASNLASGVPSRFRKSGSGTDFTLT ISS
LPEDFATYYCQNNYGI AAGATFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKV
DNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 36A

>XENP34389 6A1[B7H3] H1L1 Fab-6A1[B7H3] H1L1 Fab (G4S)2 1A7[CD28] H1.14 L1 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - 6A1[B7H3]_H1_Fab_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S SEQ ID NO:992

EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSIISTGGGSTYYRDSVKGRFTISRDNKSKS
 TLYLQMNSLRAEDTAVYYCTTDL~~SA~~LAATPFAYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDS~~SGS~~FFLYSKLTVDKSRWEQGDVFC~~SV~~MHEALHNHYTQKSLSLSPGK

Chain 2 -

6A1[B7H3]_H1_Fab_(G4S)2_1A7[CD28]_H1.14_L1_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q SEQ ID NO:993

EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSIISTGGGSTYYRDSVKGRFTISRDNKSKS
 TLYLQMNSLRAEDTAVYYCTTDL~~SA~~LAATPFAYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GGGS
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLPQVGF~~Q~~WQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMT
 QSPSSLSASVGDRTTITCRASQSISSYL~~NWY~~QOKPGKAPKLLIYAASSLQSGVPSRFRSGSGSGDFTLTISLQPED
 FATYYCQQSYSTPFFFGQGTKLEIK/GGGSGGGSKTHTCPCP/APPVAGPSVFLFPPKPKDTLMISRTPEVTCV
 VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKA~~
 KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDS~~SGS~~FFLYSKLTVDKSR
 WQQGNVFC~~SV~~MHEALHNHYTQKSLSLSPGK

Chain 3 - 6A1[B7H3]_L1 Light Chain SEQ ID NO:994

DIQMTQSPSSLSASVGDRTTITCRASQNIYTS~~LA~~WYQOKPGKAPKLLIYN~~AS~~LSLQTFGIPSRFRSGSGSGADFTLTIS
 LQPEDFATYFCQQYYSGLTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 36B

>XENP34395 6A1[B7H3] H1L1 Fab-6A1[B7H3] H1L1 Fab (G4S)2 1A7[CD28] H1.14 L1 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - 6A1[B7H3]_H1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S SEQ ID NO: 995

EVQLLES GGGGLVQP GGS LRLSCAAS GFTFSNYYMAWVRQAPGKGLEWVSSI STGGGSTYYRDSVKGRFTISRDN SKS
TLYLQMNSLRAEDTAVYYCTTDL SAI AATPFAYWGQGT LVT VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSDTKVDK KVEPKSCDKTHTC
PPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN AKTKPREEEYNSTYRVVS
VLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESD GQ PENNYKTT P PVLDS DGSFFLYSKLTVDKSRWEQGDFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 6A1[B7H3]_H1_Fab_(G4S)2_1A7[CD28]_H1.14_L1_scFv(GKPGS)4_(G4S)2-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S SEQ ID NO: 996

EVQLLES GGGGLVQP GGS LRLSCAAS GFTFSNYYMAWVRQAPGKGLEWVSSI STGGGSTYYRDSVKGRFTISRDN SKS
TLYLQMNSLRAEDTAVYYCTTDL SAI AATPFAYWGQGT LVT VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCGGGGS
GGGGS/ EVQLLES GGGGLVQP GGS LRLSCAAS GFTFSNYYMSWVRQAPGKGLEWVSTI SESGDSTYYADSVKGRFTIS
RDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGT LVT VSS/GKPGSGKPGSGKPGSGKPGS/DIQMT
QSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTITSSLPQPED
FATYYCQQSYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCP/APPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLT V LHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT P PVLDS DGSFFLYSKLTVDKSR
WQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 36C

Chain 3 - 6A1[B7H3]_L1 SEQ ID NO:997

DIQMTQSPSSLSASVGDRVTITCRASQNIYTS~~LA~~WYQQKPGKAPKLLIYN~~AH~~SLQTGIPSRFSGSGSGADFTLTIS
 LQPEDFATYFCQQYYSGITFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKDS~~TY~~SLSS~~LT~~LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP34728 6A1[B7H3] H1L1 Fab-1A7[CD28] H1.14 L1 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - 6A1[B7H3]_H1_Fab_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S SEQ ID NO:998

EVQLLES~~GG~~GLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSI~~ST~~GGG~~ST~~YYRDSVKGRFTISRDN
 SKS
 TLYLQMN~~SL~~RAEDTAVYYCTTDL~~SA~~IAATPFA~~Y~~WGQGT~~LV~~TVSS/ASTKGP~~SV~~FPLAPSSKSTSGGTAALGCLVKDY
 FPEPVT~~SV~~WNSGALTSGVHTFPAVLQSSGLYSLSSVTV~~PS~~SLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT~~VL~~HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSV~~M~~HEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q SEQ ID NO:999

EVQLLES~~GG~~GLVQPGGSLRLSCAASGFTFS~~SY~~MSWVRQAPGKGLEWVSTI~~ES~~GDSTYYADSVKGRFTISRDN
 SKN
 TLYLQMN~~SL~~RAEDTAVYYCAKSGFGLRQVGF~~Y~~WGQGT~~LV~~TVSSGKPGSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSA
 SVGDRVTITCRASQSE~~SS~~YLNWYQQKPGKAPKLLIYA~~AS~~SLQSGVPSRFSGSGSGTDFTLTIS~~SL~~QPEDFATYYCQQ
 SYSTPFTFGQGT~~KL~~EIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFN
 WYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VL~~HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV~~M~~HE
 ALHNHYTQKSLSLSPGK

Chain 3 - 6A1[B7H3]_L1 Light Chain SEQ ID NO:1000

DIQMTQSPSSLSASVGDRVTITCRASQNIYTS~~LA~~WYQQKPGKAPKLLIYN~~AH~~SLQTGIPSRFSGSGSGADFTLTIS
 LQPEDFATYFCQQYYSGITFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKDS~~TY~~SLSS~~LT~~LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 37

**>XENP34717 1A7[CD28] H1.14 L1 Fab-2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 pl(-)
Isosteric A PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q**

Chain 1 - 1A7[CD28]_H1.14_Fab_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S SEQ ID NO:1001

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISSESGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCAKSGFGLRQVGFEDYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - 2E4A3.189[B7H3]_H1.22_Fab_IgG1_PVA_/S267K/S364K/E357Q SEQ ID NO:1002

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNNYMHWVRQAPGQGLEWMGIISPSVGRITAYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARGGGSEPRLDYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFPYPSDIAVEWES
NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - 1A7[CD28]_L1 Light Chain SEQ ID NO:1003

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 38A

>XENP34336 1A7[CD28] H1.14 L1 Fab-

2E4A3.189[B7H3] H1.3 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.3 1A7[CD28] L1 Fab-IgG1 pl(-)
Isosteric A PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q

Chain 1 -1A7[CD28]_H1.14_L1_Fab-IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S SEQ ID NO:1004

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKLEWVSTISESGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCAKSGFGLRQVGFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 2 -2E4A3.189[B7H3]_H1.3_1A7[CD28]_L1_Fab_(GKPGS)2_2E4A3.189[B7H3]_H1.3_1A7[CD28]_L1_Fab-
IgG1_PVA_/S267K/S364K/E357Q SEQ ID NO:1005

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNHYMHWRQAPGQGLEWMGIISPSAGSTDYAQKRFQGRVTMTRDTSTIS
TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCKASGYIFTNHYMHWRQAPGQGLEWMGIISPSAGSTDYAQKRFQGRVTMTRD
TSTSTVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 3 -1A7[CD28]_L1 SEQ ID NO:1006

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38B

**>XENP34339 1A7[CD28] H1.14 L1 Fab-
 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 pl(-)
) Isosteric A PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q**

Chain 1 - 1A7[CD28]_H1.14_Fab_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S SEQ ID NO:1007

EVQLLES~~GGGLVQPGGSLRL~~SCAASGFTFSSYYMSWVRQAPGKLEWVSTI~~ESGDSTYYADSVKGRFTISRDN~~SKN
 TLYLQMN~~SLRAEDTAVYYCAKSGPGLPQVGF~~YWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY~~
 FPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC~~
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN~~AKTKPREEEYNSTYRVVS~~
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEK~~TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYP~~SDIAVEW
 ESDGQ~~PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDV~~FSCSV~~MHEALHNHYTQKSLSLSPGK~~

Chain 2 -

2E4A3.189[B7H3]_H1.22_Fab_(GKPGS)2_2E4A3.189[B7H3]_H1.22_Fab_IgG1_PVA_/S267K/S364K/E357Q

SEQ ID NO:1008

QVQLVQSGAEVKKPGASVKV~~SCASGYIFTNNYMHWVRQAPGQGLEWMGIISPSV~~GRTAY~~AQKFQGRVTMTRDTSTS~~
 TVY~~MELSSLR~~SEDTAVYYCARGGGSS~~PRLDYWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
 EPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK~~
 PGS/QVQLVQSGAEVKKPGASVKV~~SCASGYIFTNNYMHWVRQAPGQGLEWMGIISPSV~~GRTAY~~AQKFQGRVTMTRD~~
 TSTSTVY~~MELSSLR~~SEDTAVYYCARGGGSS~~PRLDYWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH~~
 TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN~~AKTKPREEQYNSTYRV~~
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK~~TISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKG~~FYP~~SDIAV~~
 EWESNGQ~~PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK~~

Chain 3 - 1A7[CD28]_L1 Light Chain SEQ ID NO:1009

DIQMTQSPSSLSASVGDRVTITC~~RAQSIS~~SYLNWYQ~~QKPGKAPKLLIYAASSLQSGVPSR~~FSGSGSGTDFTLT~~ISS~~
 LQPEDFATYYC~~QQS~~YSTP~~FTFGQ~~GTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLN~~FYPRE~~AKVQWKVDNA~~
 LQSGNSQESVTEQDSK~~DSTYLS~~STLTLSKADYE~~KHKVYACEVTHQGLSP~~VT~~KS~~FNRGEC

Figure 38C

**>XENP34398 1A7[CD28] H1.14 L1 Fab-
2E4A3.189[B7H3] H1.22 1A7 L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7 L1 Fab-IgG1 pl(-
) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S**

Chain 1 -1A7[CD28]_H1.14_L1_Fab-IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:1010

EVQLLES GGG L V Q P G G S L R L S C A A S G F T F S S Y Y M S W V R Q A P G K G L E W V S T I S E S G D S T Y Y A D S V K G R F T I S R D N S K N
T L Y L Q M N S L R A E D T A V Y Y C A K S G P G L R Q V G F D Y W G Q G T L V T V S S / A S T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y
F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S V V T V P S S S L G T Q T Y I C N V N H K P S D T K V D K K V E P K S C D K T H T C
P P C P A P P V A G P S V F L F P P K P K D T L M I S R T P E V T C V V D V K H E D P E V K F N W Y V D G V E V H N A K T K P R E E E Y N S T Y R V V S
V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C D V S G F Y P S D I A V E W
E S D G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W E Q G D V F S C S V L H E A L H S H Y T Q K S L S L S P G K

**Chain 2 -2E4A3.189[B7H3]_H1.22_1A7_L1_Fab_(GKPGS)2_2E4A3.189[B7H3]_H1.22_1A7_L1_Fab-
IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S** SEQ ID NO:1011

Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y I F T N N Y M H W V R Q A P G Q G L E W M G I I S P S V G F T A Y A Q K F Q G R V T M T R D T S T S
T V Y M E L S S L R S E D T A V Y Y C A R G G G S S P R L D Y W G Q G T L V T V S S / A S T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P
E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V / E P K S C G K P G S G K
P G S / Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y I F T N N Y M H W V R Q A P G Q G L E W M G I I S P S V G F T A Y A Q K F Q G R V T M T R D
T S T S T V Y M E L S S L R S E D T A V Y Y C A R G G G S S P R L D Y W G Q G T L V T V S S / A S T K G P S V F P L A P S S K S T S G G T A A L G C L V K
D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H
T C P P C P A P P V A G P S V F L F P P K P K D T L M I S R T P E V T C V V D V K H E D P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V
V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E Q M T K N Q V K L T C L V K G F Y P S D I A V
E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V L H E A L H S H Y T Q K S L S L S P G K

Chain 3 -1A7[CD28]_L1 SEQ ID NO:1012

D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q S I S S Y L N W Y Q Q K P G K A P K L L I Y A A S S L Q S G V P S R F S G S G S G T D F T L T I S S
L Q P E D F A T Y Y C Q Q S Y S T P E T F G Q G T K L E I K / R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A K V Q W K V D N A
L Q S G N S Q E S V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G E C

Figure 38D

>XENP35611 1A7[CD28] H1L1 Fab-

2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q

Chain 1 -1A7[CD28] H1L1 Fab-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S SEQ ID NO:1013

EVQLLESQGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISGSGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 2 -2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 PVA /S267K/S364K/E357Q SEQ ID NO:1014

QVQLVQSGAEVKKPGASVKVSCASGYIFTNMYMHVWRQAPGQGLEWMGIISPSVGRATAYAQKFEQGRVTMTTRDTST
TVYMEISSLRSEDTAVYYCARGGSSPRLDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCASGYIFTNMYMHVWRQAPGQGLEWMGIISPSVGRATAYAQKFEQGRVTMTTRD
TSTSTVYMEISSLRSEDTAVYYCARGGSSPRLDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFPYPSDIAV
EWESNGQGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 3 -1A7[CD28] L1 SEQ ID NO:1015

DIQMTQSPSSLSASVGRVITITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQSSYTFPTFGQGTLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP35612 1A7[CD28] H1.1 L1 Fab-

2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-IgG1 PVA /S267K/S364K/E357Q

Chain 1 -1A7[CD28] H1.1 L1 Fab-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S SEQ ID NO:1016

EVQLLESQGGGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVSTISGSGDSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 2 -2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 PVA /S267K/S364K/E357Q SEQ ID NO:1017

QVQLVQSGAEVKKPGASVKVSCASGYIFTNMYMHVWRQAPGQGLEWMGIISPSVGRATAYAQKFEQGRVTMTTRDTST
TVYMEISSLRSEDTAVYYCARGGSSPRLDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCASGYIFTNMYMHVWRQAPGQGLEWMGIISPSVGRATAYAQKFEQGRVTMTTRD
TSTSTVYMEISSLRSEDTAVYYCARGGSSPRLDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFPYPSDIAV
EWESNGQGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 3 -1A7[CD28] L1 SEQ ID NO:1018

DIQMTQSPSSLSASVGRVITITCRASQSISSYLNWYQOKPGKAPKLLIYAASSLSQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQSSYTFPTFGQGTLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 38E

>XENP37808 1A7[CD28] H1.1 L1 Fab-
2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.22 1A7[CD28] L1 Fab-IgG1 pl(-)
Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S
Chain 1 -1A7[CD28]_H1.1_L1_Fab-IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S
SEQ ID NO:1019
EVQLLES^{GGGLVQPGGSLRLS}CAAS^{GFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN}SKN
TLYLQMN^{SLRAEDTAVYYCAKSGPGLPQVGF}FDYWGQGT^{LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY}
FPEPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS^{CSVLHEALHSHYTQKSLSLSPGK}
Chain 2 -2E4A3.189[B7H3]_H1.22_1A7[CD28]_L1_Fab (GKPGS)2_2E4A3.189[B7H3]_H1.22_1A7[CD28]_L1_Fab-
IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S SEQ ID NO:1020
QVQLVQSGAEVKKPGASVKVSCKAS^{GYIFTNNYMHWVRQAPGQGLEWMGIISPSVGR}TAYAQKFQGRVTMT^{TRDTSTS}
TVYME^{LSSLRSEDTAVYYCARGGSSPRLDYWGQGT}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCKAS^{GYIFTNNYMHWVRQAPGQGLEWMGIISPSVGR}TAYAQKFQGRVTMT^{TRD}
TSTSTVYME^{LSSLRSEDTAVYYCARGGSSPRLDYWGQGT}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ^{QGNVFS}CSVLHEALHSHYTQKSLSLSPGK
Chain 3 -1A7[CD28]_L1 SEQ ID NO:1021
DIQMTQSPSSLSASVGRVTITCFASQ^{SISSYLNWYQKPGKAPKLLIYAAS}SLQSGVPSRFSGSGSGTDFTLT^{ISS}
LQPEDFATYYC^{QQS}YSTPFTFGQGT^{KLEIK/RTVAAPSVFI}FPPSDEQLKSGTASVVC^{LLNNFY}PREAKVQW^{KVDNA}
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP37810 1A7[CD28] H1.14 L1 Fab-
2E4A3.189[B7H3] H1.3 1A7[CD28] L1 Fab (GKPGS)2 2E4A3.189[B7H3] H1.3 1A7[CD28] L1 Fab-IgG1 pl(-)
Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S
Chain 1 -1A7[CD28]_H1.14_L1_Fab-IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S
SEQ ID NO:1022
EVQLLES^{GGGLVQPGGSLRLS}CAAS^{GFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN}SKN
TLYLQMN^{SLRAEDTAVYYCAKSGPGLPQVGF}FDYWGQGT^{LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY}
FPEPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS^{CSVLHEALHSHYTQKSLSLSPGK}
Chain 2 -2E4A3.189[B7H3]_H1.3_1A7[CD28]_L1_Fab (GKPGS)2_2E4A3.189[B7H3]_H1.3_1A7[CD28]_L1_Fab-
IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S SEQ ID NO:1023
QVQLVQSGAEVKKPGASVKVSCKAS^{GYIFTNNYMHWVRQAPGQGLEWMGIISPSAGSTDYA}QKFQGRVTMT^{TRDTSTS}
TVYME^{LSSLRSEDTAVYYCARGGSSPRLDYWGQGT}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSNTKVDKKV/EPKSCGKPGSGK
PGS/QVQLVQSGAEVKKPGASVKVSCKAS^{GYIFTNNYMHWVRQAPGQGLEWMGIISPSAGSTDYA}QKFQGRVTMT^{TRD}
TSTSTVYME^{LSSLRSEDTAVYYCARGGSSPRLDYWGQGT}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVT^{SVWNSGALTSGVHTFPAVLQSSGLYSLSSVTV}PSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ^{QGNVFS}CSVLHEALHSHYTQKSLSLSPGK
Chain 3 -1A7[CD28]_L1 SEQ ID NO:1024
DIQMTQSPSSLSASVGRVTITCFASQ^{SISSYLNWYQKPGKAPKLLIYAAS}SLQSGVPSRFSGSGSGTDFTLT^{ISS}
LQPEDFATYYC^{QQS}YSTPFTFGQGT^{KLEIK/RTVAAPSVFI}FPPSDEQLKSGTASVVC^{LLNNFY}PREAKVQW^{KVDNA}
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39A

>XENP36781 6A1[B7H3] H1L1 Fab-6A1[B7H3] H1L1 Fab-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
 IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Chain 1 - 6A1[B7H3]_H1L1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:1025

EVQLLES GGGGLVQP GGS LRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSI STGGGSTYYRDSVKGRFTISRDN SKS
 TLYLQMNSLRAEDTAVYYCTTDL SAI AATPFAYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 6A1[B7H3]_H1L1_Fab-

IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4

SEQ ID NO:1026

EVQLLES GGGGLVQP GGS LRLSCAASGFTFSNYYMAWVRQAPGKGLEWVSSI STGGGSTYYRDSVKGRFTISRDN SKS
 TLYLQMNSLRAEDTAVYYCTTDL SAI AATPFAYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYPSDIAVEW
 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVLHEALHSHYTQKSLSLSP/GGGGGSGGGSG
 GGGG/ EVQLLES GGGGLVQP GGS LRLSCAASGFTFSNYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISR
 DNSKNTLYLQMNSLRAEDTAVYYCAKSGFGLRQVGFYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
 SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
 ATYYCQSQSYSTFTFGQGTKLEIK

Chain 3 - 6A1[B7H3]_L1 SEQ ID NO:1027

DIQMTQSPSSLSASVGDRVTITCRASQNIYTSIAWYQQKPKAPKLLIYNAHSLQTFGIPSRFSGSGSGADFTLTIS
 LQPEDFATYFCQQYYSGLTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39B

>XENP37805 2E4A3.189[B7H3] H1L1 Fab-2E4A3.189[B7H3] H1L1 Fab-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Chain 1 - 2E4A3.189[B7H3]_H1L1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:1028

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNYYMHVVRQAPGQGLEWMGIIISPSAGTTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIAVEWES
DGQOPENNYKTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 2E4A3.189[B7H3]_H1L1_Fab-

IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4

SEQ ID NO:1029

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNYYMHVVRQAPGQGLEWMGIIISPSAGTTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVLHEALHSHYTQKSLSLSP/GGGGGSGGGSGGG
GS/EVQLLESGLLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKLEWVSTISESGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT
YYCQQSYSTPFTFGQGTKLEIK

Chain 3 - 2E4A3.189[B7H3]_L1 SEQ ID NO:1030

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISL
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39C

>XENP37806 2E4A3.189[B7H3] H1.3 L1 Fab-2E4A3.189[B7H3] H1.3 L1 Fab-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
 IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Chain 1 - 2E4A3.189[B7H3]_H1.3_L1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:1031

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNHYMHVWRQAPGGQGLEWMGIIISPSAGSTDYAQKFFQGRVTMTRDTSTS
 TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPP
 CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
 DGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSVLSLHEALHSHYTQKSLSLSPGK

Chain 2 - 2E4A3.189[B7H3]_H1.3_L1_Fab-

IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4

SEQ ID NO:1032

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNHYMHVWRQAPGGQGLEWMGIIISPSAGSTDYAQKFFQGRVTMTRDTSTS
 TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPP
 CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFFPSDIAVEWES
 NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVLSLHEALHSHYTQKSLSLSP/GGGGGSGGGSGGG
 GS/EVQLLESGLLVQPGGSLRLSCAASGFTTFSSYYMSWVRQAPGKLEWVSTISESGDSTYYADSVKGRFTISRDN
 SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/DIQTQSP
 SSLASVGDRTTITCPASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
 YYCQQSYSTFFTFGQGTKLEIK

Chain 3 - 2E4A3.189[B7H3]_L1 SEQ ID NO:1033

DIQTQSPSSLSASVGDRTTITCPASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
 LQPEDFATYYCQQSYSTFFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDSYSLSSITLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39D

>XENP37807 2E4A3.189[B7H3] H1.22 L1 Fab-2E4A3.189[B7H3] H1.22 L1 Fab-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Chain 1 - 2E4A3.189[B7H3]_H1.22_L1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S
SEQ ID NO:1034

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNNYMHVVRQAPGQGLEWMGIIISPSVGRATAYAQKFQGRVTMTTRDTSTS
TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIAVEWES
DGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 2E4A3.189[B7H3]_H1.22_L1_Fab-
IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4
SEQ ID NO:1035

QVQLVQSGAEVKKPGASVKVSCKASGYIFTNNYMHVVRQAPGQGLEWMGIIISPSVGRATAYAQKFQGRVTMTTRDTSTS
TVYMELSSLRSEDTAVYYCARGGGSSPRLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFVSLHEALHSHYTQKSLSLSP/GGGGGSGGGSGGG
GS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVSTISSESGDSITYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT
YYCQQSYSTPFTFGQGTKLEIK

Chain 3 - 2E4A3.189[B7H3]_L1 SEQ ID NO:1036

DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISL
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 39E

>XENP37982 3C4[B7H3] H1 L1.1 Fab-3C4[B7H3] H1 L1.1 Fab-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S/M428L/N434S-
 IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.14 L1 scFv(GKPGS)4

Chain 1 - 3C4[B7H3]_H1_L1.1_Fab-IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S/M428L/N434S

SEQ ID NO:1037

QVQLVQSGAEVKKPGASVKVSCKVS~~GFS~~LT~~SYHVS~~WVRQAPGQGLEWMGAISSGGSSYYNSK~~FQ~~GRVTMTRDTSTST
 VYME~~LSS~~LRSEDTAVYFCTG~~DLGAAISW~~FAYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~SSL~~GTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
 CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
 DGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 3C4[B7H3]_H1_L1.1_Fab-

IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4

SEQ ID NO:1038

QVQLVQSGAEVKKPGASVKVSCKVS~~GFS~~LT~~SYHVS~~WVRQAPGQGLEWMGAISSGGSSYYNSK~~FQ~~GRVTMTRDTSTST
 VYME~~LSS~~LRSEDTAVYFCTG~~DLGAAISW~~FAYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~SSL~~GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
 CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
 TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TCLVKG~~FYP~~SDIAVEWES
 NGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSVL~~HEALHSHYTQKSLSLSP/SGGGSSGGSSGGG
 GS/EVQLLES~~GGGLVQ~~PGGSLRLSCAASGFT~~FSS~~YYMSWVRQAPGKLEWVSTISESGDSTYYADSVKGRFTISRDN
 SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGT~~LVTVSS~~/GKPGSGKPGSGKPGSGKPGS/DIQTQSP
 SSLASVGD~~RV~~TITCPASQSISSYL~~NWYQ~~KPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT
 YYCQSSYSTPFTFGQGTKLEIK

Chain 3 - 3C4[B7H3]_L1.1 SEQ ID NO:1039

DIQTQSPSSLSASVGD~~RV~~TITCRTS~~QSI~~YKSLAWYQOKPGKAPKLLIYNAHSLQ~~TG~~IPSRFSGSGSGTDFTLTISS
 LQPEDFATYFCQ~~QYYSG~~LTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKDSYSLSS~~TL~~TLTKADY~~E~~KHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 40A

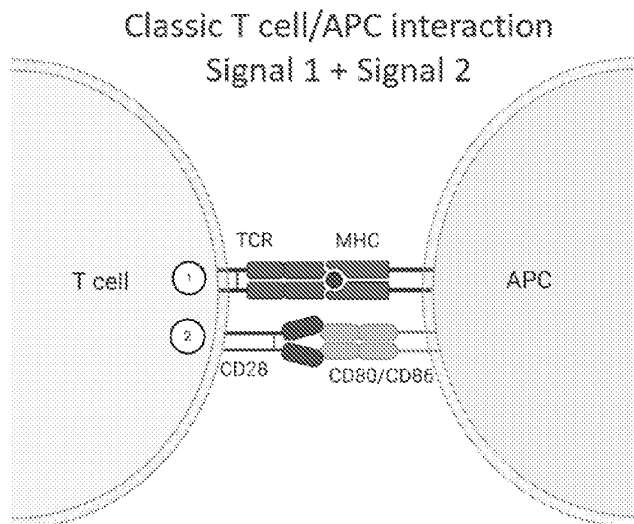


Figure 40B

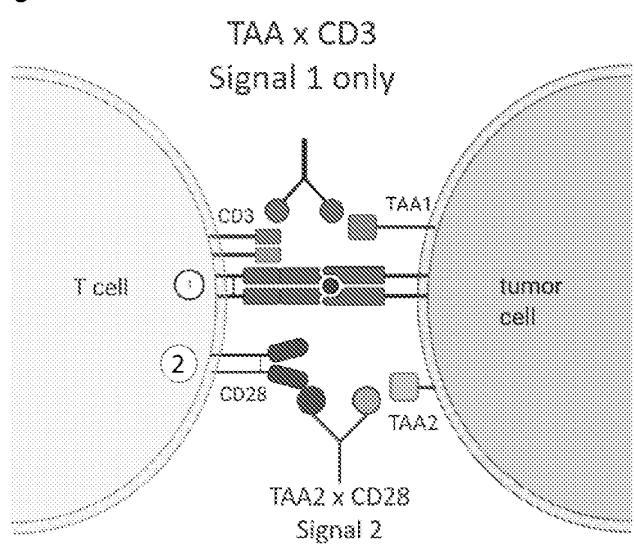


Figure 41

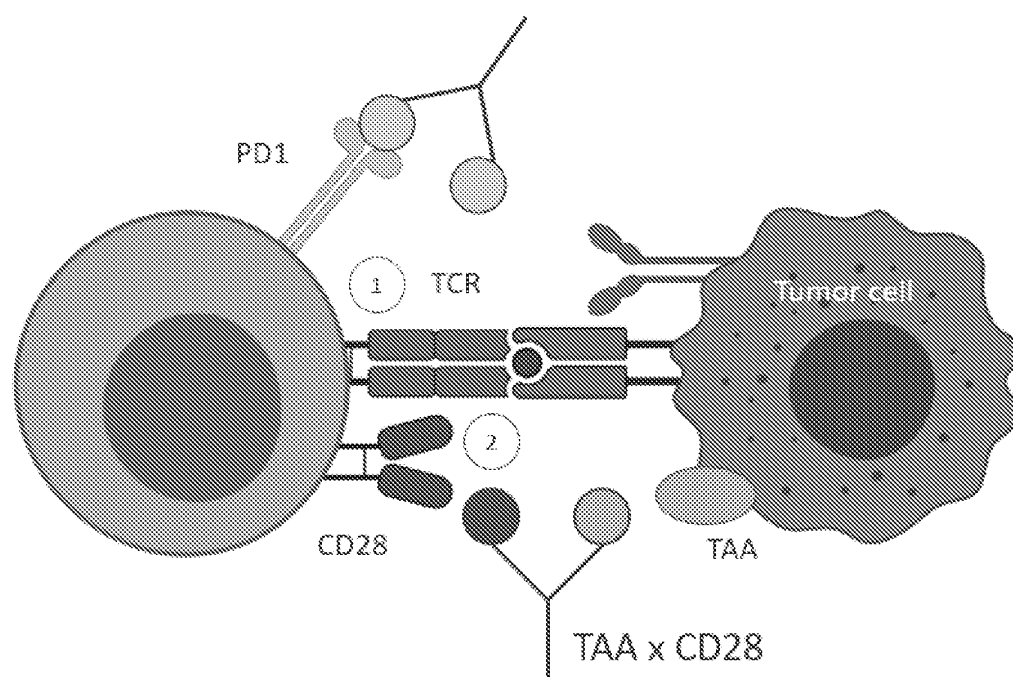


Figure 42

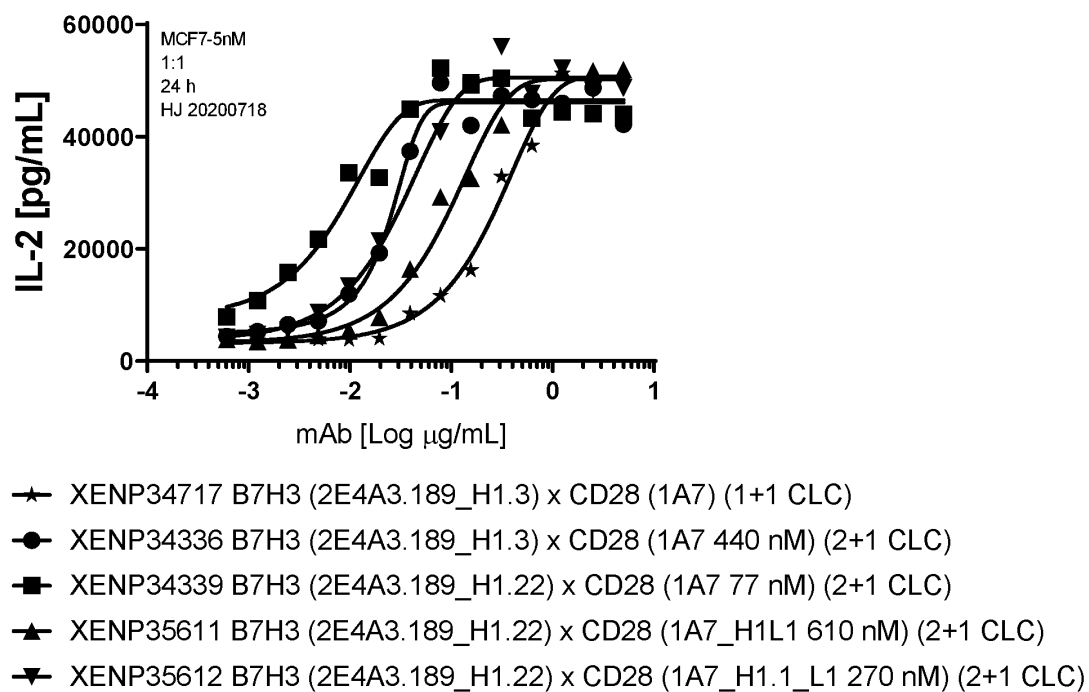


Figure 43A

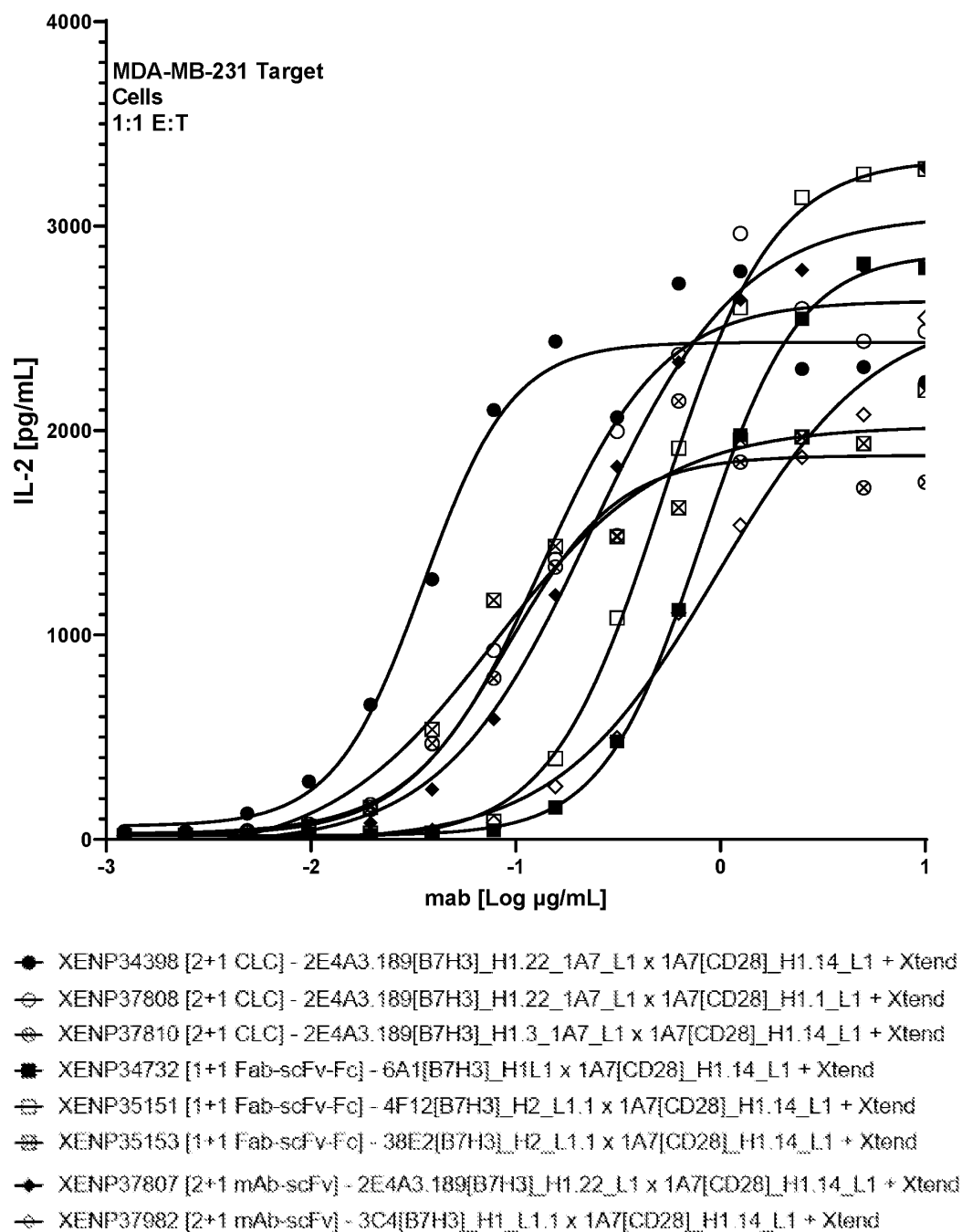
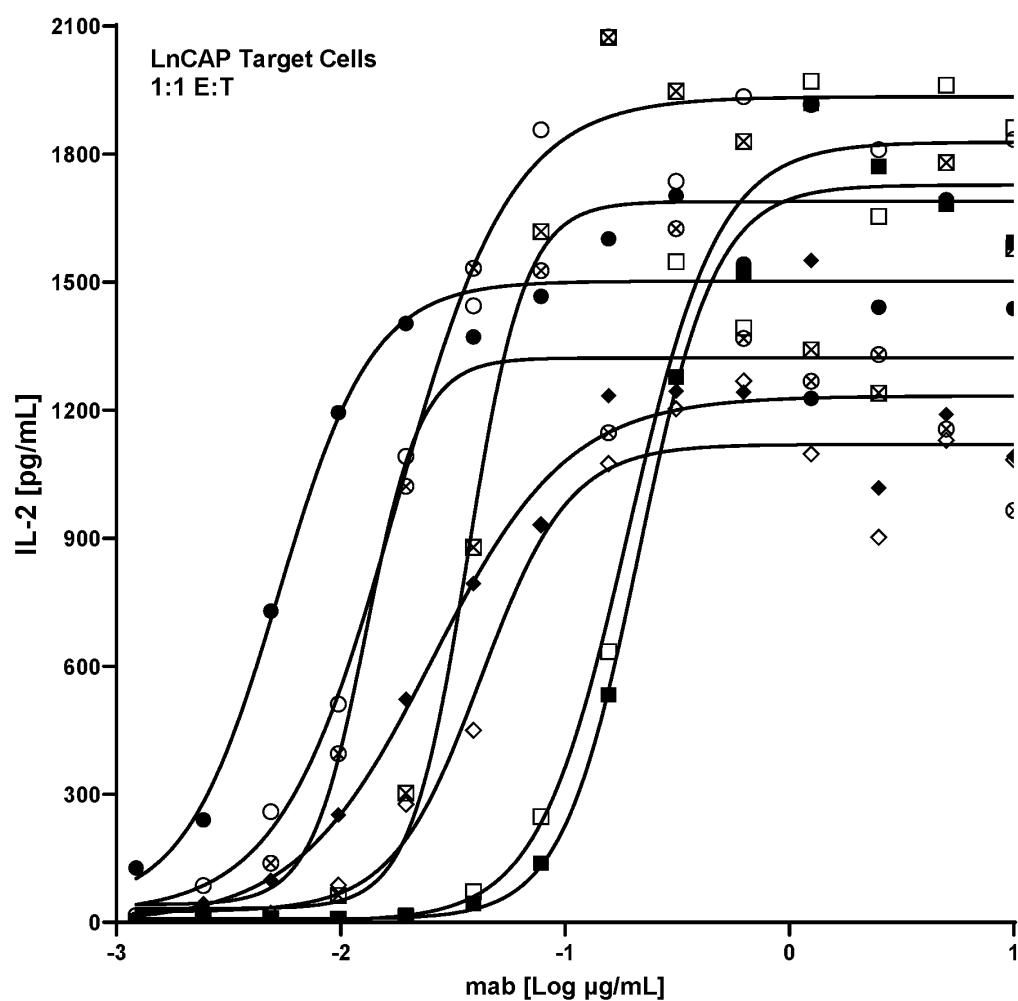
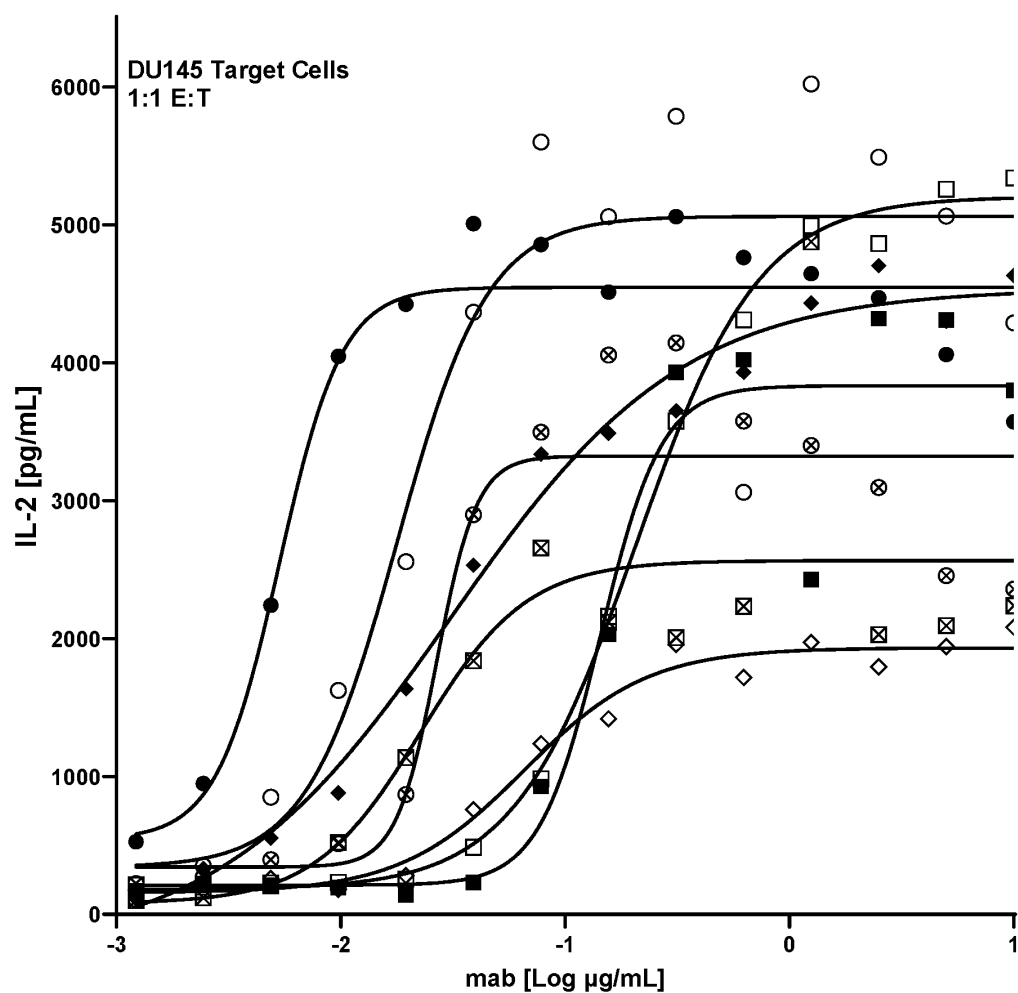


Figure 43B



- XENP34398 [2+1 CLC] - 2E4A3.189[B7H3]_H1.22_1A7_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊕ XENP37808 [2+1 CLC] - 2E4A3.189[B7H3]_H1.22_1A7_L1 x 1A7[CD28]_H1.1_L1 + Xtend
- ⊗ XENP37810 [2+1 CLC] - 2E4A3.189[B7H3]_H1.3_1A7_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- XENP34732 [1+1 Fab-scFv-Fc] - 6A1[B7H3]_H1L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊞ XENP35151 [1+1 Fab-scFv-Fc] - 4F12[B7H3]_H2_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊞ XENP35153 [1+1 Fab-scFv-Fc] - 38E2[B7H3]_H2_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend
- ◆ XENP37807 [2+1 mAb-scFv] - 2E4A3.189[B7H3]_H1.22_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊕ XENP37982 [2+1 mAb-scFv] - 3C4[B7H3]_H1_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend

Figure 43C



- XENP34398 [2+1 CLC] - 2E4A3.189[B7H3]_H1.22_1A7_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊕ XENP37808 [2+1 CLC] - 2E4A3.189[B7H3]_H1.22_1A7_L1 x 1A7[CD28]_H1.1_L1 + Xtend
- ⊗ XENP37810 [2+1 CLC] - 2E4A3.189[B7H3]_H1.3_1A7_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- XENP34732 [1+1 Fab-scFv-Fc] - 6A1[B7H3]_H1L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊞ XENP35151 [1+1 Fab-scFv-Fc] - 4F12[B7H3]_H2_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊞ XENP35153 [1+1 Fab-scFv-Fc] - 38E2[B7H3]_H2_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend
- ◆ XENP37807 [2+1 mAb-scFv] - 2E4A3.189[B7H3]_H1.22_L1 x 1A7[CD28]_H1.14_L1 + Xtend
- ⊕ XENP37982 [2+1 mAb-scFv] - 3C4[B7H3]_H1_L1.1 x 1A7[CD28]_H1.14_L1 + Xtend

Figure 44

<u>1A7 VH</u>	<u>SEQ</u>	<u>SEQ ID</u>	
HFR1	EVQLLESGGGLVQPGGSLRLSCAASGFX ₁ X ₂ X ₃	1184	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	1185	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	1186	X ₁ is selected from S, A
HCDR2	X ₁ IX ₂ X ₃ X ₄ X ₅ X ₆ X ₇ YYADSVKG	1187	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	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	1188	
HCDR3	SGPGLRQVGFDY	1189	
HFR4	WGQGTLTVSS	1190	
<u>1A7 VL</u>			
LFR1	DIQMTQSPSSLSASVGDRVTITC	1191	
LCDR1	RASQSISX ₁ X ₂ LX ₃	1192	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	1193	
LCDR2	X ₁ ASX ₂ LX ₃ X ₄	1194	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	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	1195	
LCDR3	QQX ₁ X ₂ X ₃ X ₄ PX ₅ T	1196	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	1197	

Figure 45A

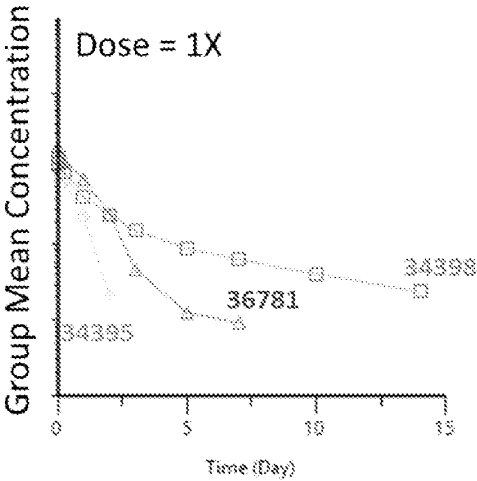


Figure 45B

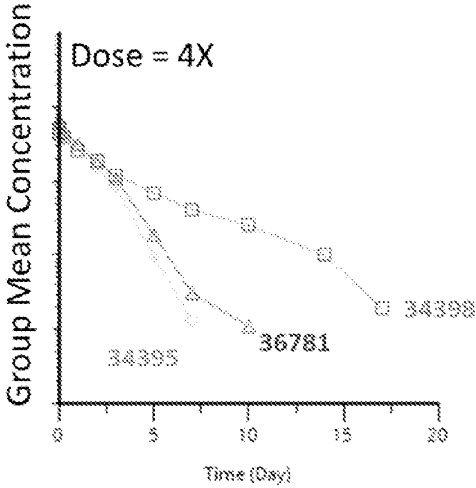


Figure 45C

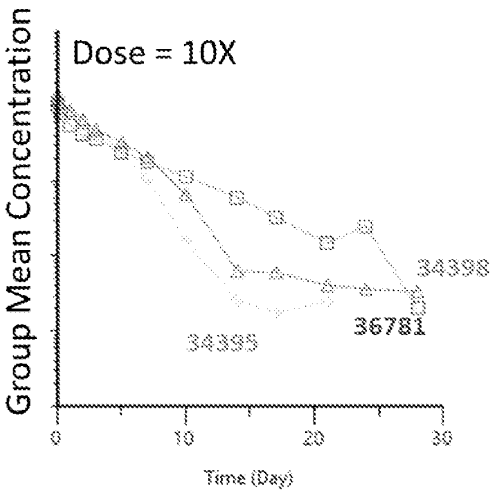


Figure 45D

XENP34398: 2 + 1 CLC
XENP36781: 2 + 1 mAb-scFv
XENP34395: 2 + 1 Fab₂-scFv-Fc

Figure 46A

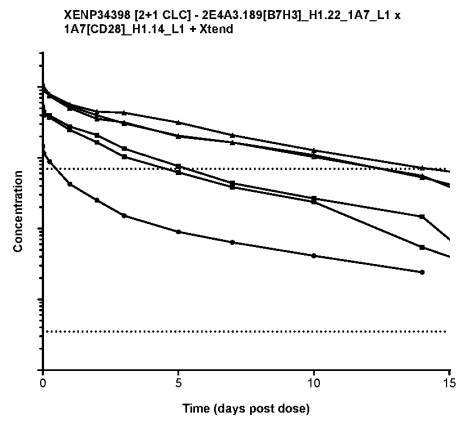


Figure 46B

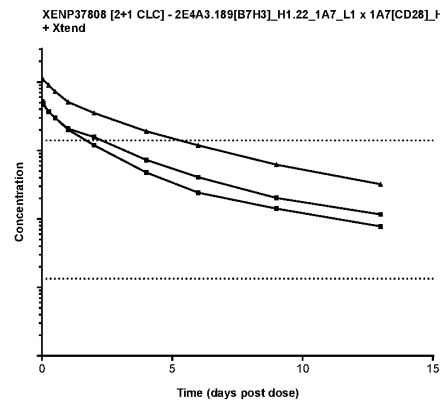


Figure 46C

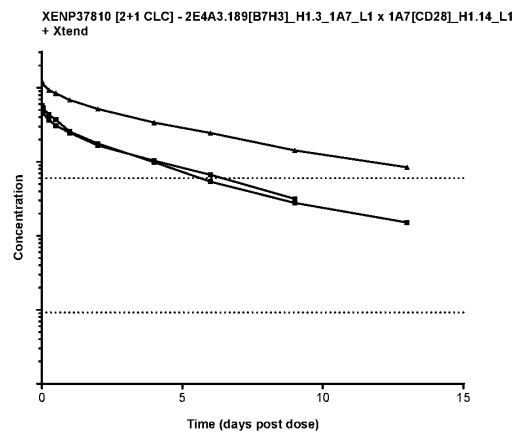


Figure 46D

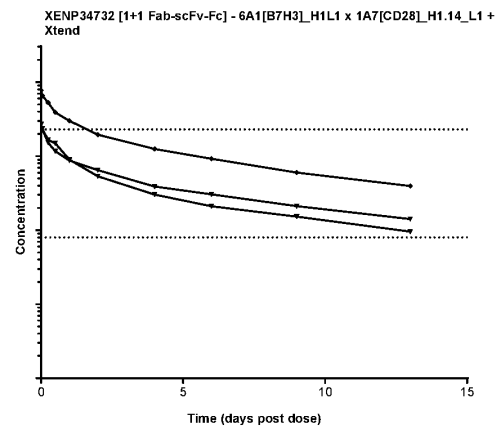


Figure 46E

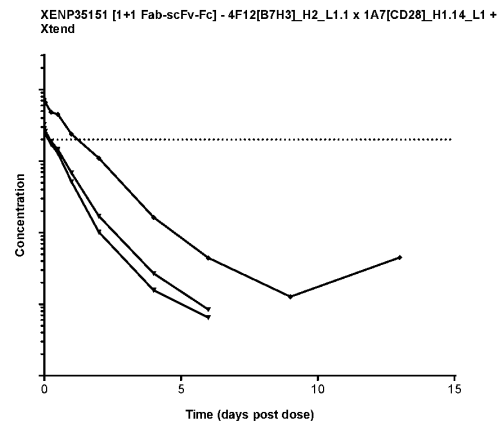


Figure 46F

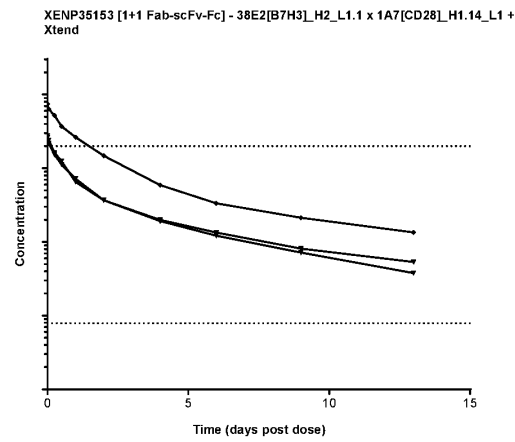


Figure 46G

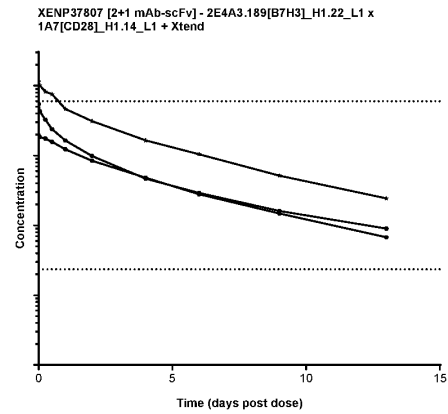


Figure 46H

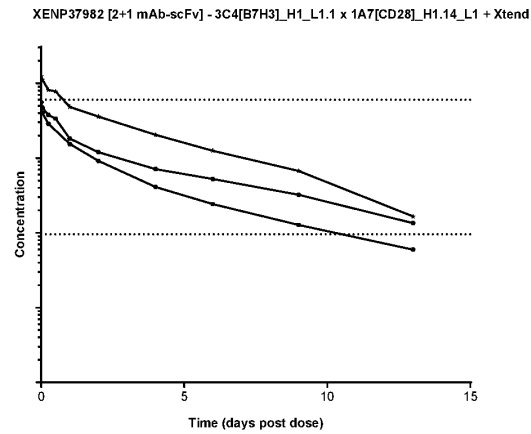


Figure 47

	<u>XENP34398</u>	<u>XENP37808</u>	<u>XENP34732</u>	<u>XENP35153</u>
Format	2+1 CLC	2+1 CLC	1 + 1 Fab-scFv-Fc	1 + 1 Fab-scFv-Fc
B7H3 Fv	2E4A3.189[B7H3]_H1.22_1A7_L1	2E4A3.189[B7H3]_H1.22_1A7_L1	6A1[B7H3]_H1_L1	4F12[B7H3]_H2_L1.1
CD28 Fv	1A7[CD28]_H1.14_L1	1A7[CD28]_H1.1_L1	1A7[CD28]_H1.14_L1	1A7[CD28]_H1.14_L1
B7H3 Fv Source	Phage	Phage	Rat	Rabbit
CD28 Fv Source	Phage	Phage	Phage	Phage
B7H3 Fv Humanness	93%	93%	85%	81%
CD28 Fv Humanness	94%	94%	94%	94%
B7H3 Monovalent KD (nM)	7.6	7.6	8.1	0.5
CD28 KD (nM)	63	230	370	360
MDA-MB-231 EC50 (nM)	0.2	0.7	6	0.6
PK t_{1/2}	3.3 to 5.0	3.4 to 4.3	5.4 to 6.1	4.2 to 5.4
DSF T_{m1} and T_{m2} (°C)	67.5, 78.5	67.5, 78.5	67.5, 80.0	67.5, 79.0
Sequence Liabilities	none	none	none	NS (HCDR3); NS (LCDR1)
Pros	most potent; high humanness	high humanness	simplest bsAb format	simplest bsAb format
Cons			weak activity	rabbit-derived

Figure 48A

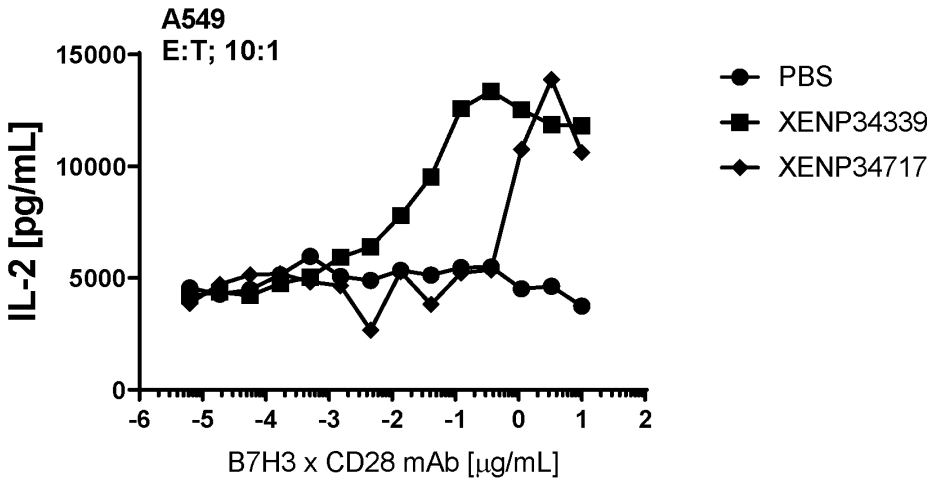


Figure 48B

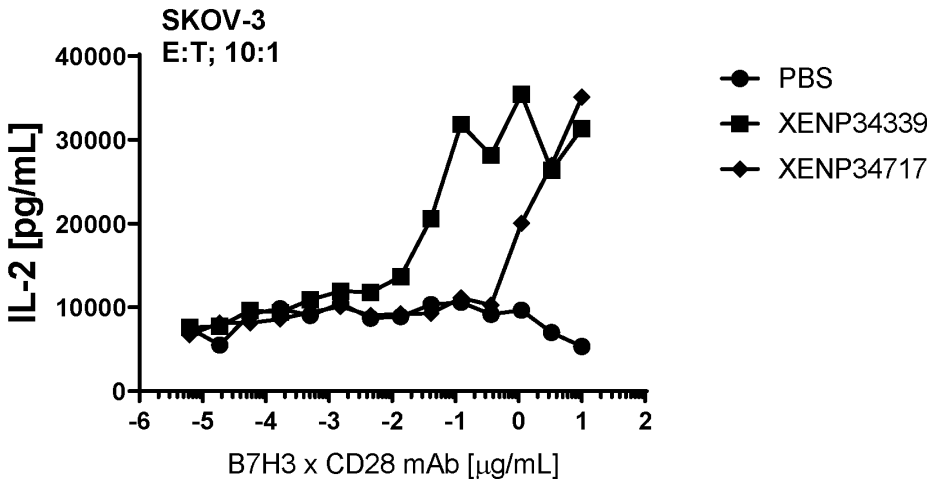


Figure 49

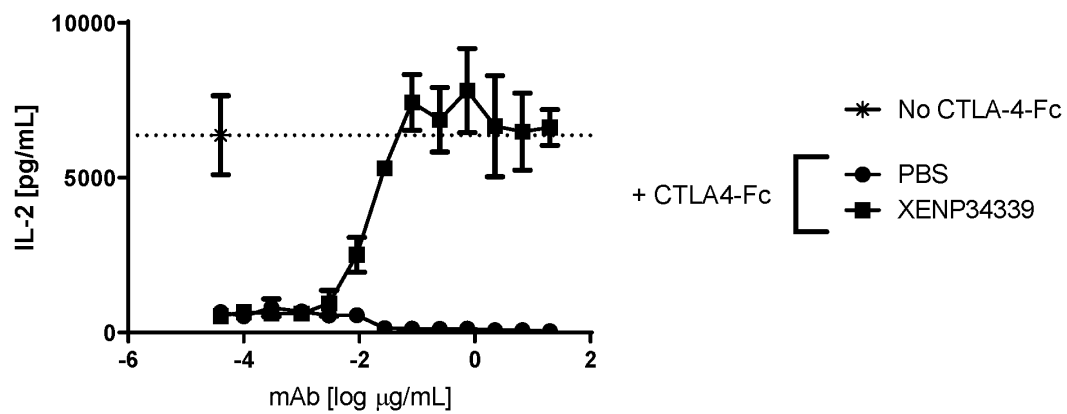


Figure 50A

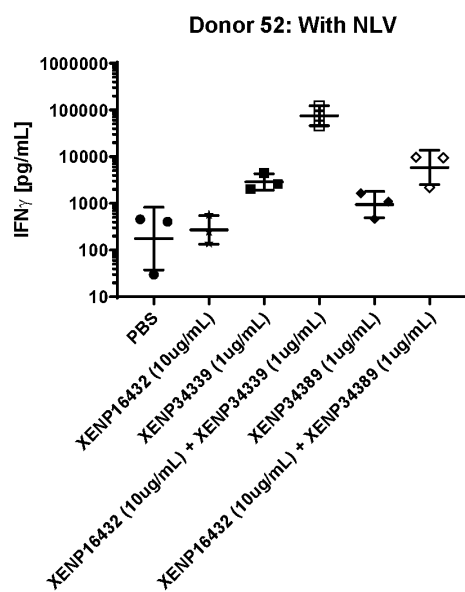


Figure 50B

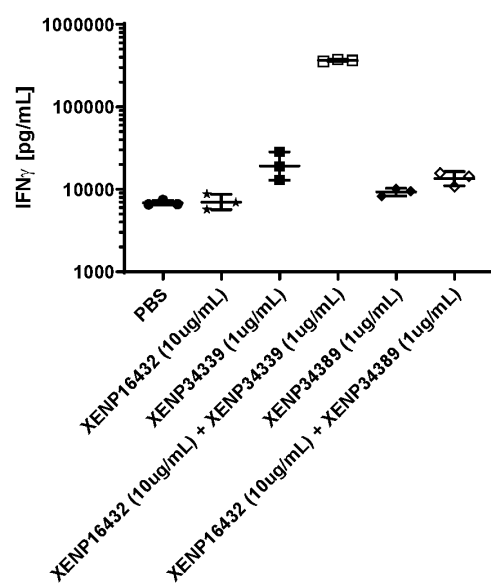


Figure 51

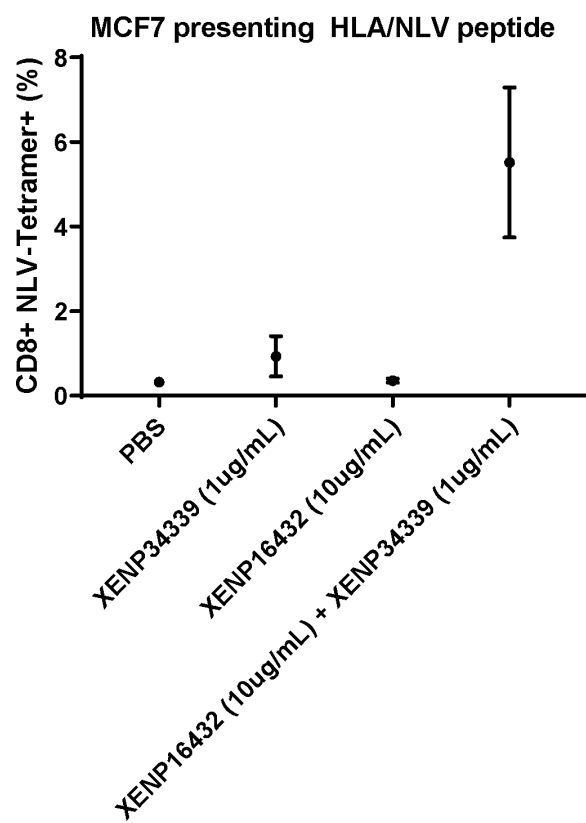


Figure 52

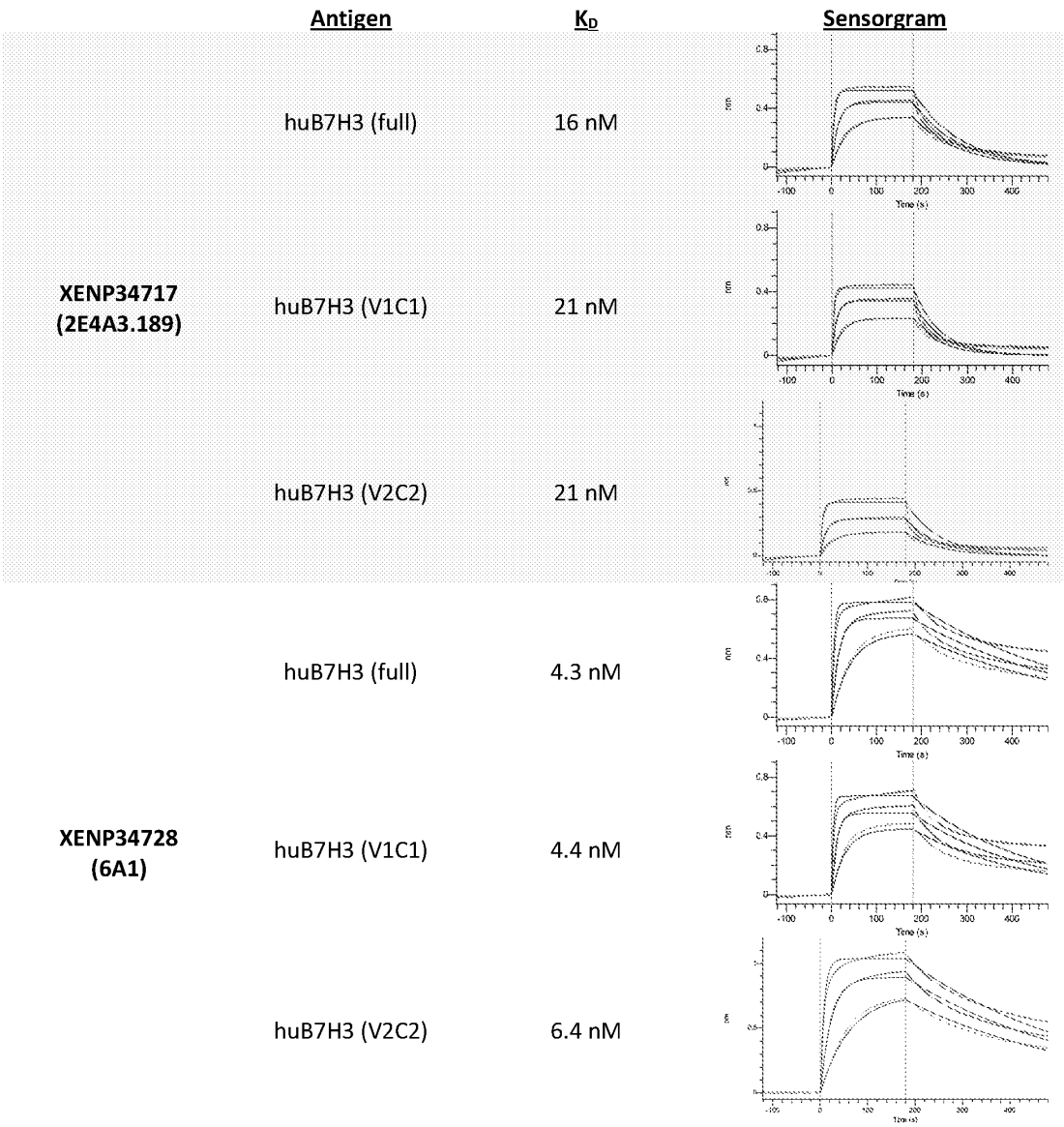


Figure 53

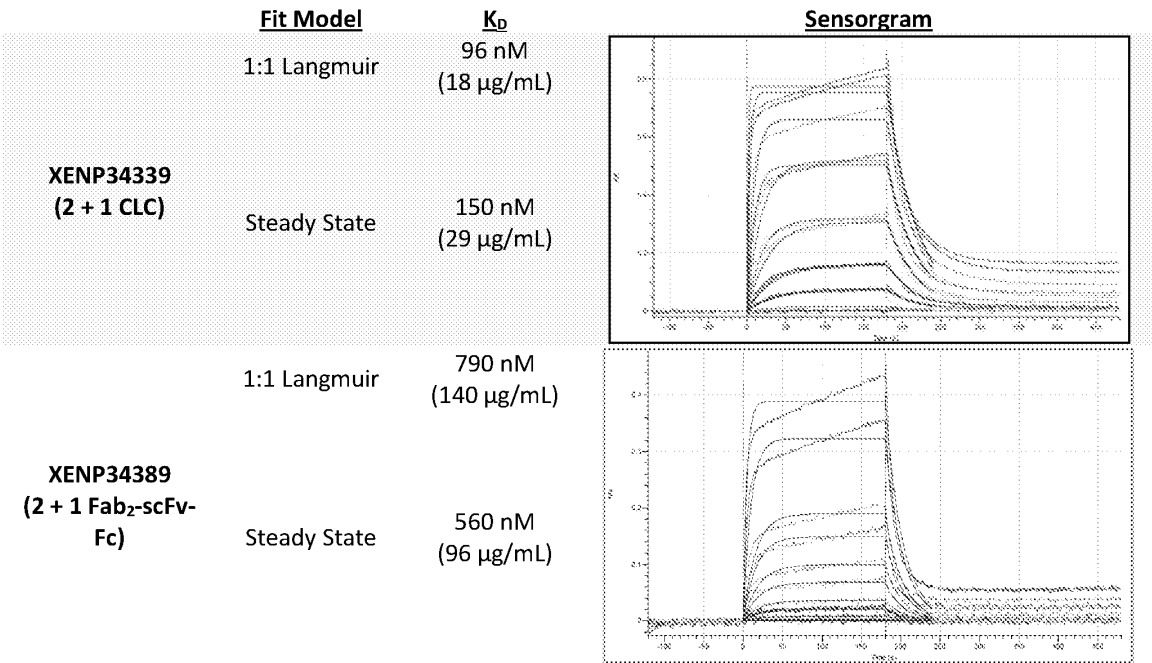


Figure 54A

>XENP31602 PSMA-H H1L1 Fab-PSMA-H H1L1 CH1 (G4S)2 [CD3] H1.30 L1.47 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - PSMA-H_H1_IgG1_pl(-)_Isosteric_A /PVA /S267K/L368D/K370S SEQ ID NO:1040

EVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQSLWMGNINPNNGGTTYNQKFQGRVTITVDKSTS
TAYMELSSLRSEDTAVYYCAAGWNFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTPPCPAP
PVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQP
ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - PSMA-

H_H1_CH1_(G4S)2_[CD3]_H1.30_L1.47_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA /S267K/S364K/E357Q

SEQ ID NO:1041

EVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQSLWMGNINPNNGGTTYNQKFQGRVTITVDKSTS
TAYMELSSLRSEDTAVYYCAAGWNFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/ GGGGSGGGGS/
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI RSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLR AEDTAVYYCVRHGNEFGDSYVSWFAYWGQGTLLTVSS/ GKPGSGKPGSGKPGSGKPGS/ QAVVTQE
PSLTVSPGGTVTLTCSSTGAVTTENYANWVQKPGKSPRGLIGQTNKRAPGVPARFSGSLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/ GGGGSGGGGS/ KTHTCTPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - PSMA-H_L1 Light Chain SEQ ID NO:1042

DIVMTQSPDLSAVSLGERATLSCRASQDVGTAVIEWYQQKPDQSPKLLIYWASTPHTGVPDRFTGSGSGTDFTLTIS
LQAEDVAVYFCQQYNSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 54B

>XENP32220 PSMA-H H1 L1.24 Fab-PSMA-H H1 L1.24 Fab (G4S) [CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - PSMA-H_H1_IgG1_pl(-)_Isosteric_A /PVA /S267K/L368D/K370S SEQ ID NO:1043

EVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQSLWMGNINPNNGGTTYNQKFQGRVTITVDKSTS
TAYMELSSLRSEDTAVYYCAAGWNFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQP
ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - PSMA-

H_H1_(G4S)_ [CD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA /S267K/S364K/E357Q

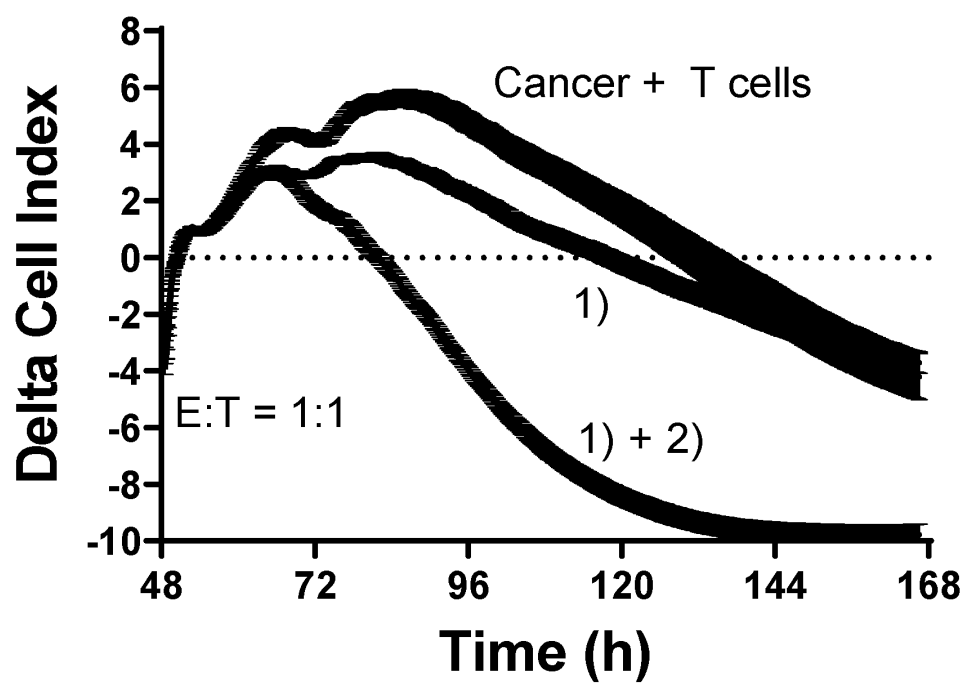
SEQ ID NO:1044

EVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTIHWVRQAPGQSLWMGNINPNNGGTTYNQKFQGRVTITVDKSTS
TAYMELSSLRSEDTAVYYCAAGWNFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/ GGGGSGGGGS/
QAVVTQEPSLTVSPGGTTLTTCGSSGTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKAALTI
SGAQPEDEADYYCALWYSNHWVFGGGKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCA
ASGFTFSTYAMNWVRQAPGKGLEWVGRIPIFSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVR
HGTFGDSYVSWFAYWGQGTLLTVSS/ GGGGSGGGGS/ KHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - PSMA-H_L1.24 Light Chain SEQ ID NO:1045

DIVMTQSPDSLAVSLGERATLSCRASQDVGTAVDWYQQKPDQSPKLLIYYASTPHTGVPDRFTGSGSGTDFTLTIS
LQAEDVAVYFCQQYNSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 55



1) 1 μ g/ml XENP31602

2) 1 μ g/ml XENP34339

Figure 56A

CD3 High – [anti-CD3] H1.30 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIISKY</u> <u>NNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVS</u> <u>WFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSTLVSPGGTV</u> <u>TLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKA</u> <u>ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL</u>	SEQ ID NO:1046
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIISKY</u> <u>NNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVS</u> <u>WFAYWGQGTLLTVSS</u>	SEQ ID NO:1047
vhCDR1	<u>TYAMN</u>	SEQ ID NO:1048
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	SEQ ID NO:1049
vhCDR3	<u>HGNFGDSYVSWFAY</u>	SEQ ID NO:1050
Variable Light (vl) Domain	<u>QAVVTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNK</u> <u>RAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL</u>	SEQ ID NO:1051
vlCDR1	<u>GSSTGAVTTSNYAN</u>	SEQ ID NO:1052
vlCDR2	<u>GTNKRAP</u>	SEQ ID NO:1053
vlCDR3	<u>ALWYSNHWV</u>	SEQ ID NO:1054
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	SEQ ID NO:1055

Figure 56B

CD3 High-Int #1 – [anti-CD3] H1.32 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFSTYAMNWVRQAPGKGLEWVGRI</u> <u>RSK</u> <u>ANNYATYYADSVKGRFTISR</u> <u>DDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFAYWGQGLTVTVSS</u> <u>/GKPGSGKPGSGKPGSGKPGS/QAVVTQEP</u> <u>SLTVSPG</u> <u>GTVTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKPAPGVPARFSGSL</u> <u>LGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL</u>	SEQ ID NO:1056
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFSTYAMNWVRQAPGKGLEWVGRI</u> <u>RSK</u> <u>ANNYATYYADSVKGRFTISR</u> <u>DDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFAYWGQGLTVTVSS</u>	SEQ ID NO:1057
vhCDR1	<u>TYAMN</u>	SEQ ID NO:1058
vhCDR2	<u>RI</u> <u>RSKANNYATYYADSVKG</u>	SEQ ID NO:1059
vhCDR3	<u>HGNFGDSYVSWFAY</u>	SEQ ID NO:1060
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGT</u> <u>VTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN</u> <u>KPAPGVPARFSGSL</u> <u>LGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	SEQ ID NO:1061
vlCDR1	<u>GSSSTGAVTTSNYAN</u>	SEQ ID NO:1062
vlCDR2	<u>GTNKPAP</u>	SEQ ID NO:1063
vlCDR3	<u>ALWYSNHWV</u>	SEQ ID NO:1064
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	SEQ ID NO:1065

Figure 56C

CD3 High-Int #2 – [anti-CD3] H1.89 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGGT~~ KLTVL	SEQ ID NO:1066
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGT ~~LVTVSS~~	SEQ ID NO:1067
vhCDR1	~~TYAMN~~	SEQ ID NO:1068
vhCDR2	<del>RI~~RSK~~YNNYATYYADSVK</del>	SEQ ID NO:1069
vhCDR3	~~HGNFGDEYVSWFAY~~	SEQ ID NO:1070
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGGT~~ KLTV L	SEQ ID NO:1071
vlCDR1	~~GSSTGAVTTSNYAN~~	SEQ ID NO:1072
vlCDR2	~~GTNKPAP~~	SEQ ID NO:1073
vlCDR3	~~ALWYSNHWV~~	SEQ ID NO:1074
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	SEQ ID NO:1075

Figure 56D

CD3 High-Int – [anti-CD3] H1.90 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGGT~~ KLTVL	SEQ ID NO:1076
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGT ~~LVTVSS~~	SEQ ID NO:1077
vhCDR1	~~TYAMN~~	SEQ ID NO:1078
vhCDR2	<del>RI~~RSK~~YNNYATYYADSVK</del>	SEQ ID NO:1079
vhCDR3	~~HGNFGDPYVSWFAY~~	SEQ ID NO:1080
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLTV L	SEQ ID NO:1081
vlCDR1	~~GSSTGAVTTSNYAN~~	SEQ ID NO:1082
vlCDR2	~~GTNKPAP~~	SEQ ID NO:1083
vlCDR3	~~ALWYSNHWV~~	SEQ ID NO:1084
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	SEQ ID NO:1085

Figure 56E

Anti-CD3-Intermediate – [anti-CD3] H1.33 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWFVGGGT ~~KLTVL~~	SEQ ID NO:1086
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGLTVTVSS	SEQ ID NO:1087
vhCDR1	~~TYAMN~~	SEQ ID NO:1088
vhCDR2	<del>RI~~RSK~~YNNYATYYADSVK~~G~~</del>	SEQ ID NO:1089
vhCDR3	~~HGNFGDSYVSWFDY~~	SEQ ID NO:1090
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWFVGGGT~~ KLTV L	SEQ ID NO:1091
vlCDR1	~~GSSTGAVTTSNYAN~~	SEQ ID NO:1092
vlCDR2	~~GTNKPAP~~	SEQ ID NO:1093
vlCDR3	~~ALWYSNHWF~~	SEQ ID NO:1094
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	SEQ ID NO:1095

Figure 56F

CD3 High-Int – [anti-CD3] H1.31 L1.47 scFv		
	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTVL	SEQ ID NO:1096
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGT ~~LVTVSS~~	SEQ ID NO:1097
vhCDR1	~~TYAMS~~	SEQ ID NO:1098
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	SEQ ID NO:1099
vhCDR3	~~HGNFGDSYVSWFAY~~	SEQ ID NO:1100
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGG~~ TVT ~~LT~~ CGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTV L	SEQ ID NO:1101
vlCDR1	~~GSSTGAVTTSNYAN~~	SEQ ID NO:1102
vlCDR2	~~GTNKPAP~~	SEQ ID NO:1103
vlCDR3	~~ALWYSNHWV~~	SEQ ID NO:1104
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	SEQ ID NO:1105

Figure 56G

CD3 High[VL-VH] – [anti-CD3] L1.47 H1.30 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAFGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	SEQ ID NO:1106
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAFGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1107
vICDR1	GSSTGAVTTSNYAN	SEQ ID NO:1108
vICDR2	GTNKPAP	SEQ ID NO:1109
vICDR3	ALWYSNHWV	SEQ ID NO:1110
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	SEQ ID NO:1111
vhCDR1	TYAMN	SEQ ID NO:1112
vhCDR2	RIRSKYNNYATYYADSVKRG	SEQ ID NO:1113
vhCDR3	HGNFGDSYVSWFAY	SEQ ID NO:1114
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1115

Figure 56H

CD3 High-Int #1[VL-VH] – [anti-CD3] L1.47 H1.32 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	SEQ ID NO:1116
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1117
vICDR1	GSSTGAVTTSNYAN	SEQ ID NO:1118
vICDR2	GTNKRAP	SEQ ID NO:1119
vICDR3	ALWYSNHWV	SEQ ID NO:1120
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	SEQ ID NO:1121
vhCDR1	TYAMN	SEQ ID NO:1122
vhCDR2	RIIRSKANNYATYYADSVKRG	SEQ ID NO:1123
vhCDR3	HGNFGDSYVSWFAY	SEQ ID NO:1124
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1125

Figure 56l

CD3 High-Int #2[VL-VH] – [anti-CD3] L1.47 H1.89 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLLTVSS	SEQ ID NO:1126
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1127
vICDR1	GSSTGAVTTSNYAN	SEQ ID NO:1128
vICDR2	GTNKRAP	SEQ ID NO:1129
vICDR3	ALWYSNHWV	SEQ ID NO:1130
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGTLLTVSS	SEQ ID NO:1131
vhCDR1	TYAMN	SEQ ID NO:1132
vhCDR2	RIRSKYNNYATYYADSVKRG	SEQ ID NO:1133
vhCDR3	HGNFGDEYVSWFAY	SEQ ID NO:1134
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1135

Figure 56J

CD3 High-Int[VL-VH] – [anti-CD3] L1.47 H1.90 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGLTVTVSS	SEQ ID NO:1136
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1137
vICDR1	GSSTGAVTTSNYAN	SEQ ID NO:1138
vICDR2	GTNKRAP	SEQ ID NO:1139
vICDR3	ALWYSNHWV	SEQ ID NO:1140
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS	SEQ ID NO:1141
vhCDR1	TYAMN	SEQ ID NO:1142
vhCDR2	RIRSKYNNYATYYADSVKRG	SEQ ID NO:1143
vhCDR3	HGNFGDPYVSWFAY	SEQ ID NO:1144
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1145

Figure 56K

Anti-CD3-Intermediate[VL-VH] – [anti-CD3] L1.47 H1.33 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAFGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLLTVSS	SEQ ID NO:1146
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KPAFGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1147
vICDR1	GSSTGAVTTSNYAN	SEQ ID NO:1148
vICDR2	GTNKPAP	SEQ ID NO:1149
vICDR3	ALWYSNHWV	SEQ ID NO:1150
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGTLLTVSS	SEQ ID NO:1151
vhCDR1	TYAMN	SEQ ID NO:1152
vhCDR2	RIRSKYNNYATYYADSVKGR	SEQ ID NO:1153
vhCDR3	HGNFGDSYVSWFDY	SEQ ID NO:1154
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1155

Figure 56L

CD3 High-Int[VL-VH] – [anti-CD3] L1.47 H1.31 scFv		
	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMSWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS	SEQ ID NO:1156
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	SEQ ID NO:1157
vlCDR1	GSSTGAVTTSNYAN	SEQ ID NO:1158
vlCDR2	GTNKRAP	SEQ ID NO:1159
vlCDR3	ALWYSNHWV	SEQ ID NO:1160
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTVTVSS	SEQ ID NO:1161
vhCDR1	TYAMS	SEQ ID NO:1162
vhCDR2	RIRSKYNNYATYYADSVKRG	SEQ ID NO:1163
vhCDR3	HGNFGDSYVSWFAY	SEQ ID NO:1164
Linker	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:1165

Figure 57A

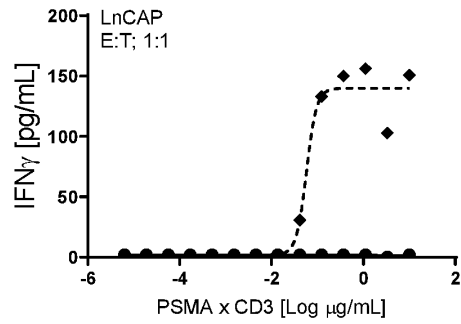


Figure 57B

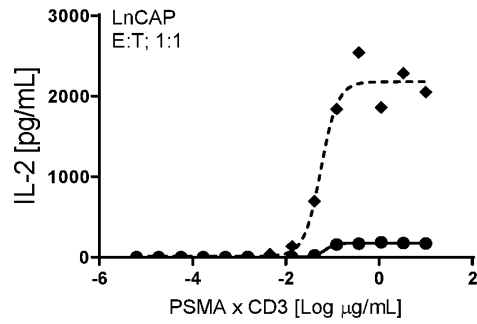


Figure 57C

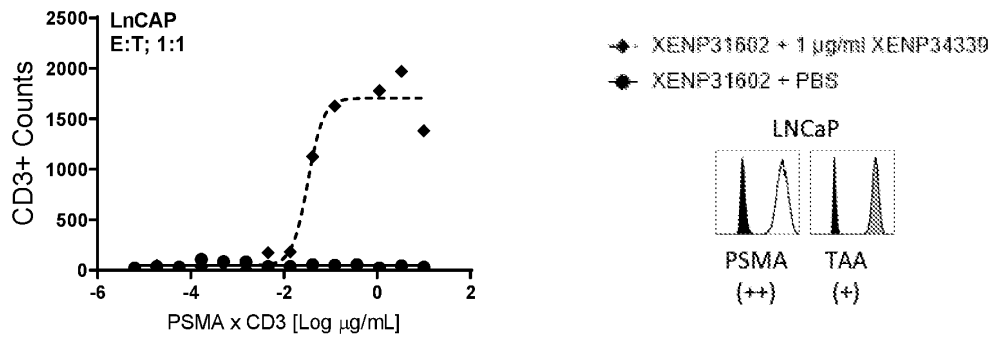


Figure 58A

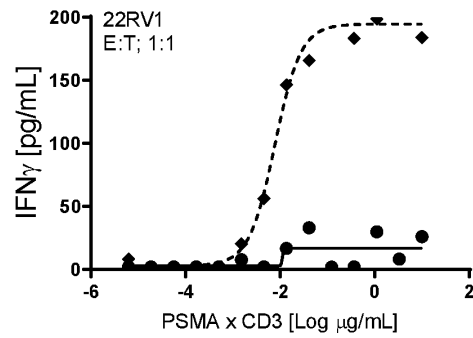


Figure 58B

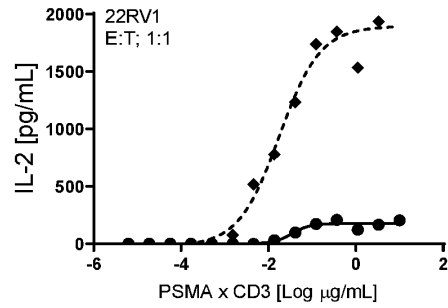


Figure 58C

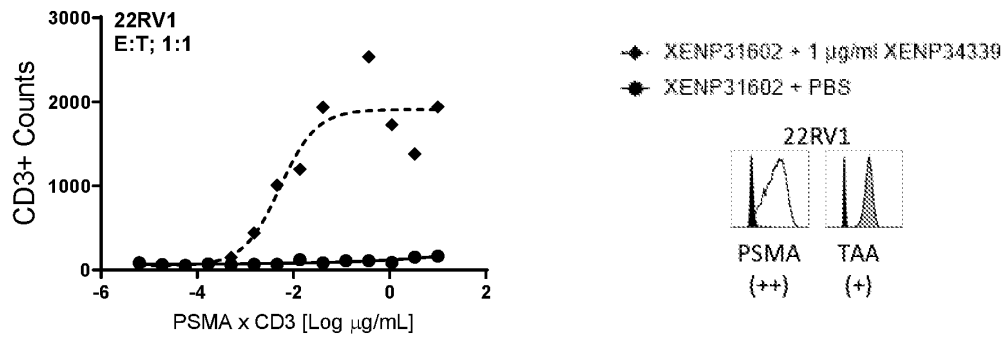


Figure 59A

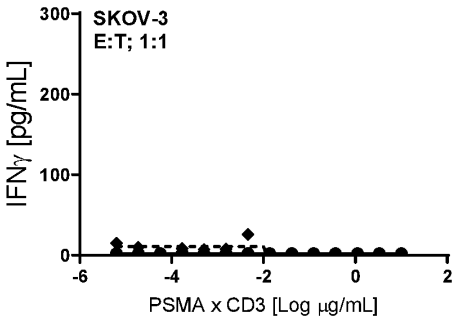


Figure 59B

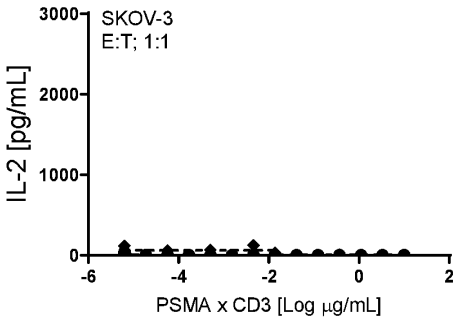


Figure 58C

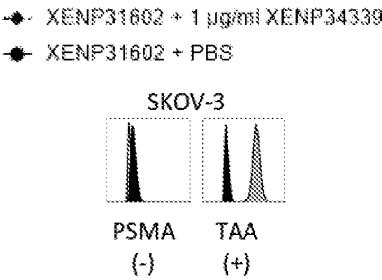
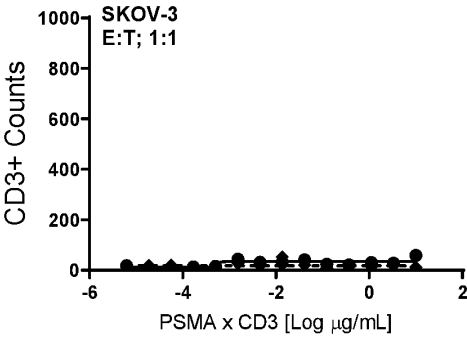


Figure 60A

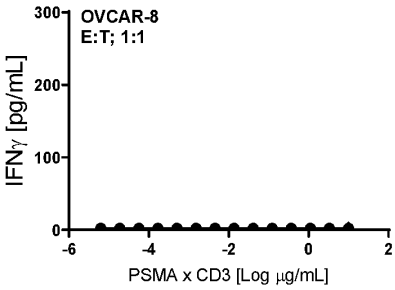


Figure 60B

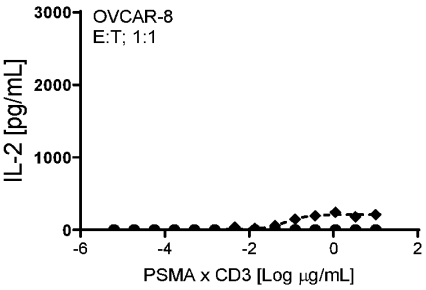


Figure 60C

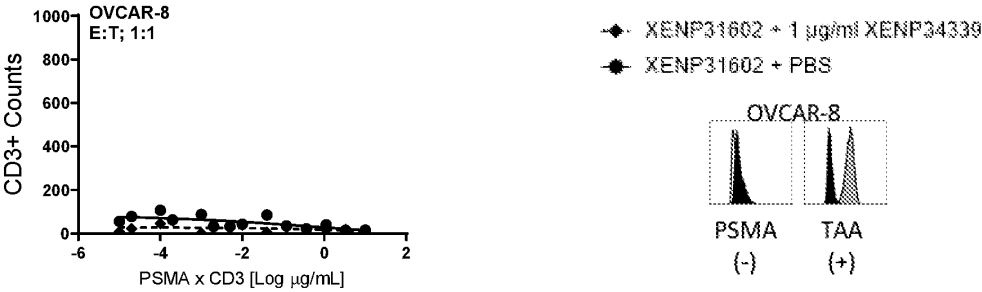


Figure 61A

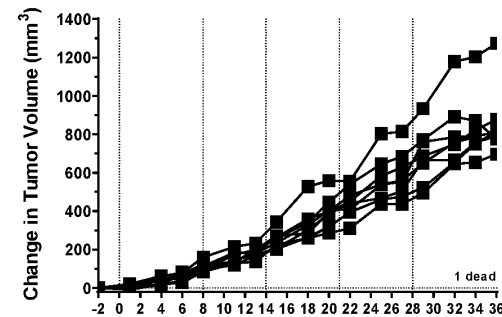


Figure 61B

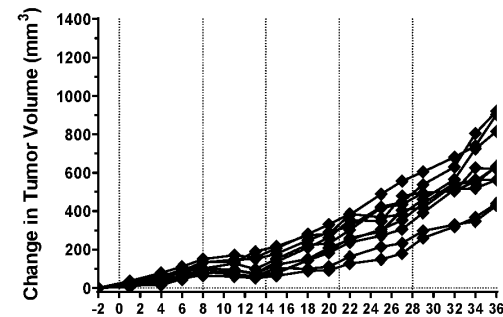


Figure 61C

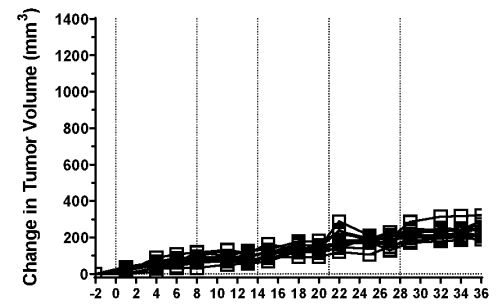


Figure 61D

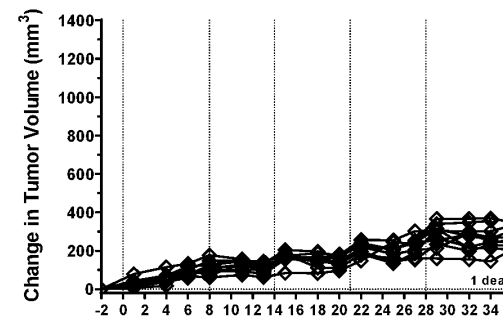
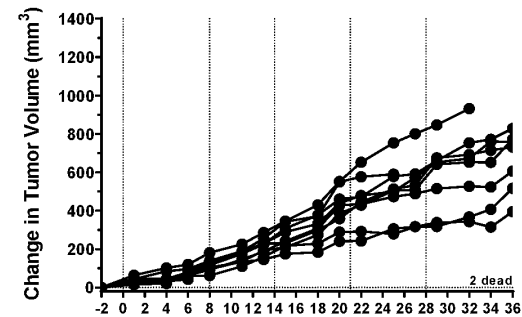


Figure 61E



- PBS
- CD3bsAb1, 0.5 mg/Kg
- ◆ CD3bsAb2, 0.5 mg/Kg
- XENP34339, 5 mg/Kg + CD3bsAb1, 0.5 mg/Kg
- ◇ XENP34339, 5 mg/Kg + CD3bsAb2, 0.5 mg/Kg

Figure 62

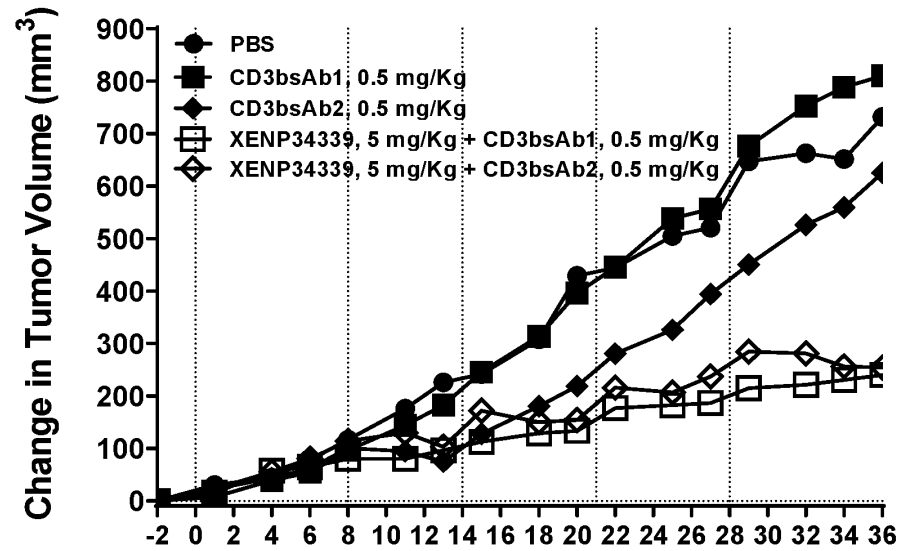


Figure 63

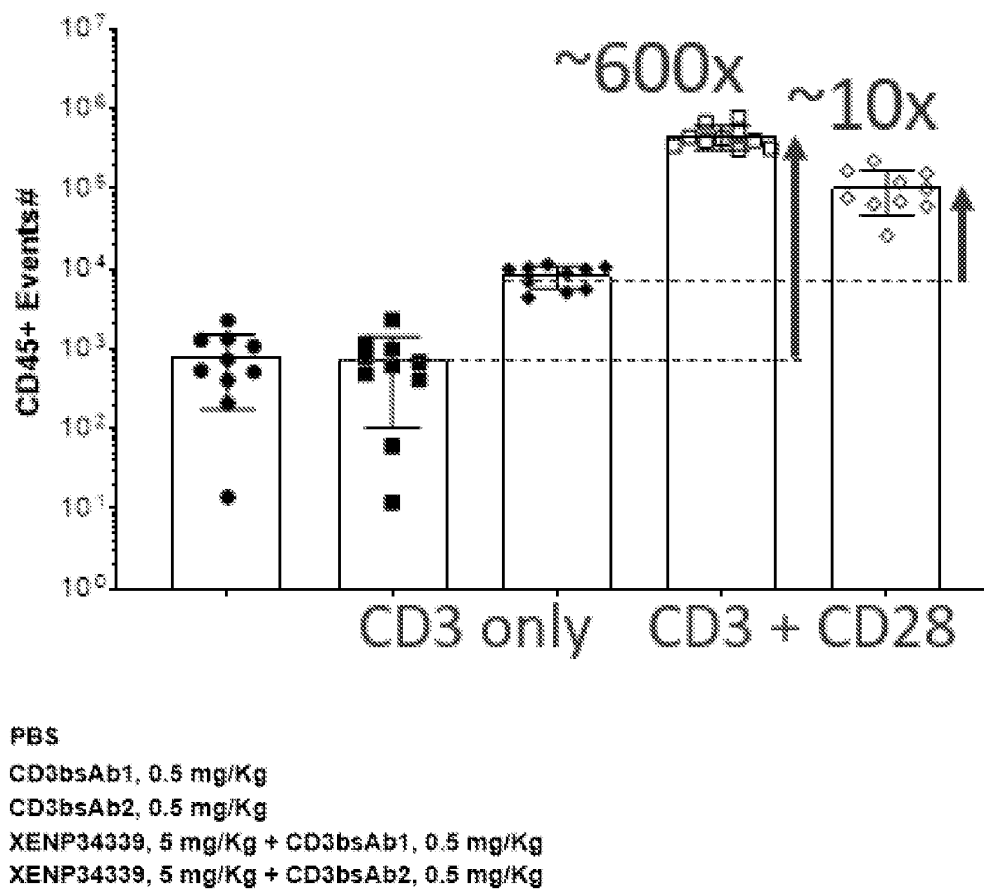


Figure 64A

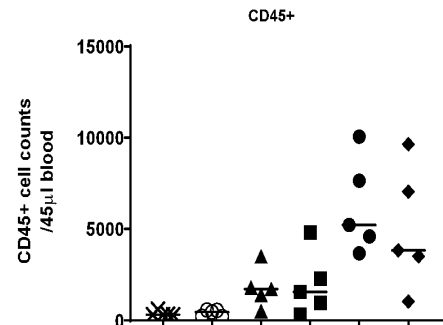


Figure 64B

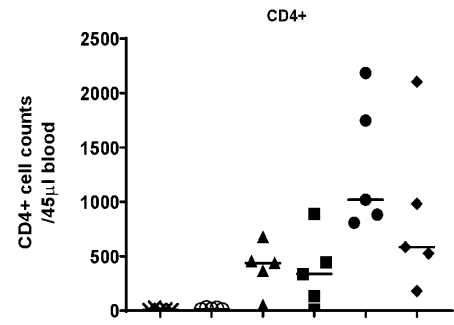


Figure 64C

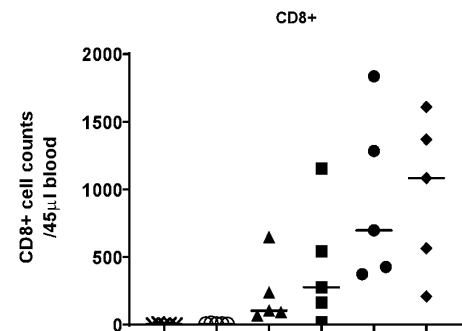


Figure 64D

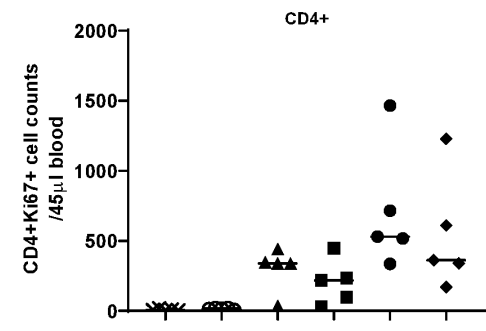
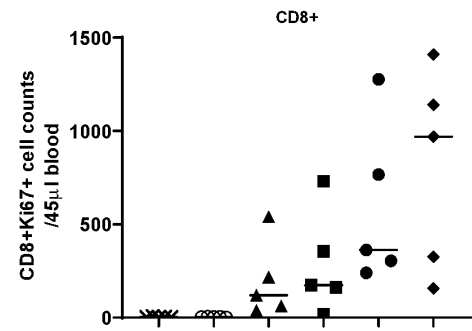


Figure 64E



- × (A) huPBMC + PBS
- (B) XENP34339 - 0.3 mg/kg
- PSMAxCD3**
- ▲ (D) XENP32220 - 1 mg/kg
- (F) XENP 32220 - 6 mg/kg
- PSMAxCD3 + B7H3xCD28**
- (G) XENP32220, 1 mg/kg + XENP34339, 0.3 mg/Kg
- ◆ (H) XENP32220, 6 mg/kg + XENP34339, 0.3 mg/Kg

Figure 65A

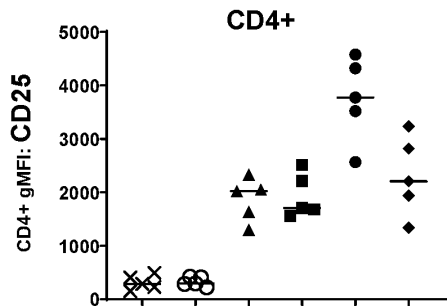


Figure 65B

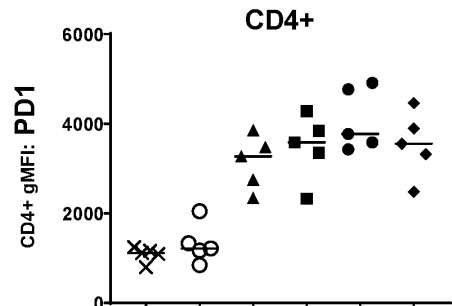


Figure 65C

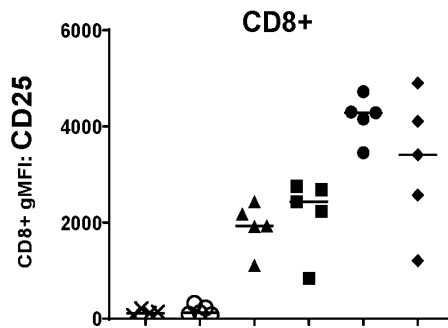
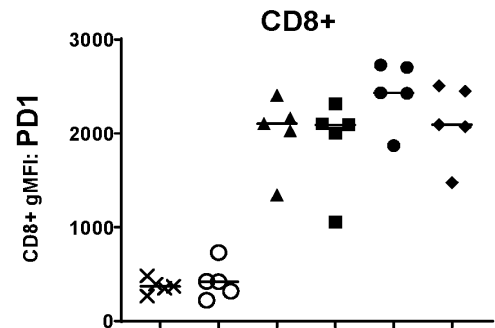


Figure 65D



PSMAxCD3

PSMAxCD3 + B7H3xCD28

X (A) huPBMC + PBS ▲ (D) XENP32220 - 1 mg/kg ● (G) XENP32220, 1 mg/kg + XENP34339, 0.3 mg/Kg
O (B) XENP34339 - 0.3 mg/kg ■ (F) XENP 32220 - 6 mg/kg ◆ (H) XENP32220, 6 mg/kg + XENP34339, 0.3 mg/Kg

Figure 66

Baseline-corrected Group Median TM Caliper vs time

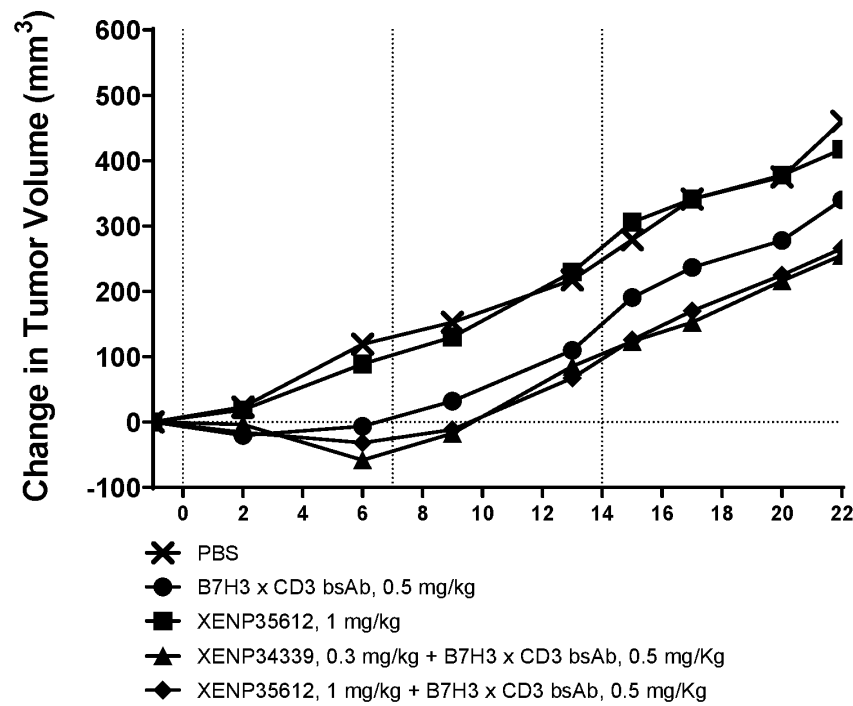


Figure 67A

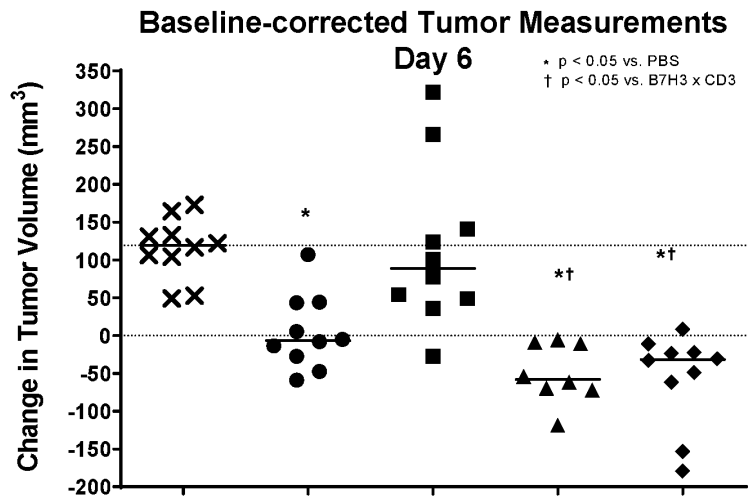


Figure 67B

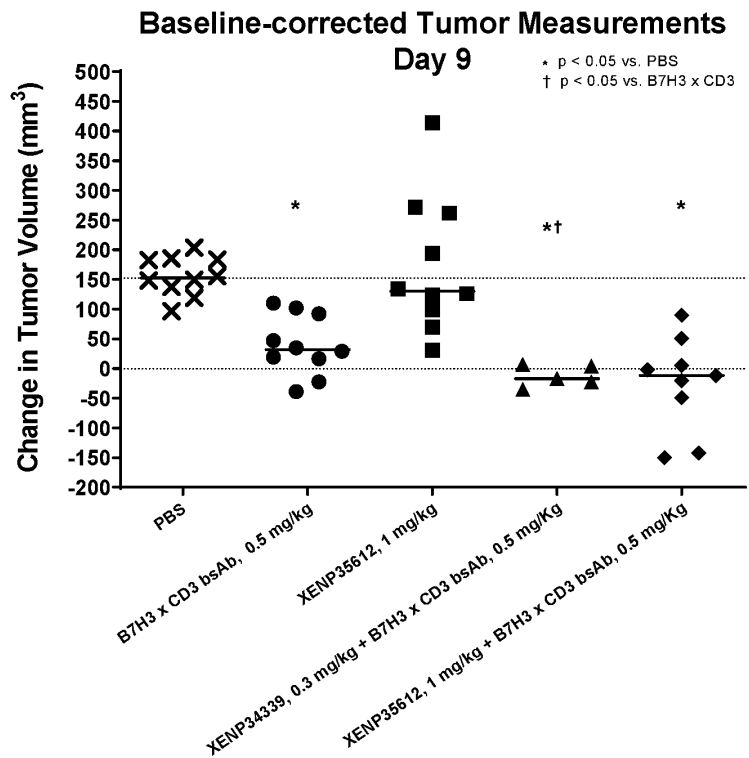


Figure 69

>XENP29154 TGN1412 hu5.11A1[CD28] H1L1 IgG4 K447del**XENP29154_TGN1412_hu5.11A1[CD28]_H1_IgG4_K447del Heavy Chain** SEQ ID NO:1166

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDSWIHWRQAPGKGLEWVAVISPYGGSTYYADSVKGRFTI
SADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGG
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

XENP29154 TGN1412_hu5.11A1[CD28]_L1 Light Chain SEQ ID NO:1167

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTD
FTLTISSLQPEDFATYYCQQYLYHPATFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC

Figure 70A

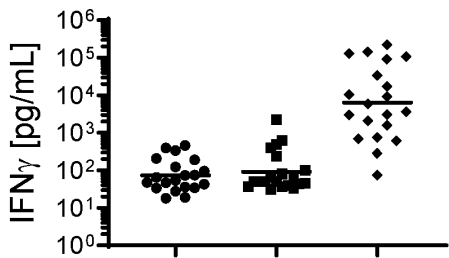


Figure 70B

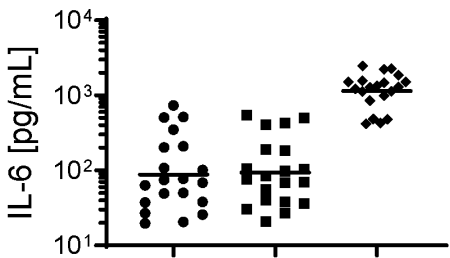
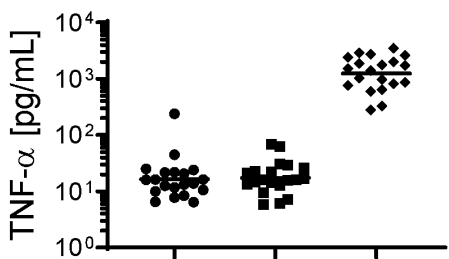


Figure 70C



- PBS
- XENP34339
- ◆ TGN1412 (XENP29154)

Figure 71A

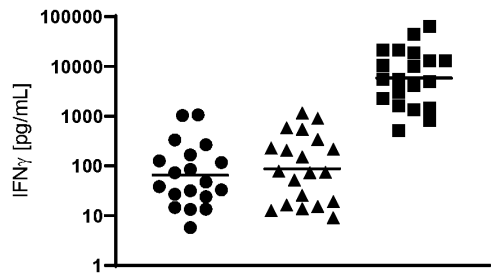


Figure 71B

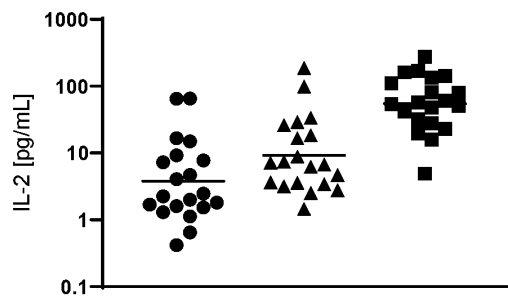
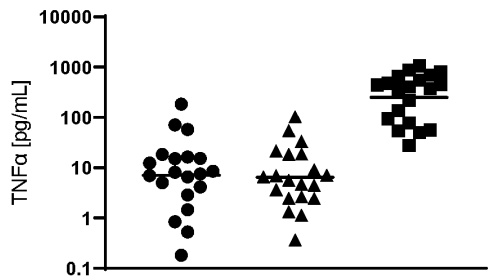


Figure 71C



- PBS
- ▲ XENP37808 [10ug/well]
- TGN1412 IgG4 [10ug/well]

Figure 72A

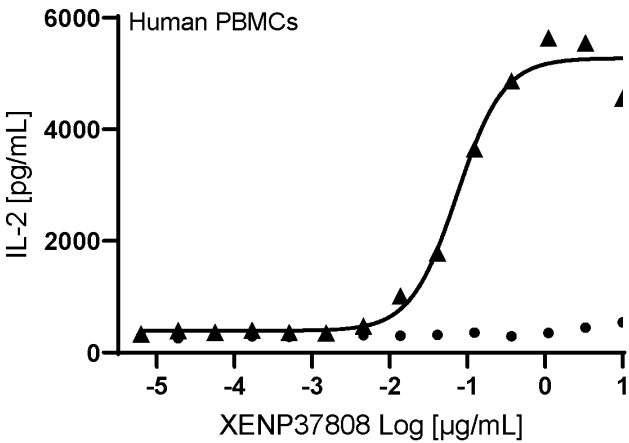
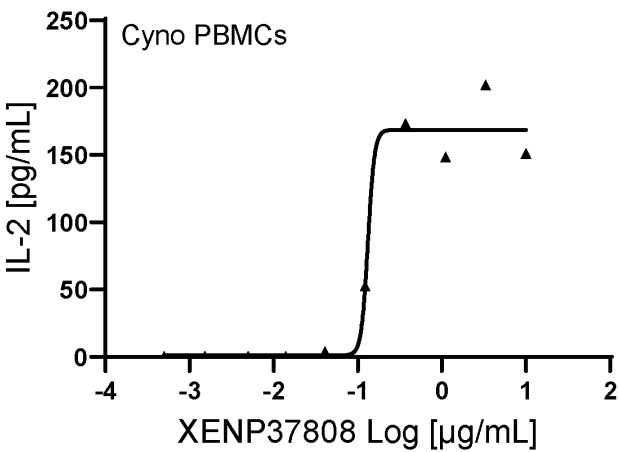


Figure 72B



- ▲ anti-CD3 scFv transfected HEK cells B7H3⁺
- anti-CD3 scFv transfected HEK cells B7H3⁻

Figure 73A

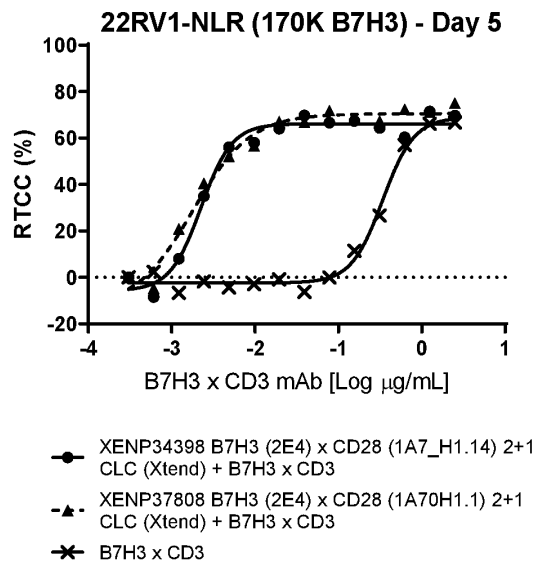


Figure 73B

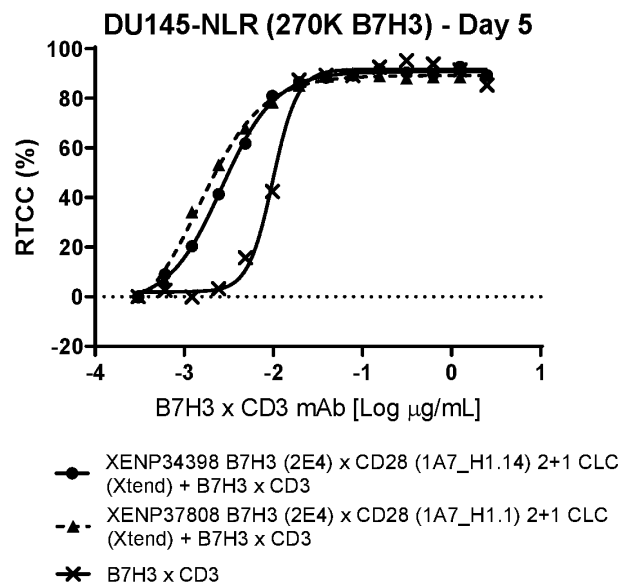


Figure 74A

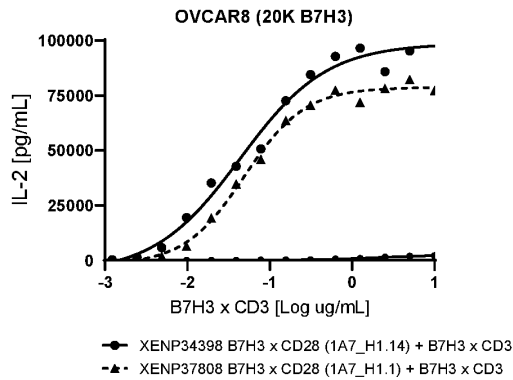


Figure 74B

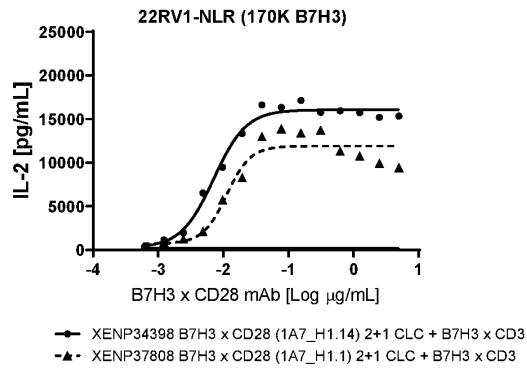


Figure 74C

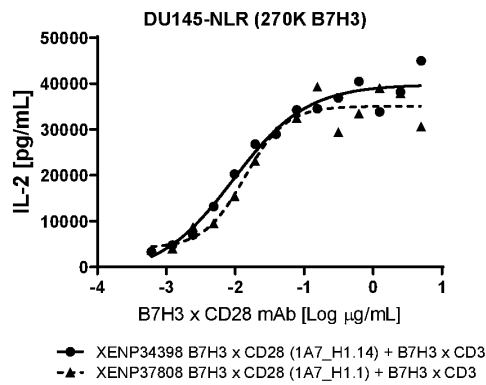


Figure 75

2E4A3.189 VH	SEQ	SEQ ID	
HFR1	QVQLVQSGAEVKKPGASVKVSCKASGX ₁ X ₂ FX ₃	1168	X ₁ is selected from Y, L; X ₂ is selected from I, T, P, A, S, G, L, F; and X ₃ is selected from T, I, V, K, E, S
HCDR1	X ₁ X ₂ YMH	1169	X ₁ is selected from N, D, Q, E, I, F; and X ₂ is selected from Y, N, H, F, V
HFR2	WVRQAPGQGLEWMG	1170	
HCDR2	IX ₁ X ₂ PX ₃ X ₄ GX ₅ X ₆ X ₇ YAKKFQG	1171	X ₁ is selected from I, L; X ₂ is selected from S, A, F, G; X ₃ is selected from S, I, V, L, Q, A, G; X ₄ is selected from A, S, V, G, T; X ₅ is selected from T, R, S; X ₆ is selected from T, W, I; and X ₇ is selected from S, D, A, N, I, L, Q
HFR3	RX ₁ TMTRDTSTSTVYMELSSLRSEDTAVYYCAR	1172	X ₁ is selected from V, F
HCDR3	X ₁ GX ₂ SSPRX ₃ DY	1173	X ₁ is selected from G, A; X ₂ is selected from G, F, W, L, M; and X ₃ is selected from L, S, V, G, Q
HFR4	WGQGTLVTVSS	1174	
2E4A3.189 VL			
LFR1	DIQMTQSPSSLSASVGDRVTITC	1175	
LCDR1	RASQSISSYLN	1176	
LFR2	WYQQKPGKAPKLLIY	1177	
LCDR2	AASSLOS	1178	
LFR3	GVPSRFGSGSGTDFTLTISLQPEDFATYYC	1179	
LCDR3	QQSYSTPYT	1180	
LFR4	FGQGTKLEIK	1181	