

Figure 1A

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 1B

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 1C

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 1D

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 1E

Monomer 1	Monomer 2
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/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
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/N276K
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	
E269Q/E272Q/E283Q/E357Q	
E269Q/E272Q/E283Q	
E269Q/E272Q	
E269Q/E283Q	
E272Q/E283Q	
E269Q	

Figure 2

<u>Variant constant region</u>	<u>Substitutions</u>
pI-ISO(-)	I199T/N203D/K274Q/R355Q/N384S/K392N/N397M/Q419E/K447_
pI_ISO(-)-Fc only	K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_
pI_(-)_isosteric_A	N208D/Q295E/N384D/Q418E/N421D
pI_(-)_isosteric A-Fc only	Q295E/N384D/Q418E/N421D
pI_(-)_isosteric_B	N208D/Q295E/Q418E/N421D
pI_(-)_isosteric_B-Fc only	Q295E/Q418E/N421D
pI_ISO(+RR)	Q196K/I199T/P217R/P228R/N276K
pI_ISO(+RR)-Fc only	P217R/P228R/N276K
pI_ISO(+)	Q196K/I199T/N276K
pI_ISO(+)-Fc only	N276K
pI_(+)_isosteric_A	E269Q/E272Q/E283Q/E357Q
pI_(+)_isosteric_B	E269Q/E272Q/E283Q
pI_(+)_isosteric_E269Q/E272Q	E269Q/E272Q
pI_(+)_isosteric_E269Q/E283Q	E269Q/E283Q
pI_(+)_isosteric_E272Q/E283Q	E272Q/E283Q
pI_(+)_isosteric_E269Q	E269Q

Figure 3

Ablation Variants

G236R
S239G
S239K
S239Q
S239R
V266D
S267K
S267R
H268K
E269R
299R
299K
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
267K/P329K

Figure 4

Heavy Chain 1 (-) e.g. Fab-Fc	Heavy Chain 2 (+) e.g. scFv-Fc or Fab-scFv-Fc
	C220S
Heterodimeric skew variants L368D/K370S	Heterodimeric skew variants S364K/E357Q
Isosteric pl substitutions N208D/Q295E/N384D/Q418E/N421D	
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure 5

Positive Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGS GGGGS GGGGS	15	0	7
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	8
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	9
+B	GKGGSGKGGSGKGGGS	15	+3	10
+C	GGKGS GGGKGS GGGKGS	15	+3	11
+D	GGGKS GGGKGS GGGKGS	15	+3	12
+E	GKGKSGKGKSGKGKS	15	+6	13
+F	GGGKS GGGKGS GGGKGS	15	+3	14
+G	GKPGSGKPGSGKPGS	15	+3	15
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	1
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	16

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 20	GGGGS GGGGS GGGGS GGGGS	20	0	17
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	18
-B	GEGGS GEGGS GEGGS	15	-3	19
-C	GGEGS GEGGS GEGGS	15	-3	20
-D	GGGES GGGES GGGES	15	-3	21
-E	GEGES GEGES GEGES	15	-6	22
-F	GGGES GGGES GEGGS	15	-3	23
-G	GEGES GEGES GEGES GEGES	20	-8	24

Additional scFv Linkers

GGGGS GGGGS GGGGS	SEQ ID NO: 7
GGGGS GGGGS GGGGS GGGGS	SEQ ID NO: 17
GSTSGSGKPGSGEGSTKG	SEQ ID NO: 8
PRGASKSGSASQTGSAPGS	SEQ ID NO: 25
GTAAAGAGAAGGAAAGAAG	SEQ ID NO: 26
GTSGSSGSGSGSGSGGGG	SEQ ID NO: 27
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 1

Figure 6

Useful domain linkers

Name	Sequence	SEQ ID NO:
(GGGGS) ₁ or GGGGS	GGGGS	2
(GGGGS) ₂	GGGGSGGGGS	28
(GGGGS) ₃	GGGGSGGGGSGGGGS	7
(GGGGS) ₄	GGGGSGGGGSGGGGSGGGGS	17
(GGGGS) ₅	GGGGSGGGGSGGGGSGGGGSGGGGS	29
(GGGGS) ₆	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	30
(GGGGS) ₇	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	31
(GGGGA) ₁ or GGGGA	GGGGA	32
(GGGGA) ₂	GGGAGGGGA	33
(GGGGA) ₃	GGGAGGGGAGGGGA	34
(GGGGA) ₄	GGGAGGGGAGGGGAGGGGA	35
(GGGGA) ₅	GGGAGGGGAGGGGAGGGGAGGGGA	36
(GGGGA) ₆	GGGAGGGGAGGGGAGGGGAGGGGAGGGGA	37
(GGGGA) ₇	GGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	38
30AA-linker	DPALVHQRPAAPPGGGSGGGSGGGSGGG	39
(GKPGS) ₁ or GKPGS	GKPGS	40
(GKPGS) ₅	GKPGSGKPGSGKPGSGKPGSGKPGS	41
(GKPGS) ₆	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	42
(GGGES) ₁ or GGGES	GGGES	43
“half hinge”	KTHTCPPCP	44
“full hinge C220S variant”	EPKSSDKTHTCPPCP	45
“flex half hinge”	GGGSGGGGSKTHTCPPCP	6
“charged half hinge1”	GKPGSGKPGSKTHTCPPCP	46
“charged half hinge2”	GKPGSKTHTCPPCP	47

Figure 7A

1 + 1 Fab-scFv-Fc Backbone 1**>Fab-Fc Side (SEQ ID NO: 48)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 49)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 2**>Fab-Fc Side (SEQ ID NO: 50)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 51)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 3**>Fab-Fc Side (SEQ ID NO: 52)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 53)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

Figure 7B

1 + 1 Fab-scFv-Fc Backbone 4**>Fab-Fc Side (SEQ ID NO: 54)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 55)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 5**>Fab-Fc Side (SEQ ID NO: 56)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 57)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 6**>Fab-Fc Side (SEQ ID NO: 58)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 59)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

Figure 7C

1 + 1 Fab-scFv-Fc Backbone 7**>Fab-Fc Side (SEQ ID NO: 60)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 61)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTKLVK
 GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 8**>Fab-Fc Side (SEQ ID NO: 62)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TKTYTCNVDPKPSDTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDPEVQ
 FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
 PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSRLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 63)

ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNAKTKPREEQ
 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVCLTKLVKGF
 YPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 9**>Fab-Fc Side (SEQ ID NO: 64)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
 TQTYTCNVDPKPSDTKVDKTVKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
 NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTL
 PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 65)

ERKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
 NSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTKLVKGFY
 PSDIAVEWESNGQPNENYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

Figure 7D

1 + 1 Fab-scFv-Fc Backbone 10**>Fab-Fc Side (SEQ ID NO: 66)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
 TQYTCNVDHKPSDTKVDKTVKCCVECPPECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
 NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
 PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 67)

ERKCCVECPPECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQF
 NSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
 PSDIAVEWESNGQPEENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 11**>Fab-Fc Side (SEQ ID NO: 68)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSGSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVLHEALHSHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 69)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPEENNYKTTTPVLDSGSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVLHEALHSHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 12**>Fab-Fc Side (SEQ ID NO: 70)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPEENNYKTTTPVLDSGSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGK

>scFv-Fc Side (SEQ ID NO: 71)

ERKSSDKTHTCPPRPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPEENNYKTTTPVLDSGSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGK

Figure 8A

2 + 1 Fab2-scFv-Fc Backbone 1**>Fab-Fc Side (SEQ ID NO: 72)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 73)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 2**>Fab-Fc Side (SEQ ID NO: 74)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 75)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 3**>Fab-Fc Side (SEQ ID NO: 76)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 77)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNHYTQKSLSLSPGK

Figure 8B

2 + 1 Fab2-scFv-Fc Backbone 4**>Fab-Fc Side (SEQ ID NO: 78)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDFVSCS
 VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 79)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 5**>Fab-Fc Side (SEQ ID NO: 80)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCS
 VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 81)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 6**>Fab-Fc Side (SEQ ID NO: 82)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCS
 VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 83)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

Figure 8C

2 + 1 Fab2-scFv-Fc Backbone 7**>Fab-Fc Side (SEQ ID NO: 84)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 85)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 8**>Fab-Fc Side (SEQ ID NO: 86)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VLHEALHSHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 87)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVLHEALHSHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 9**>Fab-Fc Side (SEQ ID NO: 88)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 89)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

Figure 9

Constant Light Domain – Kappa (SEQ ID NO: 90)

RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

Constant Light Domain – Lambda (SEQ ID NO: 91)

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 10A

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEPSTLVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	92
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	93
vhCDR1	<u>TYAMN</u>	94
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	95
vhCDR3	<u>HGNFGDSYVSWFAY</u>	96
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	97
vlCDR1	<u>GSSTGAVTTSNYAN</u>	98
vlCDR2	<u>GTNKRAP</u>	99
vlCDR3	<u>ALWYSNHWV</u>	100
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	101

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEPSTLVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	102
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	103
vhCDR1	<u>TYAMN</u>	104
vhCDR2	<u>RIRSKANNYATYYADSVKG</u>	105
vhCDR3	<u>HGNFGDSYVSWFAY</u>	106
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	107
vlCDR1	<u>GSSTGAVTTSNYAN</u>	108
vlCDR2	<u>GTNKRAP</u>	109
vlCDR3	<u>ALWYSNHWV</u>	110
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	111

Figure 10B

CD3 High-Int #2 – [anti-CD3] H1.89 L1.47 scFv

	Sequence	SEQ ID NO:
scFv	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY</u> <u>VSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSTVSPG</u> <u>GTVTLTGSSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL</u> <u>GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL</u>	112
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY</u> <u>VSWFAYWGQGTLLTVSS</u>	113
vhCDR1	<u>TYAMN</u>	114
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	115
vhCDR3	<u>HGNFGDEYVSWFAY</u>	116
Variable Light (vl) Domain	<u>QAVVTQEPSTVSPGGTTLTLCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	117
vlCDR1	<u>GSSTGAVTTSNYAN</u>	118
vlCDR2	<u>GTNKRAP</u>	119
vlCDR3	<u>ALWYSNHWV</u>	120
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	121

CD3 High-Int – [anti-CD3] H1.90 L1.47 scFv

	Sequence	SEQ ID NO:
scFv	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY</u> <u>VSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSTVSPG</u> <u>GTVTLTGSSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL</u> <u>GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL</u>	122
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY</u> <u>VSWFAYWGQGTLLTVSS</u>	123
vhCDR1	<u>TYAMN</u>	124
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	125
vhCDR3	<u>HGNFGDPYVSWFAY</u>	126
Variable Light (vl) Domain	<u>QAVVTQEPSTVSPGGTTLTLCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	127
vlCDR1	<u>GSSTGAVTTSNYAN</u>	128
vlCDR2	<u>GTNKRAP</u>	129
vlCDR3	<u>ALWYSNHWV</u>	130
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	131

Figure 10C

Anti-CD3-Intermediate – [anti-CD3] H1.33 L1.47 scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGTLLTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEPSTLVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	132
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGTLLTVSS	133
vhCDR1	<u>TYAMN</u>	134
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	135
vhCDR3	<u>HGNFGDSYVSWFDY</u>	136
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	137
vLCDR1	<u>GSSTGAVTTSNYAN</u>	138
vLCDR2	<u>GTNKRAP</u>	139
vLCDR3	<u>ALWYSNHWV</u>	140
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	141

CD3 High-Int – [anti-CD3] H1.31 L1.47 scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEPSTLVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	142
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	143
vhCDR1	<u>TYAMS</u>	144
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	145
vhCDR3	<u>HGNFGDSYVSWFAY</u>	146
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	147
vLCDR1	<u>GSSTGAVTTSNYAN</u>	148
vLCDR2	<u>GTNKRAP</u>	149
vLCDR3	<u>ALWYSNHWV</u>	150
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	151

Figure 10D

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

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS/</u> <u>EVQLVESGGGLVQPGGSLRLSCAASGFTFST</u> <u>YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS</u>	152
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	153
vCDR1	<u>GSSTGAVTTSNYAN</u>	154
vCDR2	<u>GTNKRAP</u>	155
vCDR3	<u>ALWYSNHWV</u>	156
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFAYWGQGLTVTVSS</u>	157
vhCDR1	<u>TYAMN</u>	158
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	159
vhCDR3	<u>HGNFGDSYVSWFAY</u>	160
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	161

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

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS/</u> <u>EVQLVESGGGLVQPGGSLRLSCAASGFTFST</u> <u>YAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS</u>	162
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	163
vCDR1	<u>GSSTGAVTTSNYAN</u>	164
vCDR2	<u>GTNKRAP</u>	165
vCDR3	<u>ALWYSNHWV</u>	166
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFAYWGQGLTVTVSS</u>	167
vhCDR1	<u>TYAMN</u>	168
vhCDR2	<u>RIRSKANNYATYYADSVKG</u>	169
vhCDR3	<u>HGNFGDSYVSWFAY</u>	170
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	171

Figure 10E

CD3 High-Int #2[VL-VH] – [anti-CD3] L1.47 H1.89 scFv

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTTFST <u>YAMNWVRQAPGKGLEWVGRI</u> RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM <u>NSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGLTVTVSS</u>	172
Variable Light (vl) Domain	<u>QAVVTQEP</u> SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	173
vCDR1	<u>GSSTGAVTTSNYAN</u>	174
vCDR2	<u>GTNKRAP</u>	175
vCDR3	<u>ALWYSNHWV</u>	176
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI</u> RSK <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY</u> <u>VSWFAYWGQGLTVTVSS</u>	177
vhCDR1	<u>TYAMN</u>	178
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	179
vhCDR3	<u>HGNFGDEYVSWFAY</u>	180
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	181

CD3 High-Int[VL-VH] – [anti-CD3] L1.47 H1.90 scFv

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTTFST <u>YAMNWVRQAPGKGLEWVGRI</u> RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM <u>NSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGLTVTVSS</u>	182
Variable Light (vl) Domain	<u>QAVVTQEP</u> SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	183
vCDR1	<u>GSSTGAVTTSNYAN</u>	184
vCDR2	<u>GTNKRAP</u>	185
vCDR3	<u>ALWYSNHWV</u>	186
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI</u> RSK <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY</u> <u>VSWFAYWGQGLTVTVSS</u>	187
vhCDR1	<u>TYAMN</u>	188
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	189
vhCDR3	<u>HGNFGDPYVSWFAY</u>	190
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	191

Figure 10F

Anti-CD3-Intermediate[VL-VH] – [anti-CD3] L1.47 H1.33 scFv

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS/</u> <u>EVQLVESGGGLVQPGGSLRLSCAASGFTFST</u> <u>YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGLTVTVSS</u>	192
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	193
vCDR1	<u>GSSTGAVTTSNYAN</u>	194
vCDR2	<u>GTNKRAP</u>	195
vCDR3	<u>ALWYSNHWV</u>	196
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFDYWGQGLTVTVSS</u>	197
vhCDR1	<u>TYAMN</u>	198
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	199
vhCDR3	<u>HGNFGDSYVSWFDY</u>	200
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	201

CD3 High-Int[VL-VH] – [anti-CD3] L1.47 H1.31 scFv

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS/</u> <u>EVQLVESGGGLVQPGGSLRLSCAASGFTFST</u> <u>YAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS</u>	202
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV</u> <u>L</u>	203
vCDR1	<u>GSSTGAVTTSNYAN</u>	204
vCDR2	<u>GTNKRAP</u>	205
vCDR3	<u>ALWYSNHWV</u>	206
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY</u> <u>VSWFAYWGQGLTVTVSS</u>	207
vhCDR1	<u>TYAMS</u>	208
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	209
vhCDR3	<u>HGNFGDSYVSWFAY</u>	210
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	211

Figure 11A

Human ENPP3 sequence

>sp|O14638 (SEQ ID NO: 212)

MESTLTATEQPVKKNTLKKYKIACIVLLALLVIMSLGLGLGLRLEKQGSCRKKCFDASFRGLENCRCDVACKD
 RGDCWDFEDTCVESTRIWMCNKFRCGETRLEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDAQQSQCP
 EGFDLPPVILFSGDFRAEYLYTWDTLMPNINKLKTGHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDV
 NLNKNFSLSSKEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEEERISTLLKWL
 DLPAERPRFYTYMYFEEDSSGHAGGPVSARVIKALQVVDHAFGLMEGLKQRLNHNVCNIIILLADHGMDQTYCNKMEY
 MTDYFPRINFFYMYEGPAPRIAHNIPHDFFSFNSEEIVRNLSCKRPDQHFKPYPYLPDLKRLHYAKNVRIDKVHLF
 VDQQLAVRSKSNNTNCGGNHGYNNEFRSMEAIFLAHGPFKEKTEVEPFENIEVYNLMCDLLRIQAPNNGTHGSL
 NHLLKVPFYEP SHAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLFPGRPRVL
 QKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPLQGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLADKNITHGFL
 YPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLA
 NTDVPIPTHYFVVLTSCKNKSHTPENCPGWLDPFIIIPHRPTNVESCEGKPEALWVEERFQAHARVRDVELLTGL
 DIFYQDKVQPVSEILQLKTYLPTFETII

Human ENPP3 sequence, extracellular domain

>sp|O14638|31-875 (SEQ ID NO: 213)

LLVIMSLGLGLGLRLEKQGSCRKKCFDASFRGLENCRCDVACKDRGDCWDFEDTCVESTRIWMCNKFRCGETR
 LEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDAQQSQCPGFDLPPVILFSGDFRAEYLYTWDTLMPNI
 NKLKTGHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDVNLNKNFSLSSKEQNNPAWWHGQPMWLTAMY
 QGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEEERISTLLKWLDPKAERPRFYTYMYFEEDSSGHAGGPVSARV
 IKALQVVDHAFGLMEGLKQRLNHNVCNIIILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRIAHNIPHDF
 FSNSEEIVRNLSCKRPDQHFKPYPYLPDLKRLHYAKNVRIDKVHLFVDQQLAVRSKSNNTNCGGNHGYNNEFRSM
 EAIFLAHGPFKEKTEVEPFENIEVYNLMCDLLRIQAPNNGTHGSLNHLLKVPFYEP SHAEVSKFSVCGFANPLP
 TESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSY
 TVPLQGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRK
 MWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVP IPTHYFVVLTSCKNKSHTPENCPGW
 LDVLPFIIIPHRPTNVESCEGKPEALWVEERFQAHARVRDVELLTGLDIFYQDKVQPVSEILQLKTYLPTFETII

Mouse ENPP3 sequence

>sp|Q6DYE8 (SEQ ID NO: 214)

MDSRLALATEEPIKKDSLKKYKILCVVLLALLVIVSLGLGLGLRKPPEEQGSCRKKCFDSSHRGLEGCRCDSGCTG
 RGDCWDFEDTCVKSTQIWTCNLFRCGENRLETALCSCADDCLQRKDCCADYKTVCGESPVWTEACASSQEPQCP
 PEGFDLPPVILFSGDFRAEYLQTWSTLLPNINKLKTGHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDV
 HLNKNFSLSSVEKSNPAWWSGQPIWLTAMYQGLKAACYWPGSDVAVNGSFPTIYRNYSNSVPYERRITLLQWLDL
 PKADRPSTFYTYVEEPDSAGHSSGPVSAGVIKALQSVDNAFGLMEGLKQRLNHNVCNIIVLADHGMDQTS
 CDRVEYMTDYFPPKINFYMQGPAPRIIRTRNIPQDFFTFNSEEIVRNLSCKRPDQHFKPYPYLPDLKRLHYAKNVRIDKAHLMV
 DRQWLAFRSKGSNCGGTHGYNNEFKSMEAIFLAHGPFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLN
 HLLKTPFYKPSHAGELSTPADCGFTTLPDPLDCSPALQNTPGLEEQAQRLNLSEGEVAATVKANLPFGRPRVM
 QKNGDHCLLYHRDYISGYKAMKMPMWSSYTVLKP GDTSPLPPTVPDCLRADVRVAPSESQKCSFYLADKNITHGFL
 YPAIKGTNESRYDALITSNLVPMYKEFKKMWDYFHEVLLIKYAIERNGLNVVSGPIFDYNYDGHFDAPDEITQYVAG
 TDVPIPTHYFVVLTSCKDQHTPDSCPGWLDPFIIIPHRPTNIESCSENKTEDLWVEERFQAHARVRDVELLTGL
 DIFYQEKAQPVSQLQLKTYLPTFETII

Figure 11B

Mouse ENPP3 sequence, extracellular domain

>sp|Q6DYE8|31-874 (SEQ ID NO: 215)

LLVIVSLGLGLGLRKP EEGSGCRKKCFDSSHRGLEGCRCDSGCTGRGDCCWDFEDTCVKSTQIWT CNLFR CGENR
 LETALCSCADDCLQRKDCCADYKTV CQGESPWVTEACASSQEPQCPPGFDLPPVILFSMDGFRAEYLQTWSTLLPNI
 NKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGII DN NMYDVHLNKNFSLSSVEKSNPAWWSGQPIWLTAMY
 QGLKAACYWP GSDVAVNGSFPTIYR NYSNSVPYERRITTLQWLDLPKADRP SFYTIYVEEPDSAGHSSGFPVSAGV
 IKALQSDNAFGMLMEGLKQRNLHNCVNIIVLADHGMDQTSCDRVEYMTDYFPKINFYMYQGPAPRIRTRNIPQDFF
 TFNSEEIVRNLS CRKPDQHF KPYLTPDL PKRLHYAKNVRIDKAHLMVDRQWLAFRSKGSSNCGGTHGYNNEFKSME
 AIFLAHGPFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLNHL LKTPFYKPSHAGELSTPADCGFTTLPPT
 DPLDCSCPALQNTPGLEE QANQRNLN SEGEVAATVKANLPFGRPRVMQKNGDHCLLYHRDYISGYKAMKMPMWSSY
 TVLKPGDTSSLPPTVPDCLRADVRVAPSESQKCSFY LADKNITHGFLYPAIKGTNESRYDALITSNL VPMYKEFKKM
 WDYFHEVLLIKYAIERNGLNVVSGPIFDYNYDGHFDAPDEITQYVAGTDVIP THYFVVLTSCKDQTHTPDSCP GWL
 DVL PFI VPHRPTNIESCSENKTEDLWVEERFQAHAARVRDV ELLTGLDFYQEKAPV SQIILQLKTYLPTFETII

Macaca fascicularis ENPP3 sequence

>tr|A0A2K5TKP4 (SEQ ID NO: 216)

MESMLTLATEQP VKNTLKKYKIACIVLLALLVIMSLGLGLGLRKLKLEKQSGCRKKCFDASFRGLENCRCDVACED
 RGDCCWDFEDTCVESTRIWTCNKFRCGETRLEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDTAQQSQCPE
 GFDLPPVILFSMDGFRAEYLYTWDTLMPNINKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGII DN NMYDV
 NLNKNFSLSSEEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEERISTLLKWL DL
 PKAERP SFYTYMYFEEDSSGHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEY
 MTDYFPRINFYMYEGPAPRIRALNVPHDFFSCKYEDTYMKKRCKRPDQHF KPYLTPDL PKRLHYAKNVRIDKVHLFV
 DRQWLAVGSKSNTNCGGNGHGYNNEFRSMEAIFLAHGPFSEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLN
 HLLKVPFYEP SHAEEVSKFSVCGFANPLPTNNLSCLCPHLQNSIQLEQVNQMLNLTQEEITATVKVNL PFGPRVLQ
 KNVDNCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRVPPSESQKCSFY LADENITHGFLY
 PPAINRTSDSQYDALIMSNL VPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPEEITKHIAN
 TDIPITHYFVVLTSCKNKSHTPENCPGWL DVL PFI I PHRPTNVESCEPGKPEALWVEERFATAHARVRDV ELLTGL
 DFYQDKAQPVSEILQLKTYLPTFETII

Macaca fascicularis PD-1 sequence, extracellular domain (predicted)

>tr|A0A2K5TKP4|31-874 (SEQ ID NO: 217)

LLVIMSLGLGLGLRKLKLEKQSGCRKKCFDASFRGLENCRCDVACEDRGDCCWDFEDTCVESTRIWTCNKFRCGETR
 LEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDTAQQSQCPEGFDLPPVILFSMDGFRAEYLYTWDTLMPNI
 NKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGII DN NMYDVNLNKNFSLSSEEQNNPAWWHGQPMWLTAMY
 QGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEERISTLLKWL DL PKAERP SFYTYMYFEEDSSGHAGGPVSARV
 IKALQVVDHAFGMLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEYMTDYFPRINFYMYEGPAPRIRALNVPHDFF
 SCKYEDTYMKKRCKRPDQHF KPYLTPDL PKRLHYAKNVRIDKVHLFVDRQWLAVGSKSNTNCGGNGHGYNNEFRSME
 AIFLAHGPFSEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLNHL LKVPFYEP SHAEEVSKFSVCGFANPLPT
 NNLSCLCPHLQNSIQLEQVNQMLNLTQEEITATVKVNL PFGPRVLQKNVDNCLLYHREYVSGFGKAMRMPMWSSYT
 VPQLGDTSPLPPTVPDCLRADVRVPPSESQKCSFY LADENITHGFLYPPAINRTSDSQYDALIMSNL VPMYEEFRKM
 WDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPEEITKHIAN TDIPITHYFVVLTSCKNKSHTPENCPGWL
 DVL PFI I PHRPTNVESCEPGKPEALWVEERFATAHARVRDV ELLTGLDFYQDKAQPVSEILQLKTYLPTFETII

Figure 12

AN1[ENPP3] H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVS ^Y ISSGGGT ^{TY} YLD ^{SV} KGRFTISRDN ^{AK} NSLYLQMN ^{SL} RAEDTAVY ^Y CARHRRV ^{YY} GYYFDYWGQ ^{GL} TVTVSS	218
vhCDR1	NYGMS	219
vhCDR2	<u>YISSGGGT^{TY}YLD^{SV}KG</u>	220
vhCDR3	<u>HRRVYYGYYFDY</u>	221
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ^{WY} QQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW ^{PYT} FGGGTKLEIK	222
vlCDR1	<u>RASQSIGTSIH</u>	223
vlCDR2	<u>YASESIS</u>	224
vlCDR3	<u>QQSNSWPYT</u>	225

>XENP28278 AN1[αENPP3] H1L1 IgG1 PVA /S267K**Chain 1 - AN1[αENPP3]_H1L1_IgG1_PVA_/S267K (SEQ ID NO: 226)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVS^YISSGGGT^{TY}YLD^{SV}KGRFTISRDN^{AK}NSLYLQMN^{SL}RAEDTAVY^YCARHRRV^{YY}GYYFDYWGQ^{GL}TVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQD^{WL}NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP^{SD}IAVEWESNGQPENNYK^{TT}PPVLDSDGSFFLYSKLTV^{DK}SRWQQGNV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 2 - AN1[αENPP3]_H1L1_IgG1_PVA_/S267K (SEQ ID NO: 227)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^{WY}QQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW^{PYT}FGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFY^{PR}EAKVQWKVDNALQSGNSQESVTEQDSK^{DS}TYSLSSTLTLSKADY^EKKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 13A

AN1[ENPP3] H1 L1.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGT ^T YYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGY ^F FDYWGQGTLVTVSS	228
vhCDR1	<u>NYGMS</u>	229
vhCDR2	<u>YISSGGGT^TYYLDSVKG</u>	230
vhCDR3	<u>HRRVYYGY^FFDY</u>	231
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ^W YQQKPDQSPKLL IEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQ ^S NSW PYTFGGG ^T TKLEIK	232
vlCDR1	<u>RASQSIGTSIH</u>	233
vlCDR2	<u>YASESIS</u>	234
vlCDR3	<u>QQSNSWPYT</u>	235

AN1[ENPP3] H1 L1.77

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGT ^T YYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGY ^F FDYWGQGTLVTVSS	236
vhCDR1	<u>NYGMS</u>	237
vhCDR2	<u>YISSGGGT^TYYLDSVKG</u>	238
vhCDR3	<u>HRRVYYGY^FFDY</u>	239
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ^W YQQKPDQSPKLL IEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQ ^S NSW PYTFGGG ^T TKLEIK	240
vlCDR1	<u>RASQSIGTSIH</u>	241
vlCDR2	<u>YESESIS</u>	242
vlCDR3	<u>QQSNSWPYT</u>	243

Figure 13B

AN1[ENPP3] H1.8 L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFATSNYGMSWVRQAPGQRLEW VSYISSGGGTYYLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGTLLTVSS	244
vhCDR1	<u>NYGMS</u>	245
vhCDR2	<u>YISSGGGTYYLDSVTG</u>	246
vhCDR3	<u>HRRVYYGYFDY</u>	247
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLL IKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	248
vlCDR1	<u>RASQSIGTSIH</u>	249
vlCDR2	<u>YASESIS</u>	250
vlCDR3	<u>QQSNSWPYT</u>	251

AN1[ENPP3] H1.8 L1.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFATSNYGMSWVRQAPGQRLEW VSYISSGGGTYYLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGTLLTVSS	252
vhCDR1	<u>NYGMS</u>	253
vhCDR2	<u>YISSGGGTYYLDSVTG</u>	254
vhCDR3	<u>HRRVYYGYFDY</u>	255
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLL IEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	256
vlCDR1	<u>RASQSIGTSIH</u>	257
vlCDR2	<u>YASESIS</u>	258
vlCDR3	<u>QQSNSWPYT</u>	259

AN1[ENPP3] H1.8 L1.77

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFATSNYGMSWVRQAPGQRLEW VSYISSGGGTYYLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGTLLTVSS	260
vhCDR1	<u>NYGMS</u>	261
vhCDR2	<u>YISSGGGTYYLDSVTG</u>	262
vhCDR3	<u>HRRVYYGYFDY</u>	263
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLL IEYESEISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	264
vlCDR1	<u>RASQSIGTSIH</u>	265
vlCDR2	<u>YESESIS</u>	266
vlCDR3	<u>QQSNSWPYT</u>	267

Figure 14A

H16-7.213

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSISTAYMELSR ~~SR~~ SDDTAVYYCARELRYFGWLLS SLDYWGQGT ~~LT~~ LVTVSS	268
vhCDR1	<u>GYMH</u>	269
vhCDR2	<u>WINPNSGGTNYAQKFQG</u>	270
vhCDR3	<u>ELRYFGWLLSSLDY</u>	271
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWFQQKPGKAPKLL IYAASSLQSGVPSRFSGSESGTDFTLTIS ~~SL~~ QPEDFATYSCQ ~~Q~~ SYSF PLTFGGG ~~TK~~ VEIK	272
vlCDR1	<u>RASQSISSYLN</u>	273
vlCDR2	<u>AASSLQS</u>	274
vlCDR3	<u>Q~~Q~~SYSFPLT</u>	275

H16-9.69

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTSYDIHWVRQATGQGLEWMGWMNPNSGNTVYA QKFQGRVTMTRNTSISTAYMELSSLRSED ~~T~~ AVYYCARTVLLWPFDYW GQGT ~~LT~~ LVTVSS	276
vhCDR1	<u>SYDIH</u>	277
vhCDR2	<u>WMNPNSGNTVYAAQKFQG</u>	278
vhCDR3	<u>TVLLWPFDY</u>	279
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSKNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS ~~SL~~ QAEDVAVYYC Q ~~Q~~ YYSTPPWTFGQGT ~~TK~~ VEIK	280
vlCDR1	<u>KSSQSVLYSSKNKNYLA</u>	281
vlCDR2	<u>WASTRES</u>	282
vlCDR3	<u>Q~~Q~~YYSTPPWT</u>	283

H16-1.52

	sequence	SEQ ID NO:
Variable heavy (vh) domain	SGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISG SDGSPYYADSVKGRFTISRDN ~~SKNT~~ LYLQMNSLRAEDTAVYYCAKDG YSSGWN ~~Y~~ FDYWGQGT ~~LT~~ LVTVSS	284
vhCDR1	<u>SYAMS</u>	285
vhCDR2	<u>AISGSDGSPYYADSVKG</u>	286
vhCDR3	<u>DGYSSGWN~~Y~~FDY</u>	287
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS ~~SL~~ QAEDVAVYYC Q ~~E~~ YYSTMCSFGQGT ~~KL~~ EIK	288
vlCDR1	<u>KSSQSVLYSSNNKNYLA</u>	289
vlCDR2	<u>WASTRES</u>	290
vlCDR3	<u>Q~~E~~YYSTMCS</u>	291

Figure 14B

Ha16-1(1)23

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEWVAVI WSDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR EGYYGSGSYYYYYGMDVWGQGTITVTVSS	292
vhCDR1	<u>SYGMH</u>	293
vhCDR2	<u>VIWSDGSNKYYADSVKG</u>	294
vhCDR3	<u>EGYYGSGSYYYYYGMDV</u>	295
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGTQGA ~~AWL~~ QQHQGHPPKL LSYRNNNRPSGISERLSASTSGNTASLTITGLQPEDEADYYCSA ~~WDS~~ SLSA ~~VVF~~ GGGTKLTVL	296
vlCDR1	<u>TGNSNNVGTQGA</u>	297
vlCDR2	<u>RNNNRPS</u>	298
vlCDR3	<u>SAWDSSLSAVV</u>	299

H16-9.44

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LSLTCTVSGGSISSYYWSWIRQSAGKGLEWIGRIYTG ~~VST~~ NYNPSLK SRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDYYDSSGYYPFDYW GQGTITVTVSS	300
vhCDR1	<u>SYYWS</u>	301
vhCDR2	<u>RIYTG~~VST~~NYNPSLKS</u>	302
vhCDR3	<u>DYYDSSGYYPFDY</u>	303
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTISCRASQGISNYLAWFQQKPGKAPKSL IYAASSLENGVPSKFSGSGSGTDFTLT ~~TI~~ SSLQPEDFATYYCQQYNSS PFTFGPGTKVDIR	304
vlCDR1	<u>RASQGISNYLA</u>	305
vlCDR2	<u>AASSLEN</u>	306
vlCDR3	<u>QQYNSSPFT</u>	307

H16-1.67

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSQTL ~~SLT~~ CTVSGGSINSFGYYWSWIRQYPGKGLEWIG FLYFTGSTYYNPSLKSRVTISVDTSK ~~SQ~~ SLKLSSVTAADTAVYYCA RAGTMVRGAHYYGMDVWGQGTITVTVSS	308
vhCDR1	<u>SFGYYWS</u>	309
vhCDR2	<u>FLYFTGSTYYNPSLKS</u>	310
vhCDR3	<u>AGTMVRGAHYYGMDV</u>	311
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQ ~~SIS~~ NYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLT ~~TI~~ SSLQPEDFATYYCQQIYST PPEWTFGQGTKVEIK	312
vlCDR1	<u>RASQ~~SIS~~NYLN</u>	313
vlCDR2	<u>AASSLQ~~S~~</u>	314
vlCDR3	<u>QQIYSTPPEWT</u>	315

Figure 14C

Ha1 6-1 (3,5)36

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGPGLVKPSSETLSLTCTVSGGSISSSSYWGWIRQPPGKGL EWIGSMYYSGSTYHNPSLKS RVIIISVDTSKNQFSLKLSSVTAADTAV YYCARHYITVAGIFDYWGQGLTVTVSS	316
vhCDR1	<u>SSSYWG</u>	317
vhCDR2	<u>SMYYSGSTYHNPSLKS</u>	318
vhCDR3	<u>HYITVAGIFDY</u>	319
Variable light (vl) domain	QSVLTQPPSASGTPGQRATISCSGSSTNIGSTIVN WYQQVPGTAPKL LIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDA SLNGPVFGGGTKLTVL	320
vlCDR1	<u>SGSSTNIGSTIVN</u>	321
vlCDR2	<u>SNNQRPS</u>	322
vlCDR3	<u>AAWDASLNGPV</u>	323

H16-1.86

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSSETLSLTCTVSGGSISSSYWSWIRQPPGKGLEWIGYI YYSGSTNYNPSLKS RVTIISVDTSKNQFSLKLSSVTAADTAVYYCARA YGYYYYGMDVWGQGLTVTVSS	324
vhCDR1	<u>SYYS</u>	325
vhCDR2	<u>YIYYSGSTNYNPSLKS</u>	326
vhCDR3	<u>AYGYYYYGMDV</u>	327
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCRISQSISSYLN WYQQKPGKAPNLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSS PPWTFGQGTKVEIK	328
vlCDR1	<u>RTSQSISSYLN</u>	329
vlCDR2	<u>AASSLQS</u>	330
vlCDR3	<u>QQTYSSPPWT</u>	331

H16-9.10

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LLES GPGLVKPSQTL SLTCAISGDSVSSNSAAWN WIRQSPSRGLEWL GRYYRSKWYNAYAVSVKSRMTINPDT SKNQFSLQLNSVTPEDTAVY YCAREAGGWFD PWGQGLTVTVSS	332
vhCDR1	<u>SNSAAWN</u>	333
vhCDR2	<u>RTYYRSKWYNAYAVSVKS</u>	334
vhCDR3	<u>EAGGWFD</u>	335
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITCRASQGIRSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQANSF PPTFGGGTKVEIK	336
vlCDR1	<u>RASQGIRSWLA</u>	337
vlCDR2	<u>AASSLQS</u>	338
vlCDR3	<u>QQANSFPPT</u>	339

Figure 14D

H16-9.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLES ^G PG ^L LVKPSQ ^T LSLTCAISGDSVSSNSA ^A WNWIRQSPSRGL EWLGRTYYRSKY ^N AYPVSVKSRITINPDTSKNQ ^F SLQLNSVTPEDT AVYYCAREAGGW ^F DPWGQ ^T GLVTVSS	340
vhCDR1	<u>SNSAAWN</u>	341
vhCDR2	<u>RTYYRSKY^NAYPVSVKS</u>	342
vhCDR3	<u>EAGGW^FDP</u>	343
Variable light (vl) domain	DIQMTQSPSSVSASVGD ^R VTITCRANQ ^G GIRSWLA ^W YQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLT ^I SSLPEDFATYYCQQANS ^F PPTFGGGTKVEIK	344
vlCDR1	<u>RANQ^GGIRSWLA</u>	345
vlCDR2	<u>AASSLQ^S</u>	346
vlCDR3	<u>QQANSFPPT</u>	347

H16-1.68

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVH ^L VESGGGVVQ ^P GRSLRLSCAASGFTFRSYGMH ^W VRQAPGKGLEW VAVIWDGSNKYYADSVKGRFTISRDN ^S KNTLYLQMNSLRAEDMAMY YCARSRITIFGVVHYGMDVWGQ ^T TTTVSS	348
vhCDR1	<u>SYGMH</u>	349
vhCDR2	<u>VIWYDGSNKYYADSVKG</u>	350
vhCDR3	<u>SRITIFGVVHYGMDV</u>	351
Variable light (vl) domain	TQLTQSPSSLSASVGD ^R VTITCRASQNINSYLN ^W YQQKPGKAPKLLI YAASSLQSGVPSRFSGSGSGTDFTLT ^I SSLPEDFTTYYCQQSYSSA PTFGGGTKLEIK	352
vlCDR1	<u>RASQNINSYLN</u>	353
vlCDR2	<u>AASSLQ^S</u>	354
vlCDR3	<u>QQSYSSAPT</u>	355

Ha16-1(1)1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYI ^Y YS GSTNYNPSLKS ^R VTISVDTSKNQ ^F SLKLSSVTAADTAVYYCARAV ^S Y YYYGMDVWGQ ^T TTTVSS	356
vhCDR1	<u>SYYS</u>	357
vhCDR2	<u>YIYSGSTNYNPSLKS</u>	358
vhCDR3	<u>AVSYYYGMDV</u>	359
Variable light (vl) domain	DIQMTQSPSSLSASVGD ^R VTITCRTIQNINSYLN ^W YQRP ^G KAPKLL IYATSSLQSGVPSRFSGSGSGTDFTLT ^I SSLPEDFATYYCQQTYST LFTFGPGTKVDIK	360
vlCDR1	<u>RTIQNINSYLN</u>	361
vlCDR2	<u>ATSSLQ^S</u>	362
vlCDR3	<u>QQTYSTLFT</u>	363

Figure 14E

Ha1 6-1 (3,5)18

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVPGGSIRS ^Y FW ^{SW} IRQPAGKGLEWIGRFYFS GSTNYNPSLKS ^R VTMSVDTSKNQ ^F SLKLSSVTAADTAVYYCARDYGD HY ^Y Y ^Y GM ^D VWGQGT ^T TV ^T VSS	364
vhCDR1	<u>SYFWS</u>	365
vhCDR2	<u>RFYFSGSTNYNPSLKS</u>	366
vhCDR3	<u>DYGDHYYYGM^DV</u>	367
Variable light (vl) domain	VLTQPPSVSAAPGQKVTIS ^C SGSSSNIGNNYV ^{SW} YQQFPGTAPKFLI YDNNKRSSGIPDRFSGSKSGTSATLGITGLQTGDEADYYC ^G TWDSSL SAVIFGGG ^T TKLTVL	368
vlCDR1	<u>SGSSSNIGNNYVS</u>	369
vlCDR2	<u>DNNKRSS</u>	370
vlCDR3	<u>GTWDSSLSAVI</u>	371

Ha16-1(2,4)4

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GFTFSSYGMHWVRQAPGKGLEWVAIIWYDESNKY ^Y ADSVKGRFTISR DNSKNTLYLQMNSLRAEDTAVYYCARAYSGSYGYSY ^Y GM	372
vhCDR1	<u>SYGMH</u>	373
vhCDR2	<u>I I WYDESNKY^YADSVKG</u>	374
vhCDR3	<u>AYSGSYGYSY^YGM</u>	375
Variable light (vl) domain	QDRQPASPGSGDKLGDKYACWYQQKPGQSPVLVIYQDSKR ^P SGIPER FSGSNSGNTATLTISGTQAMDEADYYC ^Q AWDNRTAVFGGG ^T TKLTVL	376
vlCDR1	<u>PGSGDKLGDKYAC</u>	377
vlCDR2	<u>QDSKR^PS</u>	378
vlCDR3	<u>QAWDNRTAV</u>	379

Ha16-1(3,5)56

	sequence	SEQ ID NO:
Variable heavy (vh) domain	RCRLVESGA ^E VKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGI ^I YPGDS ^D TRYSPSFQ ^G QVTISADKSISTAYLQWRS ^L KASDTAMY YCARK ^D Y ^Y Y ^Y Y ^Y VMDVWGQGT ^T TV ^T VSS	380
vhCDR1	<u>SYWIG</u>	381
vhCDR2	<u>I I YPGDS^DTRYSPSFQ^G</u>	382
vhCDR3	<u>KD^YY^YY^YVMDV</u>	383
Variable light (vl) domain	DTISCTGTSSDVGN ^Y NYV ^{SW} YQQHPGKAPKLM ^I YAVNNRPSGVSNRF SGSKSGNTASLTISGLQA ^E DEADYYC ^S SYTSSRN ^L VVFGGG ^T TKLTVL	384
vlCDR1	<u>TGTSSDVGN^YNYVS</u>	385
vlCDR2	<u>AVNNRPS</u>	386
vlCDR3	<u>SSYTSSRN^LVV</u>	387

Figure 14F

H16-7.8

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGL EWIGIIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLNSTADTAV FYCARVAIVTTIPGGMDVWGQGTITVTVSS	388
vhCDR1	<u>SGGYWS</u>	389
vhCDR2	<u>IIYYSGSTYYNPSLKS</u>	390
vhCDR3	<u>VAIVTTIPGGMDV</u>	391
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLL IKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSRSF PWTFGQGTKVEIK	392
vlCDR1	<u>RASQSIGISLH</u>	393
vlCDR2	<u>YASQSF</u>	394
vlCDR3	<u>HQSRSPWT</u>	395

H16-1.93

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEW MGWISAYNGNTYYAQKLQARVTMTTDTSTSTAYMELRSLRSDDTAVY YCARDGYSSSSWSLLHYYGMDVWGQGTITVTVSS	396
vhCDR1	<u>SYGIS</u>	397
vhCDR2	<u>WISAYNGNTYYAQKLQA</u>	398
vhCDR3	<u>DGYSSSSWSLLHYYGMDV</u>	399
Variable light (vl) domain	DIQMTQSPSSLSASVGDRIITITWRSSQGIYNLSLAWYQQKPGKVPKLL IYAASLTHSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNLSA PFTFGPGTKVDIK	400
vlCDR1	<u>RSSQGIYNLSA</u>	401
vlCDR2	<u>AASLTHS</u>	402
vlCDR3	<u>QKYNLSAPFT</u>	403

Ha1 6-1(3,5)27.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LVESGAIEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGI IYPGDS TRYSPSFQGVITISADKSISTAYLQWSSLKASDTAMYCA RKDYIIYSMDVWGQGTITVTVSS	404
vhCDR1	<u>SYWIG</u>	405
vhCDR2	<u>I IYPGDS TRYSPSFQG</u>	406
vhCDR3	<u>KDYIIYSMDV</u>	407
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGQAPK LLIYGVNIRPSGVSTRFSGSKSGNTASLTISGLQAEDEADYYCSSYT RSSILVVFAGGTKLTVL	408
vlCDR1	<u>TGTSSDVGGYNYVS</u>	409
vlCDR2	<u>GVNIRPS</u>	410
vlCDR3	<u>SSYTRSSILVV</u>	411

Figure 14G

H16-1.61

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVIWYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCARSRITIFGVVHYGMDVWGQGTITVTVSS	412
vhCDR1	<u>SYGMH</u>	413
vhCDR2	<u>VIWYDGSNKYYADSVKG</u>	414
vhCDR3	<u>SRITIFGVVHYGMDV</u>	415
Variable light (vl) domain	DTQLTQSPSSLSASVGDRTITCRASQSISSYLNWYQLKPGKAPKLL IYAASSLESQVPSRFSGESGTDFTLTISLQPEDFATYYCQSYNS PITFGPGTKVDIK	416
vlCDR1	<u>RASQSISSYLN</u>	417
vlCDR2	<u>AASSLES</u>	418
vlCDR3	<u>QSYNSPIT</u>	419

H16-1 (3,5)5

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGI IYPGDS DTRYSPSFQGV TISADKSISTAYLQWSSLKASDTAMY YCAR KDYYYYTMDVWGQGTITVTVSS	420
vhCDR1	<u>SYWIG</u>	421
vhCDR2	<u>I IYPGDS DTRYSPSFQG</u>	422
vhCDR3	<u>KDYYYYTMDV</u>	423
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPK LMIYAVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYC SSYT ISRI LVVF GGGTKLTVL	424
vlCDR1	<u>TGTSSDVGGYNYVS</u>	425
vlCDR2	<u>AVSNRPS</u>	426
vlCDR3	<u>SSYTISRILVV</u>	427

H16-7.200

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSITSGDYYSWIRQHPGKGL EWF GFIYYSGSAYYNPSLKS RITISVDTSKNQFSLKLSSVTAADTAV YYCARERNYGGNSFDYWGQGTITVTVSS	428
vhCDR1	<u>SGDYYS</u>	429
vhCDR2	<u>F IYYSGSAYYNPSLKS</u>	430
vhCDR3	<u>ERNYGGNSFDY</u>	431
Variable light (vl) domain	DIVMTQSPPLSLPVTPEGPASISCRSSQSLLSNGYNYLDWYLQKPGQ SPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCM QALQTITFGQGTREIK	432
vlCDR1	<u>RSSQSLLSNGYNYLD</u>	433
vlCDR2	<u>LGSNRAS</u>	434
vlCDR3	<u>MQALQTIT</u>	435

Figure 14H

Ha16-1(3,5)42

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGI IYPGDS DTRYSPSFQGGV TISADKSISTAYLQWSSLKASDTAMY YCARKDYYYYSMDVWGQGT TTVTVSS	436
vhCDR1	<u>SYWIG</u>	437
vhCDR2	<u>I IYPGDS DTRYSPSFQG</u>	438
vhCDR3	<u>KDYYYYSMDV</u>	439
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGRFNYVSWYQQRPGKAPK LMIYAVNIRPSGVSNRFSGSKSGNTASLTISGLQAEDEAGYYC <u>SSYT</u> <u>SSSTLLVFGGGTKLTVL</u>	440
vlCDR1	<u>TGTSSDVGRFNYVS</u>	441
vlCDR2	<u>AVNIRPS</u>	442
vlCDR3	<u>SSYTSSSTLLV</u>	443

H1 6-9.65

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSRLRLSCAASGFTSSYGMHWVRQAPGKGLEW VATIWF DGSNGYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCARDSSGSYDHFDYWGQGT LTVTVSS	444
vhCDR1	<u>SYGMH</u>	445
vhCDR2	<u>TIWF DGSNGYYADSVKG</u>	446
vhCDR3	<u>DSSGSYDHFDY</u>	447
Variable light (vl) domain	DIVMTQSPPLSLPVTPGEPASISCRSSQSL LHSNGYNCLDWYLQKPGQ SPQLLIYLG SNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCM <u>QALQTPITFGQGRVEIK</u>	448
vlCDR1	<u>RSSQSL LHSNGYNCLD</u>	449
vlCDR2	<u>LGSNRAS</u>	450
vlCDR3	<u>MQALQTPIT</u>	451

Ha16-1(3,5)19

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGI IYPGDS DTRYSPSFQGGV TISADKSISTAYLQWSSLKASDTAMY YCARKDYYYYAMDVWGQGT TTVTVSS	452
vhCDR1	<u>SYWIG</u>	453
vhCDR2	<u>I IYPGDS DTRYSPSFQG</u>	454
vhCDR3	<u>KDYYYYAMDV</u>	455
Variable light (vl) domain	SALTQPASVSGSPGQSITISCTGTSSDVGRYNYVSWYQQHPGQAPKL MIYGISIRPSGVSPRFSGSKSGNTASLTISGLQAEDEADYYC <u>SSHTS</u> <u>NSTLVVFAGGTKLTVL</u>	456
vlCDR1	<u>TGTSSDVGRYNYVS</u>	457
vlCDR2	<u>GISIRPS</u>	458
vlCDR3	<u>SSHTSNSTLVV</u>	459

Figure 14I

Ha16-1.80

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSIS <u>SYYS</u> WIRQPPGKGLEW IGYVYFSGSTNYPNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYY CARATRDYYYYGMDVWGQGTTTVTVSS	460
vhCDR1	<u>SYYS</u>	461
vhCDR2	<u>YVYFSGSTNYPNPSLKS</u>	462
vhCDR3	<u>ATRDYYYYGMDV</u>	463
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITC <u>RTSHDISNYLN</u> WYQQKPGKAPKLL IYA <u>AASSLQ</u> SGVPSRFSGSRSGTDFTLTISSLQPEDFATYYC <u>QQT</u> YST <u>LF</u> TFGPGTKVDIK	464
vlCDR1	<u>RTSHDISNYLN</u>	465
vlCDR2	<u>AASSLQ</u>	466
vlCDR3	<u>QQT</u> YSTLFT	467

Figure 15A

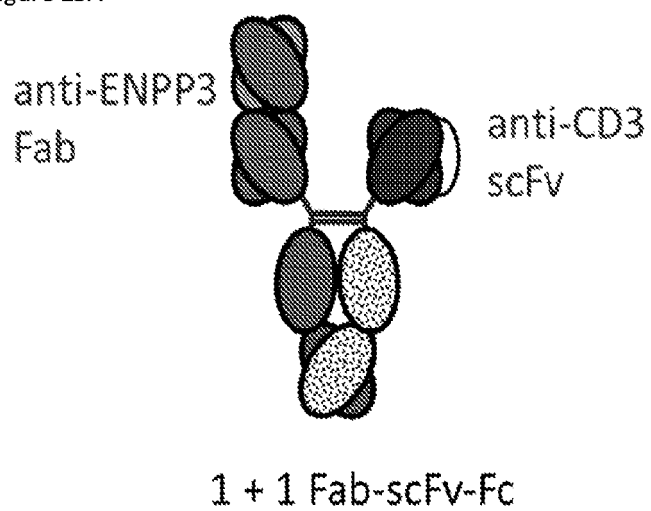


Figure 15B

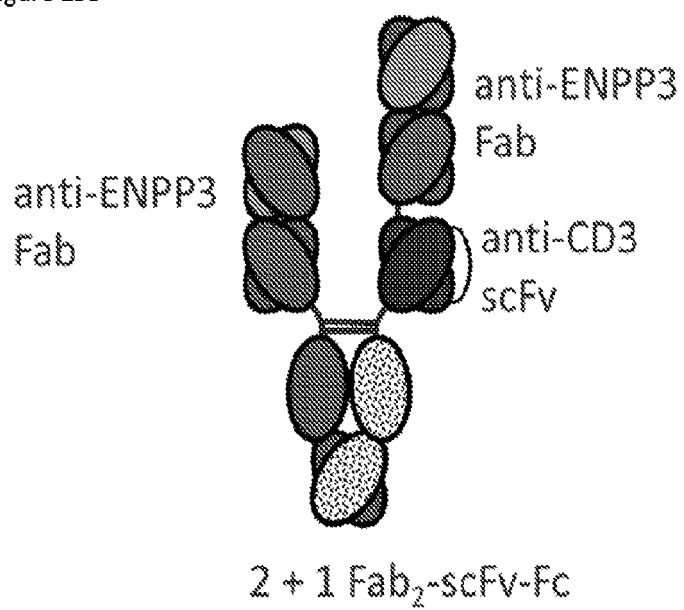


Figure 16

>XENP13245 Numax Fab-[α CD3] H1.30 L1.47 scFv(GKPGS)4 Fc(216) IgG1 PVA /S267K pl(-)
] Isosteric A L368D/K370S-IgG1 C220S/S364K/E357Q

Chain 1 - Numax_IgG1_C220S/S364K/E357Q (SEQ ID NO: 468)

QVTLRSGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYNP SLKDRLTISKDTSK
 NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTITVTSS/ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
 SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSFSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_PVA_/S267K_pl(-)_Isosteric_A_L368D/K370S (SEQ ID NO: 469)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGTITVTSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTITLTCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHVVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSFSVMHEALHNHYTQKSLSLSPGK

Chain 3 - Numax Light (SEQ ID NO: 470)

DIQMTQSPSTLSASVGRVTITCSASSRVGYMHWYQOKPGKAPKLLIYDTSKLASGVPSRFSGSGSGTEFTLTISSL
 QPDDFATYYCFQSGYPFTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17A

>XENP24804 H16-1.93[ENPP3] H1L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - H16-1.93[ENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 471)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTYYAQKLQARVTMTTDTSTS
TAYMELRSLRSDDTAVYYCARDGYSSSWSLHYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 472)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-1.93[ENPP3]_L1 (SEQ ID NO: 473)

DIQMTQSPSSLSASVGDRIITITWRSSQGIYNSLAWYQKPGKVPKLLIYAASLTLSGVP SRFSGSGSGTDFTLTIS
LQPEDVATYYCQKYNAPFTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP26820 H16-7.8[ENPP3] H1L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - H16-7.8[ENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 474)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKLEWIGIIYYSGSTYYNPSLKSRTVISVDTSK
NQFSLKLNSTAAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 475)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1 (SEQ ID NO: 476)

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQKPKDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRSPFWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17B

>XENP28287 AN1[αENPP3] H1L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 477)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSSNYGMSWVRQAPGKRLEWVS^YISSGGGTTY^YLDSVKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGY^YFDYWGQGT^YLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS^SSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT^VLVHQDWLNGKEYCKVSNKALPAPIEKTI^SSKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 478)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^RSKYNNYAT^YYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHG^NFGDSYVSWFAYWGQGT^YLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGT^VTLTLCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGV^PARFSGSLLGGKAAL^TISGAQPED
 EADYYCALWY^SNHWVFGGGTKLTVL/EPKSSDKTHTCP^PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT^VLVHQDWLNGKEYCKVSNKALPAPIEKTI^SSKAKGQPR
 EPQVYTLPPSREQMTKNQV^KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 479)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^WYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQ^QQNSNWPYTFGGG^TKTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^LLN^NFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSK^DSTYSLSS^TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP28925 AN1[αENPP3] H1.8 L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 480)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSSNYGMSWVRQAPG^RLEWVS^YISSGGGTTY^YLDSVTGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGY^YFDYWGQGT^YLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS^SSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT^VLVHQDWLNGKEYCKVSNKALPAPIEKTI^SSKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 481)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^RSKYNNYAT^YYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHG^NFGDSYVSWFAYWGQGT^YLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGT^VTLTLCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGV^PARFSGSLLGGKAAL^TISGAQPED
 EADYYCALWY^SNHWVFGGGTKLTVL/EPKSSDKTHTCP^PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT^VLVHQDWLNGKEYCKVSNKALPAPIEKTI^SSKAKGQPR
 EPQVYTLPPSREQMTKNQV^KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 482)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^WYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQ^QQNSNWPYTFGGG^TKTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^LLN^NFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSK^DSTYSLSS^TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17C

**>XENP29516 AN1[αENPP3] H1.8 L1.33 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 483)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 484)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNEGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTIVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 485)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>XENP30262 AN1[αENPP3] H1.8 L1.77 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 486)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 487)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNEGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTIVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 488)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYSESESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18A

>XENP26821 H16-7.8[ENPP3] H1L1 Fab-[α CD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - H16-7.8[ENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 489)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSTAAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 490)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNGFDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1 (SEQ ID NO: 491)

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRSPFWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP29436 AN1[α ENPP3] H1.8 L1 Fab-[α CD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 492)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPQRLWVSYISSGGGTYYLDSTVGRFTISRDNKN
SLYLYQMNSLRAEDTAVYYCARHRRVYGYFDYWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 493)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNGFDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1 (SEQ ID NO: 494)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQNSWPYTFGGGKTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18B

>XENP28390 AN1[αENPP3] H1L1 Fab-[αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 495)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSSNYGMSWVRQAPGKRLEWVSYISSGGGTTYLD~~SVKGRFTISR~~DNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFFDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~SS~~SGTQTYICNVNHKPSDTKVDK~~KVEPKSCDKTHTC~~
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT~~VLH~~QDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 496)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI~~RSKANNYATYYADSVKGRFTISR~~DDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGT~~LVTVSS~~/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGT~~VT~~TLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGV~~PARFSGSLLGGKAALTISGAQPED~~
 EADYYCALWY~~SNHW~~FGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLH~~QDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PR
 EPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 497)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~WYQ~~KPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQ~~Q~~NSNWPYTFGGGT~~KL~~EIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCL~~LN~~NF~~YPREAKVQWKVDNA
 LQSGNSQESVTEQDSK~~ST~~YSLSS~~TL~~TL~~SKADY~~EKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP29463 AN1[αENPP3] H1.8 L1.33 Fab-[αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 498)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSSNYGMSWVRQAPG~~Q~~RLEWVSYISSGGGTTYLD~~SVTGRFTISR~~DNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFFDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~SS~~SGTQTYICNVNHKPSDTKVDK~~KVEPKSCDKTHTC~~
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT~~VLH~~QDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 499)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI~~RSKANNYATYYADSVKGRFTISR~~DDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGT~~LVTVSS~~/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGT~~VT~~TLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGV~~PARFSGSLLGGKAALTISGAQPED~~
 EADYYCALWY~~SNHW~~FGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLH~~QDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PR
 EPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 500)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~WYQ~~KPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQ~~Q~~NSNWPYTFGGGT~~KL~~EIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCL~~LN~~NF~~YPREAKVQWKVDNA
 LQSGNSQESVTEQDSK~~ST~~YSLSS~~TL~~TL~~SKADY~~EKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18C

>XENP30263 AN1[αENPP3] H1.8 L1.77 Fab-[αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
)_ Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A/PVA_/S267K/L368D/K370S (SEQ ID NO: 501)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 502)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNEGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWFVGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 503)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19A

**>XENP29437 AN1[αENPP3] H1.8 L1 Fab-
AN1[αENPP3] H1.8 L1 CH1 (G4S)2 [αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 504)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1 (G4S)2 [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 505)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 506)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19B

**>XENP29520 AN1[αENPP3] H1.8 L1.33 Fab-
AN1[αENPP3] H1.8 L1.33 CH1 (G4S)2 [αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 507)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 508)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 509)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19C

**>XENP30264 AN1[αENPP3] H1.8 L1.77 Fab-
AN1[αENPP3] H1.8 L1.77 CH1 (G4S)2 [αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 510)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 511)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 512)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20A

>XENP26822 H16-7.8[ENPP3] H1L1 Fab-H16-7.8[ENPP3] H1L1 CH1 (G4S)2 [α CD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - H16-7.8[ENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 513)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSVTAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - H16-

7.8[ENPP3]_H1_CH1_(G4S)2 [α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 514)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSVTAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGG
SGGGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/
QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKKAALTI
SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1 (SEQ ID NO: 515)

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRSPFTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20B

>XENP28438 AN1[αENPP3] H1L1 Fab-AN1[αENPP3] H1L1 CH1 (G4S)2 [αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - AN1[αENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 516)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISSGGGTTYLYLDSVKGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1_CH1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 517)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISSGGGTTYLYLDSVKGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQTLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 518)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20C

**>XENP29438 AN1[αENPP3] H1.8 L1 Fab-
AN1[αENPP3] H1.8 L1 CH1 (G4S)2 [αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 519)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGQDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 520)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREOMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 521)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20D

**>XENP29467 AN1[αENPP3] H1.8 L1.33 Fab-
AN1[αENPP3] H1.8 L1.33 CH1 (G4S)2 [αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
] Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 522)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 523)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 524)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 21

**>XENP30469 AN1[αENPP3] H1.8 L1 Fab-
AN1[αENPP3] H1.8 L1 CH1 (G4S)2 [αCD3] L1.47 H1.30 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 525)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1 (G4S)2 [αCD3]_L1.47_H1.30_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 526)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFAYWGQGLVTVSS/SGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 527)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22A

**>XENP30470 AN1[α ENPP3] H1.8 L1 Fab-
 AN1[α ENPP3] H1.8 L1 CH1 (G4S)2 [α CD3] L1.47 H1.32 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 528)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLYLDSVTGRFTISRDN
 AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[α ENPP3]_H1.8_CH1_(G4S)2_[α CD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
 E357Q (SEQ ID NO: 529)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLYLDSVTGRFTISRDN
 AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
 GGGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
 AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
 RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
 YYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
 VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1 (SEQ ID NO: 530)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22B

**>XENP30819 AN1[α ENPP3] H1.8 L1.33 Fab-
 AN1[α ENPP3] H1.8 L1.33 CH1 (G4S)2 [α CD3] L1.47 H1.32 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 531)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLYLDSVTGRFTISRDN
 AKNSLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[α ENPP3]_H1.8_CH1_(G4S)2_[α CD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
 E357Q (SEQ ID NO: 532)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLYLDSVTGRFTISRDN
 AKNSLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
 GGGG/QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
 AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
 RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNLSRAEDTAV
 YYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
 VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGIFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1.33 (SEQ ID NO: 533)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22C

**>XENP30821 AN1[αENPP3] H1.8 L1.77 Fab-
AN1[αENPP3] H1.8 L1.77 CH1 (G4S)2 [αCD3] L1.47 H1.32 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 534)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 535)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 536)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23A

**>XENP31148 AN1[α ENPP3] H1.8 L1 Fab-
 AN1[α ENPP3] H1.8 L1 CH1 (G4S)2 [α CD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 537)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
 AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[α ENPP3]_H1.8_CH1_(G4S)2_[α CD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
 E357Q (SEQ ID NO: 538)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
 AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
 GGGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
 AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
 RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
 YYCVRHGNFGDEYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
 VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
 DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1 (SEQ ID NO: 539)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23B

**>XENP31149 AN1[αENPP3] H1.8 L1.33 Fab-
AN1[αENPP3] H1.8 L1.33 CH1 (G4S)2 [αCD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 540)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 541)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 542)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23C

**>XENP31150 AN1[αENPP3] H1.8 L1.77 Fab-
AN1[αENPP3] H1.8 L1.77 CH1 (G4S)2 [αCD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-)
] Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 543)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 544)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 545)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23D

**>XENP31419 AN1[αENPP3] H1.8 L1.33 Fab-
AN1[αENPP3] H1.8 L1.33 CH1 (G4S)2 [αCD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 546)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTLVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 547)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTLVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFAYWGQTLVTSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 548)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23E

**>XENP31471 AN1[αENPP3] H1.8 L1.77 Fab-
AN1[αENPP3] H1.8 L1.77 CH1 (G4S)2 [αCD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-)
] Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

Chain 1 - AN1[αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 549)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 550)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSTVGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGTGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFAYWGQGLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77 (SEQ ID NO: 551)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24A

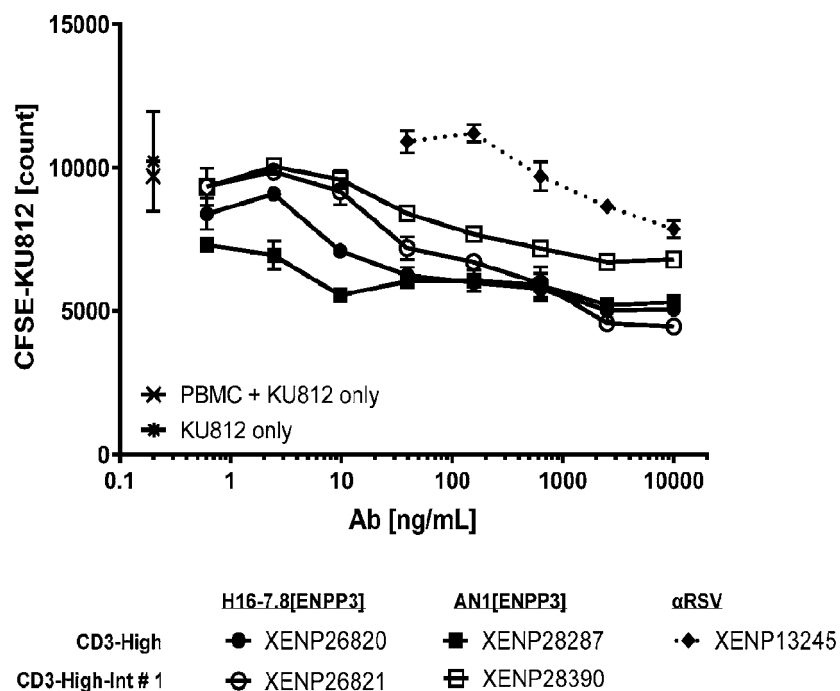


Figure 24B

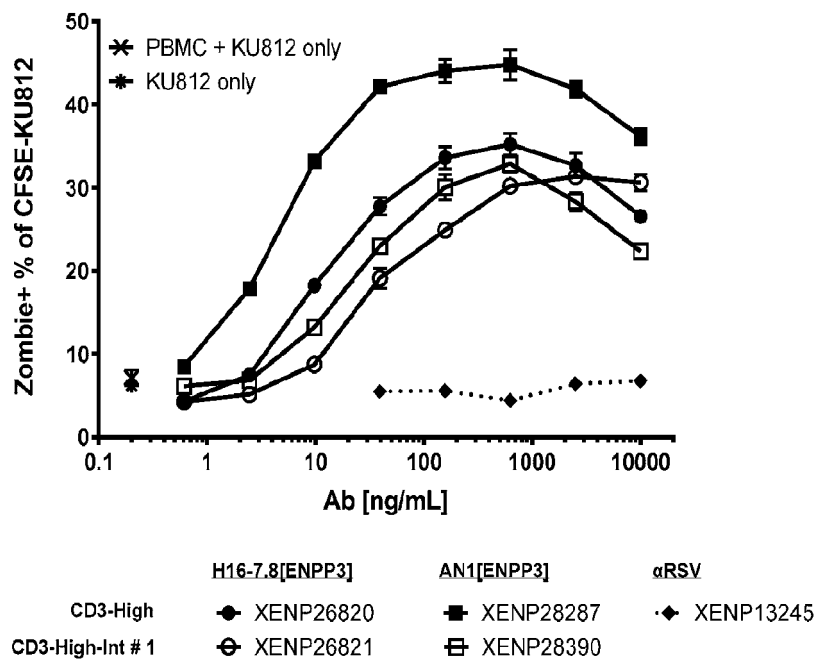


Figure 25A

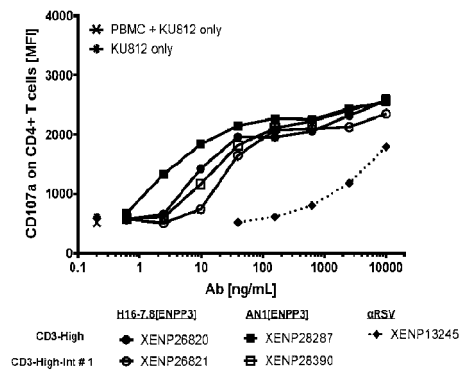


Figure 25B

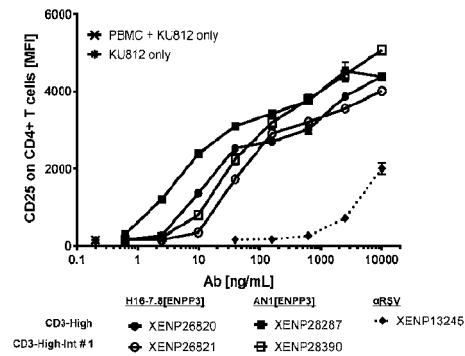


Figure 25C

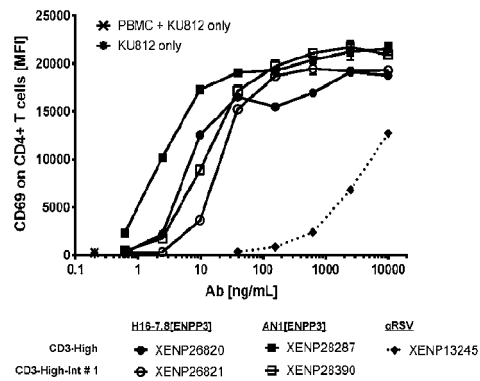


Figure 26A

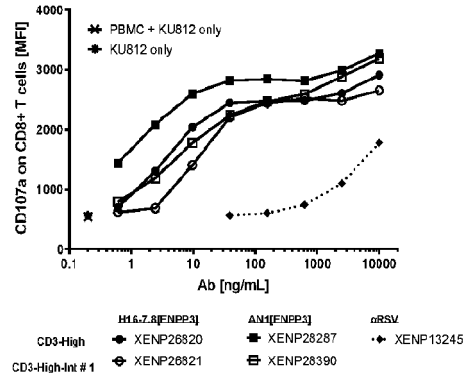


Figure 26B

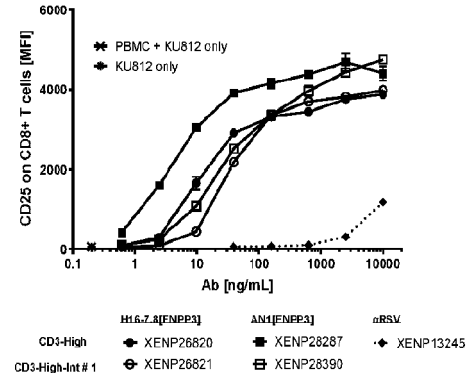


Figure 26C

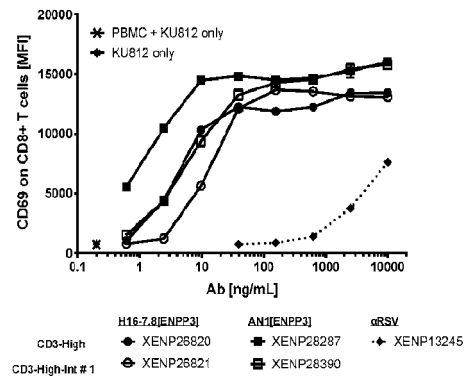


Figure 27A

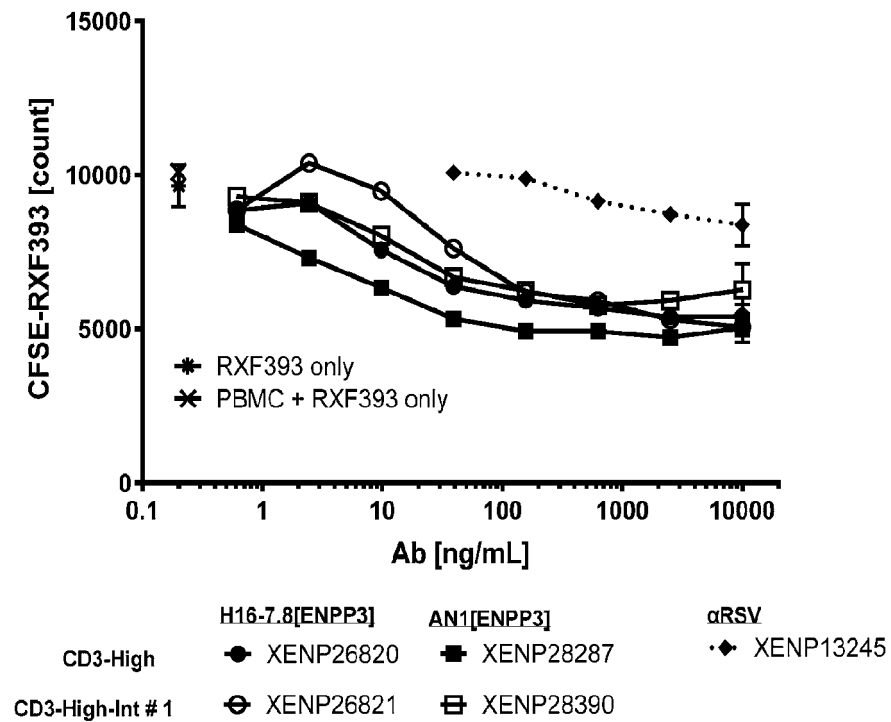


Figure 27B

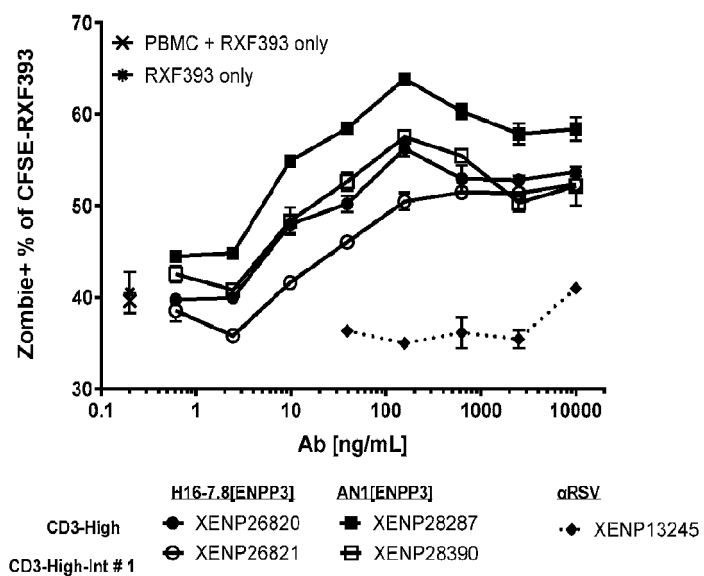


Figure 28A

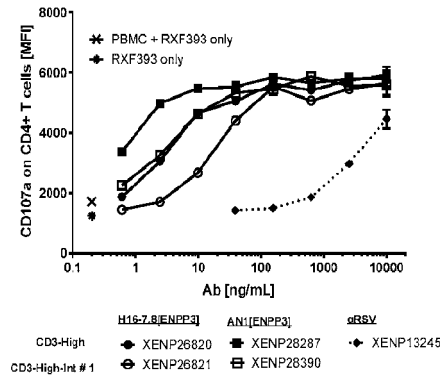


Figure 28B

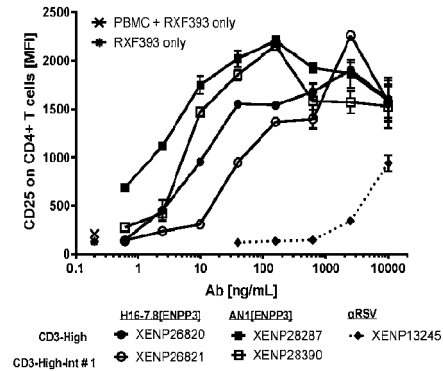


Figure 28C

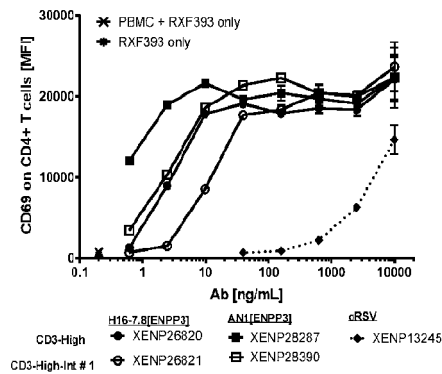


Figure 29A

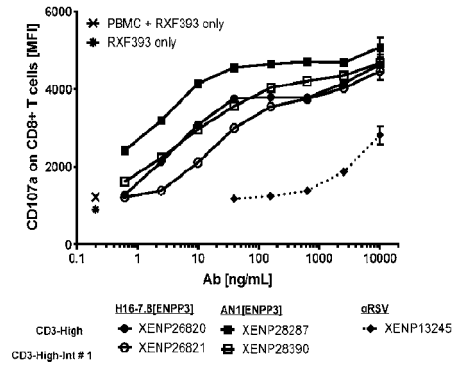


Figure 29B

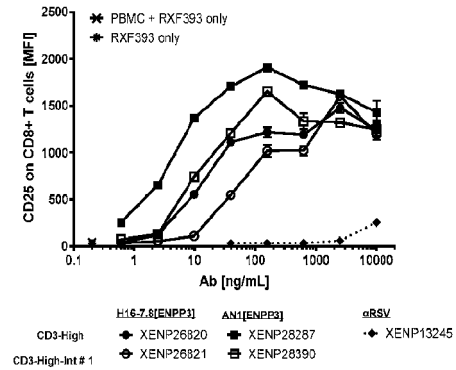


Figure 29C

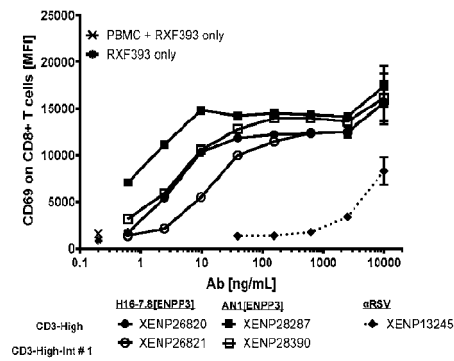
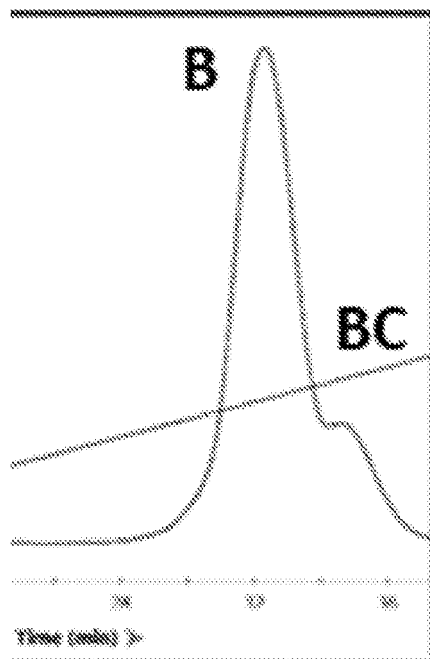


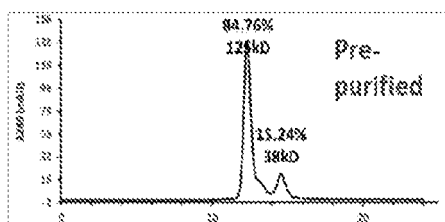
Figure 30

A)

Purification of
eluate from
Protein A
Chromatography
via Cation
Exchange
Chromatography



B) aSEC-MALS



C) aCIEX

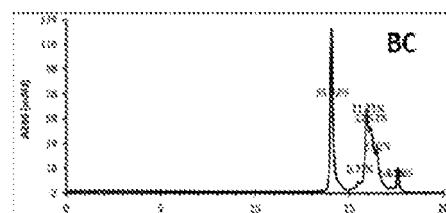
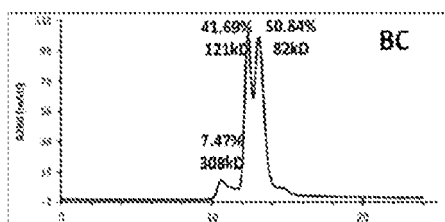
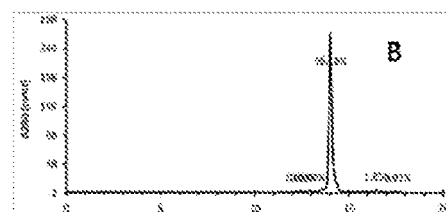
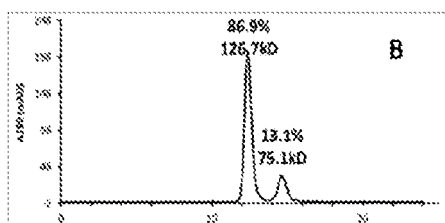


Figure 31

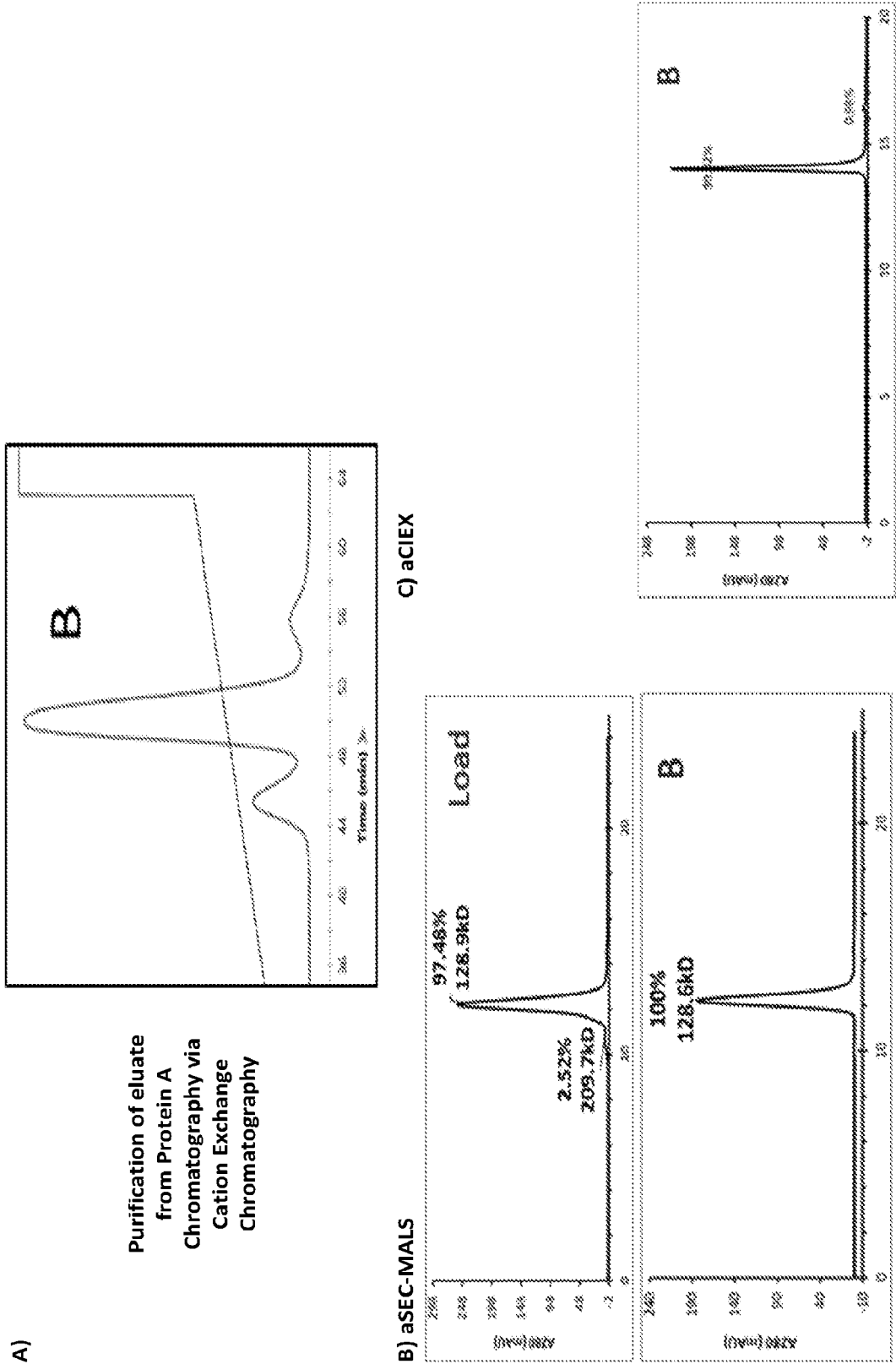


Figure 32

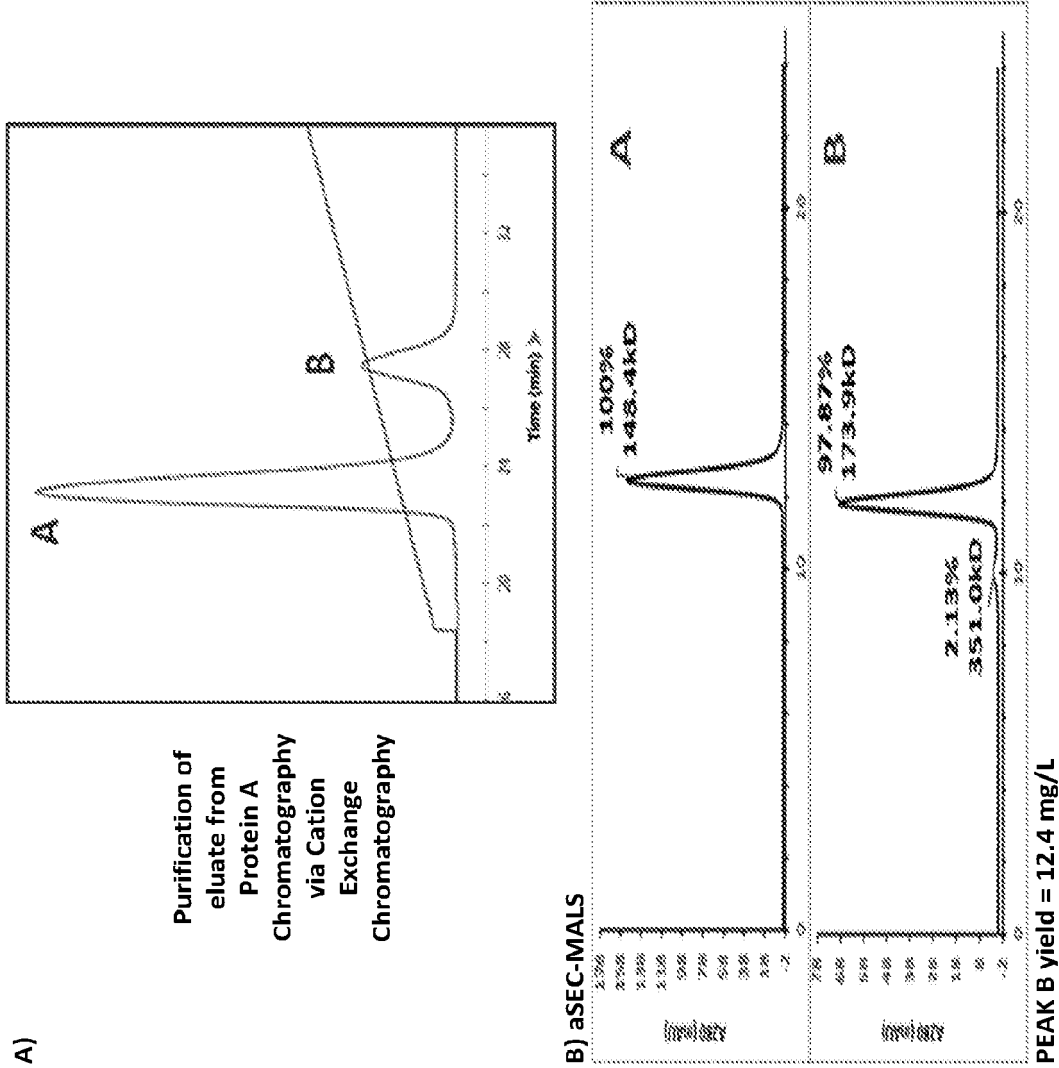


Figure 33

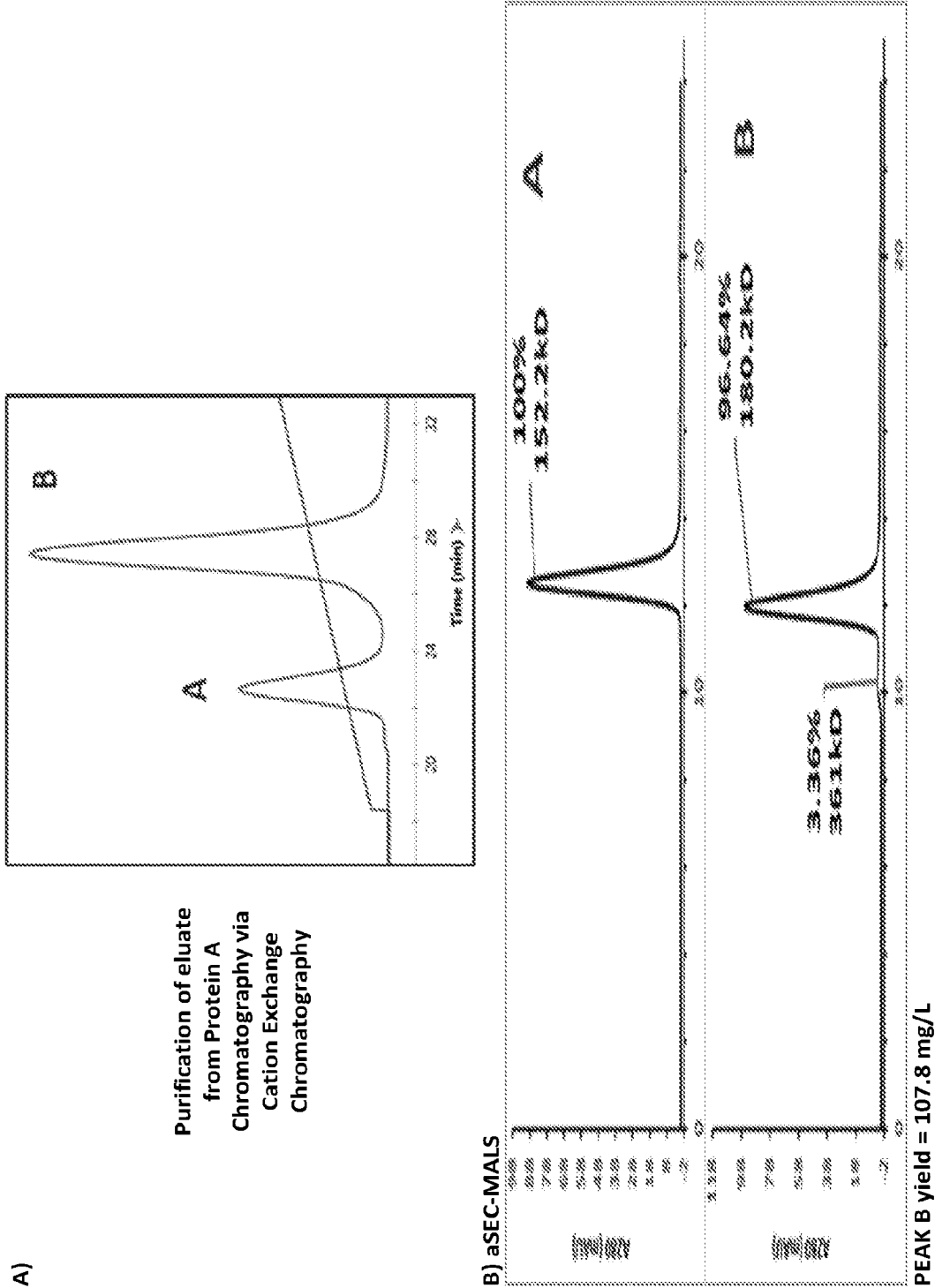


Figure 34

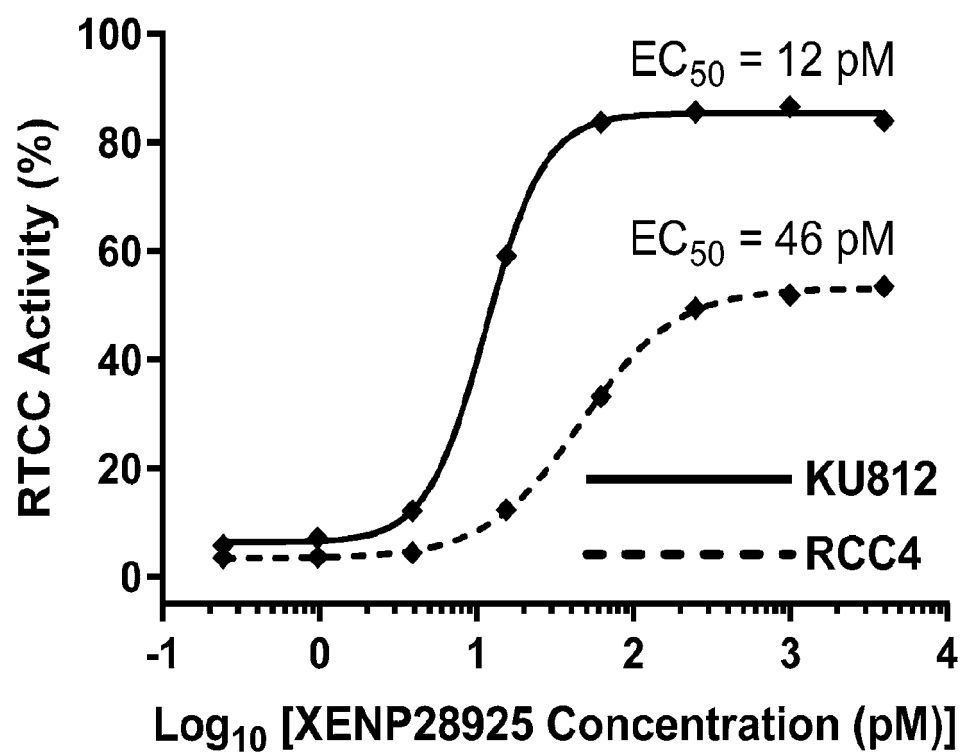


Figure 35

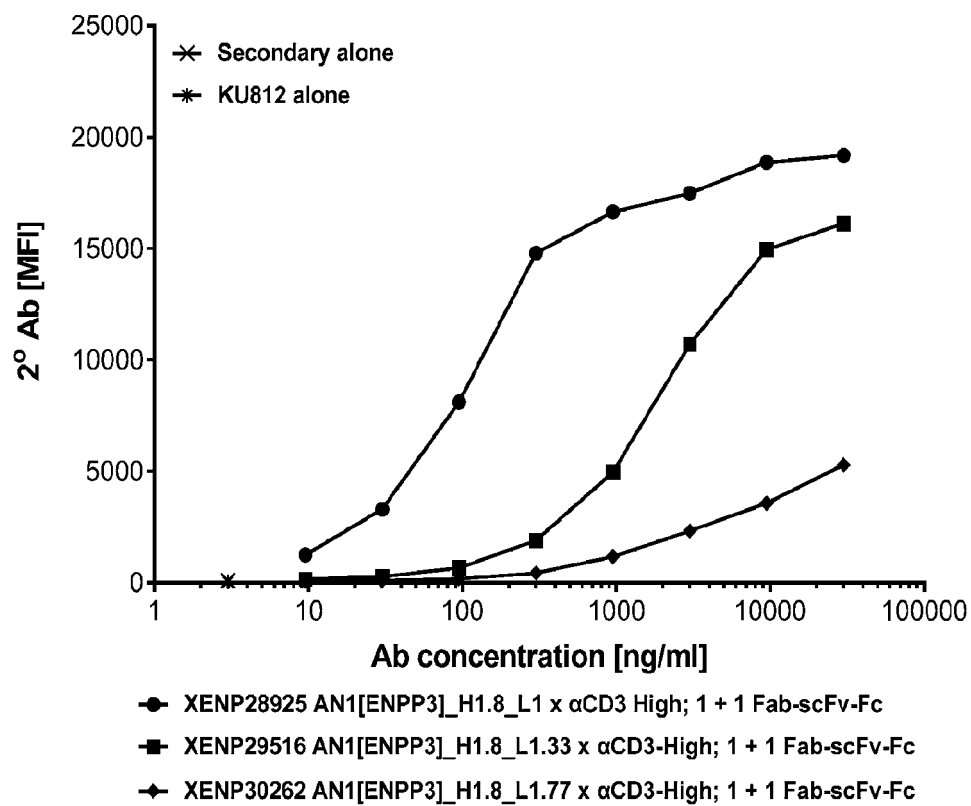


Figure 36

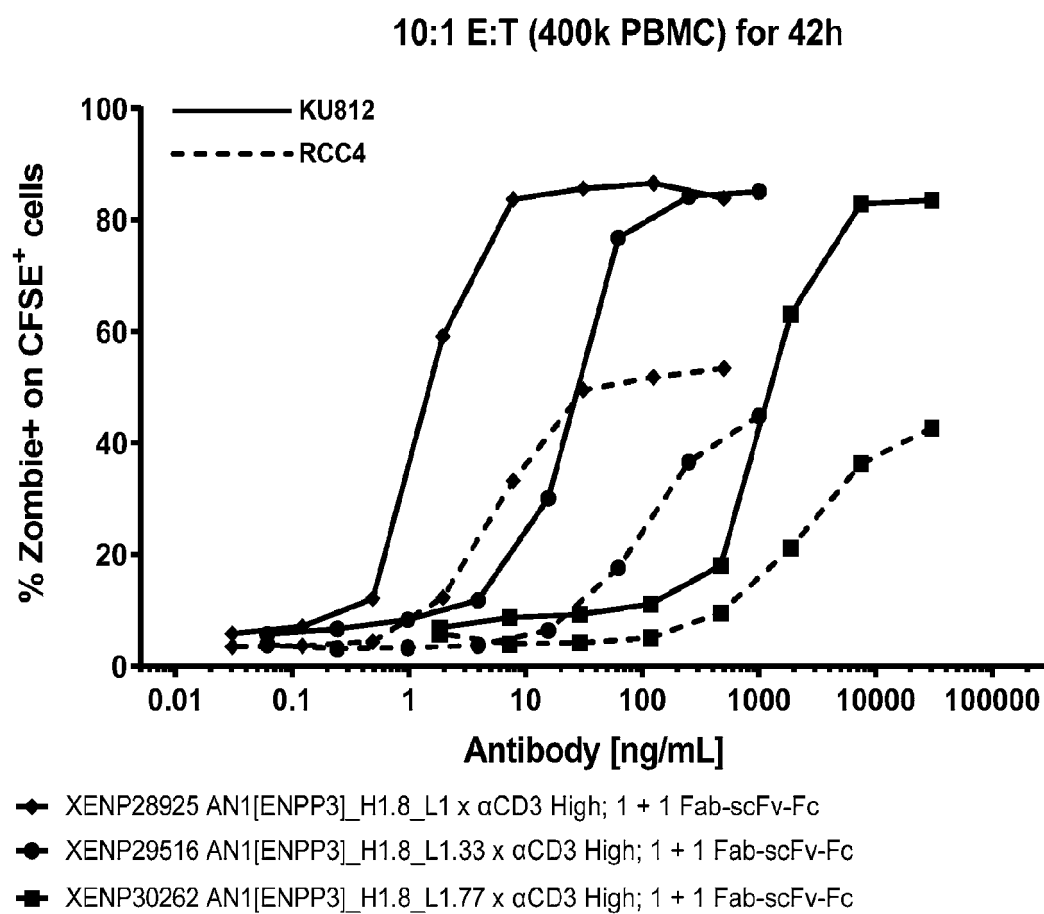


Figure 37A

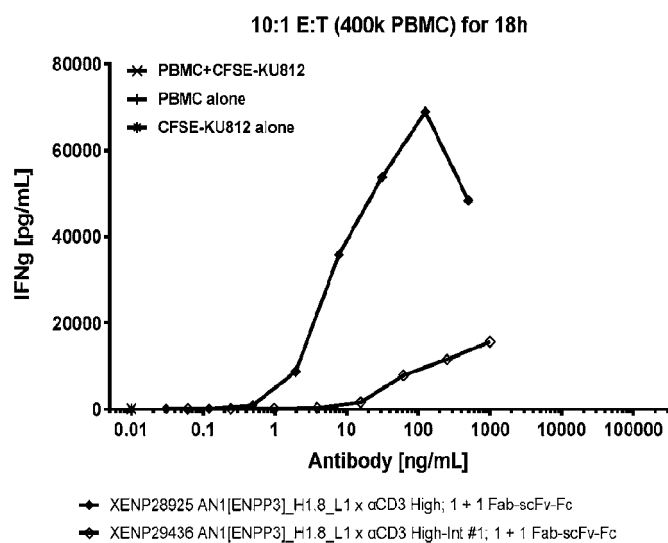


Figure 37B

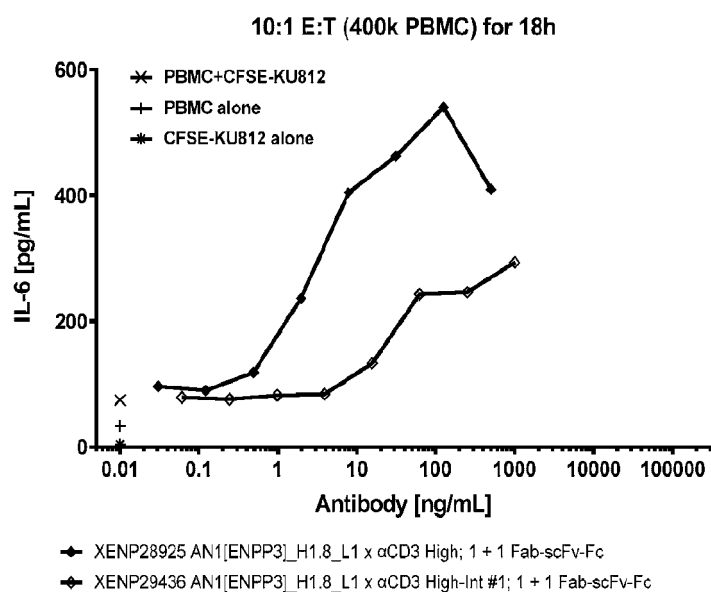


Figure 37C

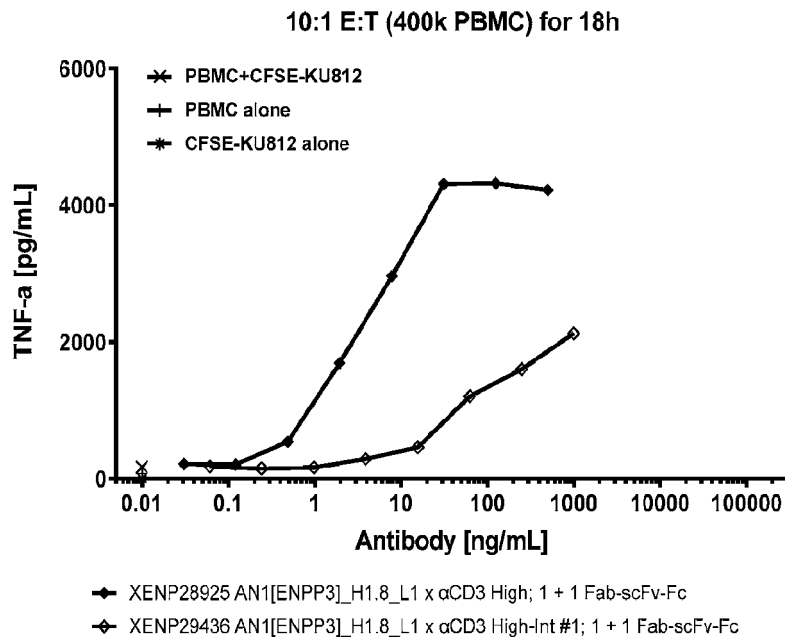


Figure 38

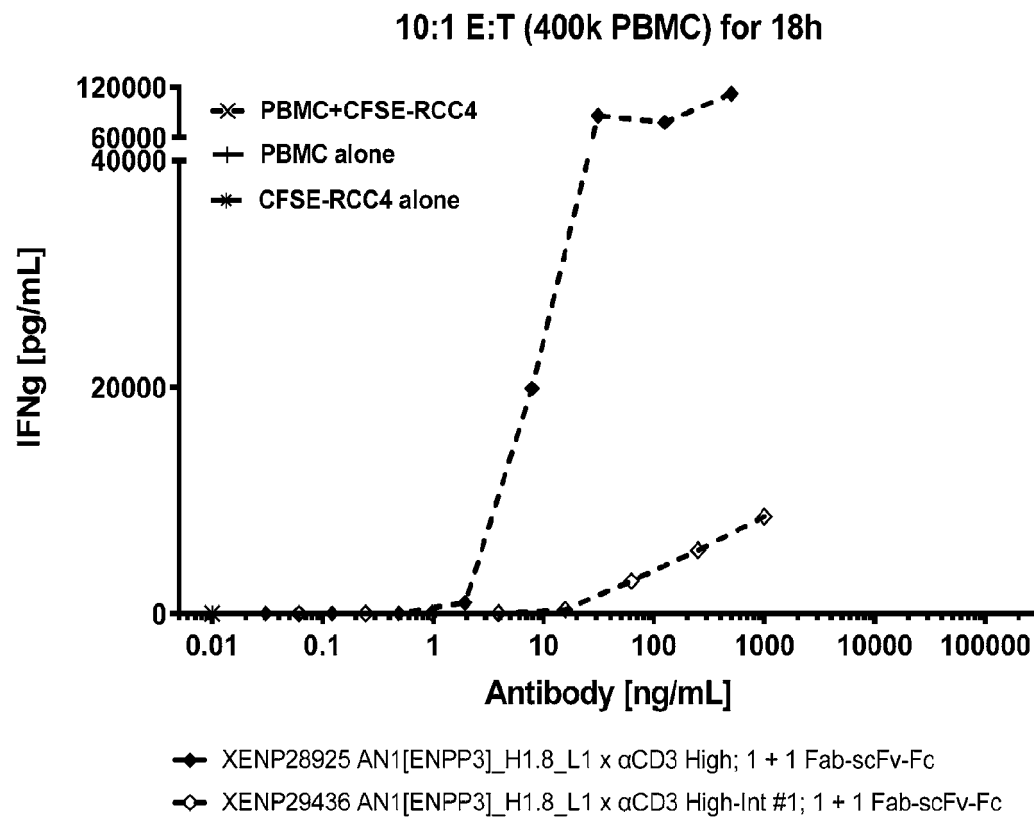


Figure 39

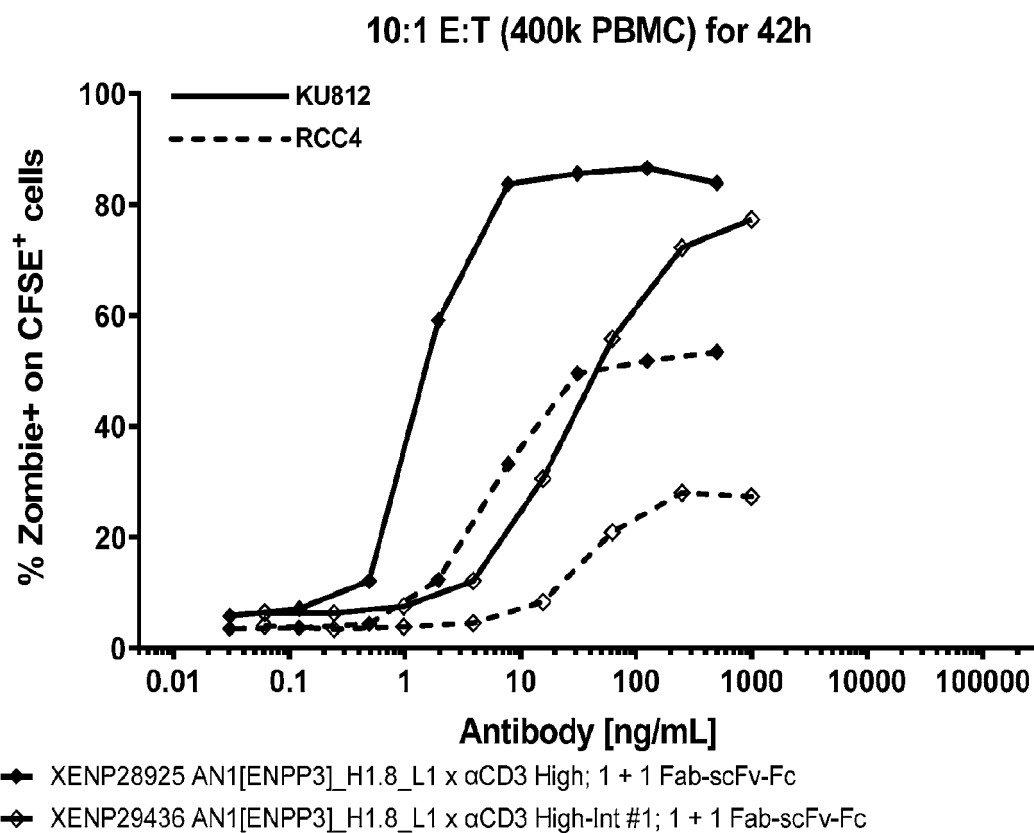


Figure 40

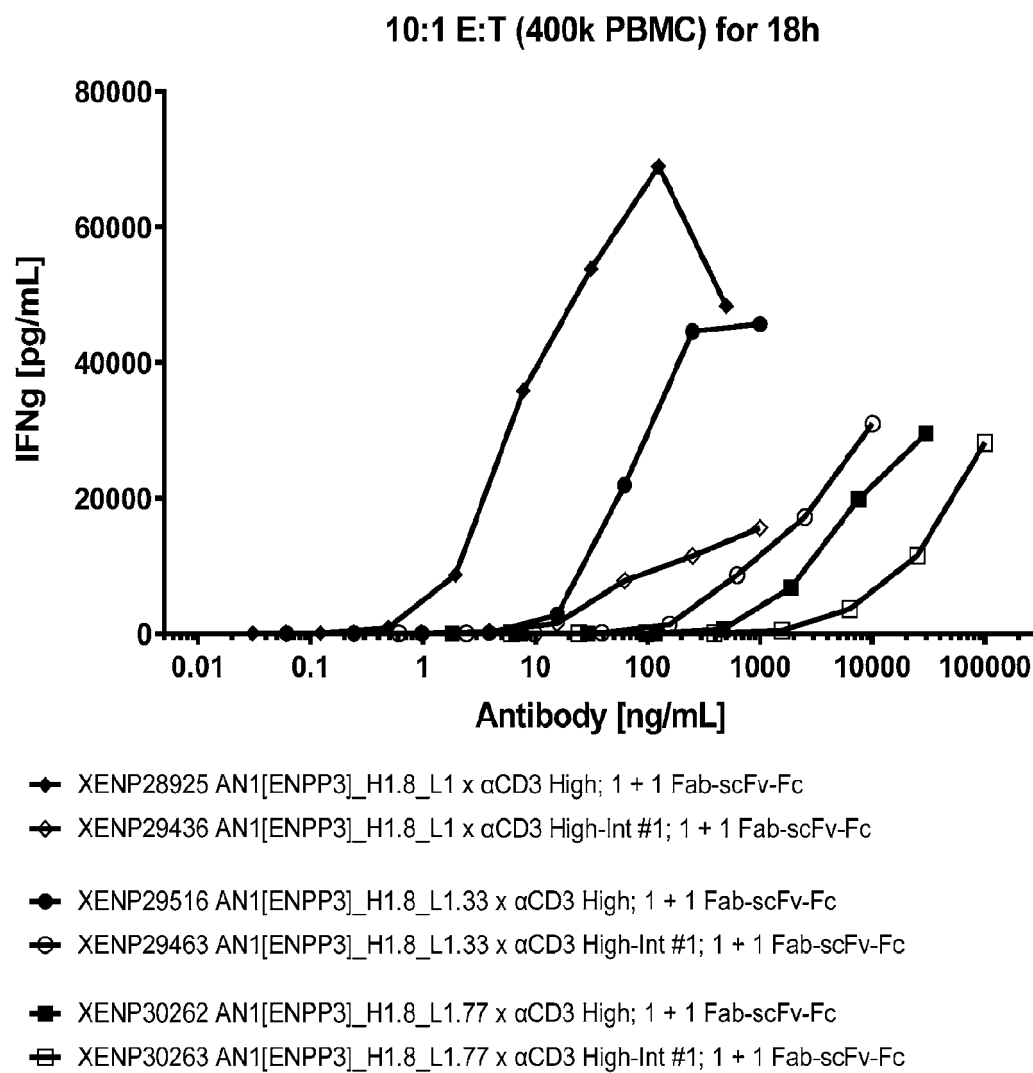


Figure 41

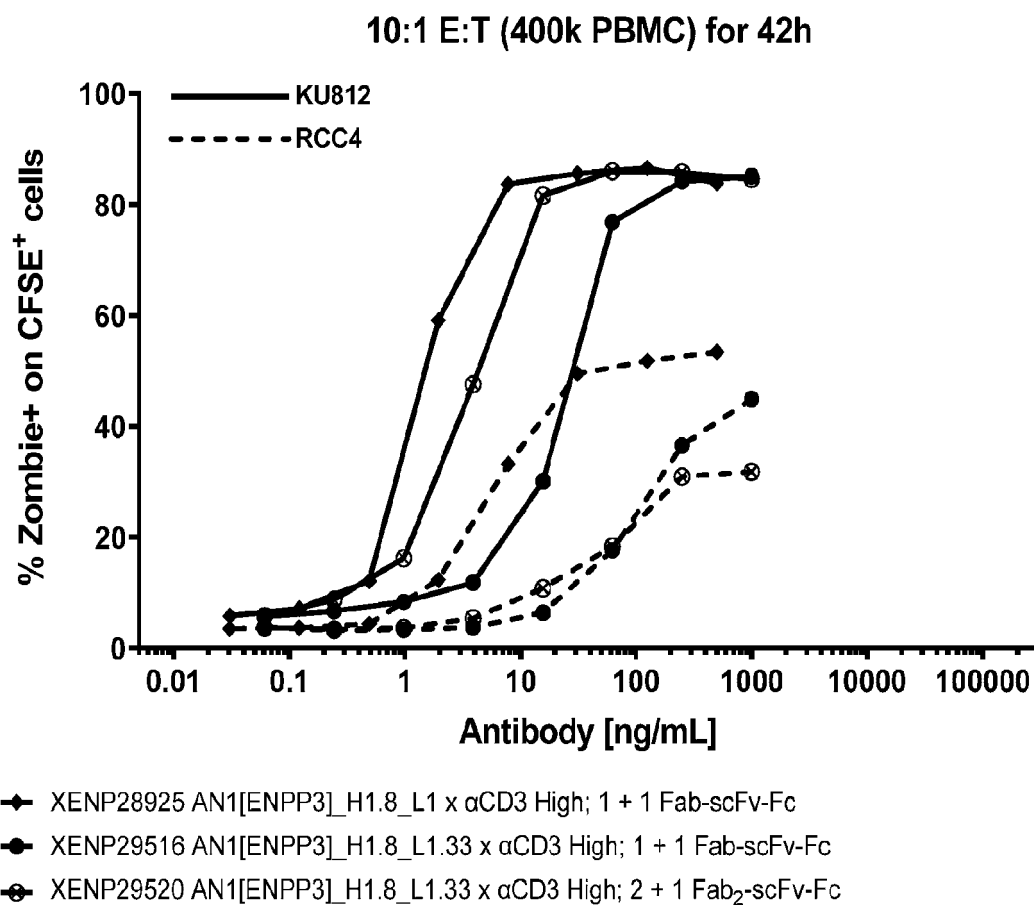


Figure 42

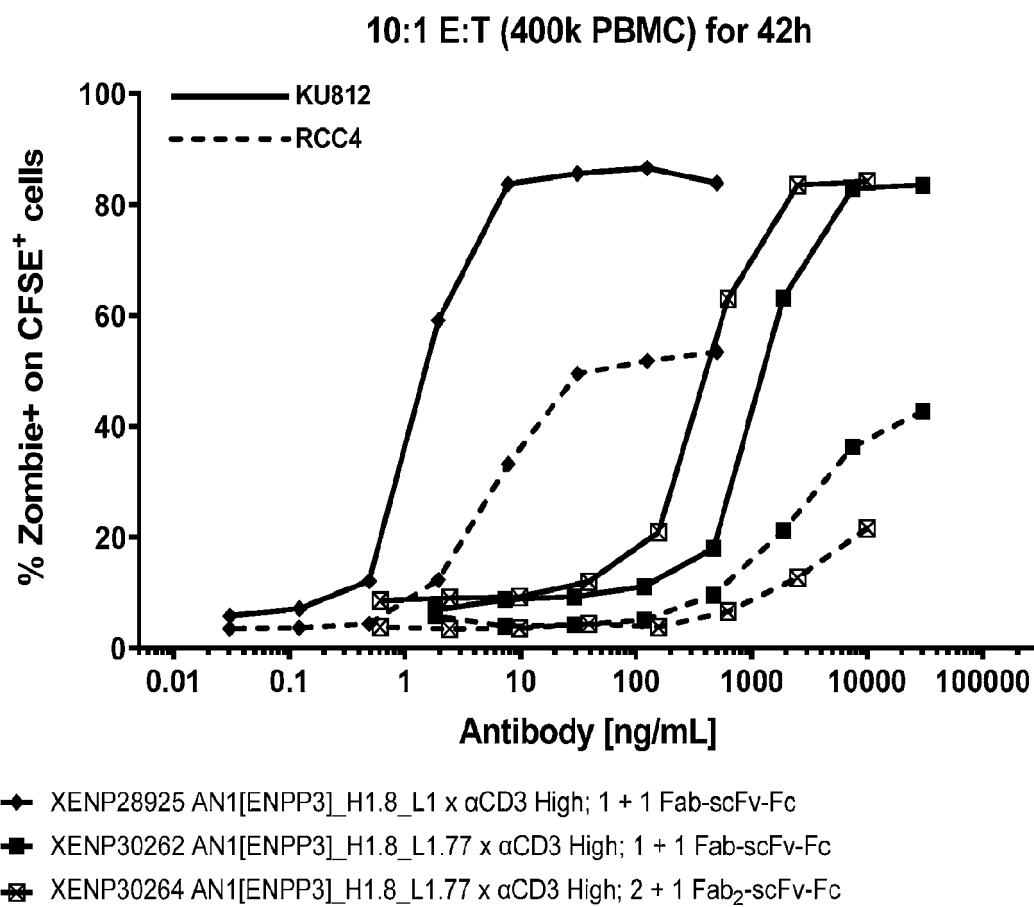


Figure 43

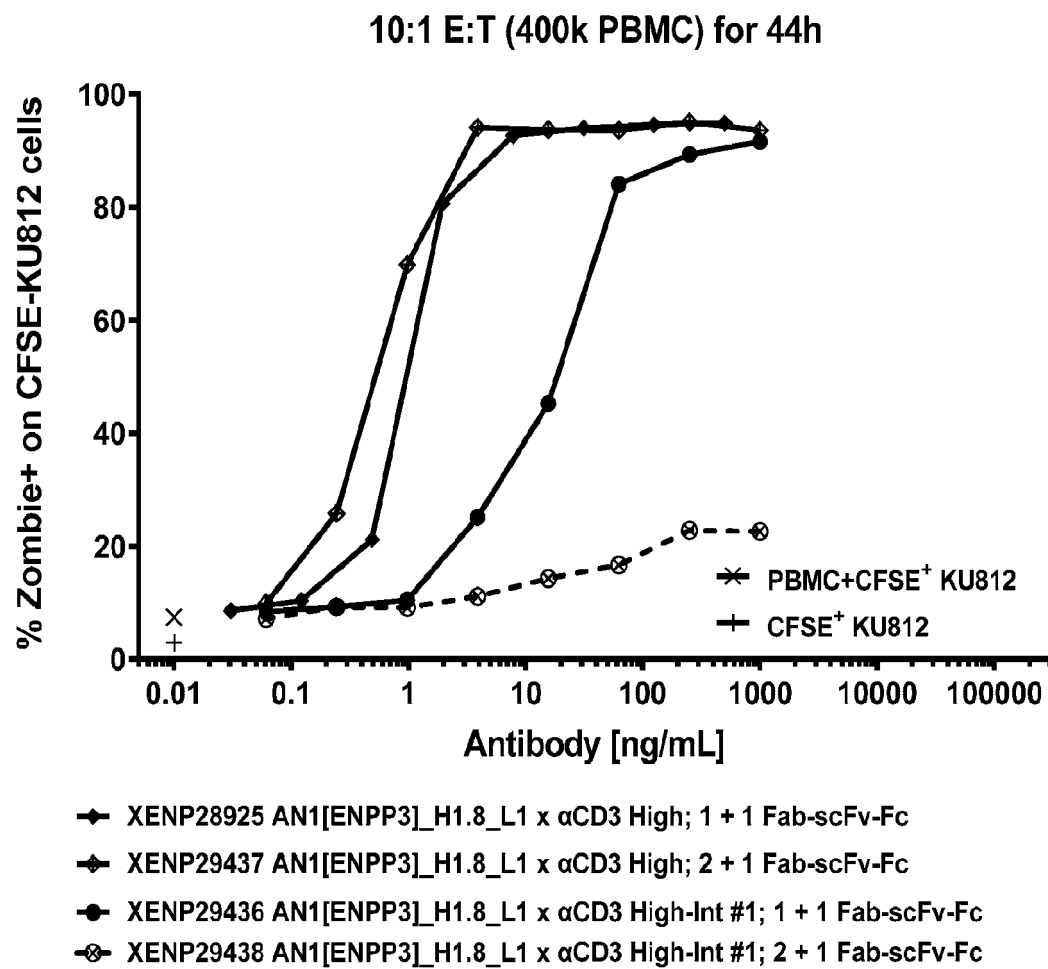


Figure 44

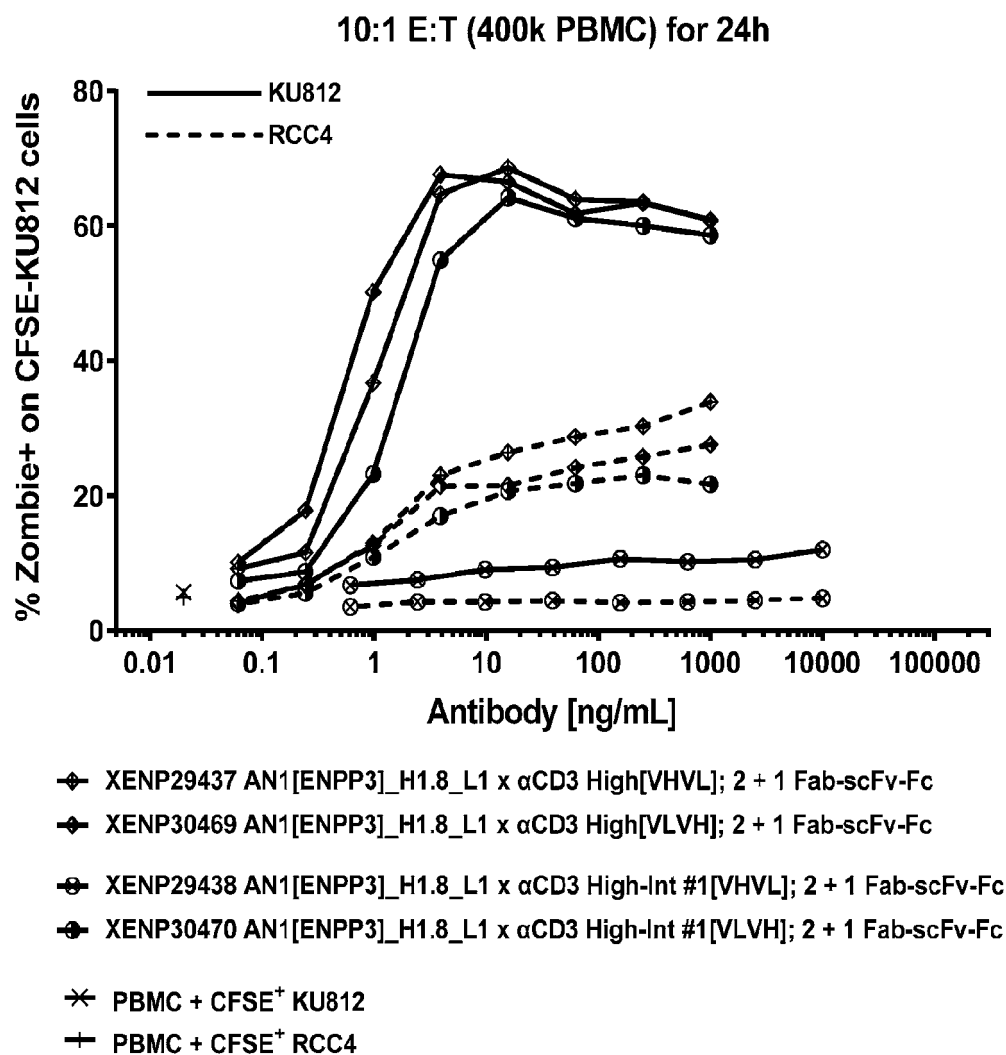


Figure 45

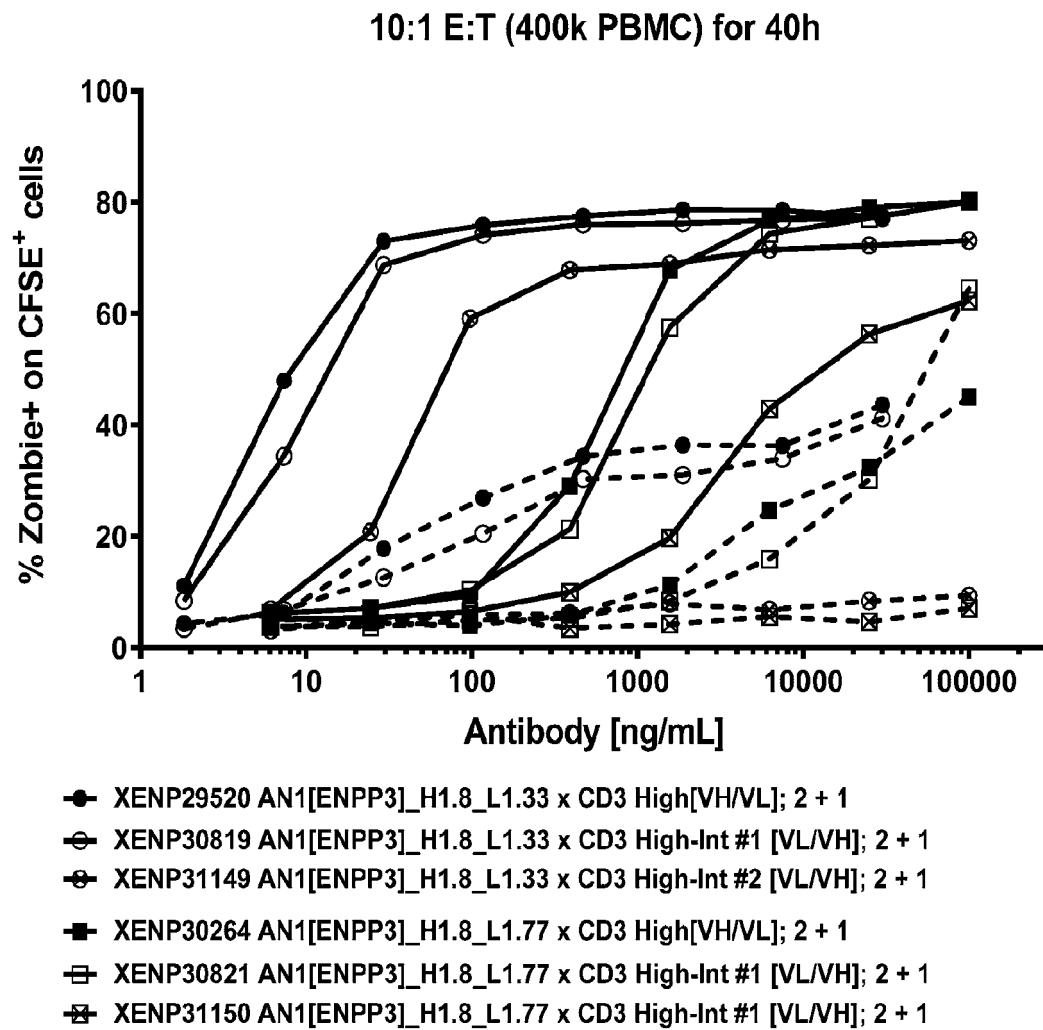


Figure 46

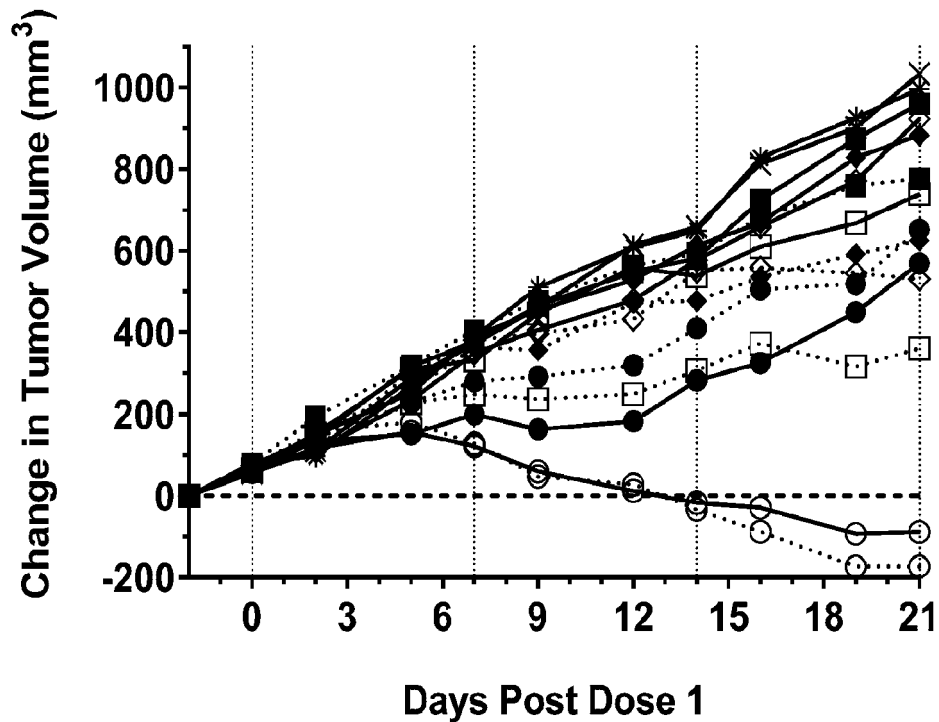
> XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K**XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NO: 552)**

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDDYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NO: 553)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGSGTDFTLTIS S
LEPEDFAVYYCQQSSNWPRTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 47

Baseline-corrected of Group median TM Caliper vs time

- ✕ PBS
 - ✱ XENP16432; 3 mg/kg
 - XENP30819 (AN1[ENPP3]_{H1.8}L1.33 x CD3 High-Int #1[VLVH] 2+1 bsAb); 1 mg/kg
 - XENP30821 (AN1[ENPP3]_{H1.8}L1.77 x CD3 High-Int #1[VLVH] 2+1 bsAb); 3 mg/kg
 - ◆ XENP31419 (AN1[ENPP3]_{H1.8}L1.33 x CD3 High-Int #2[VLVH] 2+1 bsAb); 3 mg/kg
 - ⊕ XENP30819 (AN1[ENPP3]_{H1.8}L1.33 x CD3 High-Int #1[VLVH] 2+1 bsAb); 3 mg/kg
 - ⊞ XENP30821 (AN1[ENPP3]_{H1.8}L1.77 x CD3 High-Int #1[VLVH] 2+1 bsAb); 6 mg/kg
 - ◇ XENP31419 (AN1[ENPP3]_{H1.8}L1.33 x CD3 High-Int #2[VLVH] 2+1 bsAb); 6 mg/kg
- bsAb Only
- bsAb + PD-1 blockade

Figure 48A

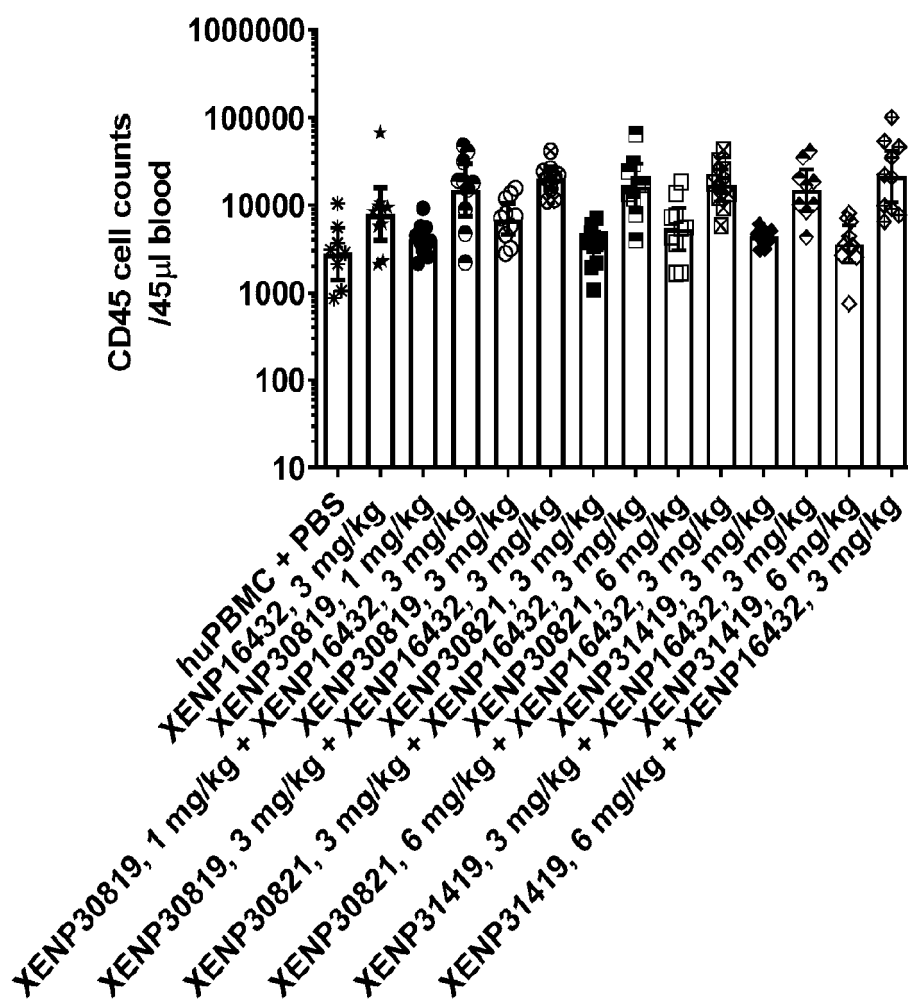


Figure 48B

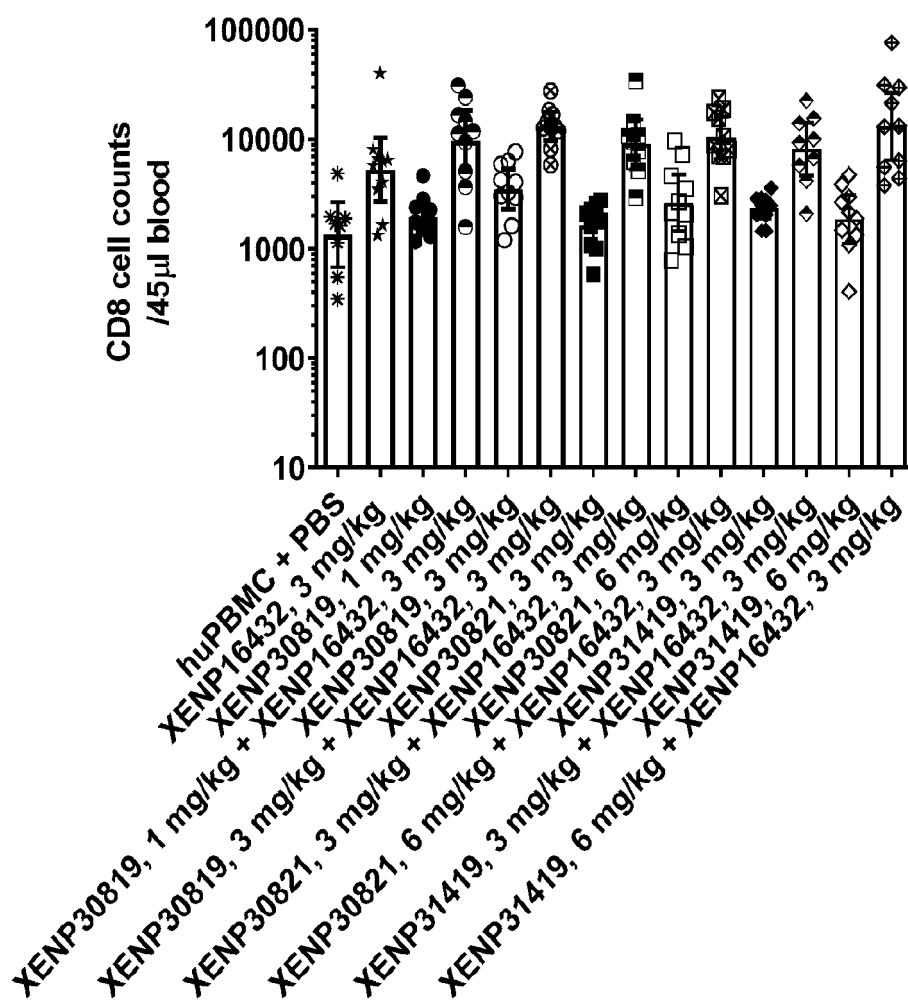


Figure 48C

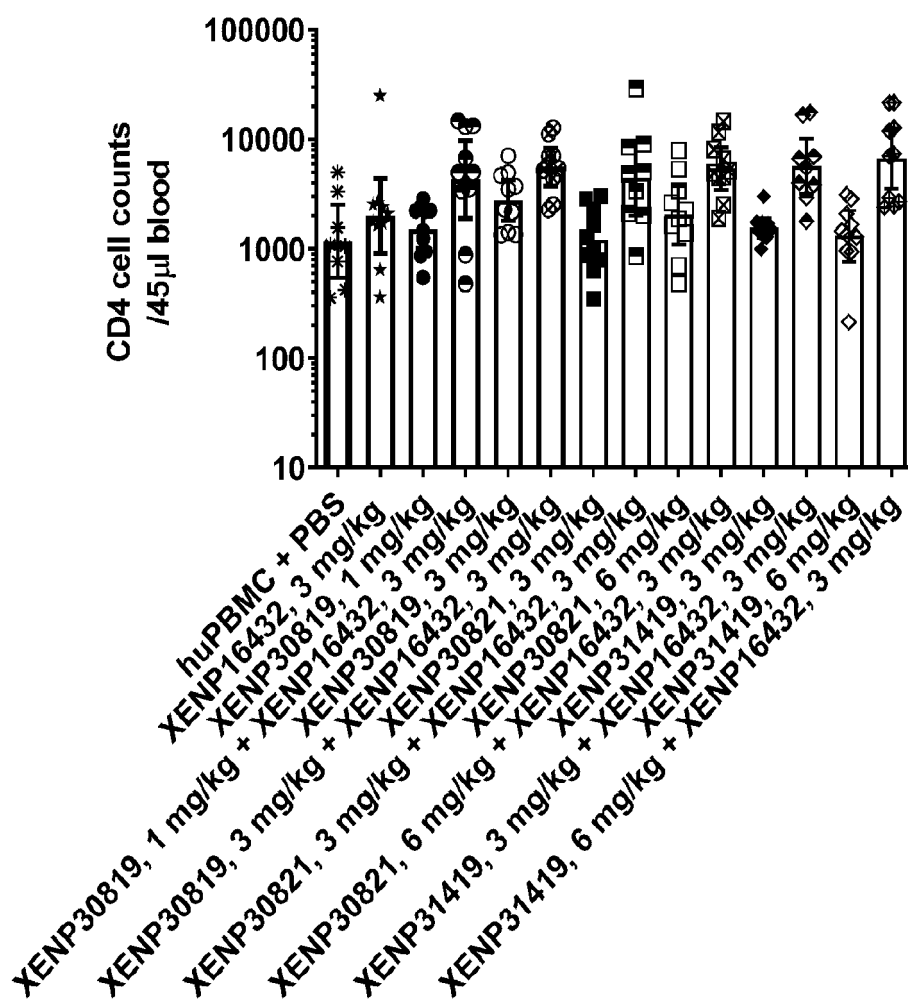
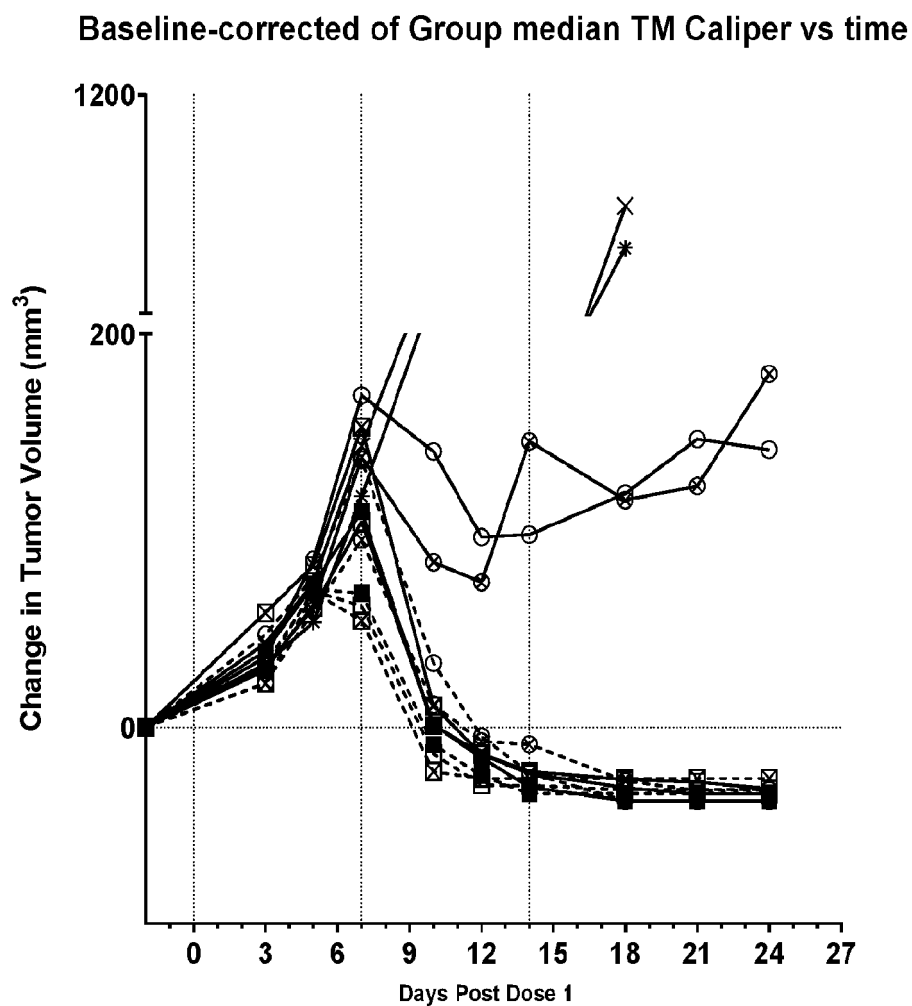


Figure 49



- ✕ huPBMC + PBS
- * XENP16432; 3 mg/kg
- ⊖ XENP31419 (AN1[ENPP3]_LH1.8_L1.33 x CD3 High-Int #2[VLVH] 2+1 bsAb); 3 mg/kg
- ⊕ XENP31419 (AN1[ENPP3]_LH1.8_L1.33 x CD3 High-Int #2[VLVH] 2+1 bsAb); 10 mg/kg
- XENP30819 (AN1[ENPP3]_LH1.8_L1.33 x CD3 High-Int #1[VLVH] 2+1 bsAb); 1 mg/kg
- ▣ XENP30819 (AN1[ENPP3]_LH1.8_L1.33 x CD3 High-Int #1[VLVH] 2+1 bsAb); 3 mg/kg
- ▤ XENP30819 (AN1[ENPP3]_LH1.8_L1.33 x CD3 High-Int #1[VLVH] 2+1 bsAb); 10 mg/kg
- bsAb Only
- bsAb + PD-1 blockade

Figure 50A

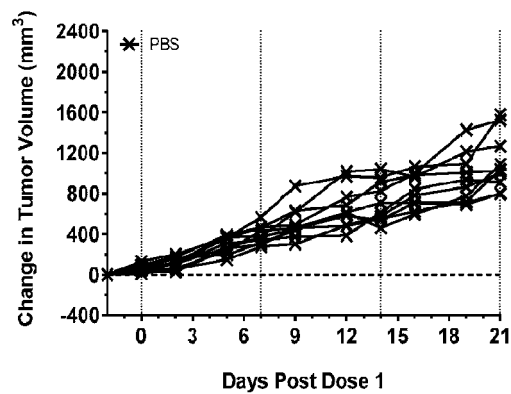


Figure 50B

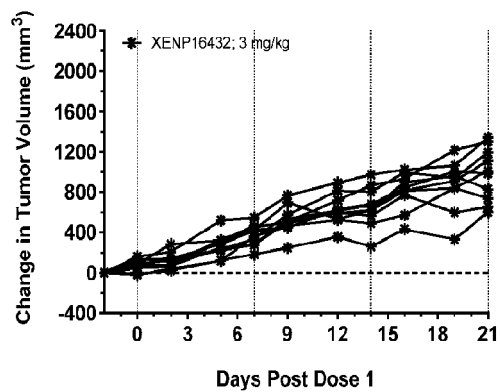


Figure 50C

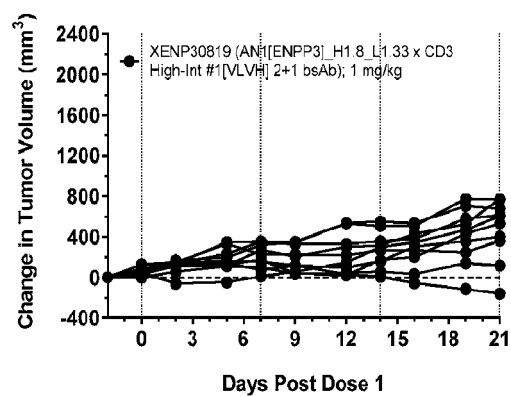


Figure 50D

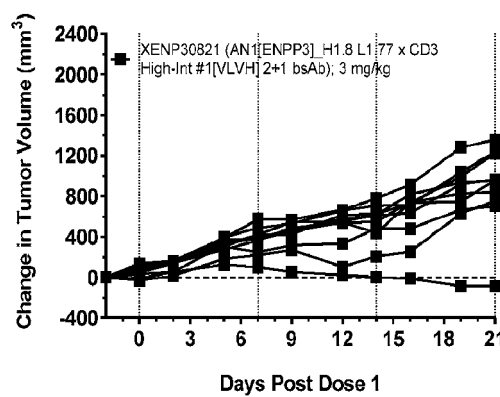


Figure 50E

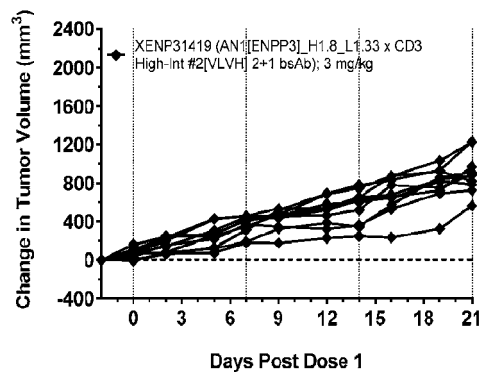


Figure 50F

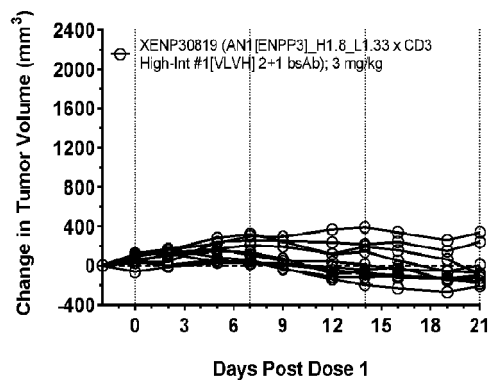


Figure 50G

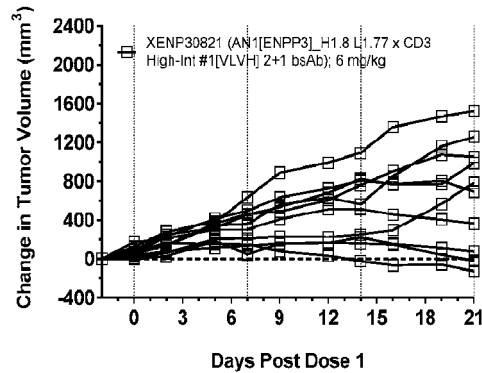


Figure 50H

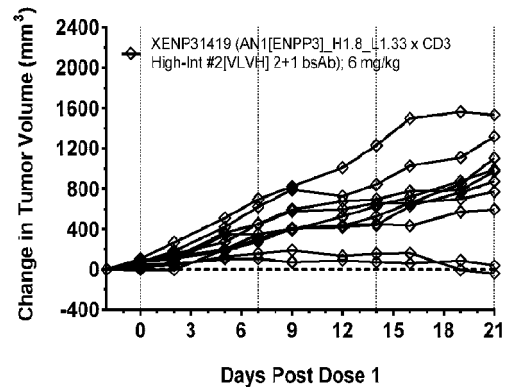


Figure 50I

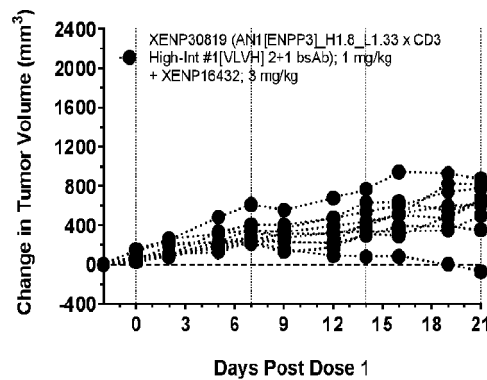


Figure 50J

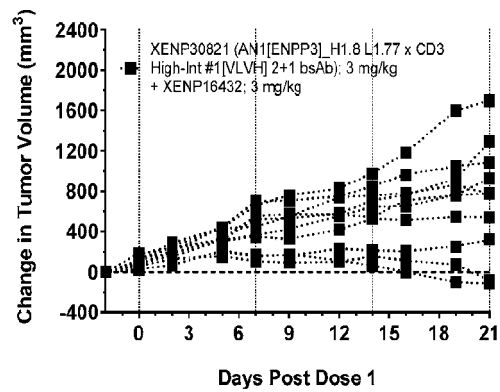


Figure 50K

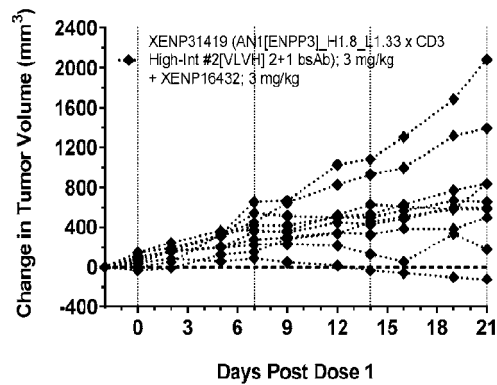


Figure 50L

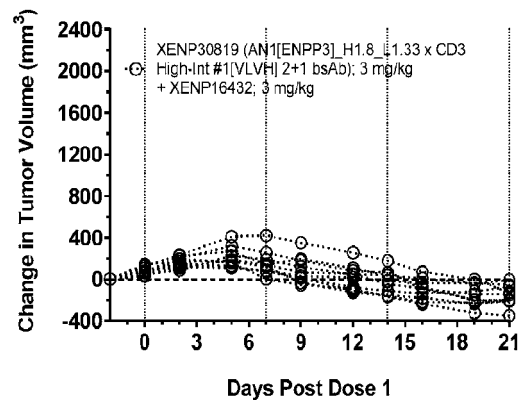


Figure 50M

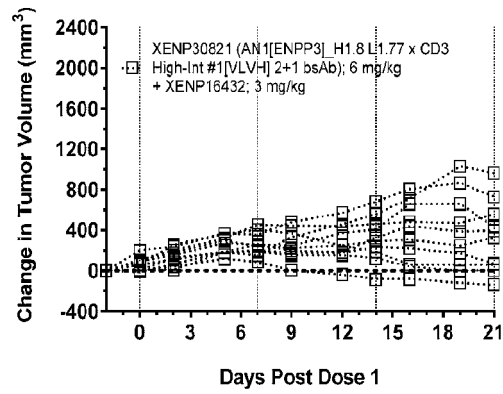


Figure 50N

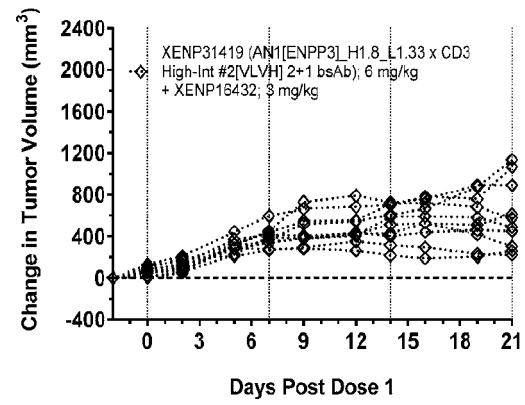


Figure 51A

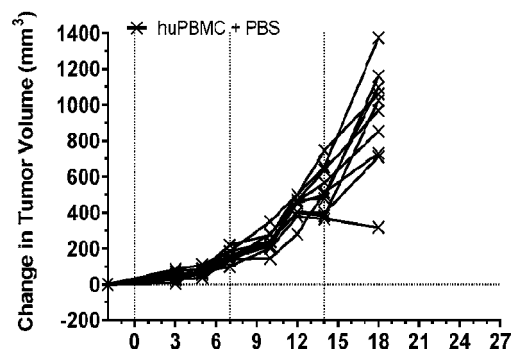


Figure 51B

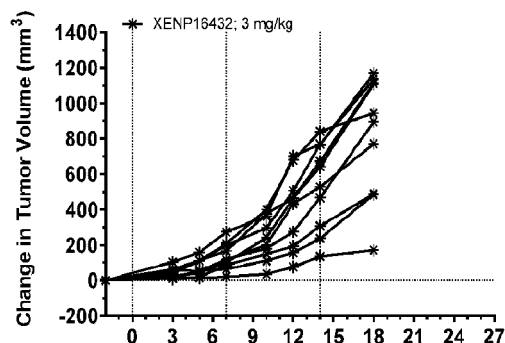


Figure 51C

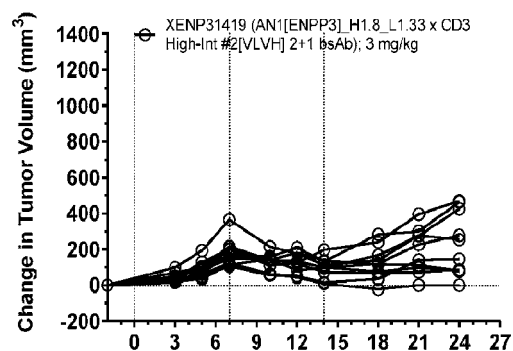


Figure 51D

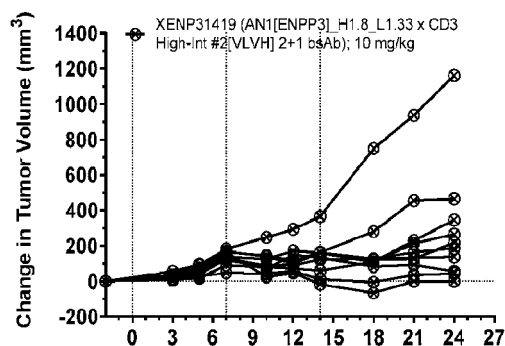


Figure 51E

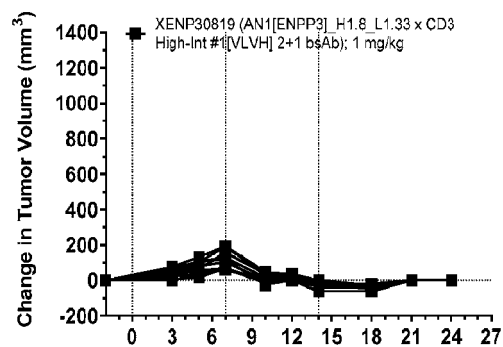


Figure 51F

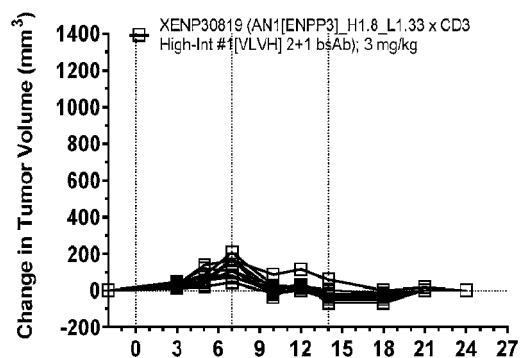


Figure 51G

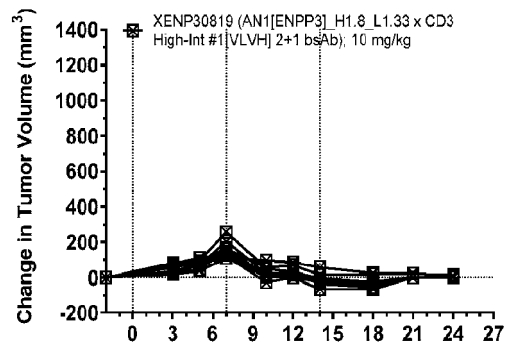


Figure 51H

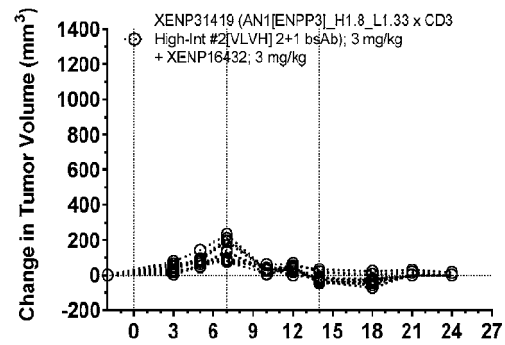


Figure 51I

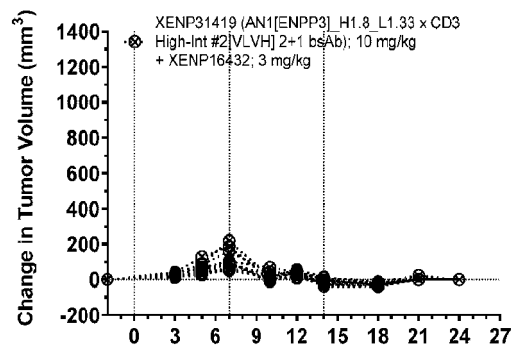


Figure 51J

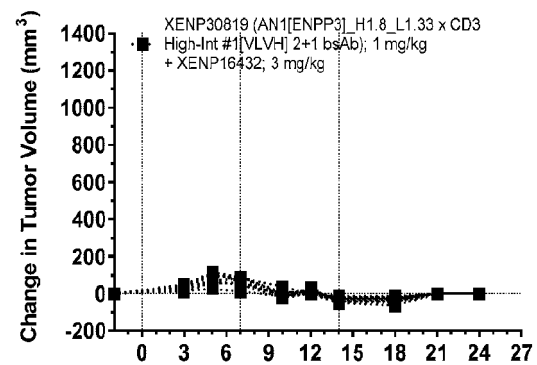


Figure 51K

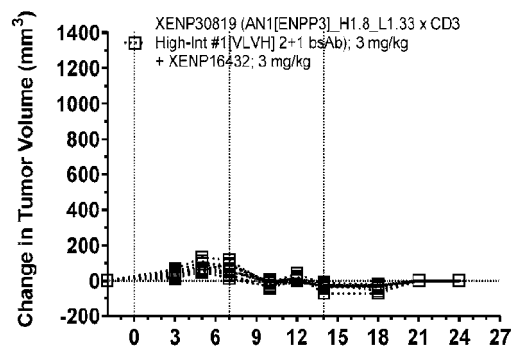
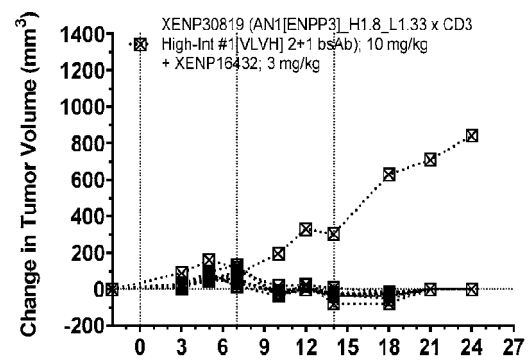


Figure 51L



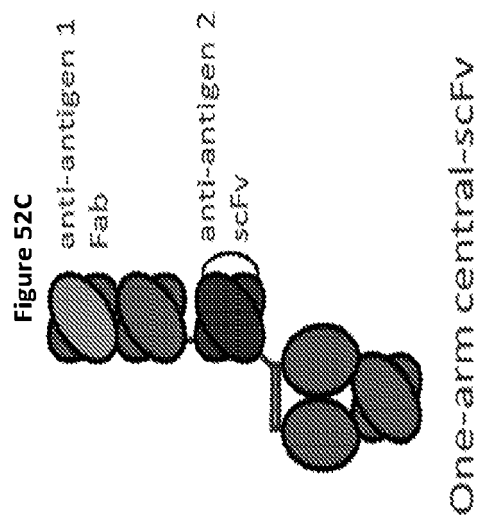
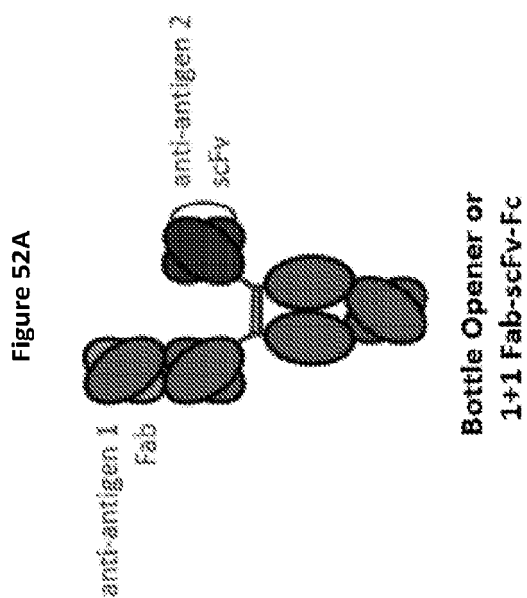
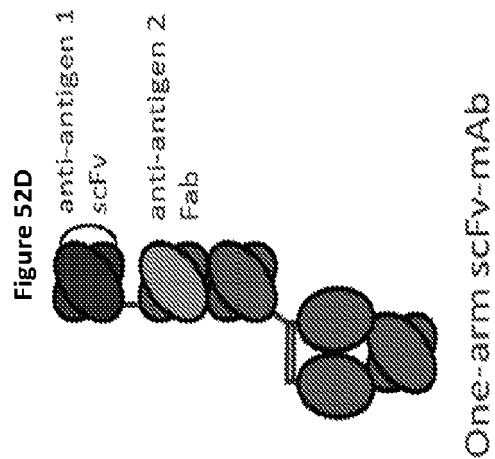
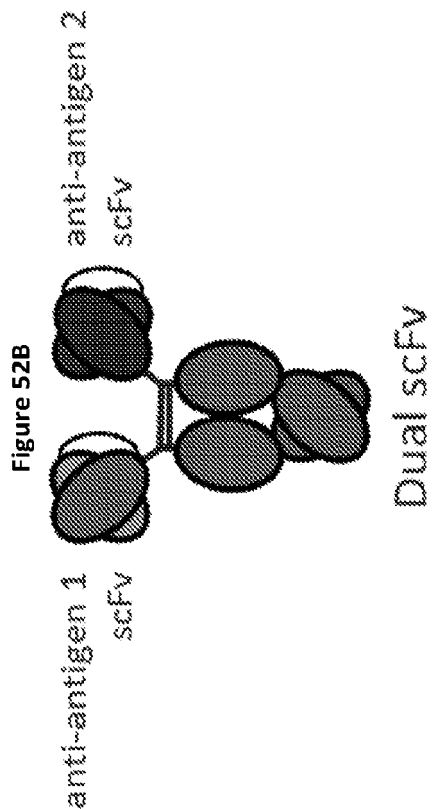


Figure 52F

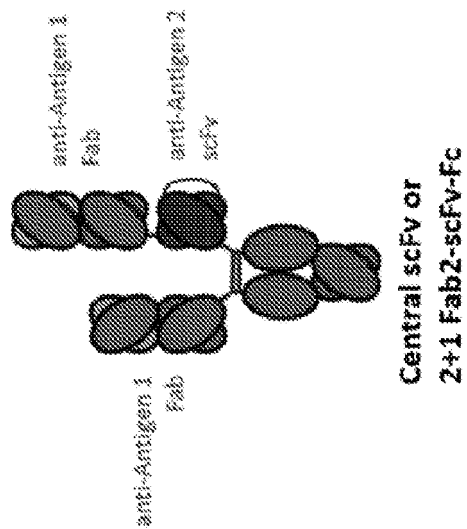


Figure 52H

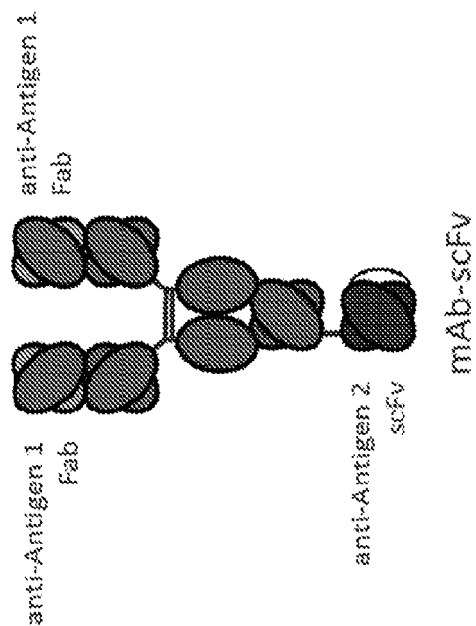


Figure 52E

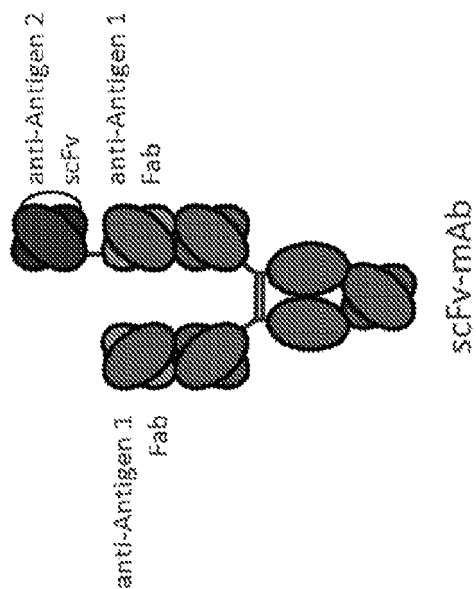
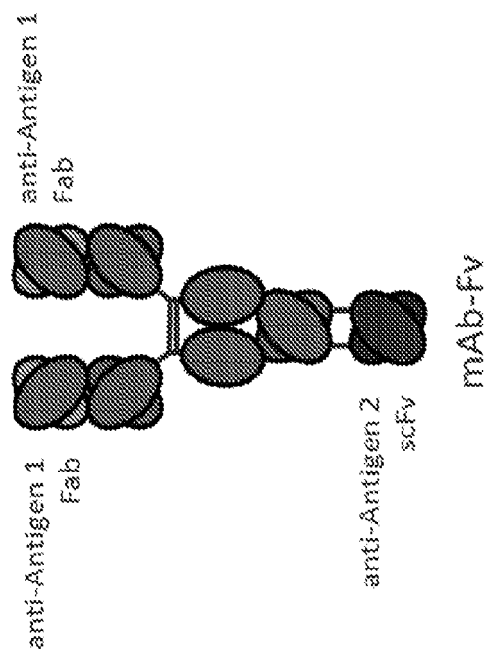


Figure 52G



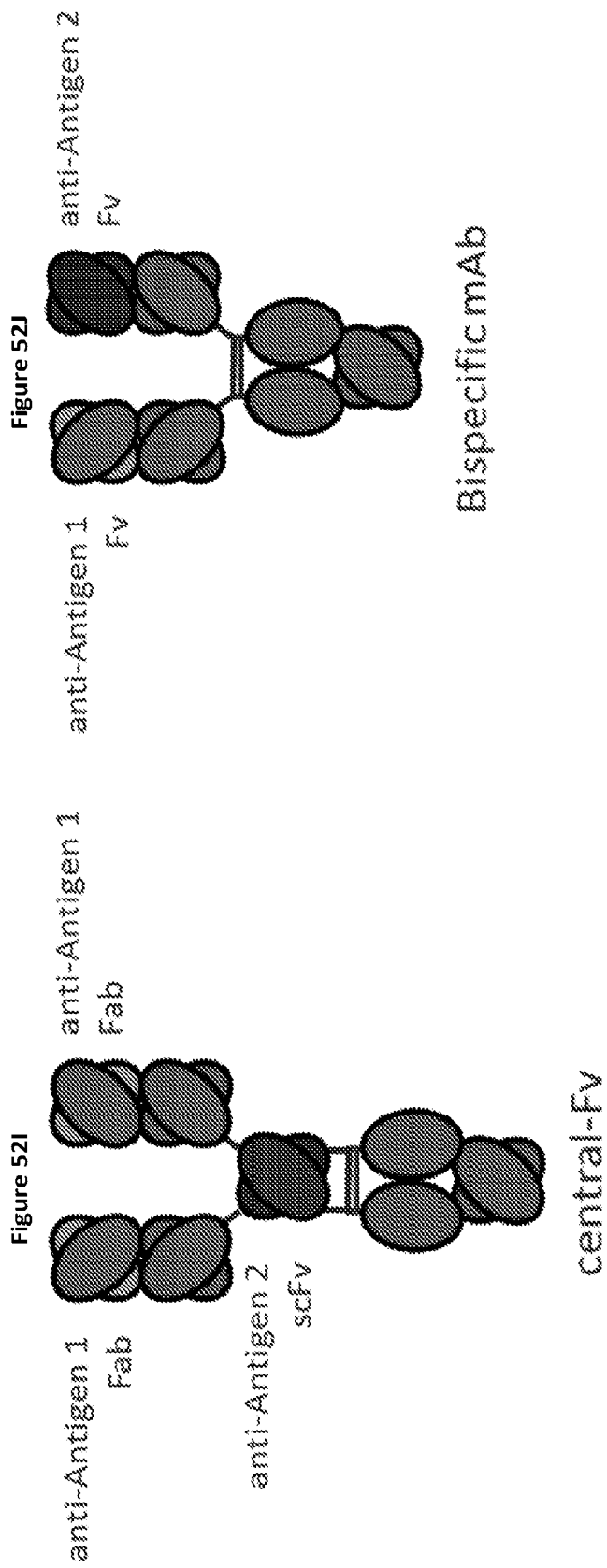


Figure 52K

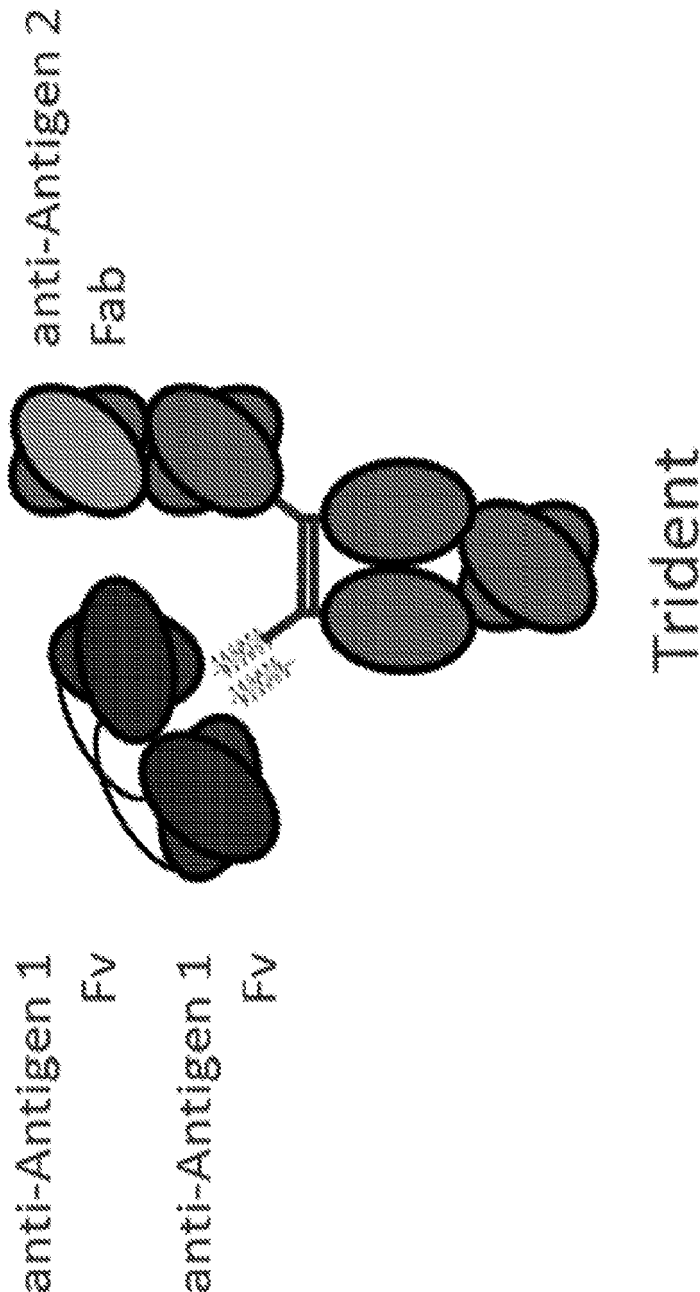


Figure 53

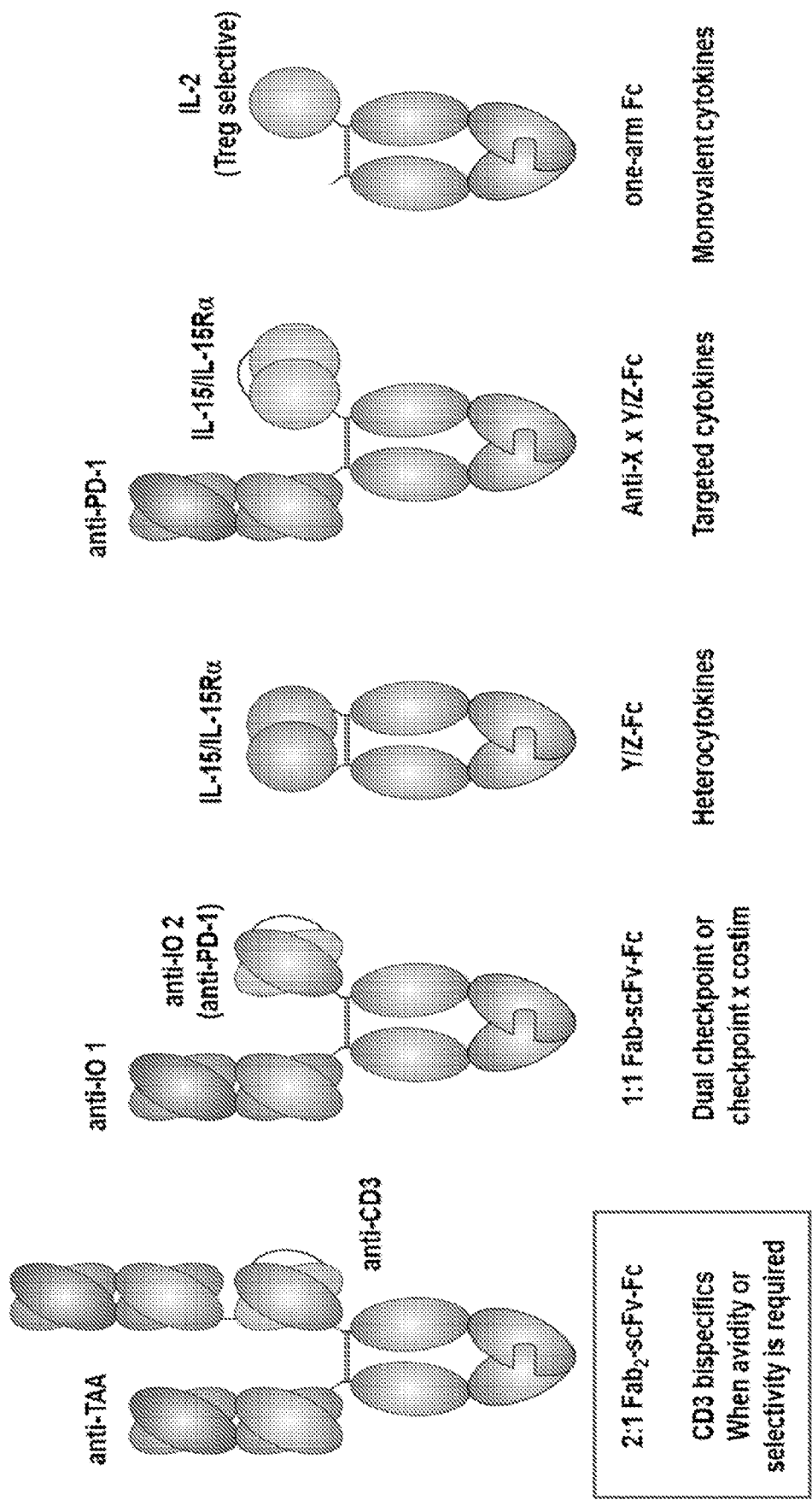


Figure 54

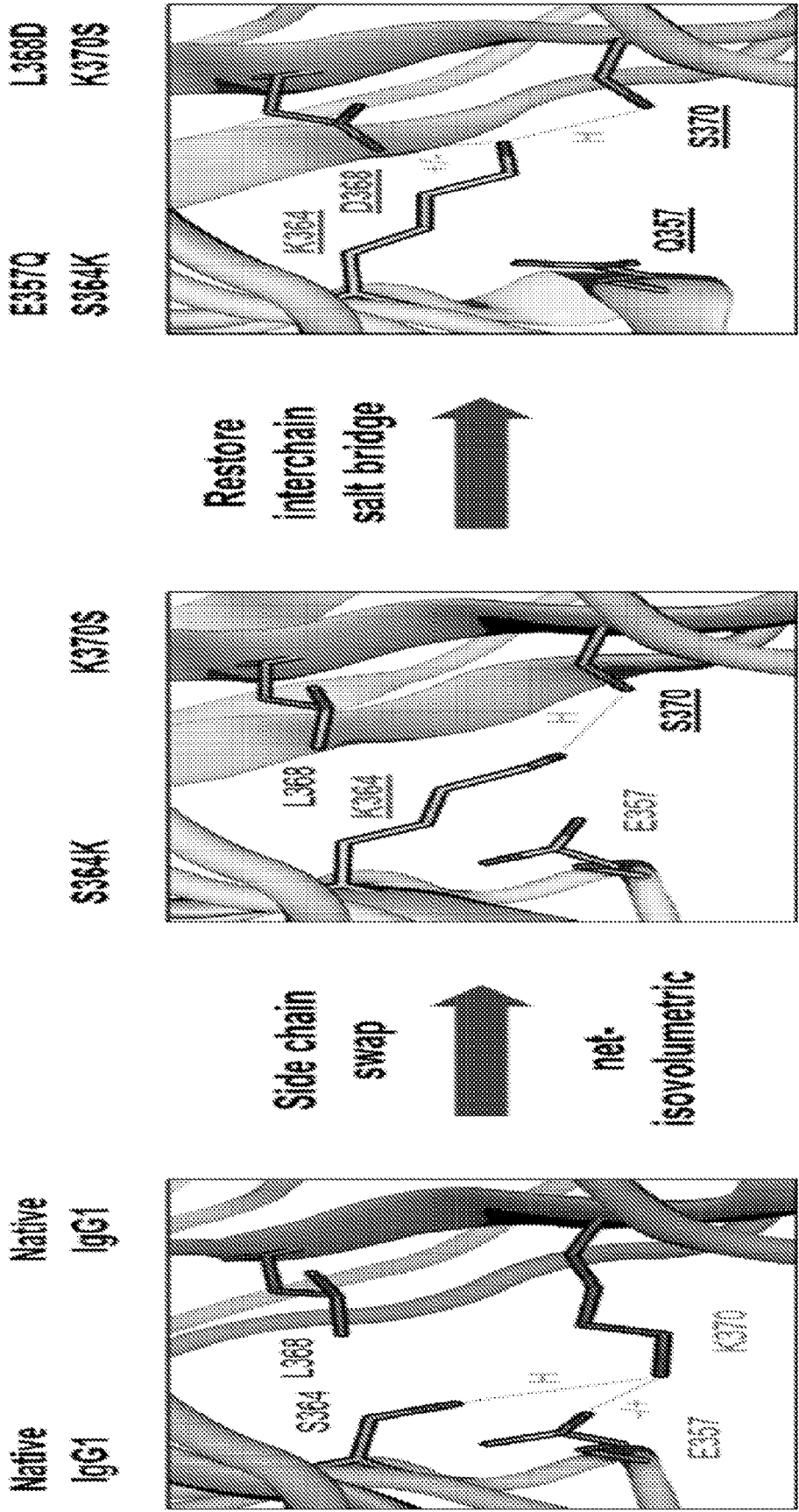
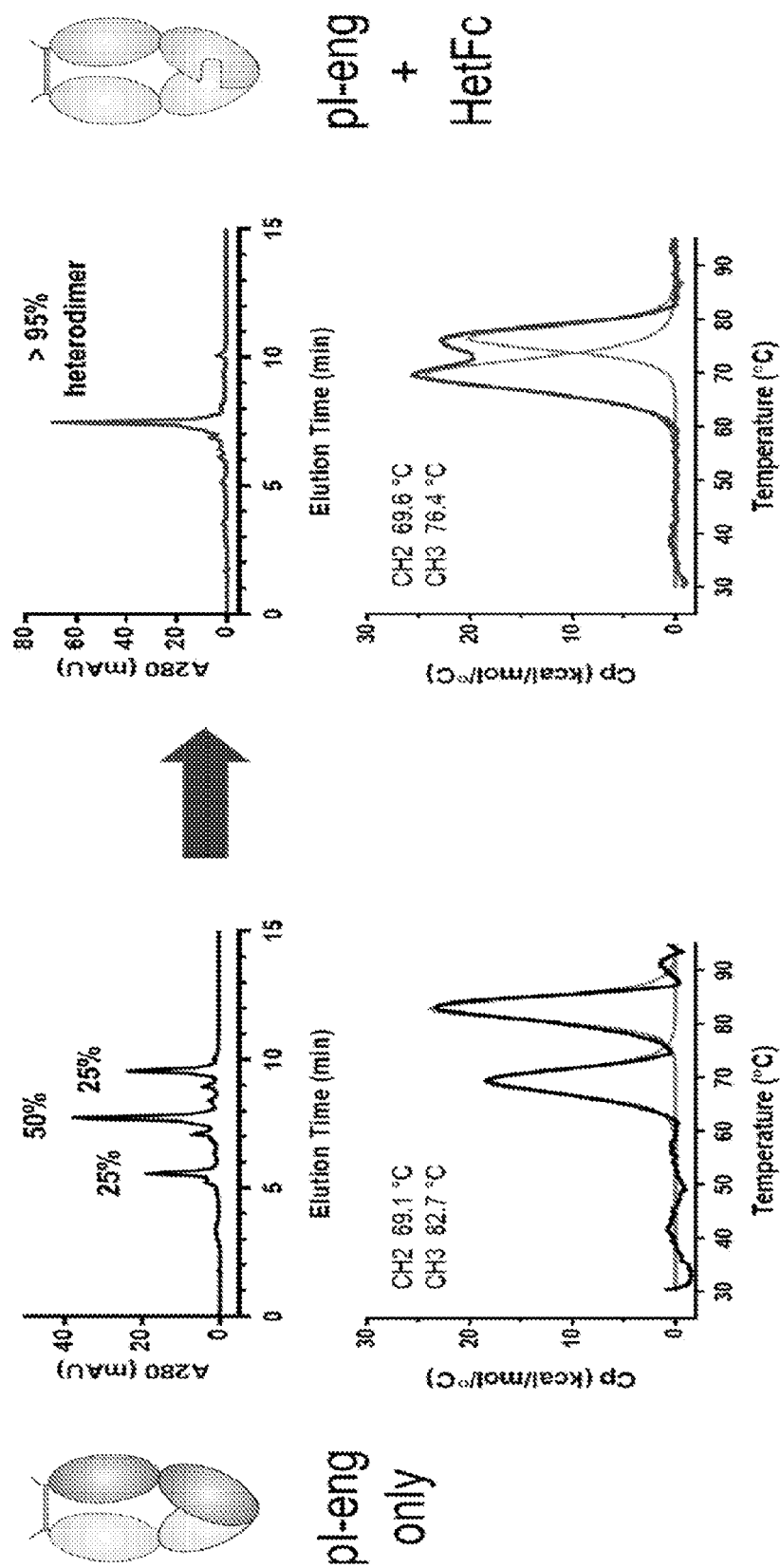


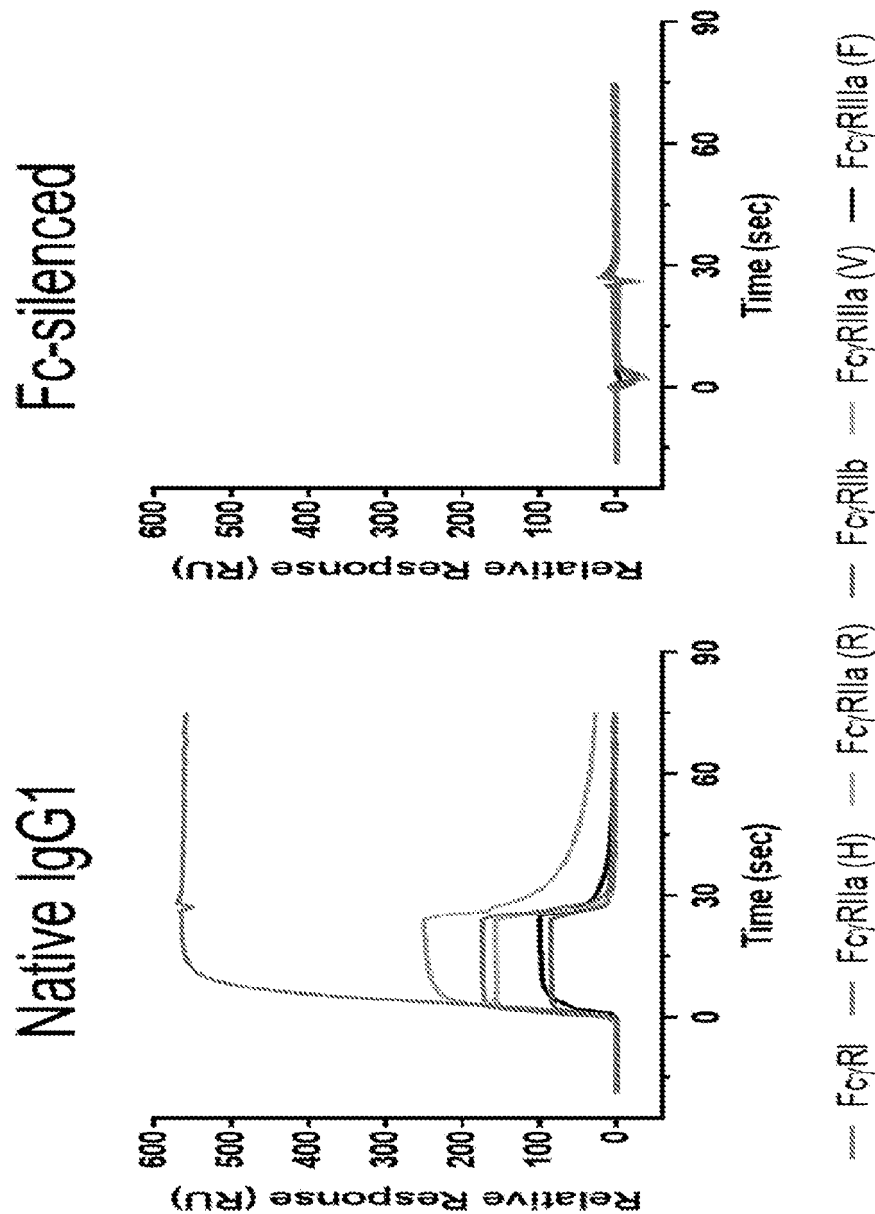
Figure 55

Distribution after standard protein A purification only (analytical IEX)



Thermostability (DSC) of purified protein after a cation exchange purification step

Figure 56



Fc γ R (1 μ M) binding measured by SPR (Biacore 3000), protein A sensor chip/antibody capture format

Figure 57A

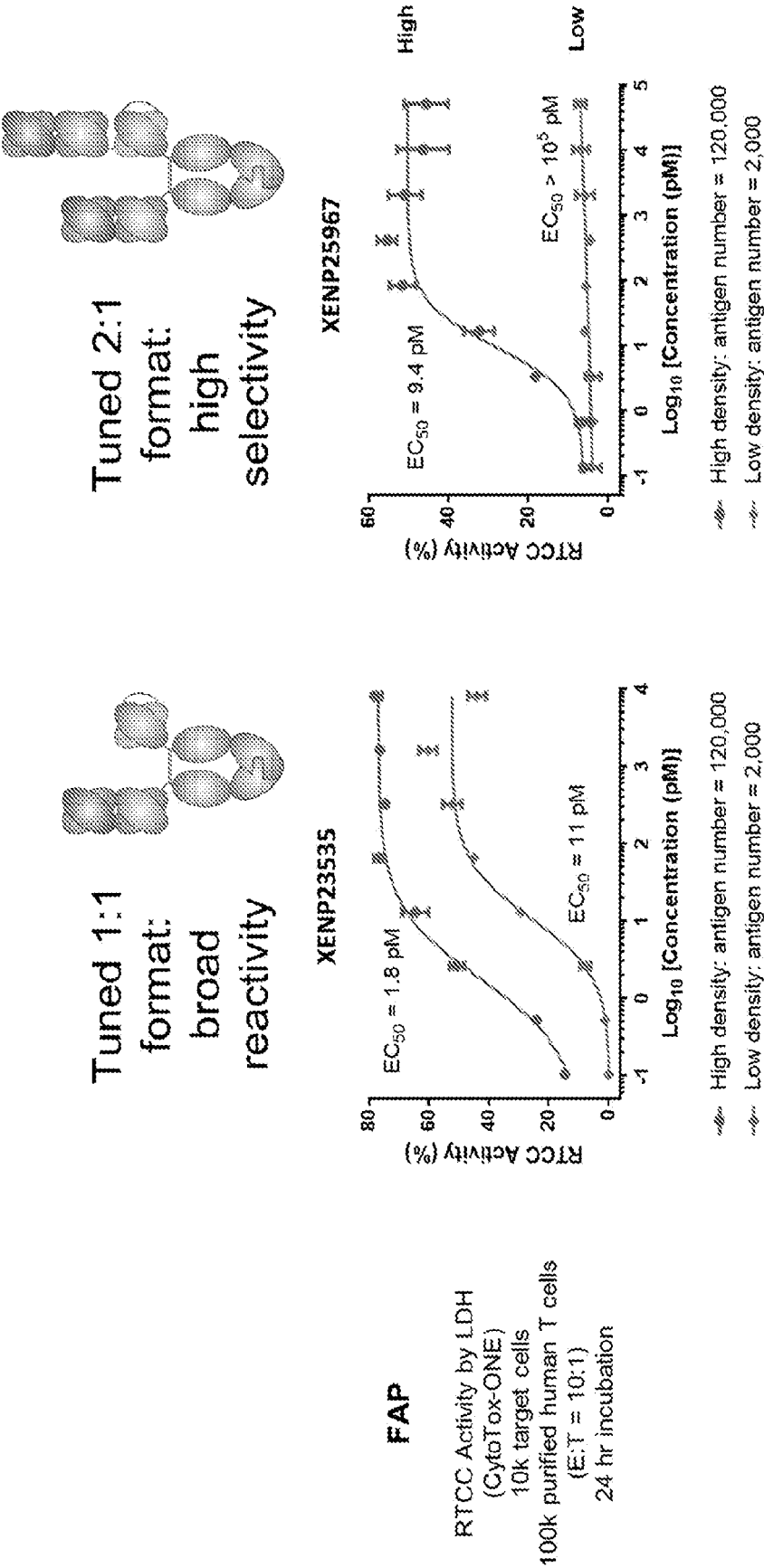


Figure 57B

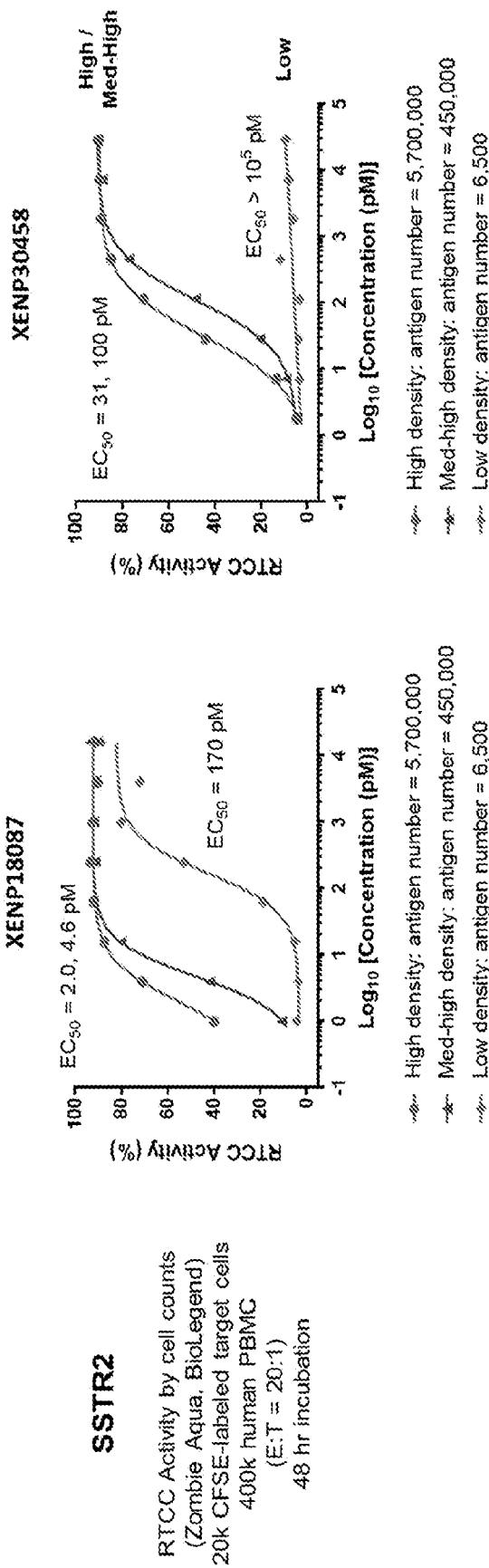


Figure 57C

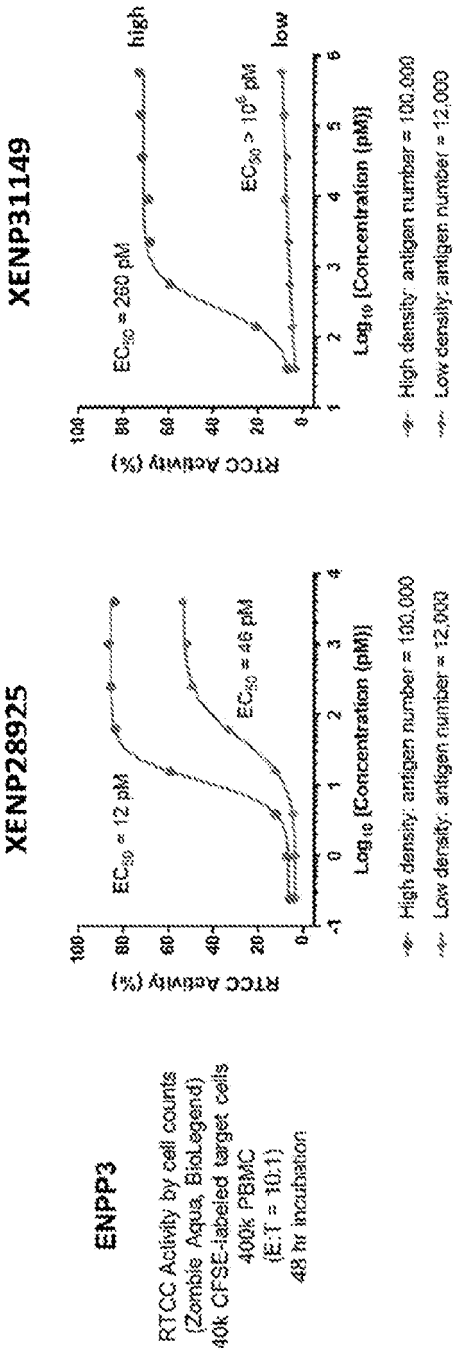
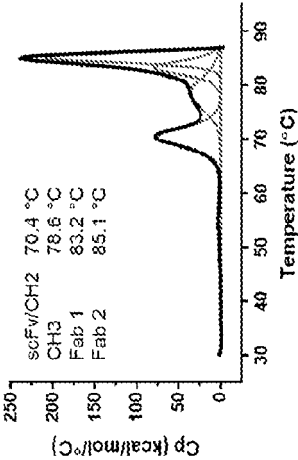


Figure 58

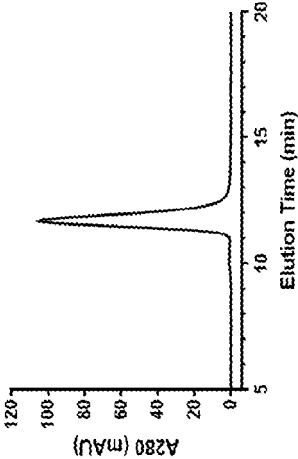
Antibody-like
thermostability (DSC)

pl-eng + HetFc + Fc-silenced



Favorable solution
properties (SEC)

After standard protein A, cation exchange purification steps



High purity
bispecific (IEX)

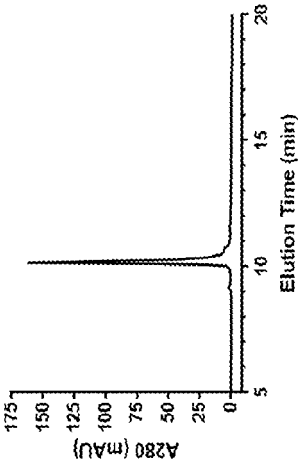


Figure 59

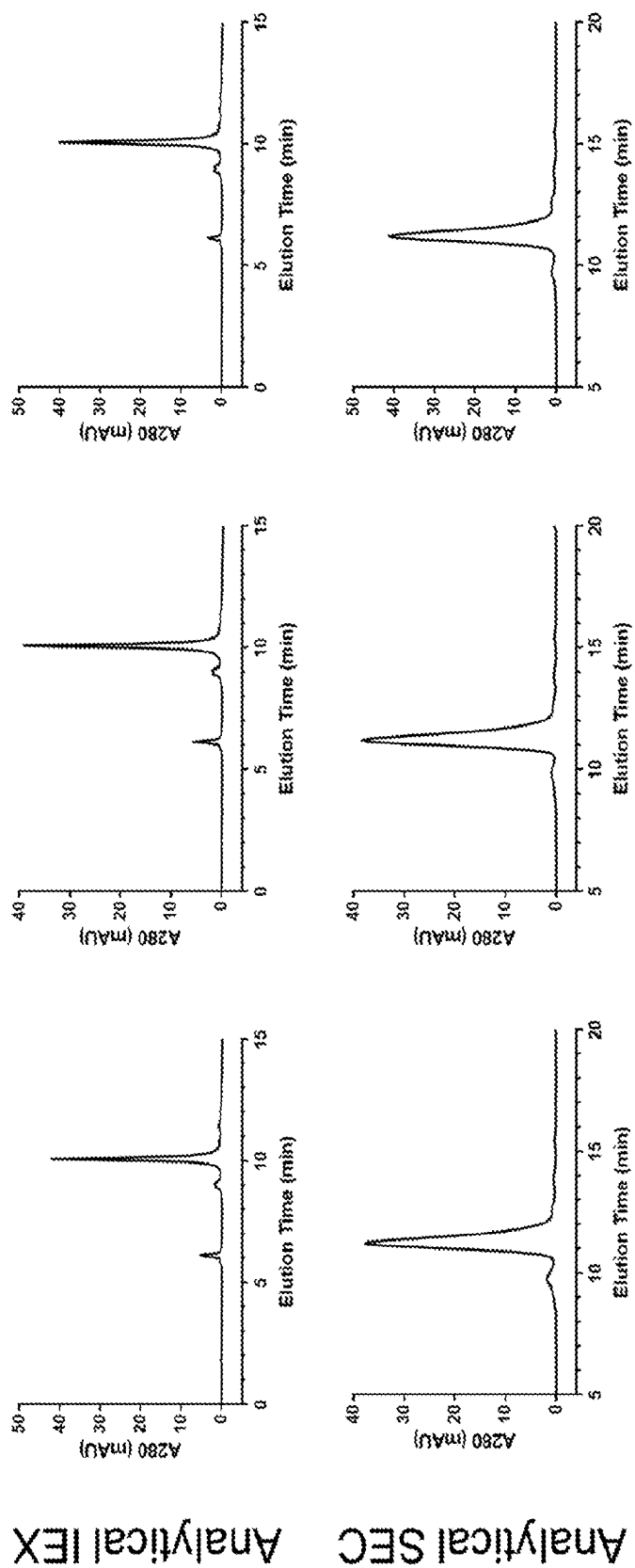
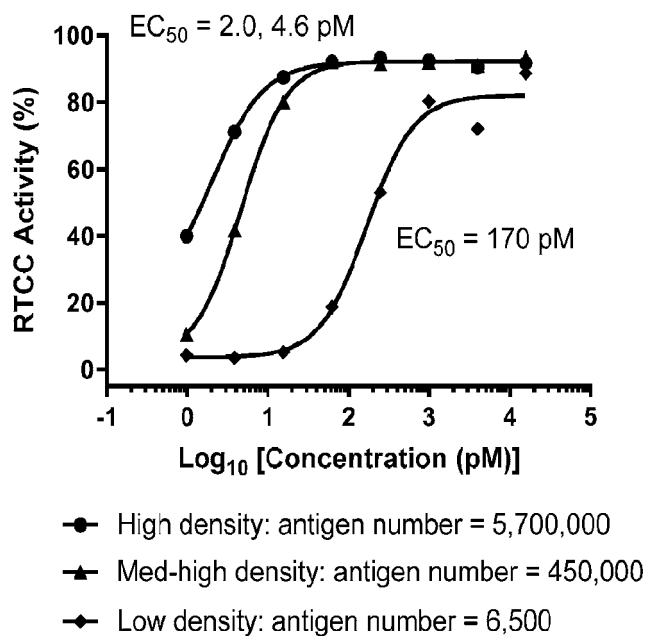


Figure 60

A)

XENP18087



B)

XENP30458

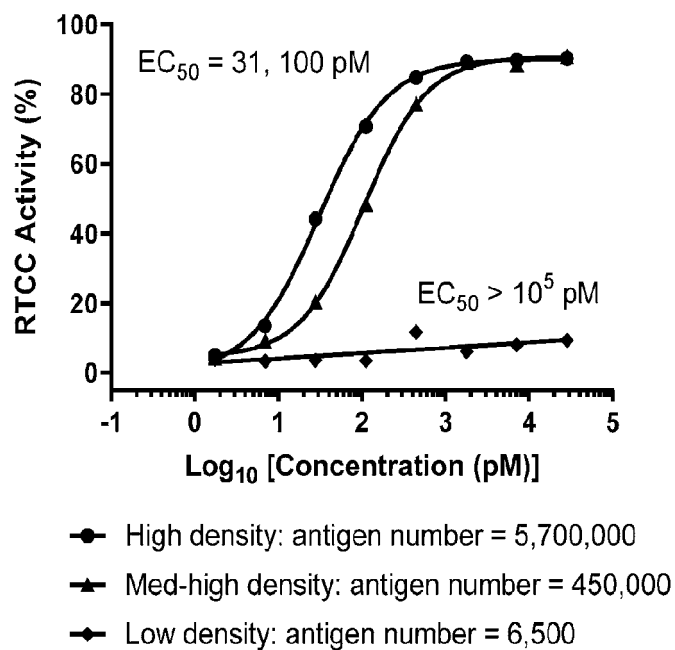


Figure 61

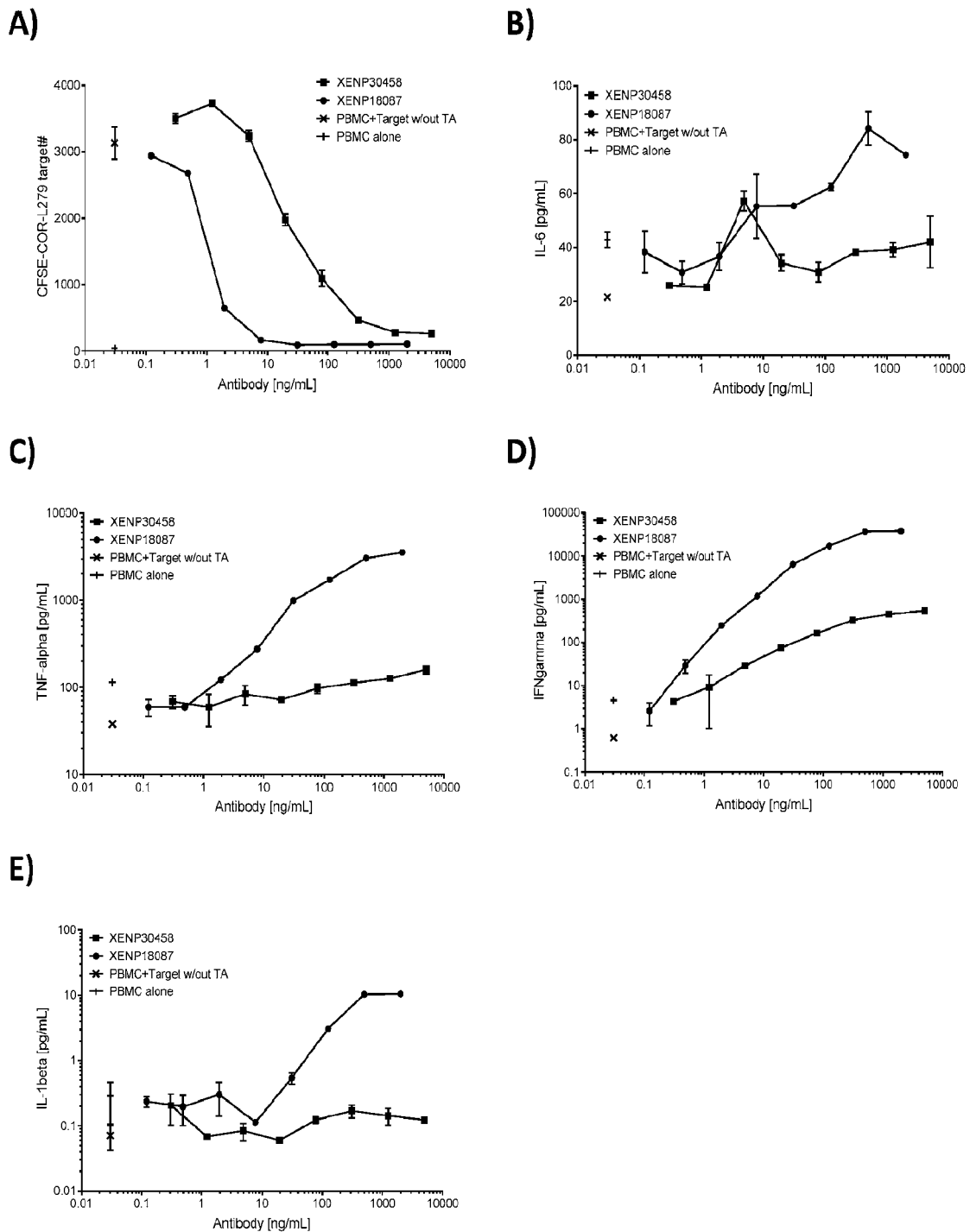


Figure 62A

>XENP18087 [αSSTR2] H1.143 L1.30 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4 Fc(216) IgG1 PVA /S267K pl(-) Isosteric A L368D/K370S-IgG1 C220S/S364K/E357Q

Chain 1 - [αSSTR2]_H1.143_IgG1_PVA_/S267K_pl(-)_Isosteric_A_L368D/K370S (SEQ ID NO: 554)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGMWFRQAPGKLEWVSFISNLGYSIYYADSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARAPYDYDSFDPMDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE
WESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/S364K/E357Q (SEQ ID NO: 555)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNEGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTIVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

Chain 3 - [αSSTR2]_L1.30 (SEQ ID NO: 556)

DIVMTQSPDLSAVSLGERATINCKSSQSLNLSNRNKNYLAWYQQKPDQSPKLLIYWASTRESGVDRFSGSGSGTDF
TLTISSLQAEDVAVYYCKQSYLWTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP23535 [αFAP] H0L0 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - [αFAP]_H0_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 557)

QVQLVQSGAEVKKPGASVKVSCKTSRYTFTETIHWVRQAPGQRLIEWIGGINPNNIGIPNYNQKFKGRVITITVDTAS
TAYMELSSLRSEDVAVYYCARRRIAYGYDEGHAMDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 558)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNEGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTIVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

Chain 3 - [αFAP]_L0 (SEQ ID NO: 559)

DIVMTQSPDLSAVSLGERATINCKSSQSLNLSNRNKNYLAWYQQKPGQPPKLLIFWASTRESGVDRFSGSGFGTDF
TLTISSLQAEDVAVYYCQQYFSYPLTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62B

**>XENP25967 [αFAP] H1L1 Fab-
[αFAP] H1L1 Fab (G4S)2 [αCD3] H1.32 L1.47 scFv(GKPGS)4 (G4S)2 IgG1 PVA /S267K-pl(-)
) Isosteric A L368D/K370S-IgG1 C220S/S364K/E357Q**

Chain 1 - [αFAP]_H1_IgG1_PVA_/S267K-pl(-)_Isosteric_A_L368D/K370S (SEQ ID NO: 560)

EVQLLES^{GGGLVQPGGSLRL}SCAASGFTFS^{SYAMSWVRQAPGKGLEWVSGISGSGG}STYYADSVKGRFTISRDN^{SKNTLYLQ}
MNSLRAEDTAVYYCAKISFY^{PGGTYFDYWGQGLTLTVSS}/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT^{SVWN}
SGALTSGVHTFPAVLQSSGLYSLSSVTV^{PPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL}
FPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD^{WLN}GEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD^{GQ}PENNYKTTTPVLDSDGSFFL
YSKLTVDKSRWEQGDV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αFAP]_H1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_(G4S)2_IgG1_C220S/S364K/E357Q (SEQ ID NO: 561)

EVQLLES^{GGGLVQPGGSLRL}SCAASGFTFS^{SYAMSWVRQAPGKGLEWVSGISGSGG}STYYADSVKGRFTISRDN^{SKNTLYLQ}
MNSLRAEDTAVYYCAKISFY^{PGGTYFDYWGQGLTLTVSS}/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT^{SVWN}
SGALTSGVHTFPAVLQSSGLYSLSSVTV^{PPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/}GGGSGGGGS/EVQLVESGG
GLVQPGGSLRLSCAASGFTFS^{TYAMNWVRQAPGKGLEWVGRI}RSKANNYATYYADSVKGRFTISRDD^{SKNTLYLQ}MNSLRAE
DTAVYYCVRHGNFGDSYVSWFAYWGQGLTLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEP^{SLTVSPGGTVTLT}CGSST
GAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSL^{LGKAA}LTI^{SGAQ}PEDEADYYCALWYSNHWVFGG^{TKLTV}
L/GGGSGGGGS/KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQD^{WLN}GEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ^{MTKNQVKLTCLV}KGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 3 - [αFAP]_L1 (SEQ ID NO: 562)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYL^{NWYQKPGKAPKLLIYAASSLQ}SGVPSR^{FS}SGSGSGTDFTLT^{TISS}LQPED
FATYYCQ^{QSYSSPYTFGGGTKLEIK}/RTVAAPSVFIFPPSDEQLKSGTASV^{VCLLNNFY}PREAKVQW^{KVDNALQSGNSQ}ESV
TEQDSKDS^{TYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR}GEC

**>XENP28925 [αENPP3] H1.8 L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A /PVA_/S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA_/S267K/S364K/E357Q**

Chain 1 - [αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 563)

EVQLVES^{GGGLVQPGGSLRL}SCAASGFAFSNYGMSWVRQAPGQ^{RLEWVS}YISSGGGTTYYLDSVTGRFTISRDN^{AKNSLYLQ}
MNSLRAEDTAVYYCARHRRVYYGY^{FDYWGQGLTLTVSS}/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT^{SVWN}
SGALTSGVHTFPAVLQSSGLYSLSSVTV^{PPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL}
FPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD^{WLN}GEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD^{GQ}PENNYKTTTPVLDSDGSFFL
YSKLTVDKSRWEQGDV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 564)

EVQLVES^{GGGLVQPGGSLRL}SCAASGFTFS^{TYAMNWVRQAPGKGLEWVGRI}RSKYN^{NYATYYADSVKGRFTISRDD}SKNTLY
LQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEP^{SLTVSPGGT}
VTLT^{CGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSL}LGKAA^{LTI}SGAQ^{PEDEADYYCALWY}SNHWV
FGGG^{TKLTVL}/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQD^{WLN}GEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ^{MTKNQVKLTCLV}
KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 3 - [αENPP3]_L1 (SEQ ID NO: 565)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^{WYQKPDQSPKLLIKYASESISGIPSRFS}SGSGSGTDFTLT^{INSLEAED}
AATYYCQ^{QNSNWPYTFGGGTKLEIK}/RTVAAPSVFIFPPSDEQLKSGTASV^{VCLLNNFY}PREAKVQW^{KVDNALQSGNSQ}ESV
TEQDSKDS^{TYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR}GEC

Figure 62C

>XENP30458 [α SSTR2] H1.24 L1.30 Fab-
 [α SSTR2] H1.24 L1.30 Fab (G4S)2 [α CD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-
 Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - [α SSTR2]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 566)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGM~~AWFRQAPGKGLEWVSFISNLA~~YSIIYADSVKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFYPM~~DYWGQ~~GLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
 CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIAVE
 WESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGQDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 -

[α SSTR2]_H1.24_[α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
 (SEQ ID NO: 567)

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGM~~AWFRQAPGKGLEWVSFISNLA~~YSIIYADSVKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFYPM~~DYWGQ~~GLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/~~GGGG~~
~~SGGGGS~~/EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
 TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/~~GKPGSGKPGSGKPGSGKPGS~~/
 QAVVTQEPSTLVSPGGTVTLT~~CGSS~~TGAVTTSNYANWVQKPGKSPRGLIGGTNKR~~APGV~~PARFSGSLLGKKAALTI
 SGAQPEDEADYYCALWYSNHWF~~GGG~~TKLTVL/~~GGGGSGGGGS~~/KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
 TPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
 EKTISKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYP~~SDIAVE~~WESNGQPPENNYKTTTPVLDSDGSFFLYSK
 LTVDKSRWQQGNV~~FSCSVL~~HEALHSHYTQKSLSLSPGK

Chain 3 - [α SSTR2]_L1.30 (SEQ ID NO: 568)

DIVMTQSPDSLAVSLGERATINCKSSQSLN~~SRNRK~~NYLAWYQQKPDQSPKLLIYWASTRESGV~~PD~~DRFSGSGSGTDF
 TLTIS~~SL~~QAEDVAVYYCKQSY~~YL~~WTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
 KVDNALQSGNSQESVTEQDSKDS~~TY~~SLSTLTLSKADY~~E~~KKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62D

>**XENP31149 [αENPP3] H1.8 L1.33 Fab-**
[αENPP3] H1.8 L1.33 CH1 (G4S)2 [αCD3] L1.47 H1.89 scFv(GKPGS)4-IgG1 pl(-
) Isosteric A /PVA /S267K/L368D/K370S-Fc(222) IgG1 C220S/PVA /S267K/S364K/E357Q

Chain 1 - [αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 569)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTITYYLDSTGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 570)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTITYYLDSTGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GGGGS
 GGGGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGG
 KAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGS
 LRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTA
 VYYCVRHGNFGDEYVSWFAYWGQGTLLTVSS/GGGGSGGGGS/KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
 PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSREMQTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - [αENPP3]_L1.33 (SEQ ID NO: 571)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHYYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 63

[α SSTR2] H1.24 L1.30

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYGM ~~AWFRQAPGKGLEW~~ VSFISNLAYSIIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARAPYDYDSFYPM ~~DYWGQGTLVTVSS~~	572
vhCDR1	<u>DYGM</u>	573
vhCDR2	<u>FISNLAYSIIYYADSVKG</u>	574
vhCDR3	<u>APYDYDSFYPM</u>	575
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSL ~~LNSRNRKNYLAWYQQKPD~~ QSPKLLIYWASTRESGVPDRFSGSGSGTDFTLT ~~ISSLQAEDVAVYYC~~ KQSY ~~YLWTFGGGTKVEIK~~	576
vlCDR1	<u>KSSQSLNSRNRKNYLA</u>	577
vlCDR2	<u>WASTRES</u>	578
vlCDR3	<u>KQSYYLWT</u>	579