

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>
pl-ISO(-)	I199T/N203D/K274Q/R355Q/N384S/K392N/N397M/Q419E/K447_
pl_ISO(-)-Fc only	K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_
pl_(-)_isosteric_A	N208D/Q295E/N384D/Q418E/N421D
pl_(-)_isosteric A-Fc only	Q295E/N384D/Q418E/N421D
pl_(-)_isosteric_B	N208D/Q295E/Q418E/N421D
pl_(-)_isosteric_B-Fc only	Q295E/Q418E/N421D
pl_ISO(+RR)	Q196K/I199T/P217R/P228R/N276K
pl_ISO(+RR)-Fc only	P217R/P228R/N276K
pl_ISO(+)	Q196K/I199T/N276K
pl_ISO(+)-Fc only	N276K
pl_(+)_isosteric_A	E269Q/E272Q/E283Q/E357Q
pl_(+)_isosteric_B	E269Q/E272Q/E283Q
pl_(+)_isosteric_E269Q/E272Q	E269Q/E272Q
pl_(+)_isosteric_E269Q/E283Q	E269Q/E283Q
pl_(+)_isosteric_E272Q/E283Q	E272Q/E283Q
pl_(+)_isosteric_E269Q	E269Q

Figure 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 pI 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	GGGGSGGGSGGGGS	15	0	
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	
+B	GKGGSGKGGSGKGGGS	15	+3	
+C	GGKSGGKSGGGKGS	15	+3	
+D	GGKSGGKSGGGKGS	15	+3	
+E	GKKGSGKKGSGKGKS	15	+6	
+F	GGKSGGKSGKGGGS	15	+3	
+G	GKPGSGKPGSGKPGS	15	+3	
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	
+I	GKKGSGKKGSGKGSGKGKS	20	+8	

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 20	GGGGSGGGSGGGSGGGGS	20	0	
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	
-B	GEGSGEGSGEGGS	15	-3	
-C	GEGSGEGSGEGGS	15	-3	
-D	GGGSGGGESGGGES	15	-3	
-E	GEGSGEGSGEGES	15	-6	
-F	GGGSGGEGSGEGGS	15	-3	
-G	GEGSGEGSGEGSGEGES	20	-8	

Additional scFv Linkers

GGGGSGGGSGGGGS	SEQ ID NO:XXX
GGGGSGGGSGGGSGGGGS	SEQ ID NO:XXX
GSTSGSGKPGSGEGSTKG	SEQ ID NO:XXX
PRGASKSGSASQTGSAPGS	SEQ ID NO:XXX
GTAAAGAGAAGGAAAGAAG	SEQ ID NO:XXX
GTSGSSGSGSGSGSGGGG	SEQ ID NO:XXX
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:XXX

Figure 6

Useful domain linkers

<u>Name</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
(GGGGS) ₁ or GGGGS	GGGGS	
(GGGGS) ₂	GGGGSGGGS	
(GGGGS) ₃	GGGGSGGGSGGGS	
(GGGGS) ₄	GGGGSGGGSGGGSGGGS	
(GGGGS) ₅	GGGGSGGGSGGGSGGGSGGGS	
(GGGGS) ₆	GGGGSGGGSGGGSGGGSGGGSGGGS	
(GGGGS) ₇	GGGGSGGGSGGGSGGGSGGGSGGGSGGGS	
(GGGGA) ₁ or GGGGA	GGGGA	
(GGGGA) ₂	GGGAGGGGA	
(GGGGA) ₃	GGGAGGGAGGGGA	
(GGGGA) ₄	GGGAGGGAGGGAGGGGA	
(GGGGA) ₅	GGGAGGGAGGGAGGGAGGGGA	
(GGGGA) ₆	GGGAGGGAGGGAGGGAGGGAGGGGA	
(GGGGA) ₇	GGGAGGGAGGGAGGGAGGGAGGGAGGGGA	
30AA-linker	DPALVHQRPAAPPGGGSGGGSGGGSGGG	
(GKPGS) ₁ or GKPGS	GKPGS	
(GKPGS) ₅	GKPGSGKPGSGKPGSGKPGSGKPGS	
(GKPGS) ₆	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	
(GGGES) ₁ or GGGES	GGGES	
"half hinge"	KTHTCPPCP	
"full hinge C220S variant"	EPKSSDKTHTCPPCP	
"flex half hinge"	GGGSGGGSGTHTCPPCP	
"charged half hinge1"	GKPGSGKPGSKTHTCPPCP	
"charged half hinge2"	GKPGSKTHTCPPCP	

Figure 7A

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 7B

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVFSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLEVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVFSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVFSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

Figure 7C

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVNHNKPSDTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDPEVQ
FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDQGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVM
HEALHNHYTQKSLSLSPGK

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

ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVNHNKPSDTKVDKTVKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMH
EALHNHYTQKSLSLSPGK

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

ERKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 7D

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

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVQF
NWWYDGVGEVHNAKTKPREEEFNSTFRVVSFLTIVHQQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPMLDSDGSEFLYSKLTVDKSRWEQGDVFSQVMH
EALHNHYTQKSLSLSPGK

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

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVQFNWYDGVGEVHNAKTKPREEQF
NSTFRVVSFLTIVHQQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPNENYKTTTPMLDSDGSEFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYDGVGEVHNAKTKPREEEYNSTYRVVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSEFLYSKLTVDKSRWEQGDVFSQ
VLHEALHSHYTQKSLSLSPGK

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

EPKSSDKTHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYDGVGEVHNAKTKPRE
EQYNSTYRVVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSEFLYSKLTVDKSRWQQGNVFSQVLHEALHSHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKEPKSCDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYDGVGEVHNAKTKPREEQYNSTYRVVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSEFLYSKLTVDKSRWQQGNVFSQ
VMHEALHNHYTQKSLSLSPGK

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

ERKSSDKTHTCPCPPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYDGVGEVHNAKTKPRE
EQYNSTYRVVSVLTIVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSEFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

Figure 8A

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPSSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 8B

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

Figure 8C

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSS
VLHEALHSHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

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

ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

Figure 9

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

RTVAAPSVFTIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSENRGEC

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

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 10A

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGLTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QAVVTQEP</u> SLTVSPG GTVTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAFGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTVL	XXX
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGLTVTVSS	XXX
vhCDR1	<u>TYAMN</u>	XXX
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	XXX
vhCDR3	<u>HGNFGDSYVSWFAY</u>	XXX
Variable Light (vl) Domain	QAVVTQEP ~~SLTV~~ SPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAFGV</u> PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTV L	XXX
vlCDR1	<u>GSSTGAVTTSNYAN</u>	XXX
vlCDR2	<u>GTNKRAFG</u>	XXX
vlCDR3	<u>ALWYSNHWV</u>	XXX
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	XXX

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGLTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QAVVTQEP</u> SLTVSPG GTVTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAFGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTVL	XXX
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGLTVTVSS	XXX
vhCDR1	<u>TYAMN</u>	XXX
vhCDR2	<u>RIRSKANNYATYYADSVKG</u>	XXX
vhCDR3	<u>HGNFGDSYVSWFAY</u>	XXX
Variable Light (vl) Domain	QAVVTQEP ~~SLTV~~ SPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN <u>KRAFGV</u> PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTV L	XXX
vlCDR1	<u>GSSTGAVTTSNYAN</u>	XXX
vlCDR2	<u>GTNKRAFG</u>	XXX
vlCDR3	<u>ALWYSNHWV</u>	XXX
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	XXX

Figure 10B

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSTVSPG GTVTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	XXX
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGLTVTVSS	XXX
vhCDR1	TYAMN	XXX
vhCDR2	RIRSKYNNYATYYADSVKG	XXX
vhCDR3	HGNFGDEYVSWFAY	XXX
Variable Light (vl) Domain	QAVVTQEPSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	XXX
vlCDR1	GSSTGAVTTSNYAN	XXX
vlCDR2	GTNKRAP	XXX
vlCDR3	ALWYSNHWV	XXX
Linker	GKPGSGKPGSGKPGSGKPGS	XXX

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSTVSPG GTVTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	XXX
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS	XXX
vhCDR1	TYAMN	XXX
vhCDR2	RIRSKYNNYATYYADSVKG	XXX
vhCDR3	HGNFGDPYVSWFAY	XXX
Variable Light (vl) Domain	QAVVTQEPSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	XXX
vlCDR1	GSSTGAVTTSNYAN	XXX
vlCDR2	GTNKRAP	XXX
vlCDR3	ALWYSNHWV	XXX
Linker	GKPGSGKPGSGKPGSGKPGS	XXX

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Figure 10C

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRIISK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPG GTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRIISK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGLTVTVSS	
vhCDR1	TYAMN	
vhCDR2	RIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFDY	
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTIVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vlCDR1	GSSTGAVTTSNYAN	
vlCDR2	GTNKRAP	
vlCDR3	ALWYSNHWV	
Linker	GKPGSGKPGSGKPGSGKPGS	

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVGRIISK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPG GTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVGRIISK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTVTVSS	
vhCDR1	TYAMS	
vhCDR2	RIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFAY	
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTIVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vlCDR1	GSSTGAVTTSNYAN	
vlCDR2	GTNKRAP	
vlCDR3	ALWYSNHWV	
Linker	GKPGSGKPGSGKPGSGKPGS	

Figure 10D

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS	
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vlCDR1	GSSTGAVTTSNYAN	
vlCDR2	GTNKRAP	
vlCDR3	ALWYSNHWV	
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTVTVSS	
vhCDR1	TYAMN	
vhCDR2	RIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFAY	
Linker	GKPGSGKPGSGKPGSGKPGS	

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS	
Variable Light (vl) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vlCDR1	GSSTGAVTTSNYAN	
vlCDR2	GTNKRAP	
vlCDR3	ALWYSNHWV	
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSK ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTVTVSS	
vhCDR1	TYAMN	
vhCDR2	RIRSKANNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFAY	
Linker	GKPGSGKPGSGKPGSGKPGS	

Figure 10E

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGLTVTVSS	
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vCDR1	GSSTGAVTTSNYAN	
vCDR2	GTNKRAP	
vCDR3	ALWYSNHWV	
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI RSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGLTVTVSS	
vhCDR1	TYAMN	
vhCDR2	RIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDEYVSWFAY	
Linker	GKPGSGKPGSGKPGSGKPGS	

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGLTVTVSS	
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vCDR1	GSSTGAVTTSNYAN	
vCDR2	GTNKRAP	
vCDR3	ALWYSNHWV	
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI RSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS	
vhCDR1	TYAMN	
vhCDR2	RIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDPYVSWFAY	
Linker	GKPGSGKPGSGKPGSGKPGS	

Figure 10F

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLLTVSS	
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vLCDR1	GSSTGAVTTSNYAN	
vLCDR2	GTNKRAP	
vLCDR3	ALWYSNHWV	
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGTLLTVSS	
vhCDR1	TYAMN	
vhCDR2	RIIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFDY	
Linker	GKPGSGKPGSGKPGSGKPGS	

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMSWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS	
Variable Light (vL) Domain	QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	
vLCDR1	GSSTGAVTTSNYAN	
vLCDR2	GTNKRAP	
vLCDR3	ALWYSNHWV	
Variable Heavy (vH) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGTLLTVSS	
vhCDR1	TYAMS	
vhCDR2	RIIRSKYNNYATYYADSVKG	
vhCDR3	HGNFGDSYVSWFAY	
Linker	GKPGSGKPGSGKPGSGKPGS	

Figure 11A

Human ENPP3 sequence

>sp|O14638

MESTLTLLATEQPVKKNTLKKYKIACIVLLALLVIMSLGLGLGLRLEKQGSCRKKCFDASFRGLENCRCDVACKD
RGDCCWDFEDTCVESTRIWMCNKFRCGETRLEASLSCSDDCLQRKCCADYKSVQGETSWLEENCDAQQSQCP
GFDLPPVILFSDMGFRAEYLYTWDTLMPNINKLKTGCIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII
DNNMYDVNLNKNFSLSSKEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNGSV
PFEERISTLLKWLDL PKAERPRFYTM YFEEDSSGHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCV
NIILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRI RAHNIPHDFFSFNSEIIVRNLS
CRKPDQHF KPYP LTPDL PKRLHYAKNVRIDKVHLFVDQQWLAVRSKSNTCGGGNHGYNNEFRS
MEAI FLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLKVPFYEP
SHAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEETATVKVNL
PFGPRV LQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRVPP
SESQKCSFYLDKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATER
NGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKSHTPENC
PGWLDVLPFIIPHRPTNVESCEPGKPEALWVEERFTHAIAVRDVELLTGLDFYQDKVQPVSEILQ
LKTYLPTFETII

Human ENPP3 sequence, extracellular domain

>sp|O14638|31-875

LLVIMSLGLGLGLRLEKQGSCRKKCFDASFRGLENCRCDVACKDRGDCCWDFEDTCVESTRIWMCNKFR
CGETRLEASLSCSDDCLQRKCCADYKSVQGETSWLEENCDAQQSQCPGFDLPPVILFSDMGFRAEYLY
TWDTLMPNINKLKTGCIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII DNNMYDVNLNKNFSLSS
KEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNGSV PFEERISTLLKWLDL
PKAERPRFYTM YFEEDSSGHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNIILLADHGMD
QTYCNKMEYMTDYFPRINFFYMYEGPAPRI RAHNIPHDFFSFNSEIIVRNLS
CRKPDQHF KPYP LTPDL PKRLHYAKNVRIDKVHLFVDQQWLAVRSKSNTCGGGNHGYNNEFRSM
EAI FLAHGPSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLKVPFYEP
SHAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEETATVKVNL
PFGPRV LQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPLPPTVPDCLRADVRVPP
SESQKCSFYLDKNITHGFLYPPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATER
NGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKSHTPENC
PGWLDVLPFIIPHRPTNVESCEPGKPEALWVEERFTHAIAVRDVELLTGLDFYQDKVQPVSEILQ
LKTYLPTFETII

Mouse ENPP3 sequence

>sp|Q6DYE8

MDSRLALATEEPIKKDSLKKYKILCVVLLALLVIVSLGLGLGLRKPPEEQGSCRKKCFDSSHRGLEGCRCDSGCTG
RGDCCWDFEDTCVKSTQIWTNLFRCGENRLETALCSCADDCLQRKCCADYKTVCQGESPWVTEACASSQEPQCP
GFDLPPVILFSDMGFRAEYLYTWTLLPNINKLKTGCIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII
DNNMYDVHLNKNFSLSSVEKSNPAWWSGQPIWLTAMYQGLKAACYWPGSDVAVNGSFPTIYRNYSNSV
PYERRITTLQWLDL PKADRPSFYTIYVEEPDSAGHSSGPVSAGVIKALQSVDNAFGMLMEGLKQRNLHNCV
NIIVLADHGMDQTS CD RVEYMTDYFPKINFYMYQGPAPRI RTRNIPQDFFTFNSEIIVRNLS
CRKPDQHF KPYP LTPDL PKRLHYAKNVRIDKAHLMVDRQWLAFRSKGSNCGGGTHGYNNEFKS
MEAI FLAHGPSFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLNHLKTPFYKPSHAGELST
PADCGFTTLP LTPDPLDCSCPALQNTPGLEEQAQRLNLSEGEVAATVKANLPFGPRV
MQKNGDHCLLYHRDYISGYGKAMKMPMWSSYTVLKPDTSSLPPTVPDCLRADVRVAPSESQKCSFYLD
KNITHGFLYPAIKGTNESRYDALITSNLVPMYKEFKKMWDYFHEVLLIKYAIERNGLNVVSGPIFDYNYD
GHFDAPDEITQYVAGTDVPIPTHYFVVLTSCKDQHTPDSCPGWLDVLPFIVPHRPTNIESCSENKTE
DLWVEERFQAHAARVRDVELLTGLDFYQEKAPVSQLQKTYLPTFETII

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Figure 11B

Mouse ENPP3 sequence, extracellular domain

>sp|Q6DYE8|31-874

LLVIVSLGLGLGLRKPEEQGSCRKKCFDSSHRGLEGCRCDSGCTGRGDCCWDFEDTCVKSTQIWTNCNLFRCGENR
LETALCSCADDCLQRKDCADYKTVCQGESFWVTEACASSQEPQCPPGFDLPPVILFSMDGFRAEYLQWSTLLPNI
NKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDVHLNKNFSLSSVEKSNPAWWSGQPIWLTAMY
QGLKAACYWPGSDAVNGSFPTIYRNYSNSVPYERRITTLQWLDLPKADRPSFYTIYVEEPDSAGHSSGPVSAGV
IKALQSVDNAFGMLMEGLKQRNLHNCVNIILADHGMDQTSRVEYMTDYFPKINFYMYQGAPAPRI RTRNIPQDFE
TFNSEEIVRNLSCKRPDQHF KPYP LTPDL PKRLHYAKNVRI DKAHLMVDRQWLAFRSKGSSNCGGTHGYNNEFKSME
AIFLAHGSPFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLNHLKTPFYKPSHAGELSTPADCGFTTPLPT
DPLDCSCPALQNTPGLEEQAQRLNLSSEGEVAATVKANLPFGRPRVMQKNGDHCLLYHRDYISGYGKAMKMPMWSSY
TVLKPGDTSPLPPTVPDCLRADVRVAPSESQKCSFYLDKNITHGFLYPAIKGTNESRYDALITSNLVPMYKEFKKM
WDYFHEVLLIKYAIERNGLNVVSGPIFDYNDGHDPADEITQYVAGTDVPIPTHYFVVLTSCKDQTHTPDSCPGWL
DVLFPFIVPHRPTNIESCSENKTEDLWVEERFQAHAARVRDVELLTGLDFYQEKAPVSQLQLKTYLPTFETII

Macaca fascicularis ENPP3 sequence

>tr|A0A2K5TKP4

MESMLTLATEQPVKKNTLKKYKIACIVLLALLVIMSLGLGLGLRKLEKQGSCRKKCFDASFRGLENCRCDVACED
RGDCCWDFEDTCVESTRIWTCNKFRCGETRLEASLSCSDCLQRKDCADYKSVQGETSWLEENCDAQQSQCP
GFDLPPVILFSMDGFRAEYLYTWDTLMPNINKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDV
NLNKNFSLSSSEEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEERISTLLKWL
PKAERPSTYMYFEEDPSGHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNIILADHGMDQTYCNKMEY
MTDYFPRINFYMYEGPAPRIALNVPHDFFSCKYEDTYMKKRCRKPQHF KPYP LTPDL PKRLHYAKNVRI DKVH
LFDVDRQWLAVGSKSNTNCGGNGHYNNEFRSMEAI FLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLN
HLLKVPFYEP SHAEEVSKF SVCGFANPLPTNNLSCLCPHLQNSIQLEQVNQMLNLTQEETATVKVNLFPGRPRVLQ
KNVDNCLLYHREYVSGFGKAMRMPMWSSYTPVQLGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLDENITHGFLY
PPAINRTSDSQYDALIMSNLVPMEEFKMWDFHVSLLIKHATERNGVNVVSGPIFDYNDGHDPAEEITKHIAN
TDIPIPTHYFVVLTSCKNKSHTPENCPGWL DVLFPFIIPHRPTNVESCEPGKPEALWVEERFTHAIARVRDVELLTGL
DFYQDKAPVSEILQLKTYLPTFETII

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

>tr|A0A2K5TKP4|31-874

LLVIMSLGLGLGLRKLEKQGSCRKKCFDASFRGLENCRCDVACEDRGDCCWDFEDTCVESTRIWTCNKFRCGETR
LEASLSCSDCLQRKDCADYKSVQGETSWLEENCDAQQSQCPGFDLPPVILFSMDGFRAEYLYTWDTLMPNI
NKLKTCGIHSKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDVNLNKNFSLSSSEEQNNPAWWHGQPMWLTAMY
QGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEERISTLLKWLDPKAERPSTYMYFEEDPSGHAGGPVSARV
IKALQVVDHAFGMLMEGLKQRNLHNCVNIILADHGMDQTYCNKMEYMTDYFPRINFYMYEGPAPRIALNVPHDFF
SCKYEDTYMKKRCRKPQHF KPYP LTPDL PKRLHYAKNVRI DKVH LFDVDRQWLAVGSKSNTNCGGNGHYNNEFRSME
AIFLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLNHLKVPFYEP SHAEEVSKF SVCGFANPLPT
NNLSCLCPHLQNSIQLEQVNQMLNLTQEETATVKVNLFPGRPRVLQKNVDNCLLYHREYVSGFGKAMRMPMWSSY
TPVQLGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLDENITHGFLYPPAINRTSDSQYDALIMSNLVPMEEFKMW
WDYFHSVLLIKHATERNGVNVVSGPIFDYNDGHDPAEEITKHIANTDIPIPTHYFVVLTSCKNKSHTPENCPGWL
DVLFPFIIPHRPTNVESCEPGKPEALWVEERFTHAIARVRDVELLTGLDFYQDKAPVSEILQLKTYLPTFETII

Figure 12

AN1[ENPP3]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISGGGTTYLD ~~SVKGRFTISRDN~~ AKNSLYLQMNSLRAEDTAVY YCARHRRVYGY ~~YFDYWGQ~~ GLVTVSS	XX
vhCDR1	~~NYGMS~~	XX
vhCDR2	~~YISGGGTTYLD~~ SVKG	XX
vhCDR3	~~HRRVYGY~~ FDY	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ~~WYQQKPDQSPKLL~~ IKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYC ~~QGSNSW~~ PYTFGGG ~~TKLEIK~~	XX
vlCDR1	~~RASQSIGTSIH~~	XX
vlCDR2	~~YASESIS~~	XX
vlCDR3	~~QGSNSW~~ PYT	XX

>XENP28278 AN1[αENPP3]_H1L1_IgG1_PVA_/S267K**Chain 1 - AN1[αENPP3]_H1L1_IgG1_PVA_/S267K**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISGGGTTYLD~~SVKGRFTISRDN~~AKNSLYLQMNSLRAEDTAVYYCARHRRVYGY~~YFDYWGQ~~GLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCPCPPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTFLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK

Chain 2 - AN1[αENPP3]_H1L1_IgG1_PVA_/S267K

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~WYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS~~LEAEDAATYYC~~QGSNSW~~PYTTFGGG~~TKLEIK~~/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 13A

AN1[ENPP3] H1 L1.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGTTYLD ~~SVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY~~ YCARHRRVYYGYFDYWGQGT ~~LVT~~ VSS	XX
vhCDR1	<u>NYGMS</u>	XX
vhCDR2	<u>YISSGGGTTYLD~~SVK~~</u>	XX
vhCDR3	<u>HRRVYYGYFDY</u>	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ~~WYQQKPDQSPKLL~~ IEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQ ~~QNSW~~ PYTFGGG ~~TKLEIK~~	XX
vlCDR1	<u>RASQSIGTSIH</u>	XX
vlCDR2	<u>YASESIS</u>	XX
vlCDR3	<u>QQNSWPYT</u>	XX

AN1[ENPP3] H1 L1.77

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGTTYLD ~~SVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY~~ YCARHRRVYYGYFDYWGQGT ~~LVT~~ VSS	XX
vhCDR1	<u>NYGMS</u>	XX
vhCDR2	<u>YISSGGGTTYLD~~SVK~~</u>	XX
vhCDR3	<u>HRRVYYGYFDY</u>	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH ~~WYQQKPDQSPKLL~~ IEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQ ~~QNSW~~ PYTFGGG ~~TKLEIK~~	XX
vlCDR1	<u>RASQSIGTSIH</u>	XX
vlCDR2	<u>YESESIS</u>	XX
vlCDR3	<u>QQNSWPYT</u>	XX

Figure 13B

AN1[ENPP3] H1.8 L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEW VSYISGGGTTYLLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFFDYWGQGLVTVSS	XX
vhCDR1	<u>NYGMS</u>	XX
vhCDR2	<u>YISSGGGTTYLLDSVTG</u>	XX
vhCDR3	<u>HRRVYYGYFFDY</u>	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHHWYQQKPDQSPKLL IKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQGSNSW PYTFGGGTKLEIK	XX
vlCDR1	<u>RASQSIGTSH</u>	XX
vlCDR2	<u>YASESIS</u>	XX
vlCDR3	<u>QGSNSWPYT</u>	XX

AN1[ENPP3] H1.8 L1.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEW VSYISGGGTTYLLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFFDYWGQGLVTVSS	XX
vhCDR1	<u>NYGMS</u>	XX
vhCDR2	<u>YISSGGGTTYLLDSVTG</u>	XX
vhCDR3	<u>HRRVYYGYFFDY</u>	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHHWYQQKPDQSPKLL IEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQGSNSW PYTFGGGTKLEIK	XX
vlCDR1	<u>RASQSIGTSH</u>	XX
vlCDR2	<u>YASESIS</u>	XX
vlCDR3	<u>QGSNSWPYT</u>	XX

AN1[ENPP3] H1.8 L1.77

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEW VSYISGGGTTYLLDSVTGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFFDYWGQGLVTVSS	XX
vhCDR1	<u>NYGMS</u>	XX
vhCDR2	<u>YISSGGGTTYLLDSVTG</u>	XX
vhCDR3	<u>HRRVYYGYFFDY</u>	XX
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHHWYQQKPDQSPKLL IEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQGSNSW PYTFGGGTKLEIK	XX
vlCDR1	<u>RASQSIGTSH</u>	XX
vlCDR2	<u>YESESIS</u>	XX
vlCDR3	<u>QGSNSWPYT</u>	XX

Figure 14A

H16-7.213

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTGYMHWVRQAPGGLEWMGWINPNSGGTNYA QKFQGRVTMTSDTSISTAYMELSLRSDDTAVYYCARELRYFGWLLS SLDYWGQGLTVTVSS	XX
vhCDR1	GYMH	XX
vhCDR2	WINPNSGGTNYAQKFQ	XX
vhCDR3	ELRYFGWLLSLDY	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCPASQSISSYLNWFOQKPGKAPKLL IYAASSLQSGVPSRFSGESGTDFTLTISLQPEDFATYSCQSYSEF PLTFGGGKVEIK	XX
vlCDR1	RASQSISSYL	XX
vlCDR2	AASSLQS	XX
vlCDR3	QSYSEFLT	XX

H16-9.69

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTSYDIHWVRQATGQGLEWMGWMPNSGNTVYA QKFQGRVTMTNTSISTAYMELSLRSEDVAVYYCARTVLLWFFDYW GQGLTVTVSS	XX
vhCDR1	SYDIH	XX
vhCDR2	WMNPNSGNTVYAQKFQ	XX
vhCDR3	TVLLWFFDY	XX
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSKNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYC QYYSTFPWTFGQGTVEIK	XX
vlCDR1	KSSQSVLYSSKNKNYLA	XX
vlCDR2	WASTRES	XX
vlCDR3	QYYSTFPWT	XX

H16-1.52

	sequence	SEQ ID NO:
Variable heavy (vh) domain	SGGGLVQPGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISG SDGSPYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDG YSSGWNIFYDYWGQGLTVTVSS	XX
vhCDR1	SYAMS	XX
vhCDR2	AISGSDGSPYYADSVK	XX
vhCDR3	DGYSSGWNIFYDY	XX
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYC QEYYSTMCSFGQGTLEIK	XX
vlCDR1	KSSQSVLYSSNNKNYLA	XX
vlCDR2	WASTRES	XX
vlCDR3	QEYYSTMCS	XX

Figure 14B

Ha16-1(1)23

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGGGVVQGRSLRLSCAASGFTFRSYGMHWVRQAPGKLEWVAVI WSDGSENKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR EGYYGSGSYYYGMDVWGQGT VTVSS	XX
vhCDR1	SYGMH	XX
vhCDR2	VIWSDGSENKYYADSVK	XX
vhCDR3	EGYYGSGSYYYGMDV	XX
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGTQGAAWLQQHQGHPKLL LSYRNNNRFGISERLSASTSGNTASLTITGLQPEDEADYYCSAWDS SLSAVVFGGGTKLTVL	XX
vlCDR1	TGNSNNVGTQGA	XX
vlCDR2	RNNNRFS	XX
vlCDR3	SAWDSLSAVV	XX

H16-9.44

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LSLTCTVSGGSISSYYWSWIRQSAGKLEWIGRIYTGVSSTNYNPSLK SRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDYYDSGGYYPFDYW GQGT LVTVSS	XX
vhCDR1	SSYYWS	XX
vhCDR2	RIYTGVSSTNYNPSLKS	XX
vhCDR3	DYYDSGGYYPFDY	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITSCRASQGISNYLAWFQQKPGKAPKSL IYAASSLENGVPSKFSGSGSGTDFTLTISLQPEDFATYYCQQYNSS PFTFGPGTKVDIR	XX
vlCDR1	RASQGISNYLA	XX
vlCDR2	AASSLEN	XX
vlCDR3	QQYNSSPFT	XX

H16-1.67

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSQTLSTCTVSGGSINSFGYYWSWIRQYPGKLEWIG FLYFTGSTYYNPSLKSRTISVDTSKSQFSLKLSSVTAADTAVYYCA RAGTMVRGAHYGMDVWGQGT VTVSS	XX
vhCDR1	SFGYYWS	XX
vhCDR2	FLYFTGSTYYNPSLKS	XX
vhCDR3	AGTMVRGAHYGMDV	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCRASQGISNYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQIYST PPEWTFGQGTKEIK	XX
vlCDR1	RASQGISNYLN	XX
vlCDR2	AASSLQS	XX
vlCDR3	QQIYSTPPEWT	XX

Figure 14C

Ha1 6-1 (3,5)36

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGPGLVKPSSETLSLTCTVSGGSISSSSYWGWIQPPGKGL EWIGSMYYSGSTYHNPSLKSRVVISVDTSKNQFSLKLSVTAADTAV YYCARHYITVAGIFDYWGQGLTVTVSS	XX
vhCDR1	<u>SSSYWG</u>	XX
vhCDR2	<u>SMYYSGSTYHNPSLKS</u>	XX
vhCDR3	<u>HYITVAGIFDY</u>	XX
Variable light (vl) domain	QSVLTQPPSASGTPGQRATISCSGSSTNIGSTIVNWYQQVPGTAPKL LIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDA SLNGPVFGGGTKLTVL	XX
vlCDR1	<u>SGSSTNIGSTIVN</u>	XX
vlCDR2	<u>SNNQRPS</u>	XX
vlCDR3	<u>AAWDASLNGPV</u>	XX

H16-1.86

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSSETLSLTCTVSGGSISYYWSWIRQPPGKLEWIGYI YYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARA YGYYYGMDVWGQGLTVTVSS	XX
vhCDR1	<u>SYWS</u>	XX
vhCDR2	<u>YIYYSGSTNYNPSLKS</u>	XX
vhCDR3	<u>AYGYYYGMDV</u>	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPNLL IYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCQQTYS PPWTFGQGTKVEIK	XX
vlCDR1	<u>RTSQSISSYLN</u>	XX
vlCDR2	<u>AASSLQS</u>	XX
vlCDR3	<u>QQTYSSPPWT</u>	XX

H16-9.10

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LLES GPGLVKPSQTLTLTCAISGDSVS SNSAAWN WIRQSPSRGLEWL GRYYRSKWYNAYAVSVKSRMTINPDTSKNQFSLQLNSVTPEDTAVY YCAREAGGWFDPEWGQGLTVTVSS	XX
vhCDR1	<u>SNSAAWN</u>	XX
vhCDR2	<u>RTYYRSKWYNAYAVSVKS</u>	XX
vhCDR3	<u>EAGGWFDPE</u>	XX
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQGIRSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCQQANSF PPTFGGGTKVEIK	XX
vlCDR1	<u>RASQGIRSWLA</u>	XX
vlCDR2	<u>AASSLQS</u>	XX
vlCDR3	<u>QQANSFPPT</u>	XX

Figure 14D

H16-9.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGLVQPSQTLTLTCAISGDSVSSNSAAWNWIRQSPSRGL EWLGRTYYRSKYNNAYPVSVKSRITINPDTSKNQFSLQLNSVTPEDT AVYYCAREAGGWFDWVGQGTTLTVSS	XX
vhCDR1	<u>SNSAAWN</u>	XX
vhCDR2	<u>RTYYRSKYNNAYPVSVKS</u>	XX
vhCDR3	<u>EAGGWFD</u>	XX
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCRANQGIRSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQANSE PPTFGGGTKVEIK	XX
vlCDR1	<u>RANQGIRSWLA</u>	XX
vlCDR2	<u>AASSLQS</u>	XX
vlCDR3	<u>QQANSEPT</u>	XX

H16-1.68

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVHVLVESGGGVVQPGRSRLRLSCAASGFTFRSYGMHWVRQAPGKLEW VAVIWDGSKNYADSVKGRFTISRDNKNTLYLQMNSLRAEDMAMY YCARSRTITFGVVHYGMDVWGQGTTLTVSS	XX
vhCDR1	<u>SYGMH</u>	XX
vhCDR2	<u>VIWYDGSNKYYADSVKG</u>	XX
vhCDR3	<u>SRITIFGVVHYGMDV</u>	XX
Variable light (vl) domain	TQLTQSPSSLSASVGDRTVITCRASONINSYLNWYQQKPGKAPKLLI YAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFTTYCQQSYSSA PTFGGGTKLEIK	XX
vlCDR1	<u>RASONINSYLN</u>	XX
vlCDR2	<u>AASSLQS</u>	XX
vlCDR3	<u>QQSYSSAPT</u>	XX

Ha16-1(1)1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVSGGSISYYWWSWIRQPPGKLEWIGYIYYS GSTNYNPSLKSRTVITISVDTSKNQFSLKLSSVTAADTAVYYCARAVSY YYYGMDVWGQGTTLTVSS	XX
vhCDR1	<u>SYWWS</u>	XX
vhCDR2	<u>YIYYSGSTNYNPSLKS</u>	XX
vhCDR3	<u>AVSYYYGMDV</u>	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCRITQININSYLNWYQQRPKGAPKLL IYATSSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYST LFTFGPGTKVDIK	XX
vlCDR1	<u>RTIQININSYLN</u>	XX
vlCDR2	<u>ATSSLQS</u>	XX
vlCDR3	<u>QQTYSTLFT</u>	XX

Figure 14E

Ha16-1(3,5)18

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVPGGSIRSYFWSWIRQPAGKGLEWIGRFYFS GSTNYPNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDYGD HYYYGMDVWGQGTITVTVSS	XX
vhCDR1	SYFWS	XX
vhCDR2	RFYFSGSTNYPNPSLKSR	XX
vhCDR3	DYGDHYYYGMDV	XX
Variable light (vl) domain	VLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQFPGTAPKFLI YDNNKRSSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSLSL SAVIFGGGTKLTVL	XX
vlCDR1	SGSSSNIGNNYVS	XX
vlCDR2	DNNKRSS	XX
vlCDR3	GTWDSLSLSAVI	XX

Ha16-1(2,4)4

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GFTFSSYGMHWVRQAPGKGLEWVAIIWYDESNNKYADSVKGRFTISR DNSKNTLYLQMSLRAEDTAVYYCARAYSGSYGYSYYGM	XX
vhCDR1	SYGMH	XX
vhCDR2	IIWYDESNNKYADSVKGR	XX
vhCDR3	AYSGSYGYSYYGM	XX
Variable light (vl) domain	QDRQPASPGSGDKLGDKYACWYQQKPGQSPVLVIYQDSKRPSGIPER FSGSNSGNTATLTISGTQAMDEADYYCQAWDNRTAVFGGGTKLTVL	XX
vlCDR1	PGSGDKLGDKYAC	XX
vlCDR2	QDSKRPS	XX
vlCDR3	QAWDNRTAV	XX

Ha16-1(3,5)56

	sequence	SEQ ID NO:
Variable heavy (vh) domain	RCRLVESGAEVKKPGESLKISCKSGSYRFTSYWIGWVRQMPGKGLEW MGLIYPGDSDFTRYSPSEFQGVITISADKSISTAYLQWRSCLKASDTAMY YCARNDYVVMDVWGQGTITVTVSS	XX
vhCDR1	SYWIG	XX
vhCDR2	IIYPGDSDFTRYSPSEFQGV	XX
vhCDR3	KDYVVMDV	XX
Variable light (vl) domain	DTISCTGTSSDVGNVNYVSWYQQHPGKAPKLMYAVNNRPSGVSNRF SGSKSGNTASLTISGLQAEDADYYCSSYTSSRNLVVFGGGTKLTVL	XX
vlCDR1	TGTSSDVGNVNYVS	XX
vlCDR2	AVNNRPS	XX
vlCDR3	SSYTSSRNLVV	XX

Figure 14F

H16-7.8

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLTLCTVSGGSISGGYYWSWIRQHPGKGL EWIGLIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLNSTAAADTAV FYCARVAIVTIPGGMDVWGQGTITVTVSS	XX
vhCDR1	SGGYYWS	XX
vhCDR2	IIYYSGSTYYNPSLKSR	XX
vhCDR3	VAIVTIPGGMDV	XX
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLL IKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSRSE FWIFGQGTKEIK	XX
vlCDR1	RASQSIGISLH	XX
vlCDR2	YASQSF	XX
vlCDR3	HQSRSEFWT	XX

H16-1.93

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWISAYNGNTYYAQKLQARVTMTTDTSTSTAYMELRSLRSDDTAVY YCARDCYSSSWSLHYYGMDVWGQGTITVTVSS	XX
vhCDR1	SYGIS	XX
vhCDR2	WISAYNGNTYYAQKLQA	XX
vhCDR3	DGYSSSWSLHYYGMDV	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITITWRSSQGIYNLSLAWYQQKPGKVPKLL IYAASLTHSGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNSSA FFTFGPGTKVDIK	XX
vlCDR1	RSSQGIYNLSL	XX
vlCDR2	AASLTHS	XX
vlCDR3	QKYNSSAFFT	XX

Ha1 6-1(3.5)27.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LVESGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGI IYFGDSDFTRYSPSFQGVITISADKSIISTAYLQWSSLKASDTAMYYCA RKDYIIYYSMVWGQGTITVTVSS	XX
vhCDR1	SYWIG	XX
vhCDR2	IYFGDSDFTRYSPSFQG	XX
vhCDR3	KDYIIYYSMV	XX
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSEVGGYNYVSWYQQHPGQAPK LLIYGVNIRPSGVSTRFSGSKSGNTASLTISGLQAEDEADYYCSSYT RSSILVVFAGGTKLTVL	XX
vlCDR1	TGTSSDVGGYNYVS	XX
vlCDR2	GVNIRPS	XX
vlCDR3	SSYTRSSILVV	XX

Figure 14G

H16-1.61

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVQPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEW VAVIWDGSGNRYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARSRITIFGVVHYGMDVWGQGTITVTVSS	XX
vhCDR1	SYGMH	XX
vhCDR2	VIWYDGSNKYYADSVK	XX
vhCDR3	SRITIFGVVHYGMDV	XX
Variable light (vl) domain	DTQLTQSPSSLSASVGRVTITCRASQSISSYLNWYQLKPGKAPKLL IYAASSLESQVPSRFRSGSESGTDFTLTISLQPEDFATYYCQSYNS PITFGPGTKVDIK	XX
vlCDR1	RASQSISSYLN	XX
vlCDR2	AASSLES	XX
vlCDR3	QSYNSPIT	XX

H16-1 (3,5)5

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGEISLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGIIYPGDSSTRYSPSPFQGVQVITISADKSISTAYLQWSSLKASDTAMY YCARKEYYYTMDVWGQGTITVTVSS	XX
vhCDR1	SYWIG	XX
vhCDR2	IIYPGDSSTRYSPSPFQ	XX
vhCDR3	KDYTYTMDV	XX
Variable light (vl) domain	QSALTQSPASVSGSPGQSITISCTGTSSSDVGGYNYVSWYQQHPGKAPK IMIYAVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSST ISRILVVFGGGTKLTVL	XX
vlCDR1	TGTSSDVGGYNYVS	XX
vlCDR2	AVSNRPS	XX
vlCDR3	SSYTISRILVV	XX

H16-7.200

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSITSGDYYSWIRQHPGKGL EWFGFIYYSGSAYYNPSLKSRTISVDTSKNQFSLKLSSVTAADTAV YYCAREERNYGGNSFDYWGQGTITVTVSS	XX
vhCDR1	SGDYYS	XX
vhCDR2	FIYYSGSAYYNPSLKS	XX
vhCDR3	ERNYGGNSFDY	XX
Variable light (vl) domain	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQ SPQLLIYLGSNRASGVDPDRFSGSGSDFTLTKISRVEAEDVGVYYCM QALQITITFGQTRLEIK	XX
vlCDR1	RSSQSLLHSNGYNYLD	XX
vlCDR2	LGSNRAS	XX
vlCDR3	MQALQITIT	XX

Figure 14H

Ha16-1(3,5)42

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGIITYPGDSDFRYSPSFQGGQVTISADKSISTAYLQWSSLKASDTAMY YCARNDYIIYSMDVWGQGTITVTVSS	XX
vhCDR1	SYWIG	XX
vhCDR2	IIYPGDSDFRYSPSFQGG	XX
vhCDR3	KDYIIYSMDV	XX
Variable light (vl) domain	QSALTQSPASVSGSPGQSITISCTGTSSDVGRFNYVSWYQQRPQKAPK LMIYAVNIRPSGVSNRFSKSGNTASLTISGLQAEDEAGYYCSSYT SSSTLLVFGGGTKLTVL	XX
vlCDR1	TGTSSDVGRFNYVS	XX
vlCDR2	AVNIRPS	XX
vlCDR3	SSYTSSSTLLV	XX

H1 6-9.65

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSRLSCAASGFTFSYGMHWVRQAPGKGLEW VATIEWFDGSNGYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARSSSGSYDHFDFYWGQGTITVTVSS	XX
vhCDR1	SYGMH	XX
vhCDR2	TIWFDGSNGYYADSVKGR	XX
vhCDR3	DSSSGSYDHFDFY	XX
Variable light (vl) domain	DIVMTQSPPLSLPVTGPGEPAISICRSSQSLHSNGYNCLDWYLQKPGQ SPQLLIYLGSNRASGVPRFSGSGSDFTLTKISRVEADVGVYYCM QALQTPITFGGGTRVEIK	XX
vlCDR1	RSSQSLHSNGYNCLD	XX
vlCDR2	LGSNRAS	XX
vlCDR3	MQALQTPIT	XX

Ha16-1(3,5)19

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGIITYPGDSDFRYSPSFQGGQVTISADKSISTAYLQWSSLKASDTAMY YCARNDYIIYAMDVWGQGTITVTVSS	XX
vhCDR1	SYWIG	XX
vhCDR2	IIYPGDSDFRYSPSFQGG	XX
vhCDR3	KDYIIYAMDV	XX
Variable light (vl) domain	SALTQSPASVSGSPGQSITISCTGTSSDVGRYNYVSWYQQHPGQAPKL MIYGISIRPSGVSPRFSKSGNTASLTISGLQAEDEADYYCSSHTS NSTLVVFAGGKTLTVL	XX
vlCDR1	TGTSSDVGRYNYVS	XX
vlCDR2	GISIRPS	XX
vlCDR3	SSHTSNSTLVV	XX

Figure 14I

Ha16-1.80

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSTYYWSWIRQPPGKGLEW IGYVYFSGSTNYPNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYY CARATRDYFYYGMDVWGQGTITVTVSS	XX
vhCDR1	SYYS	XX
vhCDR2	YVYFSGSTNYPNPSLK	XX
vhCDR3	ATRDYFYYGMDV	XX
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITTCRTSHDISNYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFRSGSRSGTDFTLTISLQPEDFATYYCQQTYST LETFGEGTKVDIK	XX
vlCDR1	RTSHDISNYLN	XX
vlCDR2	AASSLQ	XX
vlCDR3	QQTYSTLETF	XX

Figure 15A

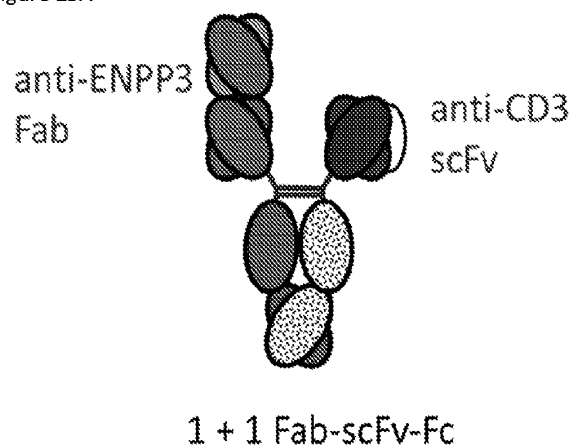


Figure 15B

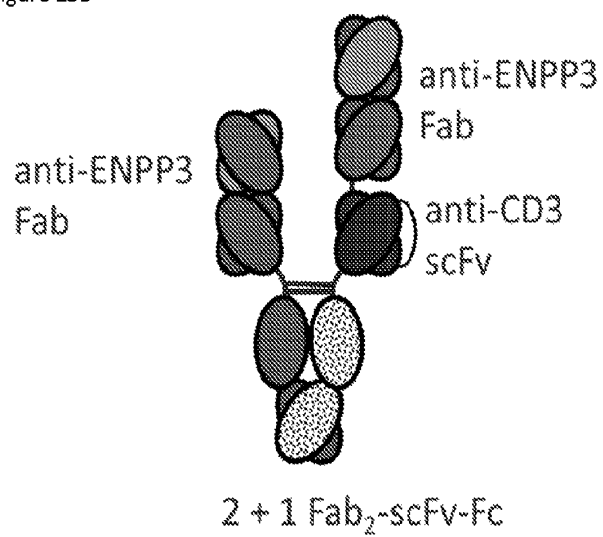


Figure 16

>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

QVTLRESGPALVKPTQTTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWDDKKHYNFSLKDRLTISKDTSK
NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTIVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQFPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_PVA_/S267K_pl(-)_Isosteric_A_L368D/K370S

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR
EPQVYTLPPSREQMTKNQVKLTCLVKGFPYPSDIAVEWESNGQFPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - Numax Light

ChainDIQMTQSPSTLSASVGDRTITCSASSRVGYMHWYQQKPGKAPKLLIYDTSKLASGVPSRFSGSGSGTEFTL
TISSLQPDDFATYYCFQGGYFFTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

QVQLVQSGAEVKKPGASVKVSCKASGYTFSTSYGISWVRQAPGQGLEWMGWI SAYNGNTYYAQKIQARVTMTTDTSTST
TAYMELRSLRSDDAVYYCARDGYSSSWSLHYYGMVWVGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCD
KTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYCKKVSINKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30 L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRI RSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCCGSSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPED
EADYYCALWYSNNHWVFGGGTKLTVL/EPKSSDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSINKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-1.93[ENPP3]_L1

DIQMTQSPSSLSASVGDRITITWRSSQGIYNSLAWYQQKPGKVPKLLIYAASLTLSHSGVPSRFSGSGSGTDFLTITSS
LQPEDVATYYCQKYNSAFPTFGPGTKVDIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSDSTYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>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

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWQWIRQHPGKGLEWIGI IYYSGSTYYNFSLKSRVTISVDTSK
NQFSLKLNLSVTAADTAVFYCARVAIVTTIPGGMVWVGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYCKKVSINKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30 L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRI RSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTITLTCCGSSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPED
EADYYCALWYSNNHWVFGGGTKLTVL/EPKSSDKTHHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSINKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFLTITNS
LEAEDAATYYCHQSRSEFPWTFGQGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSDSTYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFNSYGMSWVRQAPGKRLEWVS^{YI}SSGGGTTYLDSVKGRTTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWEQGDVF}SCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^{RSKYNNYATYYADSVK}GRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT^{CGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR}APGVPARFSGSLGGAALTI^{SGAQPED}
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCP^{PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK}
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PR
EPQVYTLPPSREQMTKNQV^{KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS}DGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGT^{SIHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS}
LEAEDAATYYCQ^{QNSWPFYF}GGGKLEIK/RTVAAPSVFI^{FPPSDEQLKSGTASVVC}LLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSK^{DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC}

**>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

EVQLVESGGGLVQPGGSLRLSCAASGFAFNSYGMSWVRQAPGQRLEWVS^{YI}SSGGGTTYLDSVTGRFTTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWEQGDVF}SCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^{RSKYNNYATYYADSVK}GRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT^{CGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR}APGVPARFSGSLGGAALTI^{SGAQPED}
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCP^{PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK}
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PR
EPQVYTLPPSREQMTKNQV^{KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS}DGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGT^{SIHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS}
LEAEDAATYYCQ^{QNSWPFYF}GGGKLEIK/RTVAAPSVFI^{FPPSDEQLKSGTASVVC}LLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSK^{DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC}

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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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGG^{TTY}YLD^{SV}TGRFTISRDNAKN
SLYLQMNSLR^{AE}DTAVYYCAR^{HR}RVY^{GY}YFYWGQ^{TL}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQ^{TY}ICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT^{VL}HDWLN^QKEYCKKVS^NKALPAPIEK^TISKAKGQPREPQVY^TLP^{PS}SREEMTKNQVSLTCDVSGFYPSDIAVEW
ESD^GQPENNYK^TTPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3] H1.30 L1.47 scFv(GKPGS)4_Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI^{RS}KYNNY^{AT}YYADSVKGRFTISRDDS
KNTLYLQMNSLR^{AE}DTAVYYCVRHGNFGDSYVSWFAYWGQ^{TL}LVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQ
PSLTVSPGGTVTLT^{CG}SS^TGAV^{TT}SNYANWVQ^QKPGKSPRGLIGGTN^KRAFGV^{PAR}FGSLLGGKAAL^{TI}SGAQPED
EADYYCALWYSN^HWVFGGGTKLT^{VL}/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT^{VL}HDWLN^QKEYCKKVS^NKALPAPIEK^TISKAKGQPR
EPQVY^TLP^{PS}SREQMTKNQV^{KL}TCLVKG^FYPSDIAVEWESNGQPENNYK^TTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^WYQKPDQSPKLLIEY^{ES}ESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ^QSN^{SW}PYTFGGGKLEIK/RTVAAPSVFI^{FP}PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDS^{TY}SLSS^{TL}TL^{SL}KADYE^KHKVYACEVTHQGLSSPVT^{KS}FN^RGEC

**>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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGG^{TTY}YLD^{SV}TGRFTISRDNAKN
SLYLQMNSLR^{AE}DTAVYYCAR^{HR}RVY^{GY}YFYWGQ^{TL}LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQ^{TY}ICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT^{VL}HDWLN^QKEYCKKVS^NKALPAPIEK^TISKAKGQPREPQVY^TLP^{PS}SREEMTKNQVSLTCDVSGFYPSDIAVEW
ESD^GQPENNYK^TTPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3] H1.30 L1.47 scFv(GKPGS)4_Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI^{RS}KYNNY^{AT}YYADSVKGRFTISRDDS
KNTLYLQMNSLR^{AE}DTAVYYCVRHGNFGDSYVSWFAYWGQ^{TL}LVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQ
PSLTVSPGGTVTLT^{CG}SS^TGAV^{TT}SNYANWVQ^QKPGKSPRGLIGGTN^KRAFGV^{PAR}FGSLLGGKAAL^{TI}SGAQPED
EADYYCALWYSN^HWVFGGGTKLT^{VL}/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT^{VL}HDWLN^QKEYCKKVS^NKALPAPIEK^TISKAKGQPR
EPQVY^TLP^{PS}SREQMTKNQV^{KL}TCLVKG^FYPSDIAVEWESNGQPENNYK^TTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.77

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH^WYQKPDQSPKLLIEY^{ES}ESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ^QSN^{SW}PYTFGGGKLEIK/RTVAAPSVFI^{FP}PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDS^{TY}SLSS^{TL}TL^{SL}KADYE^KHKVYACEVTHQGLSSPVT^{KS}FN^RGEC

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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

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYVWSWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRTISVDTSK
NQFSLKLNLSVTAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCCGSTCGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTI SGAQPED
EADYYCALWYSNNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRSEFPWTFGGQTKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPQORLEWVSYISSGGGTTYLLDSVTGRFTISRDNANK
SLYLQMNLSRAEDTAVYYCARHREVVYGYFFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCCGSTCGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTI SGAQPED
EADYYCALWYSNNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQGSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFNSYGMSWVRQAPGKRLEWVS^{YI}SSGGGTTYLDSVKGRTTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGQENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWEQGDVF}SCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^{RSKANNYATYYADSVKGR}TISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT^{CGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR}APGV^{PARFSGSL}LGKAA^{LTI}SGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKHTHTCP^{PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK}
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PR
EPQVYTLPPSREQMTKNQV^{KLTVKGFYPSDIAVEWESNGQ}ENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWQQGN}
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1

DILLTQSPDFQSVTPKEKVITITCRASQSIGTSIH^{WYQQKPDQSPKLLIKYASESISGIP}SRFSGSGSGTDFTLTINS
LEAEDAATYYCQ^{QNSWPFY}FGGGTKLEIK/RTVAAPSVFI^{FPPSDEQLKSGTASV}VCLNNFY^{PREAKVQWKVDNA}
LQSGNSQESVTEQDSK^{DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC}

**>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

EVQLVESGGGLVQPGGSLRLSCAASGFAFNSYGMSWVRQAPGQRLEWVS^{YI}SSGGGTTYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGQENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWEQGDVF}SCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI^{RSKANNYATYYADSVKGR}TISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT^{CGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR}APGV^{PARFSGSL}LGKAA^{LTI}SGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKHTHTCP^{PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK}
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI^{SKAKGQ}PR
EPQVYTLPPSREQMTKNQV^{KLTVKGFYPSDIAVEWESNGQ}ENNYKTTTPVLDS^{DGSFFLYSKLTVDKSRWQQGN}
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33

DILLTQSPDFQSVTPKEKVITITCRASQSIGTSIH^{WYQQKPDQSPKLLIEYASESISGIP}SRFSGSGSGTDFTLTINS
LEAEDAATYYCQ^{QNSWPFY}FGGGTKLEIK/RTVAAPSVFI^{FPPSDEQLKSGTASV}VCLNNFY^{PREAKVQWKVDNA}
LQSGNSQESVTEQDSK^{DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC}

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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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLIEWVSYISGGGTTYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFFDYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI RSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCCGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKKAALTI SGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPR
EPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77

DILLTQSPDFQSVTPKEKVITICRASQSIGTSIHWYQQKPDQSPKLLIEYESEISGIPSRFSGSGSGTDFLTINS
LEAEDAATYYCQSNWPFYFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSLTITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
AQPEDEADYYCALWYSNHWVFVGGGKLTVL/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPFYFVGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
AQPEDEADYYCALWYSNHWVFVGGGTKLTVL/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPTYFVGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGGTTYLD^{SV}TGRFTISRDN^{AKN}
SLYLQMNSLRAEDTAVYYCAR^{HRRVYGYFDY}WGQGT^{LV}VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT^{SV}WSNGALTSGVHTFPAVLQSSGLYSLSSVTV^{PSS}SLGTQTYICNVNHKPSDTKVDKKVEPKSCDK^{HTC}
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYN^{STY}RVVS
VLT^{VL}LHQDWLNGKEYKCKVSNKALPAPIEK^{TI}SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYP^{SDI}AVEW
ESDGPENNYKTT^{PP}VLDS^{DGS}FFLYSKLTVDKSRWEEQ^{GD}VFSCSVMEALHNHYTQ^{KS}LSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGGTTYLD^{SV}TGRFTISRDN^{AKN}
SLYLQMNSLRAEDTAVYYCAR^{HRRVYGYFDY}WGQGT^{LV}VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT^{SV}WSNGALTSGVHTFPAVLQSSGLYSLSSVTV^{PSS}SLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFS^{TYAMN}WVRQAPGKLEWVGRI^{RSKYNNYATYYADSV}KGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY^{SWFAY}WGQGT^{LV}VSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEP^{SL}TVSPGGTVTLT^{CGS}STGAVTT^{SNYAN}WVQKPGKSPRGLIG^{TN}KRAPGV^{PAR}FSGLLGKAALTISG
AQPEDEADY^{YCALWYSNHW}VFGGGTKLTVL/ GGGGSGGGGSKTHTCP^{PC}PAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN^{STY}RVVSVLT^{VL}LHQDWLNGKEYKCKVSNKALPAPIEK^{TI}
ISKAKGQPREPQVYTLPPSREQMTKNQV^{KL}TCLVKGFYPSDI^{AVE}WESNGQ^{PEN}NYKTT^{PP}VLDS^{DGS}FFLYSKLT^V
DKSRWQQGNVFSCSVMEALHNHYTQ^{KS}LSLSPGK

Chain 3 - AN1[αENPP3] L1.77

DILLTQSPDFQSVTPKEKVITICRASQSIG^{TS}SIHWYQQKPDQSPKLLIEY^{ESESIS}SGIPSRFSGSGSGTDFLT^{INS}
LEAEDAATYYCQ^{QNS}SWFYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASV^{VCL}LN^{NFY}PREAKVQWKVDNA
LQSGNSQESVTEQDSK^{STY}SLSS^{TIT}LSKADYEKHKVYACEVTHQGLSSP^{VTK}SFNRGEC

Figure 20A

>XENP26822 H16-7.8[ENPP3] H1L1 Fab-H16-

7.8[ENPP3] 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 - H16-7.8[ENPP3]_H1_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSEWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSTVAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDQGPPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - H16-

7.8[ENPP3]_H1_CH1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSEWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSTVAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGG
SGGGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIKSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/
QAVVTQEPSTVSPGGTITLTCSSTGAVTFSNYANWVQQKPGKSPRGLIGGTNKRAGVPARFSGSLLGGKAALTI
SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRT
PEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKL
TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - H16-7.8[ENPP3]_L1

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRKSFPTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYSISSGGGTTYVLDISKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYGYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1_CH1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYSISSGGGTTYVLDISKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARHRRVYGYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
 GGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI RSKANNYATYYADSVKGRFTI
 SRDTSKNTLYLQMNSLRAEDTAVYYCVREGNFGDSYVSWFAIYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
 VVTQEPSTLVSPGGTTLTCLGSGTGAFTTISNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
 AQPEDEADYYCALWYSNHWVFGGGTKLTVL/ GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
 VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFPYSDIAVEWESNGQPPENNYKTTTPVLDSGSGFFLYSKLT
 VKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSLHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFLTINS
 LEAEDAATYYCQNSWPHYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDSYSLSSLTITLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
AQPEDEADYYCALWYSNHWVFVGGGKLTVL/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPFYFVGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKT
ISKAKGQPREPQVYTLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPTYFSGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISGGGGTTYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISGGGGTTYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP SLTVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAFGVPARFSGSLGGK
AALTI SGAQPEDEADYYCALWYSNHWVFSGGKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFAFWGQGT LVTVSS/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22A

>XENP30470 AN1[αENPP3] H1.8 L1 Fab-

AN1[αENPP3] H1.8 L1 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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYGYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEPSTLTVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGK
AALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFAFWGQGTLLVTVSS/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22B

>XENP30819 AN1[αENPP3] H1.8 L1.33 Fab-

AN1[αENPP3] H1.8 L1.33 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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP SLTVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTI SGAQPEDEADYYCALWYSNHWVFSGGKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFA YWGQGTLLVTVSS/ GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP SLTVSPGGTVTLT CGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAGVVPARFSGSLGGK
AALTI SGAQPEDEADYYCALWYSNHWVFSGGKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFA YWGQGTLLTVSS/ GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.77

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYSESI SGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23A

>XENP31148 AN1[αENPP3] H1.8 L1 Fab-

AN1[αENPP3] H1.8 L1 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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISGGGGTTYLLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISGGGGTTYLLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEPSTLTVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGK
AALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFAFWGQGTLLTVSS/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTV
DKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPTYFSGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGGT^{TY}YLD^{SV}TGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT^{LV}TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT^{SV}WNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT^{VL}HLQDWLNGKEYKCKVSNKALPAPIEK^{TI}SKAKGQPREPQVY^{TL}LP^{PS}REEMTKNQVSLTCDVSGFYPSDIAVEW
ESD^{GQ}PPENNYK^{TT}PPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS^{YI}SSGGGT^{TY}YLD^{SV}TGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT^{LV}TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT^{SV}WNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP^{SL}TVSPGGTV^{TL}TCGSS^{TG}AVT^{TS}NYANWVQKPGKSPRGLIGGT^{NK}RAFGV^{PAR}FSGSLLGGK
AALTISGAQPEDEADYYCALWY^{SN}HWVFGGGTK^{LT}VL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMN^{WVR}QAPGKLEWVGRI^{RS}KYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGEYV^{SW}FAYWGQGT^{LV}TVSS/GGGSGGGGSKTHTCP^{PC}PAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS^{VL}TVLH^{QD}WLNGKEYKCKVSNKALPAPIEK^T
ISKAKGQPREPQVY^{TL}LP^{PS}REQMTKNQV^{KL}TCLVKG^{FY}PSDIAVEWESNGQPPENNYK^{TT}PPVLDSDGSFFLYSKLT
VDKSRWQQGNV^{FS}CSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGT^{SI}HWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ^QNSN^{SW}PYTFGGG^TKLEIK/RTVAAPSVFI^{FP}PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSS^{TL}TL^{SL}KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP SLTVSPGGTVTLT CGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAFGV PARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVF GGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFA YWGQGT LVTVSS/ GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPE
VTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTV
DKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.77

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYSESI SGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSLSTLTLSKADYEKKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWEQGDVFS CSVMHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS/QAVVTQEP SLTVSPGGTVTLT CGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAFGV PARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVF GGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFA YWGQGT LVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKA
KGQPREPQVYTLPPSREQMTKNQV KLTVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSR
WQQGNVFS CSVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.33

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVT VSS /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT VLVH QDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWEQGDVFS CSVMHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYYISSGGGTTYYLDSVTGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYYFDYWGQGT LVT VSS /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSG
GGGS /QAVVTQEP SLTVSPGGTVTLT CGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAFGV PARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVF GGGTKLTVL /GKPGSGKPGSGKPGSGKPGS /EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKLEWVGRI RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDEYVSWFA YWGQGT LVT VSS /EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT VLVH QDWLNGKEYKCKVSNKALPAPIEKTI SKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSR
WQQGNV FSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3] L1.77

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQQKPDQSPKLLIEYESEISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24A

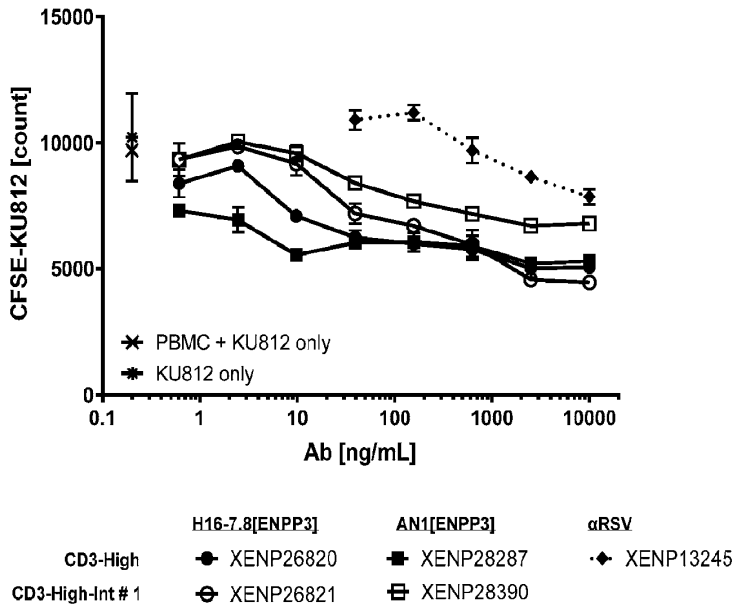


Figure 24B

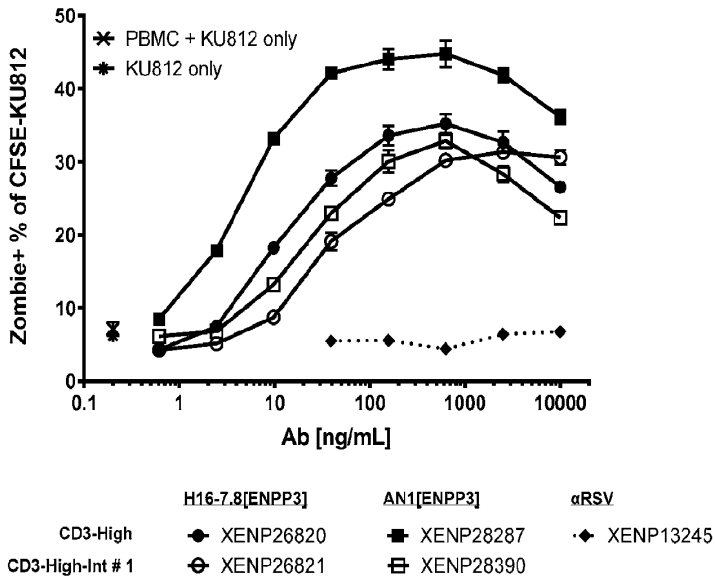


Figure 25A

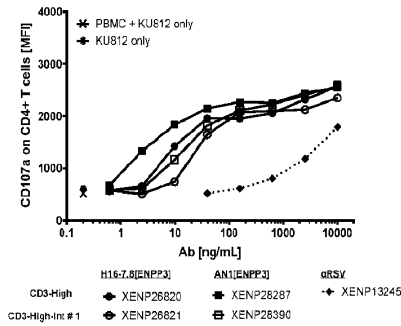


Figure 25B

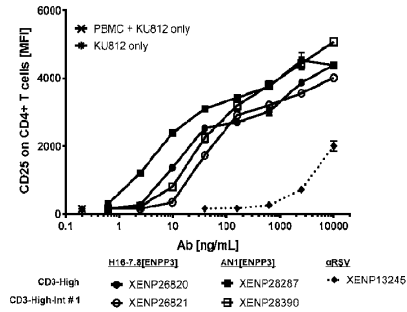


Figure 25C

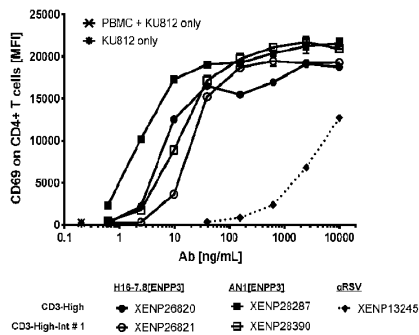


Figure 26A

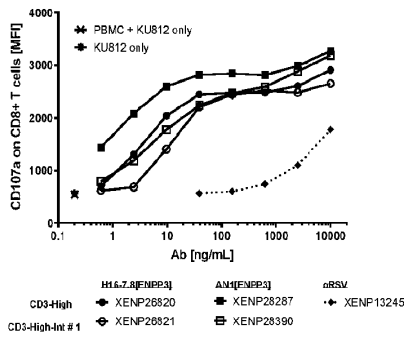


Figure 26B

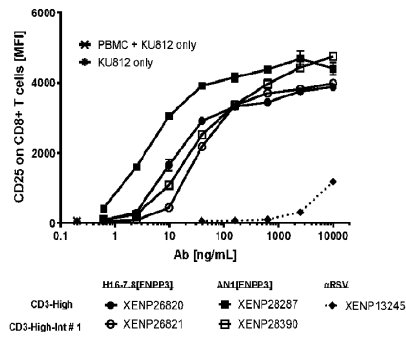


Figure 26C

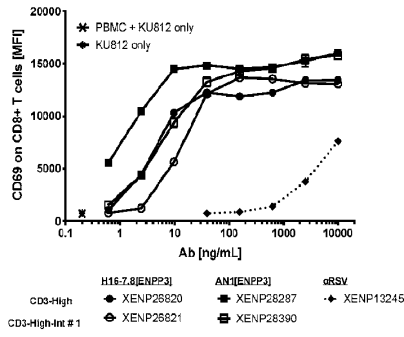


Figure 27A

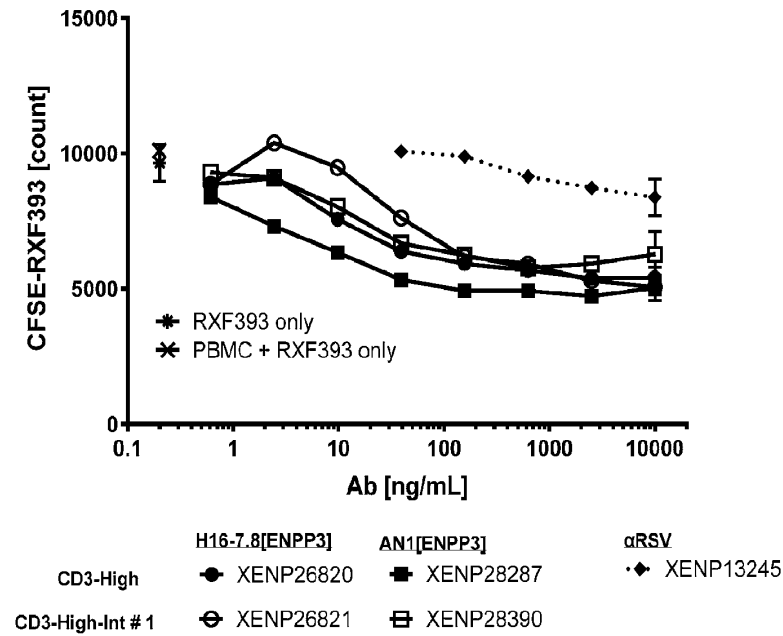


Figure 27B

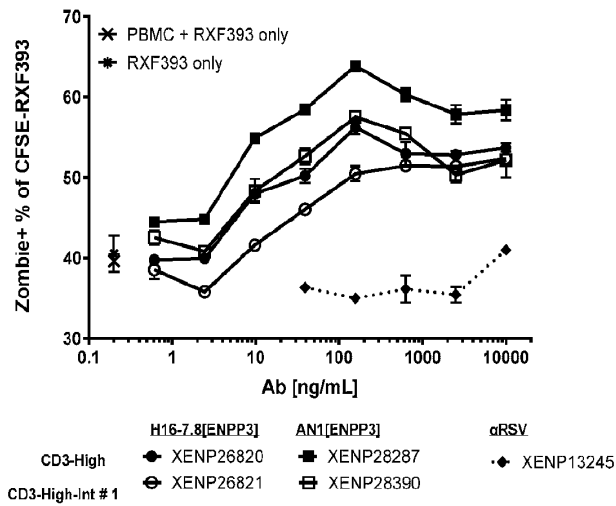


Figure 28A

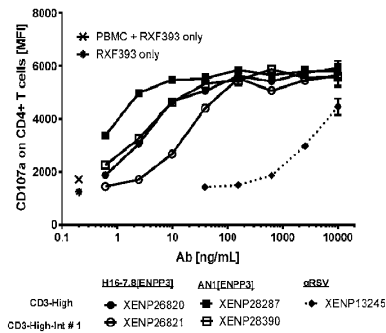


Figure 28B

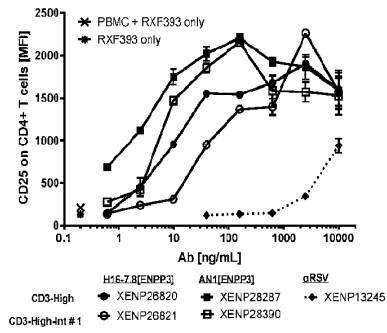


Figure 28C

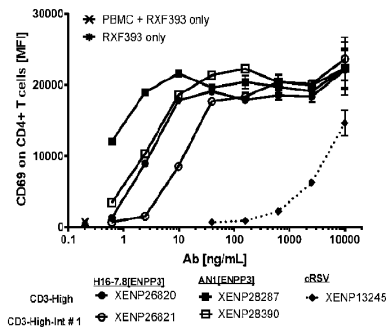


Figure 29A

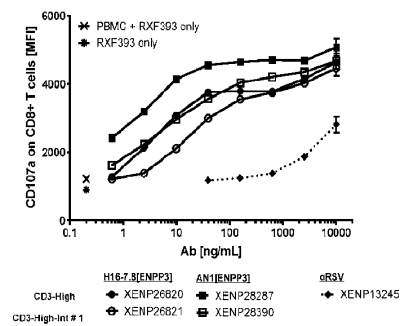


Figure 29B

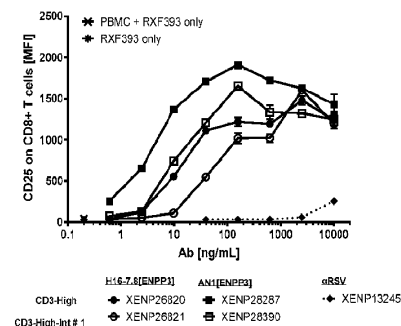


Figure 29C

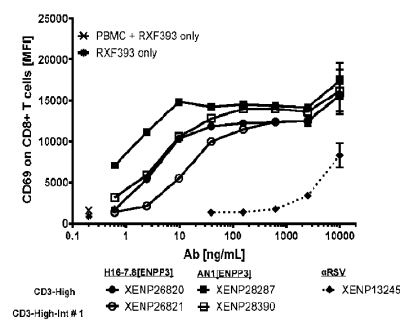
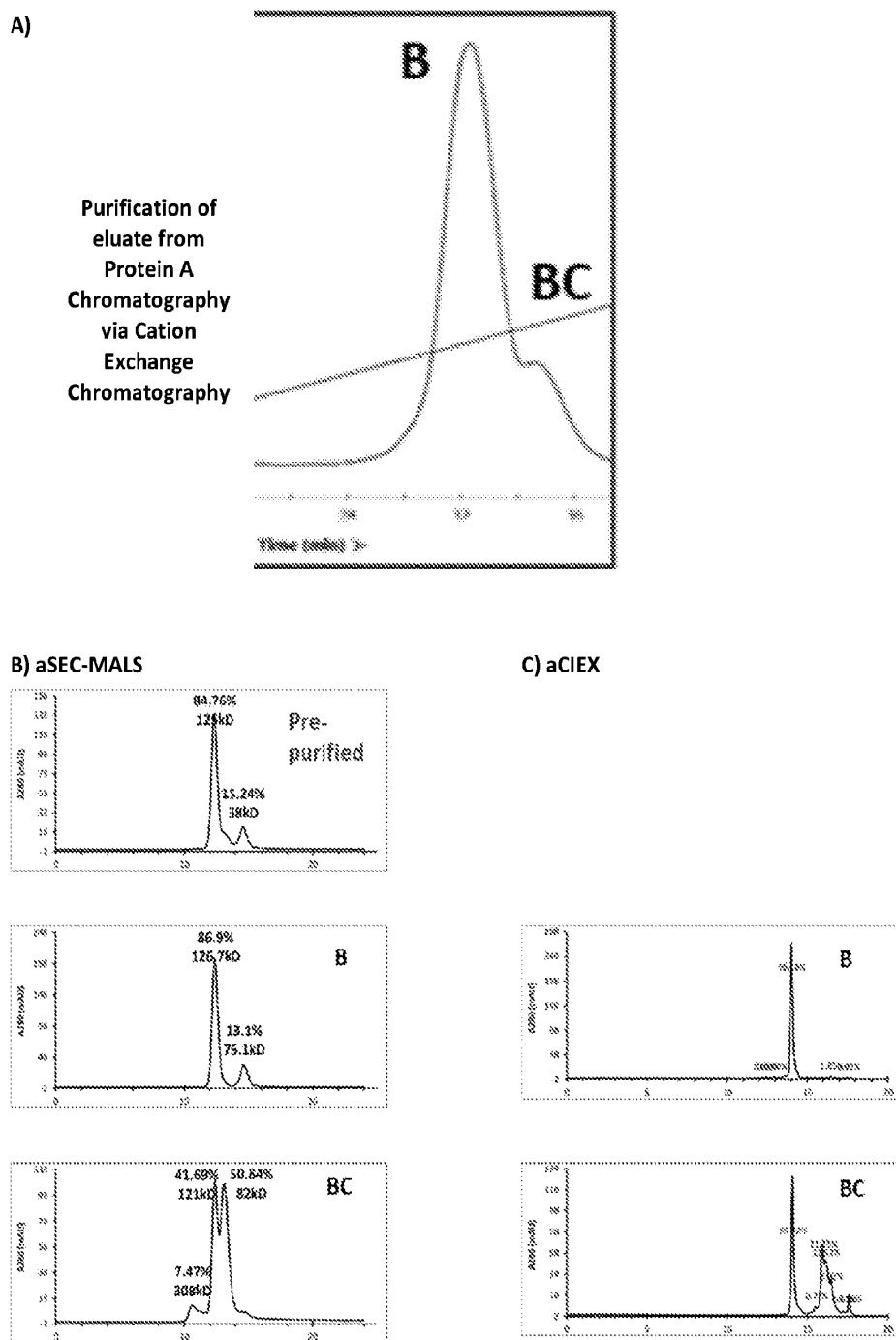


Figure 30



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Figure 31

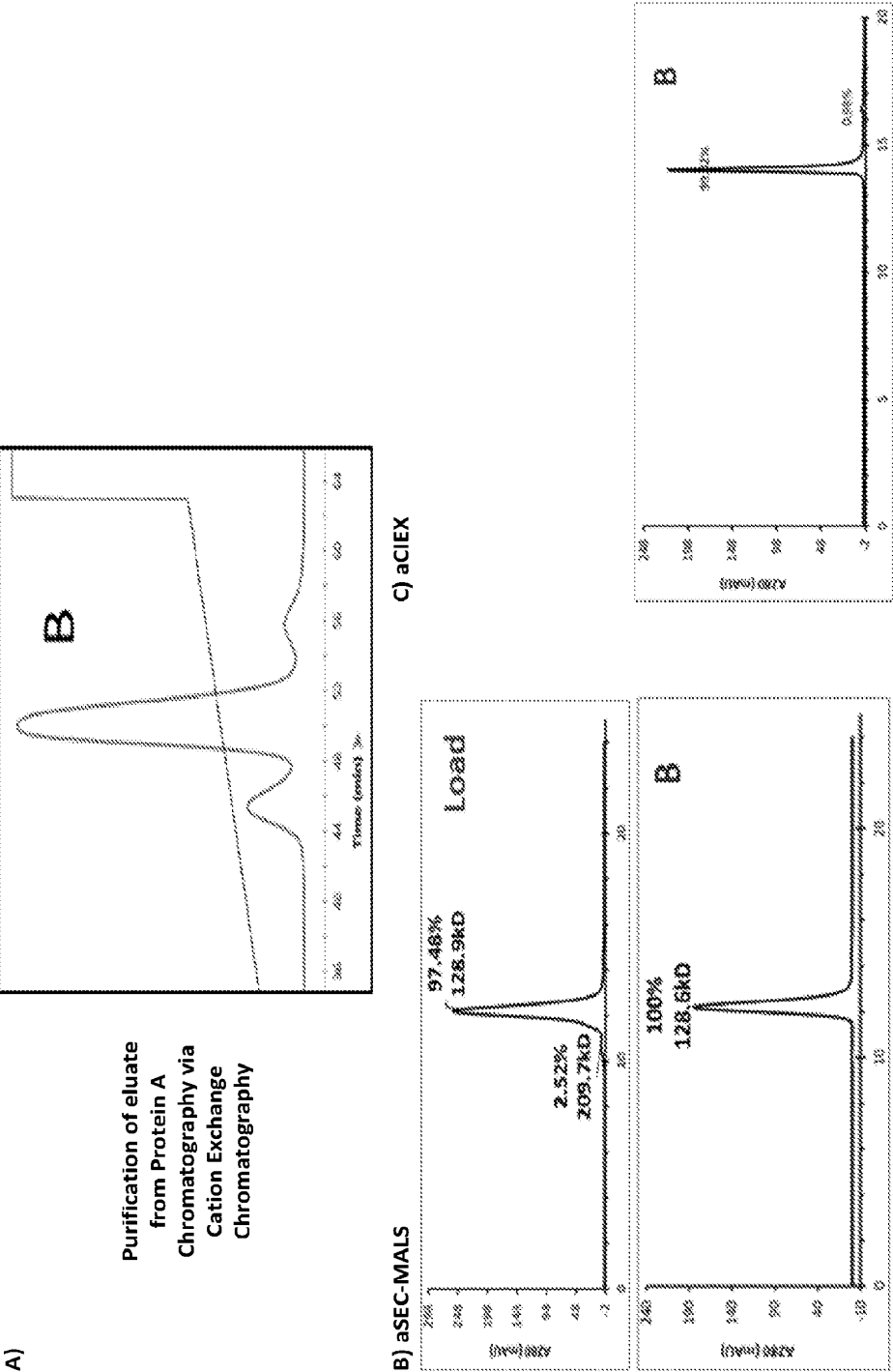


Figure 32

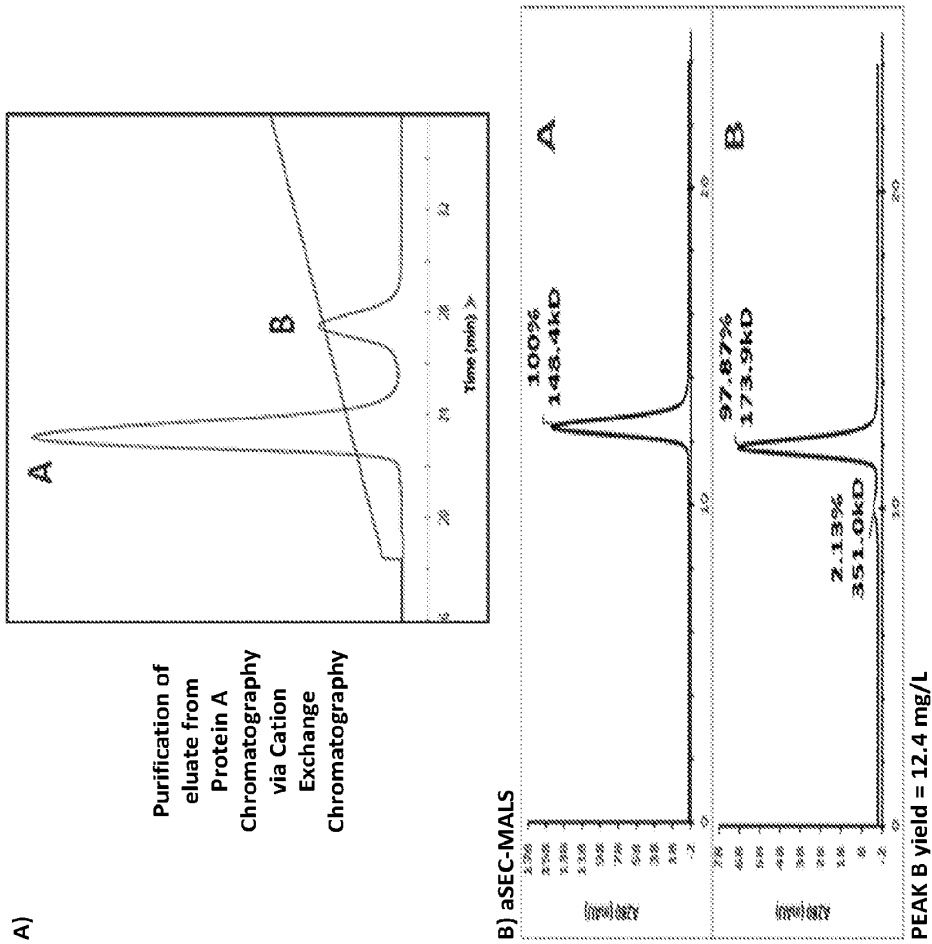
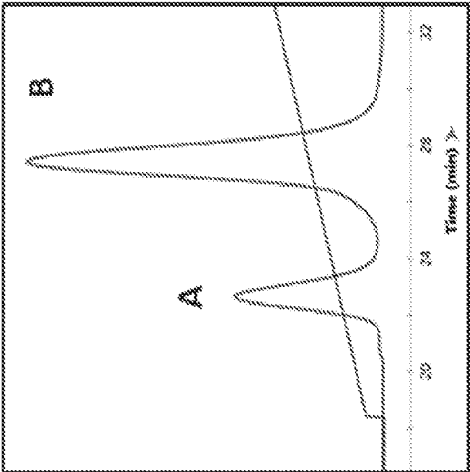


Figure 33

A)



Purification of eluate
from Protein A
Chromatography via
Cation Exchange
Chromatography

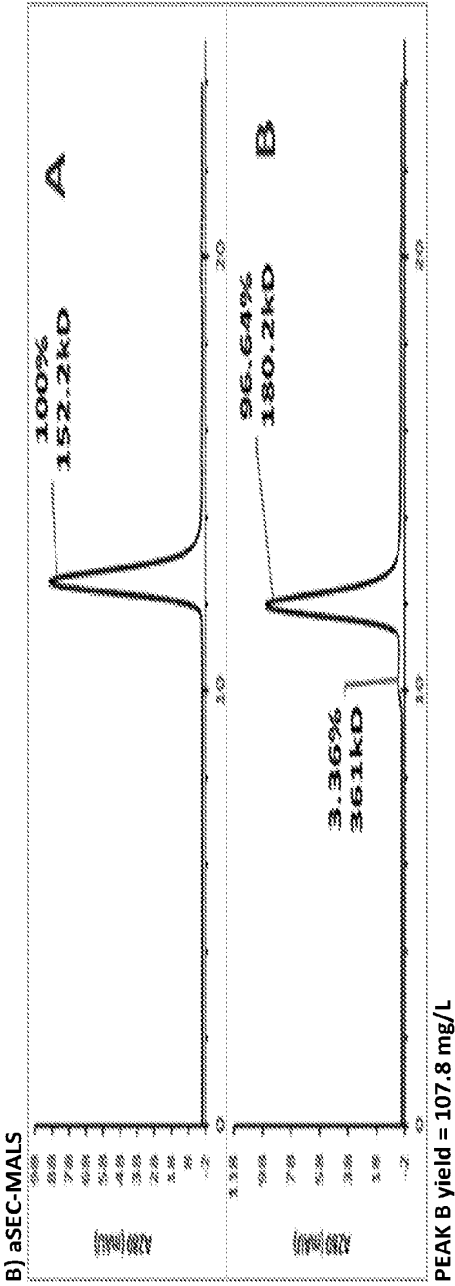


Figure 34

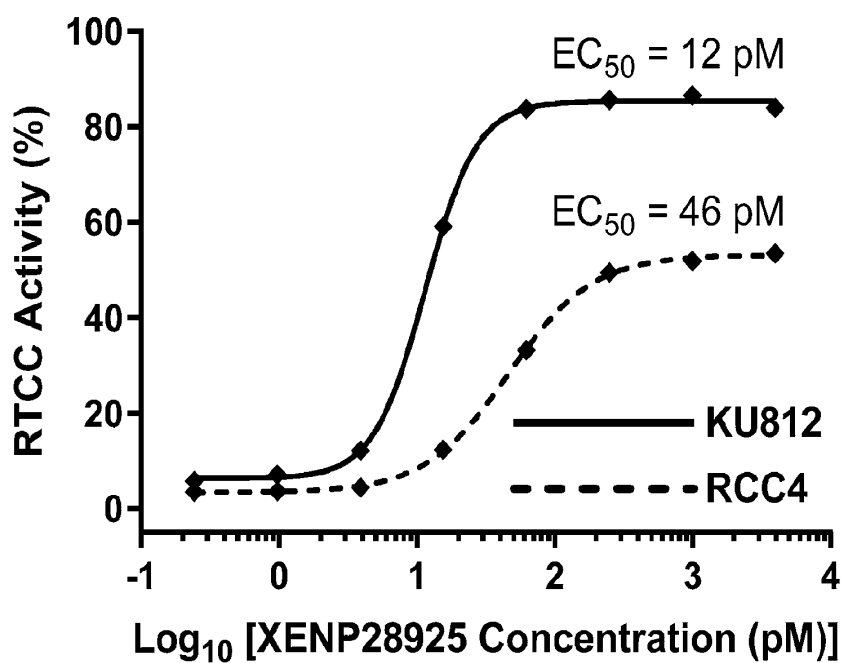


Figure 35

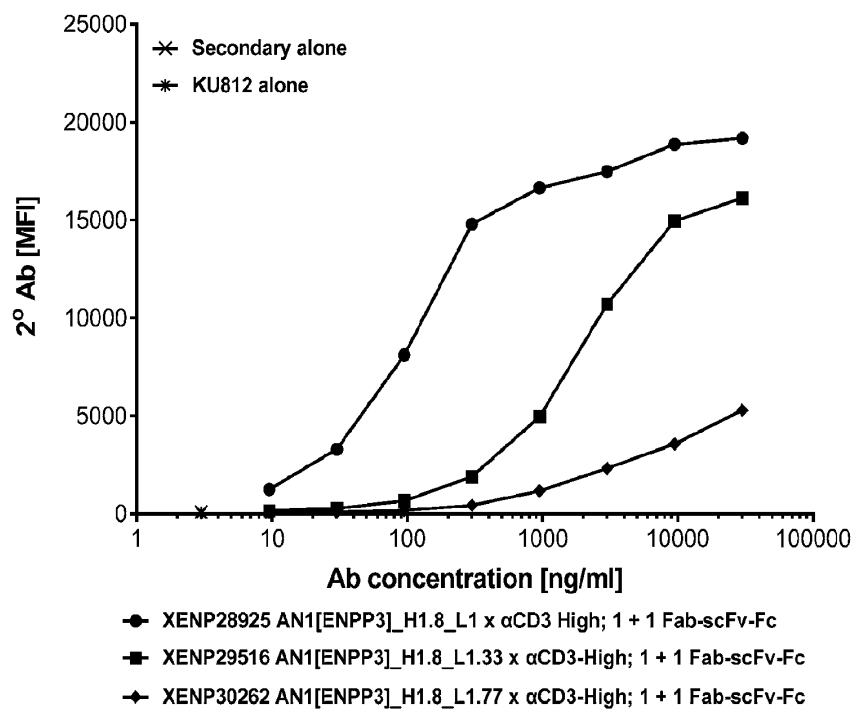


Figure 36

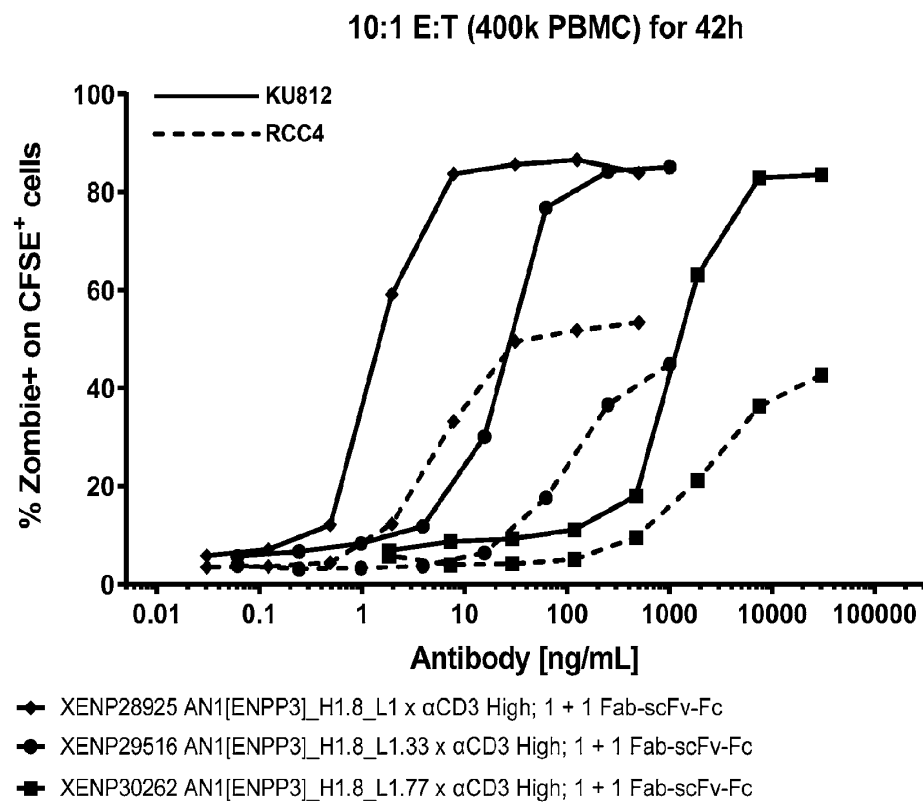


Figure 37A

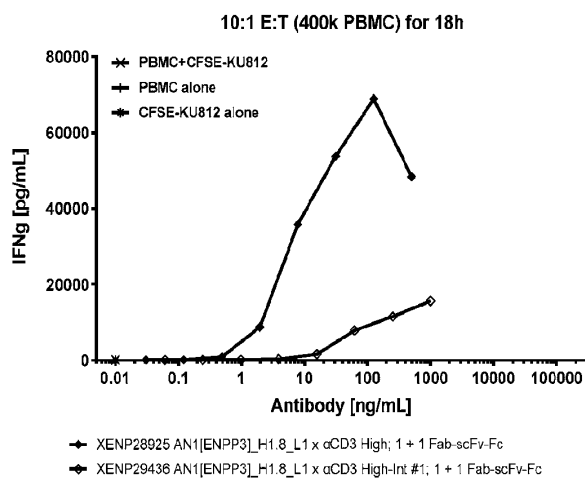


Figure 37B

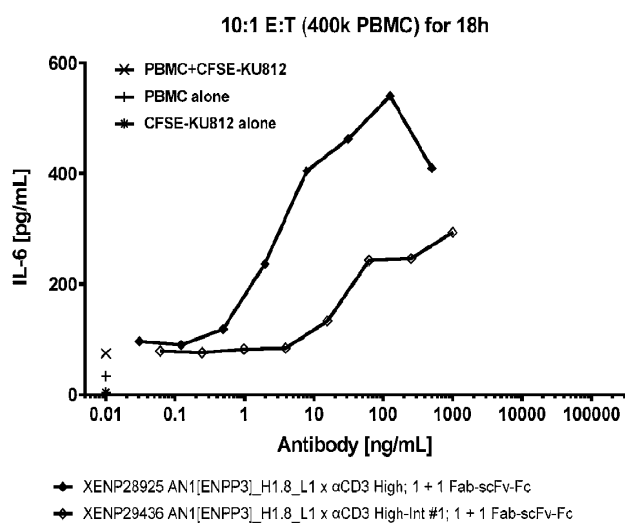


Figure 37C

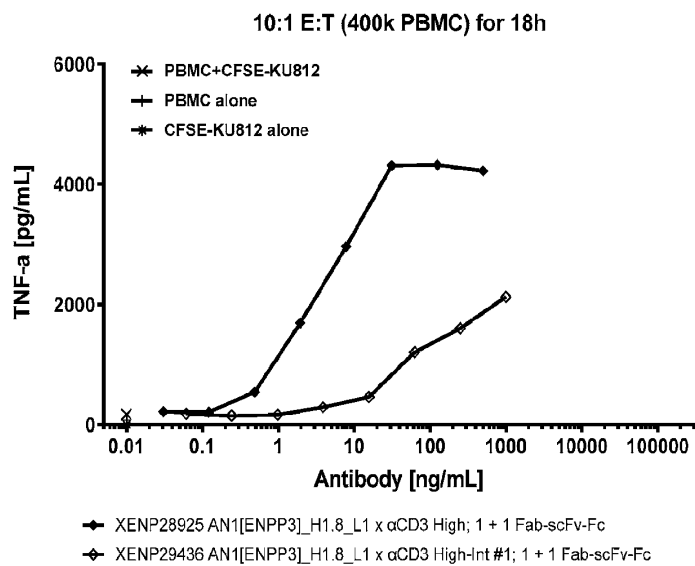


Figure 38

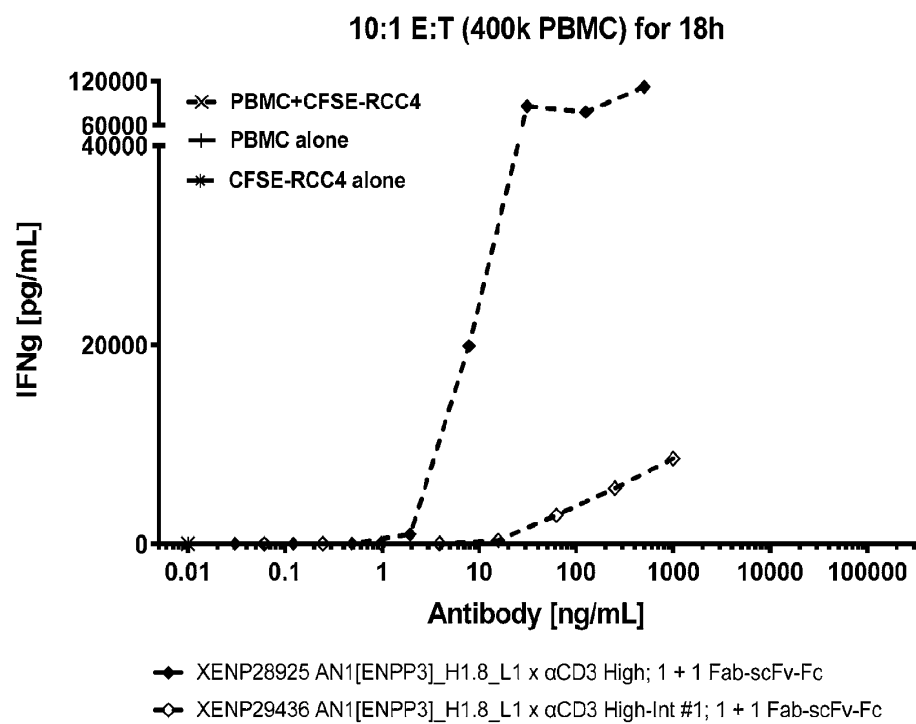


Figure 39

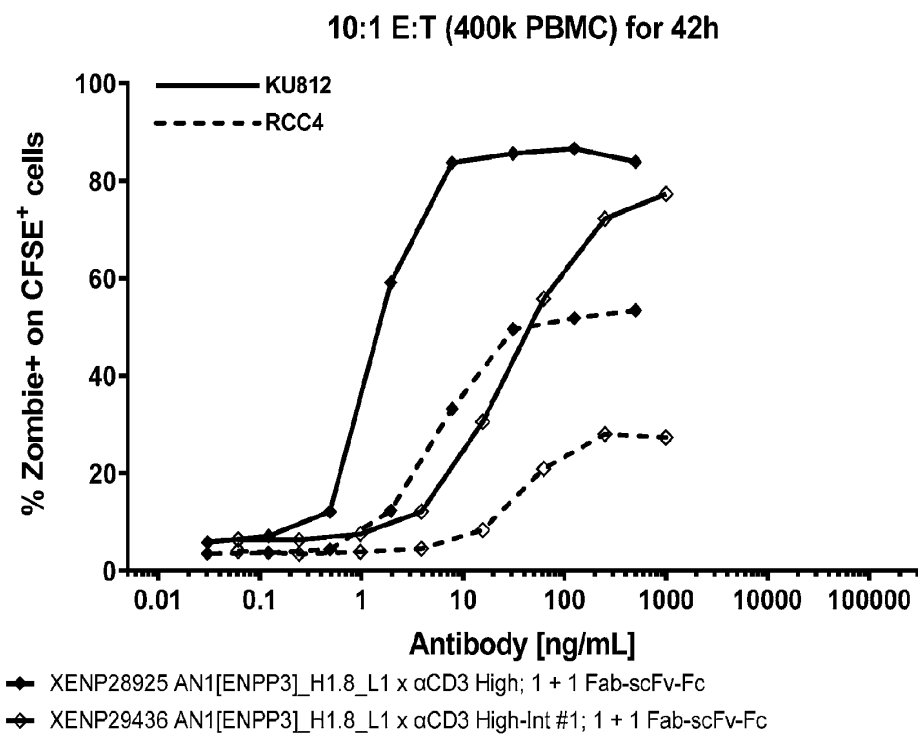


Figure 40

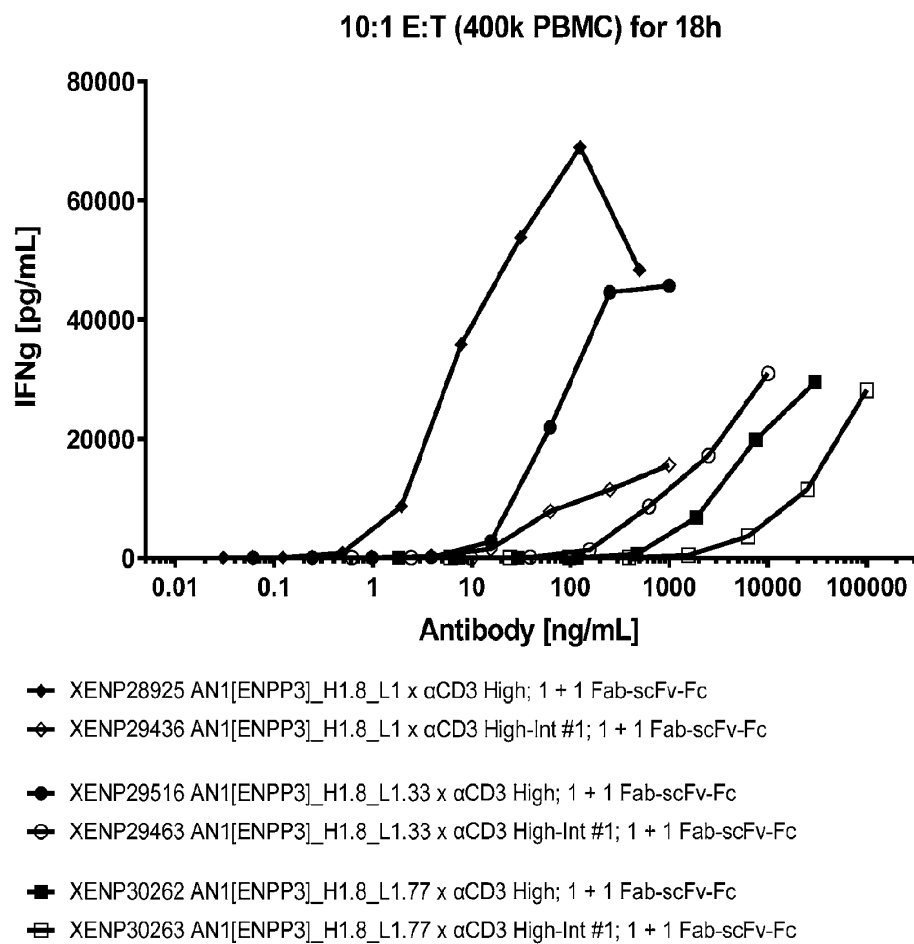


Figure 41

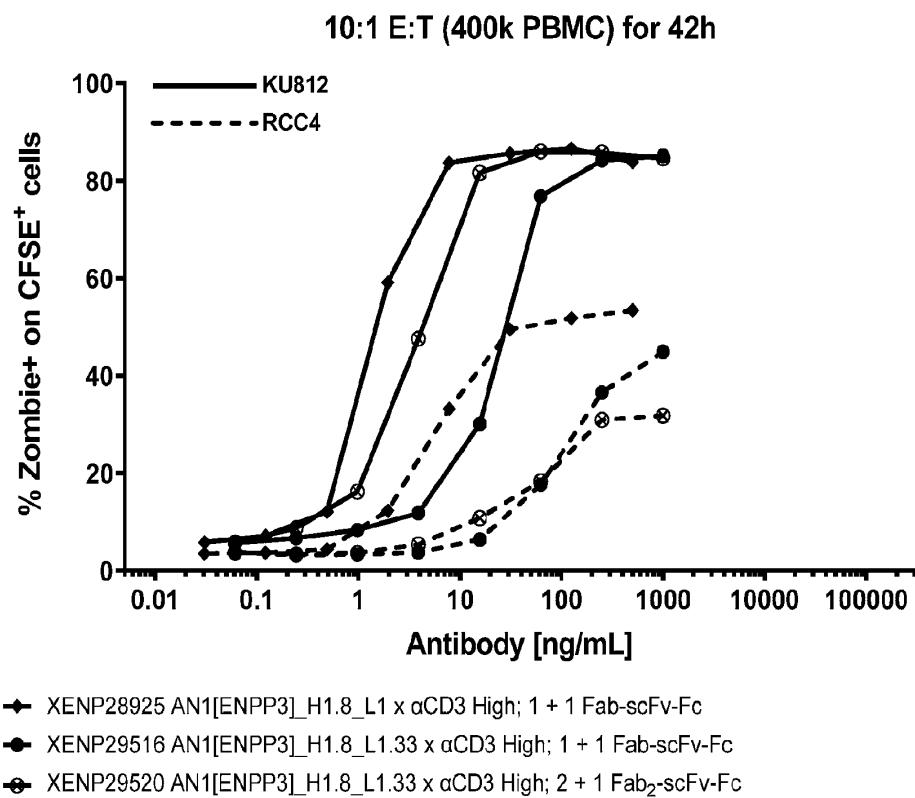


Figure 42

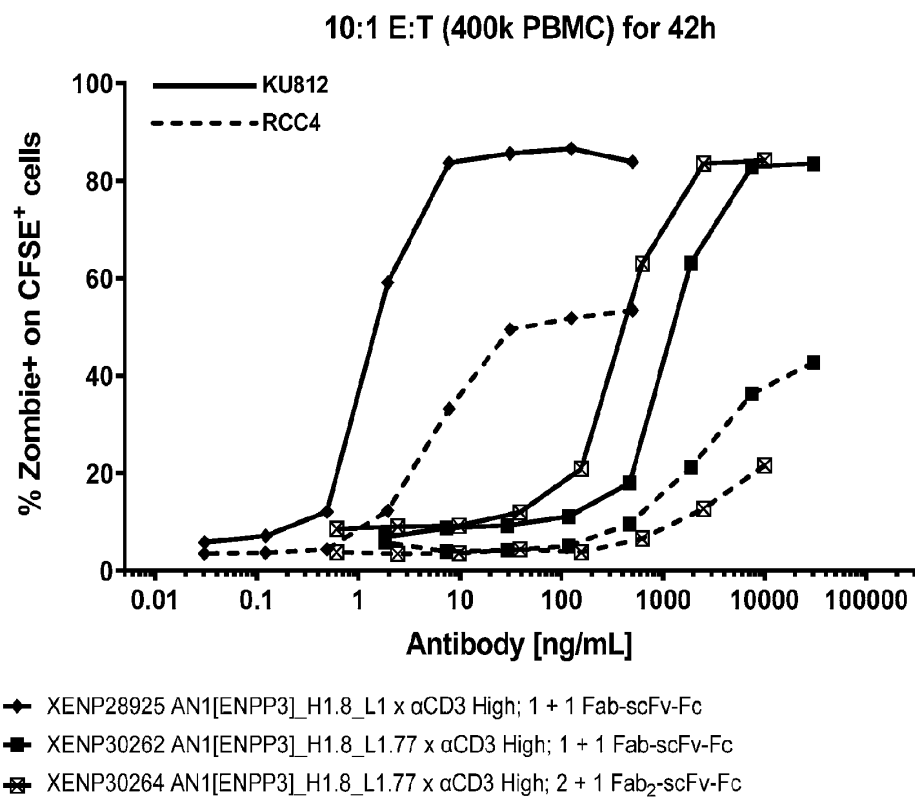


Figure 43

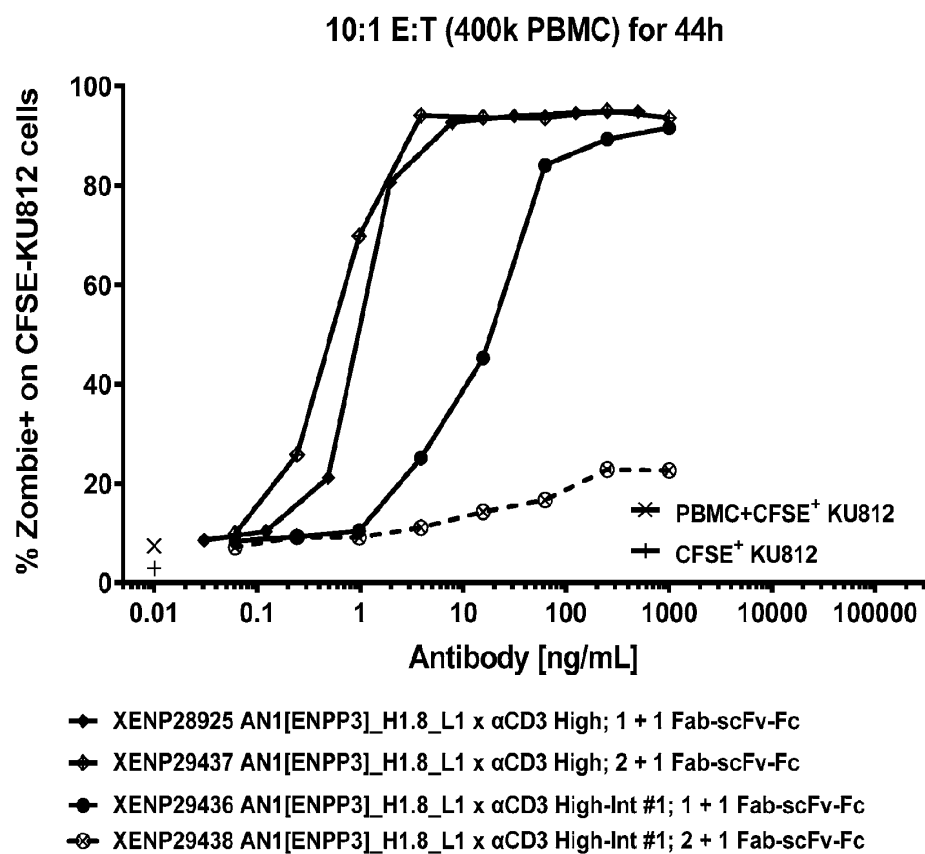


Figure 44

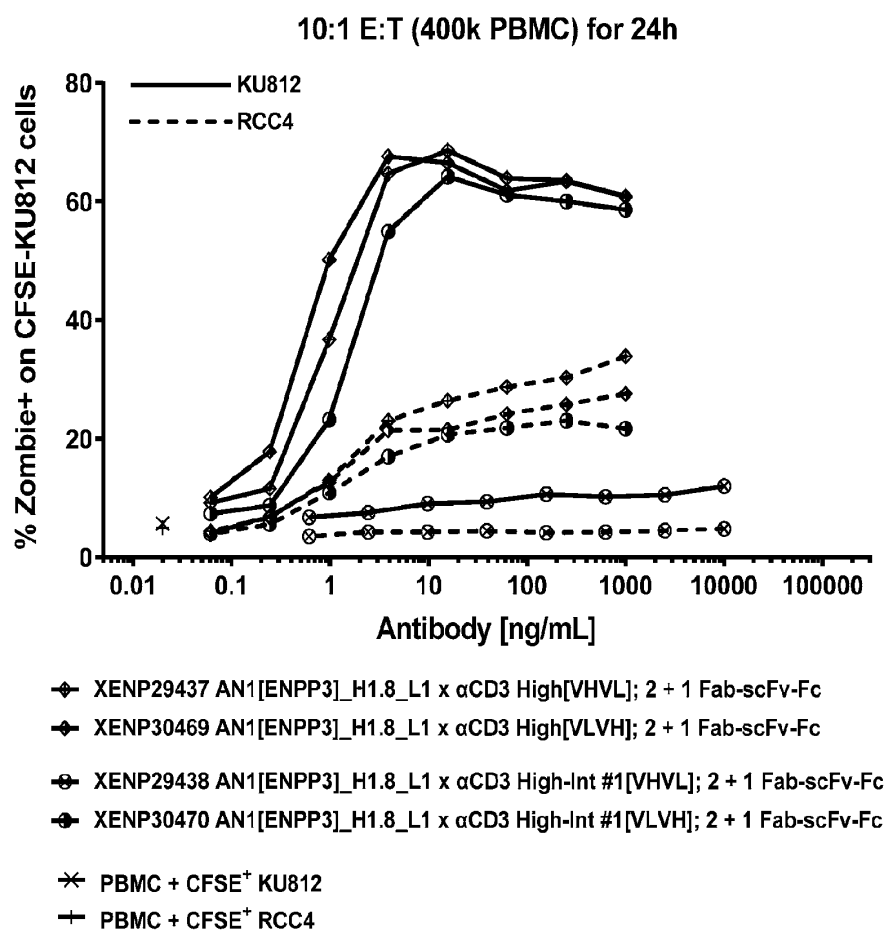


Figure 45

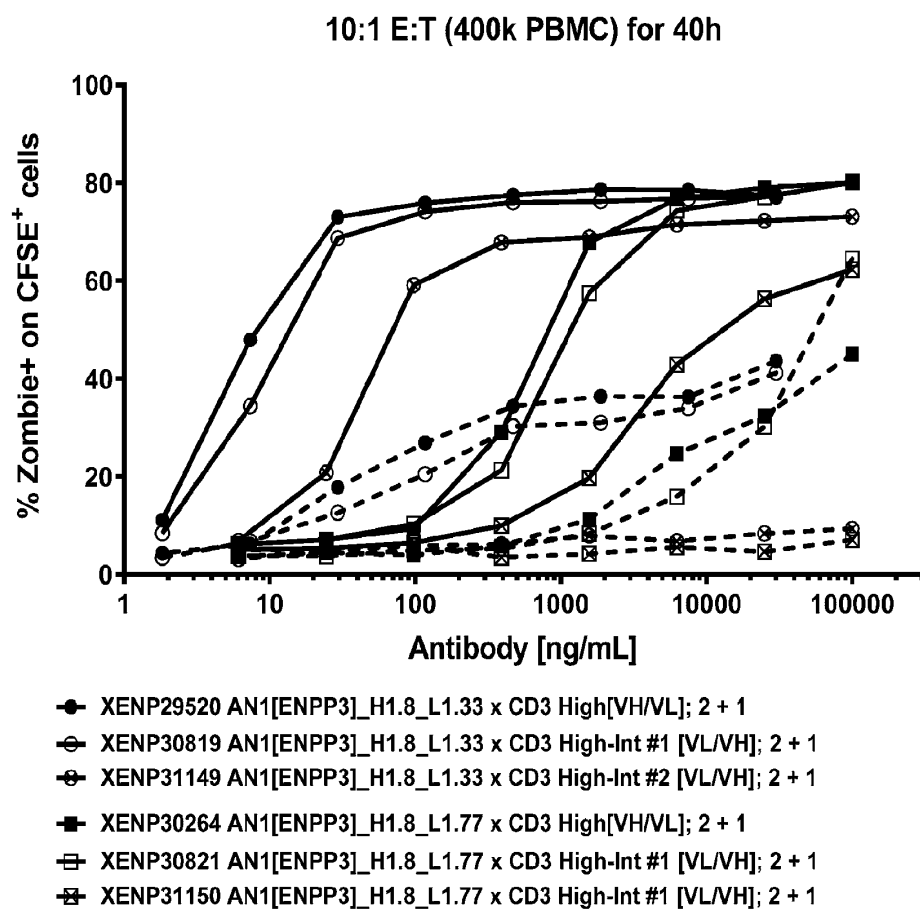


Figure 46

> XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K**XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K Heavy Chain**

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKPYYADSVKGRFTISRDN
SKN TLFLQMNSLRAEDTAVYYCATNDDYWGQTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEP
TVTS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CTPPCPAPPV AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQD WLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLT
CLVKGFYPSDIAVEWESNGQPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQK
SLSLSPGK

XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K Light Chain

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAFGIPARFSGSGSGT
DFTLTISS LEPEDFAVYYCQSSNWPRFTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC
LLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC

Figure 47

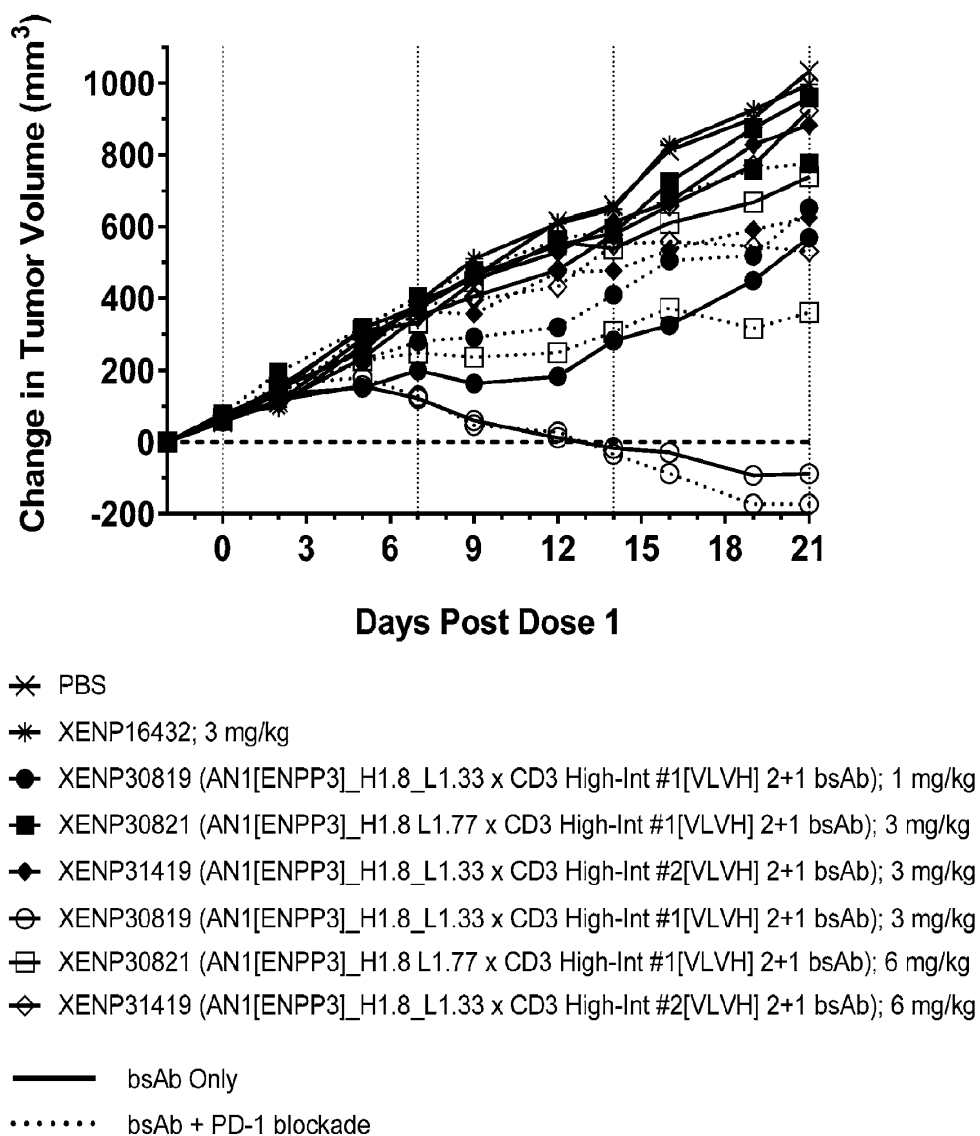
Baseline-corrected of Group median TM Caliper vs time

Figure 48A

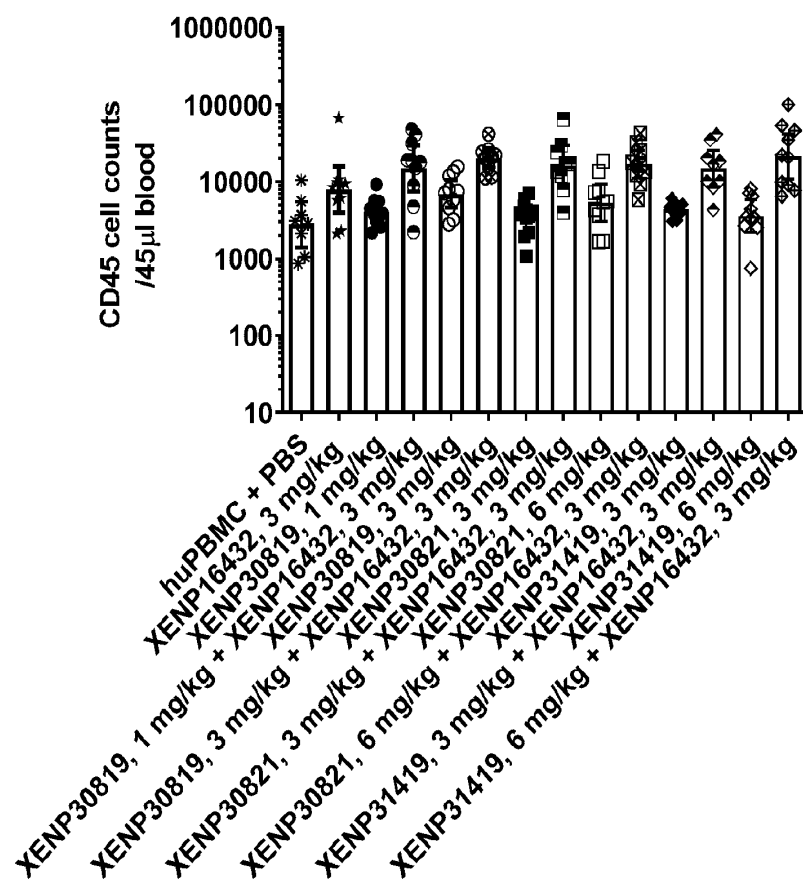


Figure 48B

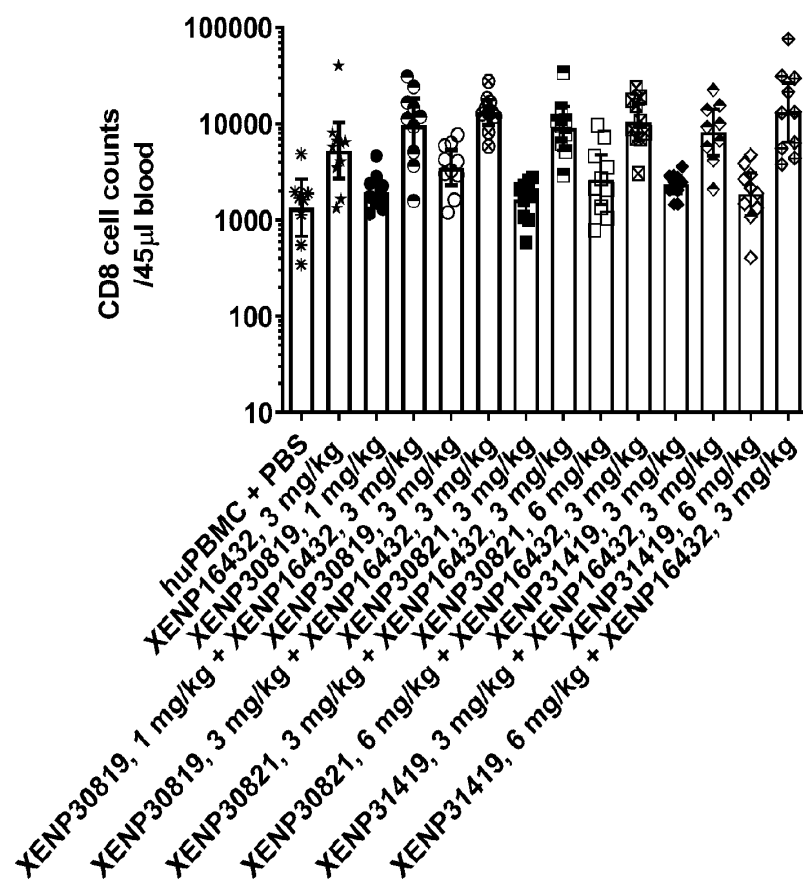


Figure 48C

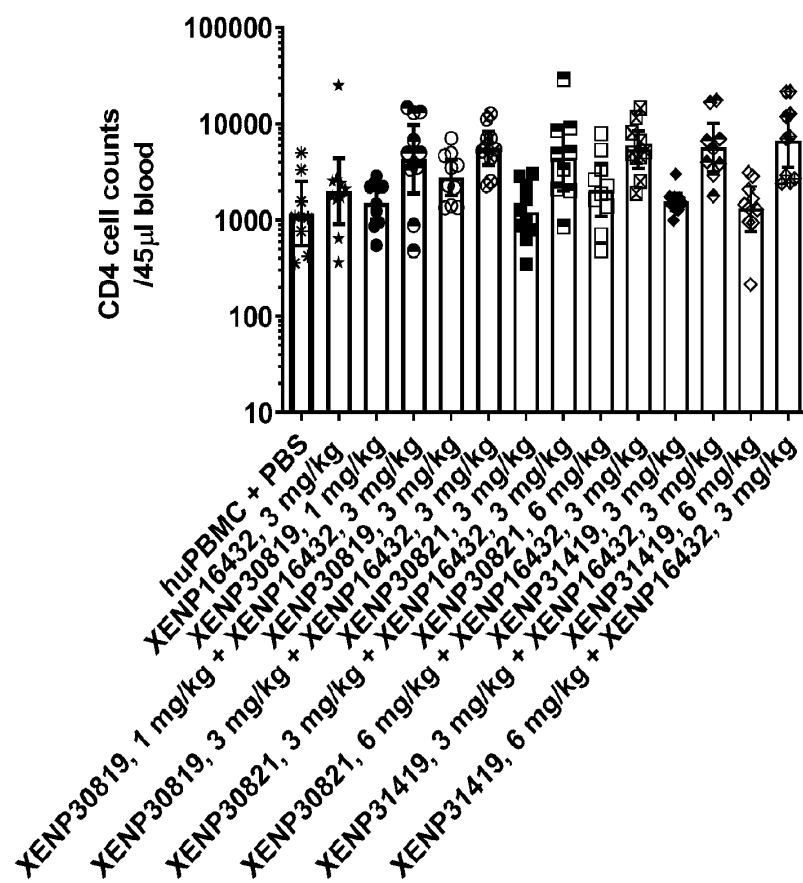
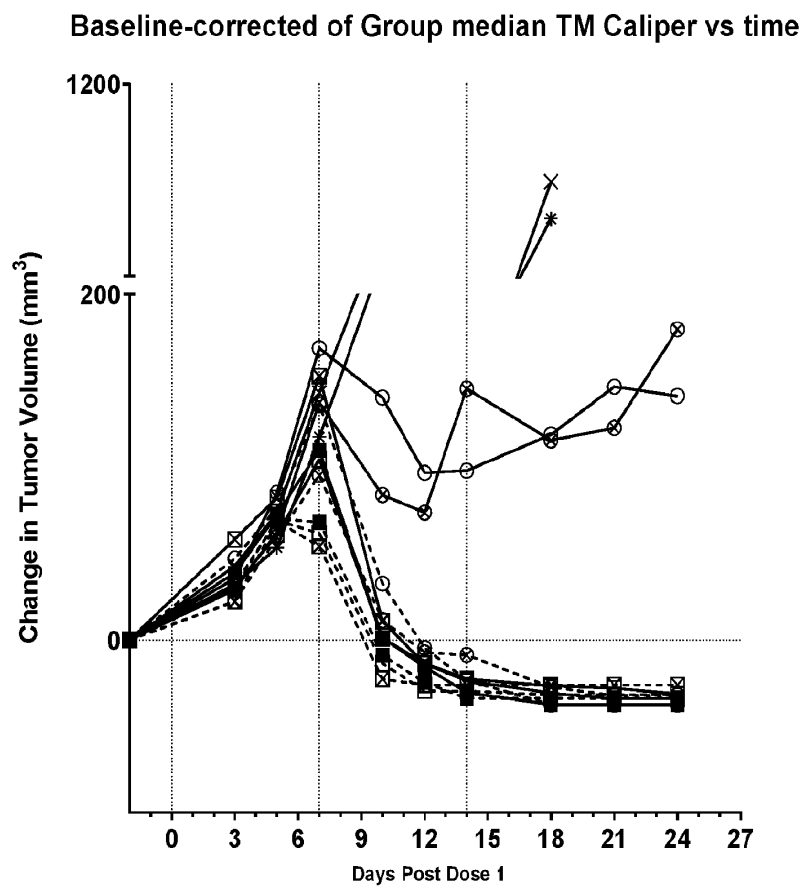


Figure 49



- ✕ huPBMC + PBS
- ✱ XENP16432; 3 mg/kg
- ⊖ XENP31419 (AN1[ENPP3]_{H1.8_L1.33} x CD3 High-Int #2[VLVH] 2+1 bsAb); 3 mg/kg
- ⊕ XENP31419 (AN1[ENPP3]_{H1.8_L1.33} x CD3 High-Int #2[VLVH] 2+1 bsAb); 10 mg/kg
- XENP30819 (AN1[ENPP3]_{H1.8_L1.33} x CD3 High-Int #1[VLVH] 2+1 bsAb); 1 mg/kg
- ⊞ XENP30819 (AN1[ENPP3]_{H1.8_L1.33} x CD3 High-Int #1[VLVH] 2+1 bsAb); 3 mg/kg
- ⊠ XENP30819 (AN1[ENPP3]_{H1.8_L1.33} x CD3 High-Int #1[VLVH] 2+1 bsAb); 10 mg/kg
- bsAb Only
- bsAb + PD-1 blockade

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Figure 50A

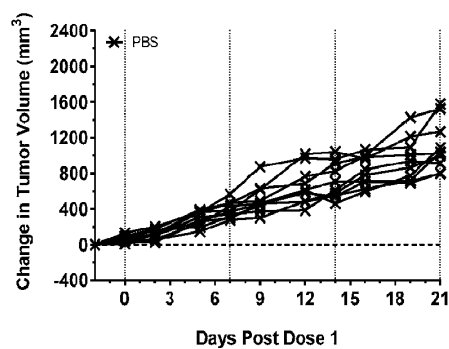


Figure 50B

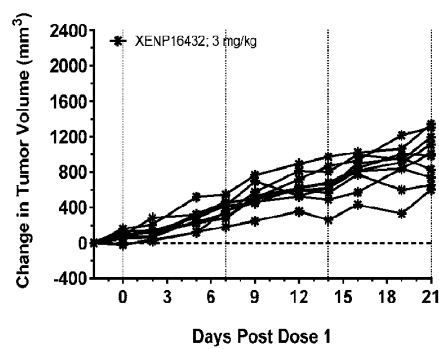


Figure 50C

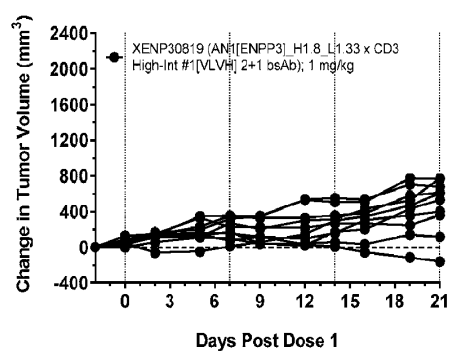


Figure 50D

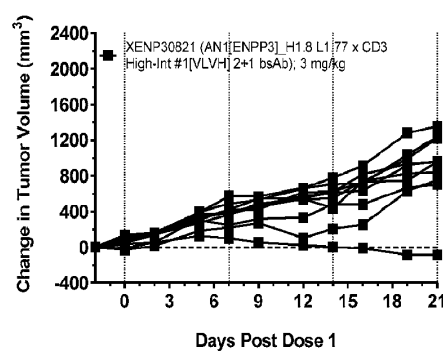


Figure 50E

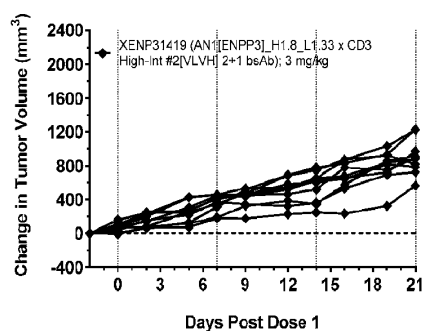


Figure 50F

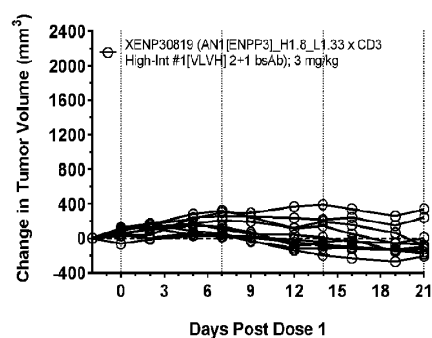


Figure 50G

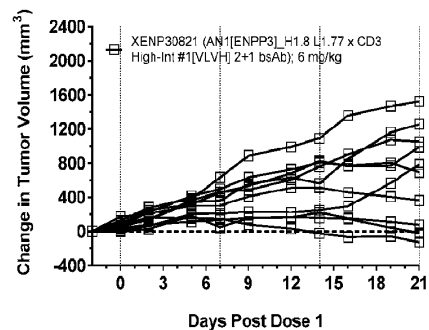


Figure 50H

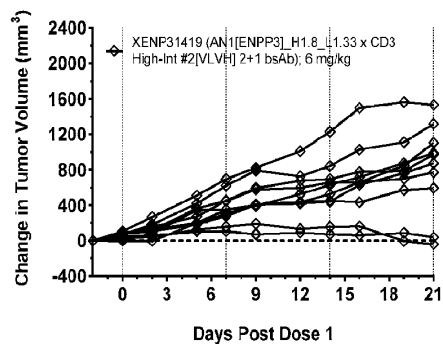


Figure 50I

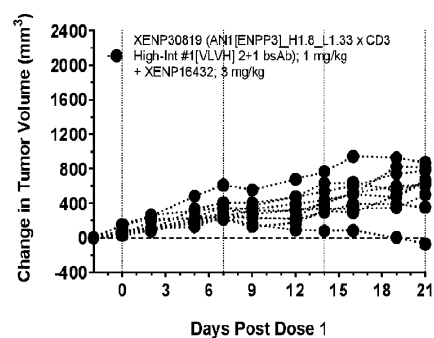


Figure 50J

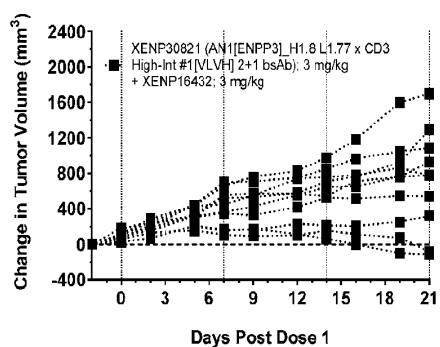


Figure 50K

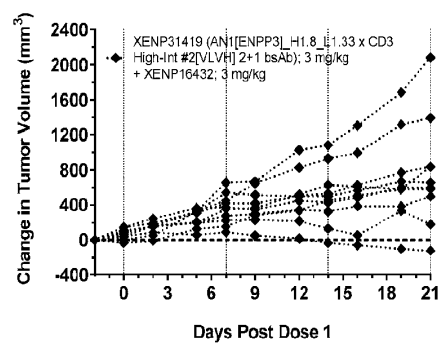


Figure 50L

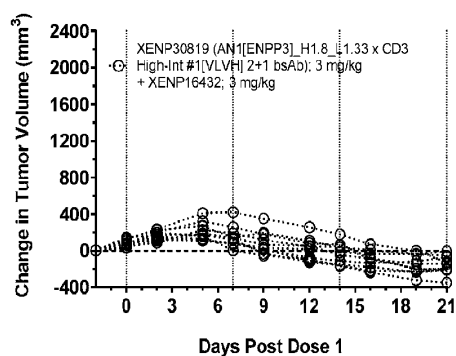


Figure 50M

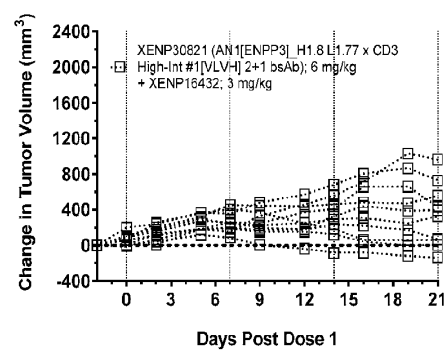


Figure 50N

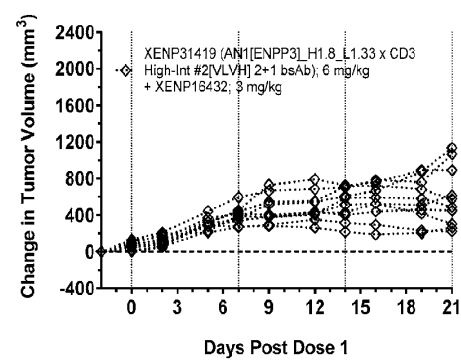


Figure 51A

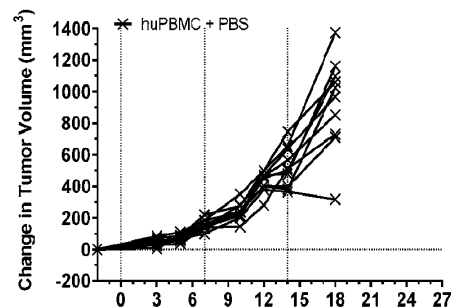


Figure 51B

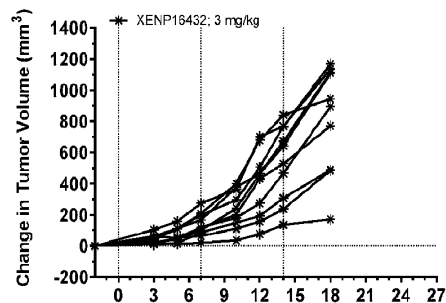


Figure 51C

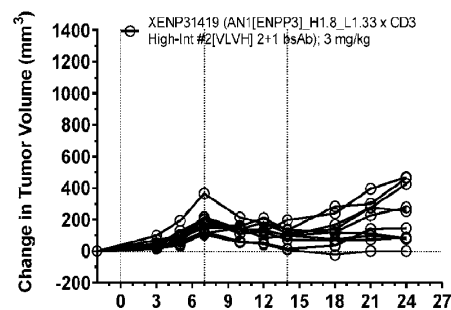


Figure 51D

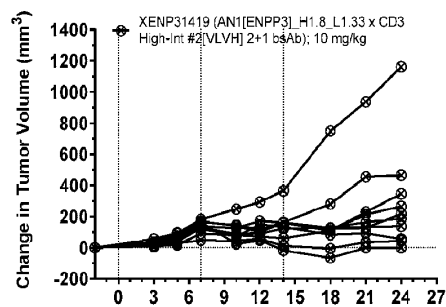


Figure 51E

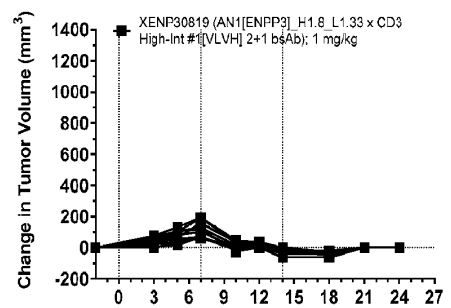


Figure 51F

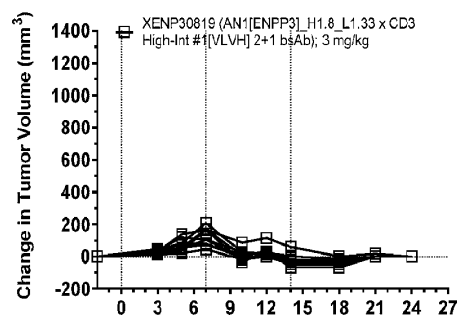


Figure 51G

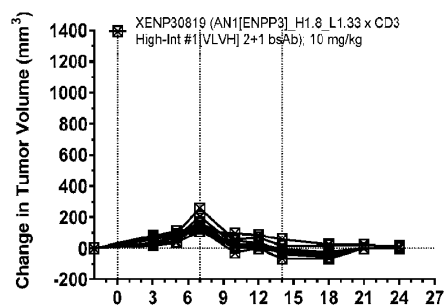


Figure 51H

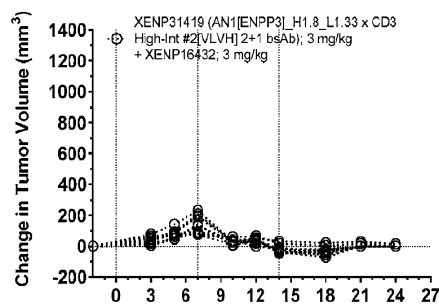


Figure 51I

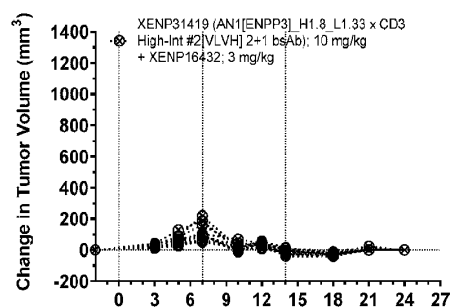


Figure 51J

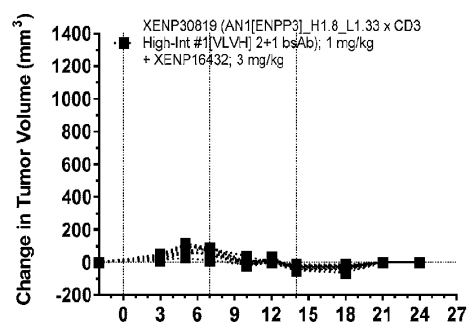


Figure 51K

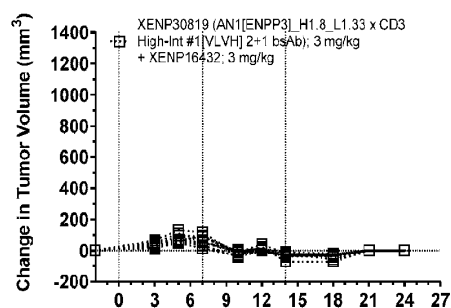
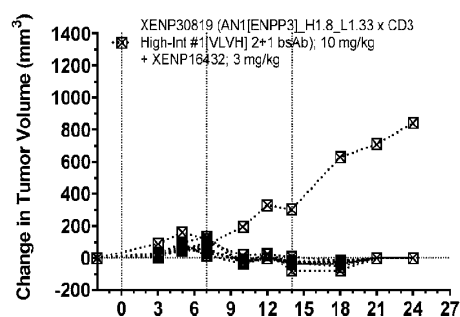
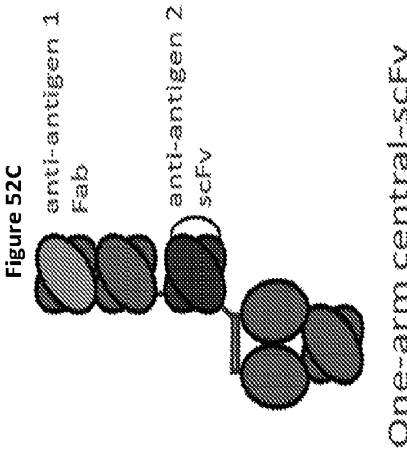
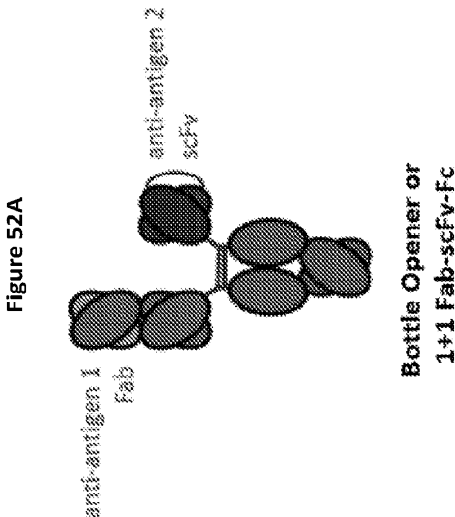
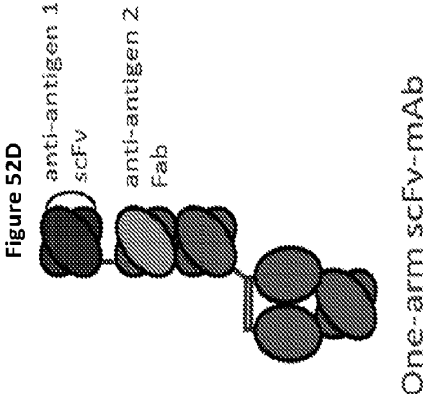
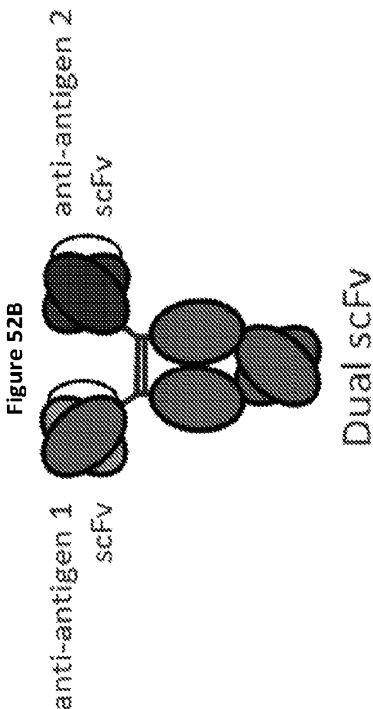
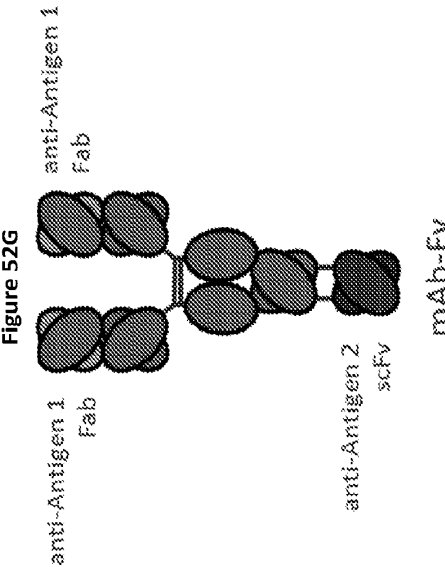
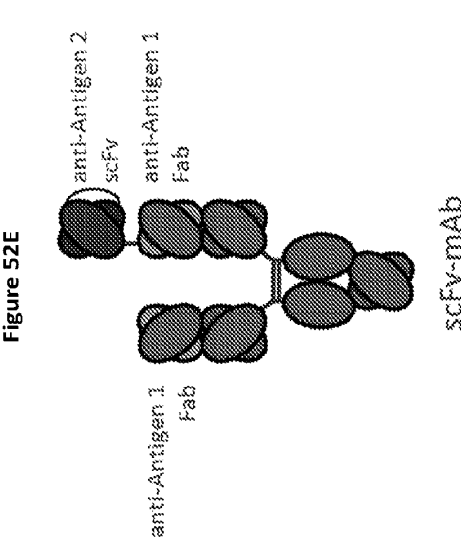
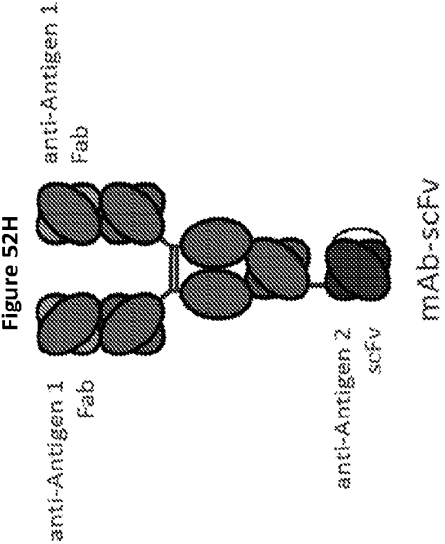
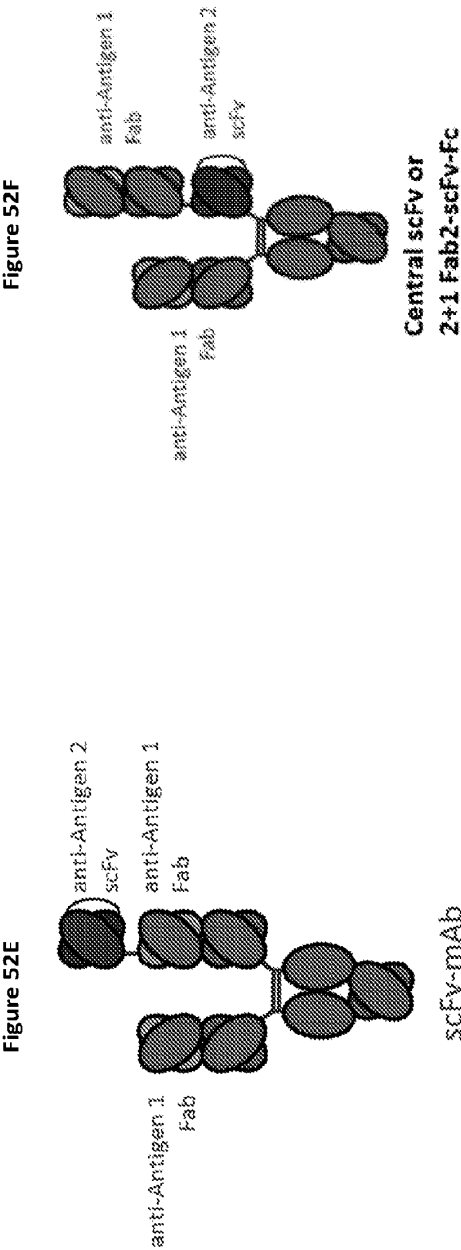
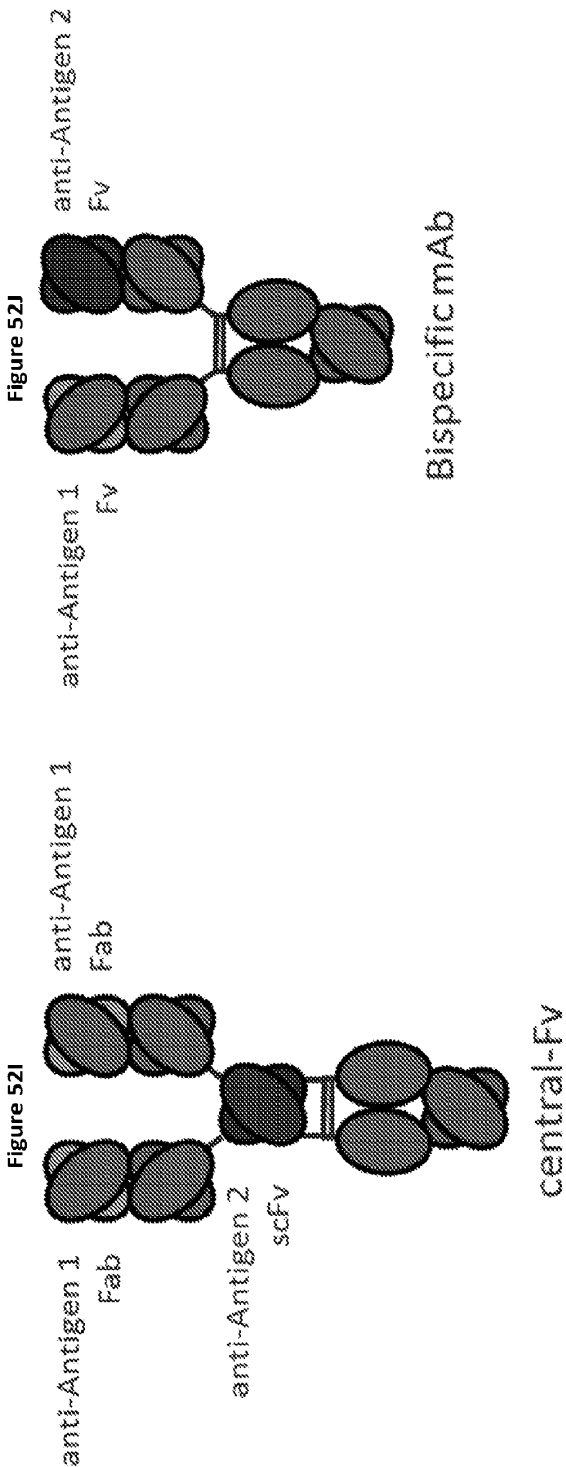


Figure 51L









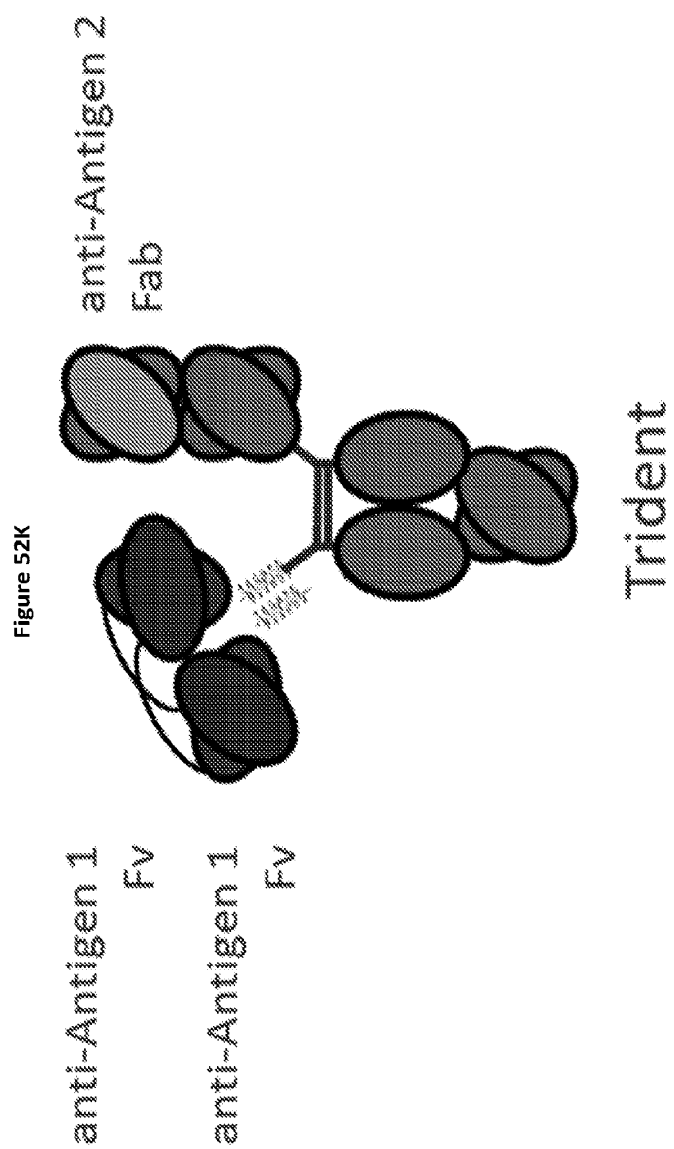


Figure 53

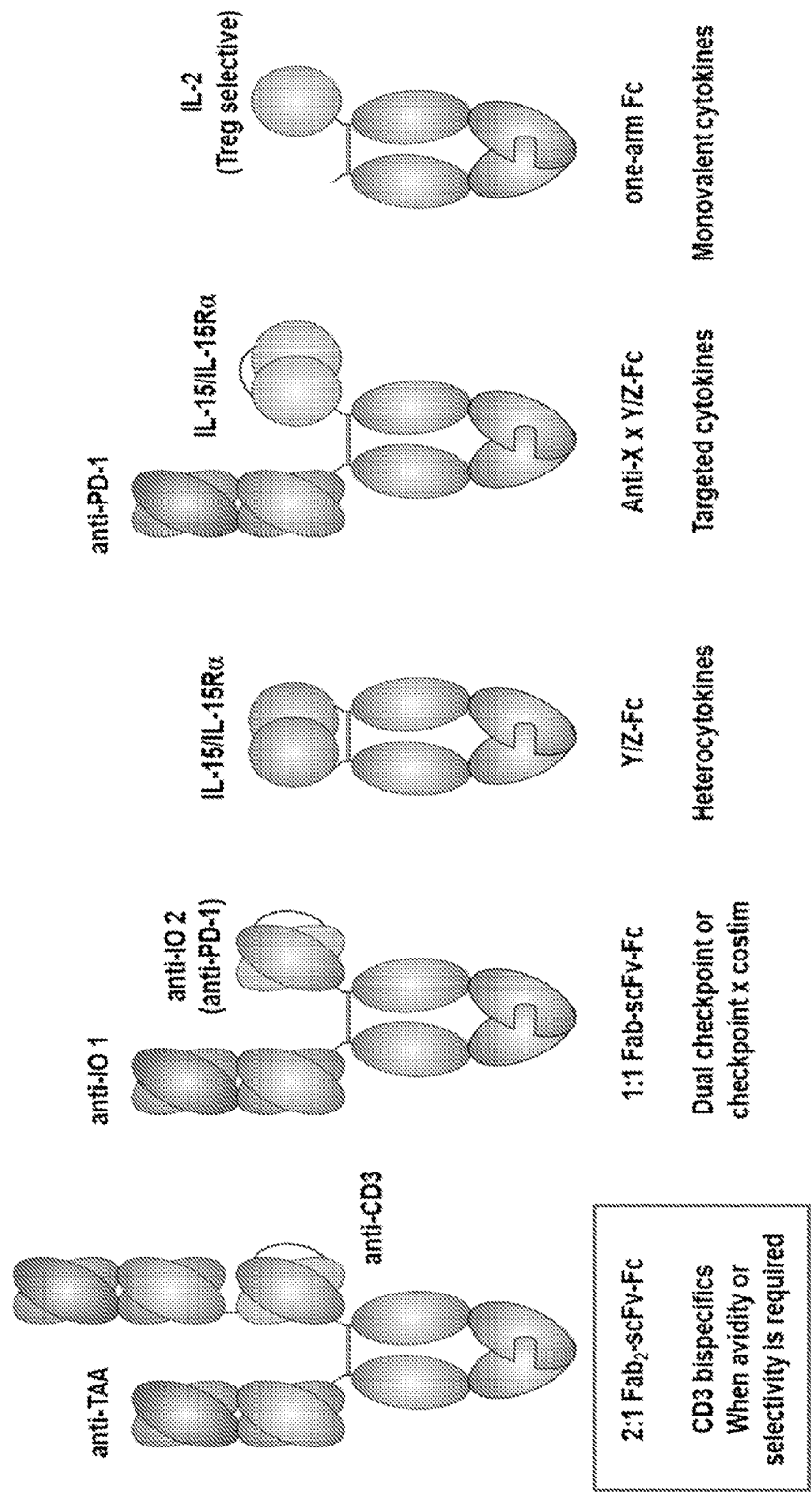


Figure 54

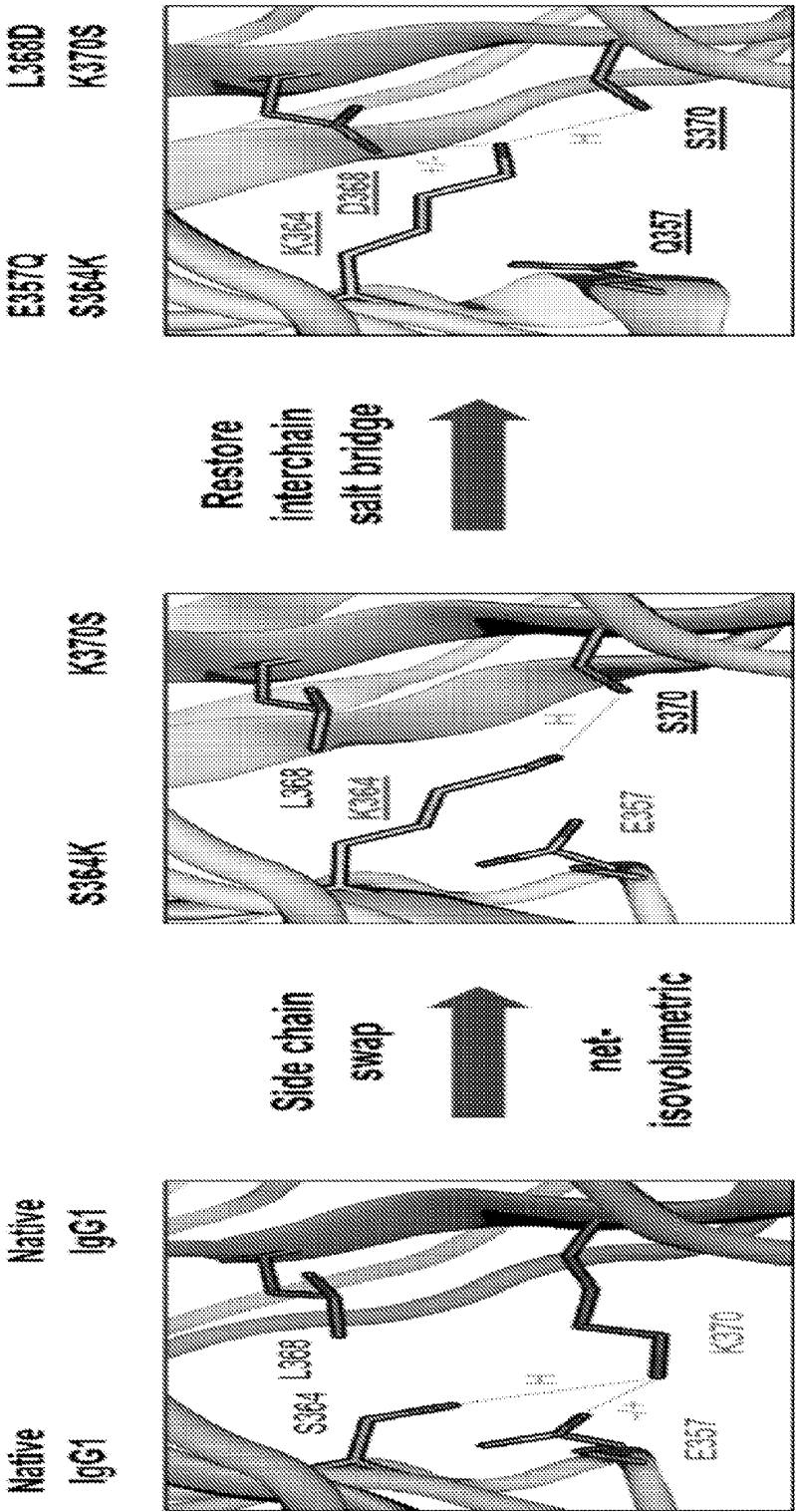
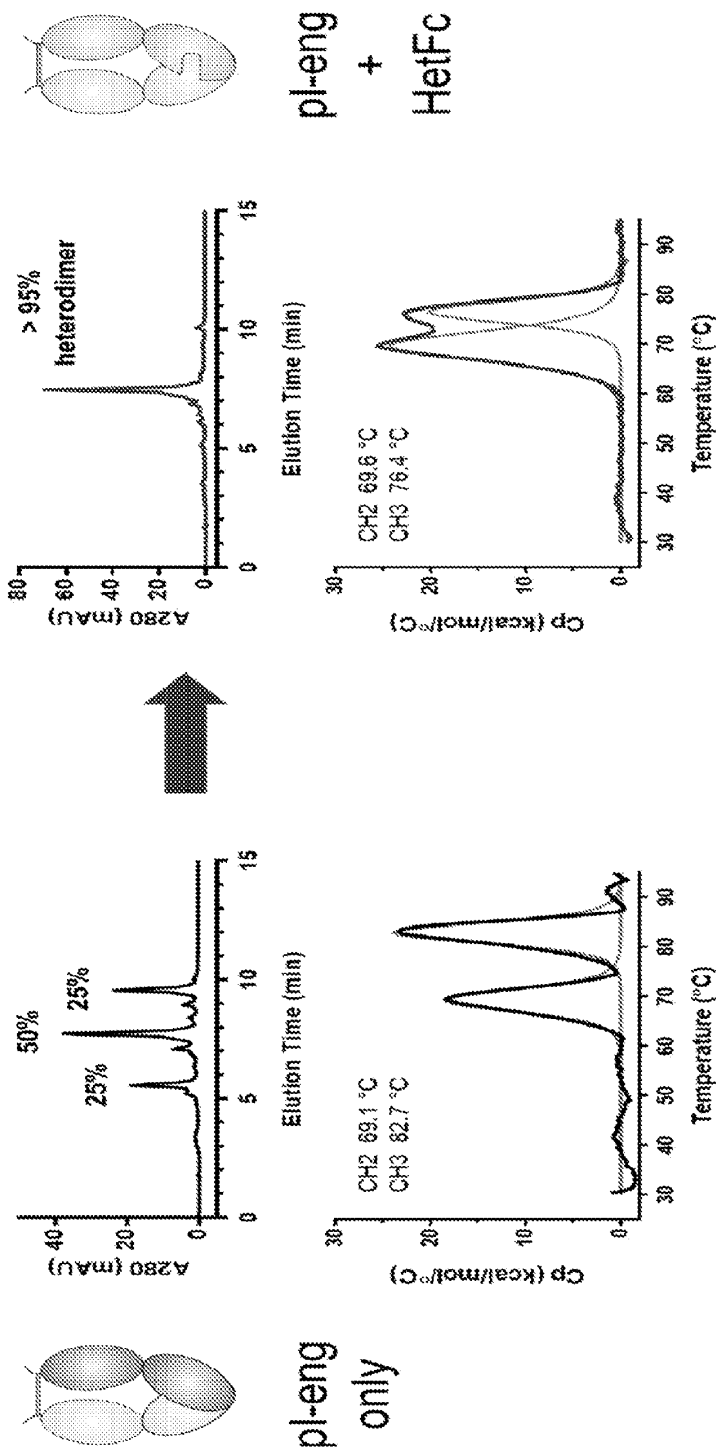


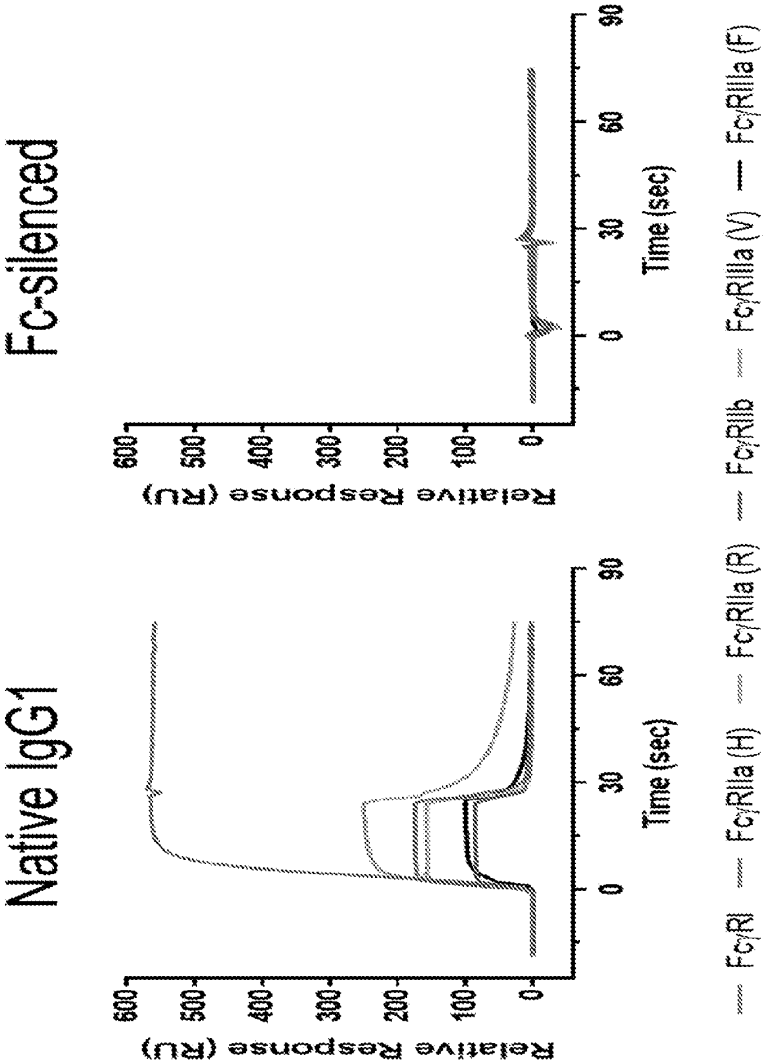
Figure 55

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

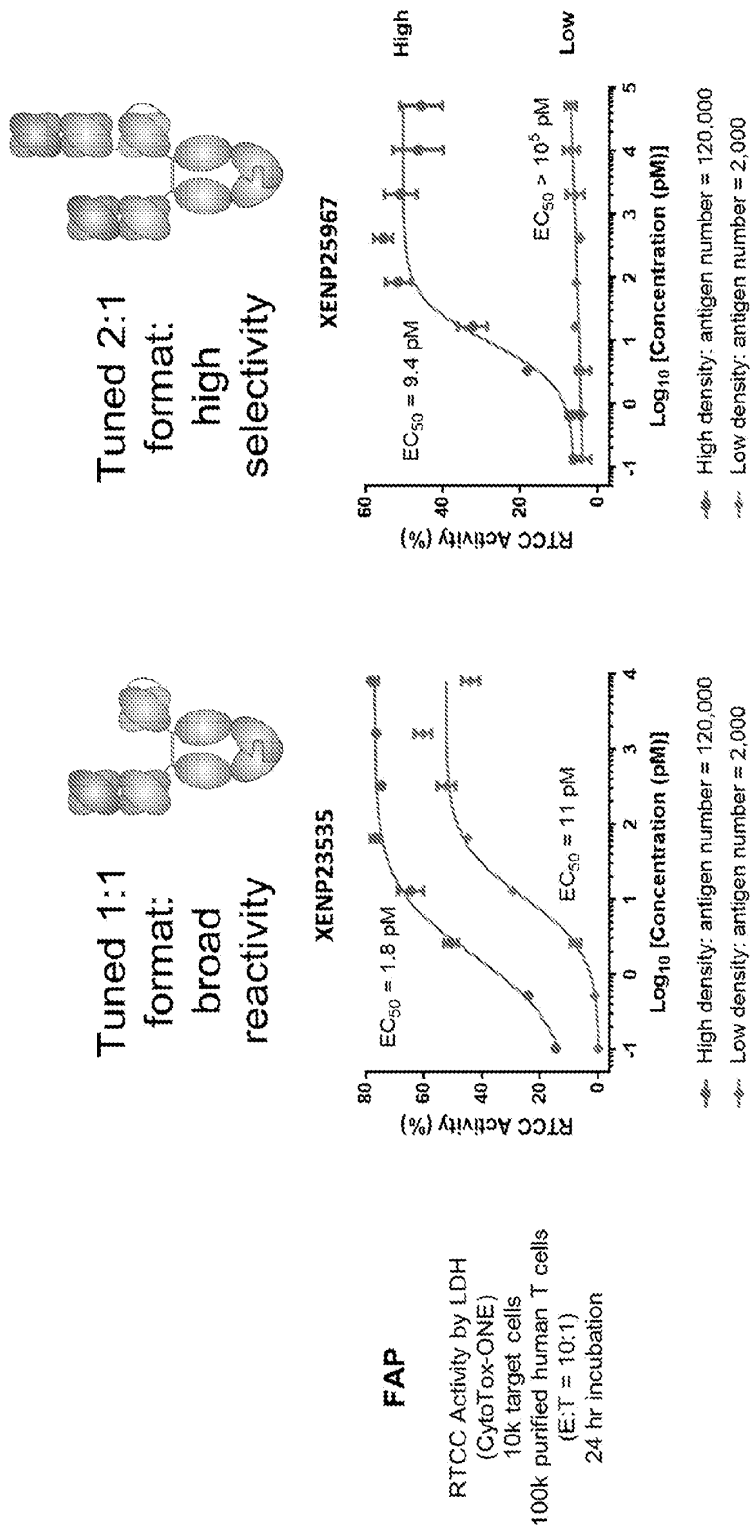


Figure 57B

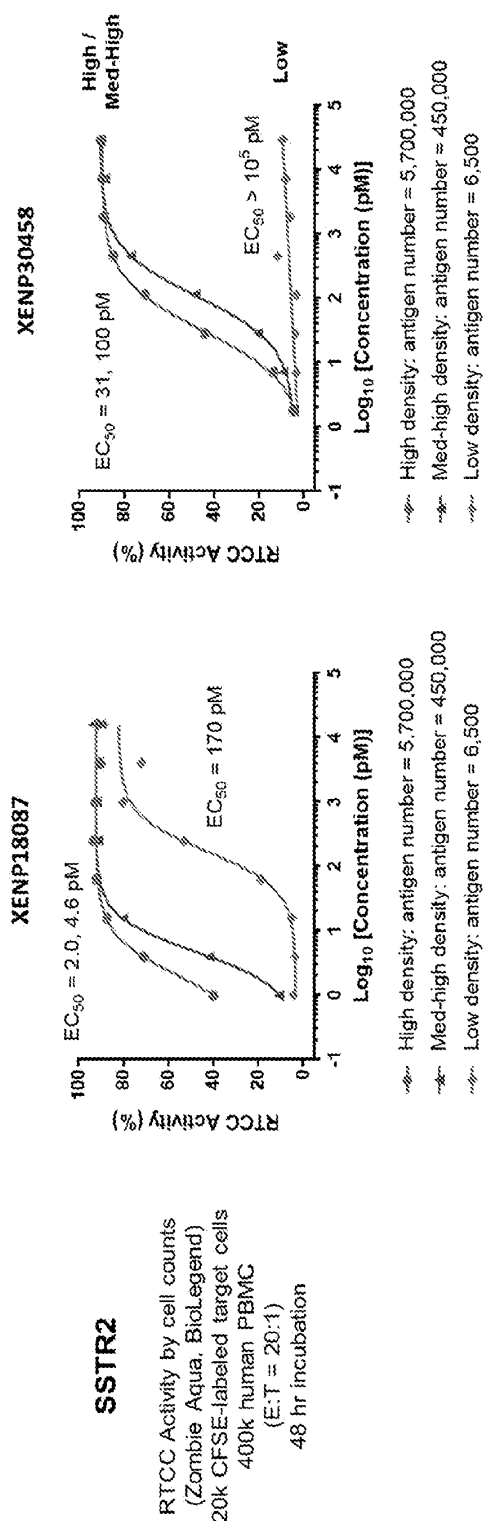


Figure 57C

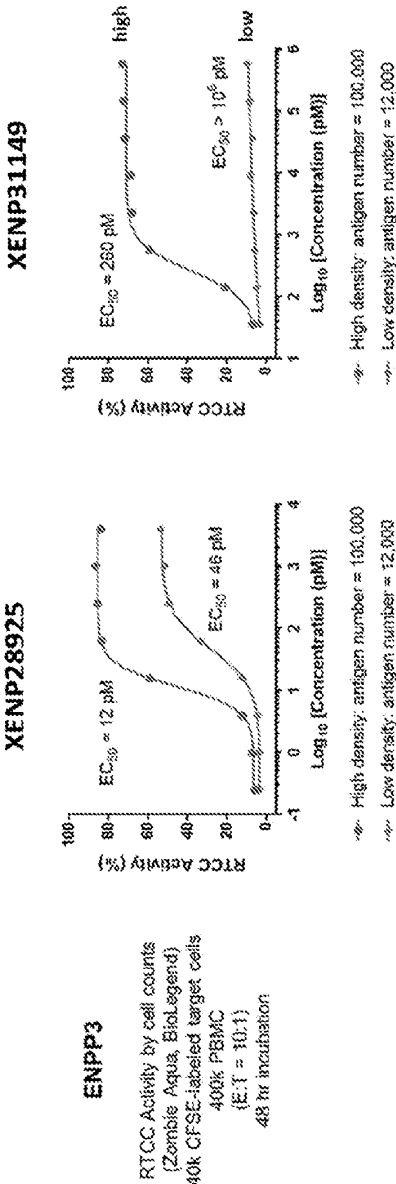


Figure 58

Antibody-like
thermostability (DSC)

Favorable solution
properties (SEC)

High purity
bispecific (IEX)

pl-eng + HetFc + Fc-silenced

After standard protein A₁ cation exchange purification steps

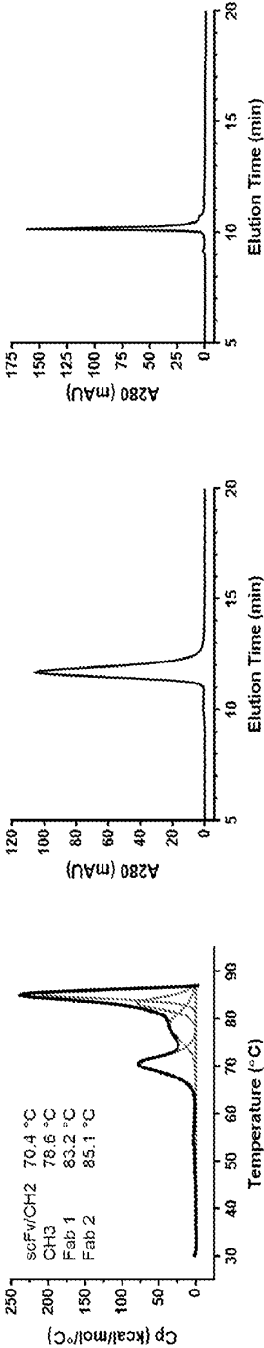


Figure 59

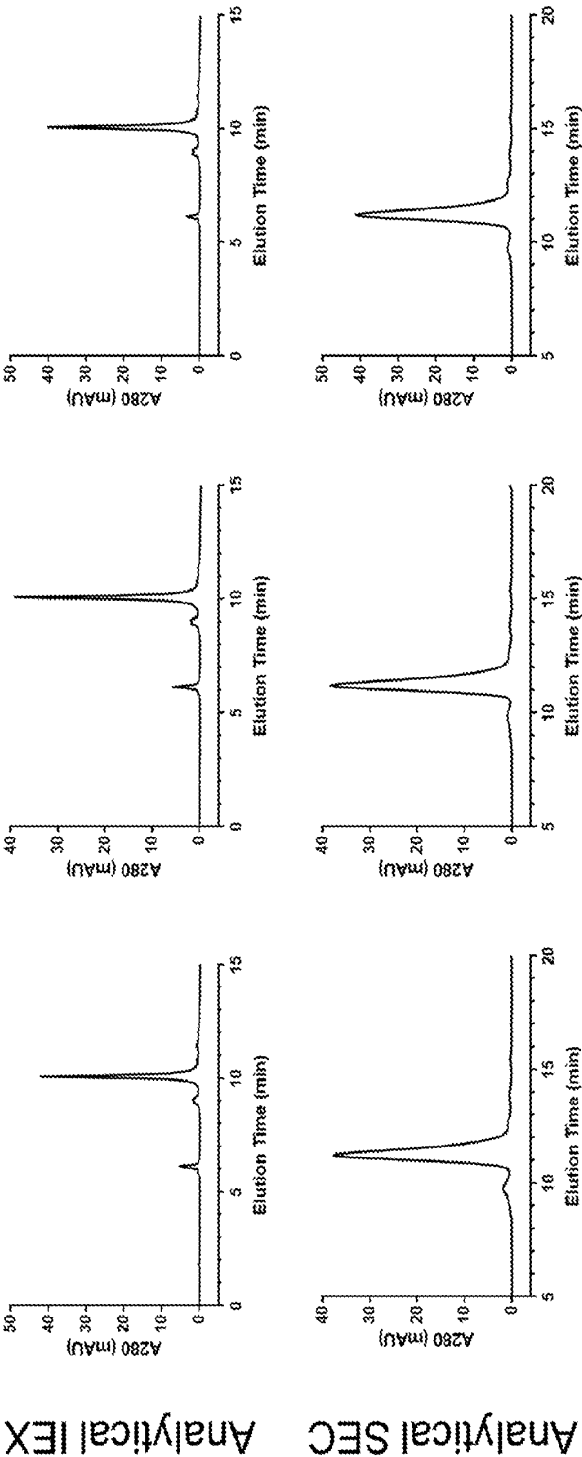
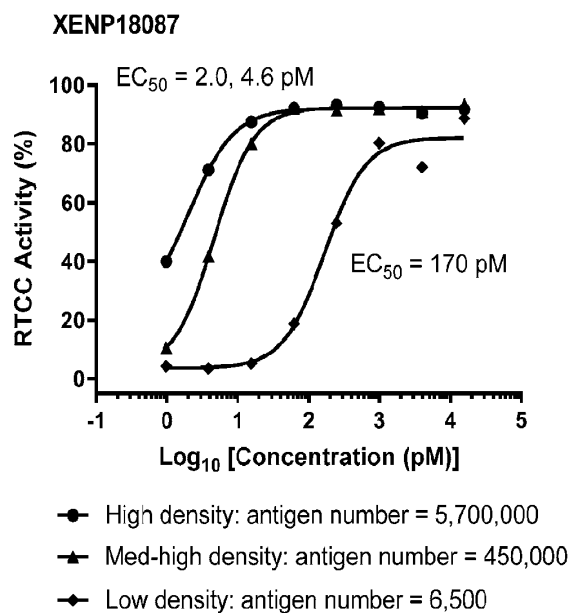


Figure 60

A)



B)

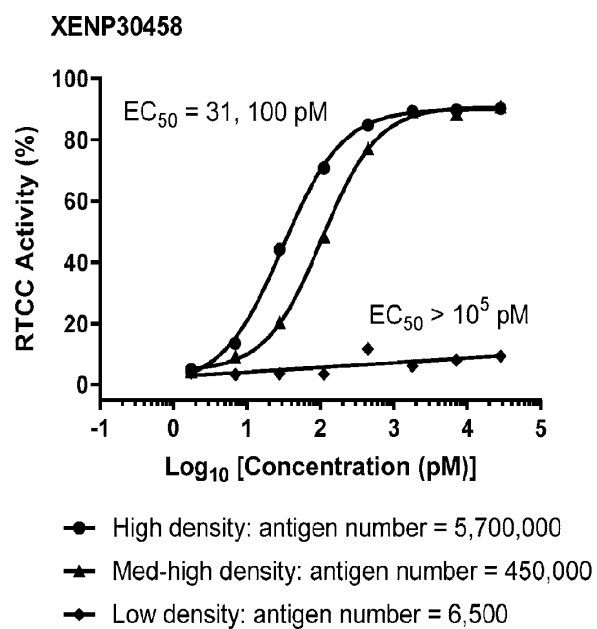


Figure 61

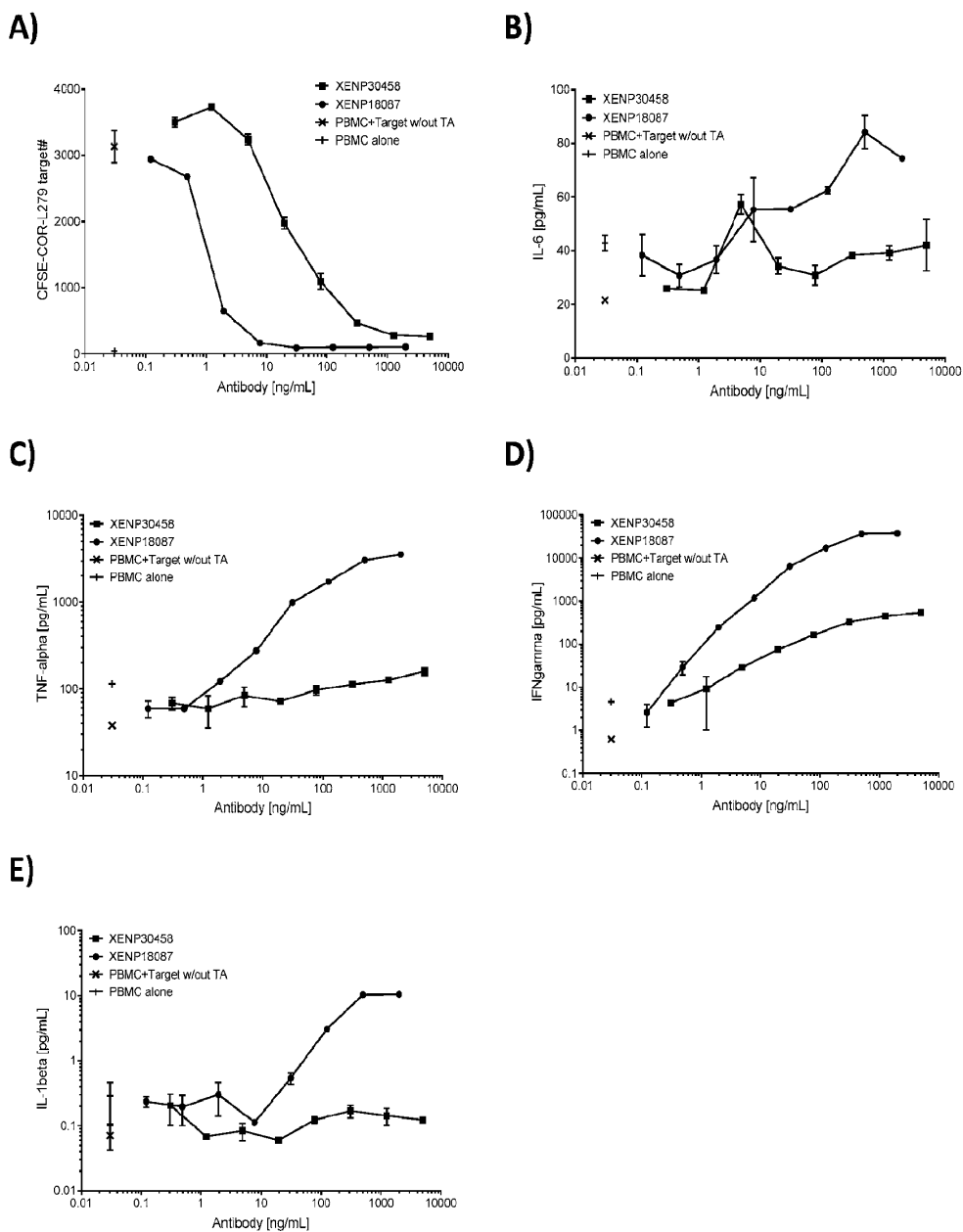


Figure 62A

>XENP18087 [α SSTR2] H1.143 L1.30 Fab-[α CD3] H1.30 L1.47 scFv(GKPGS)4 Fc(216) IgG1 PVA /S267K pl(-)
] Isosteric A L368D/K370S-IgG1 C220S/S364K/E357Q (SEQ ID NO:XX)

Chain 1 - [α SSTR2] H1.143 IgG1 PVA /S267K pl(-) Isosteric A L368D/K370S

EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~DYGM~~AWFRQAPGKGLEWVSFISNLGYSIYYADSVKGRFTISRDAKN
SLYLQMNSLRRAEDTAVYYCARAPYD~~YDSF~~DMDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAAKTKPREEEYNSTYRVV
SVLT~~VLH~~QDWLN~~Q~~KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE
WESD~~GQ~~PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3] H1.30 L1.47 scFv(GKPGS)4 Fc(216) IgG1 C220S/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~TYAM~~NWVRQAPGKGLEWVGRI~~RSKYN~~NYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRRAEDTAVYYCVRHGNF~~GDSYVSWF~~AYWGQGT~~LVTVSS~~/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT~~CGSS~~TGAVTTSN~~YANW~~VQOKPGKSPRGLIGGTN~~KRA~~PGV~~PAR~~FSGSLGGKAALTI~~SGA~~QPED
EADYYCALWYSN~~HW~~VFGGGTKLT~~VL~~/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAAKTKPREEQYNSTYRVVSVLT~~VLH~~QDWLN~~Q~~KEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - [α SSTR2] L1.30

DIVMTQSPDSLAVSLGERATINCKSSQS~~SLNS~~SRN~~RK~~NYLAWYQOKPDQSPKLLIYWASTRESGV~~PDR~~FSGSGSGTDF
TLTISS~~LQ~~AEDVAVYYC~~KQSY~~YLT~~TF~~GGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCL~~LN~~NY~~FYPREAKVQW
KVDNALQSGNSQESVTEQDSKDS~~Y~~SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP23535 [α FAP] H0L0 Fab-[α CD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
] Isosteric A /PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q (SEQ ID NO:XX)

Chain 1 - [α FAP] H0 IgG1 pl(-) Isosteric A /PVA /S267K/L368D/K370S

QVQLVQSGAEVKKPKASVKSCKTSRYTFT~~EYTI~~HWVRQAPGQRLIEWIGGINPNNGIENYNQ~~KFK~~GRVTITVDTSAS
TAYMELSSLRSEDTAVYYCARR~~RI~~AYGYDEGHAMDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAAKTKPREEEYNSTYR
VVS~~VL~~TVLH~~Q~~DWLN~~Q~~KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESD~~GQ~~PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3] H1.30 L1.47 scFv(GKPGS)4 Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~TYAM~~NWVRQAPGKGLEWVGRI~~RSKYN~~NYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRRAEDTAVYYCVRHGNF~~GDSYVSWF~~AYWGQGT~~LVTVSS~~/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLT~~CGSS~~TGAVTTSN~~YANW~~VQOKPGKSPRGLIGGTN~~KRA~~PGV~~PAR~~FSGSLGGKAALTI~~SGA~~QPED
EADYYCALWYSN~~HW~~VFGGGTKLT~~VL~~/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAAKTKPREEQYNSTYRVVSVLT~~VLH~~QDWLN~~Q~~KEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - [α FAP] L0

DIVMTQSPDSLAVSLGERATINCKSSQS~~LLYSP~~NQ~~RK~~NYLAWYQOKPGQPPKLLIFWASTRESGV~~PDR~~FSGSGFGTDF
TLTISS~~LQ~~AEDVAVYYC~~QQY~~FSY~~FL~~TFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCL~~LN~~NY~~FYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDS~~Y~~SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NO:XX)

Chain 1 - [αFAP]_H1_IgG1_PVA_/S267K-pl(-)_Isosteric_A_L368D/K370S

EVQLLES~~GGGLVQPGGSLRL~~SCAASGFTFSSYAM~~SWVRQAPGKGLEWVSGISGSGG~~STYYADSVKGRFTISRDN~~SKN~~
 TLYLQMN~~SLRAEDTAVYYCAKISFY~~PGGTYFDYWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY~~
 FPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC~~
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW~~
 ESDGQPENNYKTT~~PPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK~~

Chain 2 - [αFAP]_H1_(G4S)2_[αCD3]_H1.32_L1.47_scFv(GKPGS)4_(G4S)2_IgG1_C220S/S364K/E357Q

EVQLLES~~GGGLVQPGGSLRL~~SCAASGFTFSSYAM~~SWVRQAPGKGLEWVSGISGSGG~~STYYADSVKGRFTISRDN~~SKN~~
 TLYLQMN~~SLRAEDTAVYYCAKISFY~~PGGTYFDYWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY~~
 FPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSNTKVDKKVEPKSC/~~GGGGS
 GGGGS/ EVQLVES~~GGGLVQPGGSLRL~~SCAASGFTFSTYAM~~NWVRQAPGKGLEWVGRI~~RSKANN~~YATYYADSVKGRFT~~
 ISRDDS~~KNTLYLQMN~~SLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~LVTVSS/~~GKPGSGKPGSGKPGSGKPGS/Q
 AVVTQEP~~SLTVSPGGTVTLT~~CGSSTGAVTTSTNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKAALTIS
 GAQPEDEADYYCALWYSNHWVFGGGTKLTVL/ GGGGS~~GGGGS/~~KTHTCP~~PCPAPPVAGPSVFLFPPKPKDTLMISRT~~
 PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLHQDWLNGKEYKCKVSNKALPAPIE~~
 KTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTT~~PPVLDSDGSFFLYSKL~~
 TVDKSRWQ~~QGNVFC~~SCSVMEALHNHYTQKSLSLSPGK

Chain 3 - [αFAP]_L1

DIQMTQSP~~PSLSASVGDRVTITCRASQ~~SISSYL~~NWYQQKPKGAPKLLIYAAS~~SLQSGVPSRFSGSGSGTDFTLT~~TISS~~
 LQPEDFATYYCQ~~QSYSSPYTFGGGTKLEIK/RTVAAPSVFI~~FPPSDEQLKSGTASVVC~~LNNFY~~PREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>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 (SEQ ID NO:XX)

Chain 1 - [αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S

EVQLVES~~GGGLVQPGGSLRL~~SCAASGFAFSN~~YGM~~SWVRQAPGQ~~REWVSYIS~~SGGGT~~TYLDSVTGRFTISR~~DN~~AKN~~
 SLYLQMN~~SLRAEDTAVYYCARHRRVY~~GYFDYWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY~~
 FPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC~~
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW~~
 ESDGQPENNYKTT~~PPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK~~

Chain 2 - [αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVES~~GGGLVQPGGSLRL~~SCAASGFTFSTYAM~~NWVRQAPGKGLEWVGRI~~RSKYN~~NYATYYADSVKGRFTISR~~DDS
 KNTLYLQMN~~SLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~LVTVSS/ ~~GKPGSGKPGSGKPGSGKPGS/~~QAVVTQEP
 PS~~SLTVSPGGTVTLT~~CGSSTGAVTTSTNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCP~~PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK~~
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR~~
 EPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTT~~PPVLDSDGSFFLYSKLTVDKSRWQGN~~
 VFSCSVMEALHNHYTQKSLSLSPGK

Chain 3 - [αENPP3]_L1

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQ~~QNSWPFYTFGGGTKLEIK/RTVAAPSVFI~~FPPSDEQLKSGTASVVC~~LNNFY~~PREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSSITLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SUBSTITUTE SHEET (RULE 26)

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 (SEQ ID NO:XX)

Chain 1 - [α SSTR2]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S

EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~DY~~GMAWFRQAPGKGLEWVSEI~~SN~~LAYSIIYYADSVKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFY~~EM~~DYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
 CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAK~~GQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE
 WESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEGQGVFSCSVLHEALHSHY~~TQK~~SLSLSPGK

Chain 2 -

[α SSTR2]_H1.24_[α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
 EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~DY~~GMAWFRQAPGKGLEWVSEI~~SN~~LAYSIIYYADSVKGRFTISRDNAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFY~~EM~~DYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/ GGGG
SGGGG/EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~TY~~AMNWVRQAPGKGLEWVGRI~~RS~~KANNYATYYADSVKGRF
 TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF~~GD~~SYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/
QAVVTQEPSLTVSPGGTVTLTCGSS~~TC~~AVTTSNYANWVQKPGKSPRGLIGGTN~~KRA~~PGVPARFSGSLLGGKAALTI
 SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGS/KTH~~TC~~PPCPAPPVAGPSVFLFPPKPKDTLMISR
 TPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
 EKTISKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TLCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK
 LTVDKSRWQGNVFSCSVLHEALHSHY~~TQK~~SLSLSPGK

Chain 3 - [α SSTR2]_L1.30

DIVMTQSPDSLAVSLGERATINCKSSQSLNSRNRKNYLAWYQQKPDQSPKLLIYWASTRESGVPDRFSGSGSGTDF
 TLTIS~~SL~~QAEDVAVYYCKQ~~SYYL~~WTFGGG~~TK~~VEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQW
 KVDNALQSGNSQESVTEQDSKDS~~TY~~SLSS~~TL~~TL~~SK~~ADYEKHKVYACEVTHQGLSPVTKSFNRGEC

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 (SEQ ID NO:XX)

Chain 1 - [αENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLWVS~~YI~~SSGGGTTYLD~~SV~~TGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCAR~~HRV~~Y~~Y~~GY~~Y~~FDYWGQGT~~LV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT~~SV~~WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK

Chain 2 -

[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA_/S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLWVS~~YI~~SSGGGTTYLD~~SV~~TGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCAR~~HRV~~Y~~Y~~GY~~Y~~FDYWGQGT~~LV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT~~SV~~WNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GGGGS
GGGGS/QAVVTQEP~~SL~~TVSPGGTVTLT~~CGSSTGAVFTSNYANWVQ~~KPGKSPRGLIGGTFNKRAPGVPARFSGSLLGG
KAALTISGAQPEDEADYYCALWYS~~NHWV~~FGGGT~~KL~~TVL/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVQPGGS
LRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI~~RSKYNNYATYYADSVKGRFTISRDDSKNTLYLQ~~MNSLRAEDTA
VYYCVRHGNF~~GE~~YVSWFAYWGQGT~~LV~~TVSS/GGGGS~~GGGGS~~/KTHTCFPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQGPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQGNV~~FC~~SCSVMEALHNHYTQKSLSLSPGK

Chain 3 - [αENPP3]_L1.33

DILLTQSPDFQS~~V~~TPKEKVTITCRASQSIGTSIH~~WYQ~~KPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ~~Q~~SN~~SWP~~YTFGGG~~TK~~LEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASVVC~~LL~~NNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSK~~ST~~YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 63

[aSSTR2] H1.24 L1.30

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYCMAWFRQAPGKLEW	XX
	VSFISNLAYSIVYADSVKGRFTISRDNARNSLYIQMNSLRRAEDTAVY	
	YCAPAPYDYDSFYEMDYWGQGILVTVSS	
	DYGMA	
vhCDR1		XX
vhCDR2	FISNLAYSIVYADSVKG	XX
vhCDR3	APYDYSFYEMDY	XX
Variable light (vl) domain	DIVMTQSPDLSAVSLGERATINCKSSQSLINSRNRKNTLAWYQQKPD	XX
	QSPKLLIYWASTPESGVDPDRFSGSGGTFTLTISSLQAEIDVAVYC	
	KQSYVLTFFGGTKVEIK	
	KSSQSLINSENRRNYIA	
vlCDR1		XX
vlCDR2	WASTRES	XX
vlCDR3	KQSYVLT	XX