

Figure 5

Positive Charged scFv Linkers

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

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 20	GGGSGGGSGGGSGGGGS	20	0	17
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	18
-B	GEGSGEGSGEGGS	15	-3	19
-C	GGEGSGEGSGEGGS	15	-3	20
-D	GGGESGGGESGGGES	15	-3	21
-E	GEGESGEGESGEGES	15	-6	22
-F	GGGESGGEGSGEGGS	15	-3	23
-G	GEGESGEGESGEGESGEGES	20	-8	24

Additional scFv Linkers

GGGSGGGSGGGSGGGGS	SEQ ID NO: 7
GGGSGGGSGGGSGGGGS	SEQ ID NO: 17
GSTSGSGKPGSGEGSTKG	SEQ ID NO: 8
PRGASKSGSASQTGSAPGS	SEQ ID NO: 25
GTAAAGAGAAGGAAAGAAG	SEQ ID NO: 26
GTSGSSGSGGGSGSGGGG	SEQ ID NO: 27
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 1

Figure 6

Useful domain linkers

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

Figure 7A

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 CSVMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

Figure 7B

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVVMHEALHNHYTQKSLSLSPGK

Figure 7C

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TKTYTCNVDHKPSDTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ
 FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
 PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSRLTVDKSRWEEGDVFSVMS
 HEALHNHYTQKSLSLSPGK

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

ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVSLTCLVKGF
 YPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSVMSHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
 TQTYTCNVDHKPSDTKVDKTVERKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
 NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
 PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFSVMS
 EALHNHYTQKSLSLSPGK

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

ERKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
 NSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
 YPSDIAVEWESNGQPNENYKTTTPMLDSDGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTQKSLSLSPGK

Figure 7D

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

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
 TQTYTCNVDPKPKSDTKVDKTKVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
 NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLTP
 PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFSVSMH
 EALHNHYTQKSLSLSPGK

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

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQF
 NSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLTPPSREQMTKNQVKLTCLVKGFY
 PSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLTPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSV
 VLHEALHSHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREQMTKNQVKLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSVLHEALHSHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLTPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSV
 VMHEALHNHYTQKSLSLSPGK

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

ERKSSDKTHTCPPRPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
 EQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREQMTKNQVKLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGK

Figure 8A

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMEALHNHYTQKSLSLSPGK

Figure 8B

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

Figure 8C

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVVKLTCLVKGFIYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMSHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
 VLHEALHSHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVVKLTCLVKGFIYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMSHEALHSHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
 TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVVKLTCLVKGFIYPSDIAVEWESNG
 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVMSHEALHNHYTQKSLSLSPGK

Figure 9

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

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEEKHKVYACEVTHQG
LSSPVIKSFNRGEC

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

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 10A

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

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

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

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

Figure 10B

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGLTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEP SLTVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	112
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY VSWFAYWGQGLTVTVSS	113
vhCDR1	<u>TYAMN</u>	114
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	115
vhCDR3	<u>HGNFGDEYVSWFAY</u>	116
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGT VTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	117
vlCDR1	<u>GSSTGAVTTSNYAN</u>	118
vlCDR2	<u>GTNKRAP</u>	119
vlCDR3	<u>ALWYSNHWV</u>	120
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	121

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEP SLTVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLL GGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	122
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY VSWFAYWGQGLTVTVSS	123
vhCDR1	<u>TYAMN</u>	124
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	125
vhCDR3	<u>HGNFGDPYVSWFAY</u>	126
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGT VTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	127
vlCDR1	<u>GSSTGAVTTSNYAN</u>	128
vlCDR2	<u>GTNKRAP</u>	129
vlCDR3	<u>ALWYSNHWV</u>	130
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	131

Figure 10C

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNGFSDSY VSWFDYWGGTLVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEP SLTVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSL GGKAALTISGAQPEDEADYYCALWYSNHWFVGGGTKLTVL	132
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNGFSDSY VSWFDYWGGTLVTVSS	133
vhCDR1	<u>TYAMN</u>	134
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	135
vhCDR3	<u>HGNFGDSYVSWFDY</u>	136
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWFVGGGTKLTV L	137
vlCDR1	<u>GSSTGAVTTSNYAN</u>	138
vlCDR2	<u>GTNKRAP</u>	139
vlCDR3	<u>ALWYSNHWV</u>	140
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	141

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

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNGFSDSY VSWFAYWGQTLVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /QAVVTQEP SLTVSPG GTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSL GGKAALTISGAQPEDEADYYCALWYSNHWFVGGGTKLTVL	142
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNGFSDSY VSWFAYWGQTLVTVSS	143
vhCDR1	<u>TYAMS</u>	144
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	145
vhCDR3	<u>HGNFGDSYVSWFAY</u>	146
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWFVGGGTKLTV L	147
vlCDR1	<u>GSSTGAVTTSNYAN</u>	148
vlCDR2	<u>GTNKRAP</u>	149
vlCDR3	<u>ALWYSNHWV</u>	150
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	151

Figure 10D

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTLTVSS	152
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	153
vlCDR1	<u>GSSTGAVTTSNYAN</u>	154
vlCDR2	<u>GTNKRAP</u>	155
vlCDR3	<u>ALWYSNHWV</u>	156
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTLTVSS	157
vhCDR1	<u>TYAMN</u>	158
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	159
vhCDR3	<u>HGNFGDSYVSWFAY</u>	160
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	161

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTLTVSS	162
Variable Light (vl) Domain	QAVVTQEP SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV L	163
vlCDR1	<u>GSSTGAVTTSNYAN</u>	164
vlCDR2	<u>GTNKRAP</u>	165
vlCDR3	<u>ALWYSNHWV</u>	166
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGLTLTVSS	167
vhCDR1	<u>TYAMN</u>	168
vhCDR2	<u>RIRSKANNYATYYADSVKG</u>	169
vhCDR3	<u>HGNFGDSYVSWFAY</u>	170
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	171

Figure 10E

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

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWF</u> <u>GGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS</u> / <u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFST</u> <u>YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGT</u> <u>LVTVSS</u>	172
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWF</u> <u>GGGTKLTV</u> <u>L</u>	173
vlCDR1	<u>GSSTGAVTTSNYAN</u>	174
vlCDR2	<u>GTNKRAP</u>	175
vlCDR3	<u>ALWYSNHWF</u>	176
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEY</u> <u>VSWFAYWGQGT</u> <u>LVTVSS</u>	177
vhCDR1	<u>TYAMN</u>	178
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	179
vhCDR3	<u>HGNFGDEYVSWFAY</u>	180
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	181

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

	Sequence	SEQ ID NO:
scFv	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWF</u> <u>GGGTKLTV</u> <u>L/GKPGSGKPGSGKPGSGKPGS</u> / <u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFST</u> <u>YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM</u> <u>NSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGT</u> <u>LVTVSS</u>	182
Variable Light (vl) Domain	<u>QAVVTQEP</u> <u>SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN</u> <u>KRAPGV</u> <u>PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWF</u> <u>GGGTKLTV</u> <u>L</u>	183
vlCDR1	<u>GSSTGAVTTSNYAN</u>	184
vlCDR2	<u>GTNKRAP</u>	185
vlCDR3	<u>ALWYSNHWF</u>	186
Variable Heavy (vh) Domain	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK</u> <u>YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPY</u> <u>VSWFAYWGQGT</u> <u>LVTVSS</u>	187
vhCDR1	<u>TYAMN</u>	188
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	189
vhCDR3	<u>HGNFGDPYVSWFAY</u>	190
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	191

Figure 10F

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEP ^{SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN} KRAPGV ^{PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV} L/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGT ^{LVTVSS}	192
Variable Light (vl) Domain	QAVVTQEP ^{SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN} KRAPGV ^{PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV} L	193
vlCDR1	<u>GSSTGAVTTSNYAN</u>	194
vlCDR2	<u>GTNKRAP</u>	195
vlCDR3	<u>ALWYSNHWV</u>	196
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFDYWGQGT ^{LVTVSS}	197
vhCDR1	<u>TYAMN</u>	198
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	199
vhCDR3	<u>HGNFGDSYVSWFDY</u>	200
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	201

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

	Sequence	SEQ ID NO:
scFv	QAVVTQEP ^{SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN} KRAPGV ^{PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV} L/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGT ^{LVTVSS}	202
Variable Light (vl) Domain	QAVVTQEP ^{SLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTN} KRAPGV ^{PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV} L	203
vlCDR1	<u>GSSTGAVTTSNYAN</u>	204
vlCDR2	<u>GTNKRAP</u>	205
vlCDR3	<u>ALWYSNHWV</u>	206
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSK YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSY VSWFAYWGQGT ^{LVTVSS}	207
vhCDR1	<u>TYAMS</u>	208
vhCDR2	<u>RIRSKYNNYATYYADSVKG</u>	209
vhCDR3	<u>HGNFGDSYVSWFAY</u>	210
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	211

Figure 11A

Human ENPP3 sequence

>sp|O14638 (SEQ ID NO: 212)

MESTLTLATEQPVKKNTLKYYKIACIVLLALLVIMSLGLGLGLRLKLEKQGSCRKKCFDASFRGLENCRCDVACKD
 RGDCCWDFEDTCVESTRIWMCNKFRGETRLEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDDTAQSQCP
 GFDLPPVILFSMDGFRAEYLYTWDTLMPNINKLKTCTGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII
 DNMYDVNLNKNFSLSSKEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEE
 RISTLLKWLDLPKAERPRFYTMFYEEPDSGSHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNI
 ILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRIRAHNIPHDFFSFNSEEIVRNLSRCPDQHF
 KPYLTPDLPKRLHYAKNVRIDKVHLFVDQQLAVRSKSNNTNCGGNHGYNNEFRSMEAIFLAHG
 PSFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLKVPFYEP SHAEVSKFSVCGFANPLP
 TESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREYVSGF
 GKAMRMPMWSSYTVPLGDTSPPLPTVPDCLRADVRVPPSESQKCSFYLDKNITHGFLYPPASNRTSD
 SQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLA
 NTDVPIPTHYFVVLTSCKNKSHTPENCPGWLDVLPFIIPHRPTNVE SCPEGKPEALWVEERF
 TAIHARVRDVELLTGLDFYQDKVQPVSEILQLKTYLPTFETII

Human ENPP3 sequence, extracellular domain

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

LLVIMSLGLGLGLRLKLEKQGSCRKKCFDASFRGLENCRCDVACKDRGDCCWDFEDTCVESTRIWMCNKFR
 GETRLEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDDTAQSQCPGFDLPPVILFSMDGFRAEY
 LYTWDTLMPNINKLKTCTGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII DNMYDVNLNKNFSLSS
 KEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEE RISTLLKWLDLP
 KAERPRFYTMFYEEPDSGSHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNI ILLADHGMDQ
 TYCNKMEYMTDYFPRINFFYMYEGPAPRIRAHNIPHDFFSFNSEEIVRNLSRCPDQHF KPYLTPDL
 PKRLHYAKNVRIDKVHLFVDQQLAVRSKSNNTNCGGNHGYNNEFRSMEAIFLAHG PSFKEKTEVEPF
 ENIEVYNLMCDLLRIQPAPNNGTHGSLNHLKVPFYEP SHAEVSKFSVCGFANPLP TESLDCFCPHLQ
 NSTQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSY
 TVPLGDTSPPLPTVPDCLRADVRVPPSESQKCSFYLDKNITHGFLYPPASNRTSDSQYDALITSNLV
 PMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFV
 VLTSCKNKSHTPENCPGWLDVLPFIIPHRPTNVE SCPEGKPEALWVEERFTAIHARVRDVELLTGL
 DFYQDKVQPVSEILQLKTYLPTFETII

Mouse ENPP3 sequence

>sp|Q6DYE8 (SEQ ID NO: 214)

MDSRLALATEEPIKDSLKKYKILCVLLALLVIVSLGLGLGLRLKPPEEQGSCRKKCFDSSHRGLEGCRCDSGCTG
 RGDCCWDFEDTCVKSTQIWTCLNFRGENRLETALCSCADDCLQRKDCCADYKTVCGESPVWTEACASSQEPQCP
 P GFDLPPVILFSMDGFRAEYLQTWSTLLPNINKLKTCTGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGII
 DNMYDVHLNKNFSLSSVEKSNPAWWSGQPIWLTAMYQGLKAACYWPGSDVAVNGSFPTIYRNYSNSVPYERRIT
 TLLQWLDLPKADRSFYTIYVEEPDSAGHSSGPVSAGVIKALQSVDNAFGMLMEGLKQRNLHNCVNI I
 VLADHGMDQTSRDRVEYMTDYFPKINFYMYQGPAPRIRTRNIPQDFFTFNSEEIVRNLSRCPDQHF
 KPYLTPDLPKRLHYAKNVRIDKAHLMVDRQWLAFRSKGSSNCGGTHGYNNEFKSMEAIFLAHG
 PSFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLNHLKTPFYKPSHAGELSTPADCGFTT
 PLPTDPLDCSCPALQNTPGLEEQANQRLNLSEGEVAATVKANLPFGRPRVMQKNGDHCLLYHRDYIS
 GYGKAMKMPMWSSYTVLKP GDTSSLPTVPDCLRADVRVAPSESQKCSFYLDKNITHGFLYPAIKGT
 NESRYDALITSNLVPMYKEFKMWDYFHEVLLIKYAIERNGLNVVSGPIFDYNYDGHFDAPDEITQYVAG
 TDVPIPTHYFVVLTSCKDQHTPDSCPGWLDVLPFIIPHRPTNIESCSENKTEDLWVEERFQAHAARVR
 DVELLTGLDFYQEKAPVVSQILQLKTYLPTFETII

Figure 11B

Mouse ENPP3 sequence, extracellular domain

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

LLVIVSLGLGLGLRLKPEEQGSCRKKCFDSSHRGLEGCRCDSGCTGRGDCCWDFEDTCVKSTQIWTCNLFRCGENR
 LETALCSCADDCLQRKDCCADYKTVCQGESPWVTEACASSQEPQCPPGFDLPPVILFSMDGFRAEYLQTWSTLLPNI
 NKLKTCGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDVHLNKNFSLSSVEKSNPAWWSGQPIWLTAMY
 QGLKAACYWPGSDVAVNGSFPTIYRNYSNSVPYERRITTLQWLDLPKADRP SFYTIYVEEPDSAGHSSGPVSAGV
 IKALQSVDNAFGMLMEGLKQRNLHNCVNIIVLADHGMDQTSRVEYMTDYFPKINFYMYQGPAPRIRTRNIPQDFF
 TFNSEEIVRNLSRKPQDHFQPYLTPDLPKRLHYAKNVRIDKAHLMVDRQWLAFRSKGSSNCGGGTHGYNNEFKSME
 AIFLAHGPFIEKTVIEPFENIEVYNLLCDLLHIEPAPNNGTHGSLNHLLKTPFYKPSHAGELSTPADCGFTTPLPT
 DPLDCSCPALQNTPGLEEQANQRLNLSEGEVAATVKANLPFGRPRVMQKNGDHCLLYHRDYISGYGKAMKMPMWSSY
 TVLKPGDTSSLPTVPDCLRADVRVAPSESQKCSFYLDKNITHGFLYPAIKGTNESRYDALITSNLVP MYKEFKKM
 WDYFHEVLLIKYAIERNGLNVVSGPIFDYNYDGHFDAPDEITQYVAGTDVPIPTHYFVVLTSCKDQTHTPDSCPGWL
 DVLFPFIVPHRPTNIESCSENKTEDLWVEERFQAHAARVRDVELLTGLDFYQEKAPVVSQILQLKTYLPTFETII

Macaca fascicularis ENPP3 sequence

>tr|A0A2K5TKP4 (SEQ ID NO: 216)

MESMLTLATEQPVKNTLKKYKIA CIVLLALLVIMSLGLGLGLRLKLEKQGSCRKKCFDASFRGLENCRCDVACED
 RGDCCWDFEDTCVESTRIWTCNKFRCGETRLEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDAQQSQCPE
 GFDLPPVILFSMDGFRAEYLYTWDTLMPNINKLKTTCGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDV
 NLNKNFSLSSQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEEIRSTLLKWLDL
 PKAERP SFYTM YFEEDSSGHAGGPVSARVIKALQVVDHAFGMLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEY
 MTDYFPRINFYMYEGPAPRIRALNVPHDFFSCKYEDTYMKKRCRKPQDHFQPYLTPDLPKRLHYAKNVRIDKVHLFV
 DRQWLAVGSKSNTNCGGNHGYNNEFRSMEAIFLAHGPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLN
 HLLKVPFYEP SHAEVSKFSVCGFANPLPTNNLSCLCPHLQNSIQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQ
 KNVDNCLLYHREYVSGFGKAMRMPMWSSYTVPQLGDTSPPLPTVPDCLRADVRVPPSESQKCSFYLDENITHGFLY
 PPAINRTSDSQYDALIMSNLVP MYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPEEITKHIAN
 TDIPITHYFVVLTSCKNKSHTPENC PGWLDVLFPFIIPHRPTNVESCPEGKPEALWVEERFATAHARVRDVELLTGL
 DFYQDKAQPVSEILQLKTYLPTFETII

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

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

LLVIMSLGLGLGLRLKLEKQGSCRKKCFDASFRGLENCRCDVACEDRGDCCWDFEDTCVESTRIWTCNKFRCGETR
 LEASLCSCSDDCLQRKDCCADYKSVCQGETSWLEENCDAQQSQCPEGFDLPPVILFSMDGFRAEYLYTWDTLMPNI
 NKLKTCGIHISKYMRAMYPTKTFPNHYTIVTGLYPESHGIIIDNNMYDVNLNKNFSLSSQNNPAWWHGQPMWLTAMY
 QGLKAATYFWPGSEVAINGSFPSIYMPYNRSVPYEEIRSTLLKWLDLPKAERP SFYTM YFEEDSSGHAGGPVSARV
 IKALQVVDHAFGMLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEYMTDYFPRINFYMYEGPAPRIRALNVPHDF
 SCKYEDTYMKKRCRKPQDHFQPYLTPDLPKRLHYAKNVRIDKVHLFVDRQWLAVGSKSNTNCGGNHGYNNEFRSME
 AIFLAHGPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTRGSLNHLLKVPFYEP SHAEVSKFSVCGFANPLPT
 NNLSCLCPHLQNSIQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDNCLLYHREYVSGFGKAMRMPMWSSYT
 VPQLGDTSPPLPTVPDCLRADVRVPPSESQKCSFYLDENITHGFLYPPAINRTSDSQYDALIMSNLVP MYEEFRKM
 WDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPEEITKHIANTDIPITHYFVVLTSCKNKSHTPENC PGWL
 DVLFPFIIPHRPTNVESCPEGKPEALWVEERFATAHARVRDVELLTGLDFYQDKAQPVSEILQLKTYLPTFETII

Figure 12

AN1[ENPP3]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGTYYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGTLVTVSS	218
vhCDR1	NYGMS	219
vhCDR2	YISSGGGTYYLDSVKG	220
vhCDR3	HRRVYYGYFDY	221
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQKPDQSPKLL IKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	222
vlCDR1	RASQSIGTSIH	223
vlCDR2	YASESIS	224
vlCDR3	QQSNSWPYT	225

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISSGGGTYYLDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 13A

AN1[ENPP3] H1 L1.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGTYYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGLTVTVSS	228
vhCDR1	<u>NYGMS</u>	229
vhCDR2	<u>YISSGGGTYYLDSVKG</u>	230
vhCDR3	<u>HRRVYYGYFDY</u>	231
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLL IEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	232
vlCDR1	<u>RASQSIGTSIH</u>	233
vlCDR2	<u>YASESIS</u>	234
vlCDR3	<u>QQSNSWPYT</u>	235

AN1[ENPP3] H1 L1.77

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEW VSYISSGGGTYYLDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCARHRRVYYGYFDYWGQGLTVTVSS	236
vhCDR1	<u>NYGMS</u>	237
vhCDR2	<u>YISSGGGTYYLDSVKG</u>	238
vhCDR3	<u>HRRVYYGYFDY</u>	239
Variable light (vl) domain	DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWHYQQKPDQSPKLL IEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSW PYTFGGGTKLEIK	240
vlCDR1	<u>RASQSIGTSIH</u>	241
vlCDR2	<u>YESESIS</u>	242
vlCDR3	<u>QQSNSWPYT</u>	243

Figure 13B

AN1[ENPP3]_H1.8_L1

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

AN1[ENPP3]_H1.8_L1.33

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

AN1[ENPP3]_H1.8_L1.77

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

Figure 14A

H16-7.213

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSISTAYMELSRLSDDTAVYYCARELRYFGWLLS SLDYWGQGTLLTVTVSS	268
vhCDR1	<u>GYMH</u>	269
vhCDR2	<u>WINPNSGGTNYAQKFQG</u>	270
vhCDR3	<u>ELRYFGWLLSSLDY</u>	271
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTITCRASQSISSYLNWFQKPGKAPKLL IYAASSLQSGVPSRFSGSESGTDFTLTISLQPEDFATYSCQSYSF PLTFGGGTKVEIK	272
vlCDR1	<u>RASQSISSYLN</u>	273
vlCDR2	<u>AASSLQS</u>	274
vlCDR3	<u>QSYSFPLT</u>	275

H16-9.69

	sequence	SEQ ID NO:
Variable heavy (vh) domain	WGLSEVSCKASGYTFTSYDIHWVRQATGQGLEWMGWMNPNSGNTVYA QKFQGRVTMTRNTSISTAYMELSSLRSED TAVYYCARTVLLWPFDYW GQGTLLTVTVSS	276
vhCDR1	<u>SYDIH</u>	277
vhCDR2	<u>WMNPNSGNTVYAAQKFQG</u>	278
vhCDR3	<u>TVLLWPFDY</u>	279
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSKNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYC QQYYSTPPWTFGQGTKEIK	280
vlCDR1	<u>KSSQSVLYSSKNKNYLA</u>	281
vlCDR2	<u>WASTRES</u>	282
vlCDR3	<u>QQYYSTPPWT</u>	283

H16-1.52

	sequence	SEQ ID NO:
Variable heavy (vh) domain	SGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKLEWVSAISG SDGSPYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDG YSSGWNIFYDYWGQGTLLTVTVSS	284
vhCDR1	<u>SYAMS</u>	285
vhCDR2	<u>AISGSDGSPYYADSVKG</u>	286
vhCDR3	<u>DGYSSGWNIFYDY</u>	287
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPG QPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISLQAEDVAVYYC QEYYSTMCSFGQGTKEIK	288
vlCDR1	<u>KSSQSVLYSSNNKNYLA</u>	289
vlCDR2	<u>WASTRES</u>	290
vlCDR3	<u>QEYYSTMCS</u>	291

Figure 14B

Ha16-1(1)23

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEWVAVI WSDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR EGYYGSGSYYYYYGMDVWGQGT TTVTVSS	292
vhCDR1	<u>SYGMH</u>	293
vhCDR2	<u>VIWSDGSNKYYADSVKG</u>	294
vhCDR3	<u>EGYYGSGSYYYYYGMDV</u>	295
Variable light (vl) domain	QAGLTQPPSVSKGLRQTATLTCTGNSNNVGTQGAAWLQHQGHPPKL LSYRNNNRPSGISERLSASTSGNTASLTITGLQPEDEADYYCSAWDS SLSAVVFGGGTKLTVL	296
vlCDR1	<u>TGNSNNVGTQGAA</u>	297
vlCDR2	<u>RNNNRPS</u>	298
vlCDR3	<u>SAWDSSLSAVV</u>	299

H16-9.44

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LSLTCTVSGGSISSYYWSWIRQSAGKGLEWIGRIYTGVTNYPNPSLK SRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDYYDSSGYYPFDYW GQGT LTVTVSS	300
vhCDR1	<u>SYYS</u>	301
vhCDR2	<u>RIYTGVTNYPNPSLKS</u>	302
vhCDR3	<u>DYYDSSGYYPFDY</u>	303
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWFQQKPGKAPKSL IYAASSLENGVPSKFSGSGSGTDFTLTISLQPEDFATYYCQQYNSS PFTFGPGTKVDIR	304
vlCDR1	<u>RASQGISNYLA</u>	305
vlCDR2	<u>AASSLEN</u>	306
vlCDR3	<u>QQYNSSPFT</u>	307

H16-1.67

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSQTLSTCTVSGGSINSFGYYWSWIRQYPGKGLEWIG FLYFTGSTYYNPSLKSRTISVDTSKSQFSLKLSSVTAADTAVYYCA RAGTMVRGAHYYGMDVWGQGT TTVTVSS	308
vhCDR1	<u>SFGYYWS</u>	309
vhCDR2	<u>FLYFTGSTYYNPSLKS</u>	310
vhCDR3	<u>AGTMVRGAHYYGMDV</u>	311
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCRASQGISNYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQIYST PPEWTFGQGTKVEIK	312
vlCDR1	<u>RASQGISNYLN</u>	313
vlCDR2	<u>AASSLQS</u>	314
vlCDR3	<u>QQIYSTPPEWT</u>	315

Figure 14C

Ha1 6-1 (3,5)36

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGPGLVKPSSETLSLTCTVSGGSISSSSYYWGWRQPPGKGL EWIGSMYYSGSTYHNPSLKSRVVISVDTSKNQFSLKLSSVTAADTAV YYCARHYITVAGIFDYWGQGTLLTVSS	316
vhCDR1	<u>SSSYYWG</u>	317
vhCDR2	<u>SMYYSGSTYHNPSLKS</u>	318
vhCDR3	<u>HYITVAGIFDY</u>	319
Variable light (vl) domain	QSVLTQPPSASGTPGQRATISCSGSSTNIGSTIVNWWYQQVPGTAPKL LIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDA SLNGPVFGGGTKLTVL	320
vlCDR1	<u>SGSSTNIGSTIVN</u>	321
vlCDR2	<u>SNNQRPS</u>	322
vlCDR3	<u>AAWDASLNGPV</u>	323

H16-1.86

	sequence	SEQ ID NO:
Variable heavy (vh) domain	VESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYI YYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARA YGYYYYGMDVWGQGTITVTVSS	324
vhCDR1	<u>SYYS</u>	325
vhCDR2	<u>YIYYSGSTNYNPSLKS</u>	326
vhCDR3	<u>AYGYYYYGMDV</u>	327
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTTITCRISQSISSYLNWYQQKPGKAPNLL IYAASSLQSGVPSRFSGSGGTDFLTITSSLPEDFATYYCQQTYS PPWTFGGGTKVEIK	328
vlCDR1	<u>RTSQSISSYLN</u>	329
vlCDR2	<u>AASSLQS</u>	330
vlCDR3	<u>QQTYSPPWT</u>	331

H16-9.10

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LLES GPGLVKPSQTLSLTCAISGDSVSSNSAAWNIRQSPSRGLEWL GRYYRSKYNAYAVSVKSRMTINPDTSKNQFSLQLNSVTPEDTAVY YCAREAGGWFDPPWGQGTLLTVSS	332
vhCDR1	<u>SNSAAWN</u>	333
vhCDR2	<u>RTYYRSKYNAYAVSVKS</u>	334
vhCDR3	<u>EAGGWFDPP</u>	335
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQGIRSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGGTDFLTITSSLPEDFATYYCQQANSF PPTFGGGTKVEIK	336
vlCDR1	<u>RASQGIRSWLA</u>	337
vlCDR2	<u>AASSLQS</u>	338
vlCDR3	<u>QQANSFPPT</u>	339

Figure 14D

H16-9.33

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESQGLVKPSQTLSTCAISGDSVSSNSAAWNWIRQSPSRGL EWLGRTYYRSKYYNAYPVSVKSRITINPDTSKNQFSLQLNSVTPEDT AVYYCAREAGGWFDPPWGQGLTVTVSS	340
vhCDR1	<u>SNSAAWN</u>	341
vhCDR2	<u>RTYYRSKYYNAYPVSVKS</u>	342
vhCDR3	<u>EAGGWFDPP</u>	343
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCRANQGIRSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQANSF PPTFGGGTKVEIK	344
vlCDR1	<u>RANQGIRSWLA</u>	345
vlCDR2	<u>AASSLQS</u>	346
vlCDR3	<u>QQANSFPPT</u>	347

H16-1.68

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVHLVESGGGVVQPGRSLRLSCAASGFTFRSYGMHWVRQAPGKGLEW VAVIWDGSGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDMAMY YCARSRITIFGVVHYGMDVWGQGTITVTVSS	348
vhCDR1	<u>SYGMH</u>	349
vhCDR2	<u>VIWDGSGNKYYADSVKG</u>	350
vhCDR3	<u>SRITIFGVVHYGMDV</u>	351
Variable light (vl) domain	TQLTQSPSSLSASVGDRTVITCRASQNINSYLNWYQQKPGKAPKLLI YAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFTTYCQQSYSSA PTFGGGTKLEIK	352
vlCDR1	<u>RASQNINSYLN</u>	353
vlCDR2	<u>AASSLQS</u>	354
vlCDR3	<u>QQSYSSAPT</u>	355

Ha16-1(1)1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYS GSTNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARAVSY YYYGMDVWGQGTITVTVSS	356
vhCDR1	<u>SYYS</u>	357
vhCDR2	<u>YIYSGSTNYNPSLKS</u>	358
vhCDR3	<u>AVSYYYYGMDV</u>	359
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTVITCRTIQNINSYLNWYQQRPGKAPKLL IYATSSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQTYST LFTFGPGTKVDIK	360
vlCDR1	<u>RTIQNINSYLN</u>	361
vlCDR2	<u>ATSSLQS</u>	362
vlCDR3	<u>QQTYSTLFT</u>	363

Figure 14E

Ha1 6-1 (3,5)18

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GPGLVKPSETLSLTCTVPGGSI ¹ RSYFWSWIRQ ² PAGKGLEWIGRFYFS ³ GSTNYNP ⁴ SLKSRVTMSVDT ⁵ SKNQ ⁶ FLKLSSVTAADTAVYYCARDYGD ⁷ HY ⁸ Y ⁹ Y ¹⁰ Y ¹¹ Y ¹² Y ¹³ GMDVWGQGT ¹⁴ TVTVSS	364
vhCDR1	<u>SYFWS</u>	365
vhCDR2	<u>RFYFSGSTNYNP⁴SLKS</u>	366
vhCDR3	<u>DYGDHY⁸Y⁹Y¹⁰Y¹¹GMDV</u>	367
Variable light (vl) domain	VLTQPPSVSAAPGQKVT ¹ ISCSGSSSNIGNNYVSWYQQ ² FPGTAPKFLI ³ YDNNKRSSG ⁴ IPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL ⁵ SAVIFGGG ⁶ TKLTVL	368
vlCDR1	<u>SGSSSNIGNNYVS</u>	369
vlCDR2	<u>DNNKRSS</u>	370
vlCDR3	<u>GTWDSSLSAVI</u>	371

Ha16-1(2,4)4

	sequence	SEQ ID NO:
Variable heavy (vh) domain	GFTFSSYGMHWVRQAPGKGLEWVAI ¹ IWYDESNKYYADSVKGRFTISR ² DNSKNTLYLQMNSLRAEDTAVYYCARAYS ³ SGSYGYSYYGM ⁴	372
vhCDR1	<u>SYGMH</u>	373
vhCDR2	<u>I¹IWYDESNKYYADSVKG</u>	374
vhCDR3	<u>AYS³SGSYGYSYYGM</u>	375
Variable light (vl) domain	QDRQPASPGSGDKLGDKYACWYQQ ¹ KPGQSPVLVIYQDSKRPSGIPER ² FSGSNSGNTATLTISGTQAMDEADYYCQAWDNRTAVFGGGTKLTVL ³	376
vlCDR1	<u>PGSGDKLGDKYAC</u>	377
vlCDR2	<u>QDSKRPS</u>	378
vlCDR3	<u>QAWDNRTAV</u>	379

Ha16-1(3,5)56

	sequence	SEQ ID NO:
Variable heavy (vh) domain	RCRLVESGA ¹ EVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW ² MGI ³ IYPGSDTRYSPSFQ ⁴ GQVTISADKSISTAYLQWRS ⁵ LKASDTAMY ⁶ YCARKD ⁷ Y ⁸ Y ⁹ Y ¹⁰ Y ¹¹ Y ¹² VMDVWGQGT ¹³ TVTVSS	380
vhCDR1	<u>SYWIG</u>	381
vhCDR2	<u>I³IYPGSDTRYSPSFQ⁴G</u>	382
vhCDR3	<u>KD⁷Y⁸Y⁹Y¹⁰Y¹¹VMDV</u>	383
Variable light (vl) domain	DTISCTGTSSDVGN ¹ NYVSWYQQHPGKAPK ² LM ³ IYAVNNRPSGVS ⁴ NR ⁵ F ⁶ SGSKSGNTASLTISGLQA ⁷ EDEADYYC ⁸ SSYTSSRN ⁹ LVVFGGGTKLTVL ¹⁰	384
vlCDR1	<u>TGTSSDVGN¹NYVS</u>	385
vlCDR2	<u>AVNNRPS</u>	386
vlCDR3	<u>SSYTSSRN⁹LVV</u>	387

Figure 14F

H16-7.8

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGL EWIGIIYYSGSTYYNP SLKSRVTISVDTSKNQFSLKLSVTAADTAV FYCARVAIVTTIPGGMDVWGQGTITVTVSS	388
vhCDR1	<u>SGGYYWS</u>	389
vhCDR2	<u>IIYYSGSTYYNP SLKS</u>	390
vhCDR3	<u>VAIVTTIPGGMDV</u>	391
Variable light (vl) domain	EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLL IKYASQSFSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSRSF PWTFGQGTKVEIK	392
vlCDR1	<u>RASQSIGISLH</u>	393
vlCDR2	<u>YASQSFS</u>	394
vlCDR3	<u>HQSRSF PWT</u>	395

H16-1.93

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGISWVRQAPGQGLEW MGWISAYNGNTYYAQKLQARVTMTTDTSTSTAYMELRSLRSDDTAVY YCARDGYSSSWSL LHYYGMDVWGQGTITVTVSS	396
vhCDR1	<u>SYGIS</u>	397
vhCDR2	<u>WISAYNGNTYYAQKLQA</u>	398
vhCDR3	<u>DGYSSSWSL LHYYGMDV</u>	399
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITITWRSSQGIYNSLAWYQQKPGKVPKLL IYAAS TLHSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYN SA PFTFGPGTKVDIK	400
vlCDR1	<u>RSSQGIYNSLA</u>	401
vlCDR2	<u>AAS TLHS</u>	402
vlCDR3	<u>QKYN SAPFT</u>	403

Ha1 6-1(3,5)27.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	LVESGAEVKKPGESL KISCKGSGYRFTSYWIGWVRQMPGKGLEWMGI IYPGSDSTRYSPSFQGV TISADKSISTAYLQWSSLKASDTAMY YCA RKDY YYYSMDVWGQGTITVTVSS	404
vhCDR1	<u>SYWIG</u>	405
vhCDR2	<u>IIYPGSDSTRYSPSFQG</u>	406
vhCDR3	<u>KDY YYYSMDV</u>	407
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGQAPK LLIYGVNIRPSGVSTRFSGSKSGNTASLTISGLQAEDADYYC SSYT RSSILVVFAGGTKLTVL	408
vlCDR1	<u>TGTSSDVGGYNYVS</u>	409
vlCDR2	<u>GVNIRPS</u>	410
vlCDR3	<u>SSYTRSSILVV</u>	411

Figure 14G

H16-1.61

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVIWDGSGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVY YCARSRITIFGVVHYGMDVWGQGTTTIVTVSS	412
vhCDR1	<u>SYGMH</u>	413
vhCDR2	<u>VIWYDGSNKYYADSVKG</u>	414
vhCDR3	<u>SRITIFGVVHYGMDV</u>	415
Variable light (vl) domain	DTQLTQSPSSLSASVGDRTTITCRASQSISSYLNWYQLKPGKAPKLL IYAASSLES ~~G~~ VPSRFSGSESGTDFTLTIS ~~S~~ LQPEDFATYYCQ ~~S~~ SYNS PITFGPGTKVDIK	416
vlCDR1	<u>RASQSISSYLN</u>	417
vlCDR2	<u>AASSLES</u>	418
vlCDR3	<u>Q~~S~~SYNSPIT</u>	419

H16-1 (3,5)5

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGI ~~I~~ YPGDS ~~D~~ TRYSPSFQ ~~G~~ QVTISADKSISTAYLQWSSLKASDTAMY YCARKDY ~~Y~~ YYTMDVWGQGTTTIVTVSS	420
vhCDR1	<u>SYWIG</u>	421
vhCDR2	<u>I~~I~~YPGDS~~D~~TRYSPSFQ~~G~~</u>	422
vhCDR3	<u>KDY~~Y~~YYTMDV</u>	423
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQ ~~Q~~ HPGKAPK LMIYAVSNRPSGVSNR ~~F~~ SGSKSGNTASLTISGLQAEDEADY ~~C~~ SSYT ISRILVVFGGGTKLTVL	424
vlCDR1	<u>TGTSSDVGGYNYVS</u>	425
vlCDR2	<u>AVSNRPS</u>	426
vlCDR3	<u>SSYTISRILVV</u>	427

H16-7.200

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTL ~~S~~ LTCTVSGGSITSGDYYWSWIRQHPGKGL EWF ~~G~~ FIYYSGSAYYNPSLKSRITISVDTSKNQFSLKLSSVTAADTAV YYCAR ~~E~~ ERNYGGNSFDYWGQGT ~~L~~ TVTVSS	428
vhCDR1	<u>SGDYYWS</u>	429
vhCDR2	<u>FIYYSGSAYYNPSLKS</u>	430
vhCDR3	<u>ERNYGGNSFDY</u>	431
Variable light (vl) domain	DIVMTQSPLSLPVTPGEPASISCRSSQSL ~~L~~ HSNGYNYLDWYLQKPGQ SPQLLIYLGSNRASGV ~~P~~ DRFSGSGSGTDFTLKISRVEAEDVGVYYCM QALQTITFGQGT ~~R~~ LEIK	432
vlCDR1	<u>RSSQSL~~L~~HSNGYNYLD</u>	433
vlCDR2	<u>LGSNRAS</u>	434
vlCDR3	<u>MQALQTIT</u>	435

Figure 14H

Ha16-1(3,5)42

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGIIYPGDS DTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMY YCARKDYIIYSMDVWVGQGTITVTVSS	436
vhCDR1	<u>SYWIG</u>	437
vhCDR2	<u>IIYPGDS DTRYSPSFQG</u>	438
vhCDR3	<u>KDYIIYSMDV</u>	439
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGRFNYVSWYQQRPGKAPK LMIYAVNIRPSGVSNRFSGSKSGNTASLTISGLQAEDEAGYYCSSYT SSSTLLVFGGGTKLTVL	440
vlCDR1	<u>TGTSSDVGRFNYVS</u>	441
vlCDR2	<u>AVNIRPS</u>	442
vlCDR3	<u>SSYTSSSTLLV</u>	443

H1 6-9.65

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VATIWF DGSNGYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVY YCARDSSGSYDHF DYWGQGTITVTVSS	444
vhCDR1	<u>SYGMH</u>	445
vhCDR2	<u>TIWF DGSNGYYADSVKG</u>	446
vhCDR3	<u>DSSGSYDHF DY</u>	447
Variable light (vl) domain	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNCLDWYLQKPGQ SPQLLIYLG SNRASGV PDRFSGSGSGTDFTLKISRVEAEDVGVYYCM QALQTPITFGQGT RVEIK	448
vlCDR1	<u>RSSQSLLHSNGYNCLD</u>	449
vlCDR2	<u>LGSNRAS</u>	450
vlCDR3	<u>MQALQTPIT</u>	451

Ha16-1(3,5)19

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEW MGIIYPGDS DTRYSPSFQGVTTISADKSISTAYLQWSSLKASDTAMY YCARKDYIIYAMDVWVGQGTITVTVSS	452
vhCDR1	<u>SYWIG</u>	453
vhCDR2	<u>IIYPGDS DTRYSPSFQG</u>	454
vhCDR3	<u>KDYIIYAMDV</u>	455
Variable light (vl) domain	SALTQPASVSGSPGQSITISCTGTSSDVGRYNYVSWYQQHPGQAPKL MIYGISIRPSGVSPRFSGSKSGNTASLTISGLQAEDEADYYCSHTS NSTLVVFAGGTKLTVL	456
vlCDR1	<u>TGTSSDVGRYNYVS</u>	457
vlCDR2	<u>GISIRPS</u>	458
vlCDR3	<u>SSHTSNSTLVV</u>	459

Figure 14I

Ha16-1.80

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEW IGYVYFSGSTNYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYY CARATRDYYYYGMDVWGQGTTTVTVSS	460
vhCDR1	<u>SYYWS</u>	461
vhCDR2	<u>YVYFSGSTNYNPSLKS</u>	462
vhCDR3	<u>ATRDYYYYGMDV</u>	463
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRTSHDISNYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSRSGTDFLTITISLQPEDFATYYCQQTYST LFTFGPGTKVDIK	464
vlCDR1	<u>RTSHDISNYLN</u>	465
vlCDR2	<u>AASSLQS</u>	466
vlCDR3	<u>QQTYSTLFT</u>	467

Figure 16

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

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

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWDDKKHYNPSLKDRLTISKDTSK
 NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
 SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFCFSVMHEALHNHYTQKSLSLSPGK

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

DIQMTQSPSTLSASVGDRVTITCSASSRVGYMHWYQQKPGKAPKLLIYDTSKLASGVPSRFSGSGSGTEFTLTISSL
 QPDDFATYYCFQGSYPFTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17A

**>XENP24804 H16-1.93[ENPP3] H1L1 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**

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

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNGNTYYAQKLQARVTMTTDTSTS
 TAYMELRSLRSDDTAVYYCARDGYSSWSLLHHYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
 LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
 KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
 IAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 472)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTITLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

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

DIQMTQSPSSLSASVGDRITITWRSSQGIYNSLAWYQQKPKGKPKLLIYAASTLHSGVPSRFSGSGSGTDFTLTIS
 LQPEDVATYYCQKYNAPFTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>XENP26820 H16-7.8[ENPP3] H1L1 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**

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

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHPGKGLEWIGIIYYSGSTYYNPSLKSRTVISVDTSK
 NQFSLKLNVSVAADTAIFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
 TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
 EWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 475)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTITLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK

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

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCHQSRSPFWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17B

**>XENP28287 AN1[αENPP3] H1L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISSGGGTYYLDSVKGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQNSNWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>XENP28925 AN1[αENPP3] H1.8 L1 Fab-[αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
Isosteric A/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQNSNWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 17C

**>XENP29516 AN1[α ENPP3] H1.8 L1.33 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**

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 483)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 484)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1.33 (SEQ ID NO: 485)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**>XENP30262 AN1[α ENPP3] H1.8 L1.77 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**

Chain 1 - AN1[α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 486)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 487)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSVMSVMEALHNHYTQKSLSLSPGK

Chain 3 - AN1[α ENPP3]_L1.77 (SEQ ID NO: 488)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18A

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

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

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYSWIRQHHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
 NQFSLKLNSTVAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
 TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
 EWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSVMSVMEALHNHYTQKSLSLSPGK

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

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCHQSRSPFTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRQAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLWVSYISSGGGTTYLDVSGRFTISRDNKN
 SLYLQMNSLRAEDTAVYYCARHRRVYGYFDYWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSVMSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQNSNWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRQAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18B

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVSYISSGGGTYYLDSVKGRFTISRDN
 AKNSLYLQMNLSRAEDTAVYYCARHRRVYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
 KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI
 SGAQPED EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSVMSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQNSNWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLWVSYISSGGGTYYLDSVTGRFTISRDN
 AKNSLYLQMNLSRAEDTAVYYCARHRRVYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSVMSVMEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
 KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI
 SGAQPED EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSVMSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQNSNWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 18C

**>XENP30263 AN1[αENPP3] H1.8 L1.77 Fab-[αCD3] H1.32 L1.47 scFv(GKPGS)4-IgG1 pl(-)
)_Isosteric A_/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDNANK
 SLYLQMNSLRAEDTAVYYCARHRRVYGYFDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
 PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
 ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSFSVMHEALHNHYTQKSLSLSPGK

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

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
 KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPED
 EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSFSVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
 LEAEDAATYYCQQNSWPTYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 19A

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWQGQTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

**AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/
E357Q (SEQ ID NO: 505)**

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWQGQTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNLSRAEDTAVYYCVRHGNGFDSYVSWFAYWGQTLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTVSPGGTVTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTISG
AQPEDEADYYCALWYSNHWVFGGGLTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYAPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19B

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNLSRAEDTAVYYCVRHGNGFDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTISG
AQPEDEADYYCALWYSNHWVFGGKTLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 19C

**>XENP30264 AN1[αENPP3] H1.8 L1.77 Fab-
AN1[αENPP3] H1.8 L1.77 CH1 (G4S)2 [αCD3] H1.30 L1.47 scFv(GKPGS)4-IgG1 pl(-)
)_Isosteric_A_/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
AKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
AKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGGQGLTVTVSS/ GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLTVSPGGTVTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/ GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYESESISGIPSRFSGSGGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NO: 513)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSTVAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

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 (SEQ ID NO: 514)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHHPGKGLEWIGIIYYSGSTYYNPSLKSRVTISVDTSK
NQFSLKLNSTVAADTAVFYCARVAIVTTIPGGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGG
SGGGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTITVTVSS/GKPGSGKPGSGKPGSGKPGS/
QAVVTQEPSTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI
SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL
TVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

EIVLTQSPDFQSVTPKEKVTITCRASQSIGISLHWYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYYCHQSRSPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20B

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVS~~Y~~ISSGGGTTYYLDSVKGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGY~~Y~~FDYWGQGT~~L~~TVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS~~C~~SVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGKRLEWVS~~Y~~ISSGGGTTYYLDSVKGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGY~~Y~~FDYWGQGT~~L~~TVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~L~~TVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTLVSPGGTVTLT~~C~~GSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKAALTISG
AQPEDEADYYCALWYSNHWVFGG~~T~~KLTVL/GGGGSGGGGSKTHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFS~~C~~SVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~W~~YQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ~~Q~~SNWPYTFGGG~~T~~KL~~E~~IK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLN~~N~~FYPREAKVQWKVDNA
LQSGNSQESVTEQDSK~~D~~STYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20C

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGAALTISG
AQPEDEADYYCALWYSNHWVFGGGTKLTVL/GGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYAPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20D

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNLSRAEDTAVYYCARHRRVYYGYFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTI
SRDDSKNTLYLQMNLSRAEDTAVYYCVRHGNGFDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QA
VVTQEPSTVSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKKAALTISG
AQPEDEADYYCALWYSNHWVFGGKTLTVL/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYAPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 21

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGT~~L~~VTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~S~~SLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT~~V~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD~~G~~QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.30_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 526)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGT~~L~~VTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS~~S~~SLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGS/QAVVTQEP~~S~~LTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI~~S~~KYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~L~~VTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~V~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~W~~YQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPS~~V~~IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS~~T~~YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NO: 528)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVHLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 529)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGG/ QAVVTQEPSTLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGGQGLTVTVSS/ GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 530)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NO: 531)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.32_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 532)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGS/QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1.33 (SEQ ID NO: 533)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~WY~~QQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPS~~V~~IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS~~T~~YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 22C

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAV
YYCVRHGNFGDSYVSWFAYWQGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQGPENNYKTTTPVLDSDGSFFLYSKLTV
DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NO: 537)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVHLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

AN1[αENPP3]_H1.8_CH1_(G4S)2_[αCD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 538)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGG/ QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQTLVTVSS/ GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 3 - AN1[αENPP3]_L1 (SEQ ID NO: 539)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23B

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVHLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGS/QAVVTQEPSTLTVSPGGTVTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23C

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGT~~L~~VTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT~~V~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD~~G~~QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGTTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGT~~L~~VTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGS/QAVVTQEP~~S~~LTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI~~S~~KYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGT~~L~~VTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~V~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~W~~YQQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQ~~S~~NSWPYTFGGGTKLEIK/RTVAAPS~~V~~IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS~~T~~YLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23D

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGT~~TY~~YLD~~SV~~TGRFTISRDAKN
SLYLQMNSLR~~AE~~DTAVYYCARHRRVYYGY~~Y~~FDYWGQGT~~LV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT~~SV~~SWNSGALTSGVHTFPAVLQSSGLYSLSSV~~VT~~VPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT~~VL~~HLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESD~~G~~QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVS~~Y~~ISSGGGT~~TY~~YLD~~SV~~TGRFTISRDAKN
SLYLQMNSLR~~AE~~DTAVYYCARHRRVYYGY~~Y~~FDYWGQGT~~LV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVT~~SV~~SWNSGALTSGVHTFPAVLQSSGLYSLSSV~~VT~~VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QAVVTQEP~~SL~~TVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSL
RLSCAASGFTFSTYAMNWRQAPGKGLEWVGRI~~RS~~KYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLR~~AE~~DTAV
YYCVRHGNFGDEYVSWFAYWGQGT~~LV~~TVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VL~~HLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIH~~WY~~QQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQ~~Q~~SN~~SW~~PYTFGGGTKLEIK/RTVAAPS~~VF~~IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSK~~ST~~YSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 23E

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Chain 2 -

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

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDAKNSLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWQGQTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGGGS/QAVVTQEPSTLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWWYQKPDQSPKLLIEYESESISGIPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNSWPYTFGGGTKLEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 46

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

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDYWGQGT LVT VSS /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAPPV
AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

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

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS S
LEPEDFAVYYCQQSSNWPRTFGQG TKVEIK /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62A

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

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

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGM~~AWFRQ~~APGKGLEWVSFI~~SNL~~GYSIYYADSVKGRFTISRDN~~AKN~~
SLYLQMNSLR~~AEDTAVYYCAR~~APYDYDSFDPMDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT~~
CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
SVLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE~~
WESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSV~~MHEALHNHYTQKSLSLSPGK~~

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

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI~~RSKYNNYATYYADSVKGRFTISRDDS~~
KNTLYLQMNSLR~~AEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~LVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLT~~VS~~PGGT~~VT~~LT~~CGSSTGAVTTSNYANWVQ~~QKPGKSPRGLIGGT~~NKRAPGV~~PARFSGSLLGGKAALTISGAQPED
EADYYC~~ALWYSNHWVFGGGTK~~LT~~VL~~/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR~~
EPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSV~~MHEALHNHYTQKSLSLSPGK~~

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

DIVMTQSPD~~SLAVSLGERATINCKSSQSL~~LSNRNKNYLAWYQQKPDQSPKLLIYWASTRESGVPDRFSGSGSGTD~~F~~
TLTIS~~SLQAEDVAVYYCKQSY~~YLWTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLN~~NFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDS~~TYLS~~SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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

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

QVQLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQ~~RL~~EWIGGINPNNGIPN~~YNQ~~KFKGRVTITVDT~~SAS~~
TAYMELSSLR~~SED~~TAVYYCARRIAYGYDEGHAMDYWGQGT~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVT~~SVWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT~~
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVS~~VT~~VL~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA~~
VEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSV~~MHEALHNHYTQKSLSLSPGK~~

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

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI~~RSKYNNYATYYADSVKGRFTISRDDS~~
KNTLYLQMNSLR~~AEDTAVYYCVRHGNFGDSYVSWFAYWGQGT~~LVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLT~~VS~~PGGT~~VT~~LT~~CGSSTGAVTTSNYANWVQ~~QKPGKSPRGLIGGT~~NKRAPGV~~PARFSGSLLGGKAALTISGAQPED
EADYYC~~ALWYSNHWVFGGGTK~~LT~~VL~~/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR~~
EPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSV~~MHEALHNHYTQKSLSLSPGK~~

Chain 3 - [αFAP]_L0 (SEQ ID NO: 559)

DIVMTQSPD~~SLAVSLGERATINCKSSQSL~~LYSRNQNKNYLAWYQQKPGPPKLLIFWASTRESGVPDRFSGSGFGTD~~F~~
TLTIS~~SLQAEDVAVYYCQ~~QYFSYPLTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLN~~NFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDS~~TYLS~~SLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62B

>XENP25967 [α FAP] H1L1 Fab-

[α FAP] H1L1 Fab (G4S)2 [α CD3] H1.32 L1.47 scFv(GKPGS)4 (G4S)2 IgG1 PVA /S267K-pl(-)
) Isosteric A L368D/K370S-IgG1 C220S/S364K/E357Q

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

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGISGSGGSTYYADSVKGRFTISRDN SKNTLYLQ
 MNSLRAEDTAVYYCAKISFYPPGGTYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
 SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL
 FPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
 NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFL
 YSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α FAP]_H1_(G4S)2_[α CD3]_H1.32_L1.47_scFv(GKPGS)4_(G4S)2_IgG1_C220S/S364K/E357Q (SEQ ID NO: 561)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSGISGSGGSTYYADSVKGRFTISRDN SKNTLYLQ
 MNSLRAEDTAVYYCAKISFYPPGGTYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
 SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/ GGGGSGGGGS/ EVQLVESGG
 GLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAE
 DTAVYYCVRHGNFGDSYVSWFAYWGQGTLLVTVSS/ GKPGSGKPGSGKPGSGKPGS/ QAVVTQEP SLTVSPGGT VTLTCSST
 GAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTV
 L/ GGGGSGGGGS/ KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREOMTKNQVKTCLVKGFY
 PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - [α FAP]_L1 (SEQ ID NO: 562)

DIQMTQSPSSLSASVGRVTITCRASQSISSYLNWYQQKPKGAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTITISLQPED
 FATYYCQQSYSSPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
 TEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP28925 [α ENPP3] H1.8 L1 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

Chain 1 - [α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 563)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSSNYGMSWVRQAPGQRLEWVSYISSGGGTTYLDSVTGRFTISRDN AKNSLYLQ
 MNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
 SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL
 FPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
 NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFL
 YSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

Chain 2 - [α CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 564)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDD SKNTLY
 LQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLLVTVSS/ GKPGSGKPGSGKPGSGKPGS/ QAVVTQEP SLTVSPGGT
 VTLTCSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWV
 FGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNA
 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREOMTKNQVKTCLV
 KGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK

Chain 3 - [α ENPP3]_L1 (SEQ ID NO: 565)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQQKPDQSPKLLIKYASESISGIPSRFSGSGSGTDFLTITINSLEAED
 AATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
 TEQDSKDYSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62C

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

Chain 1 - [α SSTR2]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 566)
 EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGMWFRQAPGKGLEWVSFISNLAISIYYADSVKGRFTISRDAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFYPMQYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHT
 CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVV
 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE
 WESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVLHEALHSHYTQKSLSLSPGK

**Chain 2 -
 [α SSTR2]_H1.24_[α CD3]_H1.32_L1.47_scFv(GKPGS)4_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
 (SEQ ID NO: 567)**
 EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYGMWFRQAPGKGLEWVSFISNLAISIYYADSVKGRFTISRDAKN
 SLYLQMNSLRAEDTAVYYCARAPYDYDSFYPMQYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/SGGG
 SGGGS/ EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
 TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/ GKPGSGKPGSGKPGSGKPGS/
 QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGKKAALTI
 SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/SGGGSGGGGS/KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
 TPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK
 LTVDKSRWQGNVFCSSVLHEALHSHYTQKSLSLSPGK

Chain 3 - [α SSTR2]_L1.30 (SEQ ID NO: 568)
 DIVMTQSPDSLAVSLGERATINCKSSQSLNSRNRKNYLAWYQKPDQSPKLLIYWASTRESGVPRFSGSGSGTD
 FLTISSLQAEDVAVYYCKQSYLWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRFAKQW
 KVDNALQSGNSQESVTEQDSKDSSTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 62D

**>XENP31149 [α ENPP3] H1.8 L1.33 Fab-
[α ENPP3] H1.8 L1.33 CH1 (G4S)2 [α CD3] 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 - [α ENPP3]_H1.8_IgG1_pl(-)_Isosteric_A_/PVA_/S267K/L368D/K370S (SEQ ID NO: 569)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 2 -

[α ENPP3]_H1.8_CH1_(G4S)2_[α CD3]_L1.47_H1.89_scFv(GKPGS)4_Fc(222)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 570)

EVQLVESGGGLVQPGGSLRLSCAASGFAFSNYGMSWVRQAPGQRLEWVSYISSGGGTYYLDSVTGRFTISRDN
SLYLQMNSLRAEDTAVYYCARHRRVYYGYFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GGGGS
GGGGS/QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLLGG
KAALTISGAQPEDEADYYCALWYSNHWFVGGGKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGG
LRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTA
VYYCVRHGNGFDEYVSWFAYWGQGTLLTVSS/GGGSGGGGS/KTHCTPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL
TVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK

Chain 3 - [α ENPP3]_L1.33 (SEQ ID NO: 571)

DILLTQSPDFQSVTPKEKVTITCRASQSIGTSIHWYQKPDQSPKLLIEYASESISGIPSRFSGSGSGTDFTLTINS
LEAEDAATYYCQQSNSWPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 63

[αSSTR2] H1.24 L1.30

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYGM ~~AWFRQAPGKGLEW~~ VSFISNLAYSIIYADSVKGRFTISRDN ~~AKNSLYLQMNSLRAEDTAVY~~ YCARAPYDYDSFYPM ~~DYWGQGLTVSS~~	572
vhCDR1	<u>DYGMA</u>	573
vhCDR2	<u>FISNLAYSIIYADSVKG</u>	574
vhCDR3	<u>APYDYDSFYPM~~DY~~</u>	575
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSL ~~LNSRNRKNYLAWYQQKPD~~ QSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS ~~SLQAEDVAVYYC~~ <u>KQSY~~YL~~WTFGGG</u> TKVEIK	576
vlCDR1	<u>KSSQSL~~LNSRNRKNYL~~A</u>	577
vlCDR2	<u>WASTRES</u>	578
vlCDR3	<u>KQSY~~YL~~WT</u>	579