

Figure 1A

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

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Figure 1B

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

Figure 1C

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

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Figure 1D

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

Figure 1E

Monomer 1	Monomer 2
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/N276K
N384S/K392N/V397M/Q419E	N276K
D221E/P228E/L368E	D221R/P228R/K409R
C220E/P228E/L368E	C220R/E224R/P228R/K409R
F405L	K409R
T366I/K392M/T394W	F405A/Y407V
T366V/K409F	L351Y/Y407A
T366A/K392E/K409F/T411E	D399R/S400R/Y407A
L351K	L351E
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/N276K
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	
N208D/Q295E/N384D/Q418E/N421D	
N208D/Q295E/Q418E/N421D	
Q196K/I199T/P217R/P228R/N276K	
Q196K/I199T/N276K	
E269Q/E272Q/E283Q/E357Q	
E269Q/E272Q/E283Q	
E269Q/E272Q	
E269Q/E283Q	
E272Q/E283Q	
E269Q	

Figure 2

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

Figure 3

Ablation Variants

G236R
S239G
S239K
S239Q
S239R
V266D
S267K
S267R
H268K
E269R
299R
299K
K322A
A327G
A327L
A327N
A327Q
L328E
L328R
P329A
P329H
P329K
A330L
A330S/P331S
I332K
I332R
V266D/A327Q
V266D/P329K
S267R/A327Q
S267R/P329K
G236R/L328R
E233P/L234V/L235A/G236_/S239K
E233P/L234V/L235A/G236_/S267K
E233P/L234V/L235A/G236_/S239K/A327G
E233P/L234V/L235A/G236_/S267K/A327G
E233P/L234V/L235A/G236_
S239K/S267K
267K/P329K

Figure 4

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

Figure 5

Positive Charged scFv Linkers

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

Negative Charged scFv Linkers

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

Additional scFv Linkers

GGGSGGGSGGGGS	SEQ ID NO:25
GGGSGGGSGGGSGGGGS	SEQ ID NO:26
GSTSGSGKPGSGEGSTKG	SEQ ID NO:27
PRGASKSGSASQTGSAPGS	SEQ ID NO:28
GTAAAGAGAAGGAAAGAAG	SEQ ID NO:29
GTSGSSGSGSGSGSGGGG	SEQ ID NO:30
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO:15

Figure 6

Useful domain linkers

<u>Name</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>
(GGGGS) ₁ or GGGGS	GGGGS	5
(GGGGS) ₂	GGGSGGGGS	31
(GGGGS) ₃	GGGSGGGSGGGGS	32
(GGGGS) ₄	GGGSGGGSGGGSGGGGS	33
(GGGGS) ₅	GGGSGGGSGGGSGGGSGGGGS	34
(GGGGS) ₆	GGGSGGGSGGGSGGGSGGGSGGGGS	35
(GGGGS) ₇	GGGSGGGSGGGSGGGSGGGSGGGSGGGGS	36
(GGGGA) ₁ or GGGGA	GGGGA	37
(GGGGA) ₂	GGGGAGGGGA	38
(GGGGA) ₃	GGGGAGGGGAGGGGA	39
(GGGGA) ₄	GGGGAGGGGAGGGGAGGGGA	40
(GGGGA) ₅	GGGGAGGGGAGGGGAGGGGAGGGGA	41
(GGGGA) ₆	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	42
(GGGGA) ₇	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	43
30AA-linker	DPALVHQRAPPPGGGSGGGSGGGSGGG	44
(GKPGS) ₁ or GKPGS	GKPGS	45
(GKPGS) ₅	GKPGSGKPGSGKPGSGKPGSGKPGS	46
(GKPGS) ₆	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	47
(GGGES) ₁ or GGGES	GGGES	48
"half hinge"	KTHTCPPCP	49
"full hinge C220S variant"	EPKSSDKTHTCPPCP	50
"flex half hinge"	GGGSGGGGSKTHTCPPCP	51
"charged half hinge1"	GKPGSGKPGSKTHTCPPCP	52
"charged half hinge2"	GKPGSKTHTCPPCP	53

Figure 7A

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
VMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 2**>Fab-Fc Side (SEQ ID NO: 56)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
VMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 3**>Fab-Fc Side (SEQ ID NO: 58)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
VMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 4**>Fab-Fc Side (SEQ ID NO: 60)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

Figure 7B

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 5**>Fab-Fc Side (SEQ ID NO: 62)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDQGPENNYKTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQ
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 6**>Fab-Fc Side (SEQ ID NO: 64)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPENNYKTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQ
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 7**>Fab-Fc Side (SEQ ID NO: 66)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPENNYKTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQ
VMHEALHNHYTQKSLSLSPGK

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

Figure 7C

1 + 1 Fab-scFv-Fc Backbone 8**>Fab-Fc Side (SEQ ID NO: 68)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDPKPSDTKVDKRVESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ
FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWEEGDFVSCSV
HEALHNHYTQKSLSLSPGK

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

ESKYGPPCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEQMTKNQVKLTCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 9**>Fab-Fc Side (SEQ ID NO: 70)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDPKPSDTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEEGDFVSCSV
HEALHNHYTQKSLSLSPGK

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

ERKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 10**>Fab-Fc Side (SEQ ID NO: 72)**

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDPKPSDTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWEEGDFVSCSV
HEALHNHYTQKSLSLSPGK

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

ERKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 11**>Fab-Fc Side (SEQ ID NO: 74)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHPKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEGDFVSCS
VLHEALHSHYTQKSLSLSPGK

Figure 7D

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

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVLHEALHSHYDTQKSLSLSPGK

1 + 1 Fab-scFv-Fc Backbone 12**>Fab-Fc Side (SEQ ID NO: 76)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV
MHEALHNHYTQKSLSLSPGK

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

ERKSSDKTHTCPPRPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSV MHEALHNHYTQKSLSLSPGK

Figure 8A

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSKVMHEALHNHYTQKSLSLSPGK

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

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSKVMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 3**>Fab-Fc Side (SEQ ID NO: 82)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSKVMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 4**>Fab-Fc Side (SEQ ID NO: 84)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLEVDKSRWEQGDVFS
VMHEALHNHYTQKSLSLSPGK

Figure 8B

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 5**>Fab-Fc Side (SEQ ID NO: 86)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 6**>Fab-Fc Side (SEQ ID NO: 88)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

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

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 7**>Fab-Fc Side (SEQ ID NO: 90)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 91)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 8C

2 + 1 Fab2-scFv-Fc Backbone 8**>Fab-Fc Side (SEQ ID NO: 92)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFPFAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VLHEALHSHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 93)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

2 + 1 Fab2-scFv-Fc Backbone 9**>Fab-Fc Side (SEQ ID NO: 94)**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSKVHTFPFAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVAGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

>Fab-scFv-Fc Side (SEQ ID NO: 95)

APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9

Constant Light Domain – Kappa (SEQ ID NO: 96)

RTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

Constant Light Domain – Lambda (SEQ ID NO: 97)

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 10A

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

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLTVL	98
scFv (VLVH)	QAVVTQEP ~~SLTVSPGGT~~ VTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLTV L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~	99
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~	100
vhCDR1	~~TYAMN~~	101
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	102
vhCDR3	~~HGNFSGSYVSWFAY~~	103
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLTV L	104
vlCDR1	~~GSSTGAVTTSNYAN~~	105
vlCDR2	~~GTNKRAP~~	106
vlCDR3	~~ALWYSNHWV~~	107
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	108

Figure 10B

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

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRI ~~RSK~~ ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGV ~~PARFSGSL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLT ~~VL~~	109
scFv (VLVH)	QAVVTQEP ~~SLTVSPGG~~ TVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLT ~~V~~ L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRI ~~RSK~~ ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~	110
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWVRQAPGKGLEWVGRI ~~RSK~~ ANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFAYWGQGT ~~LVTVSS~~	111
vhCDR1	<u>TYAMN</u>	112
vhCDR2	<u>RIRSKANNYATYYADSVKG</u>	113
vhCDR3	<u>HGNFGDSYVSWFAY</u>	114
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGG~~ TVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLT ~~V~~ L	115
vlCDR1	<u>GSSTGAVTTSNYAN</u>	116
vlCDR2	<u>GTNKRAP</u>	117
vlCDR3	<u>ALWYSNHWV</u>	118
Linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	119

Figure 10C

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

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDEY~~ VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLT ~~VL~~	120
scFv (VLVH)	QAVVTQEP ~~SLTVSPGGT~~ VTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLT ~~V~~ L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHG ~~NFGDEY~~ VSWFAYWGQGT ~~LVTVSS~~	121
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDEY~~ VSWFAYWGQGT ~~LVTVSS~~	122
vhCDR1	~~TYAMN~~	123
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	124
vhCDR3	~~HGNEFGDEYVSWFAY~~	125
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLT ~~V~~ L	126
vlCDR1	~~GSSTGAVTTSNYAN~~	127
vlCDR2	~~GTNKRAP~~	128
vlCDR3	~~ALWYSNHWV~~	129
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	130

Figure 10D

CD3 High-Int #3 – [anti-CD3] H1.90 L1.47 scFv

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDPY~~ VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR ~~APGV~~ PARFSGSLL GGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTVL~~	131
scFv (VLVH)	QAVVTQEP ~~SLTVSPGGT~~ VTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KR ~~APGV~~ PARFSGSLLGGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTV~~ L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFST YAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHG ~~NFGDPY~~ VSWFAYWGQGT ~~LVTVSS~~	132
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDPY~~ VSWFAYWGQGT ~~LVTVSS~~	133
vhCDR1	~~TYAMN~~	134
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	135
vhCDR3	~~HGNFGDPYVSWFAY~~	136
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KR ~~APGV~~ PARFSGSLLGGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTV~~ L	137
vlCDR1	~~GSSTGAVTTSNYAN~~	138
vlCDR2	~~GTNKRAP~~	139
vlCDR3	~~ALWYSNHWV~~	140
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	141

Figure 10E

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

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFDYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGV ~~PARFSGSLL~~ GGKAALTISGAQPEDEADYYCALWYSNHWVF ~~GGG~~ TKLT ~~VL~~	142
scFv (VLVH)	QAVVTQEP ~~SLTVSPGG~~ TVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLT ~~V~~ L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFST YAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFDYWGQGT ~~LVTVSS~~	143
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHG ~~NFGDSY~~ VSWFDYWGQGT ~~LVTVSS~~	144
vhCDR1	~~TYAMN~~	145
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	146
vhCDR3	~~HGNFSDSYVSWFDY~~	147
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGG~~ TVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGV ~~PARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVF~~ GGGTKLT ~~V~~ L	148
vlCDR1	~~GSSTGAVTTSNYAN~~	149
vlCDR2	~~GTNKRAP~~	150
vlCDR3	~~ALWYSNHWV~~	151
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	152

Figure 10F

CD3 Low – [anti-CD3] H1.31 L1.47 scFv

	Sequence	SEQ ID NO:
scFv (VHVL)	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGT ~~LVTVSS~~ /GKPGSGKPGSGKPGSGKPGS/QAVVTQEP ~~SLTVSPG~~ GTVTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKR ~~APGV~~ PARFSGSLL GGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTVL~~	153
scFv (VLVH)	QAVVTQEP ~~SLTVSPGGT~~ VTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KR ~~APGV~~ PARFSGSLLGGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTV~~ L/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTTFST YAMSWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQM NSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGT ~~LVTVSS~~	154
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSTYAMSWVRQAPGKGLEWVGRI ~~RSK~~ YNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNF ~~GDSY~~ VSWFAYWGQGT ~~LVTVSS~~	155
vhCDR1	~~TYAMS~~	156
vhCDR2	~~RIRSKYNNYATYYADSVKG~~	157
vhCDR3	<del>HGNF~~GDSY~~VSWFAY</del>	158
Variable Light (vl) Domain	QAVVTQEP ~~SLTVSPGGT~~ VTLTGSSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KR ~~APGV~~ PARFSGSLLGGKAALTI ~~SGAQPE~~ DEADYYCALWYSNHWVFGGGTK ~~LTV~~ L	159
vlCDR1	~~GSSTGAVTTSNYAN~~	160
vlCDR2	~~GTNKRAP~~	161
vlCDR3	~~ALWYSNHWV~~	162
Linker	~~GKPGSGKPGSGKPGSGKPGS~~	163

Figure 11

Human CLDN6 sequence

>sp|P56747
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDL
QAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAE
AQKREL GASLYLGWAASGLLLGGGLLCCTCPSSGSGQPSHYMARYSTSAPAI SRGPSEYPTKNYV (SEQ ID
NO: 164)

Human CLDN6 sequence, N-terminal extracellular domain

>sp|P56747|29-81
MWKVTAFIGNSIVVAQVVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDLQAAR (SEQ ID NO: 165)

Human CLDN6 sequence, C-terminal extracellular domain

>sp|P56747|138-160
WTAHAIIRDFYNPLVAE AQKREL (SEQ ID NO: 166)

Mouse CLDN6 sequence

>sp|Q9Z262
MASTGLQILGIVLTLLGWVNALVSCALPMWKVTAFIGNSIVVAQMVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDL
QAARALCVVTLIVLLGLLVYLAGAKCTTCVEDRNSKSRVLVLTSGIIFVISGVLTLIPVCWTAHSIIQDFYNPLVAD
AQKREL GASLYLGWAASGLLLGGGLLCACSSGGTQGPRHYMACYSTSVPHSRGPSEYPTKNYV (SEQ ID NO:
167)

Mouse CLDN6 sequence, N-terminal extracellular domain

>sp|Q9Z262|29-81
MWKVTAFIGNSIVVAQMVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDLQAAR (SEQ ID NO: 168)

Mouse CLDN6 sequence, C-terminal extracellular domain

>sp|Q9Z262|138-163
WTAHSIIQDFYNPLVADAQKREL GAS (SEQ ID NO: 169)

Macaca fascicularis CLDN6 sequence (predicted)

>tr|G7Q0B0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDL
QAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIVFVISGVLTLIPVCWTAHAIIRDFYNPLVAE
AQKREL GASLYLGWAASGLLLGGGLLCCTCPSSGSRGPSHYMARYSTSAPAI SRGPSEYPTKNYV (SEQ ID
NO: 170)

Macaca fascicularis CLDN6 sequence, N-terminal extracellular domain (predicted)

>tr|G7Q0B0|29-81
MWKVTAFIGNSIVVAQVVWEGWLWMSCVVQSTGQMCKVYDSSLALPQDLQAAR (SEQ ID NO: 171)

Macaca fascicularis CLDN6 sequence, C-terminal extracellular domain (predicted)

>tr|G7Q0B0|138-160
WTAHAIIRDFYNPLVAE AQKREL (SEQ ID NO: 172)

Figure 12

```

===== EC loop
c1dn6      MASAGNQILGVVLTLLGWVNGLVSCALPINKVTAFIGNSIVVAQVWEGLWVSCVQSTG 60
c1dn9      MA5TGLELLGMTLAVLGWLGTLVSCALPINKVTAFIGNSIVVAQVWEGLWVSCVQSTG 60
          **:*:::*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:
          =====
c1dn6      QMOCKVYD5LLALPODLQAARALCVIALLVALLVLFGLLVYLAGAKCTTCVEEKDSKARLVLT 120
c1dn9      QMOCKVYD5LLALPODLQAARALCVIALLVALLVLFGLLVVAITGAQCTTCVEDEGAKARIVLT 120
          *****:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:
          =====
c1dn6      SGIVFVISGVLTLIPVCWTAHAITIDFYNPLVAEAKKREL GASLYLGWAA5GLLLLGGGL 180
c1dn9      AGVILLLAGILVLI PVVCWTAHAITIDFYNPLVAEAKKREL GASLYLGWAAAALLMLGGGL 180
          :*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:
          =====
c1dn6      LCCTCP5GG5QG5SHMARY5TSAPAI5RGP5EYPTKNYV      220
c1dn9      LCCTCPPPQVERPRGPRLGYSIPSR---5GASGLDKRDYV      217
          ***** : * * * : * * : : *

```

Figure 13

mC6-30[CLDN6]

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSPGKSLEW IGGIDPNNNGNTHYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVY YCARIYYFGRLYFDEFWGAGTTVTVSS	175
vhCDR1	EYTMH	176
vhCDR2	GIDPNNNGNTHYNQKFKG	177
vhCDR3	IYYFGRLYDEF	178
Variable light (vl) domain	DIQMTQSSSSFSVSLGDRVTTITCKASEDIYNRLAWYQQKPGNVPRL ISGATSLETGVPSRFSGSGSGKDYTLSTISLTQTEDVTYYCQQYWS PLTFGGGTKLEIK	179
vlCDR1	KASEDIYNPLA	180
vlCDR2	GATSLET	181
vlCDR3	QQYWSPLT	182

>XENP34243 mC6-30**mC6-30 Heavy Chain**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDSNNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDEFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
183)

mC6-30 Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTISS
LQPEDATYYCQQYWSGPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO:
184)

Figure 14

C6-30[CLDN6] H1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSED TAVY YCARIYYFGRLYFDEWGAGTLVTVSS	185
vhCDR1	EYTMH	186
vhCDR2	GIDPNNNGNTHYNQKFQ	187
vhCDR3	IYYFGRLYFDE	188

C6-30[CLDN6] H2

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEWGAGTLVTVSS	189
vhCDR1	EYTMH	190
vhCDR2	GIDPNNNGNTHYNQKFQ	191
vhCDR3	IYYFGRLYFDE	192

C6-30[CLDN6] L1

	sequence	SEQ ID NO:
Variable light (vl) domain	DIQMTQSPSSLSASVGDRTITCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYTFITISLQPEDIATYYCQQYWSS PLTFGGGTKVEIK	193
vlCDR1	QASEDIYNRLA	194
vlCDR2	GATSLET	195
vlCDR3	QQYWSSPLT	196

C6-30[CLDN6] L2

	sequence	SEQ ID NO:
Variable light (vl) domain	DIQMTQSPDSLAVSLGERATINCKASEDIYNRLAWYQQKPGQVPKLL ISGATSLETGVPSRFSGSGSGKDYTLTISLQAEADVAVYYCQQYWSS PLTFGGGTKVEIK	197
vlCDR1	KASEDIYNRLA	198
vlCDR2	GATSLET	199
vlCDR3	QQYWSSPLT	200

Figure 15A

C6-30[CLDN6] H1.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGISPNNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARIYYFGRLYFDEWGAGTLVTVSS	201
vhCDR1	EYTMH	202
vhCDR2	GISPNNGNTHYNQKFQ	203
vhCDR3	IYYFGRLYFDE	204

C6-30[CLDN6] H1.2

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGINPNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARIYYFGRLYFDEWGAGTLVTVSS	205
vhCDR1	EYTMH	206
vhCDR2	GINPNNGNTHYNQKFQ	207
vhCDR3	IYYFGRLYFDE	208

C6-30[CLDN6] H1.3

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDSNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARIYYFGRLYFDEWGAGTLVTVSS	209
vhCDR1	EYTMH	210
vhCDR2	GIDSNNGNTHYNQKFQ	211
vhCDR3	IYYFGRLYFDE	212

C6-30[CLDN6] H1.4

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDANNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARIYYFGRLYFDEWGAGTLVTVSS	213
vhCDR1	EYTMH	214
vhCDR2	GIDANNNGNTHYNQKFQ	215
vhCDR3	IYYFGRLYFDE	216

C6-30[CLDN6] H1.5

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPQNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARIYYFGRLYFDEWGAGTLVTVSS	217
vhCDR1	EYTMH	218
vhCDR2	GIDPQNGNTHYNQKFQ	219
vhCDR3	IYYFGRLYFDE	220

Figure 15B

C6-30[CLDN6] H1.6

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNSGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDTAVY YCARIYYFGRLYFDEFWGAGTLVTVSS	221
vhCDR1	EYTMH	222
vhCDR2	GIDPNSGNTHYNQKFQ	223
vhCDR3	IYYFGRLYDEF	224

C6-30[CLDN6] H1.7

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNQGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDTAVY YCARIYYFGRLYFDEFWGAGTLVTVSS	225
vhCDR1	EYTMH	226
vhCDR2	GIDPNQGNTHYNQKFQ	227
vhCDR3	IYYFGRLYDEF	228

C6-30[CLDN6] H1.8

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNDNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDTAVY YCARIYYFGRLYFDEFWGAGTLVTVSS	229
vhCDR1	EYTMH	230
vhCDR2	GIDPNNDNTHYNQKFQ	231
vhCDR3	IYYFGRLYDEF	232

C6-30[CLDN6] H1.9

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNANTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDTAVY YCARIYYFGRLYFDEFWGAGTLVTVSS	233
vhCDR1	EYTMH	234
vhCDR2	GIDPNNANTHYNQKFQ	235
vhCDR3	IYYFGRLYDEF	236

C6-30[CLDN6] H1.19

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDTATY YCARIYYFGRLYFDEFWGAGTLVTVSS	237
vhCDR1	EYTMH	238
vhCDR2	GIDPNNGNTHYNQKFQ	239
vhCDR3	IYYFGRLYDEF	240

Figure 15C

C6-30[CLDN6] H1.22

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARI ~~LYFGRLYFDEF~~ WGAGTLVTVSS	241
vhCDR1	~~EYTMH~~	242
vhCDR2	~~GIDPNNNGNTHYNQKFQ~~	243
vhCDR3	~~ILYFGRLYDEF~~	244

C6-30[CLDN6] H1.24

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEW MGGIDPNNNGNTHYNQKFQGRVTITVDKSASTAYMELSSLRSEDNAVY YCARI ~~YYLGRLYFDEF~~ WGAGTLVTVSS	245
vhCDR1	~~EYTMH~~	246
vhCDR2	~~GIDPNNNGNTHYNQKFQ~~	247
vhCDR3	~~IYYLGRLYDEF~~	248

C6-30[CLDN6] H2.1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGISPNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARI ~~YYFGRLYFDEF~~ WGAGTLVTVSS	249
vhCDR1	~~EYTMH~~	250
vhCDR2	~~GISPNNNGNTHYNQKFQ~~	251
vhCDR3	~~IYYFGRLYDEF~~	252

C6-30[CLDN6] H2.2

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGITPNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARI ~~YYFGRLYFDEF~~ WGAGTLVTVSS	253
vhCDR1	~~EYTMH~~	254
vhCDR2	~~GITPNNNGNTHYNQKFQ~~	255
vhCDR3	~~IYYFGRLYDEF~~	256

C6-30[CLDN6] H2.3

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDSNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARI ~~YYFGRLYFDEF~~ WGAGTLVTVSS	257
vhCDR1	~~EYTMH~~	258
vhCDR2	~~GIDSNNNGNTHYNQKFQ~~	259
vhCDR3	~~IYYFGRLYDEF~~	260

Figure 15D

C6-30[CLDN6] H2.4

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDGNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	261
vhCDR1	EYTMH	262
vhCDR2	GIDGNNGNTHYNQKFQ	263
vhCDR3	IYYFGRLYDEF	264

C6-30[CLDN6] H2.5

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPQNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	265
vhCDR1	EYTMH	266
vhCDR2	GIDPQNGNTHYNQKFQ	267
vhCDR3	IYYFGRLYDEF	268

C6-30[CLDN6] H2.6

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNDGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	269
vhCDR1	EYTMH	270
vhCDR2	GIDPNDGNTHYNQKFQ	271
vhCDR3	IYYFGRLYDEF	272

C6-30[CLDN6] H2.7

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNQGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	273
vhCDR1	EYTMH	274
vhCDR2	GIDPNQGNTHYNQKFQ	275
vhCDR3	IYYFGRLYDEF	276

C6-30[CLDN6] H2.8

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNDNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	277
vhCDR1	EYTMH	278
vhCDR2	GIDPNDNTHYNQKFQ	279
vhCDR3	IYYFGRLYDEF	280

Figure 15E

C6-30[CLDN6] H2.9

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNANTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	281
vhCDR1	EYTMH	282
vhCDR2	GIDPNNANTHYNQKFQ	283
vhCDR3	IYYFGRLYFDF	284

C6-30[CLDN6] H2.11

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYSFTEYTMHWVRQMPGKSLEW MGGIDPNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	285
vhCDR1	EYTMH	286
vhCDR2	GIDPNNNGNTHYNQKFQ	287
vhCDR3	IYYFGRLYFDF	288

C6-30[CLDN6] H2.12

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYDFTEYTMHWVRQMPGKSLEW MGGIDPNNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	289
vhCDR1	EYTMH	290
vhCDR2	GIDPNNNGNTHYNQKFQ	291
vhCDR3	IYYFGRLYFDF	292

C6-30[CLDN6] H2.71

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDLNNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	293
vhCDR1	EYTMH	294
vhCDR2	GIDLNNGNTHYNQKFQ	295
vhCDR3	IYYFGRLYFDF	296

C6-30[CLDN6] H2.75

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPHNGNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	297
vhCDR1	EYTMH	298
vhCDR2	GIDPHNGNTHYNQKFQ	299
vhCDR3	IYYFGRLYFDF	300

Figure 15F

C6-30[CLDN6] H2.90

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNLNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	301
vhCDR1	EYTMH	302
vhCDR2	GIDPNNLNTHYNQKFQGH	303
vhCDR3	IYYFGRLYDEF	304

C6-30[CLDN6] H2.91

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNFNTHYNQKFQGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	305
vhCDR1	EYTMH	306
vhCDR2	GIDPNNFNTHYNQKFQGH	307
vhCDR3	IYYFGRLYDEF	308

C6-30[CLDN6] H2.118

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNGNTHYNQKKGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	309
vhCDR1	EYTMH	310
vhCDR2	GIDPNNGNTHYNQKKGH	311
vhCDR3	IYYFGRLYDEF	312

C6-30[CLDN6] H2.119

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEW MGGIDPNNGNTHYNQKFEGHVTISVDKSISTAYLQWSSLKASDTAMY YCARIYYFGRLYFDEFWGAGTLVTVSS	313
vhCDR1	EYTMH	314
vhCDR2	GIDPNNGNTHYNQKFEGH	315
vhCDR3	IYYFGRLYDEF	316

C6-30[CLDN6] L1.1

	sequence	SEQ ID NO:
Variable light (vl) domain	DIQMTQSPSSLSASVGRVTITCQASQDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTFTISLQPEDATYYCQYWS PLTFGGGTKVEIK	317
vlCDR1	QASQDIYNRLA	318
vlCDR2	GATSLET	319
vlCDR3	QCYWSPLT	320

Figure 15G

C6-30[CLDN6] L1.4

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTTTCQASEDVYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTISSSLQPEDATYYCQQYWS PLTFGGGTKVEIK	321
v1CDR1	QASEDVYNRLA	322
v1CDR2	GATSLET	323
v1CDR3	QQYWSPLT	324

C6-30[CLDN6] L1.7

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTTTCQASEDIYSRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTISSSLQPEDATYYCQQYWS PLTFGGGTKVEIK	325
v1CDR1	QASEDIYSRLA	326
v1CDR2	GATSLET	327
v1CDR3	QQYWSPLT	328

C6-30[CLDN6] L1.16

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTTTCQASEDIYNRLAWYQQKPGKVPKLL ISAATSLETGVPSRFSGSGSGKDYFTISSSLQPEDATYYCQQYWS PLTFGGGTKVEIK	329
v1CDR1	QASEDIYNRLA	330
v1CDR2	AATSLET	331
v1CDR3	QQYWSPLT	332

C6-30[CLDN6] L1.18

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTTTCQASEDIYNRLAWYQQKPGKVPKLL ISGTTTLETGVPSRFSGSGSGKDYFTISSSLQPEDATYYCQQYWS PLTFGGGTKVEIK	333
v1CDR1	QASEDIYNRLA	334
v1CDR2	GTTSLET	335
v1CDR3	QQYWSPLT	336

Figure 15H

C6-30[CLDN6] L1.19

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLLISGAS SLETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSSPLTFGGGTKV EIK	337
v1CDR1	QASEDIYNRLA	338
v1CDR2	GASSLET	339
v1CDR3	QQYWSSPLT	340

C6-30[CLDN6] L1.21

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATNLETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSS PLTFGGGTKVEIK	341
v1CDR1	QASEDIYNRLA	342
v1CDR2	GATNLET	343
v1CDR3	QQYWSSPLT	344

C6-30[CLDN6] L1.22

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATQLETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSS PLTFGGGTKVEIK	345
v1CDR1	QASEDIYNRLA	346
v1CDR2	GATQLET	347
v1CDR3	QQYWSSPLT	348

C6-30[CLDN6] L1.23

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATSRETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSS PLTFGGGTKVEIK	349
v1CDR1	QASEDIYNRLA	350
v1CDR2	GATSRET	351
v1CDR3	QQYWSSPLT	352

Figure 15I

C6-30[CLDN6] L1.27

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLES ~~GVPSRFSGSGSGKDYFTFTIS~~ SLQPED ~~IATYYCQQYWS~~ PLTFGGG ~~TKVEIK~~	353
v1CDR1	QASEDIYNRLA	354
v1CDR2	GATSLES	355
v1CDR3	QQYWSPLT	356

C6-30[CLDN6] L1.60

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTFTIS ~~SLQPED~~ IATYYC ~~QQYWS~~ PLTFGGG ~~TKVEIK~~	357
v1CDR1	QASEDIYNRLA	358
v1CDR2	GATSLET	359
v1CDR3	QQYWSPLT	360

C6-30[CLDN6] L1.107

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTFTIS ~~SLQPED~~ IATYYC ~~QQYWS~~ PLTFGGG ~~TKVEIK~~	361
v1CDR1	QASEDIYNRLA	362
v1CDR2	GATSLET	363
v1CDR3	QQYWSPLT	364

C6-30[CLDN6] L1.114

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVITTCQASEDIYLR ~~LAWYQQKPGKVPKLL~~ ISGATSLETGVPSRFSGSGSGKDYFTFTIS ~~SLQPED~~ IATYYC ~~QQYWS~~ PLTFGGG ~~TKVEIK~~	365
v1CDR1	QASEDIYLR	366
v1CDR2	GATSLET	367
v1CDR3	QQYWSPLT	368

Figure 15J

C6-30[CLDN6] L1.187

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSA PLTFGGGTKVEIK	369
v1CDR1	QASEDIYNRLA	370
v1CDR2	GATSLET	371
v1CDR3	QQYWSAPLT	372

C6-30[CLDN6] L1.189

	sequence	SEQ ID NO:
Variable light (v1) domain	DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLL ISGATSLETGVPSRFSGSGSGKDYFTFTISSLPEDIATYYCQQYWSG PLTFGGGTKVEIK	373
v1CDR1	QASEDIYNRLA	374
v1CDR2	GATSLET	375
v1CDR3	QQYWSGELT	376

Figure 16A

>XENP34218 C6-30[CLDN6] H1 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
377)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGKTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
378)

>XENP34219 C6-30[CLDN6] H1 L2 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
379)

Light Chain - C6-30[CLDN6]_L2

DIQMTQSPDSLAVSLGERATINCKASEDIYNRLAWYQQKPGQVPKLLISGATSLETGVPSRFSGSGSGKDYTLTISS
LQAEDVAVYYCQQYWSPLFFGGGKTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
380)

>XENP34220 C6-30[CLDN6] H2 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
381)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGKTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
382)

Figure 16B

>XENP34221 C6-30[CLDN6] H2 L2 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
383)

Light Chain - C6-30[CLDN6]_L2

DIQMTQSPDSLAVSLGERATINCKASEDIYNRLAWYQQKPGQVPKLLISGATSLETGVPSRFSGSGSGKDYTLTISS
LQAEDVAVYYCQ~~QYWSSPFL~~FGGGTKVEIK/RTVAAPSVFI~~FPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA~~
LQSGNSQESVTEQDSKDYSLSS~~TLT~~LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
384)

>XENP35044 C6-30[CLDN6] H2 L1.1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
385)

Light Chain - C6-30[CLDN6]_L1.1

DIQMTQSPSSLSASVGRVTITCQ~~ASQDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS~~
LQPEDATYYCQ~~QYWSSPFL~~FGGGTKVEIK/RTVAAPSVFI~~FPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA~~
LQSGNSQESVTEQDSKDYSLSS~~TLT~~LSKADYEKHKVYACEVTHQGLSSPVTKSF (SEQ ID NO: 386)

>XENP35047 C6-30[CLDN6] H2 L1.4 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
387)

Light Chain - C6-30[CLDN6]_L1.4

DIQMTQSPSSLSASVGRVTITCQ~~ASEDVYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS~~
LQPEDATYYCQ~~QYWSSPFL~~FGGGTKVEIK/RTVAAPSVFI~~FPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA~~
LQSGNSQESVTEQDSKDYSLSS~~TLT~~LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
388)

Figure 16C

>XENP35050 C6-30[CLDN6]_H2 L1.7 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGATLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
389)

Light Chain - C6-30[CLDN6]_L1.7

DIQMTQSPSSLSASVGDRVTITCQASEDIYSPLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
390)

>XENP35059 C6-30[CLDN6]_H2 L1.16 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGATLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
391)

Light Chain - C6-30[CLDN6]_L1.16

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISAATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
392)

>XENP35061 C6-30[CLDN6]_H2 L1.18 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGATLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
393)

Light Chain - C6-30[CLDN6]_L1.18

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGTTTSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
394)

Figure 16D

>XENP35062 C6-30[CLDN6]_H2 L1.19 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
395)

Light Chain - C6-30[CLDN6]_L1.19

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGASSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
396)

>XENP35064 C6-30[CLDN6]_H2 L1.21 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
397)

Light Chain - C6-30[CLDN6]_L1.21

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATNLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
398)

>XENP35065 C6-30[CLDN6]_H2 L1.22 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
399)

Light Chain - C6-30[CLDN6]_L1.22

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATQLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
400)

Figure 16E

>XENP35066 C6-30[CLDN6]_H2 L1.23 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
401)

Light Chain - C6-30[CLDN6]_L1.23

DIQMTQSPSSLSASVGDRVTITCQASEDIYNFLAWYQQKPGKVPKLLISGATSRETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
402)

>XENP35070 C6-30[CLDN6]_H2 L1.27 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
403)

Light Chain - C6-30[CLDN6]_L1.27

DIQMTQSPSSLSASVGDRVTITCQASEDIYNFLAWYQQKPGKVPKLLISGATSLESFVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
404)

>XENP35085 C6-30[CLDN6]_H1.1 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.1**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEWMGGISFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
405)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNFLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
406)

Figure 16F

>XENP35086 C6-30[CLDN6] H1.2 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.2**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGINFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
407)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPED~~I~~ATYYCQQY~~W~~SS~~P~~LF~~F~~GGG~~T~~KVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~T~~LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
408)

>XENP35087 C6-30[CLDN6] H1.3 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.3**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDSNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
409)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPED~~I~~ATYYCQQY~~W~~SS~~P~~LF~~F~~GGG~~T~~KVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~T~~LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
410)

>XENP35088 C6-30[CLDN6] H1.4 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.4**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDANNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
411)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPED~~I~~ATYYCQQY~~W~~SS~~P~~LF~~F~~GGG~~T~~KVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~T~~LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
412)

Figure 16G

>XENP35089 C6-30[CLDN6] H1.5 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.5**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFQNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTP~~EVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
413)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWS~~SPLFF~~GGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
414)

>XENP35090 C6-30[CLDN6] H1.6 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.6**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNSGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTP~~EVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
415)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWS~~SPLFF~~GGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
416)

>XENP35091 C6-30[CLDN6] H1.7 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.7**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNQGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTP~~EVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
417)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWS~~SPLFF~~GGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
418)

Figure 16H

>XENP35092 C6-30[CLDN6] H1.8 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.8**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNDNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
419)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
420)

>XENP35093 C6-30[CLDN6] H1.9 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.9**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNDNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
421)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
422)

>XENP35094 C6-30[CLDN6] H2.1 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.1**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGISFNNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
423)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
424)

Figure 16l

>XENP35095 C6-30[CLDN6] H2.2 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGITFNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
425)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
426)

>XENP35096 C6-30[CLDN6] H2.3 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.3**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGIDSNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
427)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
428)

>XENP35097 C6-30[CLDN6] H2.4 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.4**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGIDGNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
429)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
430)

Figure 16J

>XENP35098 C6-30[CLDN6] H2.5 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.5**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFQNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
431)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
432)

>XENP35099 C6-30[CLDN6] H2.6 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.6**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNDGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
433)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
434)

>XENP35100 C6-30[CLDN6] H2.7 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.7**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNQGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
435)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
436)

Figure 16K

>XENP35101 C6-30[CLDN6] H2.8 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.8**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNDNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
437)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
438)

>XENP35102 C6-30[CLDN6] H2.9 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.9**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNDNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
439)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
440)

>XENP35865 C6-30[CLDN6] H2 L1.60 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNDNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
441)

Light Chain - C6-30[CLDN6]_L1.60

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
442)

Figure 16L

>XENP35883 C6-30[CLDN6] H1.19 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.19**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTATYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
443)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFS~~SGSGSKDYFTT~~ISS
LQPEDATYYCQQYWS~~SPLFFGGG~~TKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA
LQSGNSQESVTEQDSK~~DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC~~ (SEQ ID NO:
444)

>XENP35886 C6-30[CLDN6] H1.22 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.22**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARI~~LYFGRLYFD~~FWGAGTL~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
445)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFS~~SGSGSKDYFTT~~ISS
LQPEDATYYCQQYWS~~SPLFFGGG~~TKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA
LQSGNSQESVTEQDSK~~DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC~~ (SEQ ID NO:
446)

>XENP35888 C6-30[CLDN6] H1.24 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.24**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARI~~YYLGRLYFD~~FWGAGTL~~LVTVSS~~/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV~~
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE~~
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCVMHEALHNHYTQKSLSLSPGK~~ (SEQ ID NO:
447)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFS~~SGSGSKDYFTT~~ISS
LQPEDATYYCQQYWS~~SPLFFGGG~~TKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLNNFY~~PREAKVQWKVDNA
LQSGNSQESVTEQDSK~~DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC~~ (SEQ ID NO:
448)

Figure 16M

>XENP35890 C6-30[CLDN6] H2.11 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.11**

EVQLVQSGAEVKKPGESLRISCKTSGYSFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
449)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
450)

>XENP35891 C6-30[CLDN6] H2.12 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.12**

EVQLVQSGAEVKKPGESLRISCKTSGYDFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
451)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
452)

>XENP35979 C6-30[CLDN6] H2 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
453)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSAPLTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
454)

Figure 16N

>XENP35981 C6-30[CLDN6]_H2 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
455)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSGFLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
456)

>XENP35929 C6-30[CLDN6]_H2 L1.107 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
457)

Light Chain - C6-30[CLDN6]_L1.107

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSGFLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
458)

>XENP35936 C6-30[CLDN6]_H2 L1.114 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
459)

Light Chain - C6-30[CLDN6]_L1.114

DIQMTQSPSSLSASVGDRVTITCQASEDIYLPALAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSGFLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
460)

Figure 160

>XENP36021 C6-30[CLDN6] H2.71 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.71**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDLNNGNTHYNQKFOGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:
461)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
462)

>XENP36022 C6-30[CLDN6] H2.72 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.72**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDANNNGNTHYNQKFOGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:
463)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
464)

>XENP36025 C6-30[CLDN6] H2.75 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.75**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDPHNGNTHYNQKFOGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:
465)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
466)

Figure 16P

>XENP36040 C6-30[CLDN6] H2.90 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.90**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNLNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
467)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
468)

>XENP36041 C6-30[CLDN6] H2.91 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.91**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNFNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
469)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
470)

>XENP36065 C6-30[CLDN6] H2.118 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.118**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNNGNTHYNQKKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
471)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
472)

Figure 16Q

>XENP36066 C6-30[CLDN6] H2.119 L1 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.119**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNNGNTHYNQKFEQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
473)

Light Chain - C6-30[CLDN6]_L1

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
474)

>XENP36956 C6-30[CLDN6] H1.22 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.22**

QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDPNNGNTHYNQKFEQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
475)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSAPLTFGGGKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
476)

>XENP36960 C6-30[CLDN6] H1.22 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.22**

QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDPNNGNTHYNQKFEQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
477)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSGFLTFGGGKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
478)

Figure 16R

>XENP36968 C6-30[CLDN6] H2.3 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.3**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDSNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVVDV~~KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTL~~PPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
479)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~FSGSG~~SGKDYFTTISS
LQPEDATYYCQQYWSG~~PLFF~~GGGKVEIK/RTVAAPSVFI~~FPPS~~DEQLKSGTASV~~VCLL~~NNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
480)

>XENP36963 C6-30[CLDN6] H1.9 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.9**

QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNANTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSED~~TAVYYCARIYYFGRLYFD~~FWGAGTLVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVVDV~~KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTL~~PPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
481)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~FSGSG~~SGKDYFTTISS
LQPEDATYYCQQYWSG~~PLFF~~GGGKVEIK/RTVAAPSVFI~~FPPS~~DEQLKSGTASV~~VCLL~~NNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
482)

>XENP36964 C6-30[CLDN6] H2.3 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.3**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDSNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FWGAGTL~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SRTPEVTCVVVDV~~KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTL~~PPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~FSCSV~~MHEALHNHYTQKSLSLSPGK (SEQ ID NO:
483)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~FSGSG~~SGKDYFTTISS
LQPEDATYYCQQYWSA~~PLFF~~GGGKVEIK/RTVAAPSVFI~~FPPS~~DEQLKSGTASV~~VCLL~~NNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
484)

Figure 16S

>XENP36965 C6-30[CLDN6] H2.12 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.12**

EVQLVQSGAEVKKPGESLRISCKTSGYDFTETMHWVRQMPGKSLLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
485)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSAPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
486)

>XENP36957 C6-30[CLDN6] H1.24 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.24**

QVQLVQSGAEVKKPGASVKVCKTSGYTFETMHWVRQAPGQSLLEWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDATVYYCARIYYLGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
487)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSAPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
488)

>XENP36958 C6-30[CLDN6] H1.19 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.19**

QVQLVQSGAEVKKPGASVKVCKTSGYTFETMHWVRQAPGQSLLEWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDATVYYCARIYYFGRLYDFDWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
489)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSAPLFFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
490)

Figure 16T

>XENP36959 C6-30[CLDN6] H1.9 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.9**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNANTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
491)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPEDATYYCQQYWSAPLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
492)

>XENP36961 C6-30[CLDN6] H1.24 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.24**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNGNTHY~~NQ~~KFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYLGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
493)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPEDATYYCQQYWSGRLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
494)

>XENP36962 C6-30[CLDN6] H1.19 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1.19**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNGNTHY~~NQ~~KFKQGRVTITVDKSAS
TAYMELSSLRSEDTATYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
495)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSR~~F~~SGSGSGKDYFTTISS
LQPEDATYYCQQYWSGRLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASV~~V~~CLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
496)

Figure 16U

>XENP36966 C6-30[CLDN6] H2.91 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.91**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGIDPNNFNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
497)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSAPLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASVCLLN~~N~~FYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~TL~~TL~~SK~~ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
498)

>XENP36967 C6-30[CLDN6] H2.118 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.118**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGIDPNNGNTHYNQKKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
499)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSAPLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASVCLLN~~N~~FYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~TL~~TL~~SK~~ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
500)

>XENP36969 C6-30[CLDN6] H2.12 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.12**

EVQLVQSGAEVKKPGESLRISCKTSGYDFTEYTMHWVRQMPGKSLLEWMGGIDPNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFD~~FW~~GAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI~~SR~~TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SK~~AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSV~~M~~HEALHNHYTQKSLSLSPGK (SEQ ID NO:
501)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSGFLFFGGGKVEIK/RTVAAPSVFI~~F~~PPSDEQLKSGTASVCLLN~~N~~FYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~TL~~TL~~SK~~ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
502)

Figure 16V

>XENP36970 C6-30[CLDN6]_H2.91 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.91**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLSEWMGGIDPNNFNTHYNQKFGQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
503)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSGPLEFGGGTKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
504)

>XENP36972 C6-30[CLDN6]_H1 L1.187 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLSEWMGGIDPNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDATAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
505)

Light Chain - C6-30[CLDN6]_L1.187

DIQMTQSPSSLSASVGDRVTITCQASEDIYNPLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSAFLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
506)

>XENP36971 C6-30[CLDN6]_H2.118 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H2.118**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLSEWMGGIDPNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
507)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQQYWSGPLEFGGGTKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
508)

Figure 16V

>XENP36973 C6-30[CLDN6] H1 L1.189 IgG1 PVA /S267K**Heavy Chain - C6-30[CLDN6]_H1**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDFNNGNTHYNQKFPQGRVTITVDKSAS
TAYMELSSLRSED TAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
509)

Light Chain - C6-30[CLDN6]_L1.189

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTISS
LQPEDIAITYYCQQYWSGPLETFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
510)

Figure 17A

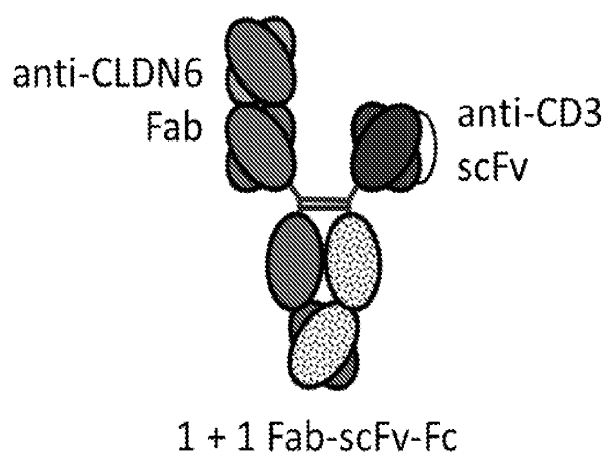


Figure 17B

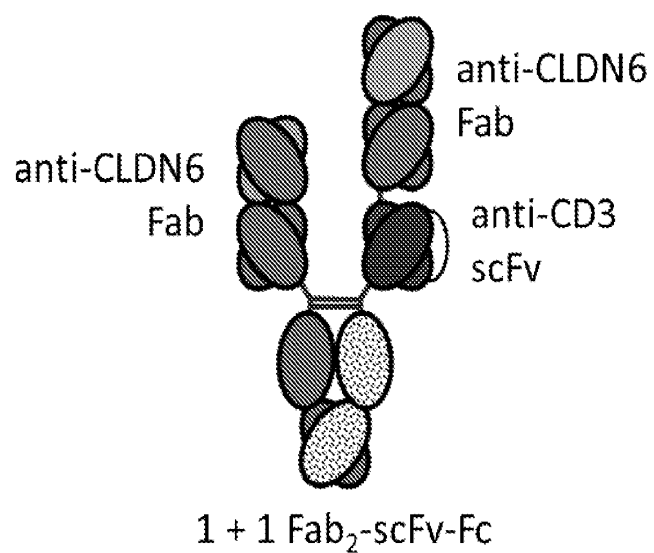


Figure 18

>XENP26863 mAb206-LCC[CLDN6] H0L0 IgG1 PVA /S267K**Heavy Chain - mAb206-LCC[CLDN6]_H0**

EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWVKQSHGKNLEWIGLINFYNGGTIYNQKFKGKATLTVDKSSS
 TAYMELLSLTSEDSAVYYCARQYGFVLDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
 APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
 QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
 511)

Light Chain - mAb206-LCC[CLDN6]_L0

QIVLTQSPAIMASAPGEKVTITCSASSSVSYLHWFOQKPGTSPKLWVYSTSNLPSGVPARFGGSGSGTSYSLTISRM
 EAEDAATYYCQQRSIYPPWTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
 512)

**>XENP26849 mAb206-LCC[CLDN6] H0L0 Fab-[ANTI-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 - mAb206-LCC[CLDN6]_H0_IgG1_pl(-)_Isosteric_A /PVA /S267K/L368D/K370S

EVQLQQSGPELVKPGASMKISCKASGYSTGYTMNWVKQSHGKNLEWIGLINFYNGGTIYNQKFKGKATLTVDKSSS
 TAYMELLSLTSEDSAVYYCARQYGFVLDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
 APPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
 QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
 513)

Chain 2 - [ANTI-CD3] H1.30 L1.47 scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA /S267K/S364K/E357Q

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKLEWVGRIPSKYNNYATYYADSVKGRFTISRDDS
 KNTLYLQMNLSRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTTLTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
 PSLTVSPGGTIVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPED
 EADYYCALWYSNEWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGN
 VFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 514)

Chain 3 - mAb206-LCC[CLDN6]_L0

QIVLTQSPAIMASAPGEKVTITCSASSSVSYLHWFOQKPGTSPKLWVYSTSNLPSGVPARFGGSGSGTSYSLTISRM
 EAEDAATYYCQQRSIYPPWTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
 515)

Figure 19

**>XENP34229 C6-30[CLDN6] H1 L1 Fab-[ANTI-CD3] L1.47 H1.30 scFv(GKPGS)4-IgG1 PVA /S267K/IgG1 pl(-)
Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**
Chain 1 - C6-30[CLDN6]_H1_IgG1_PVA_/S267K_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
516)

Chain 2 - [ANTI-CD3]_L1.47_H1.30_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q
QAVVTQEPSTLTSPGGTIVTLTCSSTGAVTTSTNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI
SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCA
ASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVR
HGNFGDSYVSWFAYWGQGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 517)

Chain 3 - C6-30[CLDN6]_L1
DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQKPGKVPKLLISGATSLETGVPSRFRSGSGSGKDYFTTIS
LQPEDATYYCQQYWSSELTFFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
518)

**>XENP34637 C6-30[CLDN6] H2 L1-[ANTI-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 - C6-30[CLDN6]_H2_L1_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNNNGNTHYNQKFGQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
519)

Chain 2 - [ANTI-CD3]_H1.30_L1.47_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWRQAPGKGLEWVGRIIRSKYNNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQE
PSLTVSPGGTIVTLTCSSTGAVTTSTNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPED
EADYYCALWYSNHWVFGGGTKLTVL/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 520)

Chain 3 - C6-30[CLDN6]_L1
DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQKPGKVPKLLISGATSLETGVPSRFRSGSGSGKDYFTTIS
LQPEDATYYCQQYWSSELTFFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
521)

Figure 20

>XENP35385 C6-30[CLDN6] H1 L1 Fab-[ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4-IgG1 PVA /S267K IgG1 pl(-)
) Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q
Chain 1 - C6-30[CLDN6] H1_IgG1_PVA_/S267K IgG1 pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
QVQLVQSGAEVKKPGASVKVSCKTSGYTFTETMHWVRQAPGQSLLEWMGGIDPNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
522)

Chain 2 - [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q
QAVVTQEPESLTVPGGTIVTLTCCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI
SGAQPEDEADYYCALWYSNHWYFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCA
ASGFTFTSTYAMNWRQAPGKGLEWVGRIFSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVR
HGNEFGDSYVSWFAYWGQGTITLVSS/EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 523)

Chain 3 - C6-30[CLDN6] L1
DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQOKPGKVPKLLISGATSLETGVPSRFRSGSGSGKDYFTTIS
LQPEDATYYCCQYWSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
524)

>XENP35387 C6-30[CLDN6] H2 L1 Fab-[ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4-IgG1 PVA /S267K IgG1 pl(-)
) Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q
Chain 1 - C6-30[CLDN6] H2_IgG1_PVA_/S267K IgG1 pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
EVQLVQSGAEVKKPGESLRISCKTSGYTFTETMHWVRQMPGKSLLEWMGGIDPNNGNTHYNQKFGQGHVTISVDKSIS
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
525)

Chain 2 - [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q
QAVVTQEPESLTVPGGTIVTLTCCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI
SGAQPEDEADYYCALWYSNHWYFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGSLRLSCA
ASGFTFTSTYAMNWRQAPGKGLEWVGRIFSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVR
HGNEFGDSYVSWFAYWGQGTITLVSS/EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 526)

Chain 3 - C6-30[CLDN6] L1
DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQOKPGKVPKLLISGATSLETGVPSRFRSGSGSGKDYFTTIS
LQPEDATYYCCQYWSPLTFGGGTKEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
527)

Figure 21A

>XENP34233 C6-30[CLDN6] H1 L1 Fab-C6-30[CLDN6] H1 L1 Fab (G4S)2 [ANTI-
CD3] L1.47 H1.30 scFv(GKPGS)4 (G4S)2 Fc(222) IgG1 PVA /S267K/S364K/E357Q-IgG1 pl(-)
) Isosteric A PVA /S267K/L368D/K370S

Chain 1 - C6-30[CLDN6]_H1_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
528)

Chain 2 - C6-30[CLDN6]_H1_Fab (G4S)2 [ANTI-

CD3] L1.47 H1.30_scFv(GKPGS)4 (G4S)2 Fc(222) IgG1_PVA_/S267K/S364K/E357Q

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSENHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIFSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDSYVSWFAYWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 529)

Chain 3 - C6-30[CLDN6]_L1_Light Chain

DIQMTQSPSSLSASVGDRVTITTCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFGSGSGKDYFTTIS
LQPEDIAITYYCQQYWSPLTFGGGKTVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
530)

Figure 21B

>XENP34638 C6-30[CLDN6] H2 L1 Fab-C6-30[CLDN6] H2 L1 Fab (G4S)2 [ANTI-
CD3] L1.47 H1.30 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-
Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H2_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGATLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
531)

Chain 2 - C6-30[CLDN6]_H2_(G4S)2_[ANTI-

CD3]_L1.47_H1.30_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLEWMGGIDFNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGATLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSENHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIFSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDSYVSWFAFWGQGLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 532)

Chain 3 - C6-30[CLDN6]_L1_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFRSGSGSGKDYFTISS
LQPEDIAITYYCQQYWSPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
533)

Figure 22A

>XENP35386 C6-30[CLDN6] H1 L1 Fab-C6-30[CLDN6] H1 L1 Fab (G4S)2 [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDPNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
534)

Chain 2 - C6-30[CLDN6]_H1_L1_Fab_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDPNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI RSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRADTAVY
YCVRHGNEFGDSYVSWFAFWGQGLTVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGSGFFLYSKLTVD
KSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 535)

Chain 3 - C6-30[CLDN6]_L1_Light Chain

DIQMTQSPFSSLSASVGRVTITCQASEDIYNPLAWYQOKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTFTISS
LQPEDIAITYYCQQYNSSPLTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
536)

>XENP35388 C6-30[CLDN6] H2 L1 Fab-C6-30[CLDN6] H2 L1 Fab (G4S)2 [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H2_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLWMGGIDPNNNGNTHYNQKFKQGHVTISVDKSI
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSGSGFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
537)

Figure 22B

Chain 2 - C6-30[CLDN6]_H2_L1_Fab_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLSEWMGGIDPNNGNTHYNQKFEQGHVTISVDKSI
TAYLQWSSLKASDTAMYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGS/QAVVTQEPSTLVSPGGTVTLTCCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNFGDSYVSWFAYWGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 538)

Chain 3 - C6-30[CLDN6]_L1_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLEFGVPSRFSGSGSGKDYFTISS
LQPEDATYYCQQYWSAPLFFGGGTKEIK/RTVAAPSVFIAPPDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
539)

**>XENP37227 C6-30[CLDN6]_H1.9_L1.187_Fab-C6-30[CLDN6]_H1.9_L1.187_Fab_(G4S)2_[ANTI-
CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2-IgG1_pl(-)_Isosteric A_PVA_/S267K/L368D/K370S-
Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

Chain 1 - C6-30[CLDN6]_H1.9_IgG1_pl(-)_Isosteric A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDPNNANTHYNQKFEQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGVDFSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
540)

Chain 2 - C6-30[CLDN6]_H1.9_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

QVQLVQSGAEVKKPGASVKVCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDPNNANTHYNQKFEQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGS/QAVVTQEPSTLVSPGGTVTLTCCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNFGDSYVSWFAYWGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 541)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLEFGVPSRFSGSGSGKDYFTISS
LQPEDATYYCQQYWSAPLFFGGGTKEIK/RTVAAPSVFIAPPDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
542)

Figure 22C

>XENP37228 C6-30[CLDN6] H1.19 L1.187 Fab-C6-30[CLDN6] H1.19 L1.187 Fab (G4S)2 [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1.19_IgG1_pl(-) Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTATYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
543)

Chain 2 - C6-30[CLDN6]_H1.19_(G4S)2 [ANTI-

CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTATYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIFSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDSYVSWFAWGGQTLVTVSS/GGGGGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEV
TCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 544)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSAPLEFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
545)

>XENP37229 C6-30[CLDN6] H1.22 L1.187 Fab-C6-30[CLDN6] H1.22 L1.187 Fab (G4S)2 [ANTI-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1.22_IgG1_pl(-) Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTATYYCARIYYFGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
546)

Figure 22D

Chain 2 - C6-30[CLDN6]_H1.22_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARI~~LYFGRLYFDF~~EWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGG/QAVVTQEP~~SLTV~~SPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAGVGPAPRFSGSLGGKA
ALTISGAQPEDEADYYCALWY~~SNHWV~~FGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAM~~NHWVRQ~~APGKGLEWVGRI~~R~~SKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNF~~GD~~SYVS~~WFAY~~WGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TLCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNV~~FSC~~VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 547)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQ~~QYWSA~~PLTFGGGTKVEIK/RTVAAPSVFI~~FPP~~SDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
548)

>XENP37230 C6-30[CLDN6]_H1.22_L1.189_Fab-C6-30[CLDN6]_H1.22_L1.189_Fab_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2-IgG1_pl(-)_Isosteric A_PVA_/S267K/L368D/K370S-****Fc(222)_IgG1_PVA_/S267K/S364K/E357Q****Chain 1 - C6-30[CLDN6]_H1.22_IgG1_pl(-)_Isosteric A_PVA_/S267K/L368D/K370S**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARI~~LYFGRLYFDF~~EWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE~~
SDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGV~~FSC~~VMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
549)

Chain 2 - C6-30[CLDN6]_H1.22_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLEWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARI~~LYFGRLYFDF~~EWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGG/QAVVTQEP~~SLTV~~SPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAGVGPAPRFSGSLGGKA
ALTISGAQPEDEADYYCALWY~~SNHWV~~FGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAM~~NHWVRQ~~APGKGLEWVGRI~~R~~SKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNF~~GD~~SYVS~~WFAY~~WGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TLCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNV~~FSC~~VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 550)

Chain 3 - C6-30[CLDN6]_L1.189_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQ~~QYWSA~~PLTFGGGTKVEIK/RTVAAPSVFI~~FPP~~SDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
551)

Figure 22E

>XENP37231 C6-30[CLDN6] H1.24 L1.187 Fab-C6-30[CLDN6] H1.24 L1.187 Fab (G4S)2 [ANTI-
CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-
Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
552)

Chain 2 - C6-30[CLDN6]_H1.24_(G4S)2_[ANTI-

CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMNHWVRQAPGKGLEWVGRIFSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRADTAVY
YCVRHGNEFGDSYVSWFAWGGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 553)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTISS
LQPEDATYYCQYYWSAPLTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO:
554)

>XENP37232 C6-30[CLDN6] H1.24 L1.189 Fab-C6-30[CLDN6] H1.24 L1.189 Fab (G4S)2 [ANTI-
CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S-
Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNNGNTHYNQKFGQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCTP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
555)

Figure 22F

Chain 2 - C6-30[CLDN6]_H1.24_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDPNNNGNTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAGVGPAPRFSGLLGGA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMHWVRQAPGKGLEWVGPIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDSYVSWFAYWGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 556)

Chain 3 - C6-30[CLDN6]_L1.189_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSGLPFGGGTKVEIK/RTVAAPSVFIAPPDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
557)

>XENP37233 C6-30[CLDN6]_H2.91_L1.187_Fab-C6-30[CLDN6]_H2.91_L1.187_Fab_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S-****Fc(222)_IgG1_PVA_/S267K/S364K/E357Q****Chain 1 - C6-30[CLDN6]_H2.91_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLWMGGIDPNNFNTHYNQKFKQGHVTISVDKSIS
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:
558)

Chain 2 - C6-30[CLDN6]_H2.91_(G4S)2_[ANTI-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q**

EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLWMGGIDPNNFNTHYNQKFKQGHVTISVDKSIS
TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAGVGPAPRFSGLLGGA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFSTYAMHWVRQAPGKGLEWVGPIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDSYVSWFAYWGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 559)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDATYYCQQYWSGLPFGGGTKVEIK/RTVAAPSVFIAPPDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
560)

Figure 22G

>XENP37547 C6-30[CLDN6] H2.91 L1.187 Fab-C6-30[CLDN6] H2.91 L1.187 Fab (G4S)2 [anti-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - C6-30[CLDN6]_H2.91_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
 EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNNFNTHYNQKFKQGHVTISVDKSIS
 TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
 SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:
 561)

Chain 2 - C6-30[CLDN6]_H2.91_(G4S)2 [anti-CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S
 EVQLVQSGAEVKKPGESLRISCKTSGYTFTEYTMHWVRQMPGKSLLEWMGGIDPNNFNTHYNQKFKQGHVTISVDKSIS
 TAYLQWSSSLKASDTAMYYCARIYYFGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
 GGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGA
 ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
 LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRI RSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
 YCVRHGNEFGDSYVSWFAWGGQTLVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEV
 TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
 KSRWQQGNVFCFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 562)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain
 DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
 LQPEDIAITYYCQQYWSAPLEFGGGTKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
 563)

>XENP37545 C6-30[CLDN6] H1.24 L1.187 Fab-C6-30[CLDN6] H1.24 L1.187 Fab (G4S)2 [anti-CD3] L1.47 H1.32 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - C6-30[CLDN6]_H1.24_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S
 QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDPNNFNTHYNQKFKQGRVTITVDKSAS
 TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
 SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:
 564)

Figure 22H

Chain 2 - C6-30[CLDN6]_H1.24_(G4S)2_[anti-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDFNNGNTHYNQKFKQGRVTITVDKSAS
 TAYMELSSLRSEDTAVYYCARIYYLGRLYFDFWAGAGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
 GGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
 ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
 LSCAASGFTFSTYAMHWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
 YCVRHGNEFGDSYVSWFAYWGQTLTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
 TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTI
 SKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVD
 KSRWQQGNVFCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 565)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQOKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
 LQPEDATYYCQQYWSAPLTFGGGKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
 566)

>XENP37541 C6-30[CLDN6]_H1.9_L1.187_Fab-C6-30[CLDN6]_H1.9_L1.187_Fab_(G4S)2_[anti-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2-IgG1_pi(-)_Isosteric A_PVA_/S267K/L368D/K370S/M428L/N434S-
Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S****Chain 1 - C6-30[CLDN6]_H1.9_IgG1_pi(-)_Isosteric A_PVA_/S267K/L368D/K370S**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDFNNANATHYNQKFKQGRVTITVDKSAS
 TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGAGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
 LTVLHQDWLNGKEYCKKVSNAKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
 SDGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGDFVFCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:
 567)

Chain 2 - C6-30[CLDN6]_H1.9_(G4S)2_[anti-**CD3]_L1.47_H1.32_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDFNNANATHYNQKFKQGRVTITVDKSAS
 TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWAGAGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGSGG
 GGS/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQOKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
 ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
 LSCAASGFTFSTYAMHWVRQAPGKGLEWVGRIIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
 YCVRHGNEFGDSYVSWFAYWGQTLTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
 TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNAKALPAPIEKTI
 SKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVD
 KSRWQQGNVFCSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO: 568)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQOKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
 LQPEDATYYCQQYWSAPLTFGGGKVEIK/RTVAAPSVFI FPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
 569)

Figure 23B

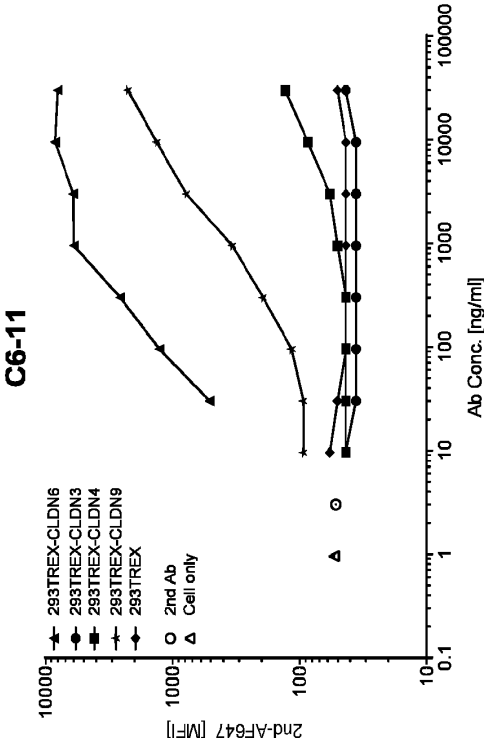


Figure 23D

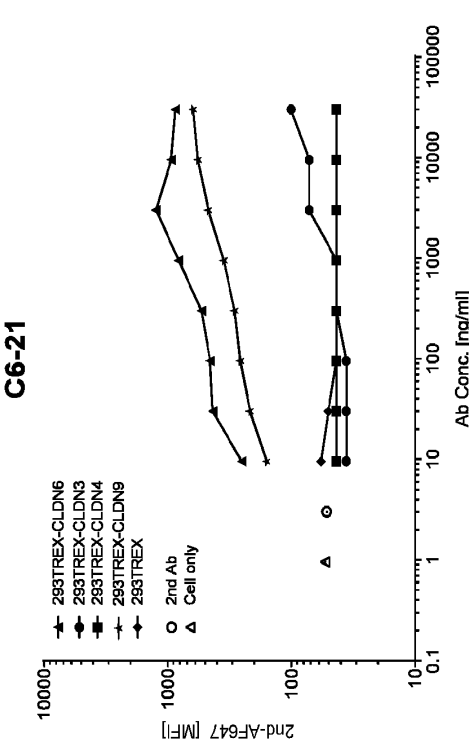


Figure 23A

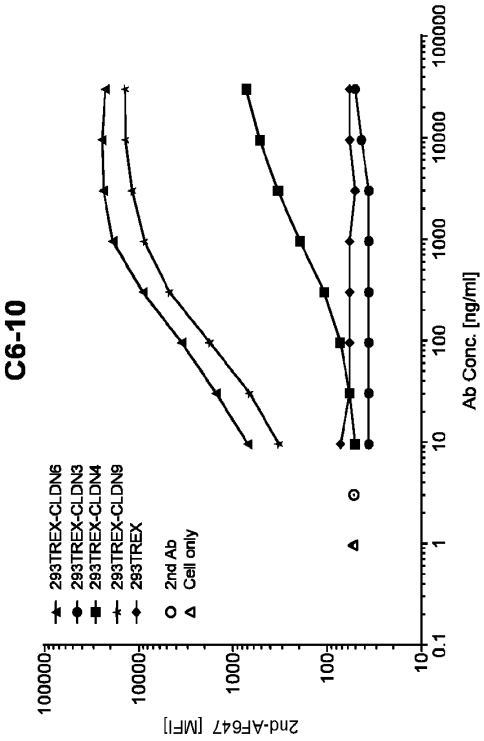


Figure 23C

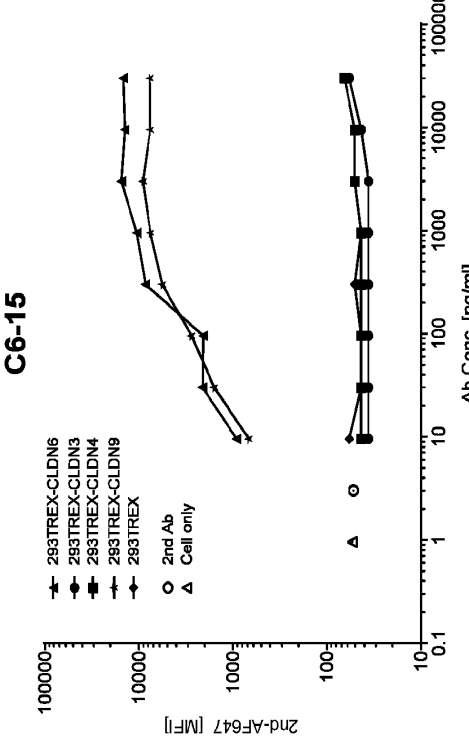


Figure 23F

C6-30

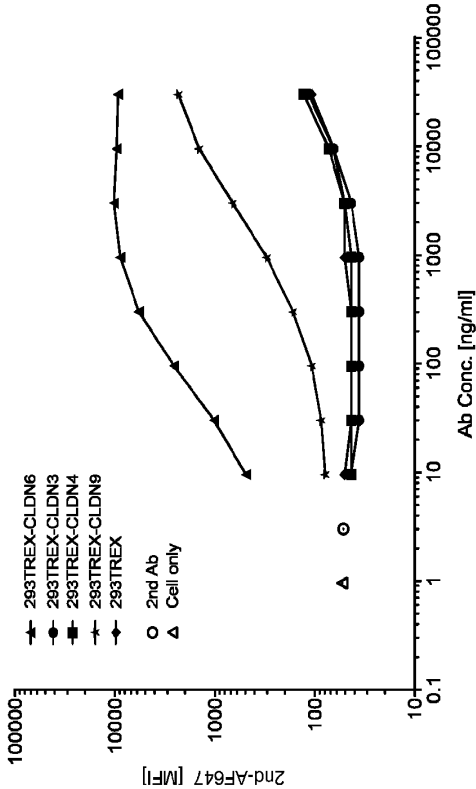


Figure 23E

C6-24

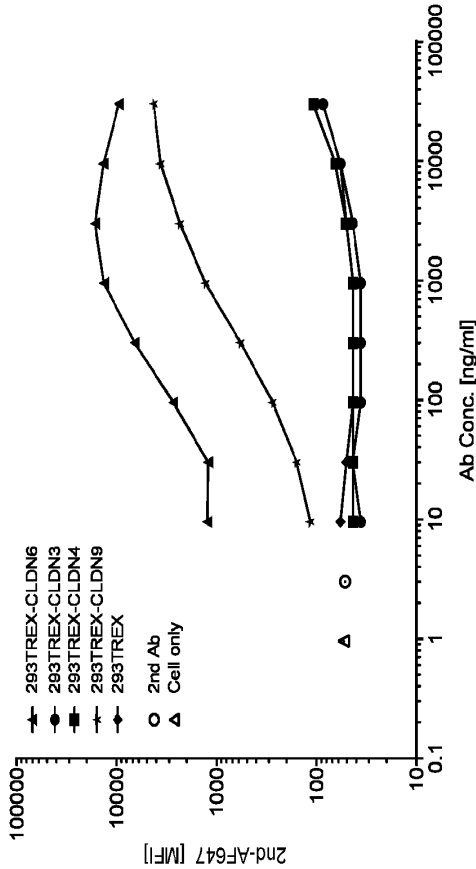


Figure 24B

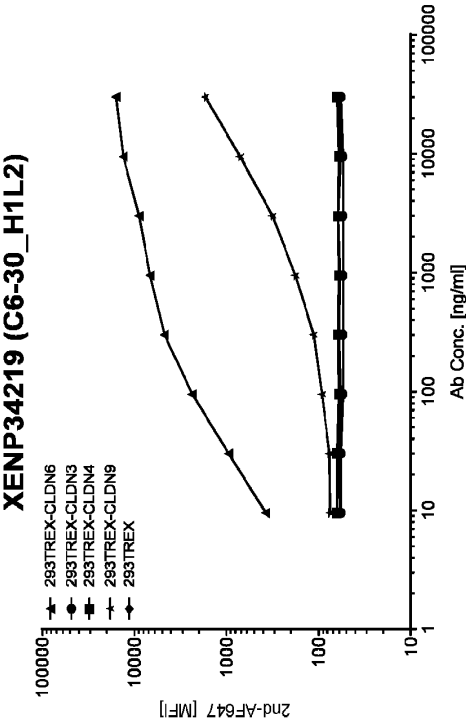


Figure 24A

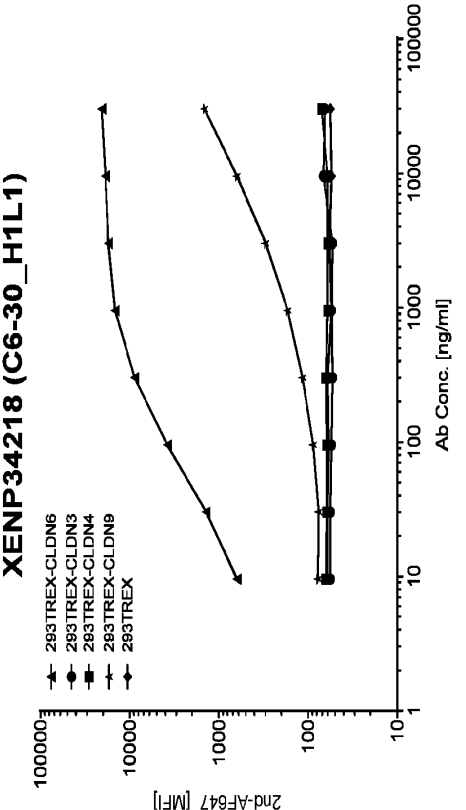


Figure 24D

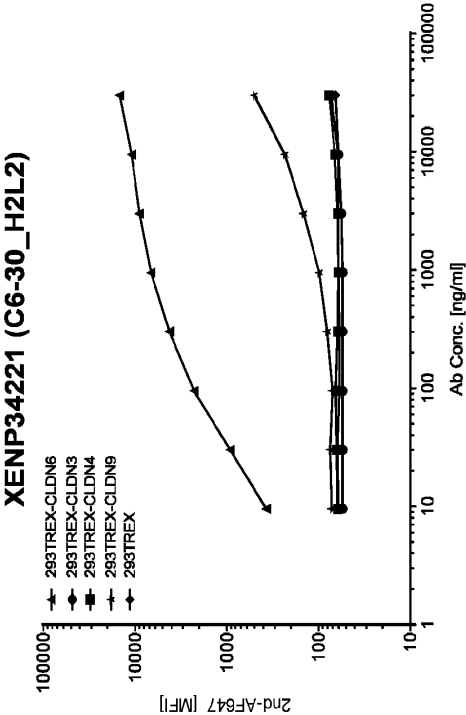


Figure 24C

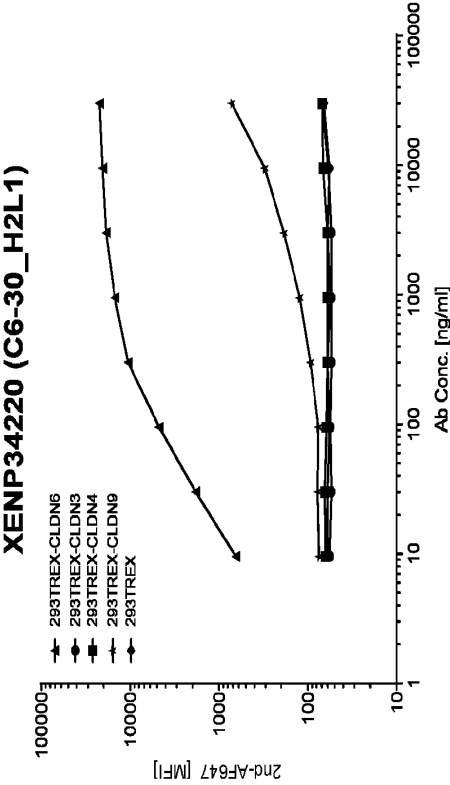
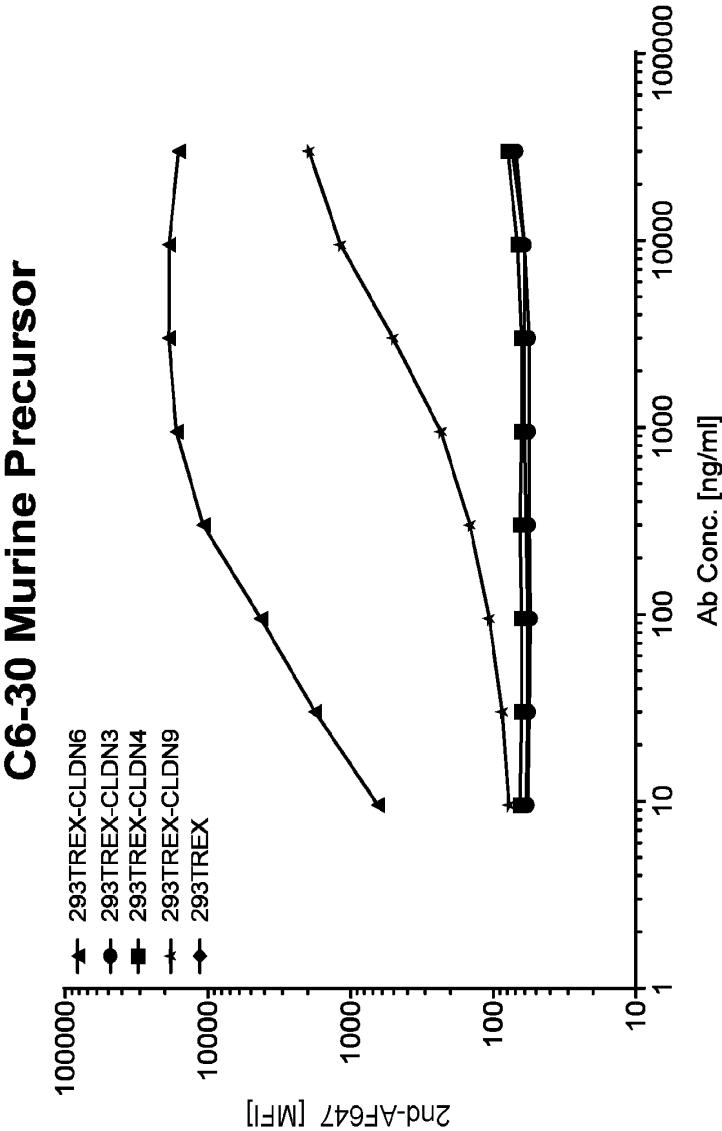


Figure 24E



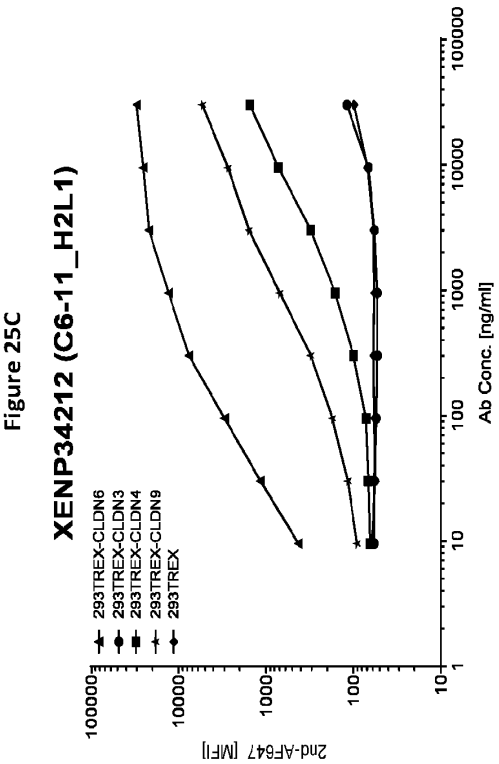
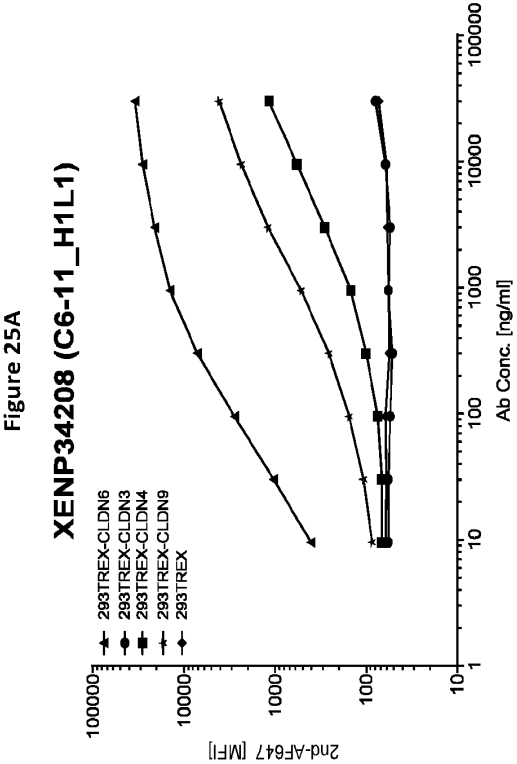
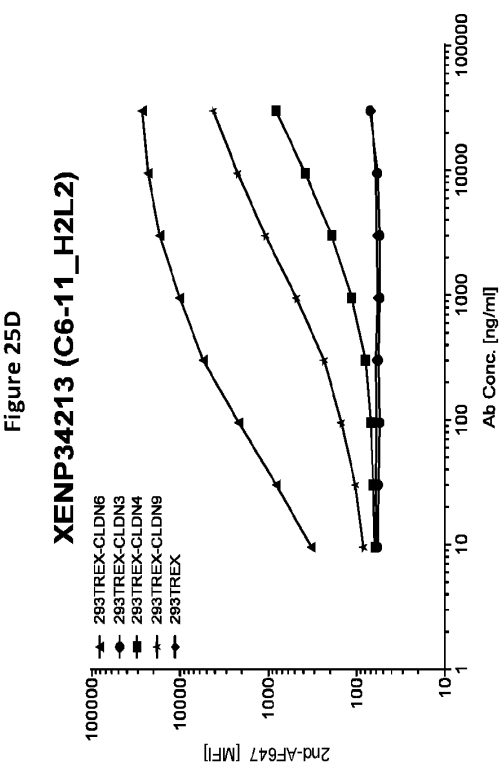
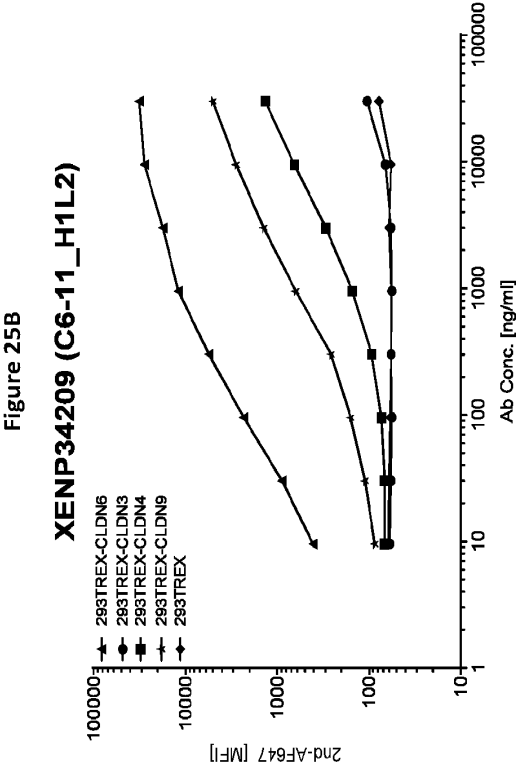
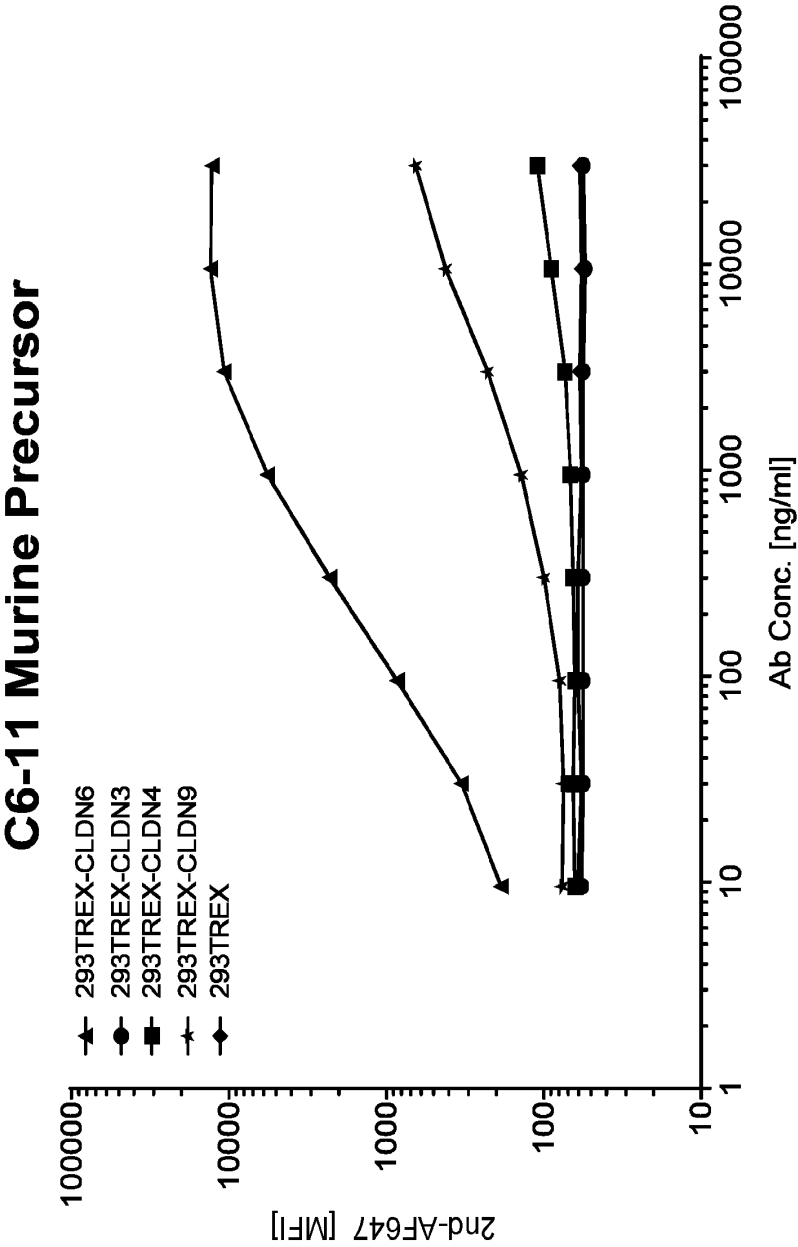


Figure 25E



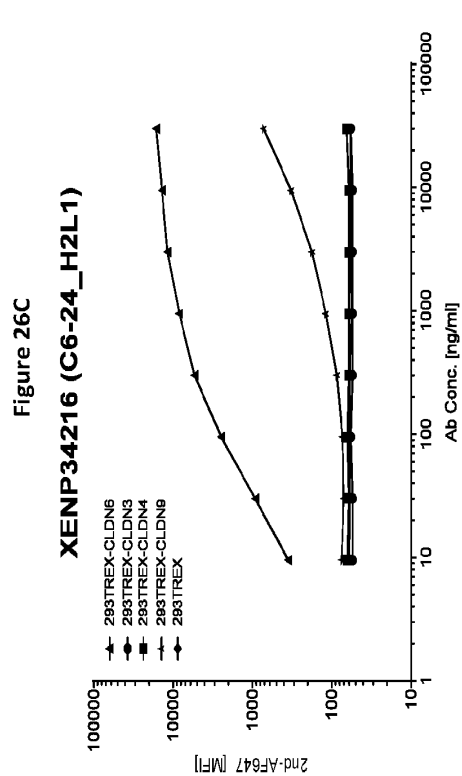
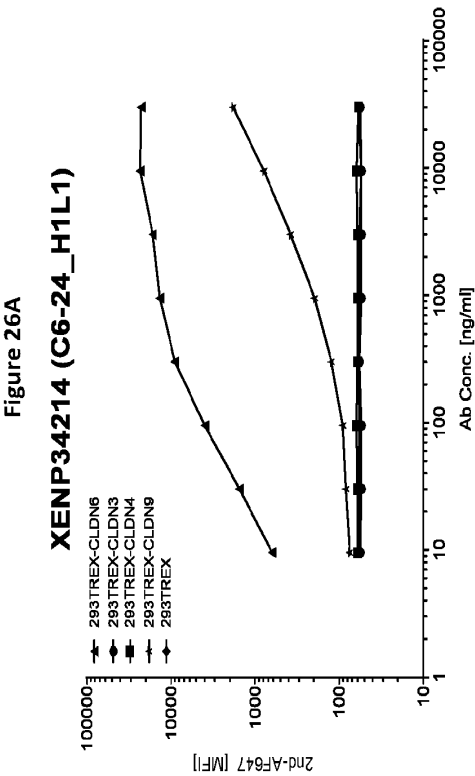
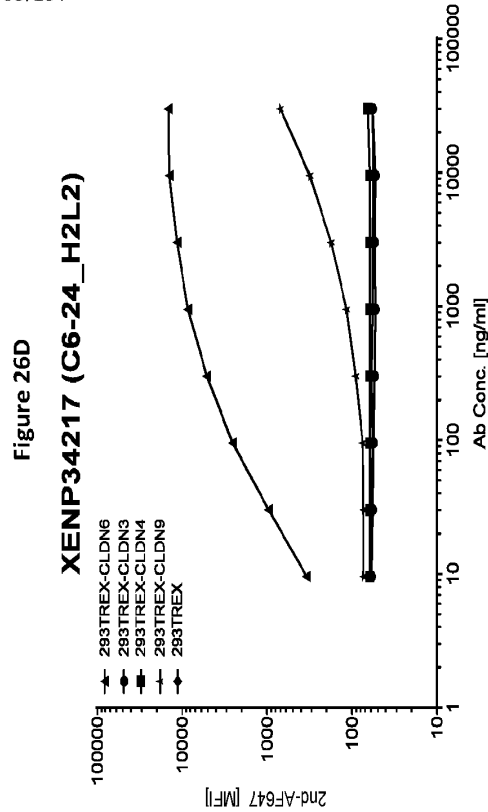
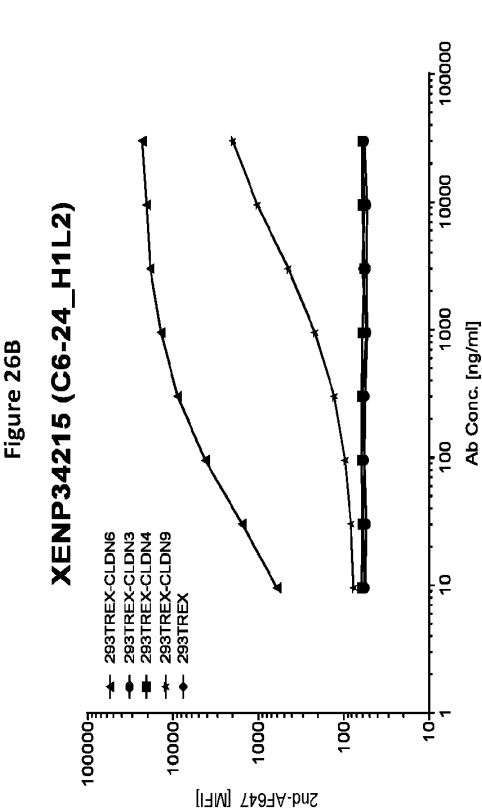


Figure 26E

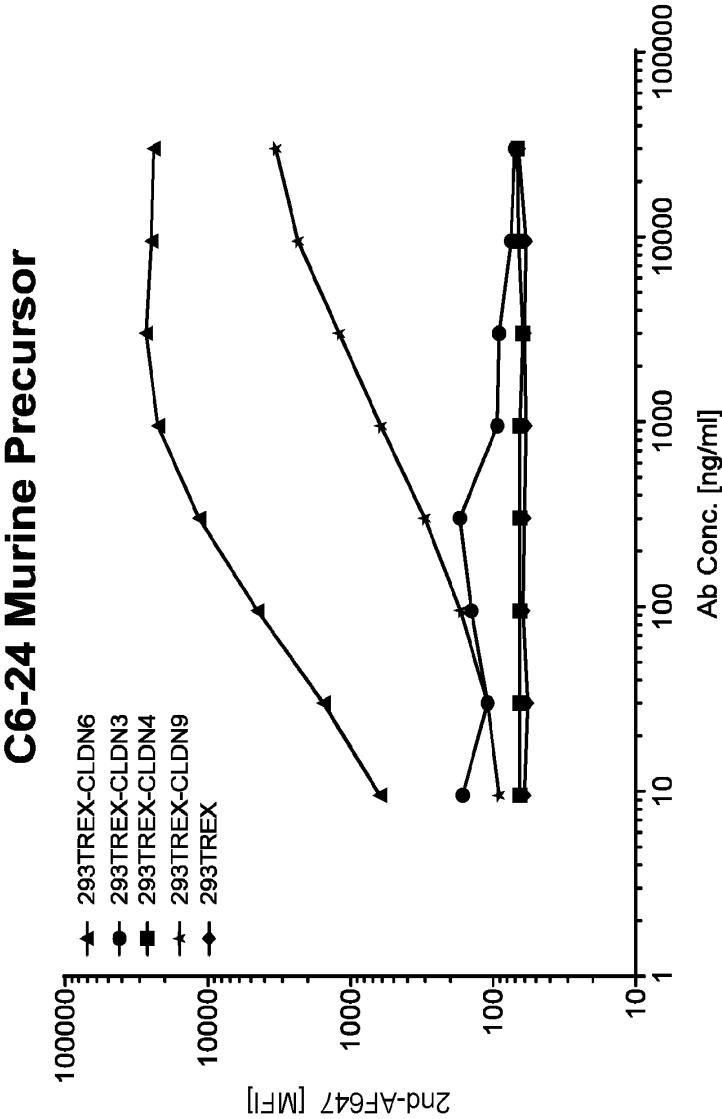


Figure 27

	<u>C6-30 Variant</u>	<u>VH mutation (Kabat)</u>	<u>Estimated CLDN6 EC50 (ng/mL)</u>	<u>Estimated CLDN9 EC50 (ng/mL)</u>	<u>Estimated CLDN9/CLDN6 EC50 ratio</u>	<u>CLDN9/CLDN6 EC50 ratio normalized to 30.1 H2L1</u>
XENP34220	H2L1	-	870.8	5821.0	6.7	1.0
XENP35085	H1.1_L1	D52S	2509.0	15452.5	6.2	0.9
XENP35086	H1.2_L1	D52N	1459.0	12133.9	8.3	1.2
XENP35087	H1.3_L1	P52aS	685.5	2818.4	4.1	0.6
XENP35088	H1.4_L1	P52aA	1124.0	5333.3	4.7	0.7
XENP35089	H1.5_L1	N53Q	1696.0	12560.3	7.4	1.1
XENP35091	H1.7_L1	N54Q	666.9	3357.4	5.0	0.8
XENP35092	H1.8_L1	G55D	2017.0	7261.1	3.6	0.5
XENP35093	H1.9_L1	G55A	1042.0	7430.2	7.1	1.1
XENP35094	H2.1_L1	D52S	1802.0	9817.5	5.4	0.8
XENP35095	H2.2_L1	D52T	2111.0	11912.4	5.6	0.8
XENP35096	H2.3_L1	P52aS	1001.0	5116.8	5.1	0.8
XENP35097	H2.4_L1	P52aG	1190.0	4446.3	3.7	0.6
XENP35098	H2.5_L1	N53Q	2204.0	7063.2	3.2	0.5
XENP35099	H2.6_L1	N54D	1628.0	13458.6	8.3	1.2
XENP35100	H2.7_L1	N54Q	800.6	3556.3	4.4	0.7
XENP35101	H2.8_L1	G55D	1190.0	9183.3	7.7	1.2

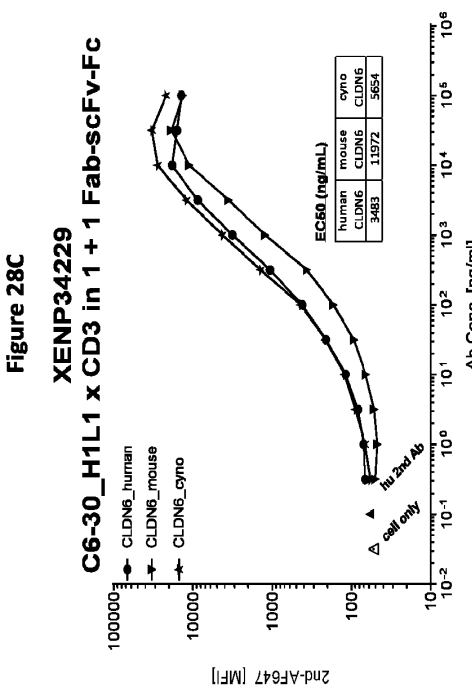
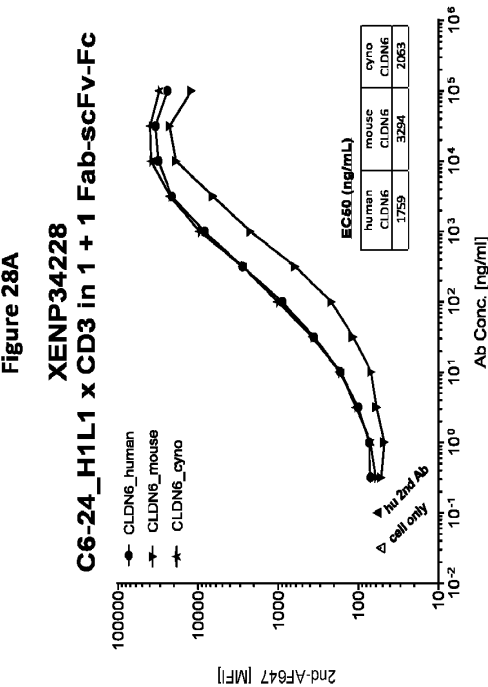
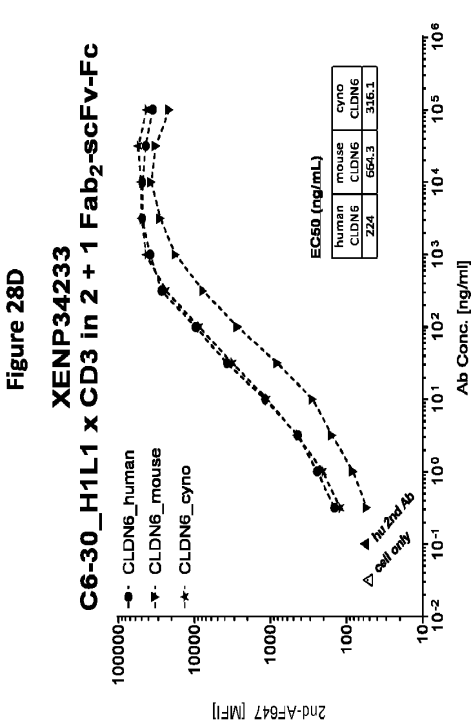
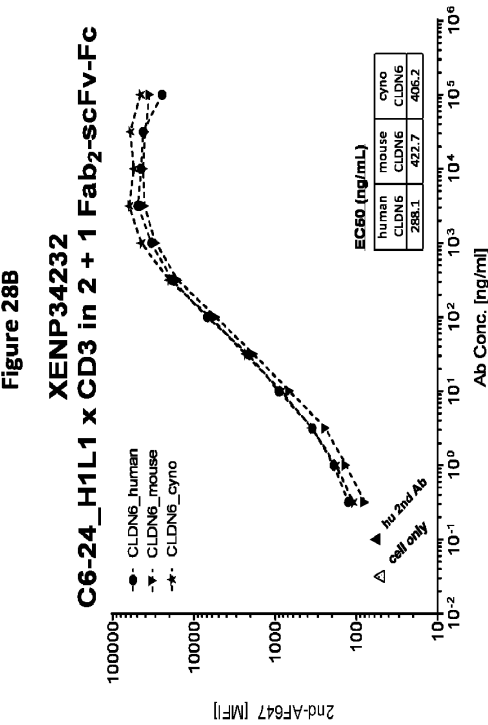


Figure 28F

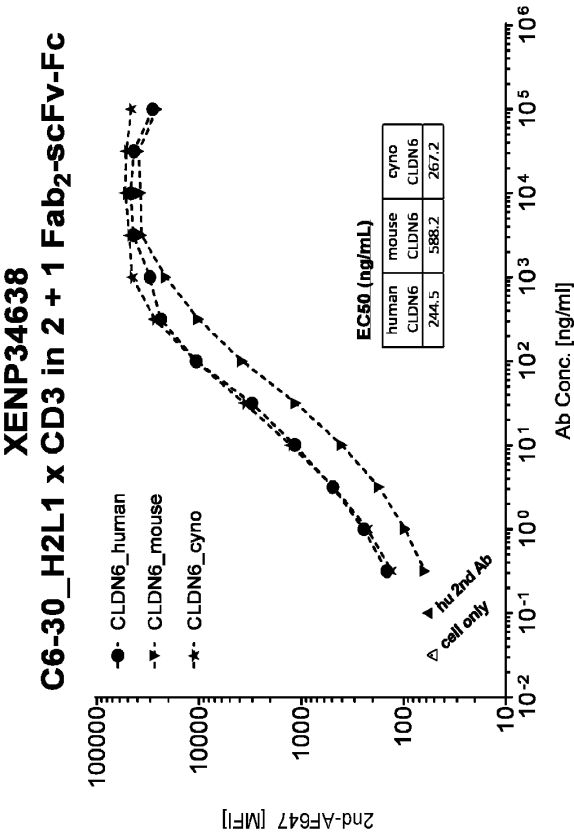
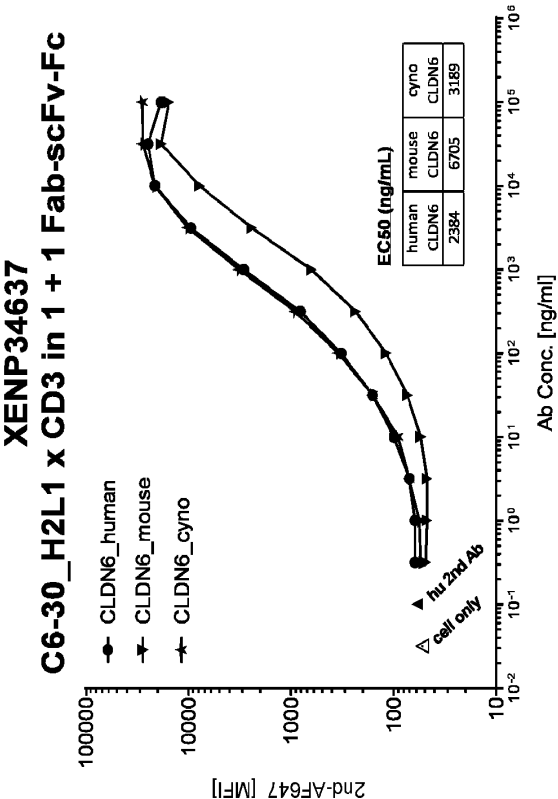


Figure 28E



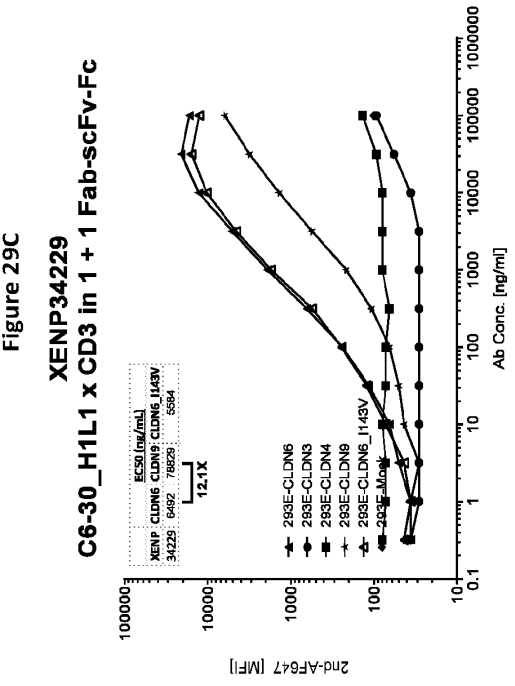
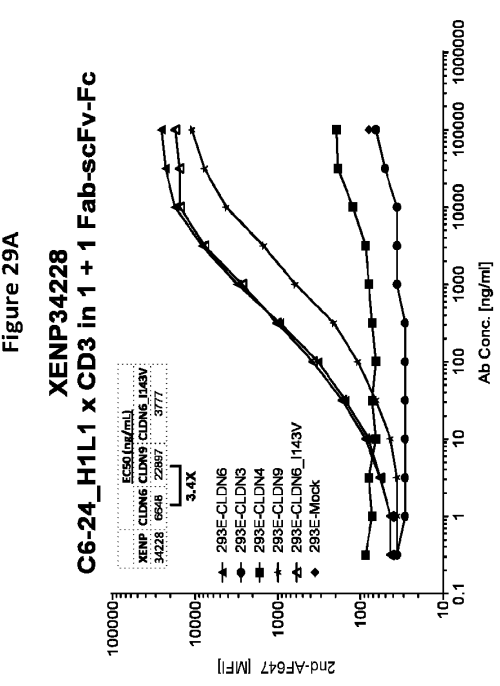
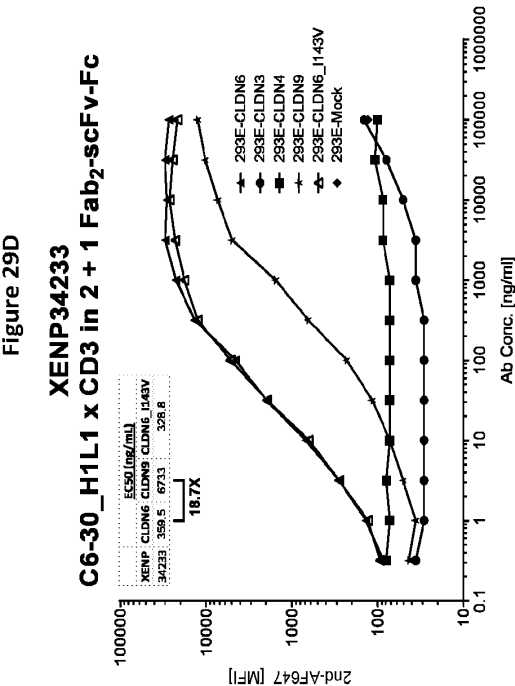
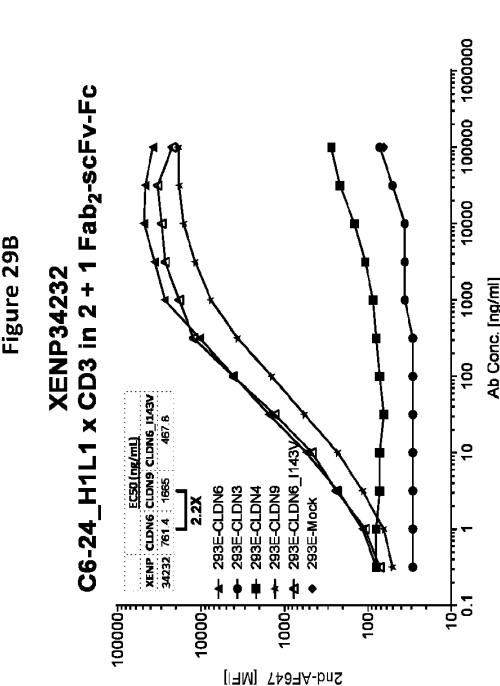


Figure 29F

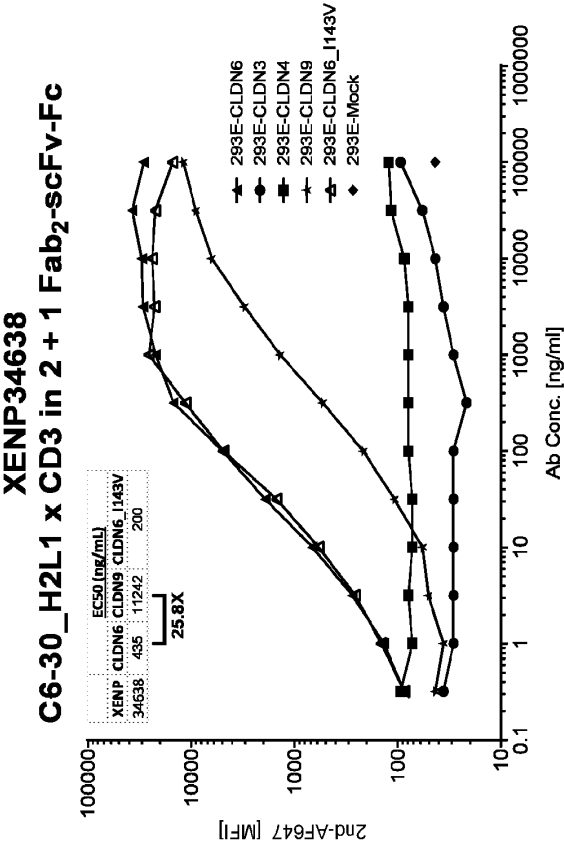


Figure 29E

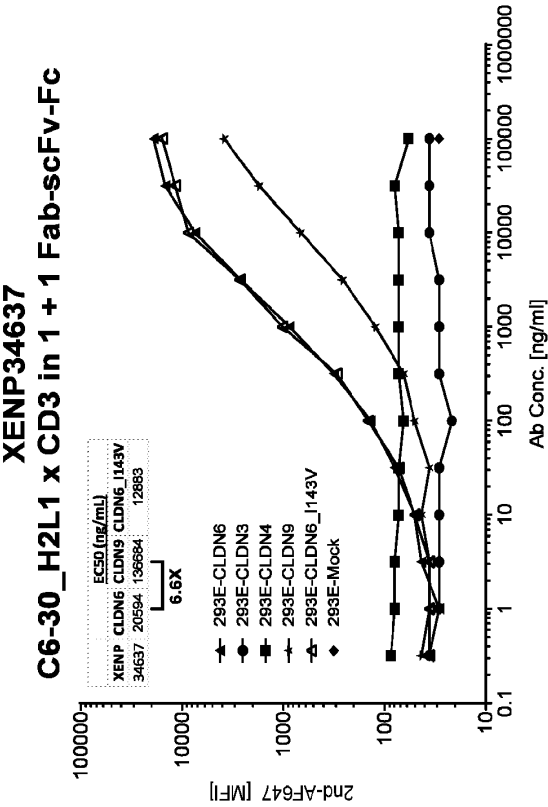


Figure 30

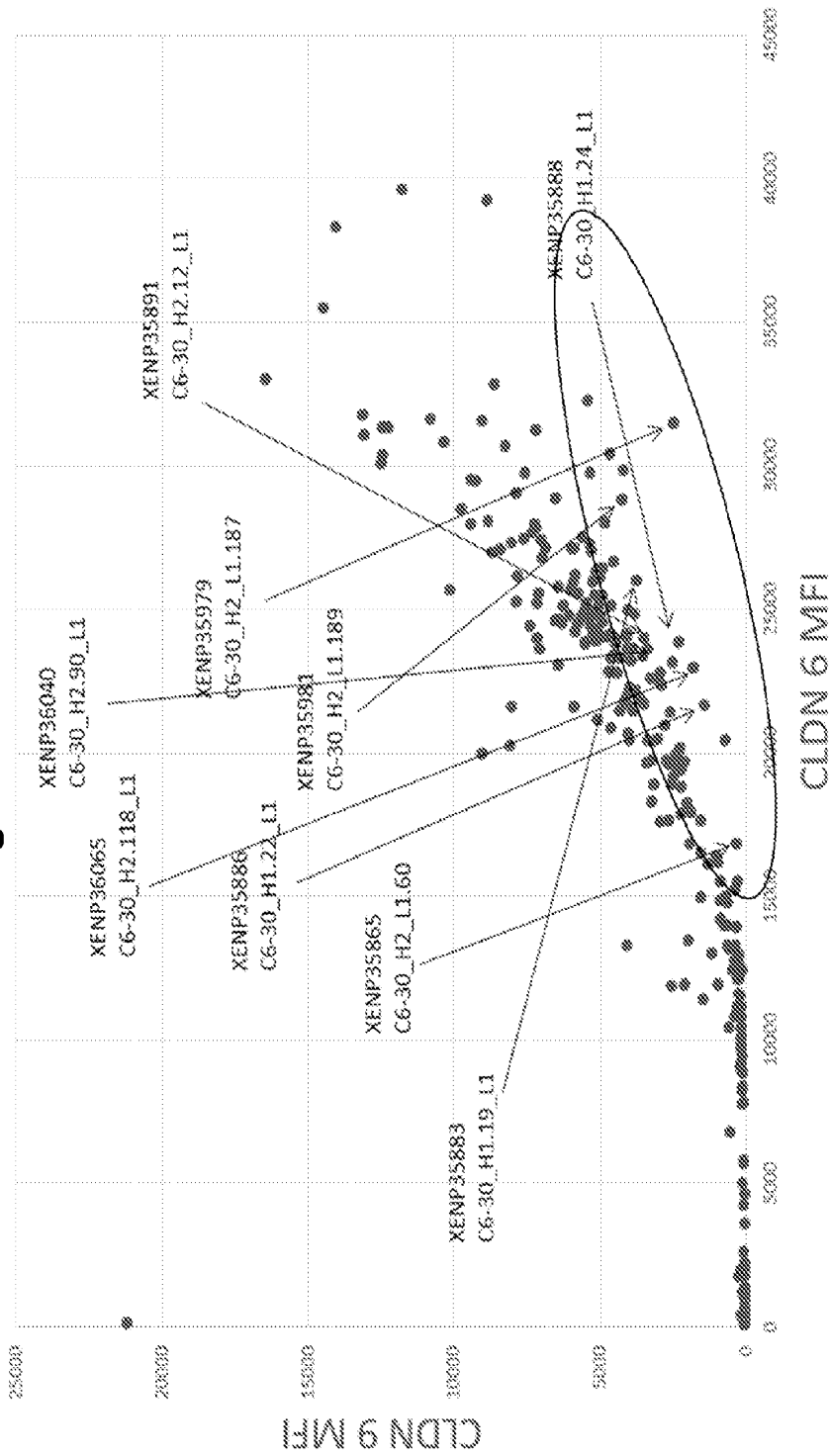


Figure 31A

A)	C6-30 Variant	EC50 (ng/ml)		CLDN9/6 ratio
		On CLDN6	On CLDN9	
XENP26863	COMPARATOR	273.8	7374	26.93
XENP34218	H1_L1	1241	54237	43.70
XENP34220	H2_L1	1632	43826	26.85
XENP35044	H2_L1.1	4338	NA	NA
XENP35047	H2_L1.4	795.2	17550	22.07
XENP35050	H2_L1.7	2218	99339	44.79
XENP35059	H2_L1.16	1276	32669	25.60
XENP35061	H2_L1.18	1248	56295	45.11
XENP35062	H2_L1.19	1225	86760	70.82
XENP35064	H2_L1.21	979.2	14147	14.45
XENP35065	H2_L1.22	1478	69069	46.73
XENP35066	H2_L1.23	1590	31803	20.00
XENP35070	H2_L1.27	1183	29684	25.09
XENP35087	H1.3_L1	1198	31760	26.51
XENP35088	H1.4_L1	1286	29242	22.74
XENP35090	H1.6_L1	1556	44628	28.68
XENP35091	H1.7_L1	1433	31427	21.93
XENP35092	H1.8_L1	1160	24998	21.55
XENP35093	H1.9_L1	978	53115	54.31
XENP35096	H2.3_L1	1241	110298	88.88
XENP35097	H2.4_L1	1103	72866	66.06
XENP35100	H2.7_L1	1139	63509	55.76
XENP35101	H2.8_L1	24783	1061	0.04
XENP35102	H2.9_L1	3526	1432	0.41

Figure 31B

B)	C6-30 Variant	EC50 (ng/ml)		CLDN9/6 ratio
		On CLDN6	On CLDN9	
XENP26863	COMPARATOR	73.97	1874	25.33
XENP34218	H1_L1	344.3	11556	33.56
XENP34220	H2_L1	390.8	11056	28.29
XENP35090	H1.6_L1	902.7	7062	7.82
XENP35865	H2_L1.60	685.7	123972	180.80
XENP35883	H1.19_L1	617.2	16767	27.17
XENP35886	H1.22_L1	941.1	24483	26.02
XENP35888	H1.24_L1	657.4	43820	66.66
XENP35890	H2.11_L1	408.1	34071	83.49
XENP35891	H2.12_L1	473.6	44135	93.19
XENP35929	H2_L1.107	791.8	99068	125.12
XENP35936	H2_L1.114	828.6	57436	69.32
XENP35979	H2_L1.187	323	29169	90.31
XENP35981	H2_L1.189	403.5	31700	78.56
XENP36021	H2.71_L1	902.4	49328	54.66
XENP36022	H2.72_L1	513.9	47177	91.80
XENP36025	H2.75_L1	1343	61089	45.49
XENP36040	H2.90_L1	705.5	66108	93.70
XENP36041	H2.91_L1	449.4	32521	72.37
XENP36065	H2.118_L1	783	491857	628.17
XENP36066	H2.119_L1	567	18031	31.80

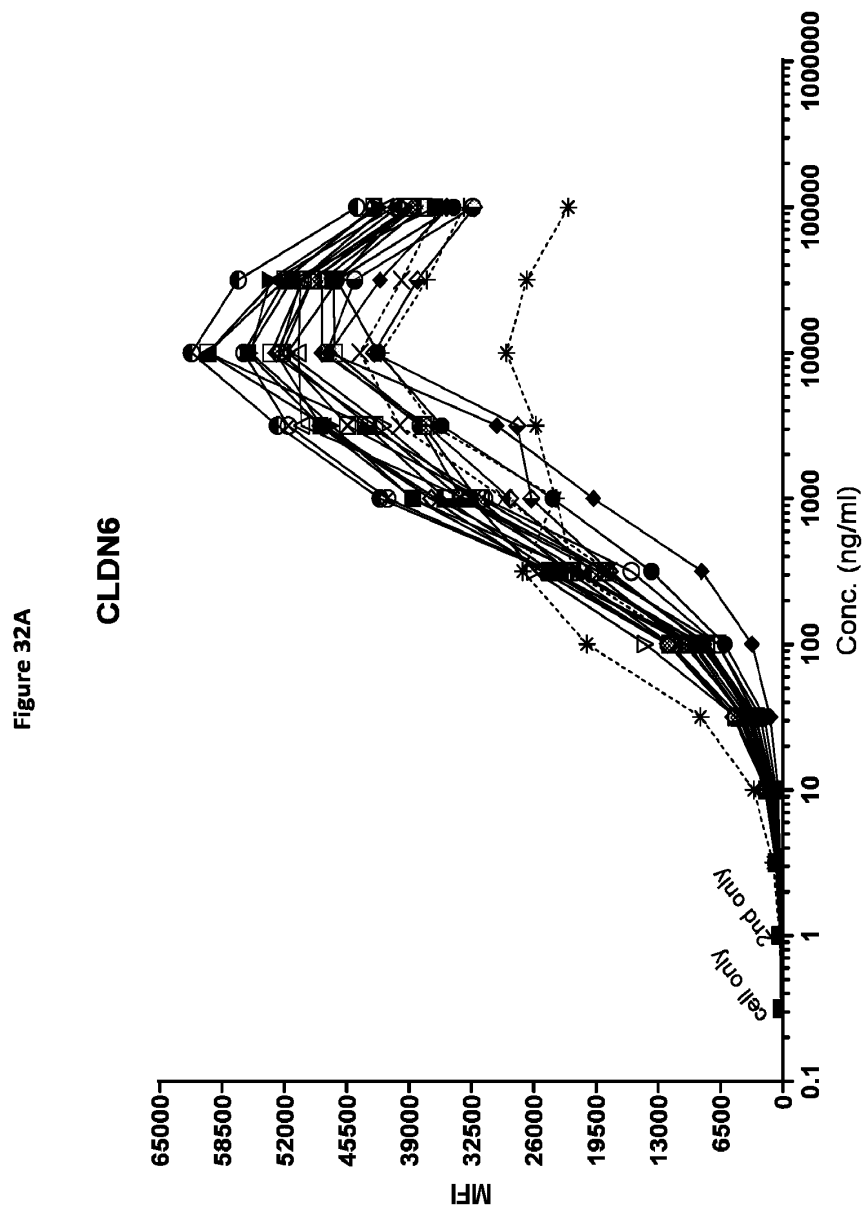


Figure 33

C6-30 Variants	CLDN6 EC50	CLDN9 EC50	CLDN9/CLDN6 EC50 Ratio	CLDN6 AUC	CLDN9 AUC	CLDN6/CLDN9 AUC Ratio
XENP34218_H1L1	373.2	8594	23.02787	3.88E+09	1.38E+09	2.802246
XENP34220_H2L1	294.7	10485	35.57855	3.62E+09	1.64E+09	2.20981
XENP26863 (COMPARATOR)	42.24	2146	50.80492	2.55E+09	1.58E+09	1.616028
XENP36956_H1.22_L1.187	658.3	29584	44.94	4.07E+09	1.61E+08	25.34196
XENP36957_H1.24_L1.187	305.3	21240	69.57091	4.63E+09	4.41E+08	10.49091
XENP36958_H1.19_L1.187	414.6	17235	41.57019	4.91E+09	4.92E+08	9.969486
XENP36959_H1.9_L1.187	392.2	18873	48.12086	4.92E+09	5.09E+08	9.67232
XENP36960_H1.22_L1.189	1072	60046	56.01306	3.93E+09	1.88E+08	20.88547
XENP36961_H1.24_L1.189	562.1	31368	55.80502	4.63E+09	4.2E+08	11.03723
XENP36962_H1.19_L1.189	450.1	15252	33.8858	4.6E+09	6.85E+08	6.710047
XENP36963_H1.9_L1.189	451.6	25916	57.38707	4.69E+09	6.73E+08	6.95726
XENP36964_H2.3_L1.187	259.5	26066	100.447	4.42E+09	4.94E+08	8.951393
XENP36965_H2.12_L1.187	279.1	16705	59.8531	4.57E+09	5.79E+08	7.881124
XENP36966_H2.91_L1.187	349.9	19604	56.02744	5.27E+09	5.24E+08	10.05439
XENP36967_H2.118_L1.187	313.6	26403	84.19324	4.29E+09	4.38E+08	9.796817
XENP36968_H2.3_L1.189	452	36292	80.29204	4.37E+09	5.86E+08	7.458967
XENP36969_H2.12_L1.189	295.1	11508	38.99695	4.02E+09	7.66E+08	5.251557
XENP36970_H2.91_L1.189	394.6	24490	62.06285	4.91E+09	6.15E+08	7.988906
XENP36971_H2.118_L1.189	378.8	14082	37.17529	3.6E+09	5.18E+08	6.948966
XENP36972_H1_L1.187	307.6	16192	52.63979	4.9E+09	5.34E+08	9.166706
XENP36973_H1_L1.189	466.5	18579	39.82637	4.55E+09	8.06E+08	5.640381

Figure 34A

CLDN6

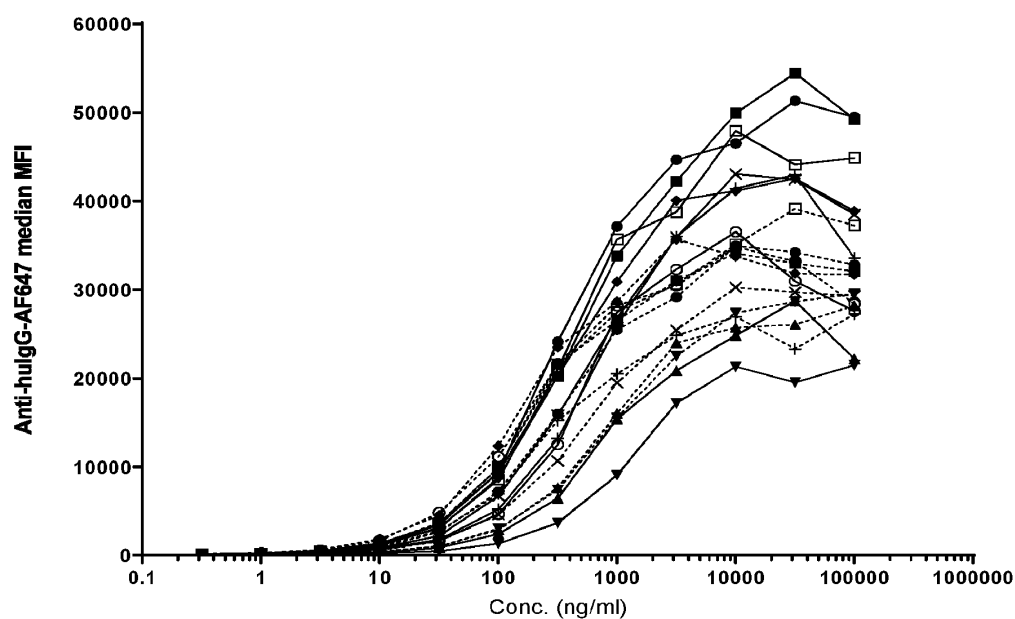


Figure 34B

CLDN9

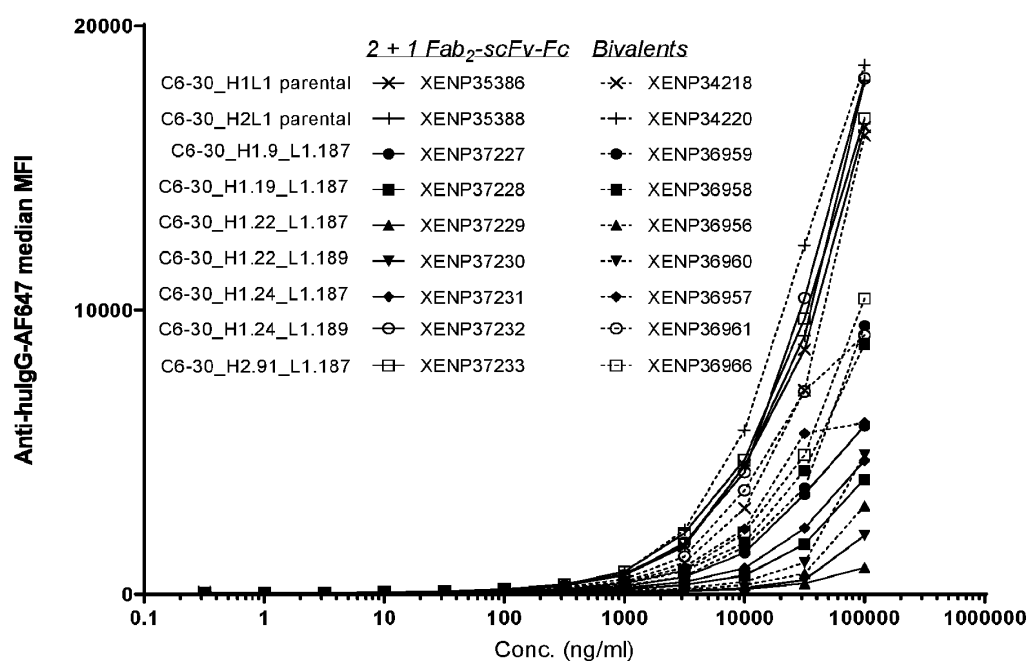


Figure 35B

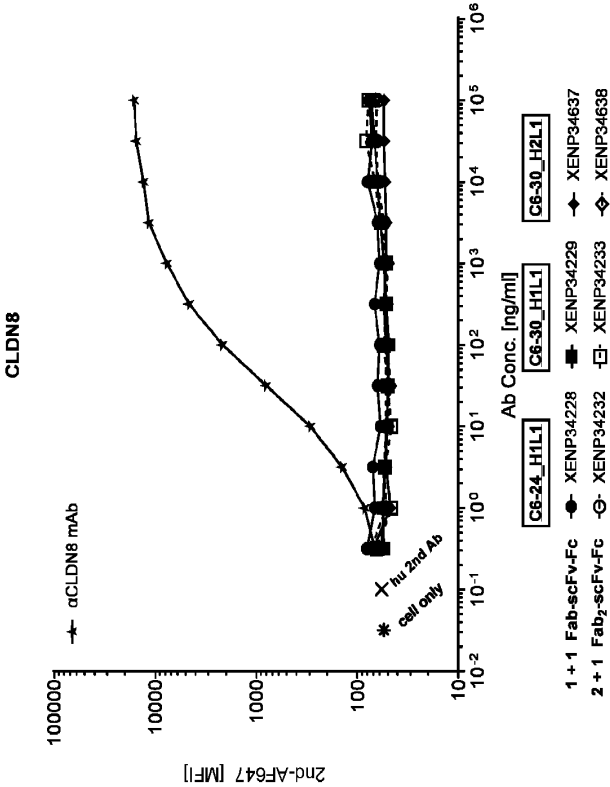


Figure 35A

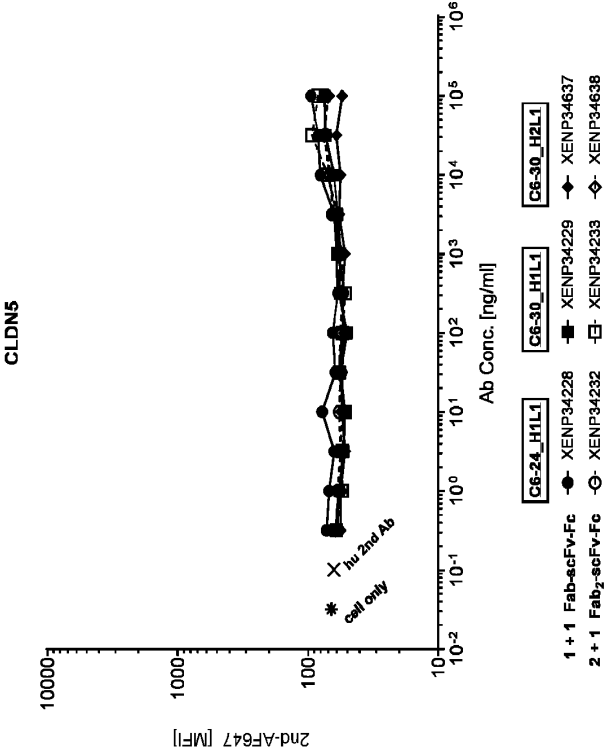


Figure 35C

CLDN17

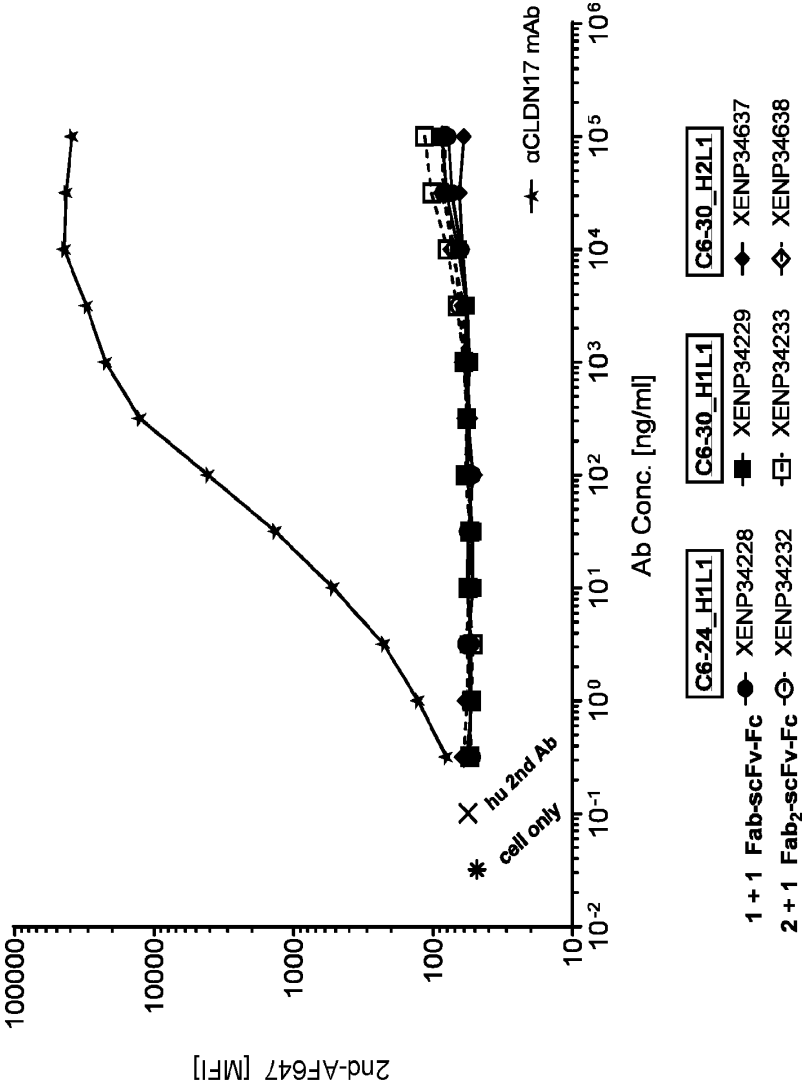
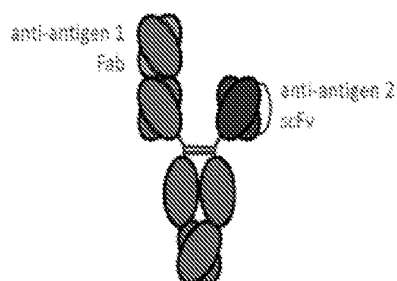


Figure 36A



Bottle Opener or
1+1 Fab-scFv-Fc

Figure 36B

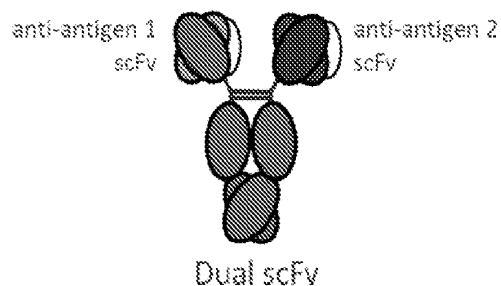
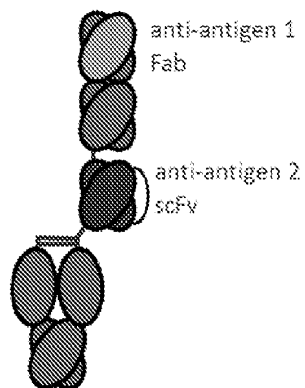
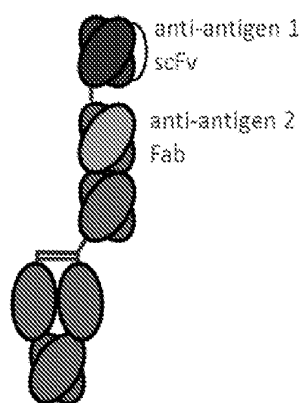


Figure 36C



One-arm central-scFv

Figure 36D



One-arm scFv-mAb

Figure 36E

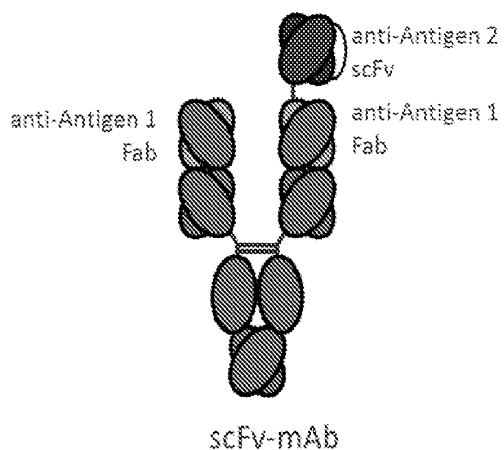
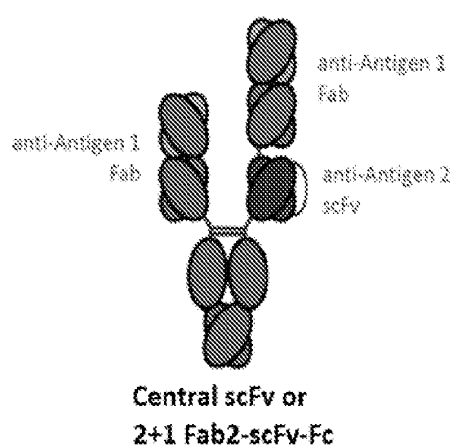


Figure 36F



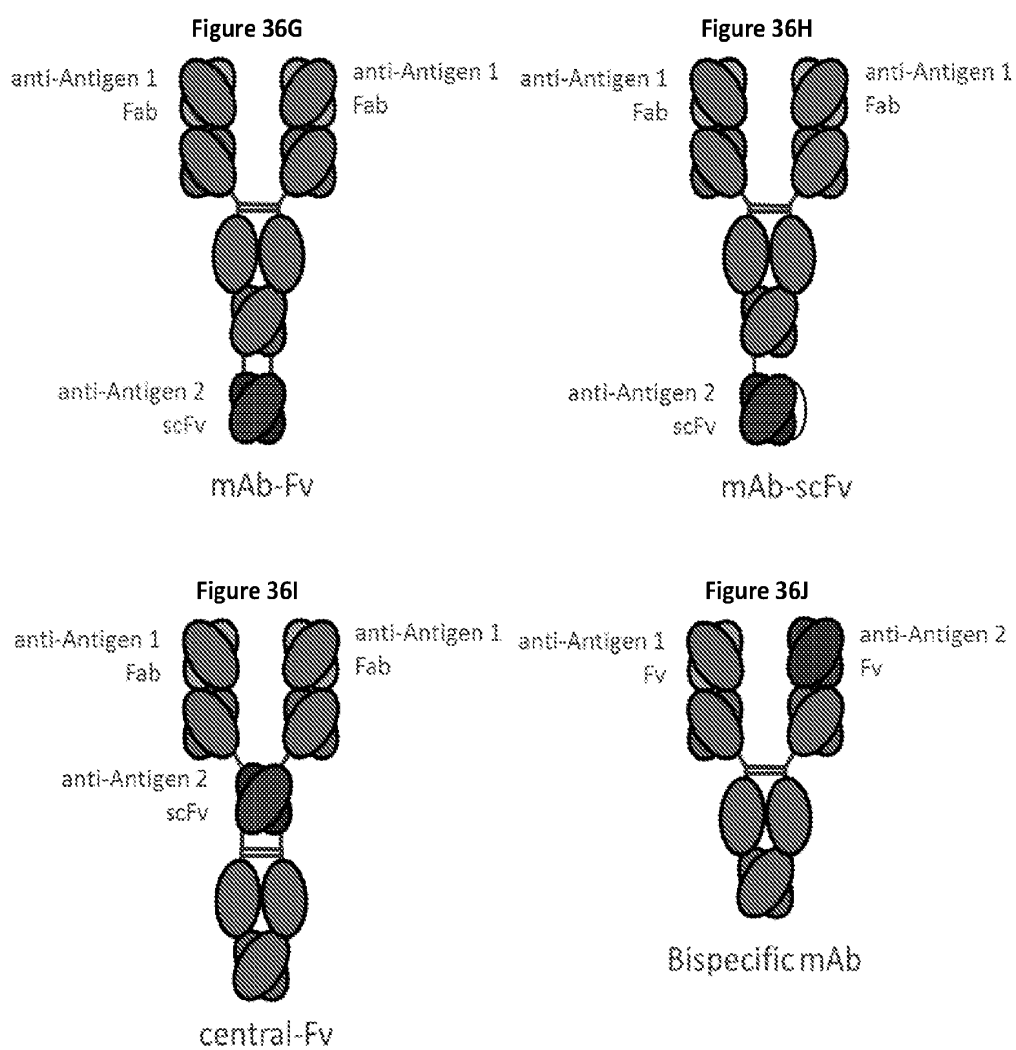
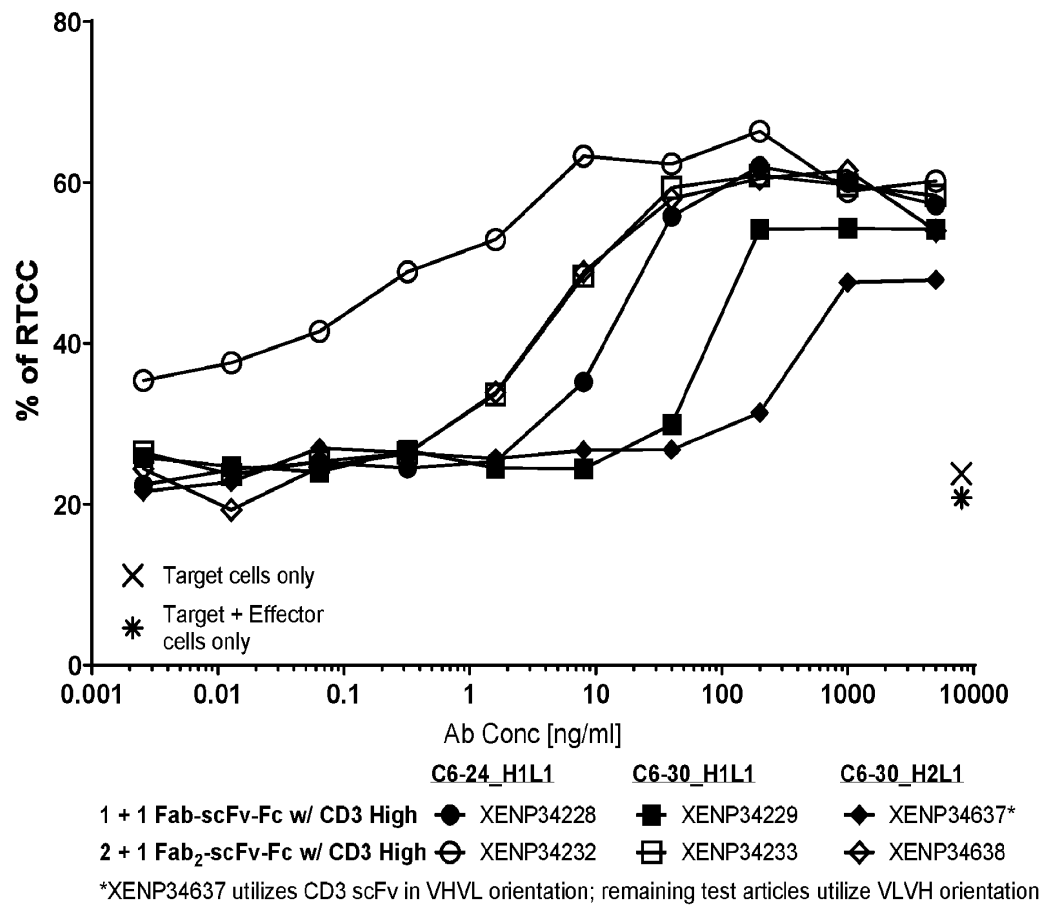


Figure 37



Sample ID	Format	FV	Humanization	PA-1 RTCC average EC50 (ng/mL)
XENP34229	1+1	C6-30	H1L1	75.6 ± 32.3
XENP34233	2+1	C6-30	H1L1	5.3 ± 1.5
XENP34637	1+1	C6-30	H2L1	205.5 ± 115.4
XENP34638	2+1	C6-30	H2L1	2.4 ± 1.2
XENP34228	1+1	C6-24	H1L1	11.4 ± 1.3
XENP34232	2+1	C6-24	H1L1	1.0 ± 0.9

Figure 38A

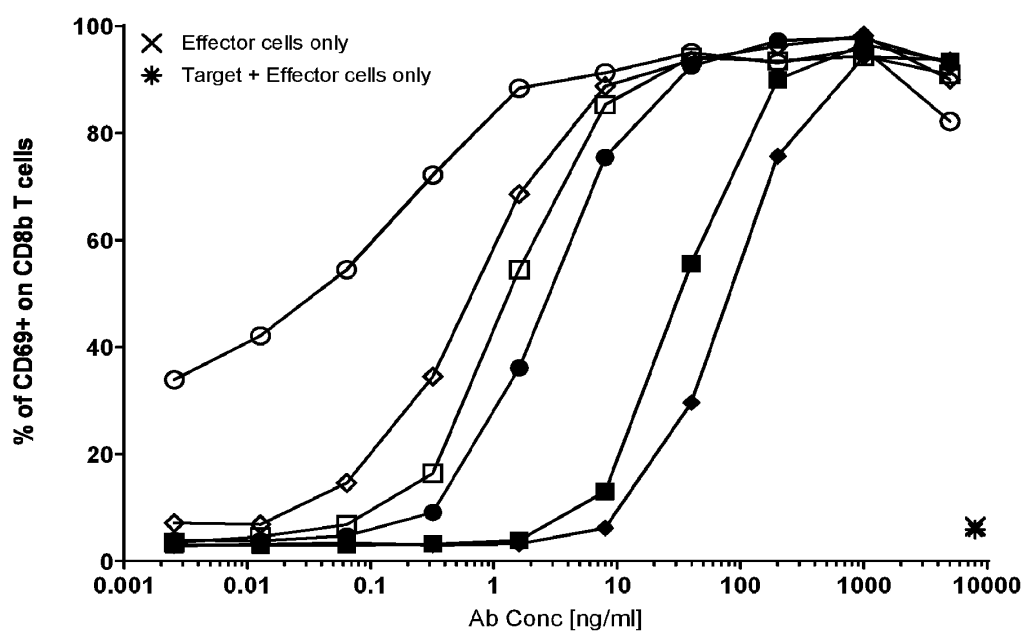
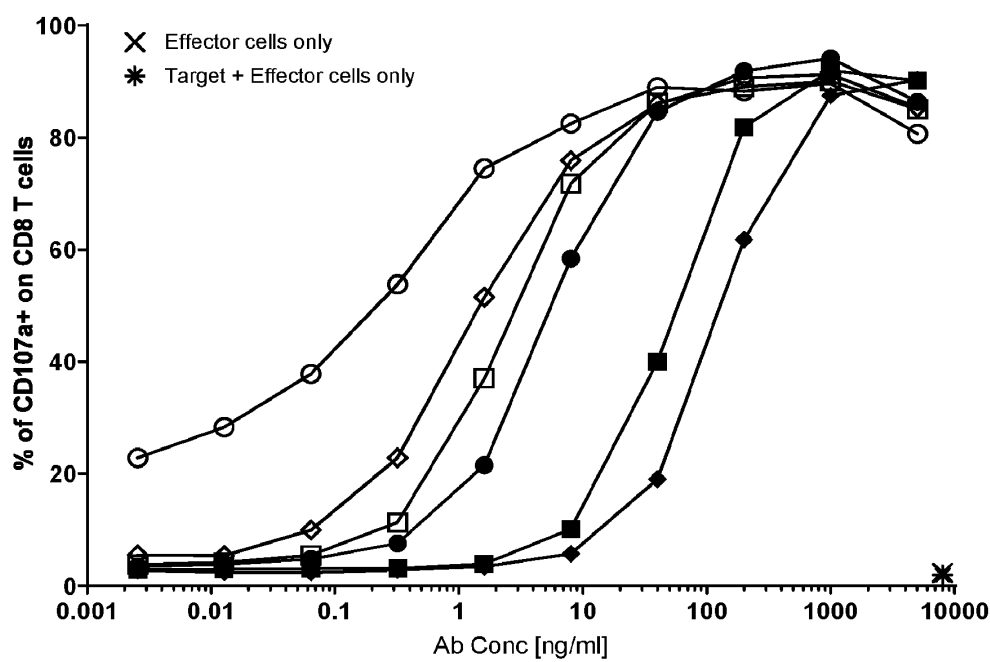
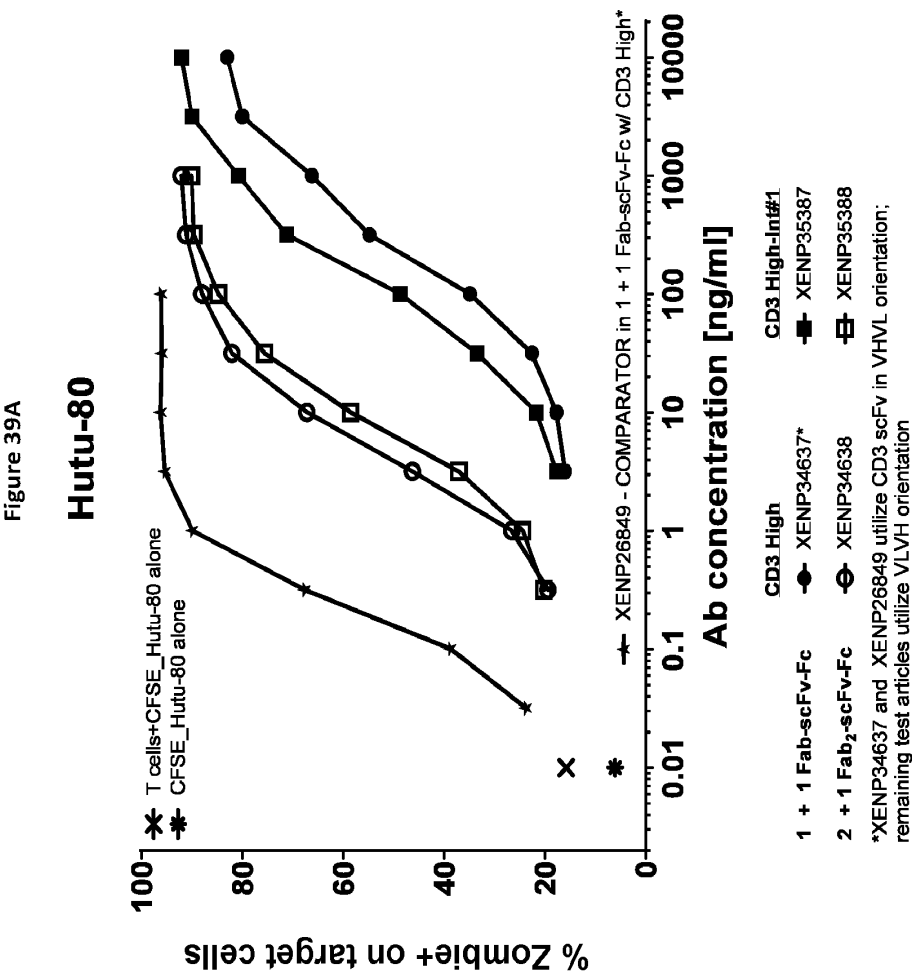
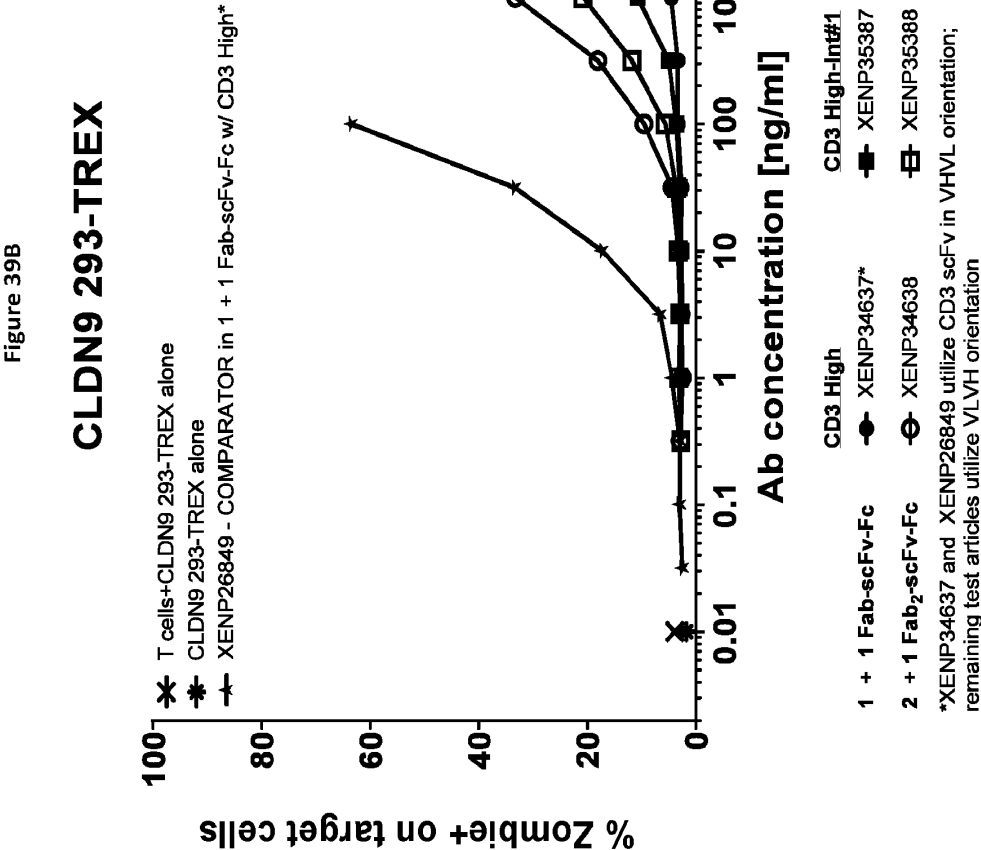


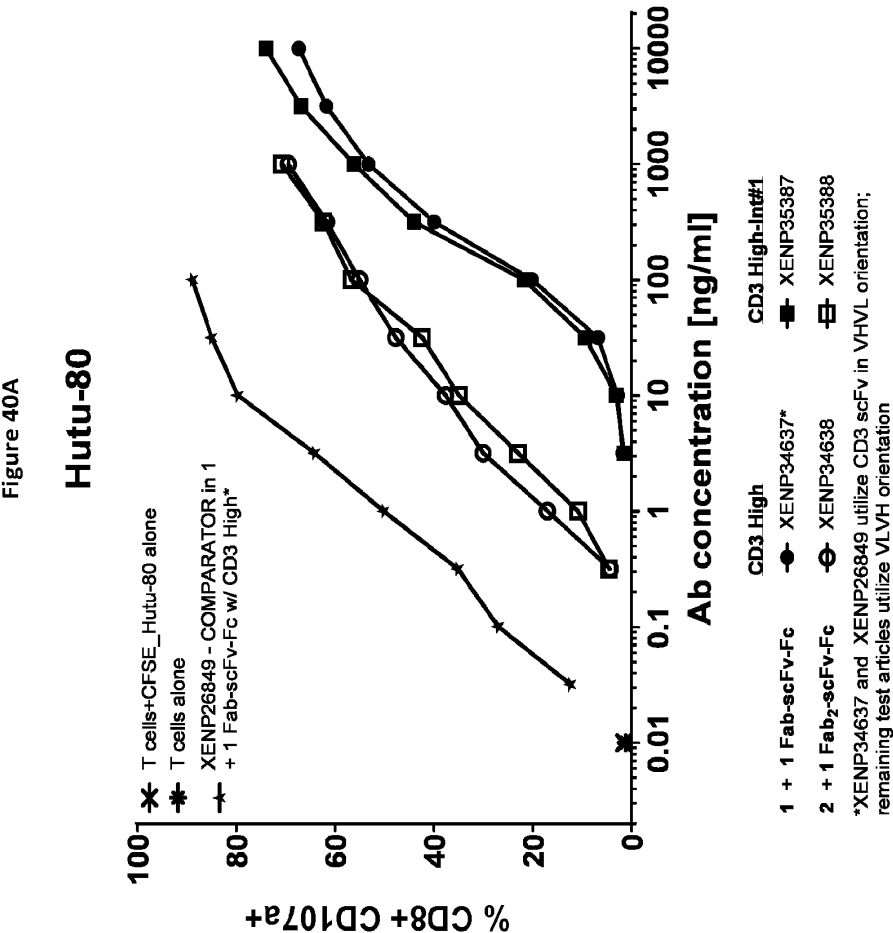
Figure 38B



C6-24_H1L1 C6-30_H1L1 C6-30_H2L1
 1 + 1 Fab-scFv-Fc w/ CD3 High ● XENP34228 ■ XENP34229 ◆ XENP34637
 2 + 1 Fab₂-scFv-Fc w/ CD3 High ○ XENP34332 □ XENP34233 ◇ XENP34638
 *XENP34637 utilizes CD3 scFv in VHVL orientation; remaining test articles utilize VLVH orientation







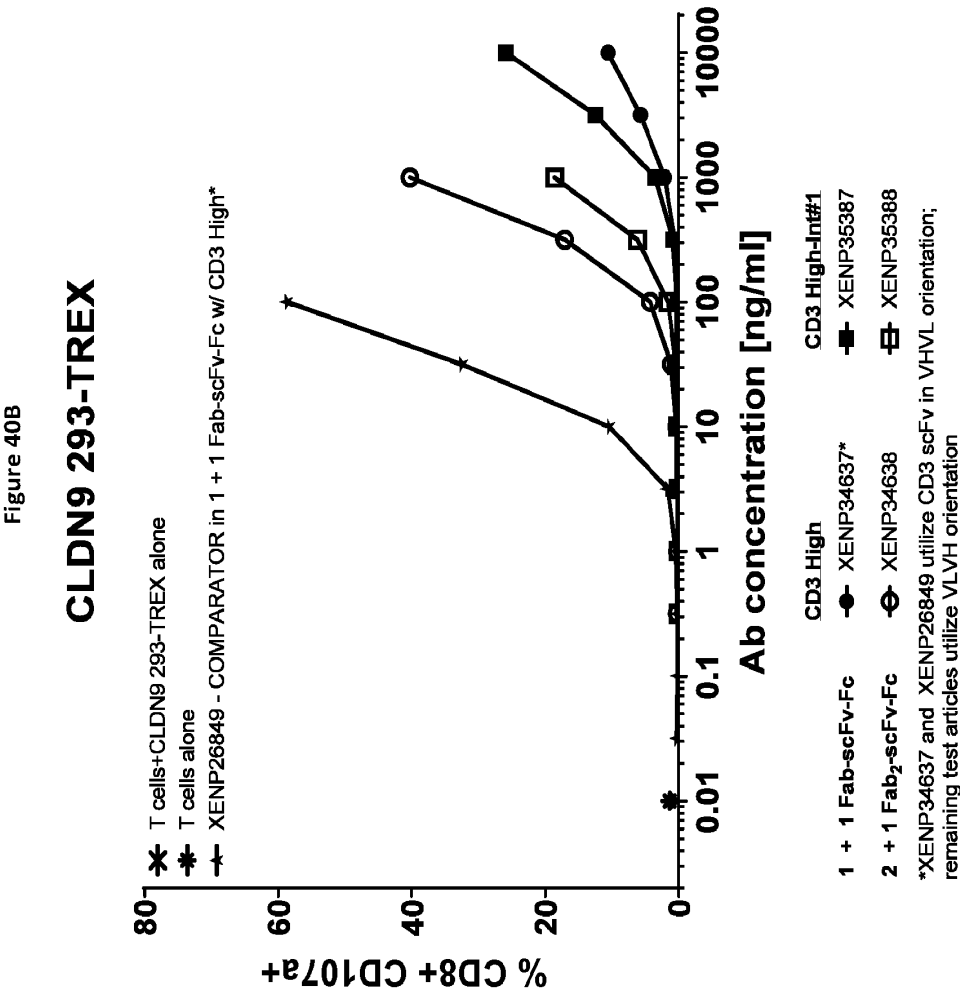


Figure 41B

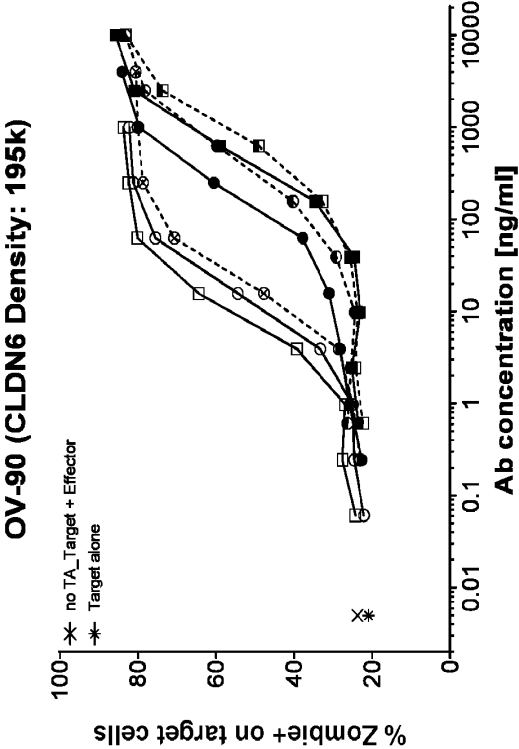
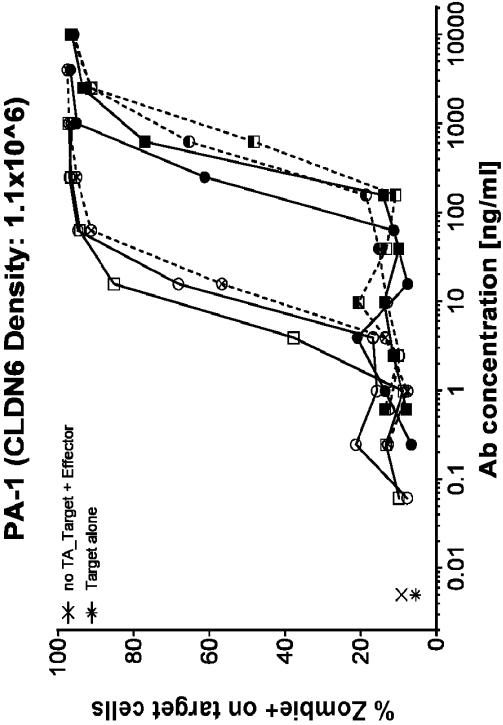


Figure 41A



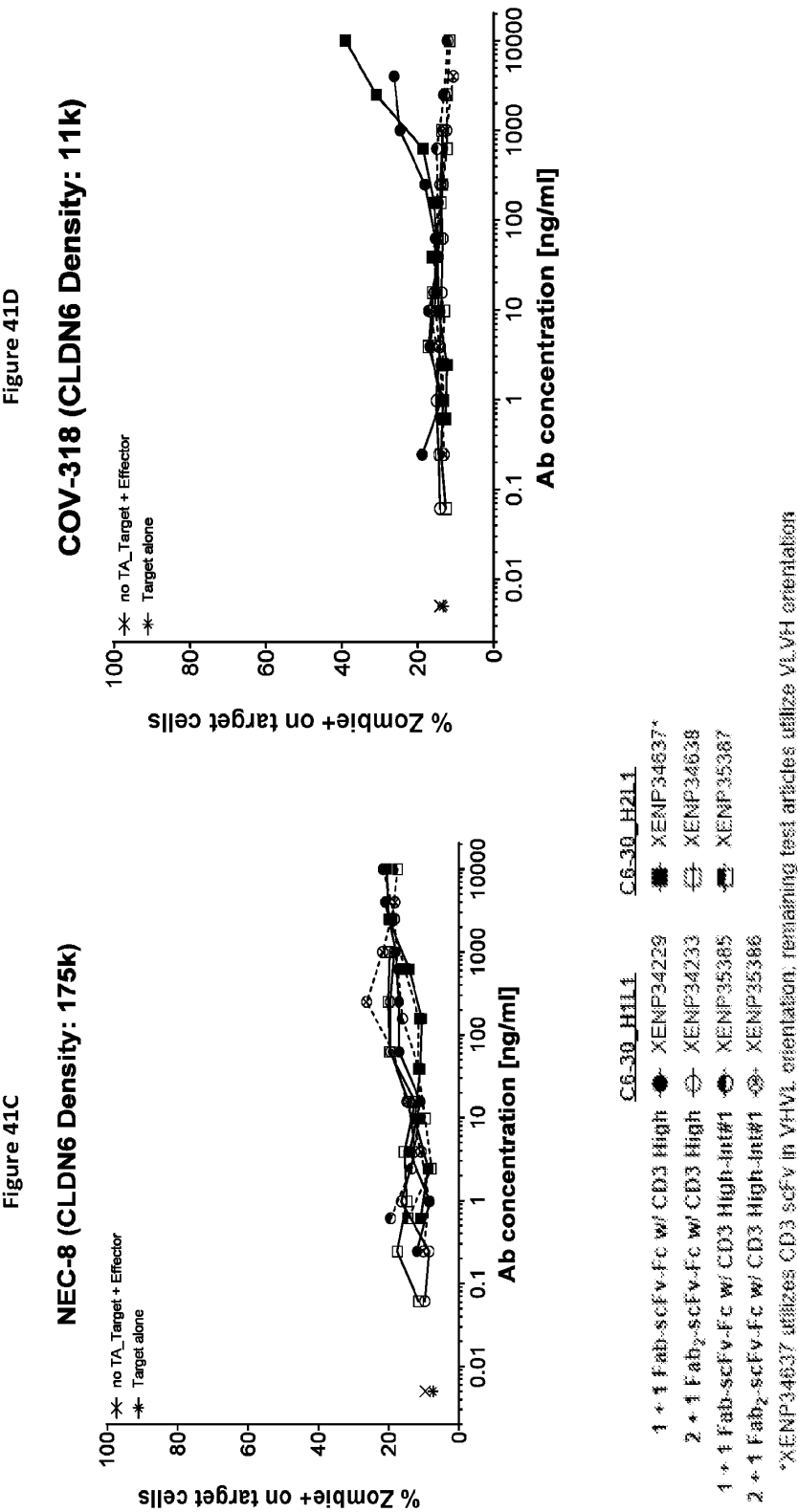


Figure 42

EC50_%Zombie+ on targets (ng/mL)		
	PA-1	OV-90
XENP34229	287	200.3
XENP34233	12.44	14.38
XENP34637	469.7	590.5
XENP34638	5.989	9.29
XENP26849	0.1084	0.299
XENP28817	1.352	5.173
XENP35385	570.1	472
XENP35386	14.26	19.19
XENP35387	1045	908.3

Figure 43B

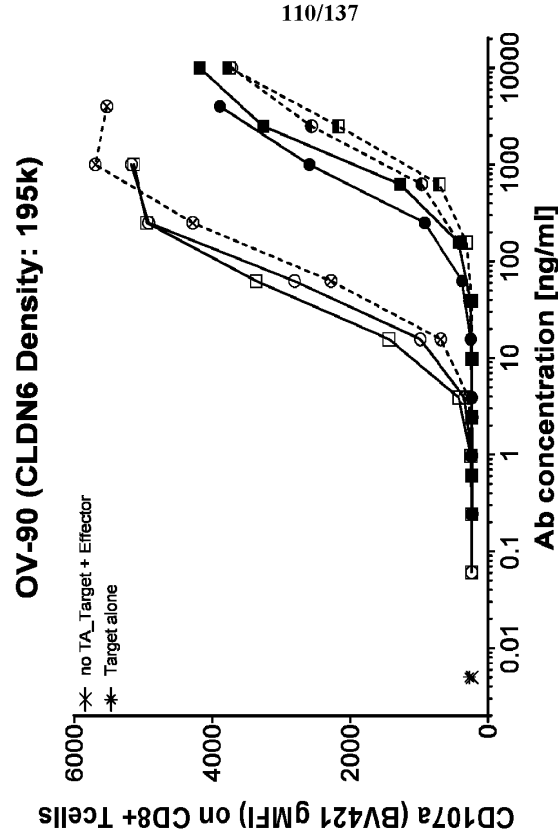
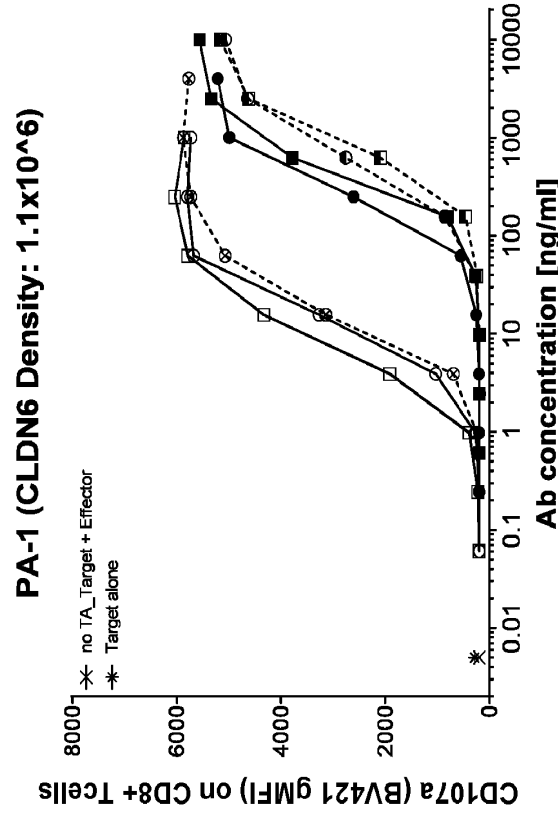
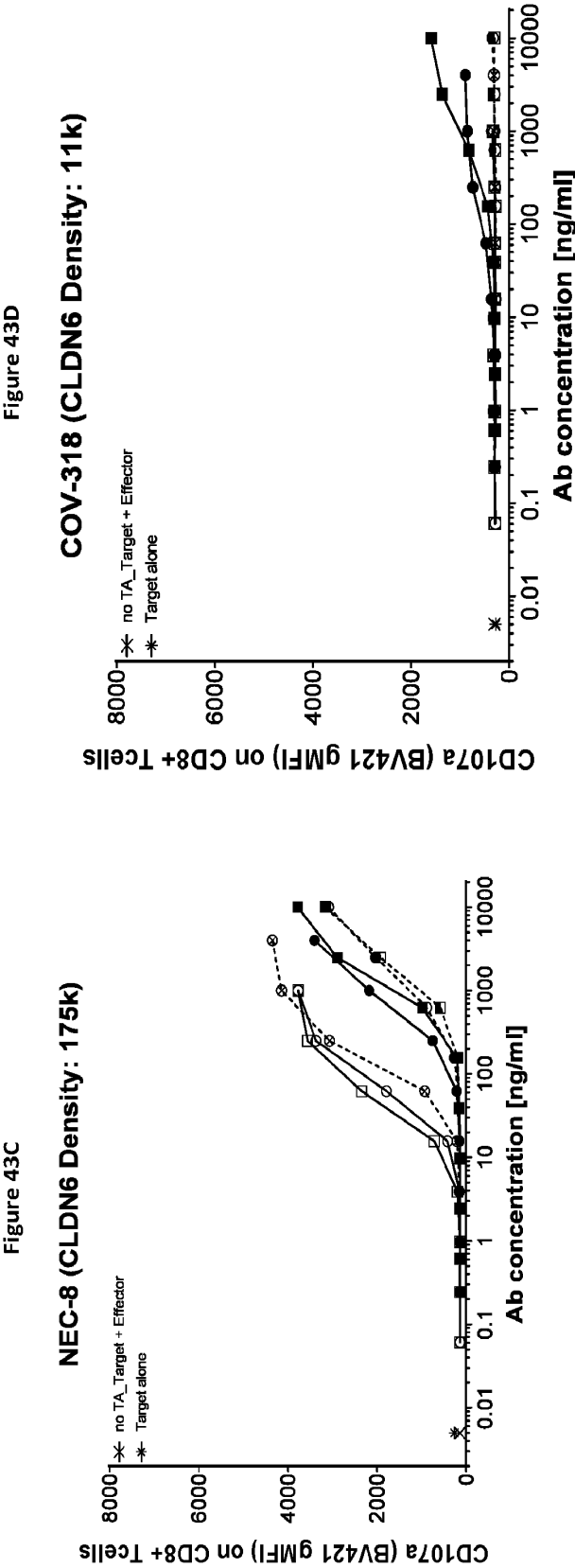


Figure 43A





C6_30_H1L1 C6_30_H2L1

1 + 1 Fab₂-scFv-Fc w/ CD3 High ● XENP34229 ■ XENP34637*

2 + 1 Fab₂-scFv-Fc w/ CD3 High ○ XENP34233 □ XENP34638

1 + 1 Fab₂-scFv-Fc w/ CD3 High-Int#1 ◆ XENP35385

2 + 1 Fab₂-scFv-Fc w/ CD3 High-Int#1 ◇ XENP35386

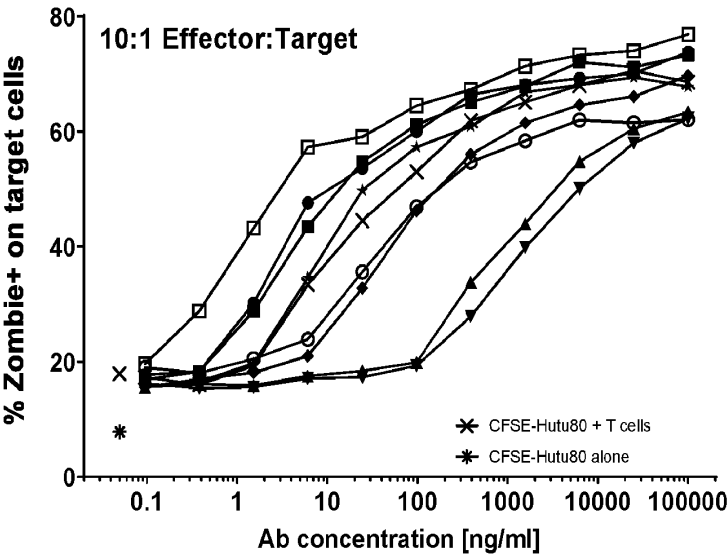
*XENP34637 utilizes CD3 scFv in VHV/L orientation; remaining test articles utilize VL/VH orientation

Figure 44

EC50_CD107a on CD8+				
	PA-1	OV-90	NEC-8	COV-318
XENP34229	322.6	1097	1178	118
XENP34233	13.18	67.02	88.68	
XENP34637	512.9	1714	1909	1012
XENP34638	7.561	44.08	54.54	
XENP26849	0.2754	2.396	2.285	22.29
XENP28817	2.064	23.56	20.21	38.66
XENP35385	686.7	2444	2383	
XENP35386	14.72	103.9	173.2	
XENP35387	1079	4280	3613	

Figure 45A

Hutu-80



%Zombie+ on Hutu-80

XENP	EC50 (ng/ml)
37227	5.4
37228	7
37229	857
37230	1426
37231	63
37232	44
37233	2.1
35386	21
35388	12

Figure 45B

CLDN9 293-TREX

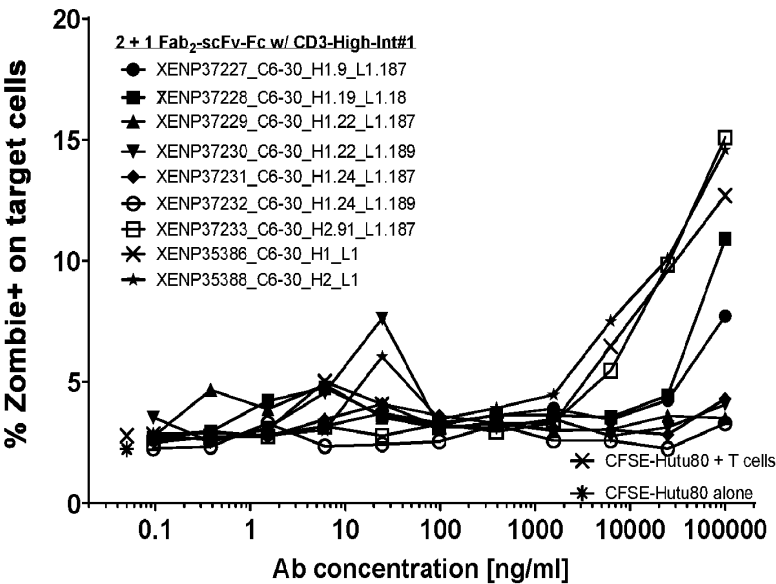
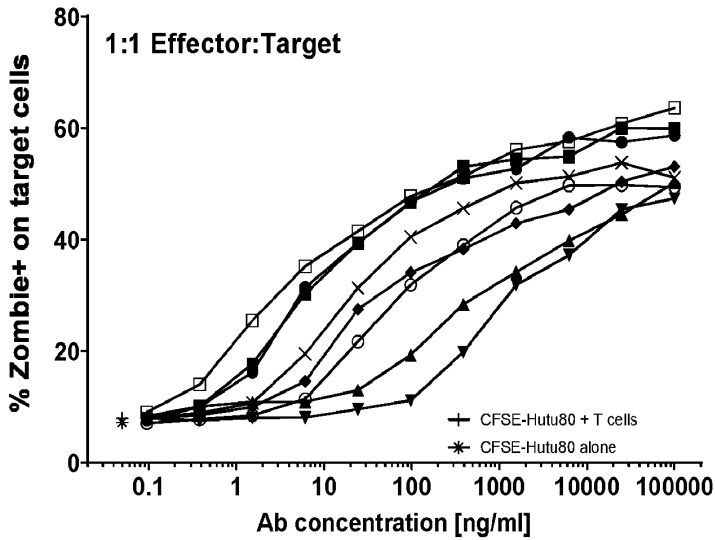


Figure 46A

Hutu-80



%Zombie+ on Hutu-80

XENP	EC50 (ng/ml)
37227	8.9
37228	10
37229	447
37230	1004
37231	38
37232	66
37233	7.2
35386	23

Figure 46B

CLDN9 293-TREX

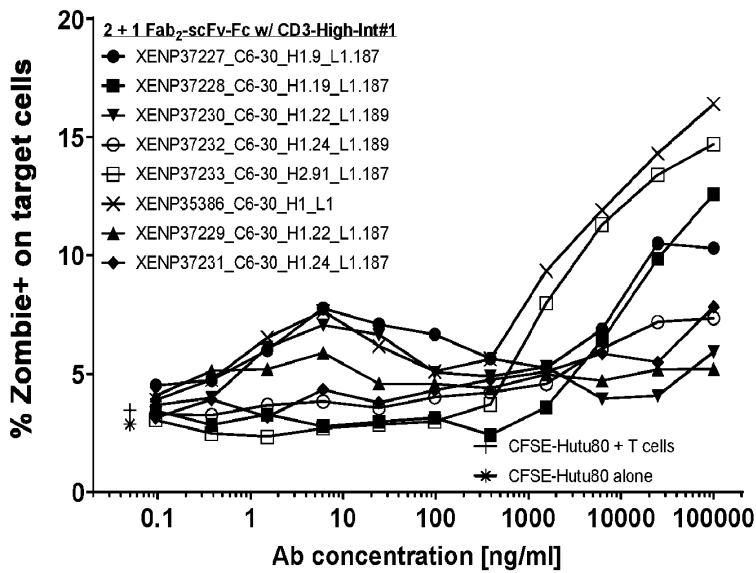


Figure 47A

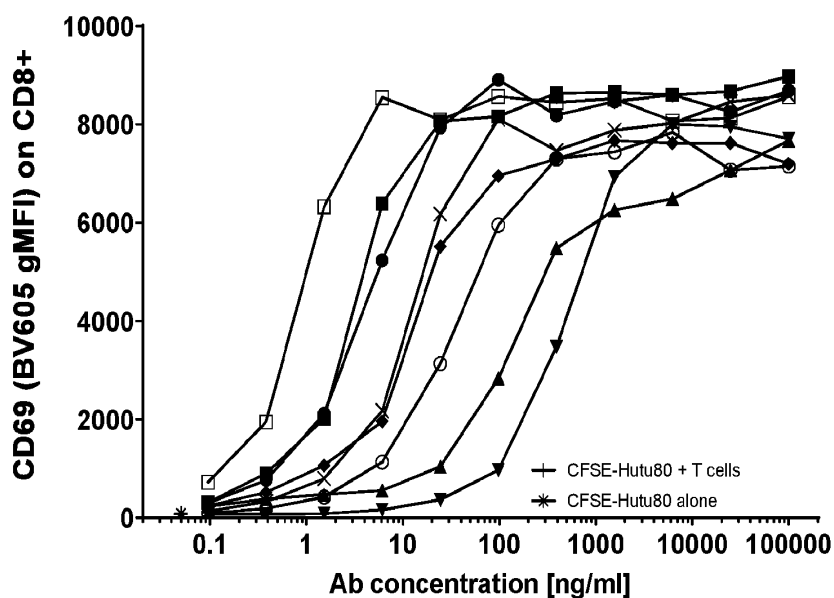
Hutu-80

Figure 47B

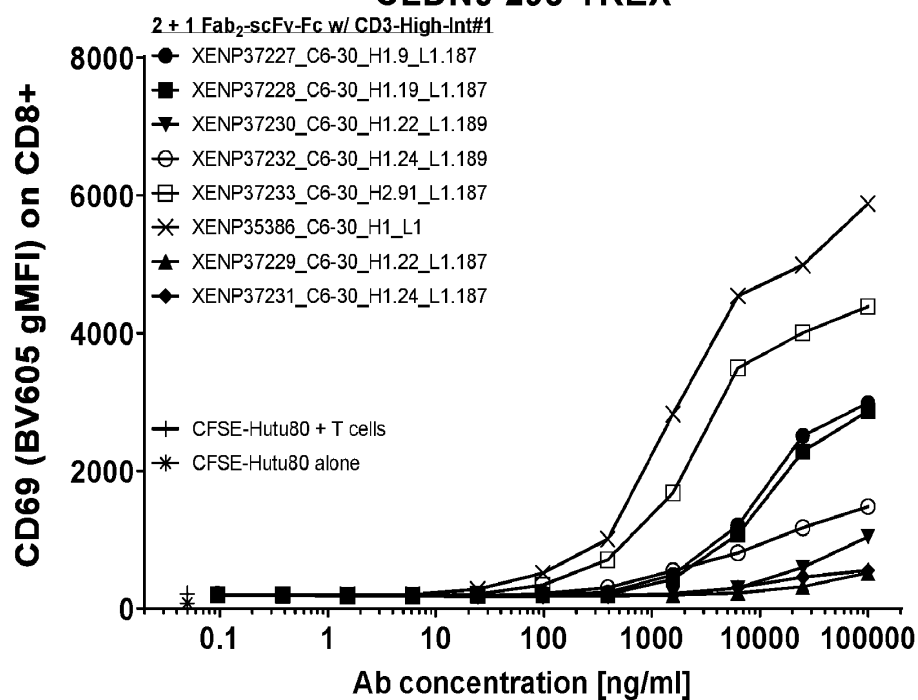
CLDN9 293-TREX

Figure 48A

Hutu-80

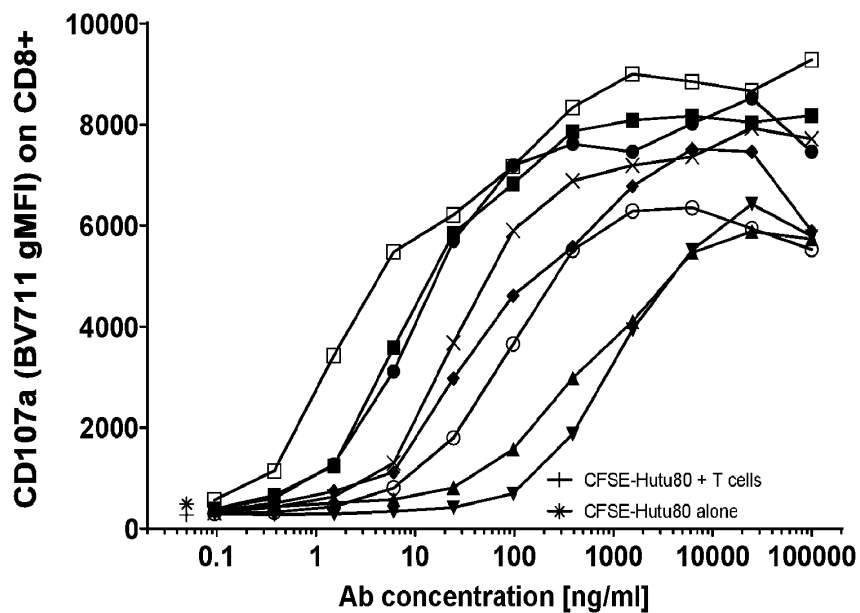


Figure 48B

CLDN9 293-TREX

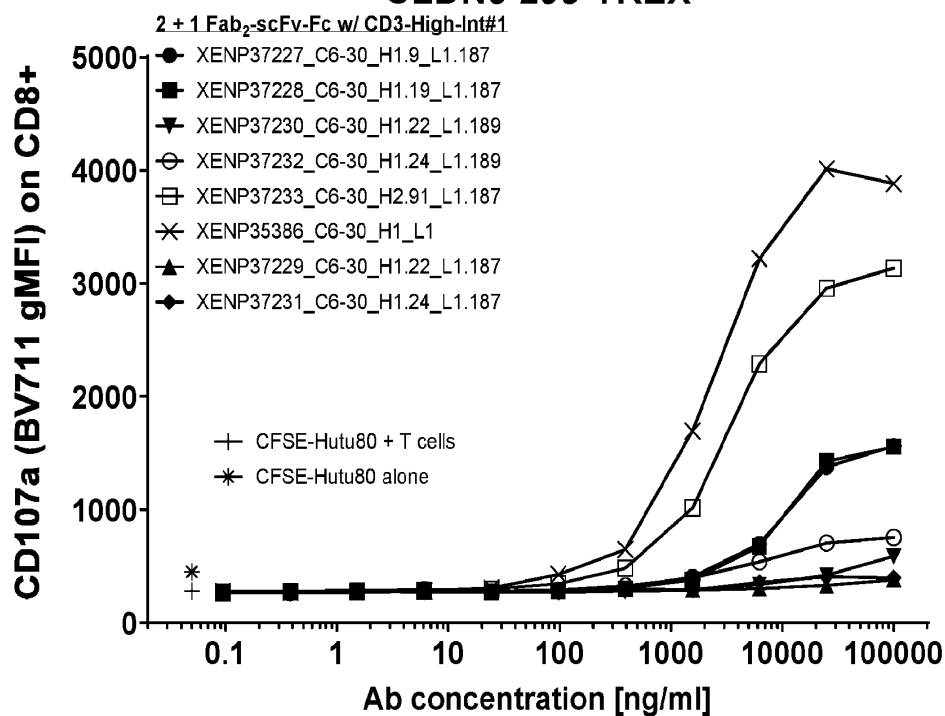


Figure 49A

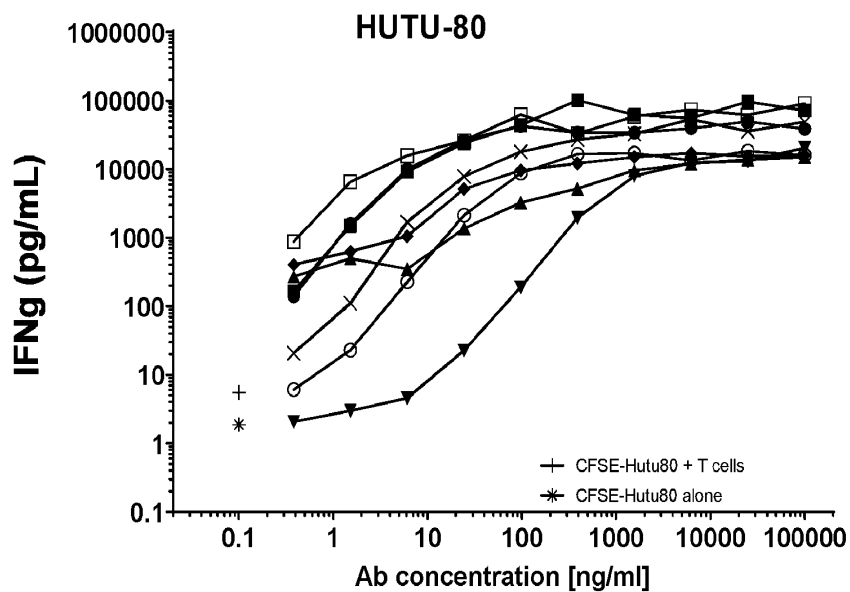


Figure 49B

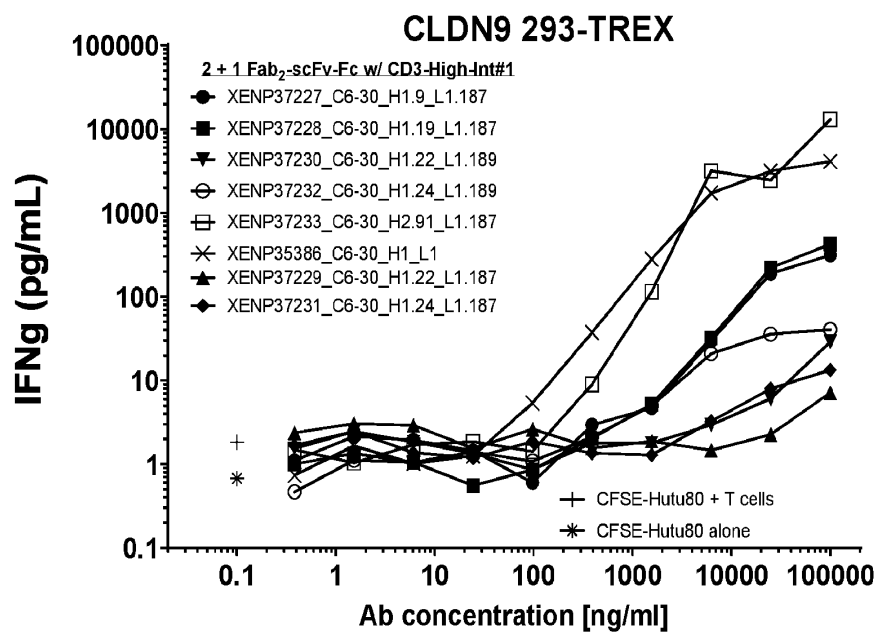


Figure 50A

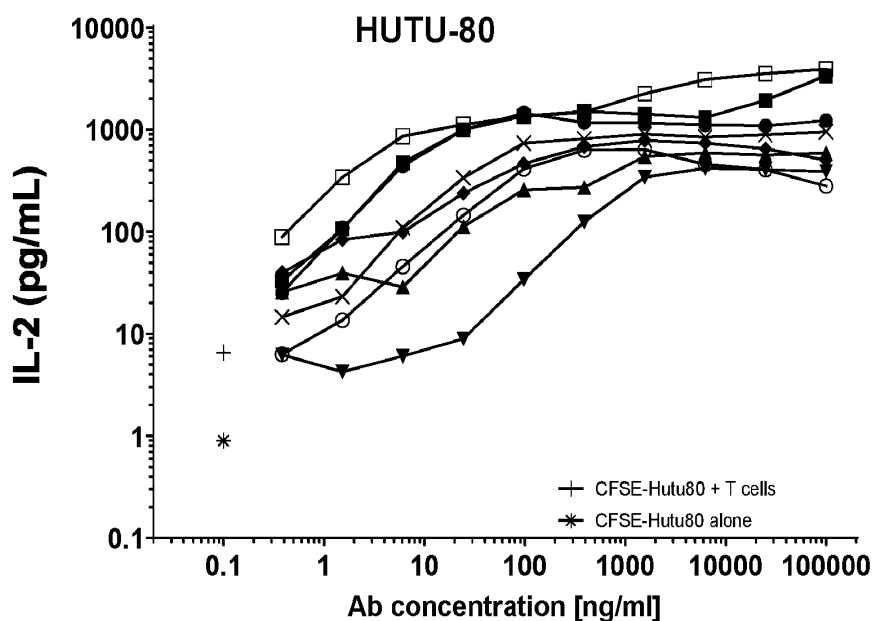


Figure 50B

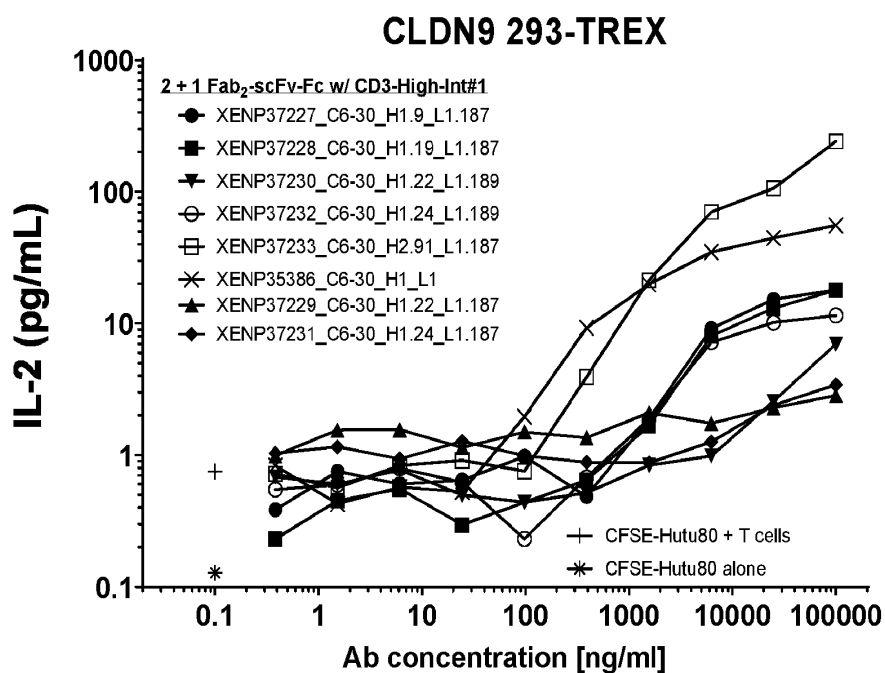


Figure 51A

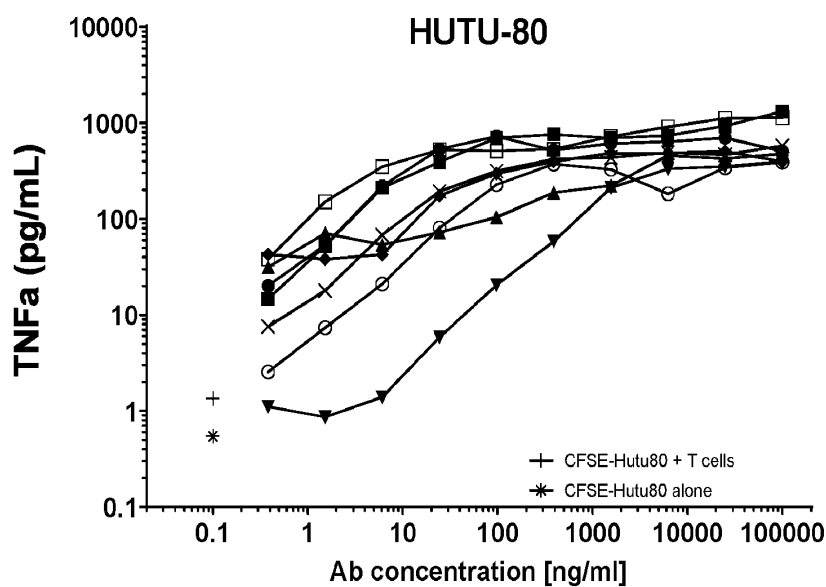


Figure 51B

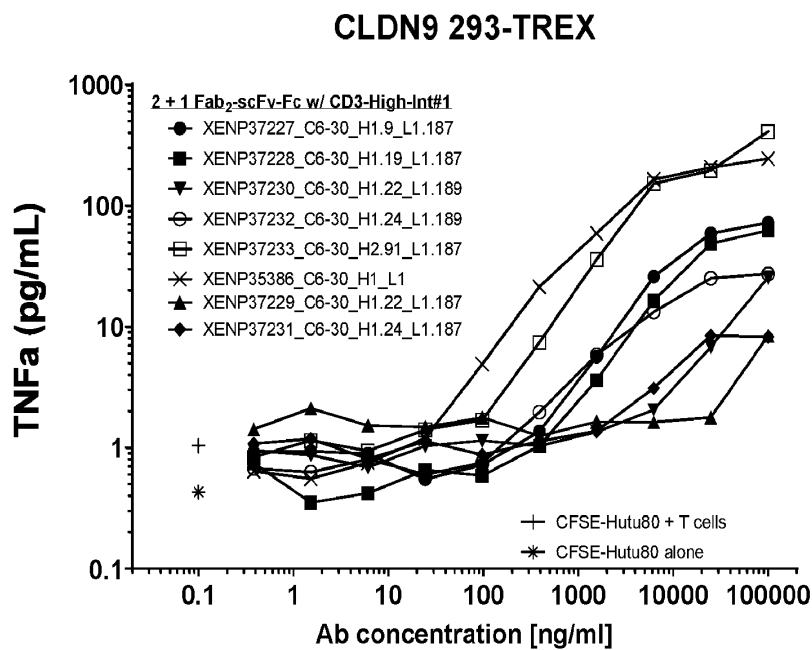


Figure 52A

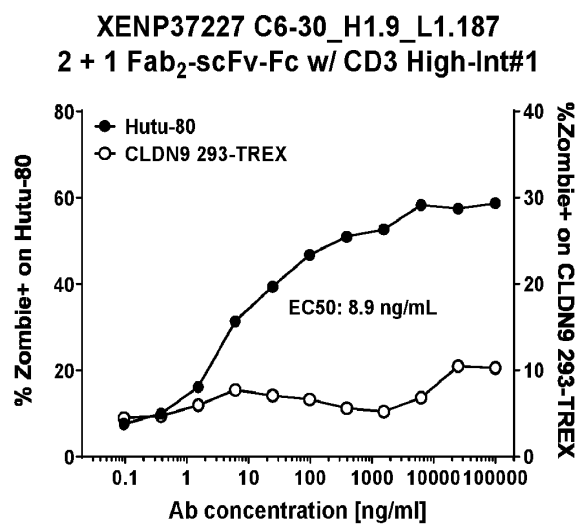


Figure 52B

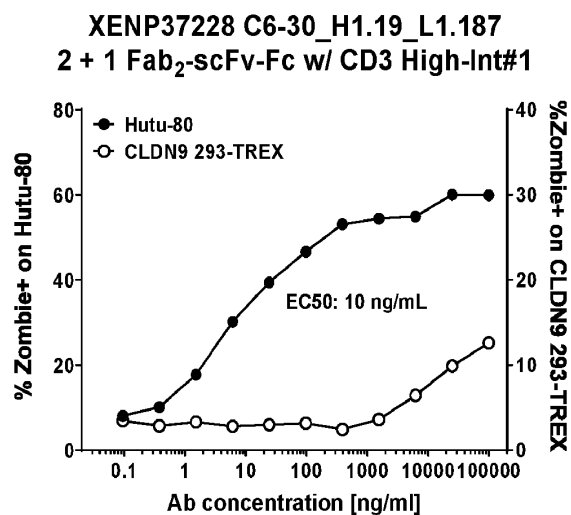


Figure 52C

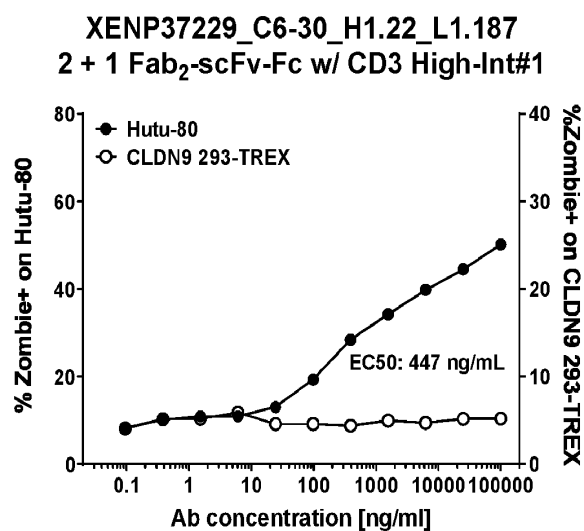


Figure 52D

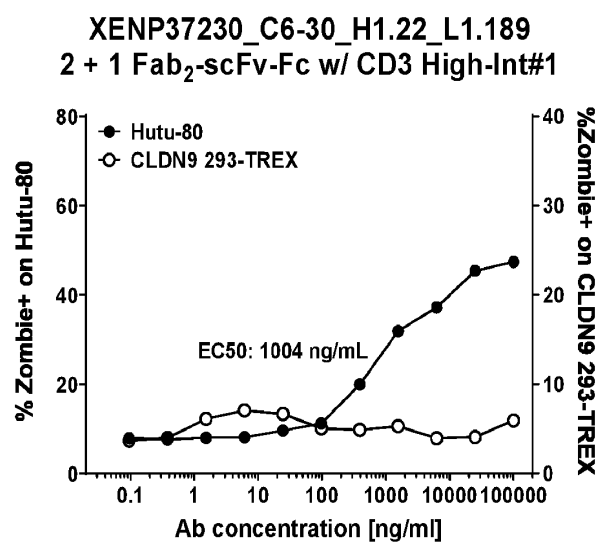


Figure 52E

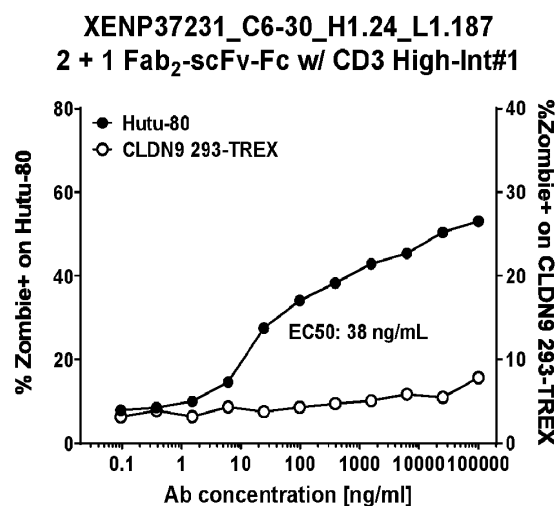


Figure 52F

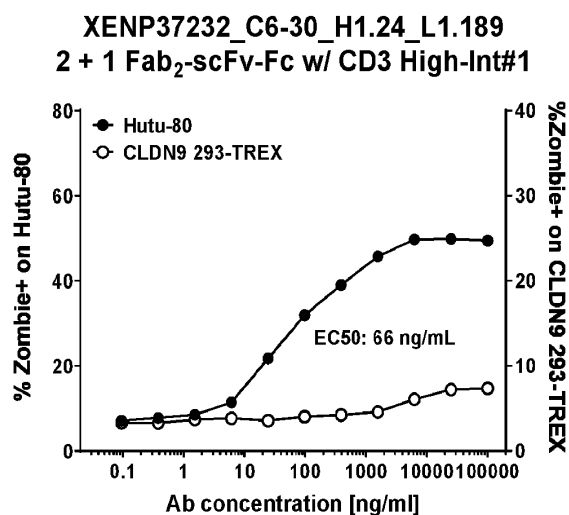


Figure 52G

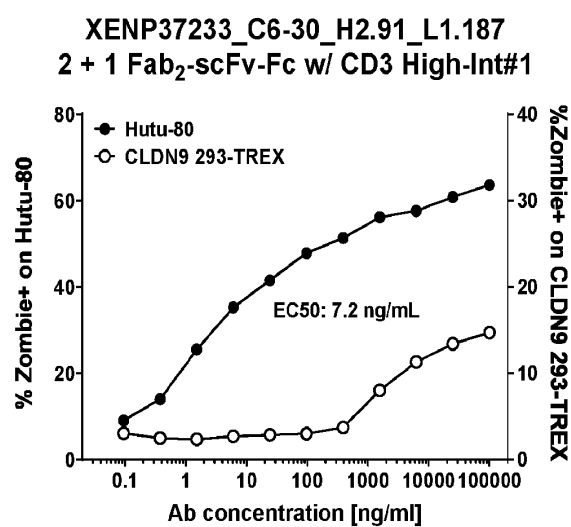


Figure 52H

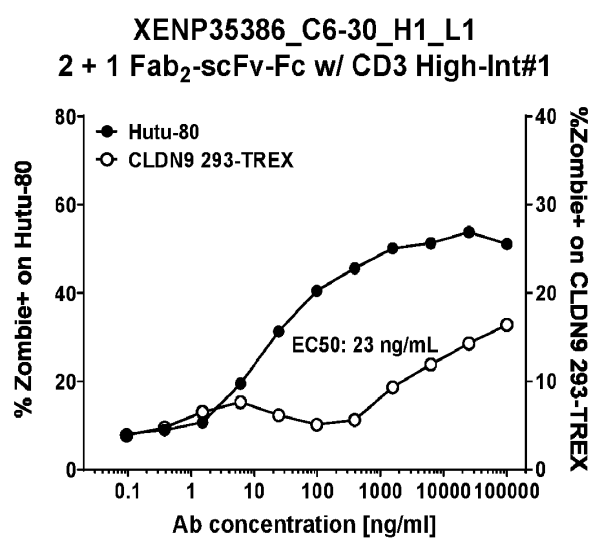


Figure 53B

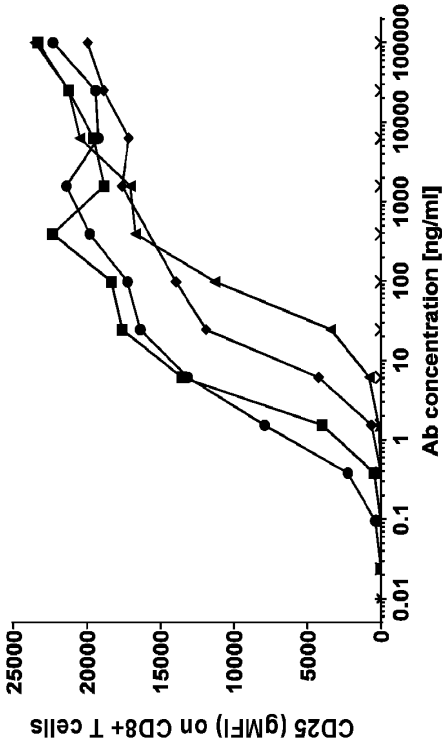


Figure 53A

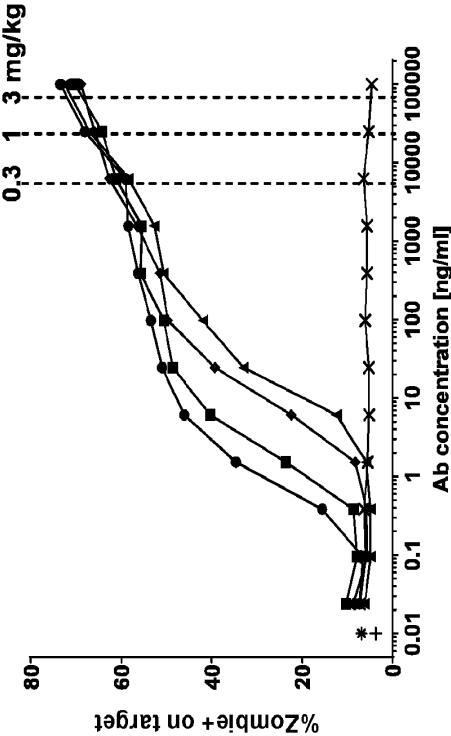


Figure 53C

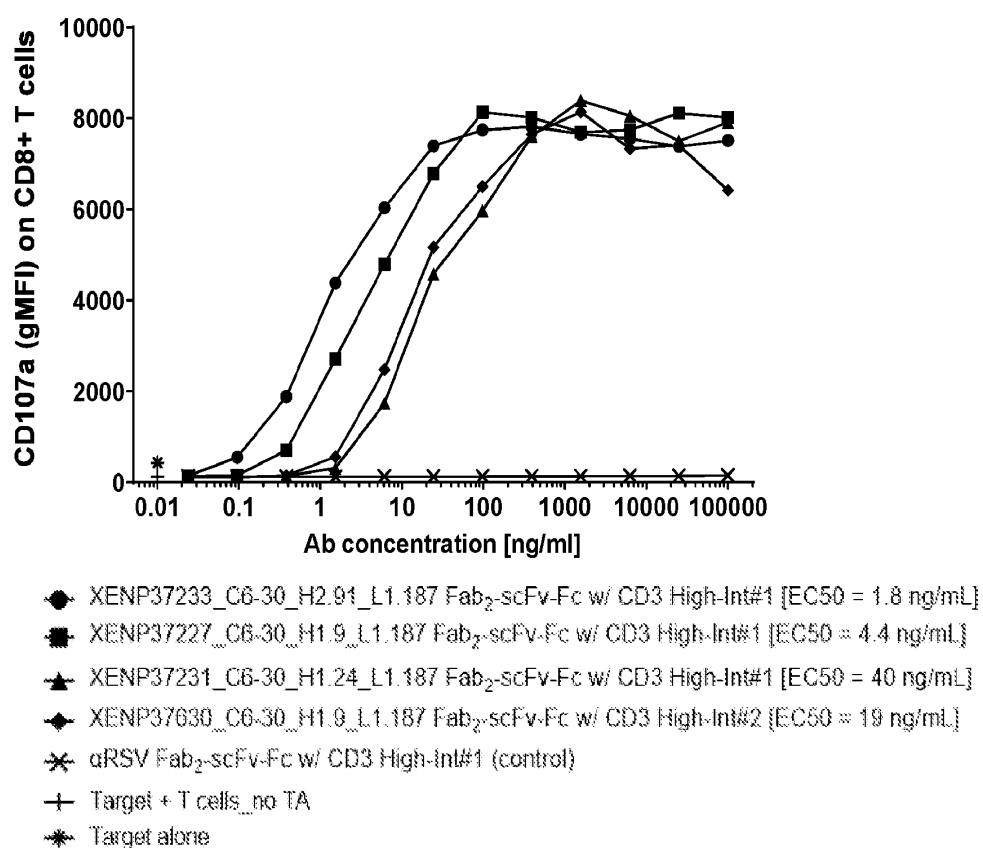


Figure 54

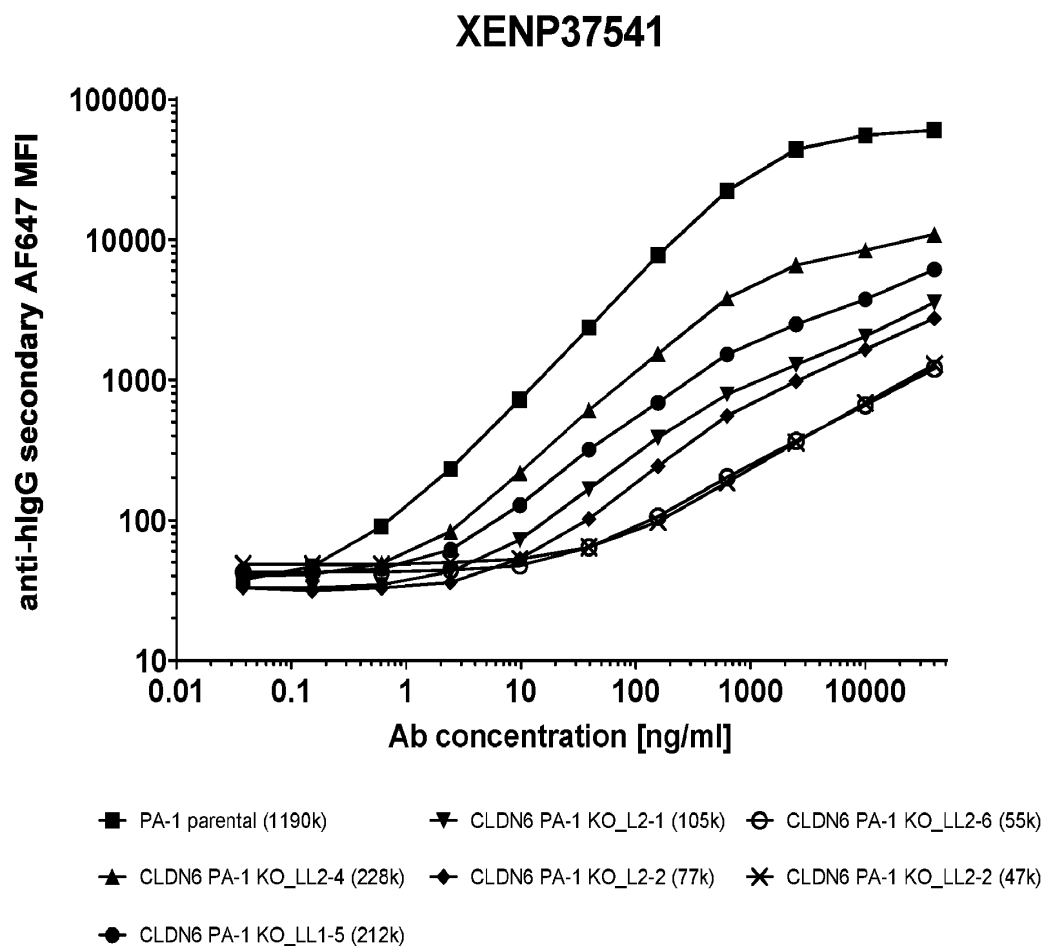
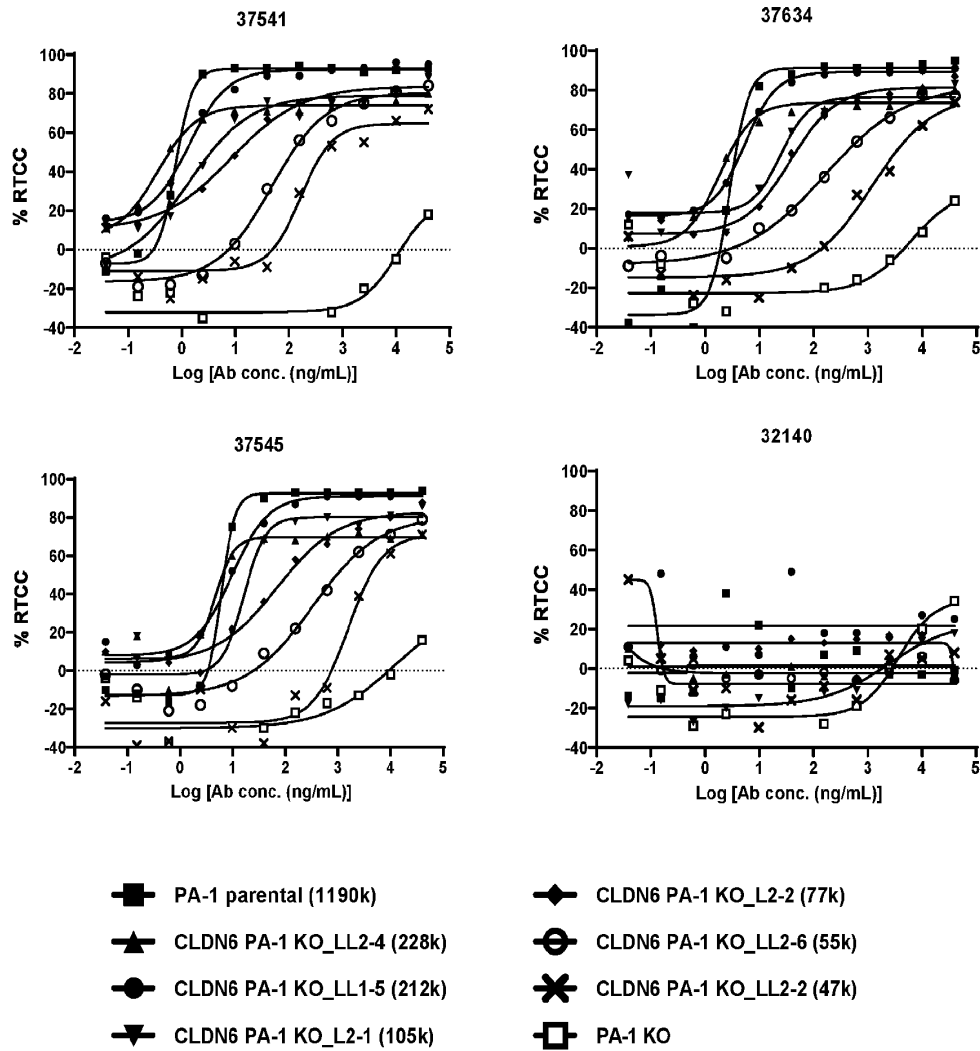


Figure 55



EC50	Parental (1190K)	LL2-4 (228K)	LL1-5 (212K)	L2-1 (105K)	L2-2 (77K)	LL2-6 (55K)	LL2-2 (47K)
<u>XENP37541</u>	0.76 ng/mL	0.35 ng/mL	1.3 ng/mL	1.4 ng/mL	8.3 ng/mL	47 ng/mL	170 ng/mL
<u>XENP37634</u>	2.8 ng/mL	1.8 ng/mL	5.3 ng/mL	24 ng/mL	37 ng/mL	160 ng/mL	1200 ng/mL
<u>XENP37545</u>	6.1 ng/mL	4.6 ng/mL	10 ng/mL	16 ng/mL	70 ng/mL	340 ng/mL	1600 ng/mL

Figure 56B

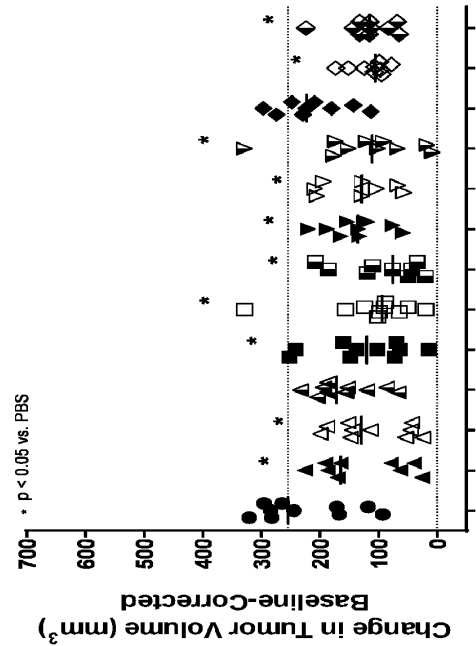


Figure 56A

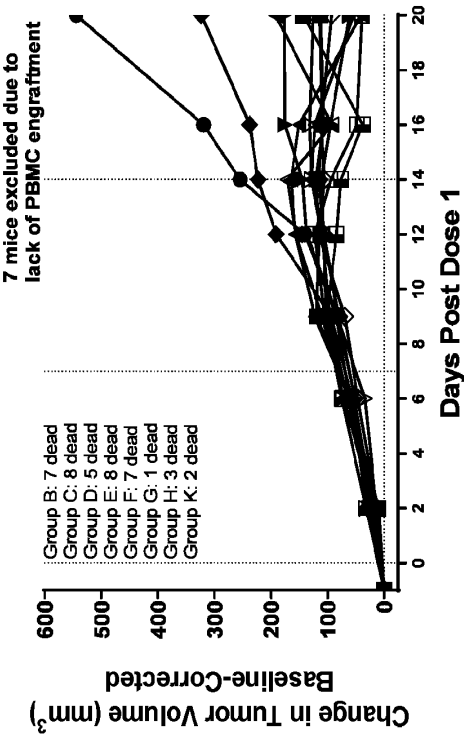


Figure 56C

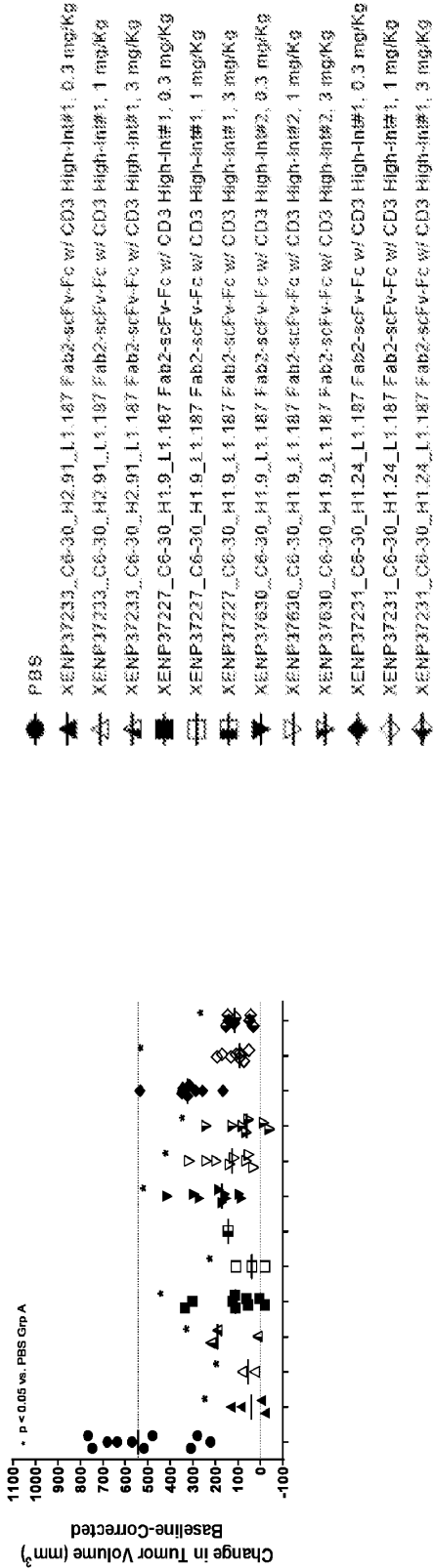


Figure 57A

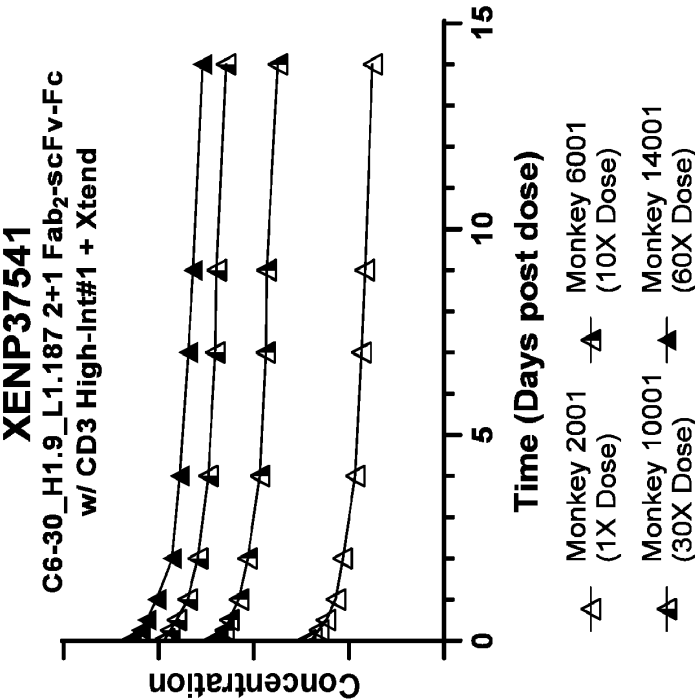


Figure 57B

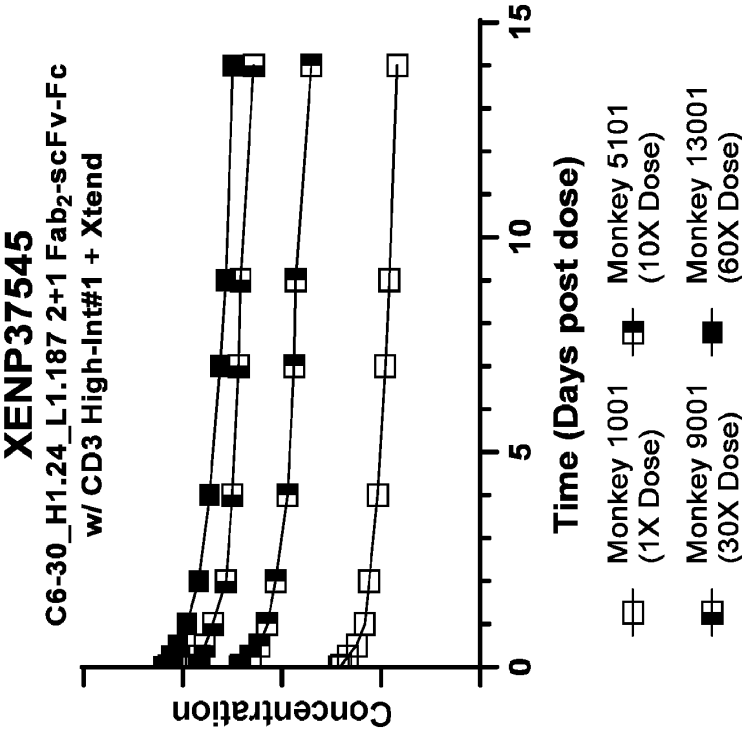


Figure 57C

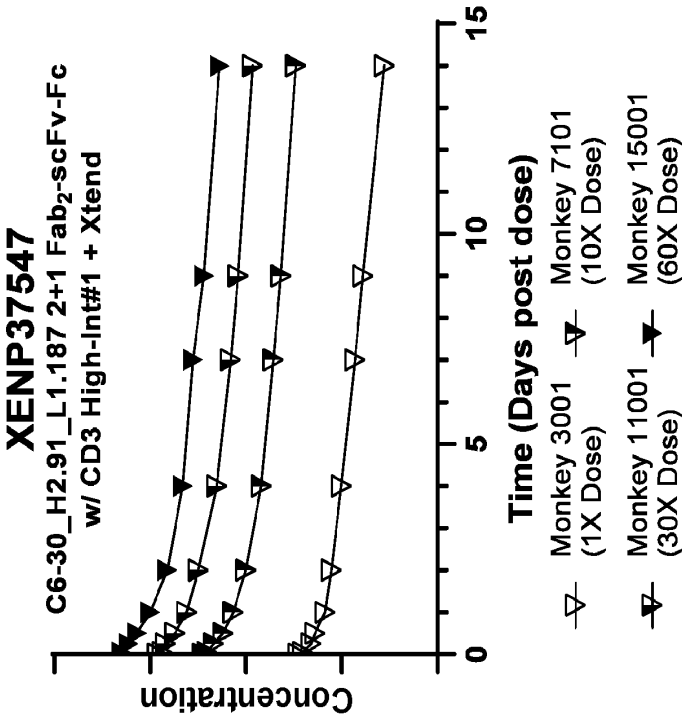


Figure 57D

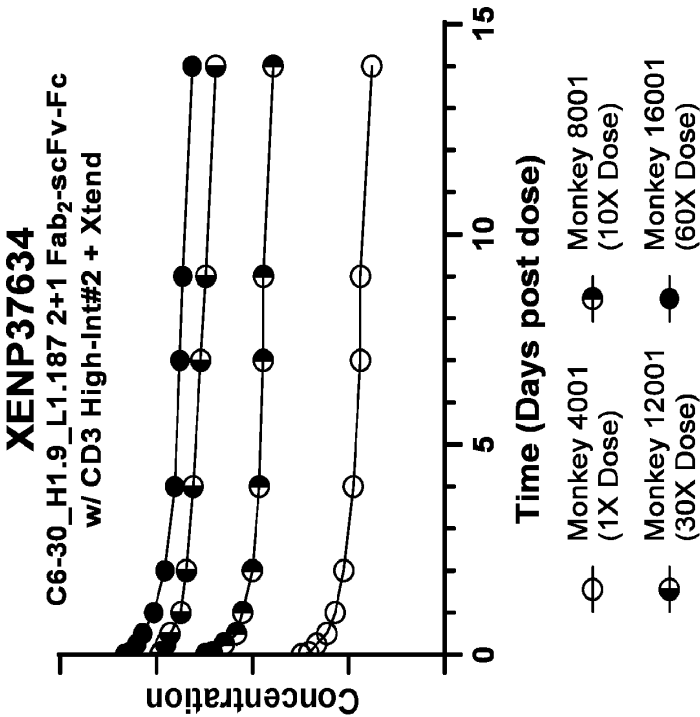


Figure 58

Blood concentration over time following high 60X dose

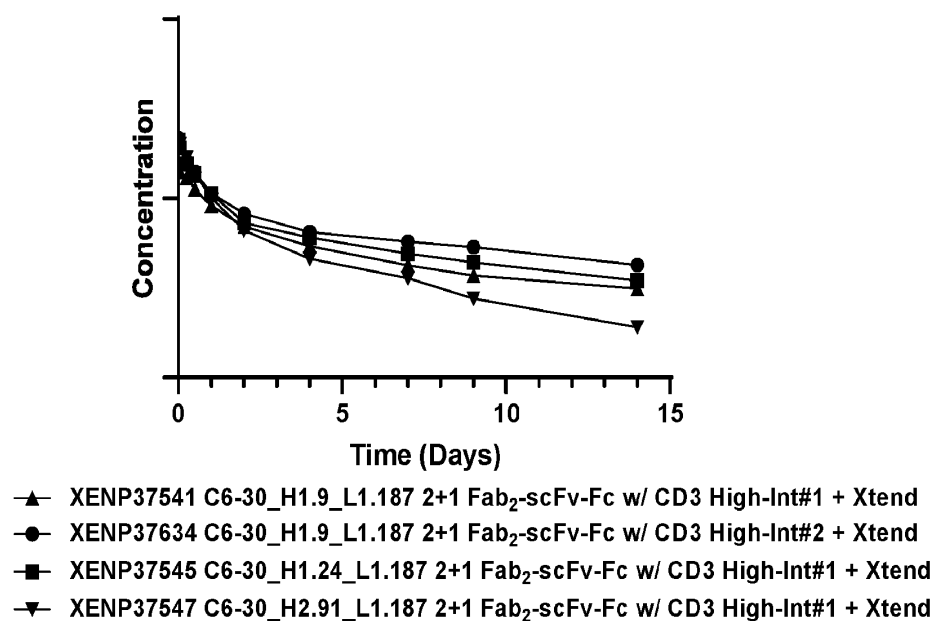


Figure 59A

>XENP37630 C6-30[CLDN6] H1.9 L1.187 Fab-C6-30[CLDN6] H1.9 L1.187 Fab (G4S)2 [anti-CD3] L1.47 H1.89 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S - Fc(222) IgG1 PVA /S267K/S364K/E357Q

Chain 1 - C6-30[CLDN6]_H1.9_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNANTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:
570)

Chain 2 - C6-30[CLDN6]_H1.9_(G4S)2_[anti-

CD3]_L1.47_H1.89_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNANTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLR
LSCAASGFTFTSYAMNWVRQAPGKGLEWVGRIIRGKYNFYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDEYVSWFAIWGQGLTVTVSS/ GGGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD
KSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 571)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETFGVPSRFSGSGSGKDYFTTIS
LQPEDIAITYYCQQYWSAPLTFGGGKTVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
572)

>XENP37634 C6-30[CLDN6] H1.9 L1.187 Fab-C6-30[CLDN6] H1.9 L1.187 Fab (G4S)2 [anti-CD3] L1.47 H1.89 scFv(GKPGS)4 (G4S)2-IgG1 pl(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S- Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

Chain 1 - C6-30[CLDN6]_H1.9_IgG1_pl(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLLEWMGGIDFNNANTHYNQKFKQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDFWGAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVLHEALHSHYTQKSLSLSPGK (SEQ ID NO:
573)

Figure 59B

Chain 2 - C6-30[CLDN6]_H1.9_(G4S)2_[anti-**CD3]_L1.47_H1.89_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S**

QVQLVQSGAEVKKPGASVKVSCKTSGYTFTEYTMHWVRQAPGQSLWMGGIDPNNANTHYNQKRFQGRVTITVDKSAS
TAYMELSSLRSEDTAVYYCARIYYFGRLYFDEFWAGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGG/QAVVTQEPSTLVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKA
ALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGLSLR
LSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVY
YCVRHGNEFGDEYVSWEAYWGQGLTVTVSS/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSQSVLHEALHSHYDTQKSLSLSPGK (SEQ ID NO: 574)

Chain 3 - C6-30[CLDN6]_L1.187_Light Chain

DIQMTQSPSSLSASVGDRVTITCQASEDIYNRLAWYQQKPGKVPKLLISGATSLETGVPSRFSGSGSGKDYFTTIS
LQPEDIAITYYCQQYWSAPLFFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
575)

Figure 60A

>XENP37217 Comp_CH02[CLDN6]_H0L0_Fab-

Comp_CH02[CLDN6]_H0L0_Fab_(G4S)2_SP34_L1.47_H1.32_scFv(GKPGS)4_(G4S)2-igG1_pi(-

)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_igG1_PVA_/S267K/S364K/E357Q

Chain 1- Comp_CH02[CLDN6]_H0_Fab_(G4S)2_SP34_L1.47_H1.32_scFv(GKPGS)4_(G4S)2 -

Fc(222)_igG1_PVA_/S267K/S364K/E357Q

EVQVEQSGLELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGNTPYINQKFKDKATLTVDKSSR
TAYMELHTLTSEDSAVYYCARCGDYDLFFFAFYWGQGLTVTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GGGGS
GGGGS/QAVVTQEPISLTIVSPGGTVTLTCGSSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKPAPGVPARFSGSLLGG
KAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/ EVQLVESGGGLVQPGGS
LRLSCAASGFTFTSYAMNWVRQAPGKGLVWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTA
VYYCVRHGNGFSDSYVSWFAYWGQGLTVTVSS/ GGGSGGGGS/KTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRT
PEVTCVVDVVRHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSQSVMSHEALHNHYTQKSLSLSPGK (SEQ ID NO: 576)

Chain 2- Comp_CH02[CLDN6]_H0_Fab-igG1_pi(-)_Isosteric_A_PVA_/S267K/L368D/K370S

EVQVEQSGLELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGNTRYINQKFKDKATLTVDKSSR
TAYMELHTLTSEDSAVYYCARCGDYDLFFFAFYWGQGLTVTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVVRHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGSQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQSVMSHEALHNHYTQKSLSLSPGK (SEQ ID
NO: 577)

Chain 3- Comp_CH02[CLDN6]_L0_Light Chain

DIVMTQFQKFMSTSVGDRVSVTKASQNVGTNVAVYQKPGQSPEALISSASSRFSGVDPDRFTGSGSGTDFTLTITN
VQSEDLADYFCQQYNSFFFTFGSGTELEIK/RTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKKVYACEVTHQGLSSPVTKSENRGEC (SEQ ID NO:
578)

>XENP38084 Comp_CH02[CLDN6]_H0_L0

Chain 1- Comp_CH02[CLDN6]_H0_Heavy Chain

EVQVEQSGLELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGNTPYINQKFKDKATLTVDKSSR
TAYMELHTLTSEDSAVYYCARCGDYDLFFFAFYWGQGLTVTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPELRGCPKVFLLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPYLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMSHEALHNHYTQESLSLSP (SEQ ID NO:
579)

Figure 60B

Chain 2- Comp_CH02[CLDN6]_H0_L0

DIVMTQFQKFMSTSVGDRVSVTCKASQNVGTNVAVYQQKPGQSPREALISSASSRFSGVDPDRFTGSGSGTDFTLTITN
VQSEDLADYFCQQVNSFPFTFGSGTELEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSITLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:
580)

Figure 61A

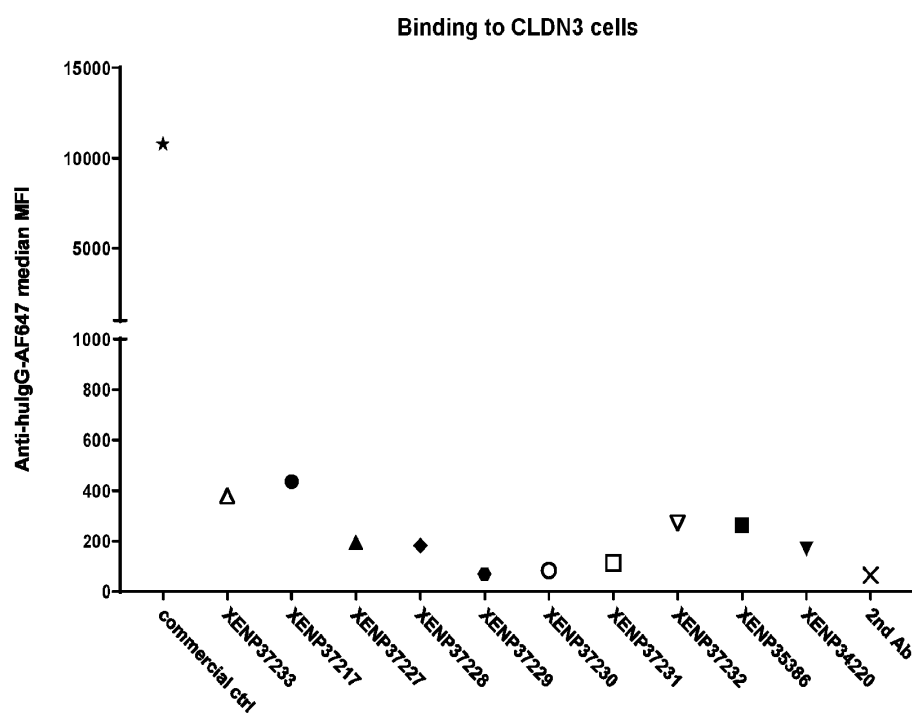


Figure 61B

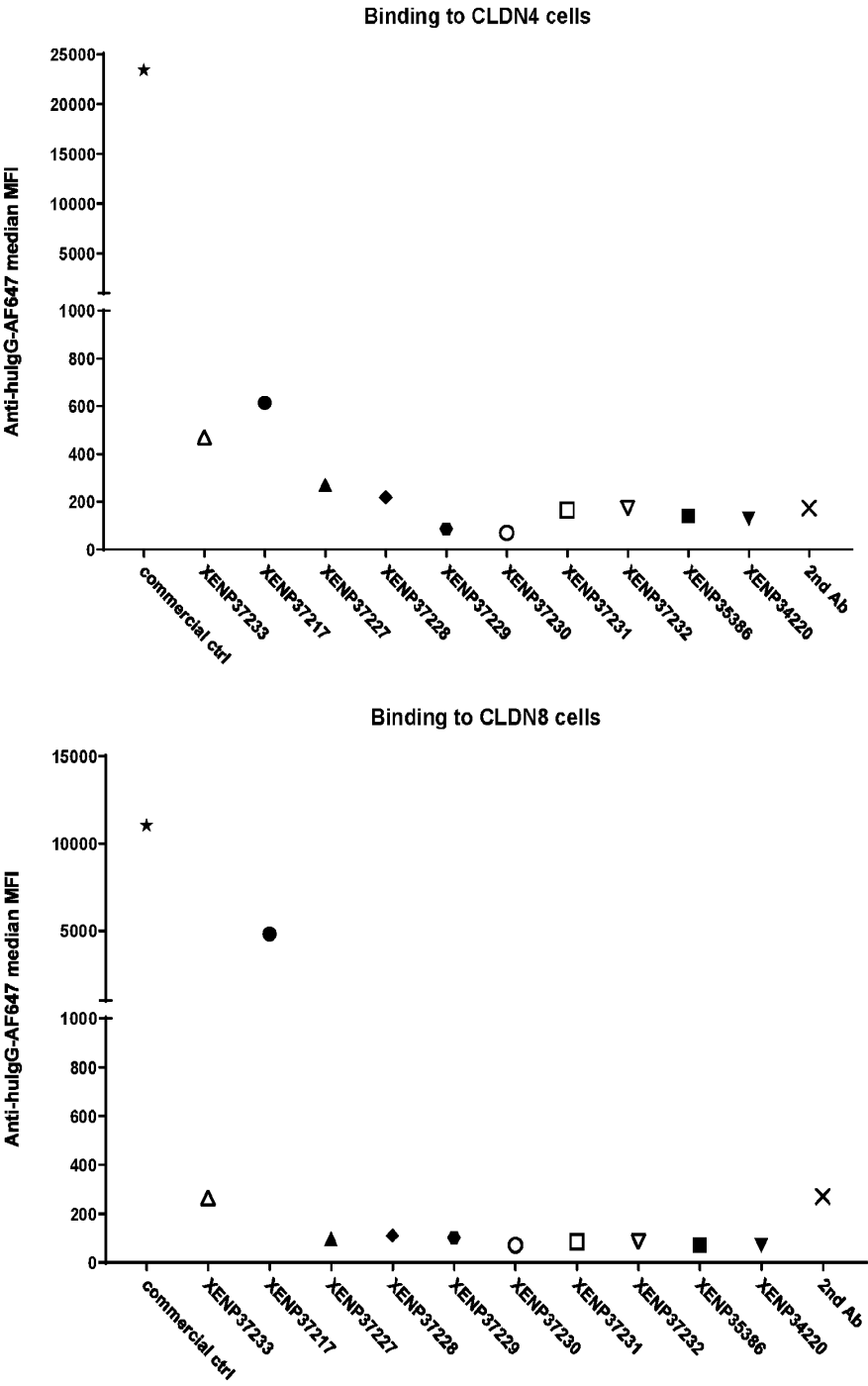


Figure 61C

