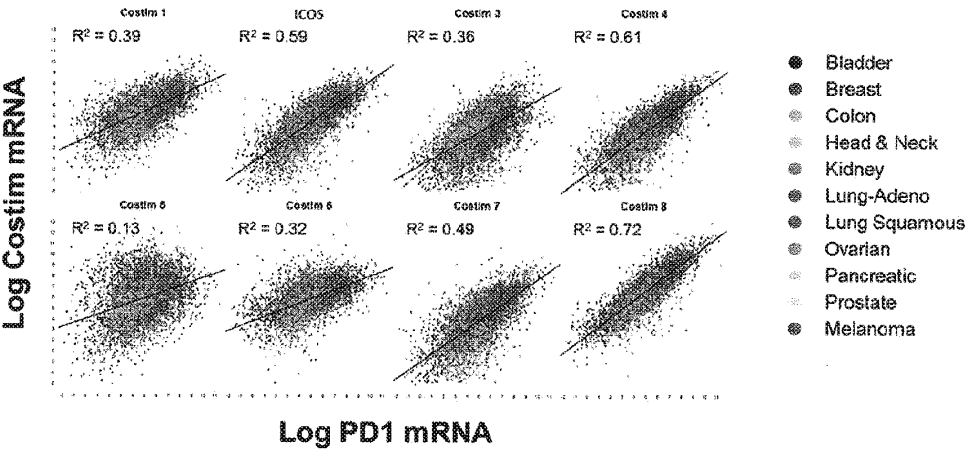
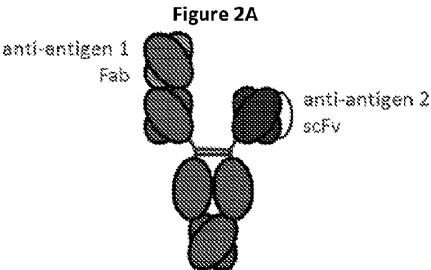
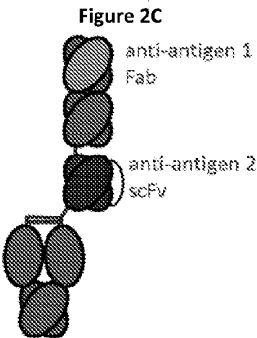


Figure 1





Bottle-opener



One-arm central-scFv

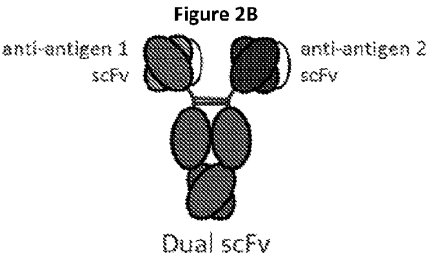
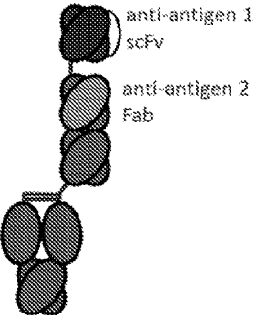
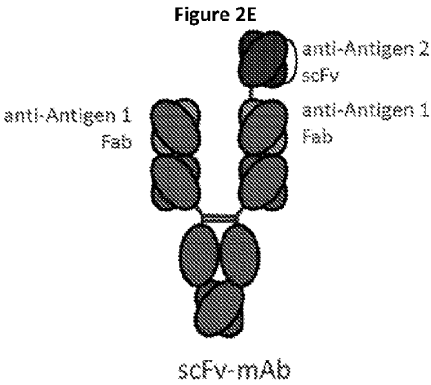
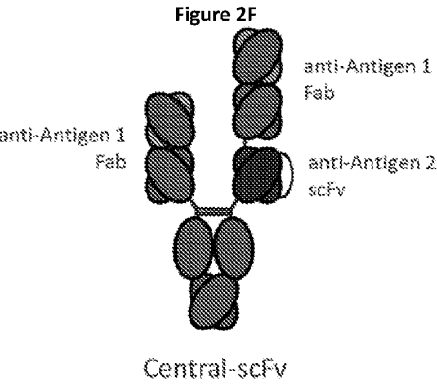
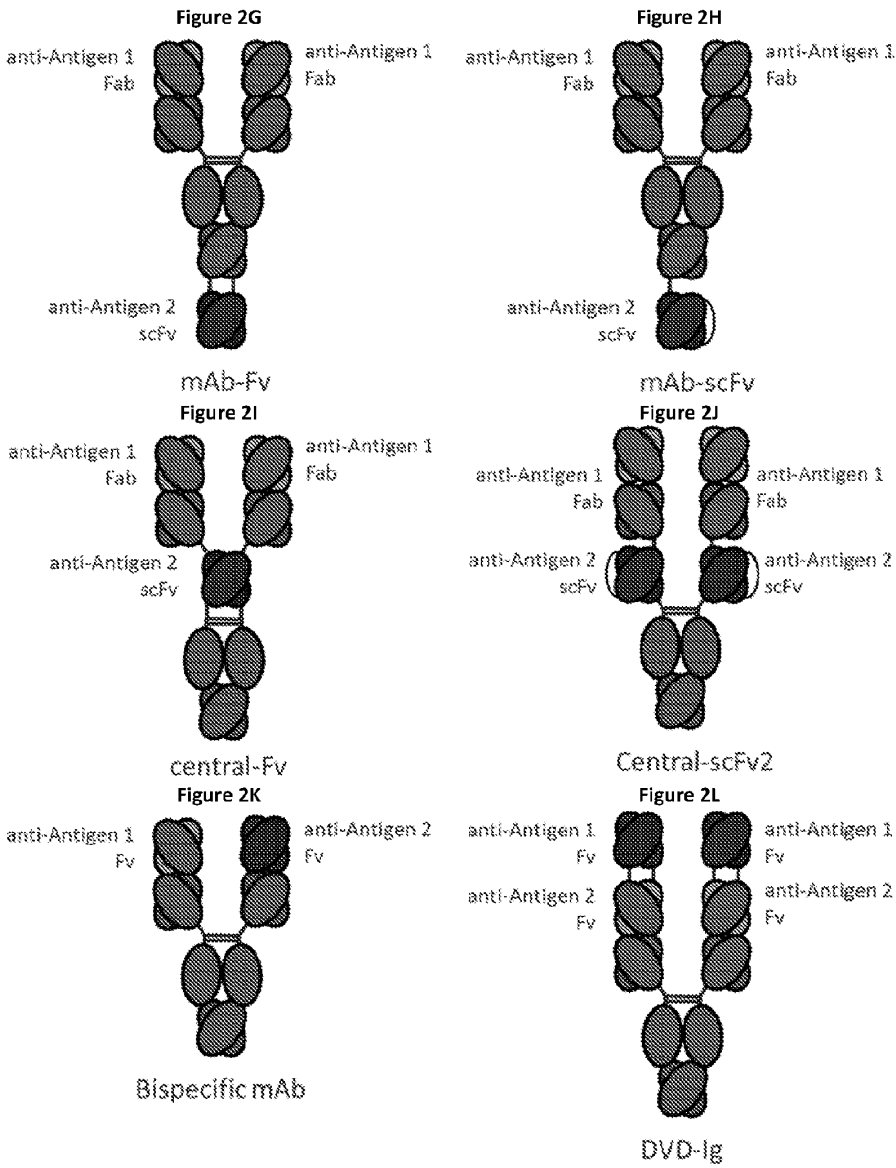


Figure 2D



One-arm scFv-mAb





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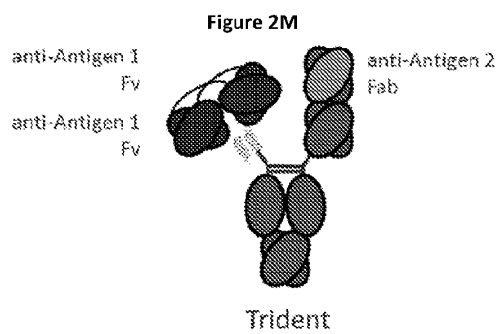
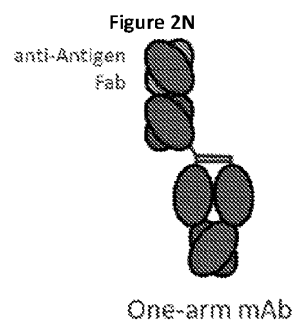


Figure 3A

>XENP023104 [ICOS]_H0.66_10_Fab-1G6_L1.194_H1.279

What	sequence	SEQ ID NO:
VH domain (Fab side)	QVQLVQSGAEVKKPGASVKVSCKASGYTF GY YMHWRAPGGQGLEWVGW INPHSGETIYAQKFG GRVTMTR DTSISTAYMELSSLRSEDTAVYVCARTYY DTSGYYHDAEDV WGQGTMTVTVSS	26643
vHCDR1 (Fab side)	<u>GYMH</u>	26644
vHCDR2 (Fab side)	<u>WINPHSGETIYAQKFG</u>	26645
vHCDR3 (Fab side)	<u>TYYDTSGYYHDAEDV</u>	26646
VL domain (Fab side)	DIQMTQSPSSVSASVGDRTITCRASQGISRLA WYQ QKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTFTLTISLQ PEDFATYYCQ QANSEFWTF GGTKVEIK	26658
vLCDR1 (Fab side)	<u>RASQGISRLA</u>	26659
vLCDR2 (fab side)	<u>VASSLSQ</u>	26660
vLCDR3 (Fab side)	<u>QANSEFPWT</u>	26661
Full length Fab HC	QVQLVQSGAEVKKPGASVKVSCKASGYTF GY YMHWRAPGGQGLEWVGW INPHSGETIYAQKFG GRVTMTR DTSISTAYMELSSLRSEDTAVYVCARTYY DTSGYYHDAEDV WGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSLSGTQTYICNVNHKPSDTKVDDKVEPKS CDKTHCTCPPCAPPAVAGPSVFLPPPKDITLMISRTPEVTCVVDVKHEDPEVKFNWVVDGVEVHNAKTKPREEY NSTYRWSVLTIVLHQDWLNGKEYCKCKVSNKALPAPIEKTKSAKAGQPREPQVYTLPPSREEMTKNQVSLTCDVS SGFYP SDIAVEWESDGGQPNNTTPPVLDSDGSFFLYSKLTVDKSRWEEQGVDFSCVIEALHSHTYQKSLSPGK	26642
Full length Fab LC	DIQMTQSPSSVSASVGDRTITCRASQGISRLA WYQ QKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTFTLTISLQ PEDFATYYCQ QANSEFWTF GGTKVEIK/RTVAAPSFIFFPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSSTYSLSLTILSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	26657

Figure 3B

What	sequence	SEQ ID NO:
VH domain (scFv side)	EIVLTQSPATLSASPGERVTLTCSRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISV QSEDFGVYVYCCQDFFSPRTFGGGRKVEIK	26648
vhCDR1 (scFv)	RASQSVGNDVA	26651
vhCDR2 (scFv)	YASHRYT	26652
vhCDR3 (scFv)	QQDFFSPRT	26653
VL domain (scFv side)	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWRQAPGKGLGWVAEIRLYSNINYNATHYAESVKGRFTISR DSKSTLYLQMNILKTEDTGVYCYTRYGNYGGYFDVWGRGTLTVSS	26649
vlCDR1 (scFv)	NYWMN	26654
vlCDR2 (scFv)	EIRLYSNINYNATHYAESVKG	26655
vlCDR3 (scFv)	YGNNGGYFDV	26656
scFv chain	EIVLTQSPATLSASPGERVTLTCSRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISV QSEDFGVYVYCCQDFFSPRTFGGGRKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCV FTFSNYWMNWRQAPGKGLGWVAEIRLYSNINYNATHYAESVKGRFTISRDSKSTLYLQMNILKTEDTGVYCYTRY GNYGGYFDVWGRGTLTVSS	
Full length scFv HC	EIVLTQSPATLSASPGERVTLTCSRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISV QSEDFGVYVYCCQDFFSPRTFGGGRKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCV FTFSNYWMNWRQAPGKGLGWVAEIRLYSNINYNATHYAESVKGRFTISRDSKSTLYLQMNILKTEDTGVYCYTRY GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCAPPVAGPSVFLPPKPKDTLMISRTPEVTCVWVDVKHEDPE VKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQV YTLPPSREQMTKNQV/KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNNVFS CSVLHEALHSHVYTKQSLSPGK	26647

Figure 4A

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

Figure 4B

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 4C

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 DEL447	
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 4D

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

Figure 4E

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

Figure 4F

Monomer 1	Monomer 2
T366S/L368A/Y407V/Y349C	T366W/S354C
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 DEL447	
N208D Q295E N384D Q418E N421D	
Q295E N384D Q418E N421D	
N208D Q295E Q418E N421D	
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 5

<u>Variant constant region</u>	<u>Substitutions</u>
pl_ISO(-)	I199T N203D K274Q R355Q N384S K392N V397M Q419E DEL447
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(+)	Q196K I199T 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 6
Ablation variants

Variant	Variant(s), cont.
G236R	P329K
S239G	A330L
S239K	A330S/P331S
S239Q	I332K
S239R	I332R
V266D	V266D/A327Q
S267K	V266D/P329K
S267R	S267R/A327Q
H268K	S267R/P329K
E269R	G236R/L328R
299R	E233P/L234V/L235A/G236del/S239K
299K	E233P/L234V/L235A/G236del/S267K
K322A	E233P/L234V/L235A/G236del/S239K/A327G
A327G	E233P/L234V/L235A/G236del/S267K/A327G
A327L	E233P/L234V/L235A/G236del
A327N	S239K/S267K
A327Q	S267K/P329K
L328E	
L328R	
P329A	
P329H	

Figure 7A

useful combinations

scFv monomer (+)	Fab monomer (-)
Heterodimer pl variants S364K/E357Q	Heterodimerization pl variants L368D/K370S
Optional scFv charged linker including but not limited to (GKPGS) ₄	Isosteric pl substitutions N208D/Q295E/N384D/Q418E/N421D
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn	± 428L/434S for FcRn
scFv of ABD of either ICOS or a checkpoint inhibitor	Fv/Fab of the other of ABD of either ICOS or a checkpoint inhibitor

Figure 7B

scFv monomer	Fab monomer
Heterodimer pl variants S364K/E357Q	Heterodimerization pl variants L368D/K370S
Optional scFv charged linker including, but not limited to (GKPGS) ₄	pl substitutions I199T N203D K274Q R355Q Q419E K447del
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn (optional)	± 428L/434S for FcRn (optional)
scFv of either ICOS or a checkpoint inhibitor	Fv/Fab of the other of ABD of either ICOS or a checkpoint inhibitor

Figure 8A

Positive charged scFv linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGSGGGGS	15	0	26200
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	26201
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	26202
+B	GKGGSGKGGSGKGGG	15	+3	26203
+C	GGKGGSGKGGSGGKGS	15	+3	26204
+D	GGKGGSGGKSGGGKS	15	+3	26205
+E	GKKGSGKKGSGKGKS	15	+6	26206
+F	GGGKSGGKGGSGKGGG	15	+3	26207
+G	GKPGSGKPGSGKPGS	15	+3	26208
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	26209
+I	GKKGSGKKGSGKKGSGKGKS	20	+8	26210

Negative charged scFv linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGSGGGSGGGGS	20	0	26211
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	26212
-B	GEGSGEGSGEGGS	15	-3	26213
-C	GGEGSGEGSGEGGS	15	-3	26214
-D	GGGESGGESGGGES	15	-3	26215
-E	GEGESGEGESGEGES	15	-6	26216
-F	GGGESGGESGEGGS	15	-3	26217
-G	GEGESGEGESGEGESGEGES	20	-8	26218

Figure 8B**scFv Linkers**

GGGGSGGGSGGGGS	(SEQ ID NO:26219)
GGGGSGGGSGGGSGGGGS	(SEQ ID NO:26220)
GSTSGSGKPGSGEGSTKG	(SEQ ID NO:26221)
PRGASKSGSASQTGSAPGS	(SEQ ID NO:26222)
GTAAAGAGAAGGAAAGAAG	(SEQ ID NO:26223)
GTSGSSGSGSGSGSGGGG	(SEQ ID NO:26224)
GKPGSGKPGSGKPGSGKPGS	(SEQ ID NO:26225)

Figure 9A**Bottle opener backbone 1**

Fab side heavy chain (SEQ ID NO:)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFFAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:)

EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKENWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

constant light chain (SEQ ID NO:)

RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Bottle opener backbone 2

Fab side heavy chain (SEQ ID NO:)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFFAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKEPKSCDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:)

EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKENWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 9B**Bottle opener backbone 3**

Fab side heavy chain (SEQ ID NO:)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 4

Fab side heavy chain (SEQ ID NO:)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTENEVSLTCLVKSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLEVDKSRWEQGDVFSC
SVMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 5 (356D/358L allotype)

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:XXX)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRQMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9C**Bottle opener backbone 6**

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:XXX)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 7

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYSSYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:XXX)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYSSYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 8

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRVESKYGPCCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQ
FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEGDVFSCSVM
HEALHNHYTQKSLSLGLGK

scFv heavy chain (SEQ ID NO:XXX)

ESKYGPCCPAPAEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEQMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGLGK

Figure 9D**Bottle opener backbone 9**

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQYITCNVDHKPSDTKVDKTVKCCVECPFCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWEQGDVFSQVMH
EALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:XXX)

ERKCSVECPFCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPENQFNWYVDGVEVHNAKTKPREEQF
NSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLFPPSREQMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 10

Fab side heavy chain (SEQ ID NO:XXX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQYITCNVDHKPSDTKVDKTVKCCVECPFCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWEQGDVFSQVMH
EALHNHYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO:XXX)

ERKCSVECPFCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTFRVSVLTVVHQDNLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLFPPSREQMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGK

Figure 10A

XENP016432 Nivolumab_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGKSLRLDCKASGITFSNGMHVVRQAPGKGLEWVAWIWDGSKRYVADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCATND DDYWGQGT LVTVSS	
vhCDR1	NSGMH	
vhCDR2	VIWYDGSKRYVADSVK G	
vhCDR3	NDDY	
Full length HC	QVQLVESGGGVVQPGKSLRLDCKASGITFSNGMHVVRQAPGKGLEWVAWIWDGSKRYVADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCATND DDYWGQGT LVTVSS/ASTKGPSVFFLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDITLMISRTPEVTCVVVDV DKH EDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMH EA LHNHYTQKSLSLSPGK	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSYLA WY QQPGQAPRLIYDASNRA T GIPARFSGSGGTDFTLTISSLEPEDFAVYYCQ QSS NWPRITFGOGTKVEIK	
vlCDR1	RASQSVSYLA	
vlCDR2	DASNRA T	
vlCDR3	QSSNWPRT	
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSYLA WY QQPGQAPRLIYDASNRA T GIPARFSGSGGTDFTLTISSLEPEDFAVYYCQ QSS NWPRITFGOGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC LL NNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDS T YSLSLTLSKADYEKHKH Y ACEVTHQGLSSPVTKSFNRGEC	

Figure 10B

XENP024120 LOPD180[PD-1]_H1L1_igG1_PVA_/S267K

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRHPGKGLWIGVIYNGNTYNP SLRS RVTSVDTSKNQFSIKLSSVTAA DTAVYYCVRASDVWGGYHYFADF L WGRGTLTVSS	
vhCDR1	<u>SGAYYWS</u>	
vhCDR2	<u>YIYNGNTYNPSLRS</u>	
vhCDR3	<u>ASDVWGGYHYFADFL</u>	
Full length HC	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRHPGKGLWIGVIYNGNTYNP SLRS RVTSVDTSKNQFSIKLSSVTAA DTAVYYCVRASDVWGGYHYFADF L WGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV TCVVDVVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLT L HQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREP QVYTLPPSREEETKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSPGK	
Variable light (vl) domain	QSVLTQPPSASGTPGQRTVISC GSNS NI GSNS VN WY QQLPGTAPKLLIYGN NQRP SGVPDRFSGSKSGTSASLAISGLQSEDEADYYC AAWDDSLNGPVFGGGTKVTL	
vlCDR1	<u>SGNSNIGSNSVN</u>	
vlCDR2	<u>GNNQRPS</u>	
vlCDR3	<u>AAWDDSLNGPV</u>	
Full length light chain	QSVLTQPPSASGTPGQRTVISC GSNS NI GSNS VN WY QQLPGTAPKLLIYGN NQRP SGVPDRFSGSKSGTSASLAISGLQSEDEADYYC AAWDDSLNGPVFGGGTKVTL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPPSKQSNKY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS	

Figure 10C

XENP024121 mAb7(1.2)[PD-1]_H1L1_igG1_PVA_/5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELMKPGASVKLSCKASGYFTFTYWMHVVWQKPGQGLEWIGEDPSDSYVNVNQNFKGKATLTVDKSSSTAVIQLSSLT SEDSAVYFCARSPDYGTSLAWFDYWGQGTLVTVST	
vhCDR1	<u>TYWMH</u>	
vhCDR2	<u>EIDPSDSYVNVNQNFKG</u>	
vhCDR3	<u>SPDYGTSLAWFDY</u>	
Full length HC	QVQLQQPGTELMKPGASVKLSCKASGYFTFTYWMHVVWQKPGQGLEWIGEDPSDSYVNVNQNFKGKATLTVDKSSSTAVIQLSSLT SEDSAVYFCARSPDYGTSLAWFDYWGQGTLVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLVSLSSVTPVSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCCPCAPPVAGPSVLEPPPKKDTLMISRTPETVC VVDVVKHEDPEVKFNWYVDGVEVHNAKTPREEEYNSTYRWSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVY TLPPSREEMTKNQVSLTCDVSIGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCVMHEALHNHYT QKSLSPGK	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASESDNYGMSEFMNWFQKPGQPPKLLIHAASINQSGSGVPSRFSGSGGTDFTLTISILEPEDFAVY FCQQSKEVPYTFGGGTKEIK	
vlCDR1	<u>RASESDNYGMSEFMN</u>	
vlCDR2	<u>AASNQGS</u>	
vlCDR3	<u>QQSKEVPYT</u>	
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASESDNYGMSEFMNWFQKPGQPPKLLIHAASINQSGSGVPSRFSGSGGTDFTLTISILEPEDFAVY FCQQSKEVPYTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWKVDNALOSGNSQESVTEQDSKDSSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 10D

XENP019686 IG6_H1.279_L1.194_IGG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYWMNWRQAPGKLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNN LKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS	
vHCDR1	<u>NYWMN</u>	
vHCDR2	<u>EIRLYSNNYATHYAESVKG</u>	
vHCDR3	<u>YYGNYGGYFDV</u>	
Full length HC	EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYWMNWRQAPGKLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNN LKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKHTCTCPCPAPPVAGPSVFLFPPKDKTLMISRTPETCV VVDVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVY TLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVNMEALHNHY TOKSLISLSPGK	
Variable light (vl) domain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVVYCC <u>QDESSPRTFGGGTKVEIK</u>	
vLCDR1	<u>RASQSVGNDVA</u>	
vLCDR2	<u>YASHRYT</u>	
vLCDR3	<u>QQDESSPRT</u>	
Full length light chain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVVYCC <u>QDESSPRTFGGGTKVEIK/RTVAAPSVFHPPSDEQLKSGTASVCLINNFPYFPAKQVQWVDNALOSGNSQESVTEQDSKDYSLST</u> LTLSKADYVEKHVYACEVTHQGLSSPVTKSFNRGEC	

Figure 10E

XENP020156 2E9_H1L1_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYFTNWLGVWRQAPGGGLEWMGNFYPGSSNTYYNEKFQGRVTMTADKSISTAYMELSR LRSDDTAVYFCARHYGTNRYFDVWGAGTLTVSS	
vhCDR1	<u>NYWLG</u>	
vhCDR2	<u>NFYPGSSNTYYNEKFQG</u>	
vhCDR3	<u>HYGTNRYFDV</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYFTNWLGVWRQAPGGGLEWMGNFYPGSSNTYYNEKFQGRVTMTADKSISTAYMELSR LRSDDTAVYFCARHYGTNRYFDVWGAGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVTVTPSSSLG TQIYICNVNHPKSTKVKDKKVEPKSCDKHTCPPCAPPVAGPSVFLFPPKPDTLISRTPEVTCV VVDVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVHLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHY TQKSLSLSPGK	
Variable light (vl) domain	DIVLTQSPGTLISLSPGERATLSCRASQSVSNDAVWYQQKPGQSPRLIYYASNRYTGVDPDRFTGSGYGTDFLTISRLEPEDFAVYFCQQ <u>DYSSPYTFGGGTKEIK</u>	
vlCDR1	<u>RASQSVSNDA</u>	
vlCDR2	<u>YASNRYT</u>	
vlCDR3	<u>QQDYSSPYT</u>	
Full length light chain	DIVLTQSPGTLISLSPGERATLSCRASQSVSNDAVWYQQKPGQSPRLIYYASNRYTGVDPDRFTGSGYGTDFLTISRLEPEDFAVYFCQQ <u>DYSSPYTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFPYBREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLSLSTL</u> TLISKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 11A XENP19690 1G6_H1.279_L1.194 anti-PD-1 Fv sequences

What	sequence	SEQ ID NO:
Vh domain	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMNMWVROAPKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYIQMN NLKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS	
vhCDR1	NYMNM	
vhCDR2	EIRLYSNNYATHYAESVKG	
vhCDR3	YYGNYGGYFDV	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Vi domain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAVYQQKGEQAPRLINVASHRYTGVDPDRFTGSGYGTFTLTISVQSEDFGVY YQQDFSSPRTFGGTKVEIK	
vICDR1	RASQSVGNDVA	
vICDR2	YASHRYT	
vICDR3	QQDFSSPRT	
scFv	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMNMWVROAPKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYIQMN NLKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSASPGERVTLTCRASQ VGNDVAVYQQKGEQAPRLINVASHRYTGVDPDRFTGSGYGTFTLTISVQSEDFGVYQQDFSSPRTFGGTKVEIK /	

Figure 11B 1G6_H1.280_L1.224 anti-PD-1 Fv sequences

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLTCVASGFTFSNYMNMWVROAPKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYIQMN NLKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS	
vhCDR1	NYMNM	
vhCDR2	EIRLYSNNYATHYAESVKG	
vhCDR3	YYGNYGGYFDV	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPATLSVSPGERVTLTCRASQSVGNDVAVYQQKGEQAPRLINVASHRYTGVDPDRFTGSGYGTFTLTISVQSEDFAVY YQQDWSSPRTFGGTKVEIK	
vICDR1	RASQSVGNDVA	
vICDR2	YASHRYT	
vICDR3	QQDWSSPRT	
scFv	EVQLVESGGGLVKPGGSLRLTCVASGFTFSNYMNMWVROAPKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYIQMN NLKTEDTGYYCTRYYGNYGGYFDVWGRGTLTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPGERVTLTCRASQ VGNDVAVYQQKGEQAPRLINVASHRYTGVDPDRFTGSGYGTFTLTISVQSEDFAVYQQDWSSPRTFGGTKVEIK	

Figure 11C XENP19692 1G6_L1.194_H1.279 anti-PD-1 Fv sequences

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EIVLTQSPATLSASPCGERVTLTCPASQSVGNDVAVYQQKPGQAPRLLIIN YASHRYTGV PDRTGSGYGTFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKVEIK	
vhCDR1	RASQSVGNDVA	
vhCDR2	YASHRYT	
vhCDR3	QQDFSSPRT	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EVQLVESGGGLVKPGGSLRLSCVSGTFTSNYMNWVRQAPGKLEWVAEIRLISNNYATHYAESVKGKFTISRDDSKSTLYLQMN NLKTEDTGYICTRYTNGYGGYFDVWGRGTLTVSS	
vlCDR1	NYWMN	
vlCDR2	EIRLISNNYATHYAESVKG	
vlCDR3	YNGYGGYFDV	
scFv	EIVLTQSPATLSASPCGERVTLTCPASQSVGNDVAVYQQKPGQAPRLLIIN YASHRYTGV PDRTGSGYGTFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKVEIK/GKPGSGKPGSGKPGSG/EEVQLVESGGGLVKPGGSLRLSCVSGTFTSNYMNWVRQAPGK CLEWVAEIRLISNNYATHYAESVKGKFTISRDDSKSTLYLQMN NLKTEDTGYICTRYTNGYGGYFDVWGRGTLTVSS	

Figure 11D XENP19669 1G6_L1.210_H1.288 anti-PD-1 Fv sequences

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EIVLTQSPATLSASPCGERVTLTCPASQSVGNDVAVYQQKPGQAPRLLIIN YASHRYTGV PDRTGSGYGTFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKVEIK	
vhCDR1	RASQSVGNDVA	
vhCDR2	YASHRYT	
vhCDR3	QQDFSSPRT	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EVQLVESGGGLVKPGGSLRLSCVSGTFTSNYMNWVRQAPGKLEWVAEIRLISNNYATHYAESVKGKFTISRDDSKSTLYLQMN NLKTEDTGYICTRYTNGYGGYFDVWGRGTLTVSS	
vlCDR1	NYWMN	
vlCDR2	EIRLISNNYATHYAESVKG	
vlCDR3	YNGYGGYFDV	
scFv	EIVLTQSPATLSASPCGERVTLTCPASQSVGNDVAVYQQKPGQAPRLLIIN YASHRYTGV PDRTGSGYGTFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKVEIK/GKPGSGKPGSGKPGSG/EEVQLVESGGGLVKPGGSLRLSCVSGTFTSNYMNWVRQAPGK CLEWVAEIRLISNNYATHYAESVKGKFTISRDDSKSTLYLQMN NLKTEDTGYICTRYTNGYGGYFDVWGRGTLTVSS	

Figure 11E XENP20162 2E9_H1L1 anti-PD-1 Fv sequences

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHWLGWVRQAPGQGLEWMGNFYPGSSNTYYNEKFGGRVTMTADKSI STAYMELSLRLSDDTAVYFCARHYGTNRYFDVWGAGTLTVSS	
vhCDR1	<u>NWLG</u>	
vhCDR2	<u>NYPGSSNTYYNEKFG</u>	
vhCDR3	<u>HYGTNRYFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DI VLTQSPGTLSLSPGERATLSCRASQSVSNDAWYQQKPGQSPRLLIYYASNRYTGVPDFRTGSGYGDFTLTIS RLEPEDFAVYFCQDYSSPYTFGGTKVEIK	
vlCDR1	<u>PASQSVSNDVA</u>	
vlCDR2	<u>YASNRYT</u>	
vlCDR3	<u>QQDYSSPYT</u>	
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYAFTNHWLGWVRQAPGQGLEWMGNFYPGSSNTYYNEKFGGRVTMTADKSI STAYMELSLRLSDDTAVYFCARHYGTNRYFDVWGAGTLTVSS/GKPGSGKPGSGKPGSGKPGS/DIVLTQSPGT LSLSPGERATLSCRASQSVSNDAWYQQKPGQSPRLLIYYASNRYTGVPDFRTGSGYGDFTLTISRLEPEDFAVY FCQDYSSPYTFGGTKVEIK	

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Figure 12A [CTLA-4]_H0.25_10 Anti-CTLA-4 Fv sequences (XENP19235 Fab, XENP19769 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QYQLVESGGGVQPGRSRLSLSCAASGFTFSYAMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNKNTLYLQMNSLRADDTAIYYCARTGWLGPFDYWGQGTLLTVSS	
vhCDR1	<u>SYAMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASOSVGSYYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSFPWTGQGTKEIK	
viCDR1	<u>RASQSVGSYYLA</u>	
viCDR2	<u>GAFSRAT</u>	
viCDR3	<u>QYGSFPWT</u>	
scFv	QYQLVESGGGVQPGRSRLSLSCAASGFTFSYAMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNKNTLYLQMNSLRADDTAIYYCARTGWLGPFDYWGQGTLLTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSLSPGERATLSCRASOSVGSYYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSFPWTGQGTKEIK /	

Figure 12B [CTLA-4]_H0.26_10 Anti-CTLA-4 Fv sequences (XENP19236 Fab, XENP19770 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QYQLVESGGGVQPGRSRLSLSCAASGFTFSYGMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNKNTLYLQMNSLRADDTAIYYCARTGWLGPFDYWGQGTLLTVSS	
vhCDR1	<u>SYGMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASOSVGSYYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSFPWTGQGTKEIK	
viCDR1	<u>RASQSVGSYYLA</u>	
viCDR2	<u>GAFSRAT</u>	
viCDR3	<u>QYGSFPWT</u>	
scFv	QYQLVESGGGVQPGRSRLSLSCAASGFTFSYGMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNKNTLYLQMNSLRADDTAIYYCARTGWLGPFDYWGQGTLLTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSLSPGERATLSCRASOSVGSYYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGSFPWTGQGTKEIK	

Figure 12C [CTLA-4]_H0.27_10 Anti-CTLA-4 Fv sequences (XENP19237 Fab, XENP19771 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSIRLSCAASGFTFSSYMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYCAETGWLGFDFYWGQGTLLTVSS	
vhCDR1	<u>YSMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	EIVLTQSPGTLISLGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISR LEPEDFAVYCCQYGSSPWTFGQGTKVEIK	
viCDR1	<u>RASQSVGSSYLA</u>	
viCDR2	<u>GAFSRAT</u>	
viCDR3	<u>QQYGSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSIRLSCAASGFTFSSYMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYCAETGWLGFDFYWGQGTLLTVSS / GKPGSGKPGSGKPGSG / EIVLTQSPGTLISLPG ERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGS SPWTFGQGTKVEIK	

Figure 12D [CTLA-4]_H0.29_10 Fab XENP19773, scFv XENP19239

What	sequence	SEQ ID NO:
Variable heavy (vh) domain		
vhCDR1		
vhCDR2		
vhCDR3		
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain		
viCDR1		
viCDR2		
viCDR3		
scFv	QVQLVESGGGVVQPGRSIRLSCAASGFTFSSYMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYCAETGWLGFDFYWGQGTLLTVSS / GKPGSGKPGSGKPGSG / EIVLTQSPGTLISLPG ERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYCCQYGS SPWTFGQGTKVEIK	

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Figure 12E [CTLA-4]_H0.38_L0 (Fab XENP19248, scFv XENP19782)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKKYADSVKGRFTISRDN SKNTL YLOMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYADSVRG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLISRL EPEDFAVYYCQQYGSSPWTFGQGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GAFSRAT</u>	
vlCDR3	<u>QQYGSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKKYADSVKGRFTISRDN SKNTL YLOMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLISLSPGER ATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLISRLLEPEDFAVYYCQQYGSSPW TFGQGTKVEIK /	

Figure 12F [CTLA-4]_H0.39_L0 (Fab XENP19249, scFv XENP19783)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKKYADSVKGRFTISRDN SKNTL YLOMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYADSVRG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLISRL EPEDFAVYYCQQYGSSPWTFGQGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GAFSRAT</u>	
vlCDR3	<u>QQYGSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKKYADSVKGRFTISRDN SKNTL YLOMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLISLSPGER ATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLISRLLEPEDFAVYYCQQYGSSPW TFGQGTKVEIK	

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Figure 12G [CTLA-4]_H0.40_L0 (Fab XENP19250, scFv XENP19784)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVVFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYYADSVK</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEFAVYYCQYGSSPWTFGQGTKVEIK	
viCDR1	<u>RASQSVGSSYLA</u>	
viCDR2	<u>GAFSRAT</u>	
viCDR3	<u>QQYGSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVVFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS / <u>GKPGSGKPGSGKPGSGKPGS</u> / EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEFAVYYCQYGSSPWTFGQGTKVEIK	

Figure 12H [CTLA-4]_H0.70_L0 (Fab XENP19280, scFv XENP19818)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVVFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYYADSVK</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEFAVYYCQYGSSPWTFGQGTKVEIK	
viCDR1	<u>RASQSVGSSYLA</u>	
viCDR2	<u>GAFSRAT</u>	
viCDR3	<u>QQYGSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVVFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS / <u>GKPGSGKPGSGKPGSGKPGS</u> / EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEFAVYYCQYGSSPWTFGQGTKVEIK	

Figure 12I [CTLA-4]_H0_L0.22 (Fab XENP19437, scFv XENP19910)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPWTFGQGTKEIK	
vICDR1	<u>RASQSVSSSYLA</u>	
vICDR2	<u>GAFSRAT</u>	
vICDR3	<u>QYQYSSPWT</u>	
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYIGSSEWTFGQGTKEIK	

Figure 12J [CTLA-4]_H2_L0 (Fab XENP_19545 scFv XENP19552)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYFGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCARTGWLGPFDYWGQGTLLTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYFGSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPWTFGQGTKEIK	
vICDR1	<u>RASQSVGSSSYLA</u>	
vICDR2	<u>GAFSRAT</u>	
vICDR3	<u>QYQYSSPWT</u>	
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYFGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCARTGWLGPFDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYIGSSEWTFGQGTKEIK	

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKGPGSIRLSCAASGFTFSYTMHWVQAQPGKGLEWVSFISYGNNTKYYADSVKGRFTISRDNAKNS LYLQMNLSLRADETAVYYCARGELLGPFDLWGQGTMTVSS	
vhCDR1	SYTMH	
vhCDR2	<u>FISYDGN</u> TKYYADSVKG	
vhCDR3	<u>GGLLG</u> PFDL	
scFv linker	<u>GKPGSGKSGKSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATISCRASQSGSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISR LEPDSFVYYCQIQGSSPWTFGQGTKVELK	
vlCDR1	<u>RASQSGSSYLA</u>	
vlCDR2	<u>GASSRAI</u>	
vlCDR3	<u>QQYGSSPWT</u>	
scFv	EVQLVESGGGLVKGPGSIRLSCAASGFTFSYTMHWVQAQPGKGLEWVSFISYGNNTKYYADSVKGRFTISRDNAKNS LYLQMNLSLRADETAVYYCARGELLGPFDLWGQGTMTVSS / GKPGSGKSGKSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSGSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISRLEPDSFVYYCQIQGS SPWTFGQGTKVELK	

Figure 12L [CTLA-4] H3.21 L0.129 (Fab XENP20423, scFv XENP20432)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLV ¹ PKPGGSLRLSCAASGFT ² SSYTHHWVRQAPGKGLEWVSFISYDGN ³ TKYYADSVKGRFTISRDNAKNSLYLQMNSLR ⁴ RAEDTAVYYCARGELLG ⁵ FDLWGQG ⁶ TMTV ⁷ TS	
vhCDR1	SYTMH	
vhCDR2	FISYDGN ³ TKYYADSVK ⁴ G	
vhCDR3	GLLGPF ⁵ DL	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	EIVLTQSPATLSL ¹ SPGERATLSCRASQSVSSYLA ² WYQKPGQAPRLLIY ³ GASSRATGIPDRFSGSGSGTDFTLTISRLEP ⁴ DFAVYYCQ ⁵ QYGS ⁶ SPWT ⁷ FGQTKV ⁸ EIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QOYGS ⁶ SPWT	
scFv	EVQLVESGGGLV ¹ PKPGGSLRLSCAASGFT ² SSYTHHWVRQAPGKGLEWVSFISYDGN ³ TKYYADSVKGRFTISRDNAKNSLYLQMNSLR ⁴ RAEDTAVYYCARGELLG ⁵ FDLWGQG ⁶ TMTV ⁷ TS / GKPGSGKPGSGKPGSG / EIVLTQSPATLSLSPGERATLSRASQSVSSYLA ² WYQKPGQAPRLLIY ³ GASSRATGIPDRFSGSGSGTDFTLTISRLEP ⁴ DFAVYYCQ ⁵ QYGS ⁶ SPWT ⁷ FGQTKV ⁸ EIK	

Figure 12M [CTLA-4]_H3.21_10.132 (Fab XENP20424, scFv XENP20433)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYTMHWVRQAPGKGLEWVSFISYDGNKYADSVKGRFTISRDNAKNS LYLQMNLSRAEDTAVYICARGGHLGPFDLWGQGTMTVTVSS	
vHCDR1	<u>SYTMH</u>	
vHCDR2	<u>FISYDGNKYADSVK</u>	
vHCDR3	<u>GGLGPFDL</u>	
scFv linker	<u>GGPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYICQYGGSSPWTFGQGTKEIK	
vLCDR1	<u>RASQSVSSYLA</u>	
vLCDR2	<u>GASSRAT</u>	
vLCDR3	<u>QQYGGSSPWT</u>	
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYTMHWVRQAPGKGLEWVSFISYDGNKYADSVKGRFTISRDNAKNS LYLQMNLSRAEDTAVYICARGGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPG EATLSCRASQSVSSYLAWYQQRPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYICQYGGSS SPWTFGQGTKEIK	

Figure 12N [CTLA-4]_H3.23_10.124 (Fab XENP20425, scFv XENP20434)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYTMHWVRQAPGKGLEWVSFISYDGNKYADSVKGRFTISRDNAKNS LYLQMNLSRAEDTAVYICARGGHLGPFDLWGQGTMTVTVSS	
vHCDR1	<u>SYTMH</u>	
vHCDR2	<u>FISYDGNKYADSVK</u>	
vHCDR3	<u>GGLGPFDL</u>	
scFv linker	<u>GGPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYICQYGGSSPWTFGQGTKEIK	
vLCDR1	<u>RASQSVSSYLA</u>	
vLCDR2	<u>GASSRAT</u>	
vLCDR3	<u>QQYGGSSPWT</u>	
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYTMHWVRQAPGKGLEWVSFISYDGNKYADSVKGRFTISRDNAKNS LYLQMNLSRAEDTAVYICARGGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSVSPG ERATLSCRASQSVSSYLAWYQQRPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYICQYGGSS SPWTFGQGTKEIK	

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Figure 120 [CTLA-4]_H3.23_10.129 (Fab XENP20426, scFv XENP20435)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYFCARGGHLGFDLWGQGTMTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYKYADSVKGR</u>	
vhCDR3	<u>GGHLGFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYYCQYGSSPWTFGQGTKEIK	
vlCDR1	<u>RASQSVSSSYLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QYGSSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYFCARGGHLGFDLWGQGTMTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPATLSLSPG ERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGS SPWTFGQGTKEIK	

Figure 12P [CTLA-4]_H3.23_L0.132 (Fab XENP20427, scFv XENP20436)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYFCARGGHLGFDLWGQGTMTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYKYADSVKGR</u>	
vhCDR3	<u>GGHLGFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYYCQYGSSPWTFGQGTKEIK	
vlCDR1	<u>RASQSVSSSYLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QYGSSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYFCARGGHLGFDLWGQGTMTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPATLSLSPG ERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGS SPWTFGQGTKEIK	

Figure 12Q [CTLA-4] H3.25 LO.124 (Fab XENP20428, scFv XENP20437)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFTSYDGNKYKYADSVKGRFTISRDNAKNS LYIQMNSLRAEDTAVYVCARGGILLGPFDLWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYKYADSVK</u> G	
vhCDR3	<u>GGLLGPFDL</u>	
scFv linker	<u>GRPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVGSSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYCCQYGGSPWTFGQGTKVEIK	
viCDR1	<u>RASQSVGSSYLA</u>	
viCDR2	<u>GASSRAT</u>	
viCDR3	<u>QYGGSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFTSYDGNKYKYADSVKGRFTISRDNAKNS LYIQMNSLRAEDTAVYVCARGGILLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGG SPWTFGQGTKVEIK	

Figure 12R [CTLA-4] H3.25 LO.129 (Fab XENP20429, scFv XENP20438)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFTSYDGNKYKYADSVKGRFTISRDNAKNS LYIQMNSLRAEDTAVYVCARGGILLGPFDLWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKYKYADSVK</u> G	
vhCDR3	<u>GGLLGPFDL</u>	
scFv linker	<u>GRPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVGSSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISR LEPEDFAVYCCQYGGSPWTFGQGTKVEIK	
viCDR1	<u>RASQSVGSSYLA</u>	
viCDR2	<u>GASSRAT</u>	
viCDR3	<u>QYGGSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFTSYDGNKYKYADSVKGRFTISRDNAKNS LYIQMNSLRAEDTAVYVCARGGILLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQYGG SPWTFGQGTKVEIK	

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Figure 125 [CTLA-4] H3.25 L0.132 (Fab XENP20430, scFv XENP20439)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLV ¹ PKGSGRL ² SLCAASGFT ³ SSYTMHWVRQAPGKGL ⁴ EWVSFISYDGN ⁵ IKYYADSVKGR ⁶ FTISRDN ⁷ AKNS LYLQMN ⁸ SLRAEDTAV ⁹ YCAR ¹⁰ GEL ¹¹ LGFDL ¹² WGQGT ¹³ MTV ¹⁴ TS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNIKYYADSVKG</u>	
vhCDR3	<u>GGLLGPFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLS ¹⁵ LPGERATL ¹⁶ SCRASQSVSS ¹⁷ YLAWYQKPGQAPRLLIYGASSRATGI ¹⁸ PDRFSGSGGT ¹⁹ DTLTISR LEPEDFAVY ²⁰ COQYGSSPWT ²¹ FGQGT ²² KVEIK	
vlCDR1	<u>RASQSVSSSYLA</u>	
vlCDR2	<u>CASSRAT</u>	
vlCDR3	<u>QOYGSSPWT</u>	
scFv	EVQLVESGGGLV ¹ PKGSGRL ² SLCAASGFT ³ SSYTMHWVRQAPGKGL ⁴ EWVSFISYDGN ⁵ IKYYADSVKGR ⁶ FTISRDN ⁷ AKNS LYLQMN ⁸ SLRAEDTAV ⁹ YCAR ¹⁰ GEL ¹¹ LGFDL ¹² WGQGT ¹³ MTV ¹⁴ TS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLS ¹⁵ LPGERATLS ¹⁶ SCRASQSVSS ¹⁷ YLAWYQKPGQAPRLLIYGASSRATGI ¹⁸ PDRFSGSGGT ¹⁹ DTLTISRLEPEDFAVY ²⁰ COQYGSSPWT ²¹ FGQGT ²² KVEIK	

Figure 12T [CTLA-4] H3.4 L0.118 (Fab XENP20341, scFv XENP20378)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLV ¹ PKGSGRL ² SLCAASGFT ³ SSYTMHWVRQAPGKGL ⁴ EWVSFISYDGN ⁵ IKYYADSVKGR ⁶ FTISRDN ⁷ AKNS LYLQMN ⁸ SLRAEDTAV ⁹ YCAR ¹⁰ TGHLG ¹¹ FDL ¹² WGQGT ¹³ MTV ¹⁴ TS	
vhCDR1	<u>SSYTMH</u>	
vhCDR2	<u>FISYDGNIKYYADSVKG</u>	
vhCDR3	<u>TGHLGPFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLS ¹⁵ VPGERATL ¹⁶ SCRASQSVGSS ¹⁷ YLAWYQKPGQAPRLLIYGAFSRATGI ¹⁸ PDRFSGSGGT ¹⁹ DTLTISR LEPEDFAVY ²⁰ COQYGSSPWT ²¹ FGQGT ²² KVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GAFSRAT</u>	
vlCDR3	<u>QOYGSSPWT</u>	
scFv	EVQLVESGGGLV ¹ PKGSGRL ² SLCAASGFT ³ SSYTMHWVRQAPGKGL ⁴ EWVSFISYDGN ⁵ IKYYADSVKGR ⁶ FTISRDN ⁷ AKNS LYLQMN ⁸ SLRAEDTAV ⁹ YCAR ¹⁰ TGHLG ¹¹ FDL ¹² WGQGT ¹³ MTV ¹⁴ TS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLS ¹⁵ VPGERATLS ¹⁶ SCRASQSVGSS ¹⁷ YLAWYQKPGQAPRLLIYGAFSRATGI ¹⁸ PDRFSGSGGT ¹⁹ DTLTISRLEPEDFAVY ²⁰ COQYGSSPWT ²¹ FGQGT ²² KVEIK	

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Figure 12U [CTLA-4] H3.4_L0.119 (Fab XENP20342, scFv XENP20379)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSPFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRILLIYGAFSRATGIPDRFSGSGGTDFTLTIISRLPEPDF AVYYCQYCGSSSEWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QYCGSSPWT	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSPFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS/GKPGSGKPGSGKPGSG/EIVLTQSPGTLISLSPGERATLSCRASQS VGSSYLAWYQOKPGQAPRILLIYGAFSRATGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYCGSSPWTFCQGTKVEIK	

Figure 12V [CTLA-4] H3.4_L0.12 (Fab XENP20071, scFv XENP20078)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSPFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRILLIYGAFSRATGIPDRFSGSGGTDFTLTIISRLPEPDF AVYYCQYCGSSSEWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QYCGSSPWT	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSPFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS/GKPGSGKPGSGKPGSG/EIVLTQSPGTLISLSPGERATLSCRASQS VGSSYLAWYQOKPGQAPRILLIYGAFSRATGIPDRFSGSGGTDFTLTIISRLPEPDFAVYYCQYCGSSPWTFCQGTKVEIK	

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Figure 12W [CTLA-4] H3.4_I0.121 (Fab XENP20344, scFv XENP20381)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVAPGQSLRLSAAAGFTTSSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQYGSSEFWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QYGSSEFWTF	
scFv	EVQLVESGGGLVAPGQSLRLSAAAGFTTSSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQS VGSSYLAWYQOKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSEFWTFGQGTKVEIK	

Figure 12X [CTLA-4] H3.4_I0.122 (Fab XENP20345, scFv XENP20382)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVAPGQSLRLSAAAGFTTSSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQYGSSEFWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QYGSSEFWTF	
scFv	EVQLVESGGGLVAPGQSLRLSAAAGFTTSSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCRASQS VGSSYLAWYQOKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYGSSEFWTFGQGTKVEIK	

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Figure 12Y [CTLA-4] H3.4_L0.123 (Fab XENP20346, scFv XENP20383)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QYGSSEWTF	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSG/EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYYCQYGSSEWTFGQGTKVEIK	

Figure 12Z [CTLA-4] H3.4_L0.124 (Fab XENP20347, scFv XENP20384)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QYGSSEWTF	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSG/EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFVAVYYCQYGSSEWTFGQGTKVEIK	

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Figure 12AA [CTLA-4] H3.4 L0.125 (Fab XENP20348, scFv XENP20385)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSAAAGFTFSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATISCRASQSVSSYLAWYQQKPGQAPRLIIYCAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QQYGSSEWTF	
scFv	EVQLVESGGGLVQPGGSLRLSAAAGFTFSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATISCRASQSVSSYLAWYQQKPGQAPRLIIYCAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSEWTFGQGTKVEIK	

Figure 12BB [CTLA-4] H3.4 L0.126 (Fab XENP20349, scFv XENP20386)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSAAAGFTFSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATISCRASQSVSSYLAWYQQKPGQAPRLIIYCAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVGSSYLA	
vlCDR2	GASRAT	
vlCDR3	QQYGSSEWTF	
scFv	EVQLVESGGGLVQPGGSLRLSAAAGFTFSYTMHWVROAPGKGLWVSVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTNVTYSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATISCRASQSVSSYLAWYQQKPGQAPRLIIYCAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSEWTFGQGTKVEIK	

Figure 12CC [CTLA-4] H3.4_I0.127 (Fab XENP20350, scFv XENP20387)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVAPGKGLSRLLSQAASGFTFSYTMHWVRQAPGKGLWVVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDE AVYYCQQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QQYGSSEWTF	
scFv	EVQLVESGGGLVAPGKGLSRLLSQAASGFTFSYTMHWVRQAPGKGLWVVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVYSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDEAVYYCQQYGSSEWTFGQGTKVEIK	

Figure 12DD [CTLA-4] H3.4_I0.128 (Fab XENP20351, scFv XENP20388)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVAPGKGLSRLLSQAASGFTFSYTMHWVRQAPGKGLWVVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVYSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGAFSRATGIPDRFSGSGGTDFLTISRLEPEDE AVYYCQQYGSSEWTFGQGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QQYGSSEWTF	
scFv	EVQLVESGGGLVAPGKGLSRLLSQAASGFTFSYTMHWVRQAPGKGLWVVFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVYSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIYGAFSRATGIPDRFSGSGGTDFLTISRLEPEDEAVYYCQQYGSSEWTFGQGTKVEIK	

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Figure 12EE [CTLA-4] H3.4_I0.129 (Fab XENP20352, scFv XENP20389)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain		
vhCDR1		
vhCDR2		
vhCDR3		
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EVQLVESGGGLVPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vlCDR1	SYTMH	
vlCDR2	FISYDGNHKYYADSVKG	
vlCDR3	TGHLGPFDL	
scFv	EVQLVESGGGLVPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EVLTQSPATLSVSPGERATLSCRAS QSVSSSYLAWYQOKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKEIK	

Figure 12FF [CTLA-4] H3.4_I0.130 (Fab XENP20353, scFv XENP20390)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNHKYYADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSGKPGS	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQYGGSSPWTFGQGTKEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QOYGGSSPWT	
scFv	EVQLVESGGGLVPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EVLTQSPATLSVSPGERATLSCRAS QSVSSSYLAWYQOKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKEIK	

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Figure 12GG [CTLA-4] H3.4 L0.131 (Fab XENP20354, scFv XENP20391)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSQAASGFTFSYTMHWVRQAPGKGLWVSVFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNHKYYADSVK</u>	
vhCDR3	<u>TGHLGPFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA ^W YQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPED FVYYCQYGGSSPMTFGQGTKEIK	
vlCDR1	<u>RASQSVSSSYLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QYGGSSPMT</u>	
scFv	EVQLVESGGGLVQPGGSLRLSQAASGFTFSYTMHWVRQAPGKGLWVSVFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSLSPGERATLSCRAS QSVSSSYLA ^W YQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFVYYCQYGGSSPMTFGQGTKEIK	

Figure 12HH [CTLA-4] H3.4 L0.132 (Fab XENP20355, scFv XENP20392)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSQAASGFTFSYTMHWVRQAPGKGLWVSVFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNHKYYADSVK</u>	
vhCDR3	<u>TGHLGPFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLA ^W YQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPED FVYYCQYGGSSPMTFGQGTKEIK	
vlCDR1	<u>RASQSVSSSYLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QYGGSSPMT</u>	
scFv	EVQLVESGGGLVQPGGSLRLSQAASGFTFSYTMHWVRQAPGKGLWVSVFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSLSPGERATLSCRAS QSVSSSYLA ^W YQOKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFVYYCQYGGSSPMTFGQGTKEIK	

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Figure 12II [CTLA-4] H3.5_L2.1 (Fab XENP20357, scFv XENP20394)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNTRYVADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGIMTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNTRYVADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYGAFSRATGIPARFSGSGSGTEFTLTISSLQSED FAVYYCQOYGSSEWTFGGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GAFSRAT	
vlCDR3	QOYGSSEWTF	
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNTRYVADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGIMTVSS / GKPGSGKPGSGKPGSG / EIVMTQSPATLSVSPGERATLSCRAS QSVSSYLAWYQQKPGQAPRLIIYGAFSRATGIPARFSGSGSGTEFTLTISSLQSEDAVYYCQOYGSSEWTFGGTKVEIK	

Figure 12IJ [CTLA-4] H3.5_L2.2 (Fab XENP20358, scFv XENP20395)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNTRYVADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGIMTVSS	
vhCDR1	SYTMH	
vhCDR2	FISYDGNTRYVADSVKG	
vhCDR3	TGHLGPFDL	
scFv linker	GKPGSGKPGSGKPGSG	
Variable light (vl) domain	EIVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYGASSRATGIPARFSGSGSGTEFTLTISSLQSED FAVYYCQOYGSSEWTFGGTKVEIK	
vlCDR1	RASQSVSSSYLA	
vlCDR2	GASSRAT	
vlCDR3	QOYGSSEWTF	
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNTRYVADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGIMTVSS / GKPGSGKPGSGKPGSG / EIVMTQSPATLSVSPGERATLSCRAS QSVSSYLAWYQQKPGQAPRLIIYGASSRATGIPARFSGSGSGTEFTLTISSLQSEDAVYYCQOYGSSEWTFGGTKVEIK	

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Figure 12KK [CTLA-4] H3.5 L2.3 (Fab XENP20359, scFv XENP20396)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVOLVEGGGLVKGGSRLSLSCAASGFTFSYTMHWVROAPGKGLWVFI SYDGNKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGFDLWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FI SYDGNKYYADSVKG</u>	
vhCDR3	<u>TGHLGFDL</u>	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSED FAVYQCQYGSSEPWTFGGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QOYGSSPWT</u>	
scFv	EVOLVEGGGLVKGGSRLSLSCAASGFTFSYTMHWVROAPGKGLWVFI SYDGNKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSG / EIVLTQSPATLSVSPGERATLSKRAS QSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPARFSGSGSGTEFTLTISLQSEDFAVYQCQYGSSEPWTFGGTKVEIK	

Figure 12LL [CTLA-4] H3 L0 (Fab XENP19546, scFv XENP19553)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVOLVEGGGLVKGGSRLSLSCAASGFTFSYTMHWVROAPGKGLWVFI SYDGNKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGWLGPFDYWGQGTMTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FI SYDGNKYYADSVKG</u>	
vhCDR3	<u>TWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTEFTLTISRLEPED FAVYQCQYGSSEPWTFGGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GAFSRAT</u>	
vlCDR3	<u>QOYGSSPWT</u>	
scFv	EVOLVEGGGLVKGGSRLSLSCAASGFTFSYTMHWVROAPGKGLWVFI SYDGNKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGWLGPFDYWGQGTMTVTVSS / GKPGSGKPGSGKPGSG / EIVLTQSPGTLSLSPGERATLSKRAS QSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTEFTLTISRLEPEDFAVYQCQYGSSEPWTFGGTKVEIK	

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Figure 12MM [CTLA-4] H3_L0.22 (Fab XENP20011)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVOLVEGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGTIVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPMTFGQGTKVEIK	
vICDR1	<u>RASQSVSSSYLA</u>	
vICDR2	<u>GAFSRAT</u>	
vICDR3	<u>QQYGGSSPMT</u>	
scFv	EVOLVEGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGTIVTVSS/ GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPMTFGQGTKVEIK	

Figure 12NN [CTLA-4] H3_L0.44 (Fab XENP20052)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVOLVEGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGTIVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLSWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPMTFGQGTKVEIK	
vICDR1	<u>RASQSVGSSYLS</u>	
vICDR2	<u>GAFSRAT</u>	
vICDR3	<u>QQYGGSSPMT</u>	
scFv	EVOLVEGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGTIVTVSS/ GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLSWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPMTFGQGTKVEIK	

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Figure 1200 [CTLA-4] H3_L0.67 (Fab XENP20018)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSVFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYDAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>DAFSRAT</u>	
vlCDR3	<u>QQYGGSSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSVFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLTVTVSS//GKPGSGKPGSGKPGSGKPGS//EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYDAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKVEIK	

Figure 12PP [CTLA-4] H3_L0.74 (Fab XENP20020)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSVFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLTVTVSS	
vhCDR1	<u>SYTMH</u>	
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	
vhCDR3	<u>TGWLGPFDY</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYCAYSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKVEIK	
vlCDR1	<u>RASQSVGSSYLA</u>	
vlCDR2	<u>GAYSRAI</u>	
vlCDR3	<u>QQYGGSSPWT</u>	
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVROAPGKGLWVSVFISYDGNKKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLTVTVSS//GKPGSGKPGSGKPGSGKPGS//EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYCAYSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSSPWTFGQGTKVEIK	

Figure 13A
7G8_H3.30_L1.34 (Fab XENP22594)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMSWVRQAPGKGLEWVAEISTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYCTRLATWDWYFDVWGQGTITVTVSS	
vhCDR1	DAWMS	
vhCDR2	EISTKANNHATYYAESVKG	
vhCDR3	LATWDWYFDV	
Variable light (vl) domain	DIVLTQSPSSLSASVGRVTITCRASQSDVDYDGDSDYMNWYQQKPKGLIYAASELESGIPARFS GSGSGTDFLTITSSLPQPEDFAFYCCQSNEDPETFGSGTKLEIK	
vlCDR1	RASQSDVDYDGDSDYMN	
vlCDR2	AASELES	
vlCDR3	QQSNEDPET	

Figure 13B
2A11_H1.144_L2.142 (Fab XENP22656)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKRPGATVKISKASGFNIKQFMHWVQQAPGKLEWGWIDPELGDTEYAPKFGQR VTITADTSTNTAIMELSLRSEDTAVYCYARGVYQALDIWGQGTITVTVSS	
vhCDR1	DYFMH	
vhCDR2	WIDPELGDTEYAPKFGQ	
vhCDR3	RGVYQALDI	
Variable light (vl) domain	DIQMTQSPAFLSVTPPEKVTITCQASQDIGNVLNWFOQKPGQIVKLLIYFTSYLHSGVPSRFSGSGS GTDYFTTISLSLEAEDAATYFCQGNLTIFYTFGGGTKEIK	
vlCDR1	QASQDIGNVLN	
vlCDR2	FTSYLHS	
vlCDR3	QQGNLTIFYT	

Figure 13C
7G8_H3.18_L1.11 (Fab XENP21670)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTDDAMDWVRQAPGKLEWVAEISTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYICTRLATWDWYFDVWGQGTIVTVSS	
vhCDR1	DAWMD	
vhCDR2	EISTKANNHATYYAESVKG	
vhCDR3	LATWDWYFDV	
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSVVDYDGSYMNWYQQKPGPKLLIYAASELESGIPARLS GSGGTDFTLTISSLQPEDFATYTCQQSNEDPFTFGSGTKLEIK	
vlCDR1	RASQSVVDYDGSYMN	
vlCDR2	AASELES	
vlCDR3	QQSNEDPFT	

Figure 13D
2A11_H010 (Fab XENP20930)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLEESGGGLVQPGGSMKLSCAASGFTTSDAMDWVRQSPKLEWVAEIRTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTGIYCTRLANWDWYFDVWGAGTIVTVSS	
vhCDR1	DAWMD	
vhCDR2	EIRTKANNHATYYAESVKG	
vhCDR3	LANWDWYFDV	
Variable light (vl) domain	DTVLTQSPASLAVSLGQRATISCKASQSVVDYDGSYMNWYQQKPGPKLLIYAASNLESGIPARLS GSGGTDFTLNIHPEVEEDAATYTCQQSNEDPFTFGSGTKLEIK	
vlCDR1	KASQSVVDYDGSYMN	
vlCDR2	AASNLES	
vlCDR3	QQSNEDPFT	

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Figure 13E
2A11_H1.125_L2.113 (Fab XENP21921)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISCKASGENIKHYFMHWQOAPGKGLWNGWIDPYLGDTEYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYCYARGVYQALDYWGQGTLLTVSS	
vHCDR1	HYFMH	
vHCDR2	WIDPYLGDTEYAPKFQGR	
vHCDR3	RGVYQALDY	
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCOASQDIGNLYLNWFQKQPDQTVKLLIYFSTSLHSGVPSRFSGSGS GTDYFTTSSLEAEDAATVFCQGNLTLPYTFGGGTVEIK	
vLCDR1	QASQDIGNYLIN	
vLCDR2	FTSLHSGVPSRFSGSGS	
vLCDR3	QQGNLTLPYT	

Figure 13F
2A11_H1L2 (Fab XENP20847)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISCKASGENIKDYFMHWQOAPGKGLWNGWIDPENGDEYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYCYARGVYQALDYWGQGTLLTVSS	
vHCDR1	DYFMH	
vHCDR2	WIDPENGDEYAPKFQGR	
vHCDR3	RGVYQALDY	
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCOASQDIGNLYLNWFQKQPDQTVKLLIYFSTSLHSGVPSRFSGSGS GTDYFTTSSLEAEDAATVFCQGNLTLPYTFGGGTVEIK	
vLCDR1	QASQDIGNYLIN	
vLCDR2	YTSRLHSGVPSRFSGSGS	
vLCDR3	QQGNLTLPYT	

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Figure 13G
2A11_H1_L2.25 (Fab XENP21372)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYIMHWQQAPGKGLWMGWIDPENGDT EYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYYCYARGVRQALDYWGQGTLLTVSS	
vhCDR1	DYYMH	
vhCDR2	WIDPENGDT EYAPKFQGR	
vhCDR3	RGVRQALDY	
Variable light (vl) domain	DIQMTQSPAPFLSVTPGKVTITCQASQDIGNHLNWFQOKPDQTVKLLIYYTSLHSGVPSRFSGSGS GTDYFTTSSLEAEDAATYFCQQGNTLPYTFGGGTKVEIK	
vlCDR1	QASQDIGNHLN	
vlCDR2	YTSRLHS	
vlCDR3	QQGNTLPYT	

Figure 13H
2A11_H1_L2.47 (Fab XENP21394)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYIMHWQQAPGKGLWMGWIDPENGDT EYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYYCYARGVRQALDYWGQGTLLTVSS	
vhCDR1	DYYMH	
vhCDR2	WIDPENGDT EYAPKFQGR	
vhCDR3	RGVRQALDY	
Variable light (vl) domain	DIQMTQSPAPFLSVTPGKVTITCQASQDIGNHLNWFQOKPDQTVKLLIYYTSLHSGVPSRFSGSGS GTDYFTTSSLEAEDAATYFCQQGNTLPYTFGGGTKVEIK	
vlCDR1	QASQDIGNHLN	
vlCDR2	YTSRLHS	
vlCDR3	QQGNTLPYT	

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Figure 13I
2A11_H1_L2.50 (Fab XENP21401)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKLSCKASGFNIKDYIMHWQQAPGKGLEMWGWDPENGDTEYAPKFGGR VTITADTSTNTAYMELSSLRSEDTAVYYCYARGVRQALDYWGQGTLLTVSS	
vHCDR1	DYIMH	
vHCDR2	WIDPENGDTTEYAPKFGG	
vHCDR3	RGVRQALDY	
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFOQKPDQTVKLLIYYTSLHSGVPSRFSGSGS GTDYFTFTISSLEAEDAATYFCQQGNLTLPYTEGGGKVEIK	
viCDR1	QASQDIGNYLN	
viCDR2	YTSYLHS	
viCDR3	QQGNLTLPYT	

Figure 13J
2A11_H1L2 (Fab XENP20847)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKLSCKASGFNIKDYIMHWQQAPGKGLEMWGWDPENGDTEYAPKFGGR VTITADTSTNTAYMELSSLRSEDTAVYYCYARGVRQALDYWGQGTLLTVSS	
vHCDR1	DYIMH	
vHCDR2	WIDPENGDTTEYAPKFGG	
vHCDR3	RGVRQALDY	
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFOQKPDQTVKLLIYYTSLHSGVPSRFSGSGS GTDYFTFTISSLEAEDAATYFCQQGNLTLPYTEGGGKVEIK	
viCDR1	QASQDIGNYLN	
viCDR2	YTSYLHS	
viCDR3	QQGNLTLPYT	

Figure 13K
7G8_H3.23_L1.11 (fab XENP21670)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTDDAWMDWVRQAAPGKGLEWVAEISTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYYCTRLATWDWYFDVWGQGTIVTVSS	
vhCDR1	DAWMD	
vhCDR2	EISTKANNHATYYAESVKG	
vhCDR3	LATWDWYFDV	
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQQKPKPKLLIYAASELESGIPARLS GSGGTDFLTITISLQPEDEATYYCQQSNEDPFTFGSGTKLEIK	
vlCDR1	RASQSDYDGDSDYNN	
vlCDR2	AASELES	
vlCDR3	QQSNEDPFT	

Figure 13L
7G8_H3.28_L1 (Fab XENP21892)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTDDAWMDWVRQAAPGKGLEWVAEISTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYYCTRLATWDWYFDVWGQGTIVTVSS	
vhCDR1	DAWMD	
vhCDR2	EISTKANNHATYYAESVKG	
vhCDR3	LATWDWYFDV	
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSDYDGDSDYNNWYQQKPKPKLLIYAASNLESGIPARLS GSGGTDFLTITISLQPEDEATYYCQQSNEDPFTFGSGTKLEIK	
vlCDR1	RASQSDYDGDSDYNN	
vlCDR2	AAASNLES	
vlCDR3	QQSNEDPFT	

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Figure 13M
7G8_H3.28_L1.11 (Fab XENP21893)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTDDAAMDWVRQAPGKLEWVAEISTKAYNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYCTR L ATWDWYFDWGQGTTVTVSS	
vhCDR1	<u>DAWMD</u>	
vhCDR2	<u>EISTKAYNHATYYAESVKG</u>	
vhCDR3	<u>LATWDWYFDV</u>	
Variable light (vl) domain	DTVLTSQSPSSLSASVGDRTVITCRASQSDVDHGDSYMNWYQOKPGKPKLLIYAASELESGLPARLS GSGGTDFTLTISLQPEDFATYYCQSNEDPFTFGSGTKLEIK	
vCDR1	<u>RASQSDVDYDGD SYMN</u>	
vCDR2	<u>AASELES</u>	
vCDR3	<u>QQSNEDPFT</u>	

Figure 13N
7G8_H3.28_L1.13 (Fab XENP21894)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTDDAAMDWVRQAPGKLEWVAEISTKAYNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYCTR L ATWDWYFDWGQGTTVTVSS	
vhCDR1	<u>DAWMD</u>	
vhCDR2	<u>EISTKAYNHATYYAESVKG</u>	
vhCDR3	<u>LATWDWYFDV</u>	
Variable light (vl) domain	DTVLTSQSPSSLSASVGDRTVITCRASQSDVDHGDSYMNWYQOKPGKPKLLIYAASELESGLPARLS GSGGTDFTLTISLQPEDFATYYCQSNEDPFTFGSGTKLEIK	
vCDR1	<u>RASQSDVDYDGD SYMN</u>	
vCDR2	<u>AASELES</u>	
vCDR3	<u>QQSNEDPFT</u>	

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Figure 14A (anti-TIM3 variable heavy and light chains + CDRs)

What: anti-TIM3 XENP21503 1D10_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLKESCAASGFAFSSFDMSWVRQTPKRLIEWVAYISSDGASTFYPDIMKGRFTI SRD NAKNTLYIQMSSLKSEDTAMYYCTRLGAYWGQGTLLVTVSA	
vhCDR1	SFDM	
vhCDR2	YISSDGASTFYPDIMKG	
vhCDR3	LGAY	
Variable light (vl) domain	DVVMQTPTLTSLVTVIGQPASISCKSSQSLSDSGKTYLNLWLLQRPQGSPKRLIYLVS KLDSGVDPDRFTGS GSGTDFTLKISRVEAEDLGVIYCWQGTHTFYTGGGTLKLEIK	
vlCDR1	KSSQSLSDSGKTYIN	
vlCDR2	VSKLDS	
vlCDR3	WQGTHTFYT	

Figure 14B

What: anti-TIM3 XENP21492 1D12_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLKESCAASGFAFSSFDMSWVRQTPKRLIEWVAYISSDGASTFYPDIMKGRFTI SRD NAKNTLYIQMSSLKSEDTAMYYCTRLGAYWGQGTLLVTVSA	
vhCDR1	SFDM	
vhCDR2	YISSDGASTFYPDIMKG	
vhCDR3	LGAY	
Variable light (vl) domain	DIVLTQSPASLAVSLGQRATISCRASESVEYYGTSIMQWYQOKPGQPPKLLIYAASNVE SGVPAFSGSG SGDFSLNHPVEEDDIAMVFCQSRKVPWTFGGTLKLEIK	
vlCDR1	RASESVEYYGTSIQ	
vlCDR2	AASNVE	
vlCDR3	QQSRKV.PWT	

Figure 14D

What: anti-TIM3	sequence	SEQ ID NO:
XENP21493 6C8_HOLO		
Variable heavy (vh)	QVQLKESGPGLVAFPSQSLITCTVSGFSLNGYGVNWFQPPGKGLMTGLMIWGDGSTDYNSALKSRLLSIS	
domain	KDKSKSQVFLKMNSLQTDTDARYCARSYTSDYWGQGLTVTVA	
vhCDR1	GYGVN	
vhCDR2	MIWGDGSTDYNSALKS	
vhCDR3	SYTSDDY	
Variable light (vl) domain	DIWMTSQKFTMSTVGDRAVSVTCASQNVGSNVAVWCQQKPGQSPKALITYSASFYSYGVFDRFTGSGSTDT FTLTISNVQSEDLAEYFCQQYNSPYTFGGGTGLEIK	
vlCDR1	KASQNVGSNVA	
vlCDR2	SASFYS	
vlCDR3	QQYNSPYT	

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Figure 14E (anti-TIM3 variable heavy and light chains + CDRs)

What: anti-TIM3 XENP21494 6D9H0_1D12_0	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGSTEYNAAFISRLSIS KDNSKSVQFFKMNLSLQADDTAIYYCARGGLSPFDYWGQGTLLTVSS	
vhCDR1	SYGVH	
vhCDR2	VIWSGGSTEYNAAFIS	
vhCDR3	GGLSPFDY	
Variable light (vl) domain	DIVLTQSPASIAVLGQRATISCRASESYEYIGTSLMQYQQKPGPPKLLIYAASNVESGVPAFESGG SGTDFSLNIHPVEEDDIAMVFCQSRKVPWTFGGCKLEIK	
vlCDR1	RASESYEYIGTSLMQ	
vlCDR2	AASNVES	
vlCDR3	QQSRKVPWT	

Figure 14F

What: anti-TIM3 XENP21495_7A9_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLLESGGGLVQPGSLKLSCAASGDFPSRYMWSVRQAPGKGLEWIGEINPDSSTINYTPSLKDKFLI SRDNKNTLYIQMSKVRSEDTALYYCARNGIYVGTITFFAYWGQGTLLTVSA	
vhCDR1	RYWMS	
vhCDR2	EINPDSSTINYTPSLKD	
vhCDR3	ENGYYVGTITFFAY	
Variable light (vl) domain	QAVVTQESALFTTSPGETVTLTCRSTGAVTTSNANWVQEKPDHIFTGLIGGTNNRAPGVPAFESGLIG DKAALTITGAQTEDEAIYFCALWYSNHWFGGKLTVLG	
vlCDR1	RSSTGAVTTSNAN	
vlCDR2	GTNNRAP	
vlCDR3	ALWYSNHWV	

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Figure 14G (anti-TIM3 variable heavy and light chains + CDRs)

What: anti-TIM3 XENP21496 7B11_HO10	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPSSLSITCTVSGFSLTSAVNWVRQSPGKLEWLGVIWGGSTDYNAAFISRLSIS KNSKRSQVFFKMNSLQANDTAIYYCVSLYRYDGFYWGQGLTVTVA	
vHCDR1	SYAVN	
vHCDR2	VIWGGSTDYNAAFIS	
vHCDR3	LYRYDGEDY	
Variable light (vl) domain	DIVLTQSQKFLSTSVGDRVSVTKASQNVGTHVARYQQKPGQSPKALVYSASYRSGVDPDRFTGSSGSTD FTLTISNVQSEDLAEYFCQQYNSYPLTFGGGTKLEIK	
vLCDR1	KASQNVGTHVA	
vLCDR2	SASYRYS	
vLCDR3	QQYNSYPLT	

Figure 14H

What: anti-TIM3 XENP21501 B11var_HO10	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPSSLSITCTVSGFSLTSAVNWVRQSPGKLEWLGVIWGGSTDYNAAFISRLSIS KNSKRSQVFFKMNSLQADDTAIYYCVSLYRYDGFYWGQGLTVTVA	
vHCDR1	SYAVN	
vHCDR2	VIWGGSTDYNAAFIS	
vHCDR3	LYRYDGEDY	
Variable light (vl) domain	DIVLTQSQKFLSTSVGDRVSVTKASQNVGTHVARYQQKPGQSPKALVYSASYRSGVDPDRFTGSSGSTD FTLTISNVQSEDLAEYFCQQYNSYPLTFGGGTKLEIK	
vLCDR1	KASQNVGTHVA	
vLCDR2	SASYRYS	
vLCDR3	QQYNSYPLT	

Figure 14I (anti-TIM3 variable heavy and light chains + CDRs)

What: anti-TIM3 XENP21502 7C2 H010	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKVVESGGGLVKPGGSLKLSCAASGFTFSRYAMSWVROTPEKRLIEWVASISSGGSTYYPDVQGRFTIS RDNARNILYLQMSSLSRSEDTAMYYCARGDYEGYFDYWGQGTSLTVSS	
vHCDR1	RYAMS	
vHCDR2	SISGGSTYYPDVQGG	
vHCDR3	GDYEGYFDY	
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMCKSSQSLNSINQKNYLAWYQQKPGQSPKLLVYFESTRESGVPDFTG SGSGTDFTLTISVYQAEDLADYFCQQHYSTELTFGAGTKLELK	
vLCDR1	KSSQSLNSINQKNYLA	
vLCDR2	FASTRES	
vLCDR3	QQHYSTPLT	

Figure 15A

XENP016434 YW243.55.S70[PD-1.1]_H0L0_IgG1_PVA_S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDSWIHWVRQAPGKGLEWAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVYYCARRHWPGGFEDYWGQGTLVTVSS	
vCDR1	<u>DSWIH</u>	
vCDR2	<u>WISPYGGSTYYADSVKG</u>	
vCDR3	<u>RHWPGGFEDY</u>	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFDSWIHWVRQAPGKGLEWAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVYYCARRHWPGGFEDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTVICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPVAGPSVFLPPKPKDITLMISRTPETVTCVVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHQDWLNKGKEYCKVSNKALPAPIEKTSISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK	
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKGKAPKLLISASFLYSGVPSRFSGSGGTDFLTITSSLPQEDFATYVCQQY <u>LYHPATFGQGTKEIK</u>	
vCDR1	<u>RASQDVSTAVA</u>	
vCDR2	<u>SASFLYS</u>	
vCDR3	<u>QQYLYHPAT</u>	
Full length light chain	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPKGKAPKLLISASFLYSGVPSRFSGSGGTDFLTITSSLPQEDFATYVCQQY <u>LYHPATFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSLTIT</u> LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	

Figure 15B

XENP024118 avelumab[PD-L1]_H1L1_1gG1_PVA_/5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPQGSLRLSCAASGFTFSYIMMMWRQAPGKGLEWVSSVPSGGITFYADTVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARIKLGTITVDYWGQGLTVTVSS	
vhCDR1	<u>SYIMM</u>	
vhCDR2	<u>SIYPSGGITFYADTVKG</u>	
vhCDR3	<u>IKLGTITVDY</u>	
Full length HC	EVQLLESGGGLVQPQGSLRLSCAASGFTFSYIMMMWRQAPGKGLEWVSSVPSGGITFYADTVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARIKLGTITVDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVWTVPSSSLGTQTYICNVNHKPSNTKVKVEPKSCDKTHCTCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDV KHEDPEVFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEALHNHTYQKSL SLSPGK	
Variable light (vl) domain	QSALTQPASVSGSPGQISITISCTGTSSDVGGYNVYVSWYQQHPGKAPKLMIVDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY <u>CSSYTSSTRVFGTGTKVTVL</u>	
viCDR1	<u>TGTSSDVGGYNVYS</u>	
viCDR2	<u>DVSNRPS</u>	
viCDR3	<u>SSYTSSSTRV</u>	
Full length light chain	QSALTQPASVSGSPGQISITISCTGTSSDVGGYNVYVSWYQQHPGKAPKLMIVDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY CSSYTSSTRVFGTGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTPPSKOSNNKYAA SSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS	

Figure 15C

XENP024119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLVTVSS	
vhCDR1	<u>RYWMS</u>	
vhCDR2	<u>NIKQDGSEKYYVDSVKG</u>	
vhCDR3	<u>EGGWFGELAFDY</u>	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCAPPVAGPSVFLPPKPKDITLMISRTPEVTCVVVDVHKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLDWLNKGKEYKCVSNKALPAPIETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSEFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLIYDASSRATIGIPDRFSGSGGTDFLTISRLEPEDFAVYVYCCQYGSLPWTFGGGTKEIK	
vlCDR1	<u>RASQRVSSSYLA</u>	
vlCDR2	<u>DASSRAT</u>	
vlCDR3	<u>QQYGSIPWT</u>	
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLIYDASSRATIGIPDRFSGSGGTDFLTISRLEPEDFAVYVYCCQYGSLPWTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLTITLSKADYKEKHVYACEVTHQGLSSPVTKSFNRGEC	

Figure 16

XENP014410 20H4.9[4-1BB]_HOLD_1gG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQWAGLLKPSSETLSLTCAVYGGSFSGYYW ⁵ WIROSPEKLEWIG ⁶ EINHGGVYTYNPSLE ⁷ SRVTISVDTSKNQ ⁸ FSIKLS ⁹ SVTAAD TAVYYCARDYGGNYDWYFDLWGRGTLTVSS	
vHCDR1	<u>GYW⁵</u>	
vHCDR2	<u>EINHGGVYTYNPSLE⁷</u>	
vHCDR3	<u>DYGGNYDWYFDL</u>	
Full length HC	QVQLQQWAGLLKPSSETLSLTCAVYGGSFSGYYW ⁵ WIROSPEKLEWIG ⁶ EINHGGVYTYNPSLE ⁷ SRVTISVDTSKNQ ⁸ FSIKLS ⁹ SVTAAD TAVYYCARDYGGNYDWYFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTPSPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHITCPPCAPPVAGPSVFLPPKPKDITLMISRTPEVTCVIVV DYKHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVSVLT ¹⁰ LDHQLNGLKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKSRWQQGNV ¹¹ VFSCVMHEALHNHYTQK SLSLSPGK	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASN ¹² RATGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQ ¹³ QRS NWPPALTFGGGTKEIK	
vLCDR1	<u>RASQSVSSYLA</u>	
vLCDR2	<u>DASN¹²RAT</u>	
vLCDR3	<u>QQRSNWPPAL¹³I</u>	
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASN ¹² RATGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQ ¹³ QRS NWPPALTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS ¹⁴ STYSLSST LTLTKADYEKHKVACEVTHQGLSSPVTKSFNRGEC	

Figure 17

XENP016437 11D4[OX40]_H0L0_IgG1_PVA_/5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMNWVRQAPGKGLEWVS YISSSS TIIDYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVVYCARESGWYLFDYWGQGTLVTVSS	
vhCDR1	<u>SYSMN</u>	
vhCDR2	<u>YISSSS</u> TIIDYADSVK G	
vhCDR3	ESGWYLF DY	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMNWVRQAPGKGLEWVS YISSSS TIIDYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVVYCARESGWYLFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV/DKKVEPKSCDKTHITCPPCPAPPVAGPSVFLPPKPKDITLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRW/SVLT/LHODWLNKGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFNCSVMHEALHNHYTQKSLSLSPGK	
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQGISWLA WYQKPEKAPKSLIYAASS LQSGVPSRFSGSGGTDFLTITSSLPEDFATYYCQQLYNSYPPTFGGGTKVEIK	
vlCDR1	<u>RASQGISWLA</u>	
vlCDR2	<u>AASSLQ</u> S	
vlCDR3	<u>QQYNSYPPT</u>	
Full length light chain	DIQMTQSPSSLSASVGDRVTITCRASQGISWLA WYQKPEKAPKSLIYAASS LQSGVPSRFSGSGGTDFLTITSSLPEDFATYYCQQLYNSYPPTFGGGTKVEIK/RTVAAPSVFHPSPDEQLKSGTASVWCLINNFYPRPAKQVQKVDNALOSGNSQESVTEODSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 18

XENP016438 ID8[GITR]_H01.0_igG1_pVA_/S267K

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPILKPSQTLSTCSFGSLTSGMGVGVIRQPSGKLEWLAHIWWDKYYSPSLKSLTISKDTSRNQVFLKITSLDTA DTATYYCVRSYYGSSGAMDYWGQGTSTVSS	
vHCDR1	<u>TSGMGVG</u>	
vHCDR2	<u>HIWWDKYYSPSLKS</u>	
vHCDR3	<u>SYYYGSSGAMDY</u>	
Full length HC	QVTLKESGPILKPSQTLSTCSFGSLTSGMGVGVIRQPSGKLEWLAHIWWDKYYSPSLKSLTISKDTSRNQVFLKITSLDTA DTATYYCVRSYYGSSGAMDYWGQGTSTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVWV DYKHEDPEVKFNWYVDGVEVHNAKTRPREEQYNSTYRVSVLTVLDHQLWLNKGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTL PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFELYSLKLTVDKSRWQQGNVFCSVNHEALHNHYTQK SLSLSPGK	
Variable light (vl) domain	DIVMTQTPLSLPVSLGDAQISCSRSSQSLVHSDGNTYLHWYLQKPGQSPKLLIYKVS KRFSGVPDRFSGSGGTDF TLKISRVEAEDLG VYFCSSQSTHVPPTFGGGTKLEIK	
vLCDR1	<u>RSSQSLVHSDGNTYLH</u>	
vLCDR2	<u>KVSKRF</u>	
vLCDR3	<u>QSSTHVPPT</u>	
Full length light chain	DIVMTQTPLSLPVSLGDAQISCSRSSQSLVHSDGNTYLHWYLQKPGQSPKLLIYKVS KRFSGVPDRFSGSGGTDF TLKISRVEAEDLG VYFCSSQSTHVPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	

Figure 19A

XENP016435 [anti-ICOS]_H0L0_IGC1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPKGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTINVAQKFGQGRVTMTDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGTMTVTSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGGTINVAQKFGQ</u>	
vHCDR3	<u>TYVDSSGGYHDAFDI</u>	
Full length HC	QVQLVQSGAEVKKPKGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTINVAQKFGQGRVTMTDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPAPPVAGPSVFLFPKPKD TLMISRTPEVTCVVDVVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFGSGSGTDFLTITSSLPQPEDFATYYCQQA NSFPWTFGGQGTKVEIK	
vLCDR1	<u>RASQGISRLLA</u>	
vLCDR2	<u>VASSLSQ</u>	
vLCDR3	<u>QQANSEFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFGSGSGTDFLTITSSLPQPEDFATYYCQQA NSFPWTFGGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

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Figure 19B

XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELIMKPGASVKLSCKASGYFTFTYWMHWWKQRPQGGLWIGIEDPSD SYVNVNQNF KGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY YGTSLAWFDY WGGGTILVTST	
vHCDR1	<u>TYWMH</u>	
vHCDR2	<u>EIDPSD</u> SYVNVNQNF KG	
vHCDR3	<u>SPDY</u> YGTSLAWFDY	
Full length HC	QVQLQQPGTELIMKPGASVKLSCKASGYFTFTYWMHWWKQRPQGGLWIGIEDPSD SYVNVNQNF KGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY YGTSLAWFDY WGGGTILVTST/ASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSQVHT FPAVLQSSGLYSLSSVTPSPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCAPPVAGPSVLEPPKPKDTLMISRTPEVTC VWVDVKHEDPEVRFNWWYDGVGVHNAKTPREEQYNSTYRVSVLTVLDHDLWGKEYKCKVSNKALPAPIEKTSKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNNYKTPPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SYVNVNQNF HEALHNH VTQKSLSLSPGK	
Variable light (vl) domain	DIVMTQAAPSPVPTPGESVSI CRSSK SP LH SN GN IYLYWFLQRPQGSPQLLI VRMSNL ASGVDPDRFSGSGSGTFTTLKISRVEAEDVGV YYCMQHLEYPYTFGGGKLEIK	
vLCDR1	<u>BSSK</u> SP <u>LH</u> SN <u>GN</u> IYLY	
vLCDR2	<u>RMSNL</u> AS	
vLCDR3	<u>MQHLE</u> YPYTF	
Full length light chain	DIVMTQAAPSPVPTPGESVSI CRSSK SP LH SN GN IYLYWFLQRPQGSPQLLI VRMSNL ASGVDPDRFSGSGSGTFTTLKISRVEAEDVGV YYCMQHLEYPYTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFYPREAKYQWVKVDNALQSGNSQESVTEQDSKSTY SLSSITLSKADYKEHKVYACEVTHQGLSSPYTKSFNRGEC	

Figure 19C

XENP021821 GSK_88.2[ICOS]_H01.0_1gG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGAELVRPGASVKLSCKASGYSTSYMINWVKQRPQGQGLEWIGNIPSDSYTNNQMFKDKATLTVDKSSNTAYMQLTSP TSEDSAVYYCTRWNLSTWYFDNYYLDYWGGQTLLTVSS	
vHCDR1	<u>SYWIN</u>	
vHCDR2	<u>NIYPSDSYTNQMFKD</u>	
vHCDR3	<u>WNLSYFDNYYLDY</u>	
Full length HC	QVQLQQPGAELVRPGASVKLSCKASGYSTSYMINWVKQRPQGQGLEWIGNIPSDSYTNNQMFKDKATLTVDKSSNTAYMQLTSP TSEDSAVYYCTRWNLSTWYFDNYYLDYWGGQTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLOSSGLYSLSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKEPKSCDKHTCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEV TCVVDVVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPRP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALH NIHTQKSLISLSPGK	
Variable light (vl) domain	DIVMTQAAPSPVPTPGESVSISSCRSSKLLHSNGNTLYLWFLQRPQSPQLLIYRMSNLASGVPRFSGSGSGTFTLRISRVEAEDVGV YYCMQHLEYPWTFGGGTLEIK	
vLCDR1	<u>RSSKSLHSNGNTLY</u>	
vLCDR2	<u>RMSNLAS</u>	
vLCDR3	<u>MQHLEYPWT</u>	
Full length light chain	DIVMTQAAPSPVPTPGESVSISSCRSSKLLHSNGNTLYLWFLQRPQSPQLLIYRMSNLASGVPRFSGSGSGTFTLRISRVEAEDVGV YYCMQHLEYPWTFGGGTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSITLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 19D

XENP021822 jMab-138[CO5]_H01.0_1gG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYPGSGVKGRFTISRENAKNSLYLQMNSLRA GDTAVYYCVRDNRKVTHEHYHYGMDVWGQGTTVTVSS	
vCDR1	<u>SYDMHW</u>	
vCDR2	<u>AI</u> GTA <u>GD</u> TYPGSGV <u>KG</u>	
vCDR3	<u>DN</u> RKVTHEHYHYGMDV	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYPGSGVKGRFTISRENAKNSLYLQMNSLRA GDTAVYYCVRDNRKVTHEHYHYGMDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPCPAPPVAGPSVLEPPPKKDTLMISRTIP EVTCVVDVYKHEDPEVKFNWYVDGVEVHNAKTRPEEQYNSTYRVSVLTVQHQQWLNQKEYKCKVSNKALPAPIEKTSKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVCSVWHEAL HNHYTQKSLSLSPGK	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQNIIRSSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQF <u>GSSPMCSFGQGT</u> KLEIK	
vCDR1	<u>RASQNIIRSSYLA</u>	
vCDR2	<u>GASSRAT</u>	
vCDR3	<u>QQFGSSPMCS</u>	
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQNIIRSSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQF <u>GSSPMCSFGQGT</u> KLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTL TLISKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC	

Figure 19E

XENP021823 jMab-139[ICOS]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSIRA GDTAVYYCVRDKRTVTTHEHYHYGMDVWGQGTITVTVSS	
vhCDR1	<u>SYDMH</u>	
vhCDR2	<u>ALGTAGDTYPGSKG</u>	
vhCDR3	<u>DKRTVTTHEHYHYGMDV</u>	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSIRA GDTAVYYCVRDKRTVTTHEHYHYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSKSTSGGTAAAGCLVKDYEPVPTVSWNSGALTSG VHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPVAGPSVFLPPKPKDTLMISRTPE VTCVVDVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDKSRWQQGNVVFSCSVNHEAL HNHYTQKLSLSPGK	
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSSSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQGE <u>GSSPMCSFGQGTLEIK</u>	
vlCDR1	<u>RASQSSSSSLA</u>	
vlCDR2	<u>GASSRAT</u>	
vlCDR3	<u>QQFGSSPMCS</u>	
Full length light chain	EIVLTQSPGTLSLSPGERATLSCRASQSSSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQGE <u>GSSPMCSFGQGTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCILNNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTL</u> <u>TLKADYEKHKVYACEVTHQGLSPVTKSNRGE</u>	

Figure 19F

XENP022346 WO2016059602_GSK([COS]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGYTFDYMAMHWVRQAPGQGLEWMGLSIYSDHTNINQKFQGRVTITADKSTSTAYMELSSLR SEDTAVYYCGRRNNGYNGWYFDVW/GQGTTTVYSS	
vHCDR1	DYAMH	
vHCDR2	LSIYSDHTNINQKFGG	
vHCDR3	NNYNGWYFDV	
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGYTFDYMAMHWVRQAPGQGLEWMGLSIYSDHTNINQKFQGRVTITADKSTSTAYMELSSLR SEDTAVYYCGRRNNGYNGWYFDVW/GQGTTTVYSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKDILMISRTPEVTC VWVDVKHEDPEVRFNWYVDGVEVHNAKTPREEQYNSTRVSVLT/LHQDWLNGKEYCKVSNKALPAPIETISKARGQPREPQV YTLPPSREEMTKNQSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH VTQKSLSLSPGK	
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLCSASSSVSYMH:WYQQKPGQAPRLIIYDTSKLAGIPARFSGSGSDTYTLTISSLEPEDFAVYYCFQSGG YPYTFGGQGTKLEIK	
vLCDR1	SASSSVSYMH	
vLCDR2	DTSKLAG	
vLCDR3	FGSGGYPTI	
Full length light chain	EIVLTQSPATLSLSPGERATLCSASSSVSYMH:WYQQKPGQAPRLIIYDTSKLAGIPARFSGSGSDTYTLTISSLEPEDFAVYYCFQSGG YPYTFGGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSLTSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	

Figure 19G

XENP023057 Jounce_37A105713[ICOS]_H0L0_IG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDYWMMDWVRQAPGKGLVWVSNIDEDGSITEYSPVKGRFTISRDNKNTLYLQMNSLR AEDTAVYCTRWGRFGDSWGQGLTVSS	
vHCDR1	<u>DYWMMD</u>	
vHCDR2	<u>NIDEDGSITEYSPVKG</u>	
vHCDR3	<u>WGFRFGDS</u>	
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFDYWMMDWVRQAPGKGLVWVSNIDEDGSITEYSPVKGRFTISRDNKNTLYLQMNSLR AEDTAVYCTRWGRFGDSWGQGLTVSS/ASTKGPSVFLPASPSSKTSGGTAALGCLVKDYEPPEPTVSWNSGALTSGVHTTTPAVL QSSGLYSLSSVAVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDV KHEDPEVFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTVLIHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFLYSKLTVDKSRWQQQGNVVFSCVMHEALHNHYTQKSL SLSPGK	
Variable light (vl) domain	DIVMTQSPDLSAVSLGERATINCKSSQSLSGSFNYLTWYQKPGQPPKLLIFVASTRHTIGVPDRFSGSGGTDFLTITSLQAEDVAVY CHHHYNAPPTFGPGTKVDIK	
vLCDR1	<u>KSSQSLSGSFNYLI</u>	
vLCDR2	<u>YASTRHT</u>	
vLCDR3	<u>HHHYNAPPT</u>	
Full length light chain	DIVMTQSPDLSAVSLGERATINCKSSQSLSGSFNYLTWYQKPGQPPKLLIFVASTRHTIGVPDRFSGSGGTDFLTITSLQAEDVAVY CHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKOSTYSL SSTLTLSKADYEKHKVYACEVTHOGLSPPVTKSFNRGEC	

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Figure 20A

XENP022091 [ICOS]_H0_10.7_Fab

What	sequence	SEQ ID NO:
Variable heavy (vH) domain	QVQLVQSGAEVKPGASVKVSKASGYTFTGYMHVYRQAPGQGLEWMGWINPHSGGTINYAKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVTSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGGTINYAKFQG</u>	
vHCDR3	<u>TYVDSSGYHDAFDI</u>	
Full length HC	QVQLVQSGAEVKPGASVKVSKASGYTFTGYMHVYRQAPGQGLEWMGWINPHSGGTINYAKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVTSS/ASTKGPSVPFLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSISLGTQTYICNVNHKPSNTKVDKKVEPKSCGS	
Variable light (vL) domain	DIQMTQSPSSVSASVGDRTVITCRASQGISSYLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFTLTISISLOPEDFATYYCQQA NSFPWTIFGQGTKEIK	
vLCDR1	<u>RASQGISSYLA</u>	
vLCDR2	<u>VASSLSQ</u>	
vLCDR3	<u>QQANSFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITCRASQGISSYLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFTLTISISLOPEDFATYYCQQA NSFPWTIFGQGTKEIK/RTVAAPSVPFIPPSDEQLKSGTASVCLINFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSNRGEK	

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Figure 20B

XENP022780 [ICOS]_HQ_L0.34_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTF ^T GYMHVWRQAPGQGLEWMGWINPHSGGTIN ^Y AQKFGQGRVTMT ^R TRDTISISTAYMELSRLRSDDTAVYYCARTYY ^D SSGGY ^H DAFDI ^W GQGTMT ^V TVSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGGTIN^YAQKFGQ</u>	
vHCDR3	<u>TY^DSSGGY^HDAFDI</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYTF ^T GYMHVWRQAPGQGLEWMGWINPHSGGTIN ^Y AQKFGQGRVTMT ^R TRDTISISTAYMELSRLRSDDTAVYYCARTYY ^D SSGGY ^H DAFDI ^W GQGTMT ^V TVSS/ASTKGPSVFLAPSKSTSGGTAALGCLVKDYFPEPVT ^V SWNSGALTSGVHTFPAVLQSSGLYSLSSV ^T VPSSSLGTQ ^T YCNVNHKPSNTK ^V DKKVEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGD ^R VTIT ^T CQASQDISRL ^L LAWYQKPKGAPK ^L LI ^V YASSLQSGVPSRFSGSGTD ^F TLT ^S ISLQPEDFAT ^Y YCQQAESEPWTFGGTK ^V EIK	
vLCDR1	<u>QASQDISRL^L</u>	
vLCDR2	<u>VASSLQ^S</u>	
vLCDR3	<u>QQAESFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGD ^R VTIT ^T CQASQDISRL ^L LAWYQKPKGAPK ^L LI ^V YASSLQSGVPSRFSGSGTD ^F TLT ^S ISLQPEDFAT ^Y YCQQAESEPWTFGGTK ^V EIK/RTVAAPSVFIFPPSDEQLKSGTASV ^V CLIN ^N FPYPREAKVQW ^K VDNALQSGNSQESVTECQ ^D SKDS ^T YSLSSTLTLSKADYEKHK ^V YACEV ^T HQGLSP ^V TKSFNRGEC	

Figure 20C

XENP022782 [ICOS]_HQ_L0.36_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFGYMHVVRQAPQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGGGTMTVTYSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGGTNYAQKFQ</u>	
vHCDR3	<u>TYDDSSGYHDAFDI</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYTFGYMHVVRQAPQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGGGTMTVTYSS/ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYCNVNHKPSNTKVDKVEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCQASQDISLLAWYQQKPGKAPKLLIYVASSLSQGVPSRFSGSGSGTDFTLTSSLPQEDFATYYCQQAESFPWTFGGGTKVEIK	
vLCDR1	<u>QASQDISLLA</u>	
vLCDR2	<u>VASSLSQ</u>	
vLCDR3	<u>QQAESFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITCQASQDISLLAWYQQKPGKAPKLLIYVASSLSQGVPSRFSGSGSGTDFTLTSSLPQEDFATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCILINFPYREAKVQWVKVDNALQSGNSQESVTEQDSKOSTYSLSTLTLSKADYKEKHVYACEVTHQGLSSPVTKSFNRGEC	

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Figure 20D

XENP022783 [ICOS]_H0_L0.37_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGGQGTMTVTSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKFGQ</u>	
vhCDR3	<u>TYDDSSGYHDAFDI</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGGQGTMTVTSS/ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKVDKVEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCQASQDISRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAESFPWTFGGGTKVEIK	
vlCDR1	<u>QASQDISRLA</u>	
vlCDR2	<u>AASSLQS</u>	
vlCDR3	<u>QQAESFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITCQASQDISRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFHPSPDEQLKSGTASVVCLLNNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSNRGEK	

Figure 20E

XENP022784 [ICOS]_HQ_L0.38_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVOSGAEVKKPGASVKVCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGGYHDAFDIWGGGTMTVTYSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKFQ</u>	
vhCDR3	<u>TYDDSSGGYHDAFDI</u>	
Full length HC	QVQLVOSGAEVKKPGASVKVCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGGYHDAFDIWGGGTMTVTYSS/ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPPSSILGTQTYICNVNHKPSNTKVDKKVEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCQASQDISSLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQAESFPWTFGGQTKVEIK	
vlCDR1	<u>QASQDISSLLA</u>	
vlCDR2	<u>AASSLQS</u>	
vlCDR3	<u>QQAESFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITTCQASQDISSLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQAESFPWTFGGQTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWIKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC	

Figure 20F

XENP023088 [ICOS]_H0.66_L0_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFKQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETIYAQKFOG</u>	
vhCDR3	<u>TYVDTSGYHDAFDV</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFKQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS/ASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCRASQGISRLLA WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGGTDFTLTIS LOPEDFATYYCQQA NSFPWTFGGGTKVEIK	
vlCDR1	<u>RASQGISRLLA</u>	
vlCDR2	<u>VASSLQS</u>	
vlCDR3	<u>QQANSEFWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITCRASQGISRLLA WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGGTDFTLTIS LOPEDFATYYCQQA NSFPWTFGGGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCCLINFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTL TLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	

Figure 20G

XENP023409 [ICOS]_H0.66_L0.34_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETIYAQKFQ</u>	
vhCDR3	<u>TYYYDTSGYHDAFDV</u>	
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS/ASTKGPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALT GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCGS	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFLTISISLPEDFATYYCQ <u>AESEFWTFGGTKVEIK</u>	
vlCDR1	<u>QASQDISRLA</u>	
vlCDR2	<u>VASSLSQ</u>	
vlCDR3	<u>QQAESFPWT</u>	
Full length light chain	DIQMTQSPSSVSASVGDRTVITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFLTISISLPEDFATYYCQ <u>AESEFWTFGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCVLLINFPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTL</u> TLISKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	

Figure 21A

depicts melting temperatures (T_m) and changes in melting temperature from the parental Fab (XENP22050) as determined by DSF of variant anti-ICOS Fabs engineered for stability.

XENP	T_m (°C)	ΔT_m (°C)
22050	72	0
22051	72.5	0.5
22052	72	0
22053	70.5	-1.5
22054	72	0
22055	72	0
22056	70.5	-1.5
22057	72.5	0.5
22058	71.5	-0.5
22059	71.5	-0.5
22060	71.5	-0.5
22061	70.5	-1.5
22062	72.5	0.5
22063	68	-4
22064	71.5	-0.5
22065	70.5	-1.5
22066	71	-1
22067	71.5	-0.5
22068	71	-1
22069	72.5	0.5
22070	73	1
22071	73	1
22072	73	1
22073	72.5	0.5
22074	71	-1
22075	66.5	-5.5
22076	71.5	-0.5
22077	70.5	-1.5
22078	70	-2
22079	74.5	2.5
22080	73.5	1.5
22081	73	1
22082	75.5	3.5
22083	76	4
22084	72	0
22085	71	-1
22086	70	-2
22087	74	2
22088	73	1
22089	70.5	-1.5
22090	70	-2
22091	72.5	0.5

Figure 21B

22092	71	-1
22093	73	1
22094	74.5	2.5
22095	74	2
22096	72	0
22101	70	-2
22102	72	0
22103	71.5	-0.5
22104	73	1
22106	71	-1
22107	68.5	-3.5
22108	71.5	-0.5
22767	74	2
22768	76.5	4.5
22769	74.5	2.5
22771	71	-1
22772	75	3
22773	75.5	3.5
22774	73	1
22775	76	4
22776	73.5	1.5
22777	75	3
22778	73	1
22779	76	4
22780	73	1
22781	75	3
22782	72.5	0.5
22783	75.5	3.5
22784	74.5	2.5
22861	76	4
22862	76	4
22863	75.5	3.5
22938	75.5	3.5
22939	76.5	4.5
22940	78.5	6.5
22941	76.5	4.5
22944	74	2
22945	76	4
22946	76.5	4.5
23086	72.5	0.5
23087	68	-4
23088	73.5	1.5
23089	69	-3
23409	74.5	2.5

Figure 22 depicts equilibrium dissociation constants (K_D), association rates (k_a), and dissociation rates (k_d) of variant anti-ICOS Fabs for murine Fc fusions of human ICOS captured on AMC biosensors as determined by Octet.

Figure 22A

XENP	Antigen	K_D (nM)	k_a (1/Ms)	k_d (1/s)
22050	huICOS	3.538	5.04E+04	1.79E-04
22051	huICOS	798.8	7.99E+02	6.38E-04
22052	huICOS	<0.001	3.32E+04	<1.0E-07
22053	huICOS	13.85	1.09E+05	1.52E-03
22054	huICOS	<0.001	4.65E+04	<1.0E-07
22055	huICOS	1.725	9.15E+04	1.58E-04
22056	huICOS	3.765	4.54E+04	1.71E-04
22057	huICOS	13.19	3.10E+04	4.09E-04
22058	huICOS	2.69	3.17E+04	8.52E-05
22059	huICOS	2.289	1.04E+05	2.38E-04
22060	huICOS	3.361	6.48E+04	2.18E-04
22061	huICOS	2.373	8.81E+04	2.09E-04
22062	huICOS	2.442	4.94E+04	1.21E-04
22063	huICOS	4.835	6.80E+04	3.29E-04
22064	huICOS	5.521	4.03E+04	2.23E-04
22065	huICOS	3.605	9.15E+04	3.30E-04
22066	huICOS	1.073	1.76E+04	1.89E-05
22067	huICOS	2.187	7.67E+04	1.68E-04
22068	huICOS	3.329	3.45E+04	1.15E-04
22069	huICOS	<0.001	2.00E+04	<1.0E-07
22070	huICOS	very weak	very weak	very weak
22071	huICOS	<0.001	2.19E+04	<1.0E-07
22072	huICOS	<0.001	2.17E+04	<1.0E-07
22073	huICOS	171.8	2.43E+03	4.17E-04
22074	huICOS	<0.001	2.04E+04	<1.0E-07
22075	huICOS	very weak	very weak	very weak
22076	huICOS	very weak	very weak	very weak
22077	huICOS	9.747	4.71E+04	4.59E-04
22078	huICOS	117	1.81E+03	2.12E-04
22079	huICOS	very weak	very weak	very weak
22080	huICOS	very weak	very weak	very weak
22081	huICOS	very weak	very weak	very weak
22082	huICOS	very weak	very weak	very weak
22083	huICOS	very weak	very weak	very weak
22084	huICOS	2.411	9.50E+04	2.29E-04
22085	huICOS	1.785	9.63E+04	1.72E-04
22086	huICOS	<0.001	4.84E+04	<1.0E-07
22087	huICOS	0.9926	8.66E+04	8.59E-05
22088	huICOS	0.606	9.51E+04	5.77E-05
22089	huICOS	5.14	8.77E+04	4.51E-04
22090	huICOS	very weak	very weak	very weak

Figure 22B

22091	hulCOS	51.33	3.29E+04	1.69E-03
22092	hulCOS	70.14	7.93E+04	5.56E-03
22093	hulCOS	19.27	3.47E+04	6.68E-04
22094	hulCOS	32.62	2.80E+04	9.13E-04
22095	hulCOS	3.472	1.24E+05	4.31E-04
22096	hulCOS	3.023	8.14E+04	2.46E-04
22101	hulCOS	2.61	6.08E+04	1.59E-04
22102	hulCOS	4.746	1.00E+05	4.77E-04
22103	hulCOS	5.838	4.94E+04	2.89E-04
22104	hulCOS	3.862	7.78E+04	3.01E-04
22105	hulCOS	2.49	9.40E+04	2.34E-04
22106	hulCOS	3.446	6.62E+04	2.28E-04
22107	hulCOS	530.3	1.06E+03	5.60E-04
22108	hulCOS	192	5.94E+03	1.14E-03

Figure 22C

XENP	Antigen	K _D (nM)	k _a (1/Ms)	k _d (1/s)
22050	hulCOS	<0.001	3.34E+04	<1.0E-07
22052	hulCOS	<0.001	4.37E+04	<1.0E-07
22053	hulCOS	13	6.83E+04	8.86E-04
22054	hulCOS	very weak	very weak	very weak
22057	hulCOS	0.00722	1.06E+05	7.65E-07
22064	hulCOS	<0.001	4.79E+04	<1.0E-07
22065	hulCOS	<0.001	3.41E+04	<1.0E-07
22069	hulCOS	<0.001	4.57E+03	<1.0E-07
22073	hulCOS	very weak	very weak	very weak
22074	hulCOS	1.31	7.57E+04	9.88E-05
22077	hulCOS	very weak	very weak	very weak
22084	hulCOS	<0.001	1.19E+04	<1.0E-07
22089	hulCOS	3.12	5.78E+04	1.80E-04
22091	hulCOS	142	1.50E+04	2.13E-03
22093	hulCOS	399	7.82E+02	3.12E-04
22094	hulCOS	14.2	7.46E+04	1.06E-03
22095	hulCOS	11	6.60E+04	7.25E-04
22102	hulCOS	0.886	9.10E+04	8.07E-05
22103	hulCOS	1.5	7.23E+04	1.09E-04
22104	hulCOS	1.33	3.66E+04	4.86E-05
22106	hulCOS	2060	4.81E+02	9.93E-04
22108	hulCOS	17.5	7.61E+04	1.33E-03

Figure 23 depicts equilibrium dissociation constants (K_D), association rates (k_a), and dissociation rates (k_d) of variant anti-ICOS Fabs for biotinylated IgG1 Fc fusions of human ICOS captured on SA biosensors as determined by Octet.

XENP	Antigen	K_D (nM)	k_a (1/Ms)	k_d (1/s)
22050	huICOS	1.936	7.65E+04	1.48E-04
22091	huICOS	54.56	3.00E+04	1.64E-03
22780	huICOS	3.131	6.41E+04	2.01E-04
22781	huICOS	14.64	1.03E+05	1.50E-03
22782	huICOS	7.457	5.62E+04	4.19E-04
22783	huICOS	39.55	3.49E+04	1.38E-03
22784	huICOS	27.81	9.13E+04	2.54E-03
22861	huICOS	5206	1.36E+03	7.07E-03
22862	huICOS	239.4	2.51E+04	6.00E-03
22863	huICOS	102.3	3.49E+04	3.57E-03
22929	huICOS	12.39	4.56E+04	5.65E-04
22938	huICOS	43.94	3.89E+04	1.71E-03
22939	huICOS	24.49	5.84E+04	1.43E-03
22940	huICOS	18.9	7.10E+04	1.34E-03
22941	huICOS	81.29	3.80E+04	3.09E-03
22944	huICOS	4.415	6.29E+04	2.78E-04
22945	huICOS	40.62	5.31E+04	2.16E-03
22946	huICOS	19.38	6.71E+04	1.30E-03

Figure 24A

XENP024352 [anti-ICOS]_{H0L0}_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTRTDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMVTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKFGQ</u>	
vhCDR3	<u>TYDDSSGYHDAFDI</u>	
scFv linker	<u>GRPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQQKPKGKAPKLLIYVASSLOSQVPSRFGSGSGTDFTLTISIQPEDFATYWCQQA NSFPWTFGQGTKVEIK	
vlCDR1	<u>RASQGISRLA</u>	
vlCDR2	<u>VASSLOS</u>	
vlCDR3	<u>QQANSEFWT</u>	
scFv	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTRTDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMVTVSS/ <u>GRPGSGKPGSGKPGSG</u> /DIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQQKPKGKAPKLLIYVASSLOSQVPSRFGSGSGTDFTLTISIQPEDFATYWCQQA NSFPWTFGQGTKVEIK/GS	

Figure 24B

XENP024353 [anti-iCOS]_10H0_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFGYTMHWVRQAPGQGLEWMGWINPHSGGTNYACKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMTVTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYACKFQG</u>	
vhCDR3	<u>TYDDSSGYHDAFDI</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLOSQVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA NSFPWTFGGGTKVEIK	
vCDR1	<u>RASQGISRLLA</u>	
vCDR2	<u>VASSLOS</u>	
vCDR3	<u>QQANSPFWT</u>	
scFv	DIQMTQSPSSVSASVGDRTVITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLOSQVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA NSFPWTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVCKASGYTFGYTMHWVRQAPGQGLEWMGWINPHSGGTNYACKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMTVTVSS/GS	

Figure 24C

XENP024354 [anti-ICOS] H0.40 L0.22 scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVOSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGEIN Y AQKFGQGRVTMTTRDTSISTAYMELS SLRSEDTAVYYCARTYYDTSGYHDAFDVWGQGTMTVTVSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGEIN</u> AQKFGQ	
vHCDR3	<u>TVYD</u> TSGYHDAFDV	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQDISRL L AWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGGTDFTLTISSLQPEDFATVYCCQA NSFPWTFGGGTKVEIK	
vLCDR1	<u>RASQDISRL</u> LA	
vLCDR2	<u>AASSLSQ</u> S	
vLCDR3	<u>QQANSFP</u> WT	
scFv	QVQLVOSGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGEIN Y AQKFGQGRVTMTTRDTSISTAYMELS SLRSEDTAVYYCARTYYDTSGYHDAFDVWGQGTMTVTVSS/ <u>GKPGSGKPGSGKPGSG</u> /DIQMTQSPSSVSASVGDRVTITCR <u>A</u> SQDISRL L AWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGGTDFTLTISSLQPEDFATVYCCQA <u>NSFPWTFGGGTKVEIK</u> /GS	

Figure 24D

XENP024355 [anti-iCOS]_H0.40_10.45_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFITYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFGGRVTMTTRDTSISTAYMELS SLRSEDTAVYYCARITYYDTSYYHDAFDVWGQGTMTVTYSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETNYAQKFGG</u>	
vhCDR3	<u>TYYDTSYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTOSPSSVSASVGDRTTTCRASQDISRLLAWYQQKPGKAPKLLIYAASSLOS GVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQA <u>QSFPWTFGGTKVEIK</u>	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLOS</u>	
vlCDR3	<u>QQAQSPWTF</u>	
scFv	QVQLVQSGAEVKKPGASVKVSKASGYTFITYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFGGRVTMTTRDTSISTAYMELS SLRSEDTAVYYCARITYYDTSYYHDAFDVWGQGTMTVTYSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /DIQMTOSPSSVSASVGDRTTTCRA <u>SQDISRLLAWYQQKPGKAPKLLIYAASSLOS</u> <u>GVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQSPWTFGGTKVEIK/GS</u>	

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Figure 24E

XENP024356 [anti-ICOS] H0.66 10.22_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTTRDTSISTAYMELSS LRSEDAVYYCARTYYDTSGYYHDAFDVWGQGTMVTSS	
vHCDR1	<u>GYMH</u>	
vHCDR2	<u>WINPHSGETIYAQKFGQ</u>	
vHCDR3	<u>TVYDTSYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITTCRASQDISRLLAWVYQKPGKAPKLLIYAASSLSQGVPSRFGSGSGTDFLTLSLQPEDFATYYCQQA NSFPWTFGGTKVEIK	
vLCDR1	<u>RASQDISRLLA</u>	
vLCDR2	<u>AASSLSQ</u>	
vLCDR3	<u>QQANSPWT</u>	
scFv	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTTRDTSISTAYMELSS LRSEDAVYYCARTYYDTSGYYHDAFDVWGQGTMVTSS/GKPGSGKPGSGKPGSG/DIQMTQSPSSVSASVGDRVTITCRAS QDISRLLAWVYQKPGKAPKLLIYAASSLSQGVPSRFGSGSGTDFLTLSLQPEDFATYYCQQA NSFPWTFGGTKVEIK/GS	

Figure 24F

XENP024357 [anti-ICOS]_H0.66_10.45_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETIYAQKFOG</u>	
vhCDR3	<u>TYYYDTSGYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSG</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCRASQDISRLLAWYQQKPGKAPKLLIYAASSLOS GVPSRFS SGSGTDFTLTISIQPEDFATYCCQA <u>QSEFWTFGQGTKEIK</u>	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLOS</u>	
vlCDR3	<u>QQAQSFPT</u>	
scFv	QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVYVCARTYYDTSGYHDAFDVWGQGTMTVSS/ <u>GKPGSGKPGSGKPGSG</u> /DIQMTQSPSSVSASVGDRTITTCRAS <u>QDISRLLAWYQQKPGKAPKLLIYAASSLOS</u> GVPSRFS SGSGTDFTLTISIQPEDFATYCCQAQSFPTFGQGTKEIK/GS	

Figure 24G

XENP024609 [anti-ICOS]_{L0.45_H0.40_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFITYYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSEDTAVVYCARITYYDTSGYYHDAFDVVGQGTMTVTYSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	
vhCDR3	<u>TYYDTSGYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQDISRLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGGTDFTLTISLQPEDFATYYCQQA <u>QSFPTFGQGTKVEIK</u>	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLQ</u>	
vlCDR3	<u>QQAQSFPT</u>	
scFv	DIQMTQSPSSVSASVGDRVTITCRASQDISRLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGGTDFTLTISLQPEDFATYYCQQA <u>QSFPTFGQGTKVEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVSKASGYTFITYYMHVVRQAPGQGLEW</u> MGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSRLRSEDTAVVYCARITYYDTSGYYHDAFDVVGQGTMTVTYSS/GS	

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Figure 24H

XENP024689 [anti-ICOS]_10.45_H0.37_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELS SLRSEDIAVYVCARTYYDTSGYHDAFDVVGQGTMTVTYSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKFQ</u>	
vhCDR3	<u>TYVDTSGYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFGSGGTDFTLTISSLQPEDFATYCCQA <u>QSFPTFGQGTKEIK</u>	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLS</u>	
vlCDR3	<u>QQAQSFPT</u>	
scFv	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFGSGGTDFTLTISSLQPEDFATYCCQA <u>QSFPTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGGLEW</u> <u>MGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLSEDIAVYVCARTYYDTSGYHDAFDVVGQGTMTVTYSS/GS</u>	

Figure 241

XENP024690 [anti-ICOS]_{10.45_H0.68}_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHVWRQAPGQGLEWMGWINPHSGETINVAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETINVAQKFQ</u>	
vhCDR3	<u>TYDDTSYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPKAPKLLIYAASSLSQGVPSRFGSGSGTDFTLTISSLQPEDFATYCCQAQSEFWTFGGGTKEIK	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLSQ</u>	
vlCDR3	<u>QQAQSEFWT</u>	
scFv	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPKAPKLLIYAASSLSQGVPSRFGSGSGTDFTLTISSLQPEDFATYCCQAQSEFWTFGGGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHVWRQAPGQGLEWMGWINPHSGETINVAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVSS/GS	

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Figure 24f

XENP024691 [anti-ICOS]_{10.45_140.35}_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGGGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKFQ</u>	
vhCDR3	<u>TYVDTSGYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPKAPKLLIYAASSLOSVPFRSGSGGTDFTLTISSLQPEDFATYYCQQAQSFPTFGQGTKEIK	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLOS</u>	
vlCDR3	<u>QQAQSFPT</u>	
scFv	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPKAPKLLIYAASSLOSVPFRSGSGGTDFTLTISSLQPEDFATYYCQQAQSFPTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGGGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTVSS/GS	

Figure 24K

XENP024692 [anti-ICOS]_L0.45_H0.34_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVVYVCARTYYDSSGGYHDAFDVWGQGTMTVTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGGTNYAQKEQG</u>	
vhCDR3	<u>TYVDSSGGYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCRASQDISRLAWYQQKPGKAPKLLIAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQSEFWTFGGGTKVEIK	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>AASSLQS</u>	
vlCDR3	<u>QQAQSEFWT</u>	
scFv	DIQMTQSPSSVSASVGDRTITTCRASQDISRLAWYQQKPGKAPKLLIAASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQQAQSEFWTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVSKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVVYVCARTYYDSSGGYHDAFDVWGQGTMTVTVSS/GS	

Figure 24L

XENP024693 [anti-ICOS]_{L0.46_H0.40}_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSEDTAVVYCAR TTTTYDTSGYYHDAFDV WGQGTMTVTVSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCRASQISRLLA WYQQKPGKAPKLLIYAASLSQSGVPSRFS SGSGTDFLTLSLQPEDFA TY YCCQA <u>QSF</u> PWTFGQGTKEIK	
viCDR1	<u>RASQISRLLA</u>	
viCDR2	<u>AASSLSQ</u>	
viCDR3	<u>QQAQSF</u> PWT	
scFv	DIQMTQSPSSVSASVGDRTVITTCRASQISRLLA WYQQKPGKAPKLLIYAASLSQSGVPSRFS SGSGTDFLTLSLQPEDFA TY YCCQA <u>QSF</u> PWTFGQGTKEIK/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QVQLVQSGAEVKKPGASVKVSKASGYFTFTGYMHWRQAPGQGLEW</u> <u>MGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSLRSEDTAVVYCAR</u> <u>TTTTYDTSGYYHDAFDV</u> WGQGTMTVTVSS/GS	

Figure 24M

XENP024694 [anti-ICOS]_10.47_H0.40_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFGTYYMHWRQAPGGGLEWMGWINPHSGETINVAQKFQGRVTMTTRDTSISTAYMELS SLRSEDVAVVYVCARTYYDTSGYYHDAFDVVGQGTMTVTYSS	
vhCDR1	<u>GYMH</u>	
vhCDR2	<u>WINPHSGETINVAQKFQ</u>	
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPGKAPKLLIYSASSLSQSGVPSRFSGSGSGTDFTLTISLIQPEDFAITYCQQA <u>QSFPWTFGQGTKEIK</u>	
vlCDR1	<u>RASQDISRLLA</u>	
vlCDR2	<u>SASSLSQ</u>	
vlCDR3	<u>QQAQSEFWT</u>	
scFv	DIQMTQSPSSVSASVGDRTVITTCRASQDISRLLAWYQQKPGKAPKLLIYSASSLSQSGVPSRFSGSGSGTDFTLTISLIQPEDFAITYCQQA <u>QSFPWTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVCKASGYTFGTYYMHWRQAPGGGLEW</u> <u>MGWINPHSGETINVAQKFQGRVTMTTRDTSISTAYMELSLRSEDVAVVYVCARTYYDTSGYYHDAFDVVGQGTMTVTYSS/GS</u>	

Figure 25 depicts melting temperatures (T_m) and changes in melting temperature from the parental scFv (XENP24352; oriented as V_H -scFv linker- V_L from N- to C-terminus) as determined by DSF of variant anti-ICOS scFvs engineered for stability.

XENP	T_m (°C)	ΔT_m (°C)
24352	56	0
24354	65.5	9.5
24353	59	3
24355	67	11
24356	64.5	8.5
24357	66	10
24609	69	13
24689	66.5	10.5
24690	69	13
24691	66.5	10.5
24692	67	11
24693	67.5	11.5
24694	68.5	12.5

Figure 26A

XENP22730

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain
 QVQLVOSGAEVKKPGASVKSCASGYTFTGYMHVWVROAPGGQGLEWMGWINPHSGGTNVAQKFGQGRVTMTSDTSISTAYMELSLRSDDTAVYVCARTYYDSSG
 YYHDAFDIHWGQGTMTVTVSS/ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYEPETVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHNKPSDT
 KVDKKVEPKSCDKTHITCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVYDGVGEVHNAAKTKPREEEYNSTYRVWVSVLTIVLHQDWLNGKEYK
 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSFGFYPSPDIAVEWESDGGQPENNYKTTTPPVLDSDGGSFFLYSKLTVDKSRWEQGGVDFSCSVLHEAL
 HSHYTKQKSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINVAASHRYTGVDPDRFTGSGYGTFTLTISSVQSEDFGVVYCCQDFSSPRTFGGKVEIK/GKPG
 SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNHWVROAPGKGLWVAEIRLYSNNYATHYAESVKGKRTFSRDDSSTLYLQMNILKTED
 TGVYCYTRYNGYGGYEDVWGRGTITVTVSS/EPKSSDKTHITCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVYDGVGEVHNAAKTKPREEQ
 YNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSFGFYPSPDIAVEWESDGGQPENNYKTTTPPVLDSDGGSFFL
 YSKLTVDKSRWQQGNVFSCSVLHEALHSHYTKQKSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain
 DIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSEFWTFGGGTKVEIK/RTVAA
 PSVFIFPPSDEQLKSGTASVVCVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 26B

XENP23377

>XENP023377 11D4[OX40]_HOL0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYSMNWVRQAPGKGLEWVSIVSSSTIDYADSVKGRFTISRDNKNSLYLQMNSLRDEDTAVVYCARESGWYLFDYWGQ
 GTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
 THITCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWVVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSFGFYPSPDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSP
 GK

>XENP023377 11D4[OX40]_HOL0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWVWYQQKPGQAPRLLINYNASHRYTGVDPDRFTGSGYGTFTLTISVSQSEDFGVVYCCQDFSSPRTFGGKTKVEIK/GKPG
 SGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAVSGFTFSNYWMNWRQAPGKGLEWVAEIRLYSNINNYATHYAESVKGRFTISRDDSKSTLYLQMNILKTED
 TGVVYCTRYGNYGGYEDVWGRGTLTVSS/EPKSSDKTHITCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWVVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023377 11D4[OX40]_HOL0_Fab-1G6_L1.194_H1.279_scFv Light Chain
 DIQMTQSPSSLSASVGDRVTITCRASQGISWLAWVYQKPEKAPKSLIYAASSLSQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNSYPPTFGGKTKVEIK/RTVAA
 PSVFIFPPSDEQLKSGTASVVCVLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 26C

XENP23378

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
 QVTLKESGPGILKPSQTLISLTCFSFGSLSTSGMGVGIWIRQPSGKGLWLAHIWDDDKYSPSLKSQLTISKDTSRNQVFLKITSIDTADTATYYCVRSYYGSSGAMDYW
 GQGTSTVTVSS/ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSSLGTQTYICNVNHHKPSDTIKVDKKVEPIK
 CDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPA
 PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCVMHEALHNHYTQKSL
 SLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPKGQAPELLINYSASHRYTGVDPDRFTGSGYGTETFTLTSSVQSEDFGVVYCCQDFESSPRTFGGGTKVEIK/GKPG
 SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNWMNWRQAPGKGLWVAEIRLYSNINNVATHYAESVKGRFTISRDDSKSTLYLQMNLLKTED
 TGVVYCTRYGNYGGYEDVWGRGTLIVTVSS/EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
 DIVMTQTPLSLPVSLGDQASISCRSSQSLVHSDGNTYLIHWYLOKPGQSPKLLIYKVSRRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSTHVPPTFGGGTKLEIK/R
 TVAAPSVFIHPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 26D

XENP23379

>XENP023379 20H4.9[4-188]_H010_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
 QVQLQQWGGAGLLKPSETLSLTCAVYGGFSGYWWSWIRQSPKEGLEWIGEINHGYYTYNPSLESRTISVDTSKNQFSILKSSVTAADTAVVYCARDYGPNGYDWYFDL
 WGRGTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAAIGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLOSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSDTKVDKKVEPK
 SCDKTHITCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVAVDVKHEDPEVKFNWVVDGVEVHNAAKTKPREEEYNSTYRVSVLTVLHQDWLNGKEYCKCKVSNKALP
 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPPVLDSDGGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHHTQKS
 LSLSPGK

>XENP023379 20H4.9[4-188]_H010_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINLYASHRYTGVPDRFTGSGYGTEFTLTISVQSEDFGVVYCCQDFSSPRTFGGGTKVEIK/GKPG
SGKPGSGRPGSGRPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWRQAPGKGLEWVAEIRLYSNINNYATHYAESVKGRFTISRDDSKSTLYLQMNNILKTED
 TGVVYCTRYGNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHITCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVAVDVKHEDPEVKFNWVVDGVEVHNAAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFL
 YSKLTVDKSRWQQGNVFCSCVMHEALHNHHTQKSLSPGK

>XENP023379 20H4.9[4-188]_H010_Fab-1G6_L1.194_H1.279_scFv Light Chain
 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRAITGIPARFSGSGGTDFLTITISLEPEDFAVYCCQQRSNWPPALTFGGGTKVEIK/RTVA
 APSVFIFPPSEQLKSGTASVTVCLNNIFPREAKYQWKVDNALQSGNSQESVTEQDSKDSSTLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 27

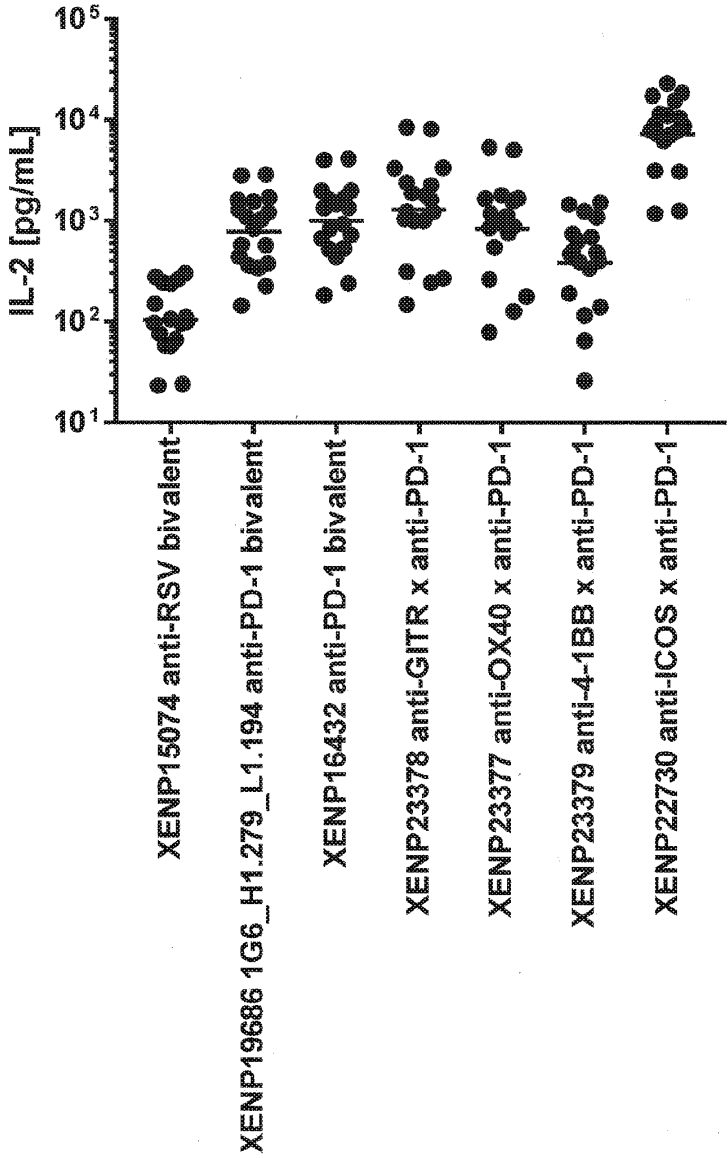


Figure 28

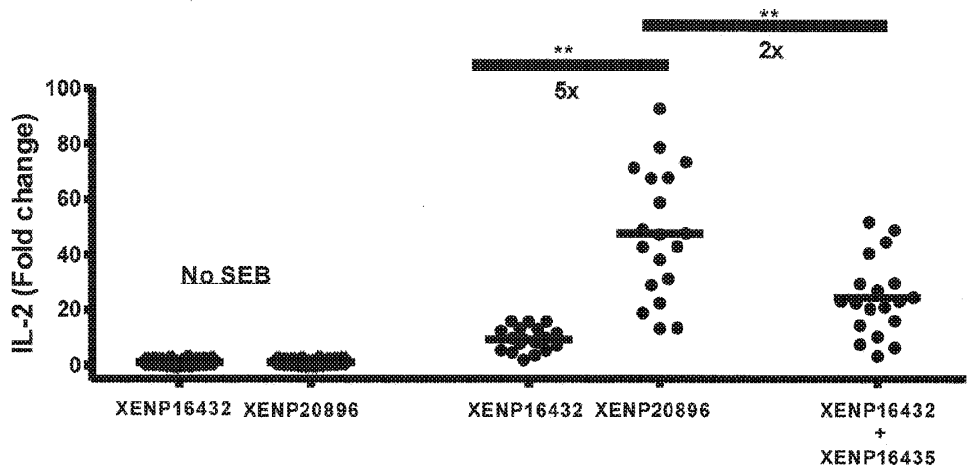


Figure 29

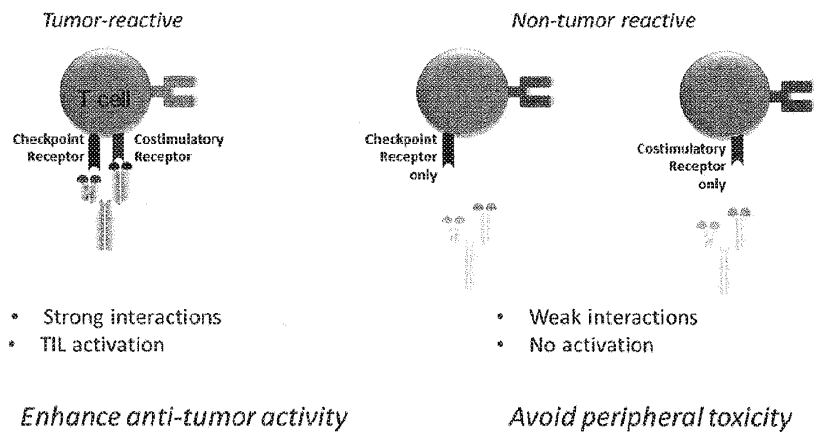


Figure 30

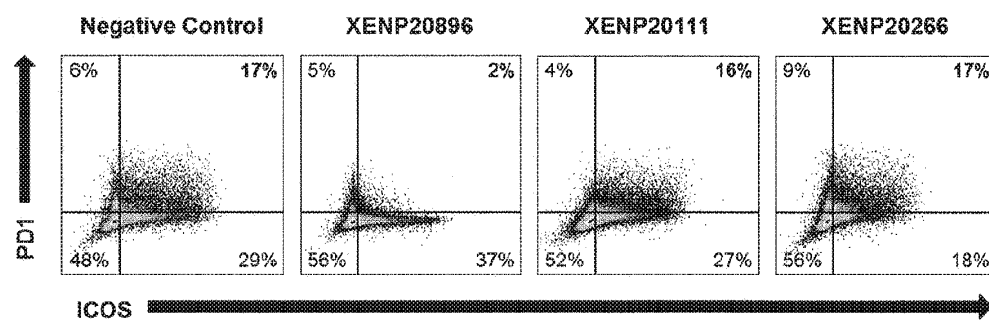


Figure 31A

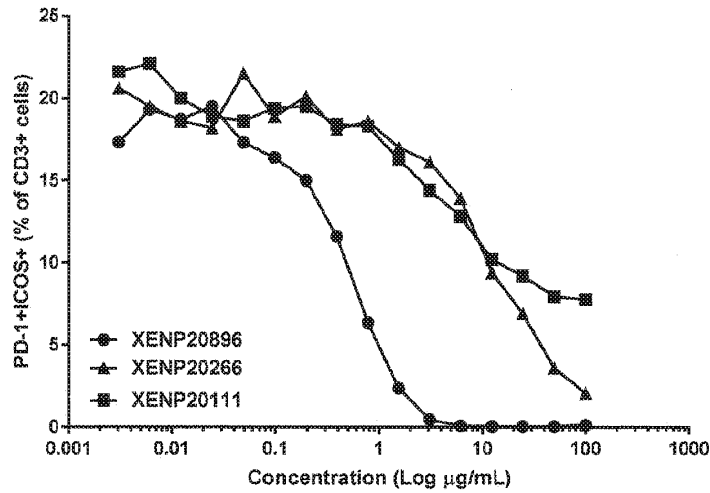


Figure 31B

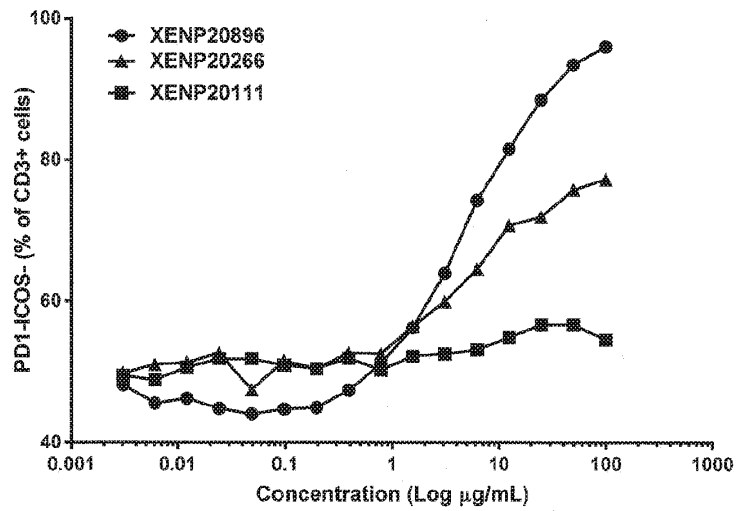


Figure 32A

XENP20896

>XENP20896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPGK

>XENP20896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTSS
VQSEDFGVYYCQDDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNHLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP20896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGRVITTCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSS
LQPEDFATYYCQQAANSFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22433

>XENP22433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPGK

>XENP22433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTSS
VQSEDFGVYYCQDDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNHLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP22433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGRVITTCRASQGISSYLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSS
LQPEDFATYYCQQAANSFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32B

XENP22744

>XENP022744 [ICOS]_HO_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSLRLSDDTAVYYCARTYYDSSGGYHDAFDIWQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNKYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022744 [ICOS]_HO_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTFTLTISS
VQSEDFGVYCCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWRQAPGKLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

>XENP022744 [ICOS]_HO_L0.34_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQAESFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22746

>XENP022746 [ICOS]_HO_L0.36_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSLRLSDDTAVYYCARTYYDSSGGYHDAFDIWQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNKYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022746 [ICOS]_HO_L0.36_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTFTLTISS
VQSEDFGVYCCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWRQAPGKLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

>XENP022746 [ICOS]_HO_L0.36_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQAESFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32C

XENP22747

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTSDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDI
AVEWESDQGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPGK

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAVWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTFTTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNNLKTEDTGYYICTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISRLAWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSGTDFTTLTISS
LQPEDFATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22748

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTSDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDI
AVEWESDQGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSQVMHEALHNHYTQKSLSLSPGK

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAVWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTFTTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNNLKTEDTGYYICTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISRLAWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSGTDFTTLTISS
LQPEDFATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32D

XENP23092

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYDDTSGLYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTFTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNHLKTEDTGYYCYTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGRVITTCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQANSEFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23410

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYDDTSGLYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQSVMEALHNHYTQKSLSLSPGK

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTFTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNHLKTEDTGYYCYTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSQS
VMHEALHNHYTQKSLSLSPGK

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGRVITTCQASQDISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 33A

XENP22730

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCFCSVLHEALHSHYTQKSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLIN~~Y~~ASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSN~~Y~~WMNWVRQAPGKLEWVAEIRLYSN~~Y~~ATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG~~V~~YYCT~~R~~YY
~~GN~~YGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQM~~T~~KNQVKLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCFCS
VLHEALHSHYTQKSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGRVTTITCRASQGISRL~~L~~AWYQQKPKAPKLLI~~Y~~VASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQANSPFTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHKVYACEVTHQGLSPVTKSFNRGEC

XENP22974

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCFCSVLHEALHSHYTQKSLSLSPGK

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLIN~~Y~~ASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSN~~Y~~WMNWVRQAPGKLEWVAEIRLYSN~~Y~~ATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG~~V~~YYCT~~R~~YY
~~GN~~YGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQM~~T~~KNQVKLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCFCS
VLHEALHSHYTQKSLSLSPGK

Figure 33B

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRTITTCQASQDISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQAESFFWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23104

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYDDTSGLYHDAFDVWGQCTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPNENYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSLHEALHSHYTQKSLSLSPGK

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGPVDRFTGSGYGTFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVPGGSLRLSCVAS
GFTFSNYYWMNWVRQAPGKGLEWVAEIRLYSNYYATHYAESEVKGRTISRDDSKSTLYLQMNHLKTEDTGVYYCTRY
GNYGGYFDVWGRGLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCF
SLHEALHSHYTQKSLSLSPGK

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRTITTCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQANSEFWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23411

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFGQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYDDTSGLYHDAFDVWGQCTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPNENYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSLHEALHSHYTQKSLSLSPGK

Figure 33C

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLIN~~Y~~ASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSN~~NY~~ATHYAESVKGRFTISRDDSKSTLYLQMNNIKTEDTGVIYCTRY~~Y~~
QNYGGYFDVWGRGTLVTVSS/EPKSSDKTHTCPGPCAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREOMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VLHEALHSHYTQKSLSLSPGK

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISRL~~L~~AWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQAESFPWTFGQGTKVEIK/RTVAAPS~~V~~FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 34A

XENP	Antigen	K _D (nM)	k _a (1/Ms)	k _d (1/s)
22438	hulCOS	2.28	2.49E+05	5.69E-04
22437	hulCOS	0.5613	2.05E+05	1.15E-04
22436	hulCOS	1.813	2.49E+05	4.52E-04
22435	hulCOS	1.411	2.27E+05	3.20E-04
22434	hulCOS	2.766	2.33E+05	6.44E-04
22433	hulCOS	3.8	1.88E+05	7.15E-04
22432	hulCOS	0.6282	2.02E+05	1.27E-04
20896	hulCOS	0.4358	2.20E+05	9.57E-05

Figure 34B

XENP	Antigen	K _D (nM)	k _a (1/Ms)	k _d (1/s)
20896	hulCOS	<0.001	8.58E+04	<1.0E-07
22432	hulCOS	1.78	8.46E+04	1.50E-04
22433	hulCOS	9.68	5.78E+04	5.59E-04
22434	hulCOS	3.99	7.48E+04	2.99E-04
22435	hulCOS	3.44	1.28E+05	4.40E-04
22436	hulCOS	1.43	1.03E+05	1.47E-04
22437	hulCOS	0.34	7.82E+04	2.66E-05
22438	hulCOS	6.2	9.80E+04	6.07E-04

Figure 34C

XENP	Antigen	K _D (nM)	k _a (1/Ms)	k _d (1/s)
20896	hulCOS	1.58	6.55E+04	1.04E-04
22433	hulCOS	11.6	6.19E+04	7.21E-04
22740	hulCOS	11.5	7.56E+04	8.68E-04
22741	hulCOS	13	8.00E+04	1.04E-03
22742	hulCOS	2.08	8.49E+04	1.76E-04
22743	hulCOS	4.41	9.21E+04	4.06E-04
22744	hulCOS	2.15	6.07E+04	1.30E-04
22745	hulCOS	9.12	7.87E+04	7.18E-04
22746	hulCOS	4.52	5.97E+04	2.70E-04
22747	hulCOS	10.1	5.56E+04	5.63E-04
22748	hulCOS	11.9	6.64E+04	7.88E-04

Figure 35

	hulCOS			cynolCOS		
XENP	K_D (nM)	k_a (1/Ms)	k_d (1/s)	K_D (nM)	k_a (1/Ms)	k_d (1/s)
20896	2.09	5.45E+04	1.14E-04	2.41	5.70E+04	1.38E-04
22433	41.30	2.64E+04	1.09E-03	35.30	3.10E+04	1.10E-03
22744	3.91	3.50E+04	1.37E-04	5.82	3.27E+04	1.90E-04
22745	17.60	6.01E+04	1.06E-03	14.50	7.84E+04	1.14E-03
22746	10.10	3.76E+04	3.81E-04	11.90	3.14E+04	3.73E-04
22747	18.40	5.05E+04	9.27E-04	21.50	4.53E+04	9.73E-04
22748	42.30	4.26E+04	1.80E-03	39.40	4.93E+04	1.94E-03
23090	2.73	5.60E+04	1.53E-04	ND	ND	ND
23091	5.62	4.75E+04	2.67E-04	ND	ND	ND
23092	4.30	5.80E+04	2.50E-04	ND	ND	ND
23093	5.43	5.70E+04	3.09E-04	ND	ND	ND
23410	9.04	3.56E+04	3.22E-04	ND	ND	ND

Figure 36A

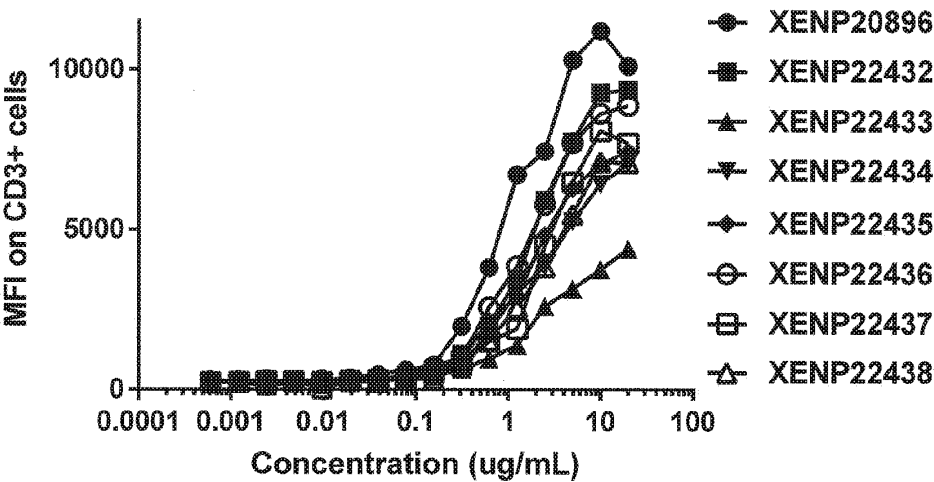


Figure 36B

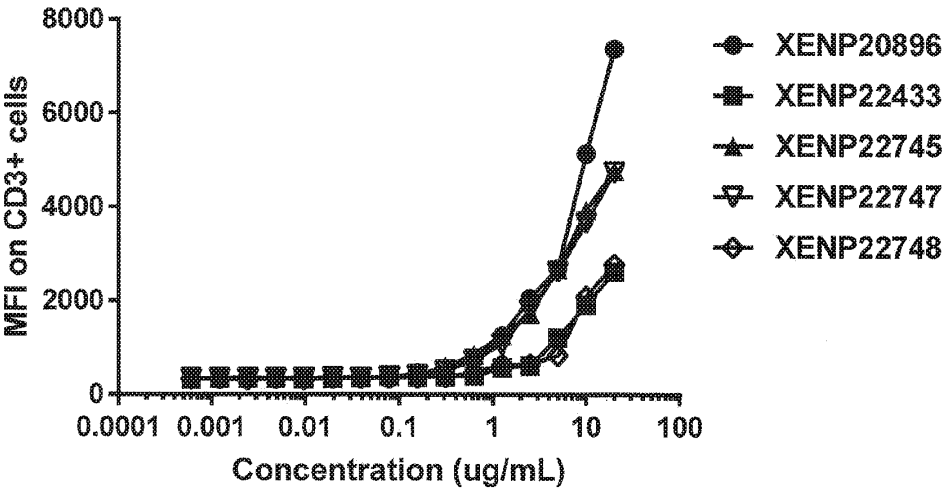


Figure 37

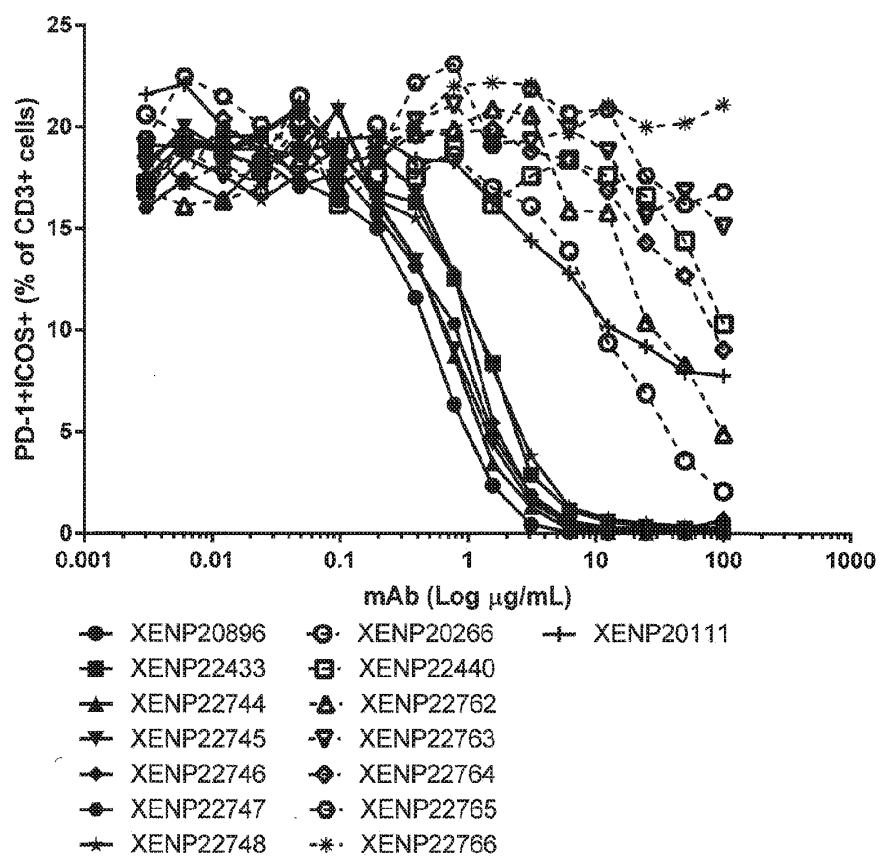


Figure 38A

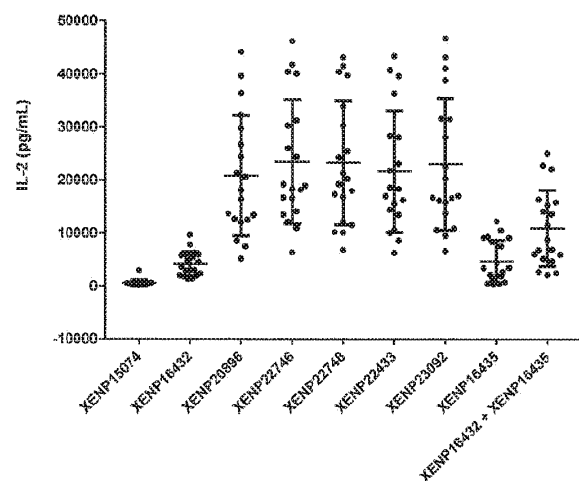


Figure 38B

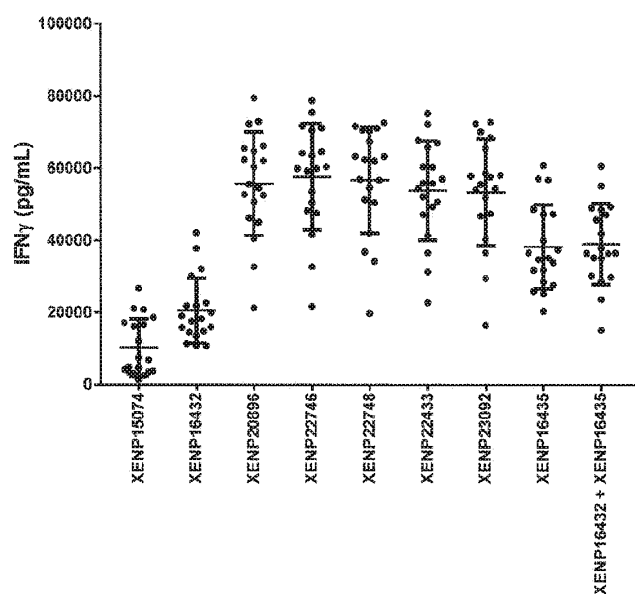


Figure 39A

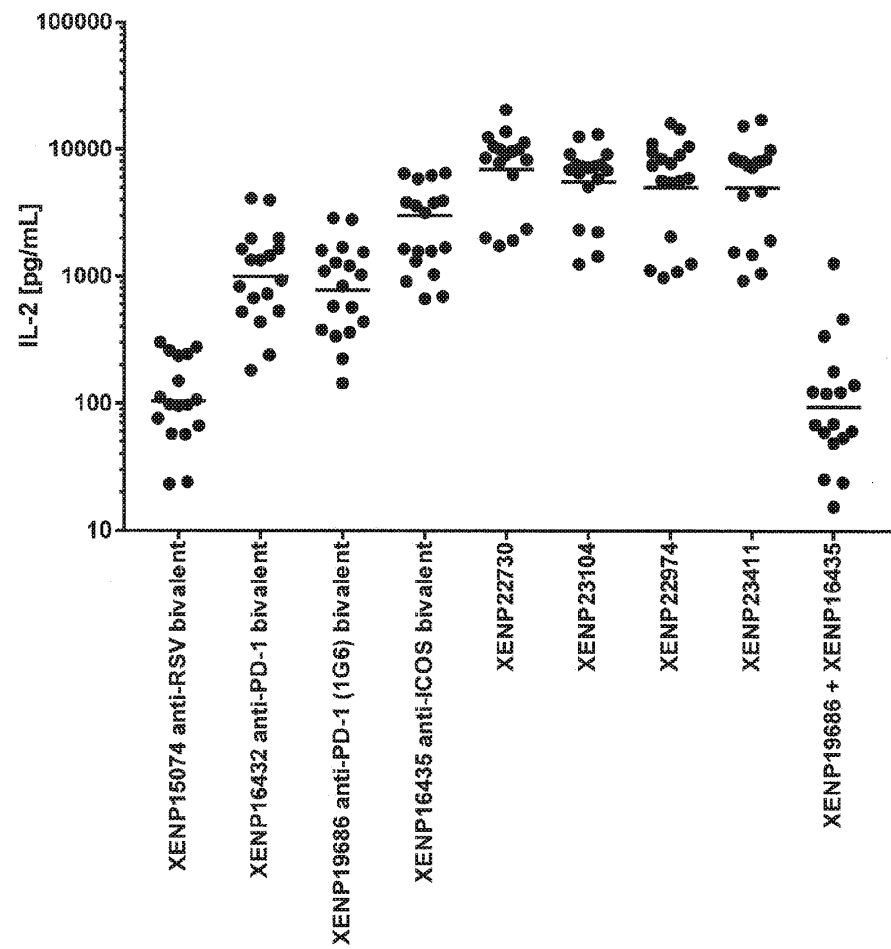


Figure 39B

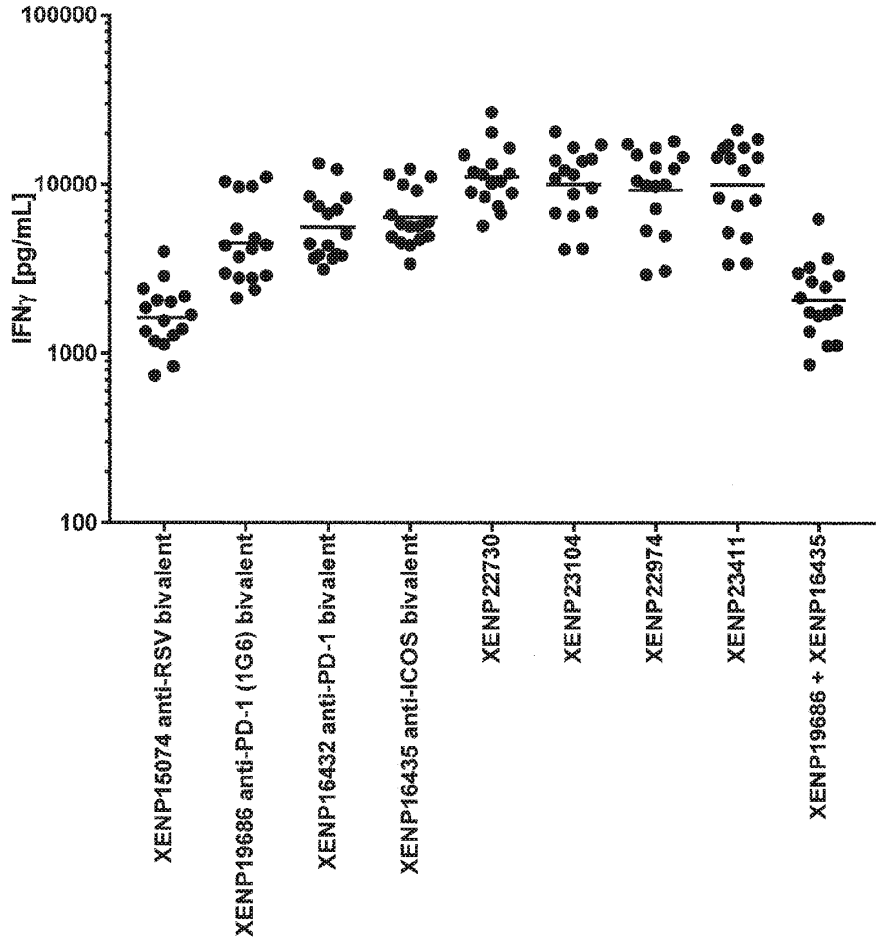


Figure 40A

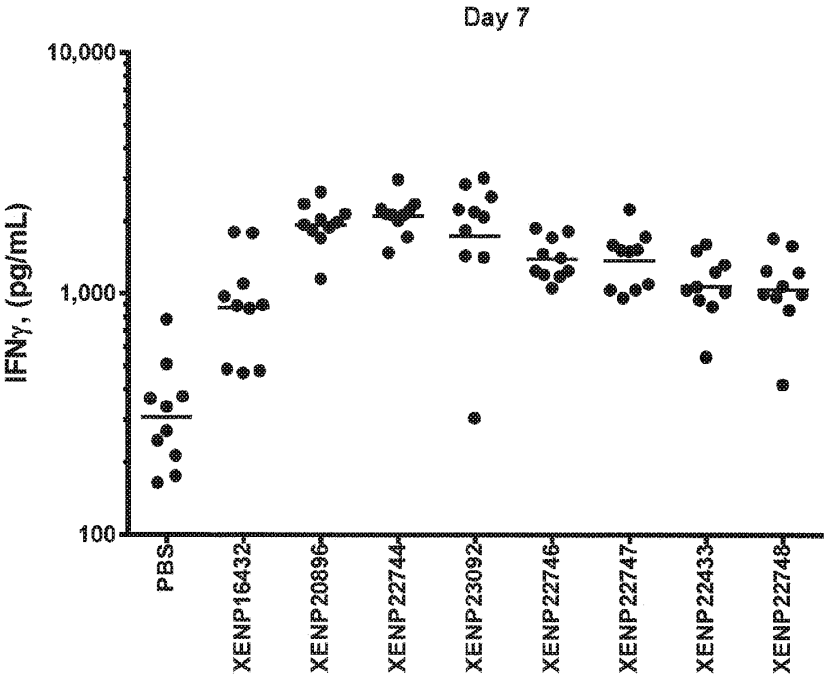


Figure 40B

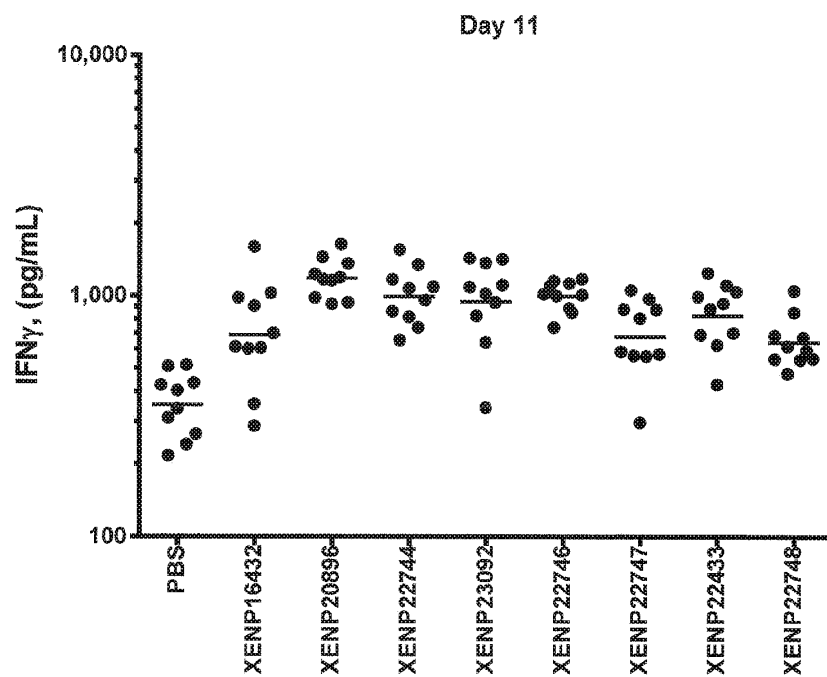


Figure 41A

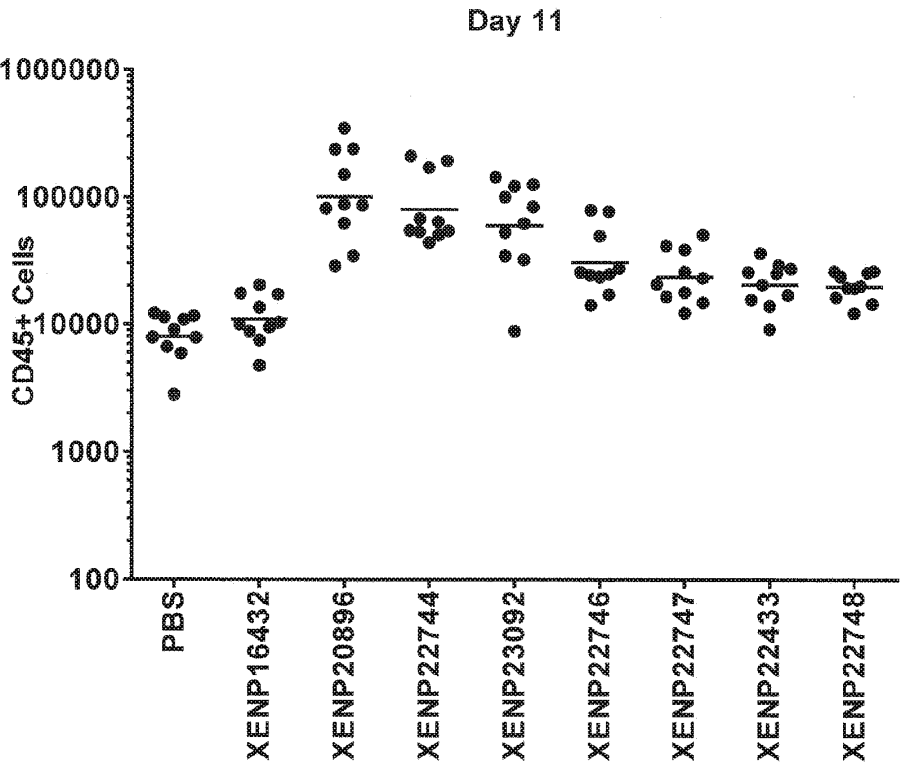


Figure 41B

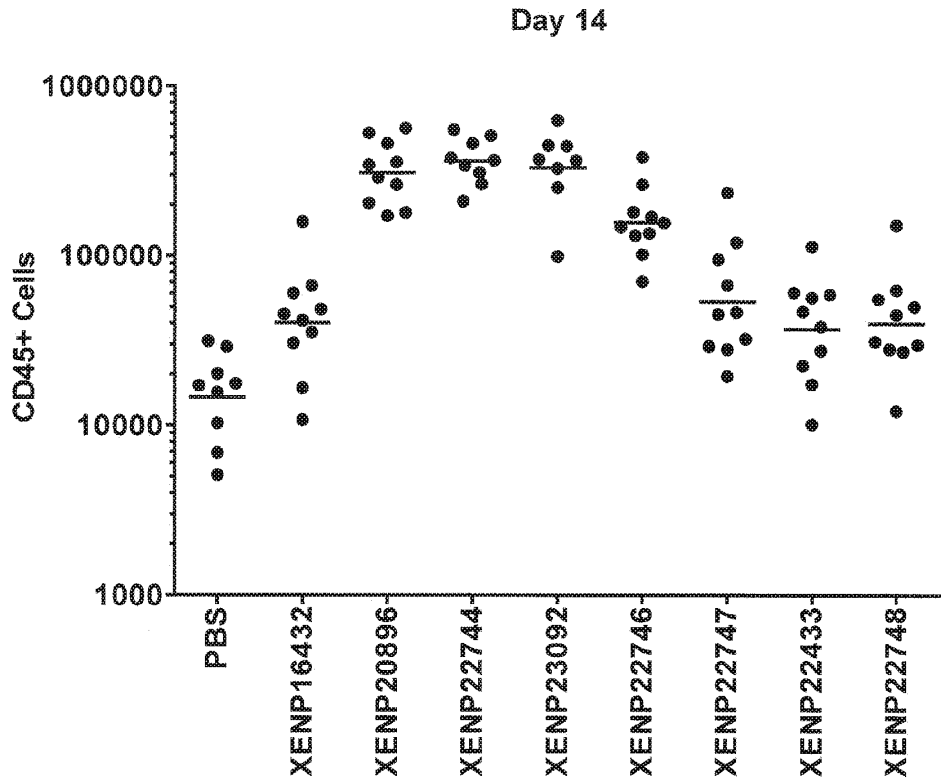


Figure 42A

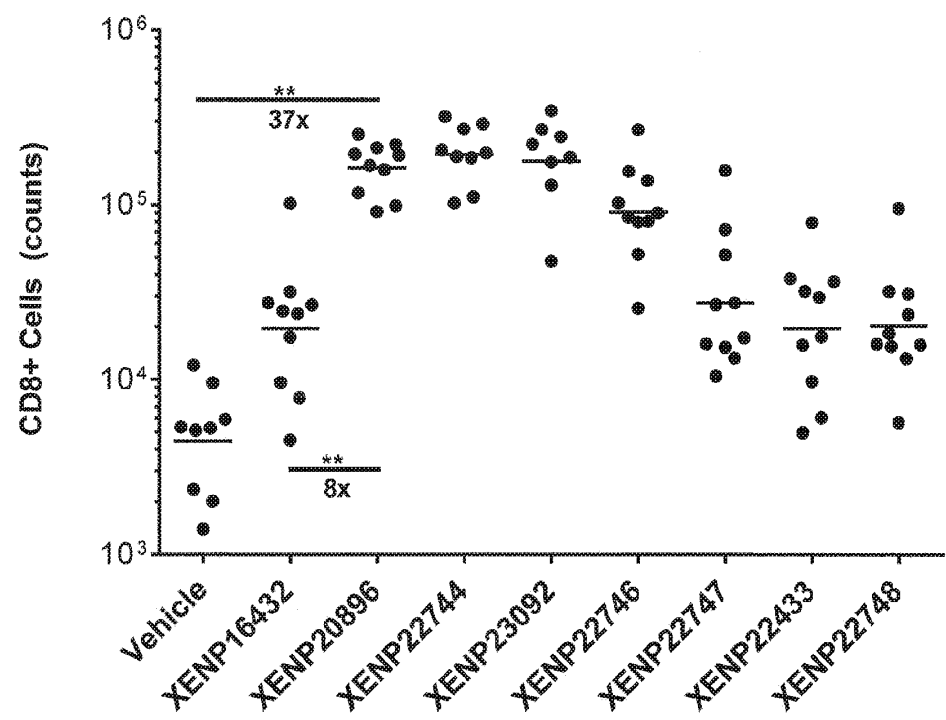


Figure 42B

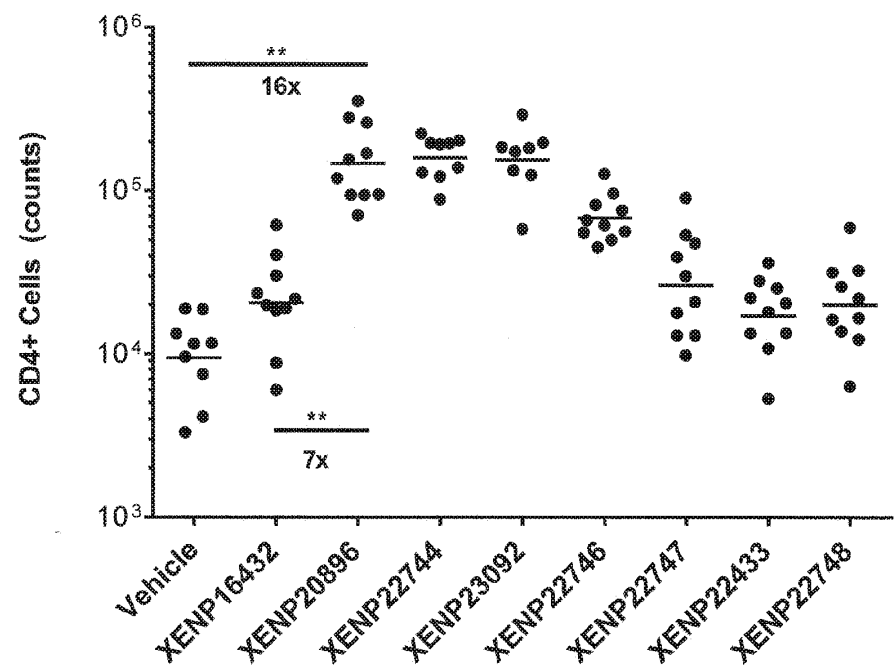


Figure 43

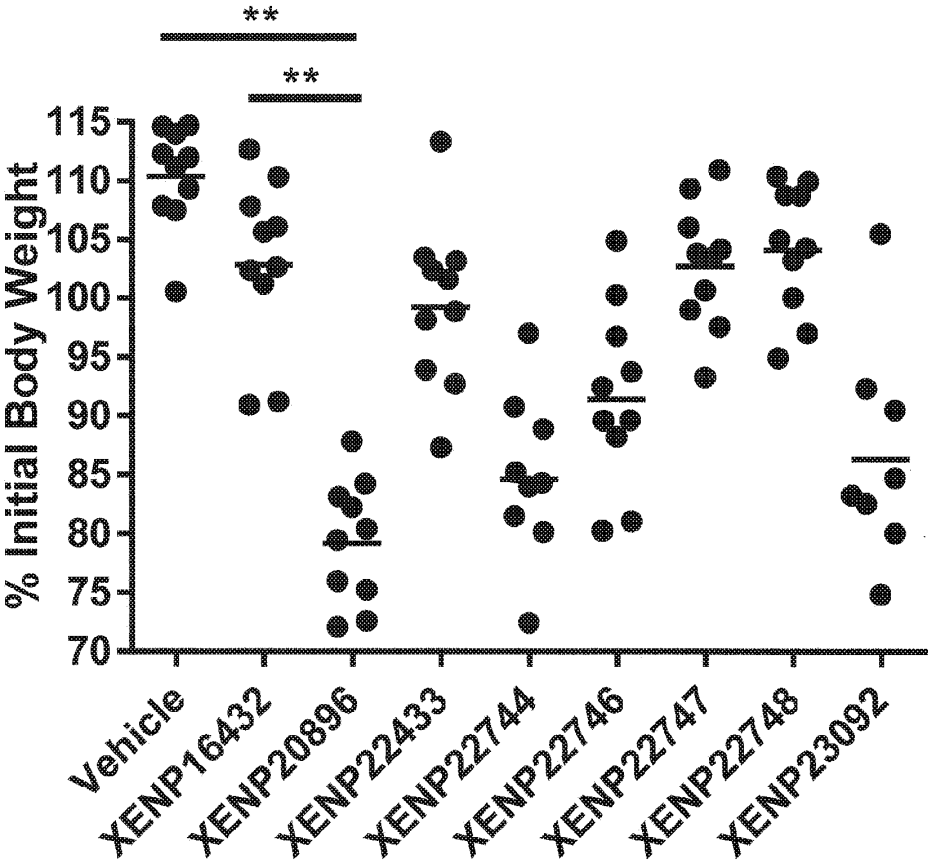


Figure 44A

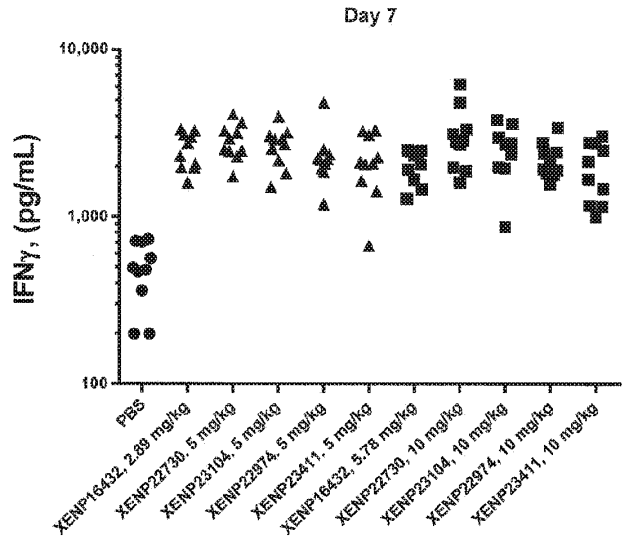


Figure 44B

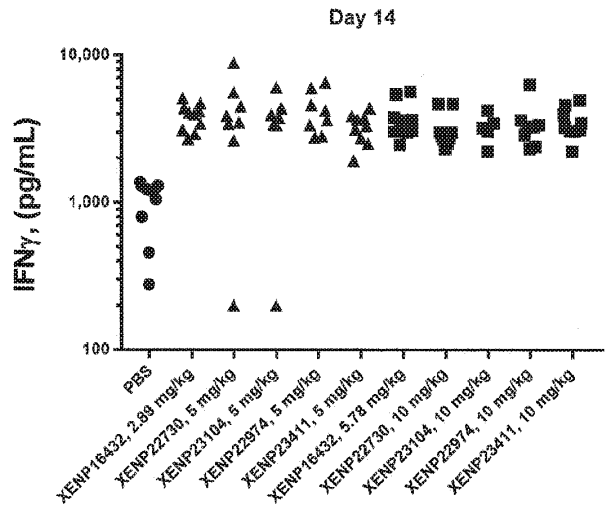


Figure 45

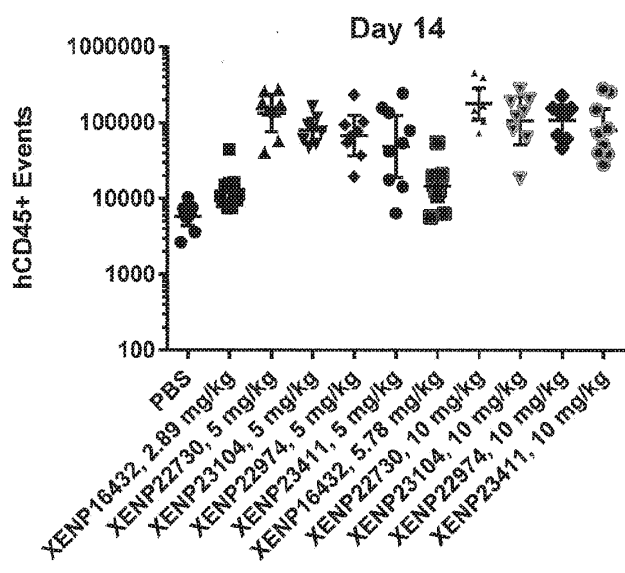


Figure 46A

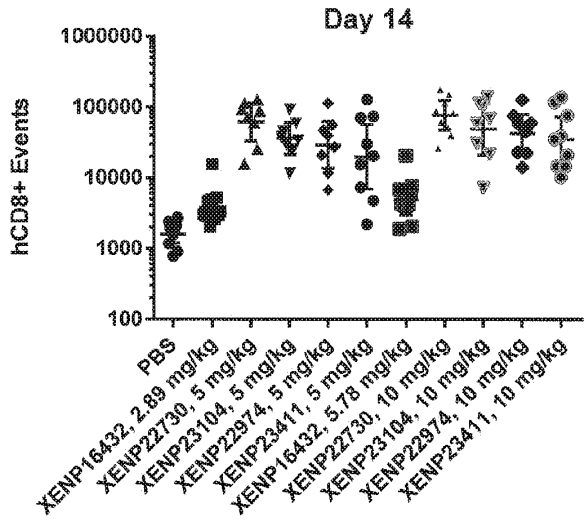


Figure 46B

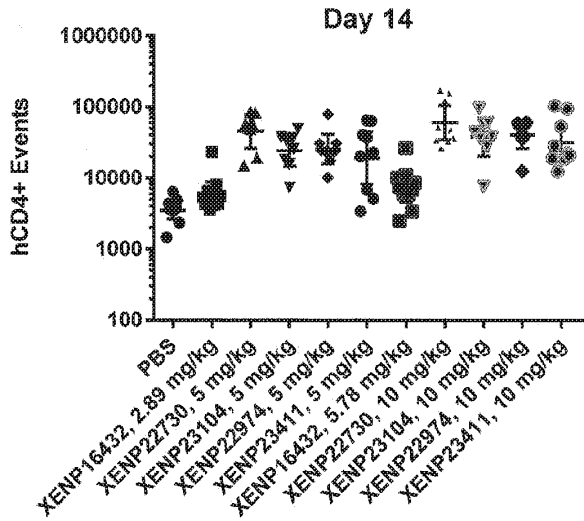


Figure 47A

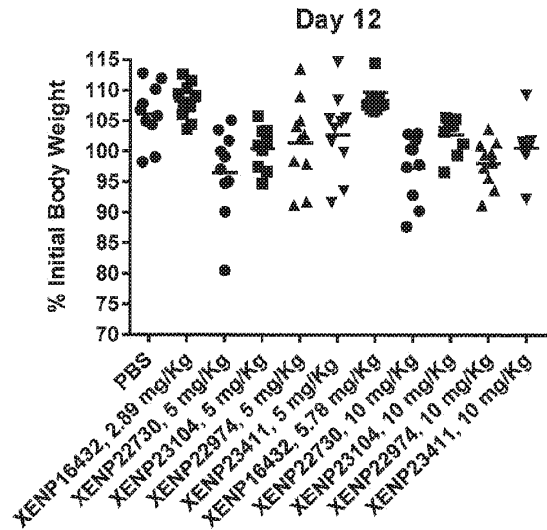


Figure 47B

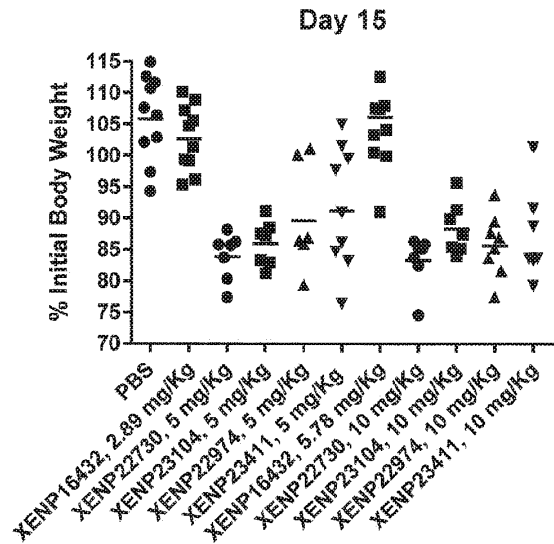


Figure 48A

XENP21828

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWKQRPQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGTLLTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDQGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGVIYYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain

DIVMTQAAPSVPTPGESVSISSCRSSKSPHNSGNIYLYWFLQRPQGSPQLLIYRMSNLASGVDPDRFSGSGSGTFTT
LKISRVEAEDVGVYYCMQHLEYPTFGGGTKLEIK/RVAAPSVEFIIPPSDEQLKSGTASVCLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21829

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

QVQLQQPGAELVRPGASVKLSCKASGYSFTSYWINWVKQRPQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTSEDSAVYYCTRWNLSTYYFDNNYYLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDQGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGVIYYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

Figure 48B

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain

DIVMTQAAPSVFVTPGESVSI~~SCRSSKSL~~HSNGNTYLYWFLQRFPGQSPQLLIYRMSNLASGVDPDRFSGSGSGTAFT
LRISRVEAEDVGVIYCMQHLEYFWTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21830

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNS
LYLQMNSLRAGDTAVYYCVRDNRKVTHEHYIYGMGVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy
Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVVYCCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDGKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain

EIVLTQSPGTLSLSPGERATLSCRASQNI~~RSSYLAWY~~QQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQDFGSSEMCSEFGGQTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21831

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNS
LYLQMNSLRAGDTAVYYCVRDKRTVTHEHYIYGMGVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 48C

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain

EIVLTQSPGTLSLSPGERATLSCRASQSISSSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQFGSSPMCSFGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22348

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGSSSVKVSCKASGYTFDYYAMHWVRQAPGQGLEWMGLISIIYSDHTNINQKFGQGRVITITADKSTS
TAYMELSSLRSEDTAVYYCGRNNGNYGWYFDVWQGQTTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRQMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSSVMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain

EIVLTQSPATLSLSPGERATLSCSASSSVSYMHYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISL
EPEDFAVYYCFQSGGYPYTFGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48D

XENP23059

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFS~~SDYWMDWVRQAPGKGLVWVSNI~~DE~~DG~~SITEYS~~PFVVKGRFTIS~~RDAKN
TLYLQMNSLRAEDTAVYYCTRW~~GRFGFDSWGQGT~~LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPEC
APFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCSV~~MHEALHNHYTQKSLS~~SPGK

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
scFv-Fc Heavy Chain

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN~~YASHRYTGVPDRFTGSGYGTEFTLT~~ISS
VQSEDFGVYYCQ~~QDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVQPGGSLRLSCVAS
GFTFSN~~YWMNVRQAPGKGLEWVAEIRLYSNNYATHAESV~~KGRFTISRDDSKSTLYLQMNNLKTEDTG~~VVYCTRY~~
~~GNVGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPECAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE~~
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQV~~KL~~TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW~~QQGNVFSCS~~
VMHEALHNHYTQKSLSLSPGK

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
Light Chain

DIVMTQSPDSLAVSLGERATINCKSSQSLSGSFNYLTWYQQKPGQPPKLLI~~FYASTRHTGVPDRFSGSGSGTDFTL~~
TISSLQAEDVAVYYCHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49

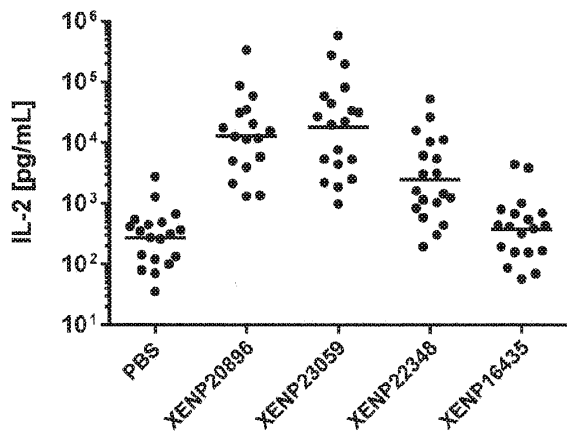


Figure 50

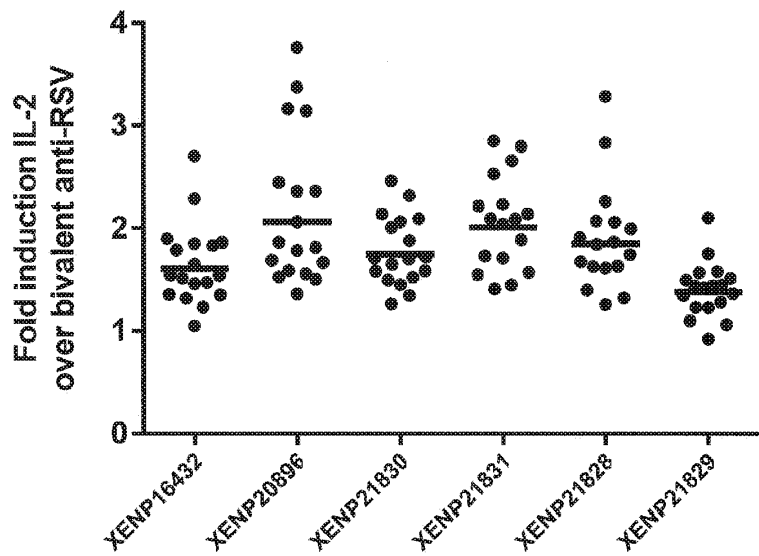


Figure 51

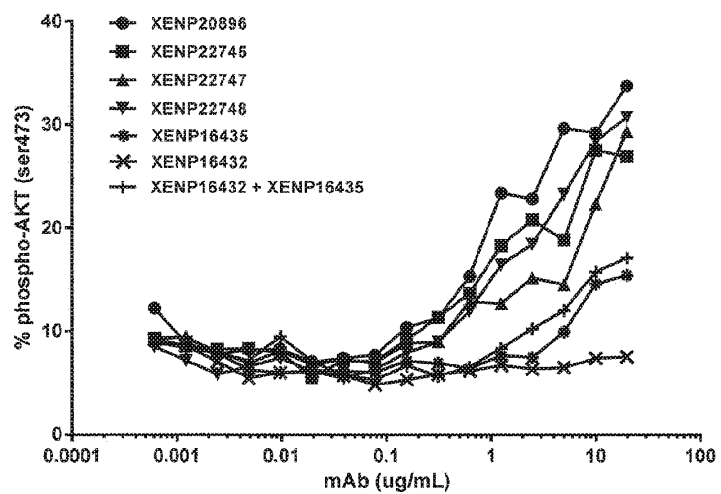


Figure 52

		XENP16435 +			
		XENP23104	XENP16435	XENP19685	XENP19686
Th17	IL17A	14.8	7.6	2.0	5.9
	IL17F	5.4	3.3	1.8	3.9
	IL22	3.6	2.5	1.3	2.7
	IL21	2.0	1.4	1.0	1.5
	CCL20	2.5	1.7	1.4	1.7
	IL1R1	1.1	1.2	1.1	1.4
	IL23R	1.2	1.2	1.1	1.1
	STAT3	1.0	0.9	1.1	0.9
	RORC	1.3	1.4	1.2	1.2
	CCR6	0.8	1.0	1.0	1.0
Th1	IFNG	13.1	3.5	1.8	5.7
	TNF	1.8	1.6	1.0	1.6
	IL12A	0.8	0.8	1.1	0.9
	IL12B	2.3	1.4	1.3	1.4
	TBX21	1.6	1.3	1.1	1.4
	STAT1	0.9	1.0	1.1	1.0
	STAT4	0.9	0.9	1.0	0.8
	IRF1	1.0	0.9	1.0	1.0
	CXCR3	0.9	1.0	1.0	0.9
	CCR5	0.8	0.8	1.0	0.7
Th2	IL4	1.2	1.1	1.2	1.2
	IL5	4.3	3.6	1.8	3.2
	IL9	10.3	3.1	2.5	5.1
	IL13	2.4	1.9	1.4	1.8
	IL24	1.7	1.3	1.3	2.0
	TNFSF4	1.0	1.1	0.7	0.9
	GATA3	1.3	1.1	1.2	1.1
	STAT6	0.9	1.0	1.0	0.9
	CCR2	0.8	0.9	1.0	0.9
	CCR3	1.0	0.8	0.8	0.9
Treg	TGFB1	1.1	1.1	1.0	1.0
	SMAD3	0.7	0.8	0.9	0.8
	ITGAE	0.9	0.8	1.0	0.8
	FOXP3	1.1	1.0	1.4	1.3

Figure 53A

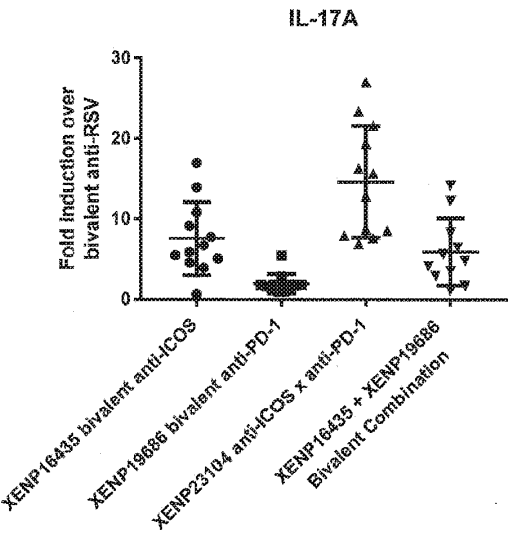


Figure 53B

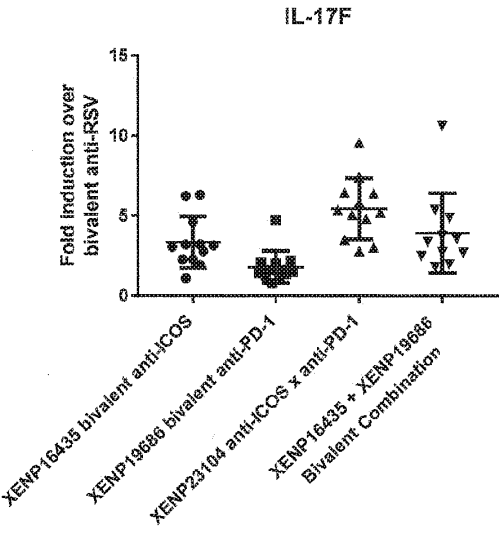


Figure 53C

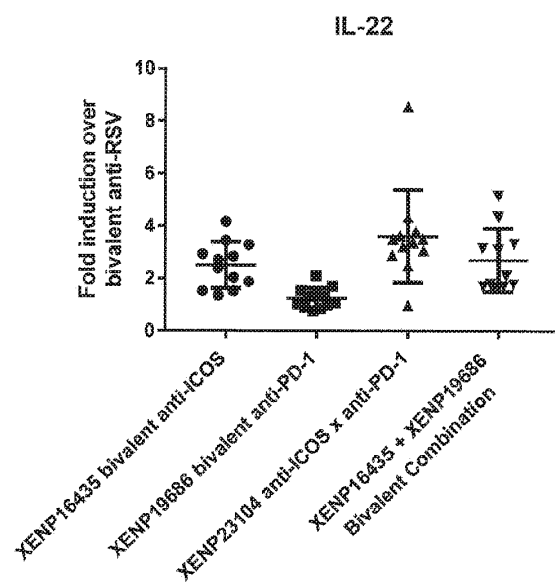


Figure 53D

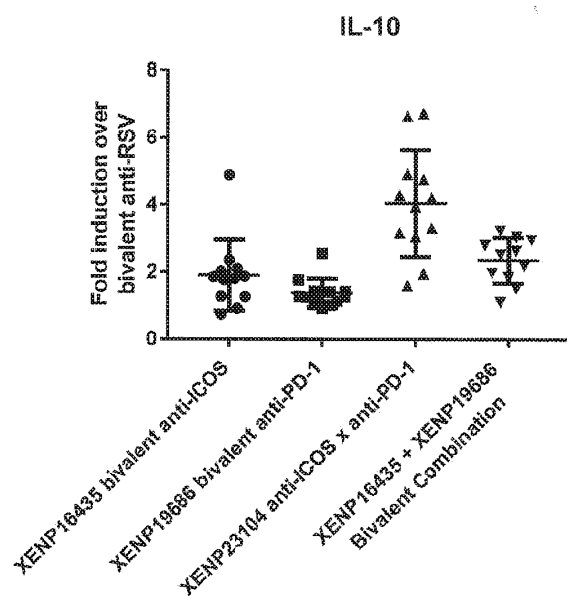


Figure 53E

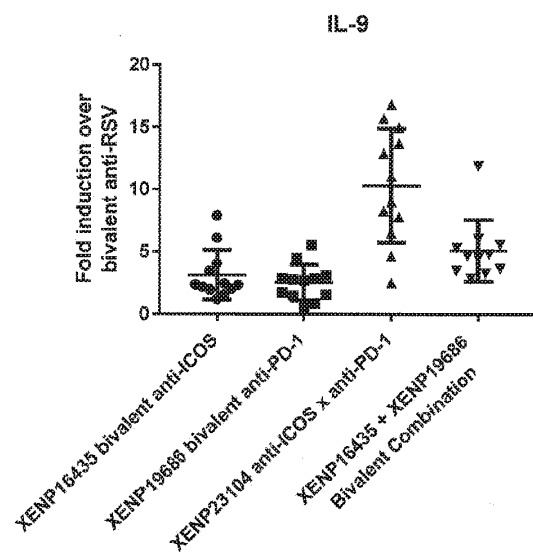


Figure 53F

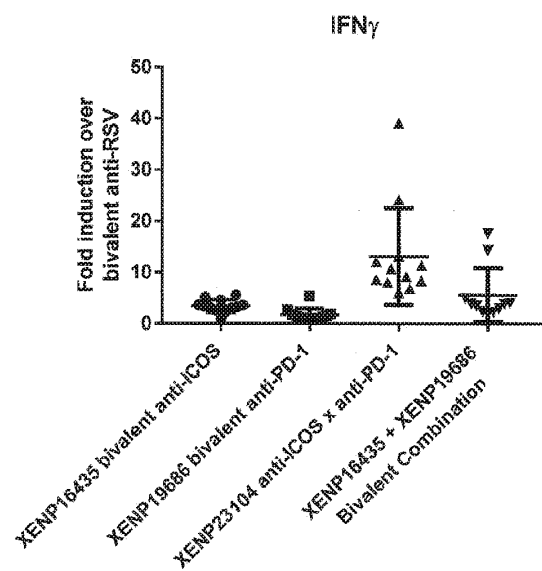


Figure 54

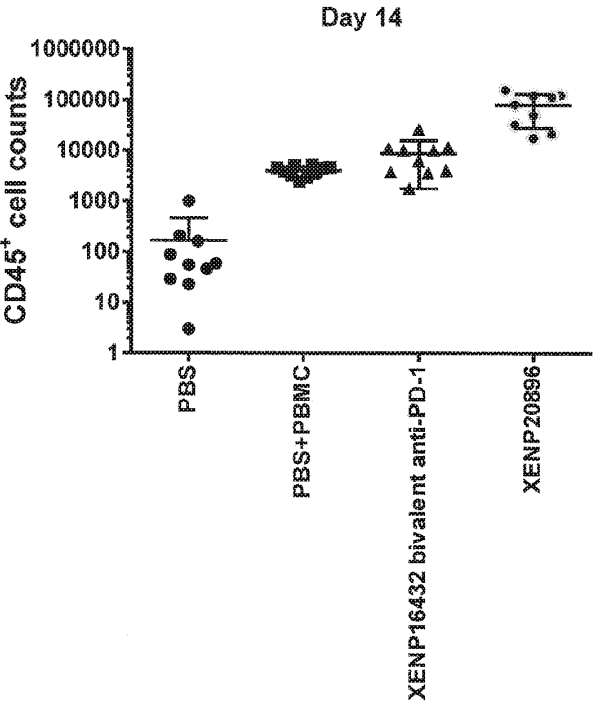


Figure 55A

Central scFv

Fab-Fc Heavy Chain

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVD
KKVEPKSCDKTHCTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYXNSTYRVVSVLTVLIHQD
WLNREYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSEFFLYSKLT
VDKSRWEQGDVFCSVMHEALHNHYTQKSLSLSPGK

Fab-scFv-Fc Heavy Chain

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCGKPGSGKPGS /**VH2-scFv linker**-
VL2 /GGGGSGGGGSKTHCTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREOMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFL
YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Light Chain

VL1 /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Central scFv2

Heavy Chain

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCGGGGGGGGGS /**VH2-scFv linker**-
VL2 /GGGGSGGGGSKTHCTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFL
YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 55B

Light Chain

VL1/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Bispecific mAb

Heavy Chain 1

VH1/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSDTKVD
KKVEPKSCDKTHCTCPRCAPAPVAGPSVFLPPKPKDITLMISRTPEVTCVVVDVCKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSEFFLYSKLT
VDKSRWEQGGVTFSCVMHEALHNHYTQKSLSLSPGK

Heavy Chain 2

VH2/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVD
KKVERKSCDKTHCTCPRCAPAPVAGPSVFLPPKPKDITLMISRTPEVTCVVVDVCKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLT
VDKSRWQGGVTFSCVMHEALHNHYTQKSLSLSPGK

Light Chain 1

VL1/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Light Chain 2

VL2/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Figure 55C

DVD-Ig

Heavy Chain

VH1 /ASTKGPSVFELAP/**VH2** /ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGEFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Light Chain

VL1 /RTVAAPSVEFIPEP/**VL2** /RTVAAPSVEFIPEPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDDSKDSYSTLSSTLTLSKA
DYEKKHYACEVTHQGLSSEFTKSFNRGEC

Trident

Heavy Chain 1

VL1 /GGGSGGGG/**VH1** /GGCGGGEVAAACEKEVAALEKEVALEKEPKSSDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQV
SLTCDVSGFYPSDIAVEWESDGPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGVFSCVMHEALHNHYTQKSLSLSPGK

Heavy Chain 2

VH2 /ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGKTYTCNVNHKPSNTKVD
KKVERKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGEFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Light Chain 1

VL1 /GGGSGGGG/**VH1** /GGCGGKVAACEKEVAALEKEKVAALKEKVAALKE

Figure 55D*Light Chain 2*

VL2/RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SFVTKSFNRGEC

Figure 56A

XENP18920

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain

QVQLVESGGGVQPGESLRLDCKASGITFSNSGMHWVRQAPGKGLEWAVIYDGSKRYAYADSVKGRFTISRDNKNTLFLQMNSLRAEDTAVYYCATNDYWGQGTLV
 TVSS/ASTRGPSVFLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTQYICNVNHNKPSDTKVKKVEPKSCD
 KTHCTPPCPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVWVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAP
 IEKTIKAKGQRPDPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFELYSKLITVDKSRWEQGDVFCSSVMHEALHNHYTQKS
 LSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain

QVQLVESGGGVQPGESLRLDCKASGITFSNSGMHWVRQAPGKGLEWAVIYDGSKRYAYADSVKGRFTISRDNKNTLFLQMNSLRAEDTAVYYCATNDYWGQGTLV
 TVSS/GKPGSGKPGSGKPGSGKEGS/EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIYDASNRAIGIPARFSGSGSGFTFTLTISLSEPEDE
 AVYICQSSNWPRTEFGQGTKEIK/EPKSSDKTHTCPECPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVWVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 RVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQRPDPQVYTLPPSREQMTKNQVKLITCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSK
 LITVDKSRWQOGNVEFCSSVMHEALHNHYTQKSLSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIYDASNRAIGIPARFSGSGSGCTDFTLTISLSEPEDEFAVYYCQSSNWPRTEFGQGTKEIK/R
 TVAAPSVEITFPSPDEQLKSGTASVTVCLLNNEFYREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 568

XENP24130

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_HOL0_scFv Fab-Fc Heavy Chain

QVQLQESGPGCLVKPSQTLSTCTVSGGSISSGAYYMSWIRQHPGKGLIEWIGIYYNGNTYYNPSLRRTVISVDTSKNQFSUKLSSVTAADTAVYYCVRASDYVMGGYH
 YFDAFDLWGRGTLTVSS/ASTKGPSVFTPLAPSSKSTSGGTAALGCLVKDYFPEPVVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPS
 DTKVDKKVEPKSCDKHTHTCPCPAPFVAGPSVFLPPPKDTHMISRPEVTCVVDVKHEDPEVKINWYVDGVEVHNAKTKPEREEYNSTYRVSVLTIVLHQDWLNGK
 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREMTKNQVSLTCDVSGFYFSDIAVEWESDQGPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWEQGDVFPSCS
 VMHEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_HOL0_scFv scFv-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPESHGGTNYAOKFGQGVMTMDRTSISTAYMELSRLESDDTAVYYCARTYYIDSSGYH
 DAFDIWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPFSSVSASVGDRTVITTCRASQGISRLLAWYQQKPKAPKLLIYVASSLSQSGVPSRFSGSGGTDF
 TLTISLQPEDFATYYCQANSEFTWTFGGGTKVEIK/EPKSSDKTHHTCPPCPAPFVAGPSVFLPPPKDTHMISRPEVTCVVDVKHEDPEVKINWYVDGVEVHNAK
 TKPREEQYNSTYRVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGIFYFSDIAVEWESNGQGPENNYKTTTPPV
 LDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_HOL0_scFv Light Chain

QSVLTQPPSASGTFGQRTVISCSSGNSNIGSNVNWYQQLPGTAPKLLIYGNQRPQGVPPRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGPVGSGGTQVTV
 L/GQPKAAPSVTLFPPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETITPPSKQSNKNKYAASSYLSTPEQWKSRSYSQVTHEGSTVEKTVAPTECS

Figure 57A

XENP23406

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDTSISTAYMELSRRLSRDDTAVYVCARTYYDSSGYYH
DAFDINGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSDT
KVDKKEPKSCDKTHCTCPCPAPFVAGPSVLEFPFKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTPREEEYNSTYRVSVLTIVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSFGYPQSDIAVEWESDGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCSCVM
HEALHNHYTQKSLSLSPGK

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-scFv Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDTSISTAYMELSRRLSRDDTAVYVCARTYYDSSGYYH
DAFDINGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNT
KVDKKEPKSCGKPGSKPGS/EIVLTQSPATLSAPEGRTVITCRASQSVGNDVAVYQKQKQAPALLINYNASHRYTGVDPDRFTGSGYGEFTLTISVQSEDEGVY
CQDFSSPRTFGGQTKVEIK/EXPGSGKPGSGKPGSG/ELVLSGSGGILVKPGSLRLSCVASEGTFSNYMNWVRQAPGKLEWVAEIRLYSNVYATHYAESVK
GRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRIYGNIGGYFDVWGRGTLTVSS/EGGSGGGGGKTHTCPPCPAPPVAGFSVFLFPPKPKDTLMISRTPEVTCVVD
VKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREOMTKNQVLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Light Chain

DIQMTQSPSSVSASVGRVTITCRASQGISRLLAWYQOKPGKAPKLLIYVASSLQSGVPSRFSGSGSDTFTLTISLQPDFAFYCCQANSFFWTFGQGTKEIK/R
TVAAPSVFIPTPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQDESVEQEDSKDSTYLSLSTLTLSKADYEXHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23407

>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDTSISTAYMELSRRLSRDDTAVYVCARTYYDSSGYYH
DAFDINGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSDT
KVDKKEPKSCDKTHCTCPCPAPFLLGGPSVLEFPFKPKDTLMISRTPEVTCVVDVEHEDEPEVKFNWYVDGVEVHNAKTPREEEYNSTYRVSVLTIVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSFGYPQSDIAVEWESDGPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFCSCV
MHEALHNHYTQKSLSLSPGK

Figure 57B

```

>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-scFv-Fc Heavy Chain
QVQLVQSGAEVKKPKGASVKVSKCASYTFTGYIMHWVRQAPGQGLRWGNTNPHSGGTNYAQKQFQRVTRTRDTSISTAYMELSLRSDDTAVYICARIYYDSSGYYH
DAFDIWGGTMTVSS/ASTKGPSVFPELAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNT
KVDKKEPKSCGKPGSGKPGS/EIVLTQSPATLSAEPGERVTLTCRASQSYGNDVAVYQQKPGQAPRLLLINVASHRITGVDPDRFTGSGYGTFTLTISSVQSEDFGVY
CQDFFSPRTFGGGTKVEIK/EGEGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASFTEFSNYMMNWVRQAPGKLEWVAEIRLYSNKYATHYAESYK
GRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRYGNYGGYFDVWGRGTLTVSS/CGGSGGGGSKTHPCPPAPELLCGPSVELFPKPKDILMISRTPEVTCVVV
DVEHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAFAPAPIEKTIISKAGQPREPQVYTLPPSREQMTKNQKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFTFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Light Chain
DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQOKPKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSSSQDEDAFYCCQANSFPTFQGTVEIK/R
TVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYERHKVYACEVTHQGLSSFPVTKSENRGEC

XENP24128
>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMMNWVRQAPGKLEWVAEIRLYSNKYATHYAESYKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRYGNYGGYF
DVWGRGTLTVSS/ASTKGPSVFPELAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSDTKVD
KKVEPKSCDKTHTCPCPAPPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVHEDPEVKFNWYVDGVEVHNAKTKPREEYINSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTIISKAGQPREPQVYTLPPSREQMTKNQVSLTCDVSGFTFSNMMNWVRQAPGKLEWVAEIRLYSNKYATHYAESYKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRYGNYGGYF
LNHYTQKSLSLSPGK

>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_H0L0_scFv Fab-scFv-Fc Heavy Chain
EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMMNWVRQAPGKLEWVAEIRLYSNKYATHYAESYKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRYGNYGGYF
DVWGRGTLTVSS/ASTKGPSVFPELAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVD
KKVEPKSCGKPGSGKPGS/QVQLVQSGAEVKKPKGASVKVSKCASYTFTGYIMHWVRQAPGQGLRWGNTNPHSGGTNYAQKQFQRVTRTRDTSISTAYMELSLRSD
TAVYICARTYYDSSGYYHDAFDIWGGTMTVSS/EGEGSGKPGSGKPGSGKPGS/DIQTQSPSSVSASVGDVITITCEASQGISRLLAWYQOKPKAPKLLIYVAS
SLQSGVPSRFSGSGSGTDFTLTISLQPEDDAFYCCQANSFPTFQGTVEIK/CGGSGGGGSKTHPCPPAPELVAGPSVFLFPKPKDILMISRTPEVTCVVVD
VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAGQPREPQVYTLPPSREQMTKNQKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSDGSFTFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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Figure 57C

>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_HOL0_scFv Light Chain
EIVLTQSEATLSASPGERVTLTCRASQSVGNDVAWYQOKPCQAPRLINYLASHRYTCVDPDRFTGSGYGTEFTLTISVQSEDFGVYCCQDFSSPRTFGGGTKVEIK/R
TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 58

XENP24123

>XENP024123 1G6_H1.279_L1.194_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Heavy Chain

EVQLVESGGGLVKPQGLKSLSCVASGFTFSNYMNMWVRQAPCKGLEWAEIKLYNNYATHVAESVKGRFTISRDSKSTIYLQNNLKTEDTGVIYCTRYKNGYGYF
 DWNGRGTLTVSS/ASTKGPSVEFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKVD
 KKVEPKSGGGSGGGGS/QVQLVQSGAEVKKPGASVKVSCKRSGYFTTGYIMHWYRQAPCGQGLEWGWINPHSGGTNYAQKFGQGRVTMTDRDTSISTAYMELSLRLSD
 TAVYICARTYYDSGGYYHDAFDIWGGQTMVTYSS/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTITCRASQGISRLAWYQQKPKAPKLLIYVAS
 SLQSGVPRFSGSGGFTLTLSLQPEDFATYYCQANSPFWTFQGTKEIK/GGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTITCRASQGISRLAWYQQKPKAPKLLIYVAS
 VKHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
 SDIAVENESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNHYTQKSLSLSPGK

>XENP024123 1G6_H1.279_L1.194_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Light Chain

EIVLTQSPATLSASGERVTITCRASQSGVNDVAVWQKPGQAPRLINYNASHRYTGVPRDFTSGYGTETLTISVSQSDFGVYVCOQDFSSPRTFGGKVEIK/R
 TVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSLTLSKADYERHKVYACEVTHQGLSPVTKSFNRGEC

XENP24125

>XENP024125 LOPD180[PD-1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Heavy Chain

QVQLQESGPGLVKPQGLKSLTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGIYYNGNTYYNFSLSRRTISVDTSKNQFSLKLSVTAADTAVYVCRASDYVWGGYH
 YFADFLLWGRGTLTVSS/ASTKGPSVEFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPS
 NTKVDKVEPKSGGGSGGGGS/QVQLVQSGAEVKKPGASVKVSCKRSGYFTTGYIMHWYRQAPCGQGLEWGWINPHSGGTNYAQKFGQGRVTMTDRDTSISTAYMELSR
 LRSDDTAVYICARTYYDSGGYYHDAFDIWGGQTMVTYSS/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTITCRASQGISRLAWYQQKPKAPKLL
 IYVASSLOSQGVSRFSGSGGFTLTLSLQPEDFATYYCQANSPFWTFQGTKEIK/GGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTITCRASQGISRLAWYQQKPKAPKLL
 CVVVDVKHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV
 KGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNHYTQKSLSLSPGK

>XENP024125 LOPD180[PD-1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Light Chain

QSVLTQPPSASGTPGQRTVISCSGSNSNIGSNSVNWYQQLPCTAPKLLIYGNORSGVPDRFSGSKSGTSASLALSGLOSEADYYCAAWDDSLNGPFGGGTKVTY
 L/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFEYFGAVTVANKADSSPVKAGVTTTPKQSNKNKYAASSYLSTPEQWKSHRYSYCCQVTHEGSTVEKTVAPTECS

Figure 59

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>XENP024134 IG6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Heavy Chain 1
EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYYMHWVRQAPKGLKWAETRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGVIYCTRIYGYNGGYF
DWNGRGTLIVTSS/ASTKGPSVFPELAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTICNVNHNKPSDKVD
KKVEPKSCDKTHTCPPCPAPVAGPSVFLFPKPKDTIMISSTPEVTCVVVDVHHDPEVFENWYVDGVEVHNAKTKPREEEYNSTIRVVSFLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDYSGFPSDIAVEWESDGPENNYKTTFPVLDSGSEFFLASKLITVDKSRWEQGVFSCSWHEA
LNHYTQKSLSLSPGK

>XENP024134 IG6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Heavy Chain 2
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMRDTSISTAYMELSRISDDTAVYICARTIYYDSSGYH
DAEDIWGQGTMTVSS/ASTKGPSVFPELAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTICNVNHNKPSNT
KVDKKVERKSCDKTHTCPPCPAPVAGPSVFLFPKPKDTIMISSTPEVTCVVVDVHHDPEVFENWYVDGVEVHNAKTKPREEQYNSTIRVVSFLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTFPVLDSGSEFFLASKLITVDKSRWEQGVFSCSWH
HEALNHYTQKSLSLSPGK

>XENP024134 IG6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Light Chain 1
EIVLTQSPATLSASPGGERVTLTCRASQSVGNDAWVYQOKPGQAPRLINYNASHRYTGVPDRFTGSGYGTETLTITISSVQSEDFGVVYCOQDFSSPRTFGGQTKVEIK/R
TVAAPSVFIFFPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHVYACEVTHQGLSSPVTIKSFNRGEC

>XENP024134 IG6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Light Chain 2
DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQOKPGKAPKLLIYVASSLSQSGVPSRFSGSGSGTDFTLTITSSLPQEDFATYYCOQANSEFWTFGGQTKVEIK/R
TVAAPSVFIFFPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHVYACEVTHQGLSSPVTIKSFNRGEC

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Figure 60

>XENP024122_1G6_H1.279_L1.194_[anti-ICOS]_H0L0_IgG1_Heavy_Chain
EVLVESGGGLVFGGSLRLSCVASEFTFSNYMNWVROAPGKGLEWAEIRLYSNVATYAEVSKGRFTISRDSKSTLYLQMNLTEDTGVYYCTRIYGNKGGYF
DVGRCITLVTVSS/ASTKCPSEVPELAP/QVQLVQSGAEVKKPCASVKVCKASCYTTTCYIMHWVROAPGQGLEWMGWINPHSGGTNYAOKFQGRVTMTPTDTSISTAYM
ELSLRSDDTAVYVCARTYYYSGGYXHDADFIDWGQGTMTVTVSS/ASTKGPSEVPELAPSSKSTSGGTAALGCLVKDYFPEPEVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVTVPESSSLGTQTYICNVNHPKSNITKVDKKVEPKSCDKTHCTCPCPAPPAVAGPSVFLFPPKPKDITLMISTRPEVTCVVVDVYKHEDPEYKFNWYVDGVEVHNATKRP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPEVLDL
DGSFFELYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024122_1G6_H1.279_L1.194_[anti-ICOS]_H0L0_IgG1_Light_Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQOKPGQAPRLINVASHRYTCVPDRFTGSGYGTETFTLTSSVQSEDFGVYCOQDFSSPRTFGGCTKVEIK/R
TVAAPSVFIIPP/DIQMTQSPSSVSASVGDRVTITCRASQGISRLLLAWYQOKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFLTITISSIQPEDFATYYCQQAISFPW
TFQGGTKVEIK/RTVAAPSVFIIPPSPDEQLKSGTASVVCLINNFIYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISSTLTLSKADYEKKHKVYACEVTHQGLSSP
VTKSENRGEC

Figure 61A

XENP24132

>XENP024132 IG6 L1.194 IG6 H1.279 DART-[anti-ICOS] H0L0 Fab-Fc IgG1 Heavy Chain 1
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDAVWYQOKPGQAPRLININASHRYTIGVPDRFTGSGYGTETLTITSSVQSGDEGVYCCQDFSSPRTFGGGTKVEIK/G
 GSGGGG/EOVLVESGGGLVKPGGSLRLSCVSGFTFSNYMNMWVRQAPGQGLEWAEIRLYSNVYATHVAESVGRFTISRDDSKSTLYLQMNLIKTEDTGVYCTRY
 YGNYGGYEDVWGRGTLTVSS/SGCGGGEVAACEKEVALEKEVALEKEPKSSDKTHTCPCPAPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVKHE
 DEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTITVLHODWLNQKEYKCKVSNKALPAPIEKTISKARGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIA
 VEWESDGPENNYKTTTPVLDSDGSFTLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024132 IG6 L1.194 IG6 H1.279 DART-[anti-ICOS] H0L0 Fab-Fc IgG1 Heavy Chain 2
 QVQLVQSGAEVKKFGASVKVSKASGYTFTGYMHWVRQAPGQGLEWMGNINPHSGGTNYAQKFGQGRVTMRDTSITAYMELSLRLSDDTAVYYCARTYYVDSGGYIH
 DAFDIWGQGTMTVTVSS/ASTKGPSVFEIAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGKTKYTCNNVHKPSNT
 KVDKKVERKSCDKTHTCPCPAPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVKHEDFEVKFWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTITVLHODWLNQKEY
 KCKVSNKALPAPIEKTISKARGQPREPQVYTLPPSREEMTKNQVSLTCLVGRGYPSDIAVEWESNQGPENNYKTTTPVLDSDGSFTLYSKLTVDKSRWQOQGNVFSCVM
 HEALHNHYTQKSLSLSPGK

>XENP024132 IG6 L1.194 IG6 H1.279 DART-[anti-ICOS] H0L0 Fab-Fc IgG1 Light Chain 1
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDAVWYQOKPGQAPRLININASHRYTIGVPDRFTGSGYGTETLTITSSVQSGDEGVYCCQDFSSPRTFGGGTKVEIK/G
 GSGGGG/EOVLVESGGGLVKPGGSLRLSCVSGFTFSNYMNMWVRQAPGQGLEWAEIRLYSNVYATHVAESVGRFTISRDDSKSTLYLQMNLIKTE
 DTGVYCTRYYGNYGGYEDVWGRGTLTVSS/SGCGGGEVAACEKEVALEKEVALEKEPKSSDKTHTCPCPAPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVKH
 EDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTITVLHODWLNQKEYKCKVSNKALPAPIEKTISKARGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDI
 AVEWESDGPENNYKTTTPVLDSDGSFTLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024132 IG6 L1.194 IG6 H1.279 DART-[anti-ICOS] H0L0 Fab-Fc IgG1 Light Chain 2
 DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQOKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDETLTITSSLPQDEDFATYYCQANSPFTFGGGTKVEIK/R
 TVAAPSVFIFPPSDEQLKSGTASVCLINNFYPREAKVQWYVDNALQSGNSQESVTEQDSKDSITSLSTLTSKADYEXHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24133

>XENP024133 mAb7 (1.2) [PD-1] L1_mAb7 (1.2) [PD-1] H1 DART-[anti-ICOS] H0L0 Fab-Fc IgG1 Heavy Chain 1
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDAVWYQOKPGQAPRLININASHRYTIGVPDRFTGSGYGTETLTITSSVQSGDEGVYCCQDFSSPRTFGGGTKVEIK/G
 GSGGGG/EOVLVESGGGLVKPGGSLRLSCVSGFTFSNYMNMWVRQAPGQGLEWAEIRLYSNVYATHVAESVGRFTISRDDSKSTLYLQMNLIKTE
 REHYGTSPTAYWGQGTITVSS/SGCGGGEVAACEKEVALEKEVALEKEPKSSDKTHTCPCPAPVAGPSVFLFPKPKDILMISRTPEVTCVVVDVKH
 EDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTITVLHODWLNQKEYKCKVSNKALPAPIEKTISKARGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDI
 AVEWESDGPENNYKTTTPVLDSDGSFTLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 61B

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>XENP024133 mAb7(1.2) [PD-1]_L1_mAb7(1.2) [PD-1]_H1_DART-[anti-ICOS]_H0L0_Fab-Fc_IgG1 Heavy Chain 2
QVQLVQSGAEVKKPGASVKVCKASGVTFTGYVMHWVRQAQCGLWMGWINPHSGGTNYAQKFGQKVTWTRDTSISTAYMELSKRLRSDDTAVVYCARVYYDSSGYYH
DAFDIWGGQTMVTVSS/ASTKGESVFEIAPSSKSTSGCTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVFPSSSLGKTKYTCNNNHKESNT
KYDKKVERKSCDKTHTCPRCPAEPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTREREQYNSTYRVSVLTIVLHQDWLNGKEY
KCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSRERQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPFVLDSDGSEFLYSKLTIVDKSRWQOQGNVFCSVN
HEALHNHYTQKSLSLSPGK

>XENP024133 mAb7(1.2) [PD-1]_L1_mAb7(1.2) [PD-1]_H1_DART-[anti-ICOS]_H0L0_Fab-Fc_IgG1 Light Chain 1
EIVLTQSFATLSLSPGERATLSCRASEVDNYGMSTFMNWFQOKPGPPKLLIHAASNOGSGVPSRFSGSGGTDFTLTITSSLEPEDFAVYFCQDSKEVYTFGGGTKVE
IK/GGGSGGGG/QVQLVQSGAEVKKPGASVKVCKASVKYCKASGYSTSYMMNWVRQAAPGQGLEWIGVTHPSDSEITWLDQKEKDRVTITVQKSTSTAYMELSSLR
SEDTAVYYCAREHYGTSFFAYWGQGLTVTVSS/GGCGGGKVAACEKVAALKEKVAALKE

>XENP024133 mAb7(1.2) [PD-1]_L1_mAb7(1.2) [PD-1]_H1_DART-[anti-ICOS]_H0L0_Fab-Fc_IgG1 Light Chain 2
DIQMTQSPSSVSASVGDRTVITCRASQGISRLIYAWYQOKPGKAPKLLIYVASSLQSGVPSRFSGSGGTDFTLTITSSLPEDFAVYFCQDSKEVYTFGGGTKVEIK/R
TVAAPSVFIFPPSDEQLKSGTASVVCCLINNEFYPREAKVQWQVKNALQSGNSQESVTEQDSKDSYSTISLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC

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Figure 62

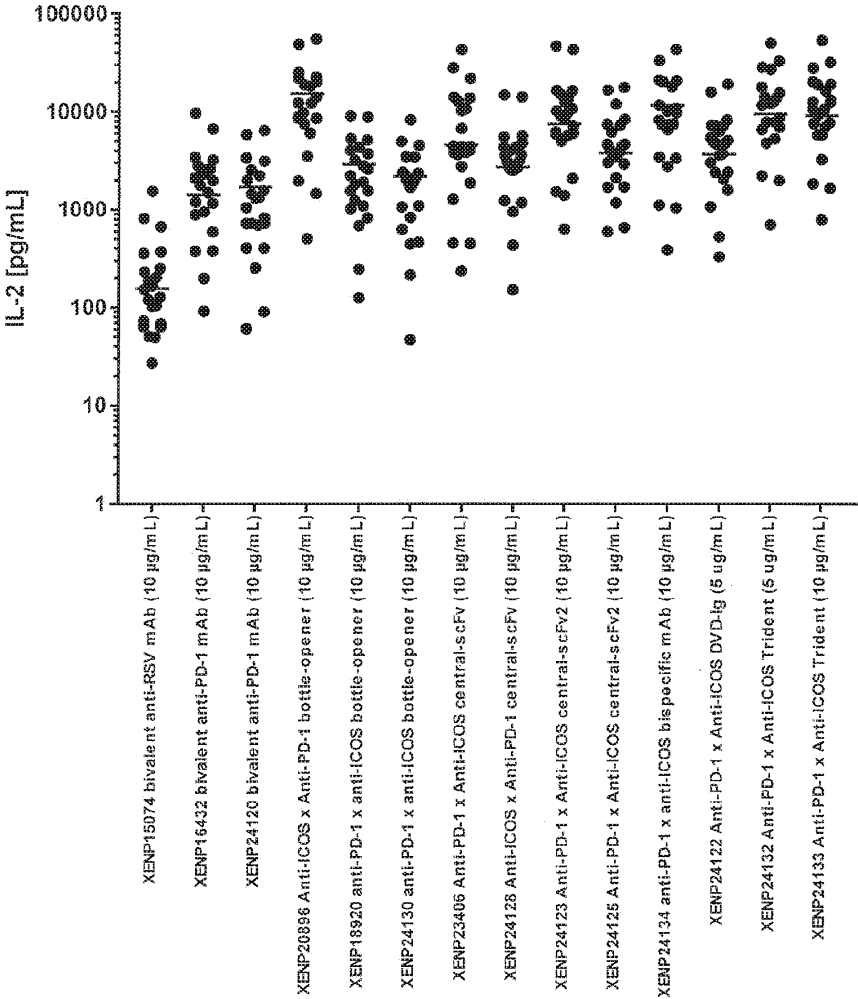


Figure 63

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQK**FO**GRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGY**YHDA**FDIWGGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI**SKAKGQ**PREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv scFv-Fc Heavy Chain

EVQLVESGGGLVKGPGSLRLSCAASGFTTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKN
SLYLQMNSLRRAEDTAVYYCARGGHLGPF**DLWGQ**TMVTVSS/**GKPGSGKPGSGKPGSGKPGS**/EIVLTQSPATLSLS
PGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQ**
YGSSPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTI**SKAKGQ**PREPQVYTL
PSREQMTKNQV**KL**TVLKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ**QGN**VFSCSVMH
EALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Light Chain

DIQMTQSPSSVSASVGDRVITTCRASQGISRL**LAWYQQKPGKAPKLLIYVASSLQSGVPSRFS**SGSGSGTDFTLTIS
LOPEDFATYYC**QQANSFPWT**FGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY**PREAKVQWKVDNA**
LQSGNSQESVTEQDSKSTYSLSSLTLSKADY**EKKHVYACEVTHQGLSSPVTKSFNRGEC**

Figure 64A

XENP24359

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1

EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMSWVRQAPGKGLEWVAEISTKANNHATYYAESVKGRFTISRDDS
KSSVYLQMNSLRAEDTAVYYCTRLATWDWYFDVWGQGTTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIAVEW
ESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGVDFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYIMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYIDSSGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVERKSCDK
THTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1

DIVLTQSPSSLSASVGDRVTITCRASQSVDDYDGDSYMNWYQQKPKGPKPKLLIYAASELESGIPAREFSGSGSGTDFTL
TISSLQPEDFATYYCQSNEDPFTFGSGTKLEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2

DIQMTQSPSSVSASVGDRVTITCRASQGISRLAWYQQKPKGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQANSFPWTFGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24360

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1

EVQLVQSGAEVKKPGATVKISCKASGFNIDYFMHWVQAPGKGLEWMGWIDPELGDTEYAPKFQGRVTTITADTSTN
TAYMELSSRLSDDTAVYYCYARGVYQALDYWGQGTTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGGFYPSDIAVEWESD
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGVDFSCSVMHEALHNHYTQKSLSLSPGK

Figure 64B

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2

QVQLVQSGAEVKKFGASVKVSCKASGYTFTGY~~YMH~~WVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTSDTSIS
TAYMELSRRLSDDTAVIYCYCART~~YYYDSSGY~~~~YHDAFDI~~WGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVNHKPSNTKVDKKVERKSCDK
THTCPRCPPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQV~~KL~~TCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV~~F~~SCSVMHEALHNHYTQKSLSLSPGK

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1

DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFOQKPGQTVKLLIYFTSYLHSGVPSRFSGSGSGTDYFTTSS
LEAEDAATYFCQ~~Q~~GN~~TLPYT~~FGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~TL~~TLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2

DIQMTQSPSSVSASVGDRVTITCRASQGISRL~~LAWY~~QKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSS
LQPEDFATYYCQ~~Q~~ANS~~FPWT~~FGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSS~~TL~~TLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 65

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1
QVTLKESGPNLVKPTETLTCTVSGFSLNGYGVNWRQPPGKGLEWLMWGDGSTDYNSALKSRILTISKDNSKSO
VVLMTNMDPVDATATYYCARSYTSDDEDYWGQGLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCF
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGVDFSCSVMHEALHNHYTQKSLSLSPCK

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2
QVQLVQSGAEVKKPGASVKVSCKASGYTFGTYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKKVERKSCDK
THTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFEYPSDI
AVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1
DIVMTQSPDLSAVSLGERATINCKSSQSLNSRTRKNYLAWYQQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2
DIQMTQSPSSVSASVGRVTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFLTITIS
LQPEDFATYYCQANSFPWTFGGGTKEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 66A

XENP21748

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPC
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIWGQGMVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSVSASVGDRTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
TYYCQQANSFFPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain

DIQMTQSPSSLSASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQLYHPATFGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24129

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKN
SLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

Figure 66B

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGYHDAFDIWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQTQS
PSSVSASVGDRTTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFA
TYYCQANSFPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQVKLTCCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSMHEALHNHYTQKSLSLSPGK

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain

EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQYGSGLPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24131

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain

EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYIMMWVRQAPGKLEWVSSIYPSGGITFYADTVKGRFTISRDNSKN
TLYLQMNSLRRAEDTAVYYCARIKLGTAVTVDYWGQGTSLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSQSMHEALHNHYTQKSLSLSPGK

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGYHDAFDIWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQTQS
PSSVSASVGDRTTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFA
TYYCQANSFPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQVKLTCCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSMHEALHNHYTQKSLSLSPGK

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain

QSALTQPASVSGSPGQSITISCTGTSSDVGYNYSWYQQHPGKAPKLMIIYDVSNRPSGVSNRFSKSGNTASLTI
SGLQAEDADYYCSSYTSSTRVFGTGKTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
ADSSPVKAGVETTTPSKQSNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS

Figure 66C

XENP24124

>XENP024124 durvalumab[PD-L1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1
Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKN
SLYLQMNSLR AEDTAVYYCAREGGWFGELAFDYWGQGT LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTR
DTSISTAYMELSR LRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVTVSS/GGGGSGGGSGGGSGGGGS/DI
QMTQSPSSVSASVGDRTITCRASQGISRL LAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCQQANSFFWTFGQGTKVEIK/GGGSGGGSGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024124 durvalumab[PD-L1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1
Light Chain

EIVLTQSPGTLSSLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQYGSLEPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYSLSSLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 67

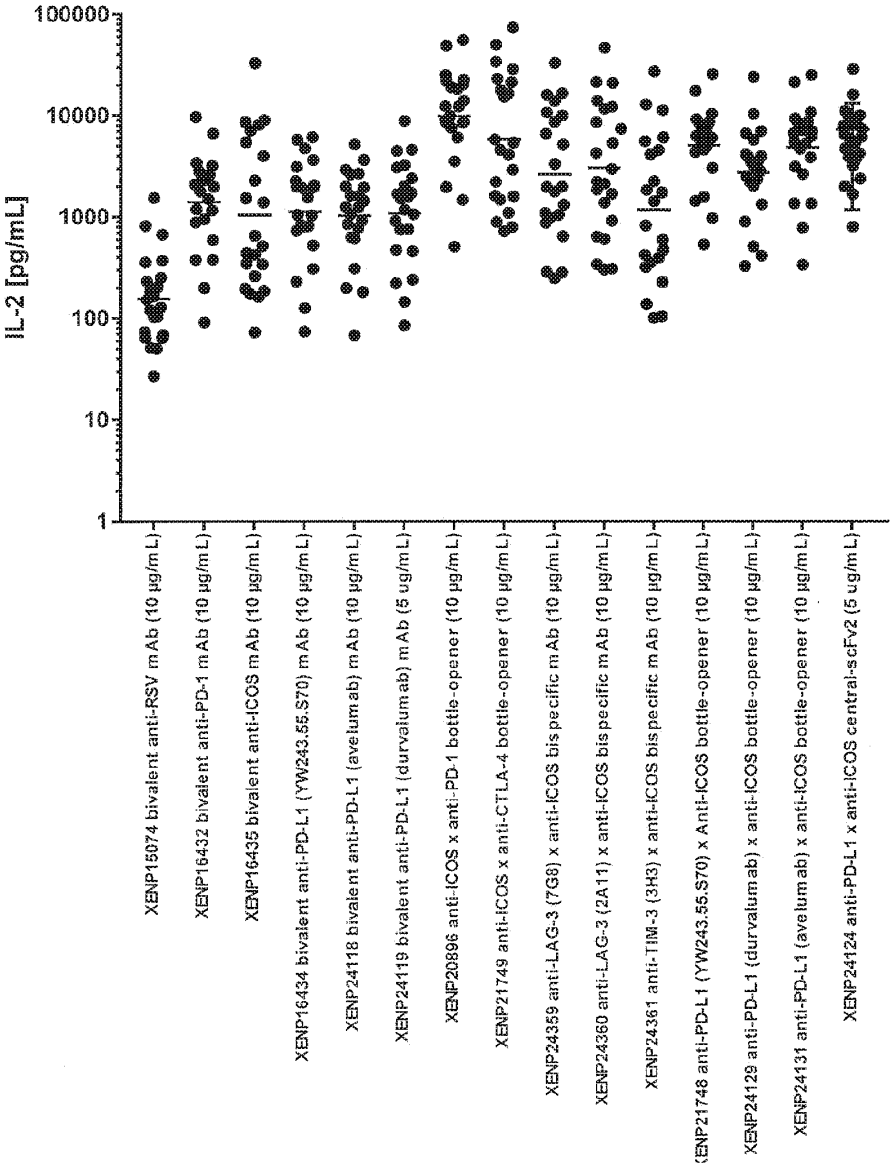


Figure 68A

XENP20266

>XENP020266 [ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYYDSSGYHDAFDIWGGTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSCFYPSDI
AVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP020266 [ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP020266 [ICOS]_H0L0 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPTFGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21861

>XENP021861 GSK_314.8 [ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGLTVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8 [ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8 [ICOS]_H0L0 one-arm mAb Light Chain

DIVMTQAAPSVPVTPGESVVISCRSSKSPHLSNGNIYLYWFLQRPQSPQLLIYRMSNLASGVDRFSGSGSGTFTFT
LKISRVEAEDVGVYYCMQHLEYPYTFGGGTKLEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCCLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68B

XENP21863

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNS
LYLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYYGMDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Light Chain

EIVLTQSPGTLISLSPGERATLSCRASQNISSYLAHWYQQKPGQAPGGLLIYGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22349

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGSSVKVCSKASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNYNQKFKQGRVITITADKSTS
TAYMELSSLRSEDVAVYYCGRNNYGNYGWYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Light Chain

EIVLTQSPATLSLSPGERATLSCSASSSVSYMHYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISSL
EPEDFAVYYCFQSGGYPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSITYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68C

XENP22439

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAFGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVTITCRASQGISLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22440

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAFGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVTITCRASQGISYLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68D

XENP22441

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVITTCRASQGISRYLAWYQQKPKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQANSFPWTFGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22442

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVITTCRASQGISRYLAWYQQKPKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQANSFPWTFGQGTKVEIK/RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68E

XENP22443

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDI AVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVITTCRASQGISRLAWYQKPKGAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSS
LQPEDFATYYCQQSNSFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22444

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDI AVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQGGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVITTCRASQGISRLAWYQKPKGAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSS
LQPEDFATYYCQQAESFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68F

XENP22445

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQQAANSYPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22766

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVTITCQASQDISLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQQAESFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68G

XENP23096

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Fab-Fc Heavy Chain

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPCGLEWMGWINPHSGETIYAQKFQGRVTMTDTSIS
TAYMELSSLRSEDTAVYYCARTYYDYDTSGYYHDAFDVWGQGMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCSMHEALHNHYTQKSLSLSPGK

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Fc-only Heavy Chain

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSMHEALHNHYTQKSLSLSPGK

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Light Chain

DIQMTQSPSSVSASVGDRVTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSDTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 69

XENP	Antigen	K _D (nM)	k _a (1/Ms)	k _d (1/s)
22445	hulCOS	3.239	2.35E+05	7.60E-04
22444	hulCOS	1.594	2.40E+05	3.83E-04
22443	hulCOS	1.415	2.69E+05	3.80E-04
22442	hulCOS	2.813	2.58E+05	7.26E-04
22441	hulCOS	5.596	2.39E+05	1.34E-03
22440	hulCOS	4.128	2.08E+05	8.57E-04
22439	hulCOS	0.6324	1.80E+05	1.14E-04
20266	hulCOS	1.502	2.34E+05	3.52E-04

Figure 70

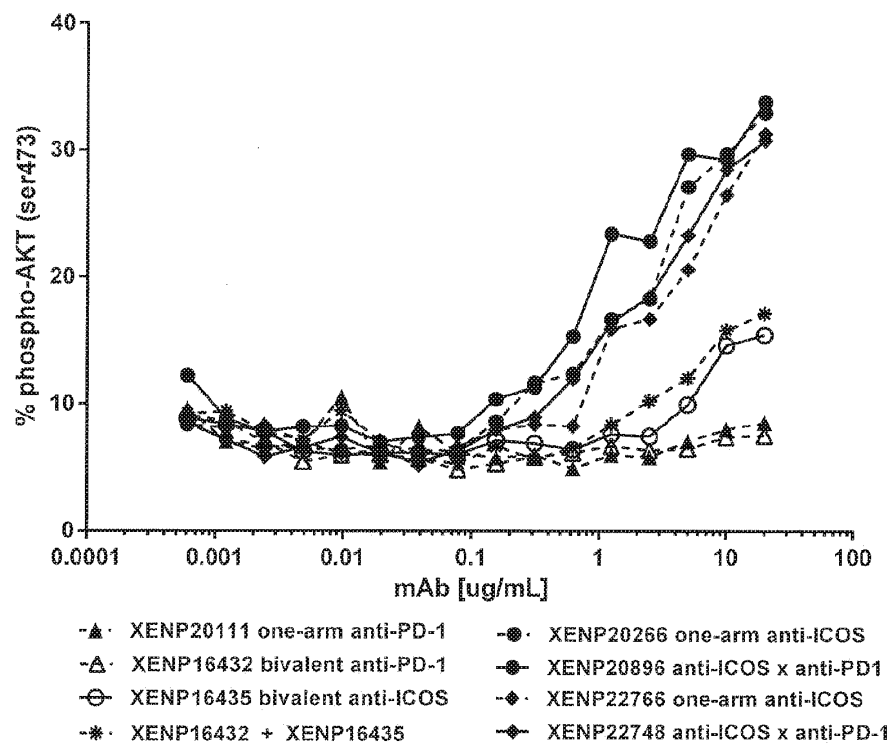


Figure 71

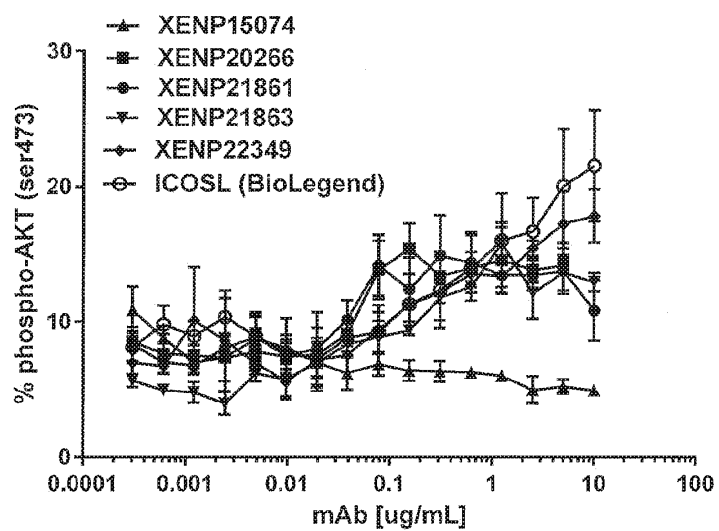


Figure 72A

Prototype Costim x PD-1 Bispecific

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLEWVSYISSSSTIDYADSVKGRFTISRDNAKNSL
YLQMNSLRDEDTAVYYCARESGWYLFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLN
GKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTT
PVLDSGGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSPGK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQS
EDFGVYYCQQDFSSPRTFGGGTKEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFS
NYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYG
GYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
MTKNQVKLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHN
HYTQKSLSLSPGK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
DIQMTQSPSSLSASVGRVTITCRASQGISWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQYNSYPPTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
QVTLKESGPGILKPSQTLSTCSFSGFSLTSGMGVGWIRQPSGKGLEWLAHIWWDDDKYSPSLKSLTISKDTSRNQ
VFLKITSLDTADTATYYCVRSYYGGSSGAMDYWGQGTSTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQD
WLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNY
KTTTPVLDSGGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQS
EDFGVYYCQQDFSSPRTFGGGTKEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFS
NYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYG
GYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
MTKNQVKLTCLVKGYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFCVMHEALHN
HYTQKSLSLSPGK

Figure 72B

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
DIVMTQTPLSLPVS LGDQASISCRSSQSLVHSDGNTYLHWYLQKPGQSPKLLIYKVSKRFSGV PDRFSGSGSGTDFTLKIS
RVEAEDLGVIYFCSTHVPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
QVQLQQWAGAGLLKPSSETLSLTCAVYGGSFSGYYWSWIRQSPKGLWIGWIGINHG GYVTYNPSLESRVTISVDTSKNQFS
LKLSVTAADTA VYYCARDYGP GNYDWYFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNY
KTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN YASHRYTGVPDRFTGSGYGTEFTLTISVQS
EDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFS
NYWMN WVRQAPGKGLEWVAEIRLYSN NYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRYGNYG
GYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
MTKNQVKLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN
HYTQKSLSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELPED
FAVYYCQQRSNWPPALTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Additional CTLA-4 x ICOS Bispecific SEQ

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv Fab-Fc Heavy Chain
QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYTMHWVRQAPGKLEWVTFISYDGN NKYYADSVKGRFTISRDN SKN
TLYLQMNSLR AEDTAIYYCARTGWLGPFDYWGQGT LTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVA
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 72C

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv scFv-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYFTFGYYMHVVRRQAPGGGLEWMGWINPHSGGTNYAQKFQGRVTMTRD
TSISTAYMELSRIRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMT
QSPSSVSASVGDRTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYY
CQQANSFPWTFGQGTKVEIK/EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREQMTKNQVKLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv Light Chain
EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQYGSSPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 73A

Prototype anti-4-1BB mAb

>XENP014410 20H4.9[4-1BB]_HOL0_IgG1_PVA_/S267K Heavy Chain
QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQSPKGLWIG~~ELNHGGYVTYNPSLES~~RVTISVDTSKNQFS
LKLSSVTAADTAVYYCARDYGP~~GN~~YDWYFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC~~SV~~MHEALHNHYTQKSLSLSPGK

>XENP014410 20H4.9[4-1BB]_HOL0_IgG1_PVA_/S267K Light Chain
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDAS~~NRAT~~GIPARFSGSGSGTDFTLTISSELPED
FAVYYCQQRSNWPPALTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-OX40 mAb

>XENP016437 11D4[OX40]_HOL0_IgG1_PVA_/S267K Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVS~~YISSSSSTIDYADSVKGRFTISRDN~~AKNSL
YLQMNSLRDEDTAVYYCARESGWYLF~~FDY~~WGQGT~~LV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFC~~SV~~MHEALHNHYTQKSLSLSPGK

>XENP016437 11D4[OX40]_HOL0_IgG1_PVA_/S267K Light Chain
DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFS~~SGSGSGTDFTLTIS~~LQPE
DFATYYCQQYNSYPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-GITR mAb

>XENP016438 1D8[GITR]_HOL0_IgG1_PVA_/S267K Heavy Chain
QVTLKESGPGILKPSQTLSTLCSFSGFSLSTSGMGVGVIRQPSGKGLWLAHIWWDDDKYYSPLSKS~~QLTISK~~DTSRNQ
VFLKITS~~LD~~TADTATYYCVRSYYYGSSGAM~~DY~~WGQGT~~SV~~TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC~~SV~~MHEALHNHYTQKSLSLSPGK

Figure 73B

>XENP016438 1D8[GITR]_H0L0_IgG1_PVA_/S267K Light Chain

DIVMTQTPLSLPVLGDOASISCRSSQSLVHSDGNTYLHWYLVKPGQSPKLLIYKVKRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDLGYYFCQSTHVPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
SGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-ICOS mAbs

>XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

QVQLQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEDPSDSYVNYNQNFKGKATLTVDKSS
STAYIQLSSTSEDSAVYFCARSPDYVGTSIAWFDYWGQGLTVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain

DIVMTQAAPSVPTPGESVSISCRSSKSLHSNGNIYLYWFLQRPQSPQLLIYRMSNLASGVPDRFSGSGSGTTFTLKIS
RVEAEDVGYYVCMQHLEYPTFTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021821 GSK_88.2[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

QVQLQPGAEIVRPGASVKLSCKASGYSTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKD KATLTVDKSSN
TAYMQLTSPTEDSAVYYCTRWNLSYYFDNNYYLDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021821 GSK_88.2[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain

DIVMTQAAPSVPTPGESVSISCRSSKSLHSNGNTYLYWFLQRPQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRIS
RVEAEDVGYYVCMQHLEYPWTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021822 jMab-138[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

Figure 73C

>XENP021822 jMab-138[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain

EIVLTQSPGTLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021823 jMab-139[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTITVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021823 jMab-139[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain

EIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQKPGQAPGLLIYFGASSRATGIPDRFSGSGSGTDFLTISRLEPED
FAVYYCQQFGSSPMCSFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP022346 WO2016059602_GSK[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

QVQLVQSGAEVKKPGSSVKVSCASGYTFTDYAMHWVRQAPGQGLEWMGLISIIYSDHTNYNQKFQGRVTITADKST
STAYMELSSLRSEDATVYYCGRNNYGNYGWYFDVWGQGTITVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPC
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022346 WO2016059602_GSK[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain

EIVLTQSPATLSLSPGERATLSCSASSVSYMHWYQQKPGQAPRLIYDTSKLASGIPARFSGSGSGTDYLTISLEPEDF
AVYYCFQGSGYPYTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023057 Jounce_37A10S713[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMDWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDNAKN
TLYLQMNSLRAGDTAVYYCTRWGRFGFDSWGQGTITVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPPVA
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 73D

>XENP023057 Jounce_37A10S713[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain
 DIVMTQSPDLSAVSLGERATINCKSSQSLSGSFNYLTWYQQKPGQPPKLLIFYASTRHTGVPDRFSGSGSGTDFTLTSS
 LQAEDVAVYYCHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
 SGNSQESVTEQDSKDYSLSTLTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-PD-L1 mAbs

>XENP016434 YW243.55.S70[PD-L1]_H0L0_IgG1_PVA_/S267K Heavy Chain
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNT
 AYLMNSLRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
 AGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
 KTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP016434 YW243.55.S70[PD-L1]_H0L0_IgG1_PVA_/S267K Light Chain
 DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGSGSGTDFTLTSSSQPE
 DFATYYCQQLYHPATFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
 QESVTEQDSKDYSLSTLTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024118 avelumab[PD-L1]_H1L1_IgG1_PVA_/S267K Heavy Chain
 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDNKNTL
 YLQMNLSLRAEDTAVYYCARIKLGTVTVDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVA
 GPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024118 avelumab[PD-L1]_H1L1_IgG1_PVA_/S267K Light Chain
 QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIDVSNRPSGVSNRFSGSKSGNTASLTISG
 LQAEDADYYCSSYSSSTRVFGTGKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV
 KAGVETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

>XENP024119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/S267K Heavy Chain
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGEKYYVDSVKGRFTISRDNK
 NSLYLQMNLSLRAEDTAVYYCAREGGWFGELAFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
 APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
 HQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
 NNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 73E

>XENP024119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/S267K Light Chain

EIVLTQSPGTLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLIYDASSRATGIPDRFSGSGSGTDFLTISRLEPE
DFAVYYCQYQYGLPWTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDSSTLSLTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-PD-1 mAbs

>XENP024120 LOPD180[PD-1]_H1L1_IgG1_PVA_/S267K Heavy Chain

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYYNGNTYYNPSLRSRVTSVDTSKNQF
SLKLSSVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024120 LOPD180[PD-1]_H1L1_IgG1_PVA_/S267K Light Chain

QSVLTQPPSASGTPGQRTVISCSSGNSNIGSNVSNWYQQLPGTAPKLLIYGNNQRPSGVPDRFSGSGSGTSASLAISGL
QSEDEADYYCAAWDDSLNGPVFGGGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS
SPVKAGVETTTPSKQSNKKAASSYLSLTPEQWKSRSYSQCQTVEGSTEKTVAPTECS

>XENP024121 mAb7(1.2)[PD-1]_H1L1_IgG1_PVA_/S267K Heavy Chain

QVQLVQSGAEVKKPGASVKVCKASGYSTSYWMNWRQAPGQGLEWIGVIHPSDSETWLDQKFKDRVTITVDKST
STAYMELSSLRSEDTAVYYCAREHYGTSFPAYWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024121 mAb7(1.2)[PD-1]_H1L1_IgG1_PVA_/S267K Light Chain

EIVLTQSPATLSLSPGERATLSCRASESVDNYGMSFMNWFQQKPGQPPKLLIHAASNQSGVPSRFSGSGSGTDFLTIS
SLEPEDFAVYFCQYQYGLPWTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSSTLSLTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 73F

Additional ICOS x PD-L1

>XENP021832 GSK_314.8[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain
QVQLQQPGTELMKPGASVKLSCKASGYFTFTYWMHWVQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSS
STAYIQLSSLTSEDSAVYFCARSPDYGYGSLAWFDYWGQGTLLTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLH
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPE
NNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021832 GSK_314.8[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVSS/GGGGSGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFG
QGTVKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENP021832 GSK_314.8[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain
DIVMTQAAPSVPTPGESVSISCRSSKSPHSNNGNIYLYWFLRPGQSPQLLIYRMSNLSAGVPDRFSGSGSGTFTLKIS
RVEAEDVGVYYCMQHLEYPYTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021833 GSK_88.2[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain
QVQLQQPGAELVRPGASVKLSCKASGYSFTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTEDSAVYYCTRWNLSYYFDNNYYLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPE
ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021833 GSK_88.2[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVSS/GGGGSGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFG
QGTVKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

Figure 73G

>XENP021833 GSK_88.2[ICOS]_HOLO_Fab-YW243.55.S70[PD-L1]_HOLO_scFv Light Chain
DIVMTQAAPSVPTPGESVSISCRSSKSLHNSNGNTYLYWFLQRPQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRIS
RVEAEDVGYYCMQHLEYPWTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021834 jMab-138[ICOS]_HOLO_Fab-YW243.55.S70[PD-L1]_HOLO_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021834 jMab-138[ICOS]_HOLO_Fab-YW243.55.S70[PD-L1]_HOLO_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAGDTAVYYCARRHWPGGFDYWGQGTITVTVSS/GGGGSGGGGSGGGGS/DIQMTQSPSSLSASVGR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLHPATFG
QGTVKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL
SPGK

>XENP021834 jMab-138[ICOS]_HOLO_Fab-YW243.55.S70[PD-L1]_HOLO_scFv Light Chain
EIVLTQSPGTLSLSPGERATLSCRASQNISSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021835 jMab-139[ICOS]_HOLO_Fab-YW243.55.S70[PD-L1]_HOLO_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 73H

>XENPO21835 jMab-139[ICOS]_HOL0_Fab-YW243.55.S70[PD-L1]_HOL0_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNLSRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSS/GGGGSGGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTSSLPEDFATYYCQQYLYHPATFG
QGKTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENPO21835 jMab-139[ICOS]_HOL0_Fab-YW243.55.S70[PD-L1]_HOL0_scFv Light Chain
EIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSSTYSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENPO21836 jMab-136[ICOS]_HOL0_Fab-YW243.55.S70[PD-L1]_HOL0_scFv Fab-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRD
TSISTAYMELSLRLSDDTAVYYCARTYYDDSSGYYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPYSDIAVEWES
DGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENPO21836 jMab-136[ICOS]_HOL0_Fab-YW243.55.S70[PD-L1]_HOL0_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNLSRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSS/GGGGSGGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTSSLPEDFATYYCQQYLYHPATFG
QGKTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENPO21836 jMab-136[ICOS]_HOL0_Fab-YW243.55.S70[PD-L1]_HOL0_scFv Light Chain
DIQMTQSPSSVSASVGDRVTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTSSLPQPE
DFATYYCQQANSFPWTFQGKTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDSSTYSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74A (have SEQ ids but not yet in)
Anti-PD-1-Fab x Anti-ICOS-scFv Bottle-openers

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain
QVQLVESGGGVVQPGRSRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTCTPPCPAPPV
AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy
Chain
QVQLVESGGGVVQPGRSRLSCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERA
TLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQSSNWPR
TFGGGTVEIK/EPKSSDKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQM
TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH
YTQKSLSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain
EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSE
LEPEDFAVYYCQQSSNWPRTFGGGTVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain
QVQLQESGPGLVKPSQTLSTCTVSGGSISGGAYYWSWIRQHPGKGLEWIGYIYYNGNTYYNPISLRVTVISVDTSK
NQFSLKLSSTVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSC
DKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVIMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSVSASVGDRTVITCRASQGISRLRLAWYQQKPKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
TYCQQANSFPWTFGGGTVEIK/EPKSSDKHTCTPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain
QSVLTQPPSASGTPGQRTISCSGSNSNIGSNVNWYQQLPGTAPKLLIYGNNQRPSCVPPDRFSGSKSGTSASLAIS
GLQSEDEADYYCAAWDDSLNGPVFGGGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
ADSSPVKAGVETSTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 74B

ICOS x PD-1 Bottle-openers with different ICOS ABDs

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGRIDPSDSYVNNYNQNEFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGTLLVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNNLKTEDTGYYCYTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
DIVMTQAAPSVPTPGESVSISSCRSSKSLHNSGNIYLYWFLQRPQGSPQLLIYRMSNLASGVDRFSGSGSGTFTT
LKISRVEAEDVGVYYCMQHLEYPTTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
QVQLQQPGAELVREGASVKLSCKASGYSTSYWLNWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTSEDSAVYYCTRWNLSTYFDNNYYLDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRTISRDDSKSTLYLQMNNLKTEDTGYYCYTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFIYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
DIVMTQAAPSVPTPGESVSISSCRSSKSLHNSGNTYLYWFLQRPQGSPQLLIYRMSNLASGVDRFSGSGSGTAFT
LRISRVEAEDVGVYYCMQHLEYPTTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74C

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNS
LYLQMNLSRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQFENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy
Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYNASHRYTGVPRDFTGSGYGTFTLTIS
VQSEDFGVYYCQDDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAS
GFTFSNYYWMNWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
EIVLTQSPGTLSLSPGERATLSCRASQNISSSLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNS
LYLQMNLSRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQFENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy
Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYNASHRYTGVPRDFTGSGYGTFTLTIS
VQSEDFGVYYCQDDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAS
GFTFSNYYWMNWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGYYCYTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
EIVLTQSPGTLSLSPGERATLSCRASQSISSSLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy
Chain
QVQLVQSGAEVKKPGSSVKVCSKASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNYNQKRFQGRVTTADKSTS
TAYMELSSLRSEDTAVYYCGRNNGYGYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQFENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

Figure 74D

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYLASHRYTGVPDRFTGSGYGEFTLTSS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKGPGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNLYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGLTVVSS/EPKSSDKTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain
EIVLTQSPATLSLSPGERATLSCASSSVSYMHYQQKPGQAPRLIYDTSKLASGIPARFSGSGSDTYTLTISSL
EPEDFAYVYCFQSGSYPTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Anti-PD-L1 x anti-ICOS Antibodies

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTTSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKN
TAYLQMNLSRAEDTAVYYCARHWPGGFDYWGQGLTVVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPC
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQFENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/DIQTQS
PSSVSASVGDRTVITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
TYCQQANSFPWTFGQGTKEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC
SCVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain
DIQTQSPSSLSASVGDRTVITCRASQDVSTAVAWYQQKPGKAPKLLIYASFLYSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQYLYHPATFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Anti-ICOS x anti-CTLA-4 Bottle Opener

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Fab-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLSDDTAVYYCARTYYDDSSGYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGVDFSCVMHEALHNHYTQKSLSLSPGK

Figure 74E

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv scFv-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSTYMHVVRQAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKN
SLYLQMNSLRAGDTAVYYCARGGHLGPPDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSL
PGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ
YGSSPWTFGGQTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NHWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREQMTKNQVLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMH
EALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Light Chain
DIQMNTQSPSSVSASVGDRVTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGGQTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

ICOS one-arm from alternative ICOS ABDs

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain
QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVQRPGGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGTTLTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPEPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGGQENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Light Chain
DIVMTQAAPSVPTPGESVVISCRSSKSPHLSNGNIYLYWFLQRPQSPQLLIYRMSNLASGVDRFSGSGSGTFTFT
LKISRVEAEDVGVYYCMQHLEYPTTFGGGTGLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSTYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRDNAKN
LYLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGGQENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Light Chain
EIVLTQSPGTLSPGERATLSCRASQNISSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISR
LEPEDFAVYYCQQFGSSPMCSFGQGTGLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74F

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fab-Fc Heavy Chain
QVQLVQSGAEVKKPGSSVKVSCKASGYTF~~FTDYAMHWVRQA~~PGQGLEWMGLIS~~ISYSDHTN~~YNQK~~FQGRVTITADK~~STS
TAYMELSSLRSEDTAVYYCGRNNYGN~~YGWYFDVWGQ~~TTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV~~TVPS~~SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV~~VVDVKHEDPEVK~~FNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLT~~VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG~~QPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYK~~TTPFVLDSDGSFFLYSKLTVDKSRWEQGDV~~FSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fc-only Heavy Chain
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV~~VVDVKHEDPEVK~~FKWYVDGVEVHNAKTKPRE
EQYNSTYRVVS~~VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG~~QPREPQVYTLPPSREQMTKNQV~~KL~~TCLVK
GFYPSDIAVEWESNGQPENNYK~~TTPVLDSDGSFFLYSKLTVDKSRWQGNV~~FSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Light Chain
EIVLTQSPATLSLSPGERATLSCSASSSVSY~~MHWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTI~~SSL
EPEDFAVYYCFQGS~~GYPYTFGQGT~~KLEIK/RTVAAPSVFIFPPSDEQLKSGTASV~~VCLLNNFYPREAKVQWKVDNAL~~
QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 75A

mAb-scFv backbone 1 (356E/358M allotype)

monomer 1 (Fab-scFv side) (SEQ ID NO:37737)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLEPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

monomer 2 (Fab side) (SEQ ID NO:37738)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLEPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

constant light chain (SEQ ID NO:37739)

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 75B

mAb-scFv backbone 2

>Fab-scFv-Hc - 356D/358L allotype (SEQ ID NO:XX)

ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSC
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - 356D/358L allotype (SEQ ID NO:XX)

ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

mAb-scFv backbone 3

>mAb-scFv Fab-scFv-Hc - N297A (SEQ ID NO:XX)

ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSC
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - N297A (SEQ ID NO:XX)

ASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VMHEALHNHYTQKSLSLSPGK

Figure 75C

mAb-scFv backbone 4

>mAb-scFv Fab-scFv-Hc - N297S (SEQ ID NO:XX)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGVFSCS
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - N297S (SEQ ID NO:XX)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKHTHTCPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYSSYTRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPGK

mAb-scFv backbone 5

>mAb-scFv Fab-scFv-IgG4-Hc (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRVESKYGPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQ
FNWYVDGVEVHNAKTKPREEEFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEGDFVSCSVM
HEALHNHYTQKSLSLGLGK

>mAb-scFv Fab-IgG4-Hc (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRVESKYGPPCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQ
FNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVM
HEALHNHYTQKSLSLGLGK

Figure 75D

mAb-scFv backbone 6

>mAb-scFv Fab-scFv-IgG2-Hc - without S267K (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQTYTCNV DHKPSDTKVDKTV ERKCCVECP PCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYITLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPMLDS DGSFFLYSKLTVDKSRWEGGDVFSCSVMH
EALHNHYTQKSLSLSPGK

>mAb-scFv Fab-IgG2-Hc - without S267K (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQTYTCNV DHKPSDTKVDKTV ERKCSVECP PCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYITLP
PSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTPPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

mAb-scFv backbone 7

>mAb-scFv Fab-scFv-IgG2-Hc - with S267K (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQTYTCNV DHKPSDTKVDKTV ERKCCVECP PCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYITLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPMLDS DGSFFLYSKLTVDKSRWEGGDVFSCSVMH
EALHNHYTQKSLSLSPGK

>mAb-scFv Fab-IgG2-Hc - with S267K (SEQ ID NO:XX)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFG
TQTYTCNV DHKPSDTKVDKTV ERKCSVECP PCPAPFVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYITLP
PSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTPPMLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

Figure 76A additional anti-PD-1 sequences

Merck Pembrolizumab VH (SEQ ID NO:)

QVQLVQSGVEVKKPGASVKVSKASGYTFTNYYMYWVRQAPGGGLEWMGGINPSNGGTNFNEKFKNRVTLTDSST
TTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTITVTVSS

Merck Pembrolizumab VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESQVPAFSGSGSGTDFTLTIS
LEPEDFAVYYCQHSRDLPLTFGGGTKVEIK

BMS nivolumab VH (SEQ ID NO:)

QVQLVESGGGVVQPGSRSLRDLCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGRFTISRDN
SKNTFLQMNLSLRAEDTAVYYCATNDDYWGQGTITVTVSS

BMS nivolumab VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTIS
SLEPEDFAVYYCQSSNWPRTFGQGTKVEIK

Teva pidilizumab VH (SEQ ID NO:)

QVQLVQSGSELKKPGASVKISKASGYTFTNYGMNWVRQAPGGLQWMGWINTDSGESTYAEFEKGRFVFLDTSV
NTAYLQITSLTAEDTGMVFCVRVGYDALDYWGQGTITVTVSS

Teva pidilizumab VL (SEQ ID NO:)

EIVLTQSPSSLSASVGDRTITCSARSSVSYMHWFQKPGKAPKLWIYRTSNLASGVPSRFSGSGSGTSYCLTIN
SLQPEDFATYYCQQRSSPEPLTFGGGTKLEIK

Pfizer MK-3475 VH (SEQ ID NO:)

QVQLVQSGVEVKKPGASVKVSKASGYTFTNYYMYWVRQAPGGGLEWMGGINPSNGGTNFNEKFKNRVTLTDSST
TTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTITVTVSS

Pfizer MK-3475 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESQVPAFSGSGSGTDFTLTIS
LEPEDFAVYYCQHSRDLPLTFGGGTKVEIK

Novartis/Dana Farber BAP049 clone E VH (SEQ ID NO:)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGGGLEWMGNIYPGTGGSNFDEKFKNRVTITADKST
S TAYMELSSLRSEDTAVYYCTRWTGTGAYWGQGTITVTVSS

Novartis/Dana Farber BAP049 clone E VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCKSSQSLDSGNQKNFLTQYQQKPGQAPRLLIYWASTRESGVPSRFSGSGSGTDFTT
ISSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK

Novartis/Dana Farber BAP049 clone B VH (SEQ ID NO:)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGGGLEWMGNIYPGTGGSNFDEKFKNRVTITADKST
S TAYMELSSLRSEDTAVYYCTRWTGTGAYWGQGTITVTVSS

Novartis/Dana Farber BAP049 clone B VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCKSSQSLDSGNQKNFLTQYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGTDFTT
ISSLPEDIATYYCQNDYSYPYTFGQGTKVEIK

Figure 76B

Regeneron H7798N VH (SEQ ID NO:)

EVQLLESGGVLVQPGGSLRLSCAASGFTFSNFGMTWVRQAPGKGLEWVSGISGGGRDITYFADSVKGRFTISRDNKNT
LYLQMNSLKGEDTAVYYCVKVGNIYFDYWGQGLVTVSS

Regeneron H7798N VH (SEQ ID NO:)

DIQMTQSPSSLSASVGDSTITTCRASLINTFLNWWYQQKPGKAPNLLIYAASSLHGGVPSRFSGSGSGTDFTLTIRTLQPED
FATYYCQQSSNTPFTFGPGTVVDFR

Medimmune h1H3 Var 6 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDGMHWVRQAPGKGLEWVAYISSGSYTIYYADSVKGRFTISRDNKNT
LYLQMNSLRAEDTAVYYCARRGYGSFYFYFDYWGQGTITVTVSS

Medimmune h1H3 Var 6 VL (SEQ ID NO:)

QIVLTQSPATLSLSPGERATLSCAASSSVSYMYWYQQKPGQAPRLIYLTNRATGIPARFSGSGSGTDYTLTISSLEPEDF
AVYYCQWSSNTPFTFGQGTKLEIK

Tesarao TSR-042/APE2058 VH (SEQ ID NO:)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSYDMSWVRQAPGKGLEWVSTISGGGSYTYQDSVKGRFTISRDNKNTL
LYLQMNSLRAEDTAVYYCASPYAMDYWGQGTITVTVSS

Tesarao TSR-042/APE2058 VL (SEQ ID NO:)

DIQLTQSPSFLSAYVGDRTITCKASQDVGTAWAYQQKPGKAPKLLIYWASTLHTGVPSRFSGSGSGTEFTLTISSLQPE
EDFATYYCQHYSSYPWTFGQGTKLEIK

Incyte Camrelizumab VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYMMSWVRQAPGKGLEWVATISGGGANTYYPDSVKGRFTISRDNKNT
LYLQMNSLRAEDTAVYYCARQLYYFDYWGQGTITVTVSS

Incyte Camrelizumab VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCLASQTIGTWLTWYQQKPGKAPKLLIYTATSLADGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQVYSIPWTFGGGTKVEIK

Beigene 317-4B6 VH (SEQ ID NO:)

QVQLQESGPGLVKPSSETLSLTCTVSGFSLTSYGVHWIRQPPGKGLEWIGVIYADGSTNYPNPSLKSRTISKDTSKNQVSL
KLSSVTAADTAVYYCARAYGNYWYIDVWGQGTITVTVSS

Beigene 317-4B6 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSSVSNDVAWYQQKPGQPPKLLINYAFHRFTGVPDRFSGSGYGTDFLTISSLQA
EDVAVYYCHQAYSSPYTFGQGTKLEIK

Beigene 326-4A3 VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKVSKASGYFTNYGMNWVRQAPGQGLKWMGWNNNAEPTYAQDFRGRFVFLDTS
STAYLQISSLKTEDTAVYYCARDVMDYWGQGLVTVSS

Beigene 326-4A3 VL (SEQ ID NO:)

DIVLTQSPASLAVSPGQRATITCRASESDNYGYSFMHWYQQKPGQPPKLLIYRASNLESGVPSRFSGSGSGTDFTLTIN
PVEAEDTANYCQSQKEYPTFGGGTKVEIK

Figure 76C

Macrogenics mAb 7 (1.2) VH (SEQ ID NO:)

QQQLVQSGAEVKKPGASVKVSCKASGYSTSYWMNWVRQAPGGLEWIGVHPDSEWLDQKFKDRVTITVDKSTS
TAYMELSSLRSEDTAVYYCAREHYGTSPFAYWGQGTILTVSS

Macrogenics mAb 7 (1.2) VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASEVDNYGMSFMNWVQKPGQPPKLLHHAASNQSGSVSRFSGSGSGTDFTLTSS
LEPEDFAVYFCQQSKEVPYTFGGGTKEIK

Junmeng Clone 38 VH (SEQ ID NO:)

QQQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPIHGLEWIGVIESETGGTAYNQKFKGRVTITADKSTST
AYMELSSLRSEDTAVYYCAREGITVATTYYWYFDVWGQGTITVTVSS

Junmeng Clone 38 VL (SEQ ID NO:)

DVVMTQSPSLPVTLGQPASISCRSSQSIHNSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHPVPLTFGQGTKEIK

Junmeng Clone 39 VH (SEQ ID NO:)

QQQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGGLEWIMGVIESETGGTAYNQKFKGRAKITADKST
STAYMELSSLRSEDTAVYYCTREGITVATTYYWYFDVWGQGTITVTVSS

Junmeng Clone 39 VL (SEQ ID NO:)

DVVMTQSPSLPVTLGQPASISCRSSQSIHNSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHPVPLTFGQGTKEIK

Junmeng Clone 41 VH (SEQ ID NO:)

QQQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGGLEWIMGVIESETGGTAYNQKFKGRVTLTADKSS
STAYMELSSLRSEDTAVYYCTREGITVATTYYWYFDVWGQGTILTVTVSS

Junmeng Clone 41 VL (SEQ ID NO:)

DVVMTQSPSLPVTLGQPASISCRSSQSIHNSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHPVPLTFGQGTKEIK

Junmeng Clone 48 VH (SEQ ID NO:)

QQQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGGLEWIMGVIESETGGTAYNQKFKGRAKITADKST
STAYMELSSLRSEDTAVYYCTREGITVATTYYWYFDVWGQGTITVTVSS

Junmeng Clone 48 VL (SEQ ID NO:)

DVVMTQSPSLPVTLGQPASISCRSSQSIHNSNGNTYLEWYLQKPGQSPRLIYKVSNRFSGVPRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHPVPLTFGQGTKEIK

Wyeth PD1-17 VH (SEQ ID NO:)

QQQLQESGPGVVKPSGTLSTCAISGGSIGSGGSIRSTRWWSWVRQSPGKLEWIGEIYHSGSTNYPNPKSRVTISLTKS
RNHPSLRNLNSVTAADTAVYYCARQDYGDSDWYFDLWGKGTMTVTVSS

Wyeth PD1-17 VL (SEQ ID NO:)

NFMLTQPHSVSESPGKTVTISCTRSSGSIASNSVQWYQQRPGSSPTTVIYEDNQRPSGVPRFSGSIDSSNSASLTVSGLK
TEDEADYYCQSSDSSAVVFGSGTKLTVL

Figure 76D

Wyeth PD1-28 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKVSCKASGYRFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVIMTTDTST
NTAYMELRSLRSDDTAVYYCARDADYSSSGSYWGQGLTVTVSS

Wyeth PD1-28 VL (SEQ ID NO:)

SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVMVIYKDTERP SGIPERFSGSSSGTKVLTISGVQAE
DEADYYCQADNSITYRVFGGGTKVTVL

Wyeth PD1-33 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVRVSCKASGYTLTSYYIHVVRQAPGQGLEWMGHINPRGATISYAQKFQGRVIMTRDTSTST
VYMELRNKSEDTALYYCATAGIYGFDFDYWGRGTLTVTVSS

Wyeth PD1-33 VL (SEQ ID NO:)

QSALTQPASVSGSPGQSITISCTGTSNDVGGYNYVSWYQHHPGKAPKLIHYDVTNRPSGVSDRFSGSKSGNTASLTISGLL
AEDEGDYCYSSYTIVNFEVLFGGGTKLTV

Wyeth PD1-35 VH (SEQ ID NO:)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYNGNTYYNPSLRSLVTISVDASKNQF
SLKLSSVTAADTAVYYCARASDYVWGGYRYMDAFDIWGRGTLTVTVSS

Wyeth PD1-35 VL (SEQ ID NO:)

QSVLTQPPSASGITPQQRVTISCSGSNSNIGSNSNVNYYQLPGTAPKLLIYGNNQRPSGVDPDRFSGSKSGTSASLAISGLQS
ENEADYYCAAWDDSLNGPVFGRGKTVTVL

Wyeth LOPD180 VH (SEQ ID NO:)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYNGNTYYNPSLRSLVTISVDTSKNQF
SLKLSSVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLTVTVSS

Wyeth LOPD180 VL (SEQ ID NO:)

QSVLTQPPSASGITPQQRVTISCSGSNSNIGSNSNVNYYQLPGTAPKLLIYGNNQRPSGVDPDRFSGSKSGTSASLAISGLQS
EDEADYYCAAWDDSLNGPVFGGGKTVTVL

UCB Ab948 VH (SEQ ID NO:)

EVQLQESGPGLVKPSQTLSTCTVTGYSITSDYAWNWIROPKPKKLEWMGYINYSGSTSYNPSLKSRTISRDTSKNQFS
LKLSSVTAADTAVYYCARWIGSSAWYFDVWGQGLTVTVSS

UCB Ab948 VL (SEQ ID NO:)

DVLMTQTPLSLVTPGQPASISCRSGQNIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFFGVDPDRISGSGSGTDFTLKIS
RVEAEDVGYYFCFGSHVPFTFGQGTKLEIK

Dana-Farber EH-12.2h7 VH (SEQ ID NO:)

QVQLVQSGHEVKKPGASVKMSCKASGYSTSSWIHWVRQAPGQGLEWIGYIYPSTGFTEYNQKFKDRATLTADKSTST
AYMELSSLRSEDTAVYYCARWRDSSGYHAMDYWGQGLTVTVSS

Dana-Farber EH-12.2h7 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGQRLTISCRASQSVSTSGYSYMHWYQQKPDQSPKLLIKFGSNLESIGIPARFSGSGSGTDFITLHISSE
PEDFATYYCQHSWEIPYTFGQGTKLEIK

Figure 76E

Sorrento RG1H10 VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKIGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10 VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-H2A-22-1S VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-H2A-22-1S VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-H2A-27-2S VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-H2A-27-2S VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-3C VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYTFSDNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-3C VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-16C VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYTFSDNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-16C VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-17C VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYKFSNGVNWVRQAPGQGLEWMGWINTKSGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-17C VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Figure 76F

Sorrento RG1H10-19C VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYKFS DNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-19C VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-21C VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYTFS DNGVNWVRQAPGQGLEWMGWINTKSGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-21C VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-23C2 VH (SEQ ID NO:)

QVQLVQSGSELKPGASVKISCKASGYKFS DNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTITVTVSS

Sorrento RG1H10-23C2 VL (SEQ ID NO:)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Rinat mAb 7 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYWINWVRQAPGQGLEWMGNIYPGSSLTNYNEKFKNRVTMTRDTSTS
TVYMELSSLRSEDVAVYYCARLSTGTFAYWGQGLTVTVSS

Rinat mAb 7 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSQSLWDSGNQKNFLTWYQKPGQPPKLLIYWTSYRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQNDYFYPHTFGGGTKVEIK

Celgene PD1AB-6 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGATVKISCKASGFNIKDTYMHVWVQAPGKGLEWMGRIDPANGDRKYDPKFQGRVTITADTSTD
TAYMELSSLRSEDVAVYYCARSGPVYYYGSSYVMDYWGQGTITVTVSS

Celgene PD1AB-6 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSGQSVLYSSNQKNFLAWYQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCHQYLYSWTFGQGTKLEIK

Figure 77A additional ICOS sequences

GSK 88.2 VH (SEQ ID NO:)

QVQLQQPGAELVRPGASVKLSCKASGYSTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTSEDSAVYYCTRWNLSTYYFDNNYYLDYWGQGTTLTVSS

GSK 88.2 VL (SEQ ID NO:)

DIVMTQAAPSVPTPGESVSISCRSSKSLHNSNGNTYLYWFLQRPQGSPQLLIYRMSNLASGVDPDRFSGSGSGTAFTLRIS
RVEAEDVGYYCMQHLEYPWTFGGGKLEIK

GSK 314.8 VH (SEQ ID NO:)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGTTLTVST

GSK 314.8 VL (SEQ ID NO:)

DIVMTQAAPSVPTPGESVSISCRSSKSLHNSNGNIYLYWFLQRPQGSPQLLIYRMSNLASGVDPDRFSGSGSGTFTLKISR
VEAEDVGYYCMQHLEYPYTFGGGKLEIK

GSK H2L5 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNYNQKFQGRVTITADKSTS
TAYMELSSLRSEDYVYYCGRNNYGNYGWYFDYWGQGTTLTVSS

GSK H2L5 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCASSVSVMHWYQQKPGQAPRLIYDTSKLASGIPARFSGSGSGTDYTLTISSLEPEDF
AVYYCFQGSGYPYTFGGGKLEIK

Jounce 37A10S713 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMDWVRQAPGKGLVWVSNIDEEDGSITEYSPFVKGRFTISRDNKNT
LYLQMNSLRSEDYVYYCTRWGRFGFDSWGQGTTLTVSS

Jounce 37A10S713 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSQSLLSGSFNLYLTWYQQKPGQPPKLLIFYASTRHTGVDPDRFSGSGSGTDFTLTISS
LQAEDYVAVYYCHHHYNAPPTFGPGTKVDIK

Japan Tobacco Jmab-136 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTS
ISTAYMELSLRSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVTVSS

Japan Tobacco Jmab-136 VL (SEQ ID NO:)

DIQMTQSPSSVSASVGDRTTICRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQANSPWTFGGGKLEIK

Japan Tobacco Jmab-138 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRRENAKNSL
LYLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTTLTVSS

Japan Tobacco Jmab-138 VL (SEQ ID NO:)

EIVLTQSPGTLISLSPGERATLSCRASQNRSSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQFGSSPMCSFGGKLEIK

Figure 77B

Japan Tobacco Jmab-139 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTITVSS

Japan Tobacco Jmab-139 VL (SEQ ID NO:)

EIVLTQSPGTLSSLSPGERATLSCRASQSISSSSLAWYQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQFGSSPMCSFGQGTKLEIK

Figure 78A additional PD-L1 sequences

AstraZeneca/Celgene/MedImmune 2.14H9 OPT VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGLTVTVSS

AstraZeneca/Celgene/MedImmune 2.14H9 OPT VL (SEQ ID NO:)

EIVLTQSPGTLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLPWTFGQGTKVEIK

Genentech atezolizumab VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGLTVTVSA

Genentech atezolizumab VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFGQGTKVEIKR

Merck/Pfizer avelumab VH (SEQ ID NO:)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPGGITFYADTVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGLTVTVSS

Merck/Pfizer avelumab VL (SEQ ID NO:)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTRVFGTGTKVTVL

Medarex 12A4 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVCKTSGDTFSTYAIWVRQAPGQGLEWMGGIPIFGKAHYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYFCARKFHFVSGSPFGMDVWGQGTITVTVSS

Medarex 12A4 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYDASNRAATGIPARFSGSGSGTDFTLTISLPEPEDFAVYYCQQRSNWPTFGQGTKVEIK

Medarex 3G10 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVCKASGYTFTDYGFVSWVRQAPGQGLEWMGWITAYNGNTNYAQKLQGRVTIMTTDTSYSTVYMELRSLRSDDTAVYYCARDYFYGMDVWGQGTITVTVSS

Medarex 3G10 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLVWYQQKPGQAPRLLIYDASNRAATGIPARFSGSGSGTDFTLTISLPEPEDFAVYYCQQRSNWPTFGQGTKVEIK

Medarex 10A5 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVCKASGYTFTSYDVHWVRQAPGQRLEWMGWLHADTGITKFSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARERIQLWFDYWGQGLTVTVSS

Medarex 10A5 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYNSYPYTFGQGTKLEIK

Figure 78B

Amplimmune/GSK/MedImmune h3D10 Var1 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGGLEWMGDIDPNYGGTNYAQKFQGRVTMTRDTS
ISTAYMELSLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var1 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQAPRLLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var2 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTRDTSI
STAYMELSLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var2 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQSPRPLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var3 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTRDTSI
STAYMELSLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var3 VL (SEQ ID NO:)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var4 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTVDRS
SSTAYMELSLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var4 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQSPRPLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var5 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var5 VL (SEQ ID NO:)

DIQLTQSPSILSASVGDRTVITCRASSSVSYIYWFQKPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var6 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYAASVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCTRGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var6 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQAPRLLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Figure 78C

Amplimmune/GSK/MedImmune h3D10 Var7 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQGLEWMGDIDPNYGGTNYAQKFQGRVTIMTRDTS
ISTAYMELSRRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var7 VL (SEQ ID NO:)

DIQLTQSPSSLSASVGDRTVITCRASSGVSYIYWFQKQPGKAPKLLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var8 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var8 VL (SEQ ID NO:)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKQPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var9 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var9 VL (SEQ ID NO:)

DIQLTQSPSSLSASVGDRTVITCRASSGVSYIYWFQKQPGKAPKPLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var10 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var10 VL (SEQ ID NO:)

DIQLTQSPSILSASVGDRTVITCRASSSVSYIYWFQKQPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var11 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTAAASVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCTRGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var11 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKQPGQAPRLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var12 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQGLEWMGDIDPNYGGTNYAQKFQGRVTIMTRDTS
ISTAYMELSRRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var12 VL (SEQ ID NO:)

DIQLTQSPSSLSASVGDRTVITCRASSGVSYIYWFQKQPGKAPKLLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Figure 78D

Amplimmune/GSK/MedImmune h3D10 Var13 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var13 VL (SEQ ID NO:)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKQPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var14 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLWVGIDIDPNYGGTNYNQKFQGRVTMTVDRA
SSTAYMELSLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var14 VL (SEQ ID NO:)

DIQLTQSPSILSASVGDRTTICRASSSVSYIYWFQKQPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYCQQWSNNPLTFGQGTKVEIK

Eli Lilly Antibody A VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGHPIFGTANYAQKFQGRVTITADKSTSTA
YMELSSLRSEDTAVYYCARSPDYSPYFYGGMDVWGQGTITVTVSS

Eli Lilly Antibody A VL (SEQ ID NO:)

QSVLTQPPSASGITPQQRVTISCSGSSNIGSNFTVNWYQQLPGTAPKLLIYGNSNRPSGVPDFRSGSGSGTSASLAISGLQSE
DEADYYCQSYDSSLSGSVFGGGIKLTVLG

Cytomx C5H9v2 VH (SEQ ID NO:)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSIWRNGIVTVYADSVKGRFTISRDNKNT
LYLQMNSLRAEDTAVYYCAKWSAAFDYWGQGTILTVTVSS

Cytomx C5H9v2 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTTICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQDNGYPSTFGGGTKVEIKR

Dana-Farber/Novartis Humanized 29E.2A3 VH (SEQ ID NO:)

CKASGYTFTSYVMHWVKAPGQRLLEWIGYVNPFDGTYNEMFKGRATLTSDKSTSTAYMELSSLRSEDTAVYYCAR
QAWGYPWGQGTILTVTVSS

Dana-Farber/Novartis Humanized 29E.2A3 VL (SEQ ID NO:)

DIVLTQSPATLSLSPGERATLSCRATESVEYYGTSLVQWYQKPGQPPKLLIYAASSVDSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYFCQSQRRVPYTFGQGTKLEIK

Dana-Farber/Novartis 1B9 VH (SEQ ID NO:)

DVQLQESGPGLVKPSQSLSTCTVTGYSTSDHAWNWRQVPGNKLEWMGYITYRGSTTYSPLKSRISITRDTSKNQFF
LQLNSVTEDTATYYCARSMITGYVMDYWGQGTSTVTVSS

Dana-Farber/Novartis 1B9 VL (SEQ ID NO:)

DIVMTQSHKFMSTSLGDRVTITCKASQDVGISVVWYQKPGQSPKLLIYWASTRHTGVPDFRFTSGSGSGTDFTLTINNVA
SEDLADYFCQYSSYPLTVGAGTKLELK

Figure 78E

Dana-Farber/Novartis 4H1 VH (SEQ ID NO:)

DVQLQESGPGGLVKPSQSLTCTVTDYSITSYAWTWIRQFPGNKLEWMGYITYRGTTIRYNPSLTSRISFTRDTSKNQLF
LQLNSVTTEDTGTGCCARSMITGYYAMDYWGQGTSTVTVSS

Dana-Farber/Novartis 4H1 VL (SEQ ID NO:)

DIVMTQSHKFMSTSVGDRVSISCKASQDVGISVAWYQKPGQSPKLLIYWASTRHTGVPVRFTGSGSGTDFLTISNVQ
SEDLADYFCQQYSSYPPTFGAGTKLELK

Dana-Farber/Novartis mAb-42 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTA
YMELSSLRSEDTAVYYCARGRMFGAGIDFWGPGTLVTVSS

Dana-Farber/Novartis mAb-42 VL (SEQ ID NO:)

NFMLTQPHSVSESPGKTVTISCTRSSGSDSNYQWYQQRPGSAPTTVIYEDNQRPSPGVDRFSGSDSSNSASLTISGLK
TEDEADYYCQSYDSNNRHVIFGGGKLTVL

Dana-Farber/Novartis BAP058-03 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGATVKISCKVSGYFTTSYWMYWVRQATGQGLEWMGRIDPNSGSKYNEKFKNRVTITADKSTS
TAYMELSSLRSEDTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-03 VL (SEQ ID NO:)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAFAWYLQKPGQSPQLLIYWASTRHTGVPDRFSGSGSGTDFTLKISRVEA
EDVGVYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-04 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGESLRISCKGSGYFTTSYWMYWVRQAPGQGLEWMGRIDPNSGSKYNEKFKNRVTISVDTSKN
QFSLKLSSTAAADTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-04 VL (SEQ ID NO:)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAFAWYLQKPGQSPQLLIYWASTRHTGVPDRFSGSGSGTDFFTISLQPE
DIATYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-06 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGESLRISCKGSGYFTTSYWMYWVRQPPGKGLEWIGRIDPNSGSKYNEKFKNRVTITADKSTSTA
YMELSSLRSEDTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-06 VL (SEQ ID NO:)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAFAWYLQKPGQSPQLLIYWASTRHTGVPDRFSGSGSGTDFFTISLQPE
DIATYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-07 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYFTTSYWMYWVRQSPRGLEWLGRIDPNSGSKYNEKFKNRFTISRDDSKNT
AYLQMNSLKTEDTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-07 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCKASQDVGTAFAWYLQKPGQSPQLLIYWASTRHTGIPPRFSGSGYGTDFLTINNIESE
DAAYYFCQYNSYPLTFGQGTKVEIK

Figure 78F

Dana-Farber/Novartis BAP058-11 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGATVKISCKVSGYTFTSYWYWVRQATGQGLEWMGRIDPNSGSTKYNEKFKNRVTITADKSTS
TAYMELSSLRSEDTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-11 VL (SEQ ID NO:)

DVVMTQSPSLSPVTLGQPASISCKASQDVGTA VAWYQQKPGQAPRLLIYWASTRHTGVPSRFSGSGSGTEFTLTISLQP
DDFATYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-13 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGATVKISCKVSGYTFTSYWYWVRQARGQRLEWIGRIDPNSGSTKYNEKFKNRFTISRDN SKNT
LYLQMNSLR AEDTAVYYCARDYRKGLYAMDYWGQGTITVTVSS

Dana-Farber/Novartis BAP058-13 VL (SEQ ID NO:)

AIQLTQSPSSLSASVGDRTITCKASQDVGTA VAWYLQKPGQSPQLLIYWASTRHTGVPSRFSGSGSGTDFLTISL EAE
DAATYYCQYNSYPLTFGQGTKVEIK

Sorrento H6 VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCKASGGTFSSY AISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTA
YMELSSLRSEDTAVYYCARGNIVATITPLDYWGQGTITVTVSS

Sorrento H6 VL (SEQ ID NO:)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLYIYYDSRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCQVWDSSDHRIFGGGTKLTVL

Sorrento RC5 VH (SEQ ID NO:)

EVQLLESGGGVVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDN SKN
TVSLQMNSLR AEDTAVYYCAKDRYYNFPLGMDVWGQGTITVTVSS

Sorrento RC5 VL (SEQ ID NO:)

AIRMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYTTSSLKSGVPSRFSGSGSGTDFLTISR LQPED
FATYYCQSYSTWTFGRGTKVEIK

Sorrento SH1A1Q VH (SEQ ID NO:)

EVQLVQSGAEVKKPGSSVKVSCKASGGTFSSY AISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTA
YMELSSLRSEDTAVYYCAREGTIYDSSGYSFDYWGQGTITVTVSS

Sorrento SH1A1Q VL (SEQ ID NO:)

QSVLTQPPSVSAAPGQKVTISCSGNNANIANNYVSWYQQLPGTAPKLLIYDNNYRPSGIPDRFSGSKSGTSA TLDITGLQT
GDEADYYCGVWDGSLTTGVFGGGTKLTVL

Sorrento SH1B3 VH (SEQ ID NO:)

QVQLVESGGGVVQPGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLR TEDTAVYYCARGWLD RDIDYWGQGTITVTVSS

Sorrento SH1B3 VL (SEQ ID NO:)

LPVLTQPASVSGSPGQSITISCTGTTSDIGGYDYVSWYQHPGKAPKLM IYDVSKRPSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYSSSTHVFGTGKLTVL

Figure 78G

Sorrento SH1D1 VH (SEQ ID NO:)

EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGTLVTVSS

Sorrento SH1D1 VL (SEQ ID NO:)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQHPGKAPKLLIYDVSNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEADYYCSSYRSSTLGPVFGGGTKLTVL

Sorrento SH1D2 VH (SEQ ID NO:)

QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGTLVTVSS

Sorrento SH1D2 VL (SEQ ID NO:)

QAGLTQPPSVSEAPRQRTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYDDLLPSGVSDRFSGSKSGTASLAISGLQS
EDEADYYCAAWDDSLNGYVFGTGKLTVL

Sorrento SH1D12 VH (SEQ ID NO:)

EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGTLVTVSS

Sorrento SH1D12 VL (SEQ ID NO:)

QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQHPGKAPKLLIYDVSKRPSGVPDRFSGSKSGNTASLTISGL
QAEDEADYYCSSYTSSTTHVFGTGKTVL

Sorrento SH1E1 VH (SEQ ID NO:)

EVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGTLVTVSS

Sorrento SH1E1 VL (SEQ ID NO:)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT
GDEADYYCGTWDSSLVWVFGGGTQLTVL

Sorrento SH1G9 VH (SEQ ID NO:)

QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGTLVTVSS

Sorrento SH1G9 VL (SEQ ID NO:)

QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQHPGRAPRLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEGDYYCSSYTSGGTLGPVFGGGTKLTVL

Sorrento SH1E6 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYGVHWVRQAPGQGLEWMGRLLPIVSMNTNYAQKFQDRVSITDKSTG
TAYMEIRSLTSEDTALYYCASVQQQLPWVFFAWGQGTLVTVSS

Sorrento SH1E6 VL (SEQ ID NO:)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT
GDEADYYCGTWDSSL SAVVFGGGTKLTVL

Figure 78H

Sorrento SH1A2 VH (SEQ ID NO:)

QMQLVQSGGGVVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKN
TLYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGT LVT VSS

Sorrento SH1A2 VL (SEQ ID NO:)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIPDRFSGSNSDTSATLGITGLQT
GDEADYYCGTWDSSLSAWVFGGGTKLTVL

Sorrento SH1B1 VH (SEQ ID NO:)

QVQLVQSGGGVVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKN
TLYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGT LVT VSS

Sorrento SH1B1 VL (SEQ ID NO:)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT
GDEADYYCGTWDSSLSAGSVVFGGGTKLTVL

Sorrento H6B1L VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAYSWVRQAPGQGLEWMGGHIPSGFTANYAQKFQGRVTITADESTST
AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGT LVT VSS

Sorrento H6B1L VL (SEQ ID NO:)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCLVWDSSSDHRIFGGGTKLTVL

Sorrento H6A1 VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAYSWVRQAPGQGLEWMGGHIPFGTANYAQKFQGRVTITADESTST
AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGT LVT VSS

Sorrento H6A1 VL (SEQ ID NO:)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCQVWDSSSDHRIFGGGTKLTVL

Sorrento H6B1 VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAYSWVRQAPGQGLEWMGGHIPSGFTANYAQKFQGRVTITADESTST
AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGT LVT VSS

Sorrento H6B1 VL (SEQ ID NO:)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCQVWDSSSDHRIFGGGTKLTVL

Sorrento H6B2 VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAISWVRQAPGQGLEWMGGHIPAFGTANYAQKFQGRVTITADESTST
AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGT LVT VSS

Sorrento H6B2 VL (SEQ ID NO:)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCQVWDSSSDHRIFGGGTKLTVL

Figure 781

Sorrento G12 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKVSCKASGYITFTGYMHVVRQAPGQGLEWMGWNPNSDNTGSAQKFQGRVFMKTTS
LNTAYMELSLRSEDTAIYYCARERSSGYFDWVGQGLTVTVSS

Sorrento G12 VL (SEQ ID NO:)

DIVMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQSYSTPIITFGQGTRLEIK

Sorrento RSA1 VH (SEQ ID NO:)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSTIYYADSVKGRFTISRDNKNSL
YLQMNSLRDEDTAVYYCARGDYGYGMDVWGQGTITVTVSS

Sorrento RSA1 VL (SEQ ID NO:)

NIQMTQSPSSVSASVGDRTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFALTISLQPE
DFATYYCQQADSPFSITFGQGTRLEIK

Sorrento RA3 VH (SEQ ID NO:)

QMQLVQSGAEVKKPGSSVKVSCKASGGTFSRYGVHVRQAPGQGLEWMGRIPVSMNTYAQKFQDRVSITTDKSTG
TAYMELRSLTSEDALYYCASVGQQLPWVFFAWGQGLTVTVSS

Sorrento RA3 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQSYSSHWTFGQGTKVEIK

Sorrento SH1E2 VH (SEQ ID NO:)

EVQLVESGAEVKKPGSSVKVSCKASGGTFSRYAISWVRQAPGQGLEWMGGHPIFGTANYAQKFQGRVTITADESTSTA
YMELSSLRSEDTAVYYCARAPYYYYYMDVWGQGTITVTVSS

Sorrento SH1E2 VL (SEQ ID NO:)

QSALTQPASVSGSLGQSVTISCTGSSSDVGSYNLVSWYQHPGKAPNLMYDVSKRSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYTGISVTVFGGGTKLTVL

Sorrento SH1E4 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRYGVHVRQAPGQGLEWMGRIPVSMNTYAQKFQDRVSITTDKSTG
TAYMELRSLTSEDALYYCASVGQQLPWVFFAWGQGLTVTVSS

Sorrento SH1E4 VL (SEQ ID NO:)

QSVLTQPPSASGSPGQSVTISCTGTSSDIGGYDSVSWYQHPGKAPKLMYDVSKRPSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYTSSIFFYVFGTGTKVTVL

Sorrento SH1B11 VH (SEQ ID NO:)

QVQLVQSGSELKKPGSSVKVSCKASGYSFSGYYIHWVRQAPGQGLEWMGWIDPNSGVNTNYVRRFQGRVTIMTRDTSLS
TAYMELSGLTADDTAVYYCARDENLWQFGYLDYWGQGLTVTVSS

Sorrento SH1B11 VL (SEQ ID NO:)

DIVMTQSPSSLSASIGDRVTITCRASQRISAYVNWYQQKPGKAPKVLIIYAASSLRSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQTYSPPWTFGQGTKVEIK

Figure 78J

Sorrento SH1C8 VH (SEQ ID NO:)

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCARGQWLVTLEDYWGQGTLLTVSS

Sorrento SH1C8 VL (SEQ ID NO:)

QSVVTQPPFSVSAAPGQKVTISCSGSSSDIGNHYVSWYQQLPGTAPKLLIYDNNQRPSGIPDRFSGSKSGTSATLAITGLQT
GDEADYYCGTWDNSLSPHLLFGGGTKLTVL

Regeneron H1H9364P2 VH (SEQ ID NO:)

EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYALHWVRQAPGKGLEWVSGISWTGGTIDYADSVKGRFTISRDN AKNS
LYLQMSLRTEDTAIYYCTRIDRGNWKYGGWFDPPWQGTLLTVSS

Regeneron H1H9364P2 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQSYSTPPITFGQGTREIK

Regeneron H1H9373P2 VH (SEQ ID NO:)

QVQLVQSGTEVKKPGASVKVSKASGYITFTAYYMHVVRQAPGQGLDWMGWISPN SGFTNYAQKFQGRVTMTTRDTSI
NTFYMELSGLRSDDTAVYYCAREGSTHNSFDPWQGTLLTVSS

Regeneron H1H9373P2 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQSYSTPPITFGQGTREIK

Regeneron H1H8314N VH (SEQ ID NO:)

EVQLVESGGGVVRPGSLRLSCAASGFTFDDYGMTWVRQAPGRGLEWVSGIHWGKRTGYADSVKGRFTISRDN AK
KSLYLQMNSLKGEDTALYHCVRGGMSTGDWFDPPWQGTLLTVSS

Regeneron H1H8314N VL (SEQ ID NO:)

DIQMTQSPSSLSASLGDRVTITCRASQSINSYLNWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTEFTLTISNLQPED
FATYYCQSYSTPPITFGQGTREIK

Inserm PDL1.3.1 VH (SEQ ID NO:)

EVQLQQSGTELVKPGASVKLSCTTSGFNIQDTYMHVVKRPEQGLEWIGWIDPANGNTKYDPKFQGGKATHIADTSSNT
AYLQLRGLTSEDTAIYYCARSGVSTAHDYWGQGTLLTVSS

Inserm PDL1.3.1 VL (SEQ ID NO:)

QIVLSQSPAILSASPGKVTMTCRASSVSFMHWYQQKPGSSPKPWYATSNLASGVPTRFSGSGSGTSYSLTISRVEAE
DAATYYCQWSSYPRTFGGGTKLEIK

Figure 79A additional CTLA-4 sequences

Medarex Ipilimumab VH (SEQ ID NO:)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNKNT
LYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLVTVSS

Medarex Ipilimumab VL (SEQ ID NO:)

EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQYVGSPWTFGQGTKVEIK

Amgen/MedImmune/Pfizer Tremelimumab VH (SEQ ID NO:)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGSKYYADSVKGRFTISRDNKNT
TLYLQMNSLRAEDTAVYYCARDPRGATLYYYYGMDVWGQGTITVTVSS

Amgen/MedImmune/Pfizer Tremelimumab VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASQSINSYLDWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQYYSTPFTFGPGTKVEIK

Agenus AGEN1884 VH (SEQ ID NO:)

EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSVKGRFTISRDNKNTSL
LYLQMNSLRAEDTAVYYCARVGLMGPFDIWGQGTMTVTVSS

Agenus AGEN1884 VL (SEQ ID NO:)

EIVLTQSPGTLSPGERATLSCRASQSVSRYLGWYQQKPGQAPRLIYGASTRATGIPDRFSGSGSGTDFTLTITRLEPED
FAVYYCQYVGSPWTFGQGTKVEIK

Tegenero 4.3F6B5 VH (SEQ ID NO:)

EVQLQSPGPVLVKPGASVKISCKASGYTFTDYKIHVVWQSHGKSLEWIGYIYPYSGSSDYNQKFKSKATLTVDNSSTTA
YMEIIRSLTSEDSAVYYCARGGDAMDYWGQGTAVTVSS

Tegenero 4.3F6B5 VL (SEQ ID NO:)

DILMTQSPASLSASVGETVTITCGASENIYGALNWWYQRKQKSPQLLIYGATNLADGMSSRFSGSGLGRQYYLKISLHP
DDVATYFCQNILGTWTFGGGTKLEIKR

Tegenero 4.8H10H5 VH (SEQ ID NO:)

DVKLVESGGGLVKLGSLKLSAASGFTFNIIYMSWVRQTPEKRLELVAAINPDGGNTYYPDYTKGRFTISRDNKNT
LYLQMSSLSKSEDSALYYCARYGGPGFDSWGQGTLLTVSS

Tegenero 4.8H10H5 VL (SEQ ID NO:)

ENVLTQSPAIMSASPGERVTMTCSASSSVSYMHWYQKSNTSPKLWIYDTSKLASGVPGRFSGSGSRNSYSLTISSMEAE
DVATYYCFPGSGFPFMYTFGGGTKLEIKR

Tegenero TGN2122.C VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYKIHVVWVRQAPGQGLEWIGYIYPYSGSSDYNQKFKSRATLTVDNSIST
AYMEISRLRSDDTAVYYCARGGDAMDYWGQGTLLTVSS

Tegenero TGN2122.C VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCGASENIYGALNWWYQRKPGKAPKLLIYGATNLADGVPSRFSGSGSGRDTLTISLQPE
EDFATYFCQNILGTWTFGGGTKVEIK

Figure 79B

Tegenero TGN2122.H VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTFNIIYMSWVRQAPGKLELVAAINPDGGNTYYPD TVKGRFTISRDN AKNS
LYLQMNSLRAEDTAVYYCARYGGPGFDSWGQGLTVTVSS

Tegenero TGN2122.H VL (SEQ ID NO:)

ENVLTQSPATLSLSPGERATLSCSASSSVSYMHVYQQKPGQAPRLWIYDTSKLASGIPARFSGSGSRNDYTLTISSEPED
FAVYYC FPGSGFPFMYTFGGGTKVEIK

Sorrento F7 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYAFDGHYMHVVRQAPGQRLEWMGWVDPHSGATNYAQNFQGGVTMTRDT
SINTVYMELSSSLKSDDTAVYYCARDFYDTSKSGAFDIWGQGTMTVTSS

Sorrento F7 VL (SEQ ID NO:)

AIQLTQSPSSVSASVGDRTTTCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQVNSFPWAFGGGTKVEIK

Sorrento E8 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCEASGYTFTNYYIHVLRQAPGQGLEWMGHNPSGGSTTYAQKFQGRITMTRDTSTNT
LYMELSSLRSEDTAIYYCARRDCRGFSCYFAYWGQGTITVTSS

Sorrento E8 VL (SEQ ID NO:)

DIVMTQSPSSLSASVGDRTTTCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPPRFSGSGSGTEFTLTISLQPED
FATYYCQQANSFPPTFGGGTKVDIK

Sorrento CT1E1 VH (SEQ ID NO:)

EVQLVESGGGLVQPGSLRLSCRGSNFNFDLAIWVRQAPGKLEWLGFVRSKAYGETTDYVASVKGRFTISRDDSK
FIAWLQMDSLKTDITAVYYCTTFNYWGQGLTVTVSS

Sorrento CT1E1 VL (SEQ ID NO:)

QPVLTPPPSVSAPGKTARISCGGNIASEAVHWYQKKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLRISVDAG
DEADYYCQVWDRITDQPVFGGGTKLTVL

Figure 80A additional LAG-3 sequences

Medarex BMS-986016 VH (SEQ ID NO:)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSDYYWNWIRQPPGKGLEWIGEINHRGSTNSNPSLKSRLVTLSDTSKNQFS
LKLRSVTAADTAVYYCAFGYSDYEYNWFDPPWGQGLTVTVSS

Medarex BMS-986016 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDF
AVYYCQQRSNWPLTFGQGTNLEIK

Immutep/INSERM/Novartis IMP731 VH (SEQ ID NO:)

QVQLKESGPGGLVAPSQSLSTCTVSGFSLTAYGVNWVRQPPGKGLEWLGMIWDDGSTDYNSALKSRLSISKDNSKSQVF
LKMNSLQTDATARYYCAREGDVAFDYWGQGTTLTVSS

Immutep/INSERM/Novartis IMP731 VH (SEQ ID NO:)

DIVMTQSPSSLAVSVGQKVTMSCKSSQSLNNGSNQKNYLAWYQQKPGQSPKLLVYFASTRDSGVPDRFIGSGSGTDFTL
TISSVQAEDLADYFCLQHFGTPPTFGGGTKLEIK

Immutep/INSERM/Novartis 13E2 VH (SEQ ID NO:)

QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGLGWIRQPSGKGLEWLTHIWDDIKRYNPDLRSRLTISKDTSSSQIFL
KIASVDATATATYYCARIVEGSYSSSYFDVWGAGTIVTVSS

Immutep/INSERM/Novartis 13E2 VH (SEQ ID NO:)

DIVMTQPHKFMSTSVEDRVTTICKASQDVIFDVAWYQQKPGQSPKLLIYSASSRVSGVPDRFTGSGSGTDFTFITISSVQA
EDLAVYYCQQHYSPTPTFGGGTKLEIK

Immutep/INSERM/Novartis 34F4 VH (SEQ ID NO:)

QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMGVGVWIRQPSGKGLEWLTHIWDDVKRYNPALKSRLTISKDTSSSQV
FLKIASVDATATATYYCARIEGDTYYDYFDYWGQGVTLTVSS

Immutep/INSERM/Novartis 34F4 VH (SEQ ID NO:)

DIVMTQSHKLMSTSVGDGLSTICKASQDVSIADVWYQQKPGQSPKLLIYSASFRTYTGVPDRFTGSGSGTDFTFITISSVQA
EDLAVYYCQQHYSIPWTFGGGKLEIK

Immutep/INSERM/Novartis IMP761 VH (SEQ ID NO:)

QITLKESGPTLVKPTQTTLTCTFSGFSLSTSGMGLGWIRQPPGKLTLEWLTHIWDDIKRYNPDLRSRLSITKDTSKNQV
VLTMTNMDPLDTGTYYCARIVEGSYSSSYFDVWGQGLTVTVSS

Immutep/INSERM/Novartis IMP761 VH (SEQ ID NO:)

DIVMTQIPSSLSASVGDRTITCKASQDVIFDVAWYQQRPQAPKLLIYSASSRVSGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQHYSPTPTFGQGTSLDIK

GSK H5L7 VH (SEQ ID NO:)

QVQLQESGPGLVKPSSETLSLTCTVSGFSLTAYGVNWIRQPPGKGLEWIGMIWDDGSTDYDSALKSRVTISVDTSKNQFS
LKLSSVTAADTAVYYCAREGDVAFDYWGQGLTVTVSS

GSK H5L7 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCKSSQSLNPSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSPRFSGSGSGTDFTLT
ISSLPQPEFATYYCLQHFGTPPTFGQGTLEIKR

Figure 80B

Merck hu22D2 VH (SEQ ID NO:)

QMQLVQSGPEVKKPGTTSVKVSKASGYTFTDYNVDWVRQARGQRLEWIGDINPNNGGTIYAQKFQERVTTITVDKSTST
AYMELSSLRSEDTAVYYCARNYRWFAMDHWGQGTITVTVSS

Merck hu22D2 VL (SEQ ID NO:)

DIVMTQTPLSLSVTPGQPASISCKASQSLDYEGSDMNWYLQKPGQPPQLLIYGASNLESGVPDRFSGSGSGTDFTLKIS
RVEAEDVGVYYCQSTEDPRITFGGGTKVEIK

Regeneron H4sH15482P VH (SEQ ID NO:)

QVQLVESGGGVVQPGSRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAIHWDGSKNYADSVKGRFTISRDNSKN
TQYLMNSLRSEDTAVYYCASVATSGDFDYGMGVWGQGTITVTVSS

Regeneron H4sH15482P VH (SEQ ID NO:)

EIVLTQSPATLSLSPGERITLSCRASQRISTYLAWYQKPGQAPRLIYDASKRATGIPARFSGSGSGTGFTLTISSEPEDF
AVYYCQQRSNWPLTFGGGTKEIK

Sorrento L35D4 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGTITVTVSS

Sorrento L35D4 VL (SEQ ID NO:)

QSVLTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQYPGKAPRLMIFEVTERASGVDPDRFSGSKSGNTASLTISGL
QTEDEAVYFCSSYSGSNPGAMFGGGTKLTVL

Sorrento L35G6 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGTITVTVSS

Sorrento L35G6 VL (SEQ ID NO:)

QAGLTQPASVSGSPGQSVTISCTGTSSDVGGYSYVSWYQKHPGKAPKLMIDVTNRPSGVSNRFSKSGNTASLTISGL
QAEDEADYYCSTYTRSNLTFGPGTKVTVL

Sorrento L33H11 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGTITVTVSS

Sorrento L33H11 VL (SEQ ID NO:)

LPVLTQPASVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIDVTNRPSGVSNRFSKSGNTASLTISGL
QAEDEADYYCSTYSSNTLLFGGGIQLTVL

Sorrento L32A9 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGTITVTVSS

Sorrento L32A9 VL (SEQ ID NO:)

QSVVTQPPSVSAAPGQKVTISCSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRHSGIPDRFSGSTSDTSATLGITRLQT
GDEADYYCGTWDSLSAYVFGTGKTVTVL

Figure 80C

Sorrento L32D10 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGILVTVSS

Sorrento L32D10 VL (SEQ ID NO:)

QSVLTQPPSASGSPGQSVTISCTGTSSDVGGYDYVSWYQQHQGKAPKLMYDVSNRPSGVSNRPSGSKSGNTASLTISGL
QAEDEADYYCSSYTSSTLVFGGGTKLTVL

Sorrento L32A4 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGILVTVSS

Sorrento L32A4 VL (SEQ ID NO:)

QSVLTQPASVSGSPGQSITISCTGTSSDIGAYNFVSWYQQHPGKAPKLMYGVSNRPSGVSSRPSGSKSGSTASLTISGLQ
AEDEADYYCSSYTTSGSAVFGTGKLTVL

Sorrento L3A1 VH (SEQ ID NO:)

EVQLLESGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGILVTVSS

Sorrento L3A1 VL (SEQ ID NO:)

QSVLTQPASVSGSPGQSITISCTGTSSDIGAYNFVSWYQQHPGKAPKLMYGVSNRPSGVSSRPSGSKSGSTASLTITGLQ
AEDEADYYCSSYTTSGSAVFGTGKLTVL

Sorrento L3A10 VH (SEQ ID NO:)

EVQLLESGGGVVPGRSLRVSCAASGFTFSNHAMHVWRQAPGKGLEWVAVISYDGSKKFYSDSVRGRFTISRDNKNT
LYLQMNLSLRPEDTAVYYCAKGAHGYTSGWHDYWGQGTILVTVSS

Sorrento L3A10 VL (SEQ ID NO:)

DVVMTQSPSSLSASVGDVRSITCRASQNIQRYLNWYQKPKGAPKLLVSAASSLQGGVPSRPSGSGSGTDFLTISRQLP
EDFATYFCQTYSSPQCTFGQGTKVDIK

Sorrento L3C5 VH (SEQ ID NO:)

QVQLVQSGSELKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGHINPSGGATNYAQKFQGRVTMTRDTSTS
STVYMELSSLRSEDTAVYYCARDSDYDLGYGMDVWGQGTILVTVSS

Sorrento L3C5 VL (SEQ ID NO:)

QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGASNRPSGSKSGNTASLTISGL
QAEDEADYYCSSYTNRTLLFGGGTKLTVL

Sorrento L3E3 VH (SEQ ID NO:)

EVQLLESGAEVKKPGASVKVSCKASGYTFTSYMHVWRQAPGQGLEWMGHINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARELMATGGFDYWGQGILVTVSS

Sorrento L3E3 VL (SEQ ID NO:)

QSVLTQPASASGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRPSGSKSGNTASLTISGL
QAEDEANYCSSYTSSTNVFGTGKVTVL

Figure 81A additional TIM-3 sequences

AnaptysBio/Tesaro APE5137 VH (SEQ ID NO:)

EVQLLESGGGLVQPGGSLRLSCAAASGFTFSYDMSWVRQAPGKGLDWVSTISGGGTYYTYYQDSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCASMDYWGQGTITVTVSSA

AnaptysBio/Tesaro APE5137 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRVTITCRASQSIRRYLNWYHQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISLQPE
DFAVYYCQSHSAPLTFGGGTKEIKR

AnaptysBio/Tesaro APE5121 VH (SEQ ID NO:)

EVQVLESGGGLVQPGGSLRLYCVASGFTFSGYAMS WVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN
TLYLQMNSLRAEDTAVYYCAKKYYVGPADYWGQGTITVTVSSG

AnaptysBio/Tesaro APE5121 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA WYQHKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQYYSSPLTFGGGTKEIVK

Dana-Farber/Novartis ABTIM3-hum03 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWIGDIYPGQGDTSYNQKFKGRATMTADKST
STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGTITVTVSS

Dana-Farber/Novartis ABTIM3-hum03 VL (SEQ ID NO:)

DIVLTQSPDSLAVSLGERATINCRASESVEYYGTS LMQWYQKPGQPPKLLIYAASNVESGVPDRFSGSGSGTDFTLTIS
LQAEDVAVYYCQQRKDPSTFGGGTKVEIK

Dana-Farber/Novartis ABTIM3-hum11 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGDIYPGNGDTSYNQKFKGRVTITADKST
STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGTITVTVSS

Dana-Farber/Novartis ABTIM3-hum11 VL (SEQ ID NO:)

AIQLTQSPSSLSASVGDRVTITCRASESVEYYGTS LMQWYQKPGKAPKLLIYAASNVESGVPDRFSGSGSGTDFTLTIS
LQPEDFATYFCQQRKDPSTFGGGTKVEIK

Dana-Farber/Novartis ABTIM3-hum21 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWIGDIYPGQGDTSYNQKFKGRATMTADKST
STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGTITVTVSS

Dana-Farber/Novartis ABTIM3-hum21 VL (SEQ ID NO:)

DIVLTQSPDSLAVSLGERATINCRASESVEYYGTS LMQWYQKPGQPPKLLIYAASNVESGVPDRFSGSGSGTDFTLTIS
LQAEDVAVYYCQQRKDPSTFGGGTKVEIK

KHK 4177 VH (SEQ ID NO:)

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFHSGSTNYPNLSKSRVTISVDTSKNQFSLK
LSSVTAADTAVYYCARDGEYFDMLTGFDYWGQGTITVTVSS

KHK 4177 VL (SEQ ID NO:)

RCDIQMTQSPSSLSASVGDRVTITCRASQGISSWLA WYQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQ
EDFATYYCQYNSYPRTFGGQTKVEIK

Figure 81B

KHK 4545 VH (SEQ ID NO:)

QVQLQESGPGLVKPSSETLSLTCTVSGGSFSRGGYYWNWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTISLDTSKNQF
SLKLSSVTAADTAVYYCARDHYSSSWTFDYWGQGLVTVSS

KHK 4545 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELPED
FAVYYCQQRSNWPPTFGQGTKLEIK

KHK 8123 VH (SEQ ID NO:)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLEWMGEINPSNGRTNYNEKFKTRVTTITADTSTS
TAYMELSSLRSEDTAVYYCARGYYLYFDYWGQGLVTVSS

KHK 8123 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTTITCHASQGIRINIGWYQQKPGKAPKLLIYHGTNLEDGVPSRFSGSGSGTDFTLTISLQPED
FATYYCVYQGQFPWTFGQGTKLEIK

Jounce mAb15 VH (SEQ ID NO:)

QVQLKESGPGLVAPSQSLTCTVSGFSLTGYGVTWVRQPPGKGLEWLGMIWGDGNTDYNGLKSRNLNISKDNSKSQV
FLKMNSLQTDATARYYCARSYYYGPPDYWGQGTTLTVSS

Jounce mAb15 VL (SEQ ID NO:)

DIVMTQSPSSLSAMSVGQKVTMSCKSSQSLNRSQKNYLAWYQRKPGQSPKLLLYFASTRESGVPDRFIGSGSGTDFTL
TISSVQAEDLADYFCHQHYNTPTTFGGGTKLEIK

Jounce mAb58 VH (SEQ ID NO:)

QIQLVQSGPELKKPGETVKISKASGYTFTTYGMSWVKQAPGKGLKLMGWINTYSGAPTYADDFKGRFAFSLETSASA
AYLQINNLKNEDTATYFCARKPPHYVNSFDYWGQGTTLTVSS

Jounce mAb58 VL (SEQ ID NO:)

DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSHESPRLLIKYASQSIGIPSRFSGSGSGSDFTLINSVEPEDV
GVYYCQNGHSFPYTFGGGTKLEIK

Roche TIM3-0433 VH (SEQ ID NO:)

QITLKESGPTLVKPTQTLTLCTFSGFSLSTSGMSVGWIRQPPGKGLEWLAHIWLNDVFFNPALKSRLTITKDTSKNQV
VLTMTNMDPVDATYYCVRANGYLYALDYWGQGLVTVSS

Roche TIM3-0433 VH (SEQ ID NO:)

ETTLTQSPAFMSATPGDKVNIACSASSSVSYTQWYQQKPGKAPKLWIYDAFKLAPGIPPRFSGSGYGTDFLTINNIESED
AAYYFCHQWSSYPWTFGQGTKLEIK

Roche TIM3-0434 VH (SEQ ID NO:)

QITLKESGPTLVKPTQTLTLCTFSGFSLSTSGMSVGWIRQPPGKGLEWLAHIWLNDVFFNPALKSRLTITKDTSKNQV
VLTMTNMDPVDATYYCVRANGYLYALDYWGQGLVTVSS

Roche TIM3-0434 VH (SEQ ID NO:)

DIQLTQSPSFLSASVGDRTTITCSASSSVSYTQWYQQKPGKAPKLWIYDAFKLAPGVPSRFSGSGSGTEFTLTISLQPEDF
ATYFCHQWSSYPWTFGQGTKLEIK

Figure 81C

Roche TIM3-0438 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKTTYMHWVRQAPGKGLEWVGRIDPADDNTKYAPKFQGKATISADTSKN
TAYLQMNSLRAEDTAVYYCVRDFGYVAWFAYWGQGLVTVSS

Roche TIM3-0438 VH (SEQ ID NO:)

DIVMTQSPLSLPVTPGEPASISCRASQSVDNVVAWYLQKPGQSPQLLIYYASNRYIGVPDRFSGSGSGTDFTLKISRVEAE
DVGVYYCQQHYSSPYTFGQGTKVEIK

Roche TIM3-0443 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKTTYMHWVRQAPGKGLEWVGRIDPADDNTKYAPKFQGKATISADTSKN
TAYLQMNSLRAEDTAVYYCVRDFGYVAWFAYWGQGLVTFSS

Roche TIM3-0443 VH (SEQ ID NO:)

DIVMTQSPLSLPVTPGEPASISCRASQSVDNVVAWYLQKPGQSPQLLIYYASNRYIGVPDRFSGSGSGTDFTLKISRVEAE
DVGVYYCQQHYSSPYTFGQGTKVEIK

Figure 82 additional BTLA sequences

Medarex 3C2 VH (SEQ ID NO:)

QVQLQESGPGLVKPSETLSLTCTISGGSISNYWNNWIRQPPGKGLEWIGYIYYSTSTKYNPSLKSRVTMSVETSKNQFSL
KLSSVTAADTAVYYCARVKVYSTGWFFDYWGQGTILVTVSS

Medarex 3C2 VL (SEQ ID NO:)

AIQLTQSPSSLSASVGDRTTTCRASQGISSALAWYQQKPGKAPKLLIYDASSLESQVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQFNSYPLTFGGGKVEIK

Medarex 11E2 VH (SEQ ID NO:)

EVQLVESGGGVIRPGGSLRLSCAASGFTFDDYGMWVVRQAPGKGLEWVSGINWNGGSTGYAASVKGRFTISRDNAKN
SLYLQMNSLRAEDSALYYCARDYYGPGSPNYFYAMDVWGQGTITVTVSS

Medarex 11E2 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTTTCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQYNSYPRTFGQGTVEIK

Medarex 4C7 VH (SEQ ID NO:)

QVQLQESGPGLVKPSETLSLTCTVHGGGINHYWVSWIRQPPGKGLEWIGYIYYSGSTKYNPSLKSRVSVSDTSKNQFSL
KLTSVTAADTAVYYCAREWPYYYEMDVWGQGTITVTVSS

Medarex 4C7 VL (SEQ ID NO:)

EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQYGGSFRTFGQGTVEIK

Medarex 8D5 VH (SEQ ID NO:)

EVQLVESGGGLVQPGGSLRLSCAASGFTISSYDMHWVRQATGKGLEWVSVIGPAGDTYYPGSVKGRFTISRRENAKNSL
YLQMNSLRAGDTAVYYCAREGMAAHNYGMDVWGQGTITVTVSS

Medarex 8D5 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPED
FAVYYCQQRSNWPPITFGQGTREIK

Figure 83A additional TIGIT sequences

Genentech 10A7 VH (SEQ ID NO:)

EVQLVESGGGLTQPGKSLKLSCEASGFTFSFTMHVVRQSPGKGLEWVAFIRSGSGIVFYADAVRGRFTISRDNAKNLL
FLQMNDLKSEDTAMYYCARRPLGHNTFDSWGQGTLLVTVSS

Genentech 10A7 VL (SEQ ID NO:)

DIVMTQSPSSLAVSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASIRFTGVPDRFTGSGSGTDYTLT
ITSVQAEDMGQYFCQQGINNPLTFGDGKLEIK

Genentech 1F4 VH (SEQ ID NO:)

EVQLQQSGPELVKPGTSMKISCKASGYSFTGHLMNWVKQSHGKNLEWIGLIIPYNGGTSYNQKFKGKATLTVDKSSST
AYMELLSLTSDSAVYFCRGLRGFYAMDYWGQGTSTVTVSS

Genentech 1F4 VL (SEQ ID NO:)

DVVLITQTPLSLSVSPGDDQVSISCRSSQSLVNSYGNFTLSWYLHKPGQSPQLLIFGISNRFSGVPDRFSGSGSGTDFTLKISTK
KPEDLGMYYCLQGTHTQPTTFGPGTKLEVK

Genentech 4.1D3 VH (SEQ ID NO:)

QVQLQQSGPGLVKPSQTLSTLCAISGDSVSSNSAAWNWIRQSPSRGLEWLGKTTYRKFYSDYAVSVKGRITINPDTSK
NQFSLQLNSVTPEDTAVFYCTRESTTYDLLAGPFDYWGQGTLLVTVSS

Genentech 4.1D3 VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSNNKKYLAWYQQKPGQPPNLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQYYSTPFTFGPGTKVEIK

Genentech 4.1D3.Q1E VH (SEQ ID NO:)

EVQLQQSGPGLVKPSQTLSTLCAISGDSVSSNSAAWNWIRQSPSRGLEWLGKTTYRKFYSDYAVSVKGRITINPDTSK
NQFSLQLNSVTPEDTAVFYCTRESTTYDLLAGPFDYWGQGTLLVTVSS

Genentech 4.1D3.Q1E VL (SEQ ID NO:)

DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSNNKKYLAWYQQKPGQPPNLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQYYSTPFTFGPGTKVEIK

Merck MEB125.31C6.A1.205 VH4/VL1 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQKFQGRVLTSDKSTS
TVYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH4/VL1 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRVITITCRASEHIYSYLSWYQQKPGKAPKLLIYNKTLAEGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQHHFGSPLTFGQGTREIK

Merck MEB125.31C6.A1.205 VH5/VL4 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQKFQGRVLTSDKSTS
TAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH5/VL4 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRVITITCRASEHIYSYLSWYQQKPGKVPKLLIYNKTLAEGVPSRFSGSGSGTQFTLTISLQPE
DVATYYCQHHFGSPLTFGQGTREIK

Figure 83B

Merck MEB125.31C6.A1.205 VH5/VL3 VH (SEQ ID NO:)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYVMHWVRQAPQGLEWIGYIDPYNDGAKYAQKFQGRVTLTDKSTS
TAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH5/VL3 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCRASEHIYSYLSWYQKPKGVKLLIYNKTLAEGVPSRFSGSGSGTDFTLTISLQPE
DVATYYCQHHFGSPLTFGQGTRLEIK

Merck Hu14D7 VH1 (SEQ ID NO:)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KSTVYLYQMNSLRAEDTAVYYCRGALYDGFYFDYWGQGTILVTVSS

Merck Hu14D7 VH2 (SEQ ID NO:)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KSSVYLYQMNSLRAEDTAVYYCRGALYDGFYFDYWGQGTILVTVSS

Merck Hu14D7 VH3 (SEQ ID NO:)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KNTVYLYQMNSLRAEDTAVYYCRGALYDGFYFDYWGQGTILVTVSS

Merck Hu14D7 VL1 (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQKPGQAPKLWIYGTSTLASGVPARFSGSGSGTDYTLTISLLEP
EDFAVYYCHQWSSFPYTFGQGTKLEIK

Merck Hu14D7 VL2 (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQKPGQAPRLWIYGTSTLASGVPARFSGSGSGTDYTLTISLLEP
EDFAVYYCHQWSSFPYTFGQGTKLEIK

Merck Hu14D7 VL3 (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQKPGQAPRLWIYGTSTLASGIPARFSGSGSGTDYTLTISLLEP
EDFAVYYCHQWSSFPYTFGQGTKLEIK

Merck Hu26B10 VH1 (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKISCKTSGYTFTEFTMHVWKQAPGKGLEWIGGLKPDNGGISYNQKFKGRATLTVDKSTNT
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTILVTVSS

Merck Hu26B10 VH2 (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKISCKTSGYTFTEFTMHVVRQAPGKGLEWIGGLKPDNGGISYNQKFKGRATLTVDKSTST
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTILVTVSS

Merck Hu26B10 VH3 (SEQ ID NO:)

EVQLVQSGAEVKKPGASVKISCKVSGYTFTEFTMHVVRQAPGKGLEWIGGLKPDNGGISYNQKFKGRATLTVDTSTST
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTILVTVSS

Merck Hu26B10 VL1 (SEQ ID NO:)

DIQLTQSPSSLSASVGDRTITCKASQDVKTAVAWYQKPKGAPKLLIYSASYRNTGVPDRFSGSGSGTDFTTISLQPE
DFATYYCQHHYSTPFTFGQGTKLEIK

Figure 83C

Merck Hu26B10 VL2 (SEQ ID NO:)

DIQLTQSPSSLSASVGDRVTITCKASQDVKTAVAWYQQKPGKAPKLLIYSASYRNTGVPSRFSGSGSGTDFTFTISLQPE
DFATYYCQGHYSTPFTFGQGTKLEIK

Merck Hu26B10 VL3 (SEQ ID NO:)

DIQLTQSPSSLSASVGDRVTITCKASQDVKTAVAWYQQKPGKAPKLLIYSASYRNTGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQGHYSTPFTFGQGTKLEIK

BMS 15A6 VH (SEQ ID NO:)

QLQLQESGPGLVKPSSETLSLTCTVSGGSISSRYFWGWIRPPGKGLEWIGYIYRGSTYYNPSLKSRTIAVDTSKNQFS
LKLSSVTAADTAVYYCASSAWYFDYWGQGNLTVSS

BMS 15A6 VL (SEQ ID NO:)

EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQYGSLYTFGQGTKLEIK

BMS 22G2 VH (SEQ ID NO:)

QVHLQESGPGLVKPSSETLSLTCTVSGGSISSYIYWSWIRPPGKGLEWIGYIYSGSTINYNPSLKSRTISVDTSKNQFS
LKLSSVTAADTAVYYCARDYYVSGNYNVDYFFGVDVWGQGTITVTVSS

BMS 22G2 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLEPED
FAVYYCQQRSNWPPLFTFGPGTKVDIK

BMS 11G11 VH (SEQ ID NO:)

QLQLQESGPGLVKPSSETLSLTCTVSGGSISSSHYWGWIWIRPPGKGLEWIGNIFYSGHTYYNPSLKSRTISVDTSKNQFS
LKLSSVTAADTAVYYCARQGLLWFGGLSPYYFDYWGQGTITVTVSS

BMS 11G11 VL (SEQ ID NO:)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLEPED
FAVYYCQQRSNWPTFGQGTKLEIK

BMS 10D7 VH (SEQ ID NO:)

QQQLVQSGAEVKKPGSSVKVSKASGGIFRNYAISWVRQAPGQGLEWMGGHPFFGTANYAQKFQGRVTTTADDESTTA
YMELSSLRSEDTAVYYCARGGAAAGTTRYGYYYGMDVWGQGTITVTVSS

BMS 10D7 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
DFATYYCQYNSYPITFGQGTREIK

Oncomed 313R19 VH (SEQ ID NO:)

QVQLQESGPGLVKPSSETLSLTCTVSGFSLSSSYMSWIRPPGKGLEWIGHGNGNTYYANWAKGRVTISKSSNQVSLKL
SSVTAADTAVYYCARGGYRTSGMDPWGQGTITVTVSS

Oncomed 313R19 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRVTITCQASQNIYSDLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQGEHLVAWIYNVFGQGTKVEIKR

Figure 83D

Oncomed 313M32 VH (SEQ ID NO:)

QVQLQESGPGLVKPSSETLSLTCAVSGYSITSDYAWNWIROP
PGKLEWIGYISYSGSTSYNPSLRSRVTISRDTSKNQFFL
KLSSVTAADTAVYYCARRQVGLGFAYWGQGT
LTVSS

Oncomed 313M32 VL (SEQ ID NO:)

DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQ
QKPGKAPKLLIYSASYRYTGVP
SRFSGSGSGTDFTFTIS
SLQPE
DIATYYCQGHYSTPWTFG

Figure 84A (anti BTLA4 variable heavy and light chains + CDRs)

What: anti-BTLA XENP20269 9C6_HOLO	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPPSQSLTCTVSGFSLTGYGVNWRQPPGKGLEWLGMIWIDGSTDYNALKSRLSIN KDNSKQVFLKMNSLQTDITARYICARDREDGRAMDYWGQGTSTVTVSS	
vhCDR1	GYGVN	
vhCDR2	MIWIDGSTDYNALKS	
vhCDR3	DRPDGRAMDY	
Variable light (vl) domain	SIVMTQTPKFLIVSAGDRVITICKASQSVSNDAVWYQQKPGQSPKLLIYYASNRYTGVDFRFTGSGYGTD FTFTISTVQAEDLAVYFCQDYSSPTEFGGKLEIK	
vlCDR1	KASQSVSNDA	
vlCDR2	YASNRYT	
vlCDR3	QQDYSSPT	

Figure 84B

What: anti-BTLA XENP20872 9C6_H1.1L1	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGAEVKKPGASVKVSCKVSGFSLTGYGVNWRQAPGQGLEWMGMIIWIDGSTDYNKFGQRTMT KDNSKSTVYMELSSLASEDIAVYICARDREDGRAMDYWGQGTMTVTVSS	
vhCDR1	GYGVN	
vhCDR2	MIWIDGSTDYNKFGQ	
vhCDR3	DRPDGRAMDY	
Variable light (vl) domain	SIVMTQSPDLSLVSLGERATINCKASQSVSNDAVWYQQKPGQSPKLLIYYASNRYTGVDFRFTGSGYGTD FTLTISLQAEDVAVYFCQDYSSPTEFGGKLEIK	
vlCDR1	KASQSVSNDA	
vlCDR2	YASNRYT	
vlCDR3	QQDYSSPT	

Figure 84C (anti BTLA4 variable heavy and light chains + CDRs)

What: anti-BTLA XENP020882 9C6 H1.11L1	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKVSGFSLTGYGVNWVRQAPGQGLEWMGMIIWIDGSTDYNKTEQGRLSIN KDNRKSTVYMELSSLRFSEDTAVYICARDRDPGRAMDIWGQGTMTVSS	
vhCDR1	GYGVN	
vhCDR2	MIWIDGSTDYNKFGQ	
vhCDR3	DRPDGRAMDY	
Variable light (vl) domain	SIVMTQSPDSLAVSLGERATINCKASQSVSNDAVWYQQKPGQSPKLLIYYASNYTGVPRDFTGSGYGT FTLTISLQAEDVAVYFCQDYSSPTFGGKLEIK	
vlCDR1	KASQSVSNDA	
vlCDR2	YASNRYT	
vlCDR3	QDYSSPT	

Figure 85

1st/2nd antigens	PD-1	PD-L1	CTLA-4	LAG-3	TIM-3	BTLA	TIGIT
ICOS	A, B, C, H, I	B, H, I	B, D, E, H, I	B, F, H, I	B, H, I	B, G, H, I	B, H, I
GHR	A, C, H, I	H, I	D, E, H, I	F, H, I	H, I	G, H, I	H, I
OX40	A, C, H, I	H, I	D, E, H, I	F, H, I	H, I	G, H, I	H, I
4-1BB	A, C, H, I	H, I	D, E, H, I	F, H, I	H, I	G, H, I	H, I

Figure 86XENP22917

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSLRLSDDTAVYYCARTYYDSSGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCSVLHEALHSHYTQKSLSLSPGK

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GTFESNYWMNVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VLHEALHSHYTQKSLSLSPGK

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Light Chain
DIQMTQSPSSVSASVGRVTITCQASQDISLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQAESFPWTFGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22977

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSLRLSDDTAVYYCARTYYDSSGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCSVLHEALHSHYTQKSLSLSPGK

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GTFESNYWMNVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VLHEALHSHYTQKSLSLSPGK

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Light Chain
DIQMTQSPSSVSASVGRVTITCQASQDISRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQAESFPWTFGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC