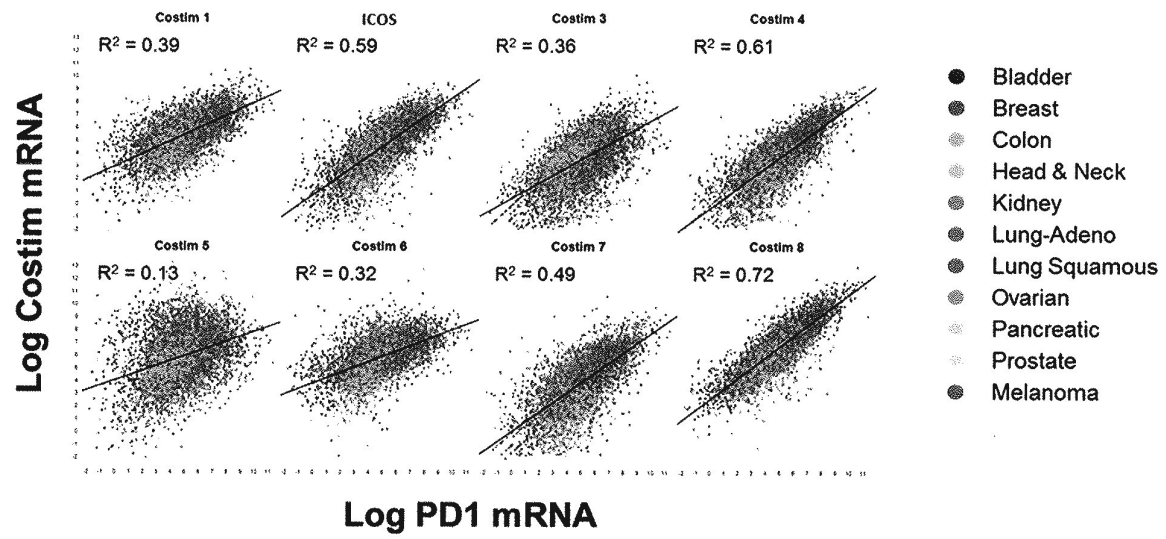
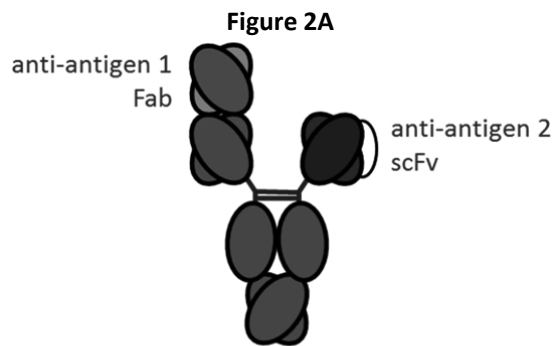
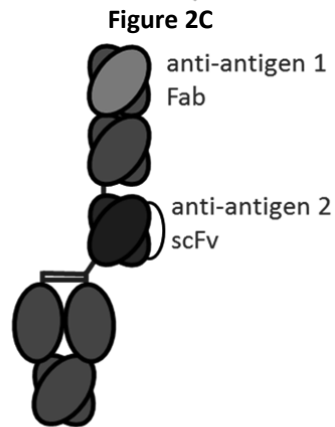


Figure 1

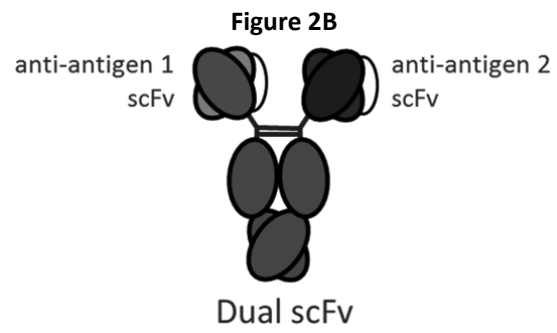
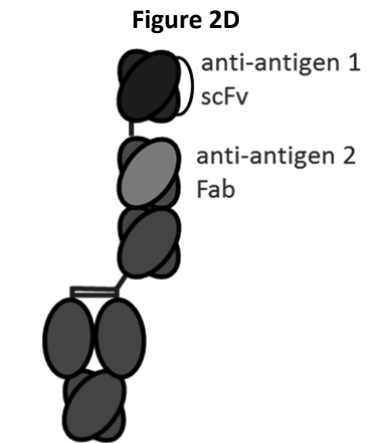




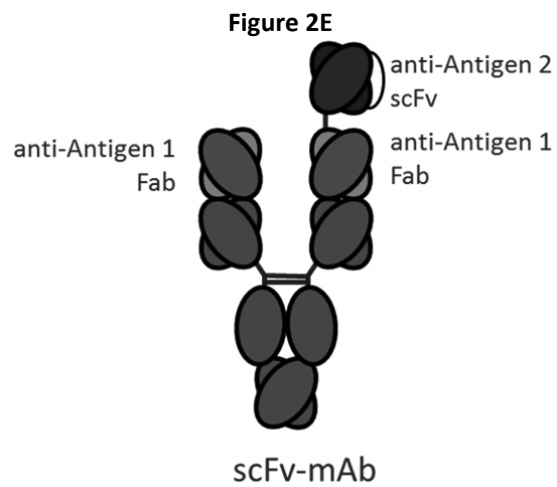
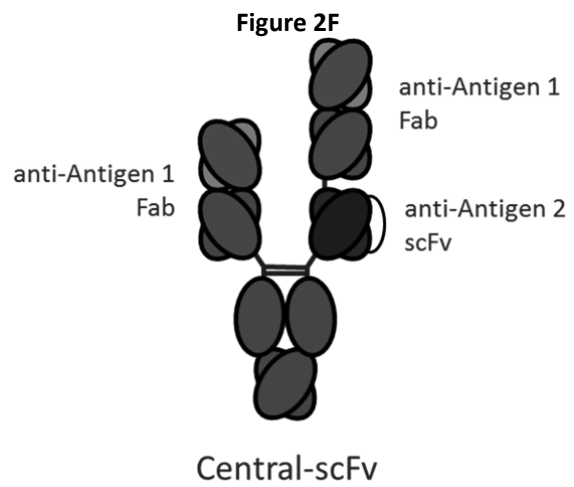
Bottle-opener

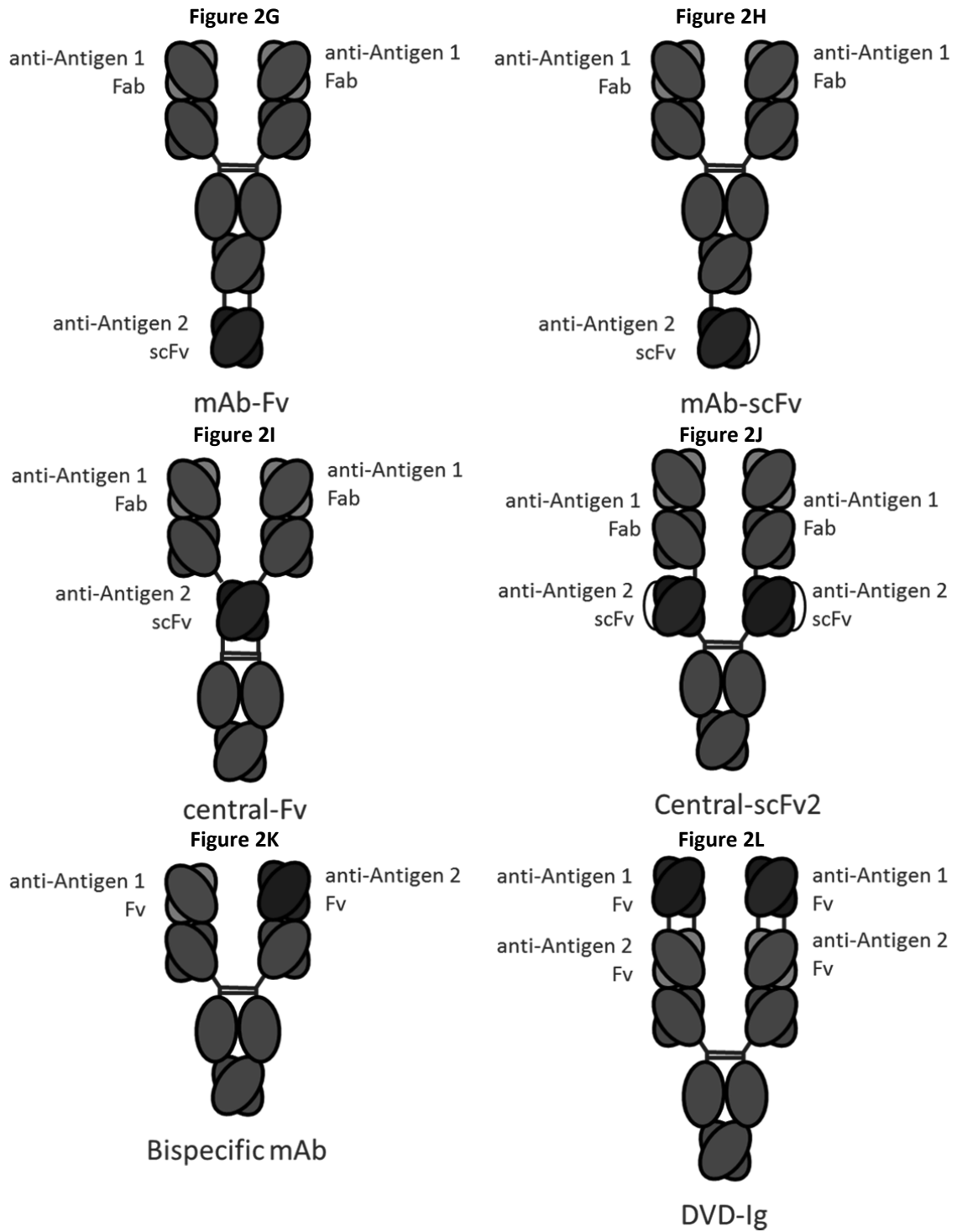


One-arm central-scFv



One-arm scFv-mAb





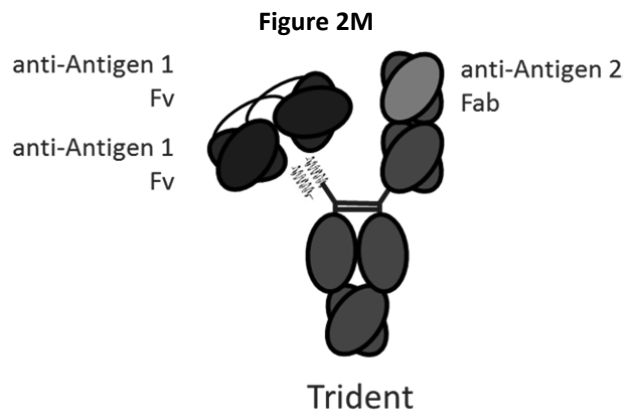
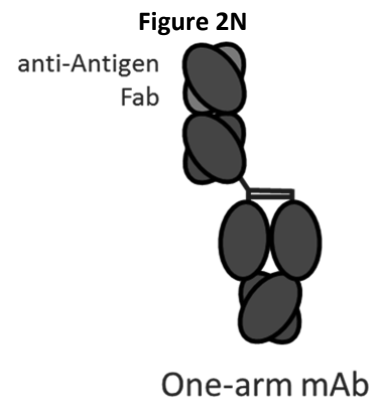


Figure 3A

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

What	sequence	SEQ ID NO:
VH domain (Fab side)	QVQLVQSGAEVKKPGASVKVCKASGYTF GYMH WVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTR DTSISTAYMELSSLRSED AVYYCARTYYDTSGYHDAFDV WGQGTMTVSS	26643
vhCDR1 (Fab side)	GYMH	26644
vhCDR2 (Fab side)	WINPHSGETIYAQKFQ	26645
vhCDR3 (Fab side)	TYYYDTSGYHDAFDV	26646
VL domain (Fab side)	DIQMTQSPSSVSASVGDRTITCRASQGISRLLA WYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGTDFTLTISSLQ PEDFATYYCQ QANSFPWTFGQGT KVEIK	26658
vLCDR1 (Fab side)	RASQGISRLLA	26659
vLCDR2 (fab side)	VASSLOS	26660
vLCDR3 (Fab side)	QANSFPWT	26661
Full length Fab HC	QVQLVQSGAEVKKPGASVKVCKASGYTF GYMH WVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTR DTSISTAYMELSSLRSED AVYYCARTYYDTSGYHDAFDV WGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV/PSSSLGTQTYICNVNHKPSDTKV/DKKVEPKS CDKHTCCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEY NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYF SDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCSVLHEALSHYTKQSLSPGK	26642
Full length Fab LC	DIQMTQSPSSVSASVGDRTITCRASQGISRLLA WYQQKPGKAPKLLIYVASSLSQSGVPSRFSGSGTDFTLTISSLQ PEDFATYYCQ QANSFPWTFGQGT KVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSSTLSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	26657

Figure 3B

What	sequence	SEQ ID NO:
VH domain (scFv side)	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN YASHRYT GVPDRFTGSGYGTEFTLTISV QSEDFGVVYCCQDFFSPRTFGGGTKVEIK	26648
vhCDR1 (scFv)	<u>RASQSVGNDVA</u>	26651
vhCDR2 (scFv)	<u>YASHRYT</u>	26652
vhCDR3 (scFv)	<u>QDFFSPRT</u>	26653
VL domain (scFv side)	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWRQAPGKGLEWVAEIRLYSN NYATHYAESVKGRFTISR D DSKSTLYLQMNNLKTEDTGVIYCTRYGNYGGYFDVWGRGTLTVSS	26649
vICDR1 (scFv)	<u>NYWMN</u>	26654
vICDR2 (scFv)	<u>EIRLYSNNYATHYAESVKG</u>	26655
vICDR3 (scFv)	<u>YGYGGYFDV</u>	26656
scFv chain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN YASHRYT GVPDRFTGSGYGTEFTLTISV QSEDFGVVYCCQDFFSPRTFGGGTKVEIK/ <u>GKPGSGKPGSGKPGS</u> /EVQLVESGGGLVKPGGSLRLSCVASG FTFSNYWMNWRQAPGKGLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMNNLKTEDTGVIYCTRY <u>YGYGGYFDVWGRGTLTVSS</u>	
Full length scFv HC	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN YASHRYT GVPDRFTGSGYGTEFTLTISV QSEDFGVVYCCQDFFSPRTFGGGTKVEIK/ <u>GKPGSGKPGSGKPGS</u> /EVQLVESGGGLVKPGGSLRLSCVASG FTFSNYWMNWRQAPGKGLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMNNLKTEDTGVIYCTRY GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVDVKHEDPE VKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLT LV HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVLHEALHSHYTKQSLSPGK	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	267K/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	GGGSGGGSGGGGS	15	0	26200
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	26201
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	26202
+B	GKGGSGKGGSGKGGGS	15	+3	26203
+C	GGKSGGGKSGGGKGS	15	+3	26204
+D	GGGKSGGGKSGGGKS	15	+3	26205
+E	GKGKSGKGKSGKGKS	15	+6	26206
+F	GGGKSGGGKSGKGGGS	15	+3	26207
+G	GKPGSGKPGSGKPGS	15	+3	26208
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	26209
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	26210

Negative charged scFv linkers

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

Figure 8B**scFv Linkers**

GGGGS	GGGGS	GGGGS	(SEQ ID NO:26219)
GGGGS	GGGGS	GGGGS	(SEQ ID NO:26220)
GSTSG	SGKPGS	GEGSTKG	(SEQ ID NO:26221)
PRGASK	SGSASQTGS	APGS	(SEQ ID NO:26222)
GTAAAG	AAGAAGGAA	AAGAAG	(SEQ ID NO:26223)
GTSGSS	SGSGSGSGSGGGG		(SEQ ID NO:26224)
GKPGSG	KPGSGKPGSGKPGS		(SEQ ID NO:26225)

Figure 9A

Bottle opener backbone 1

Fab side heavy chain (SEQ ID NO: 28669)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28670)

EPKSSDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

constant light chain (SEQ ID NO: 28671)

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYE
KHKVVYACEVTHQGLSPVTKSFNRGEC

Bottle opener backbone 2

Fab side heavy chain (SEQ ID NO: 28672)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28673)

EPKSSDKHTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9B

Bottle opener backbone 3

Fab side heavy chain (SEQ ID NO: 28674)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCEVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28675)

EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVCLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 4

Fab side heavy chain (SEQ ID NO: 28676)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTENEVSLTCLVKSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSGDSFFLYSKLEVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28677)

EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSKGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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

Fab side heavy chain (SEQ ID NO: 28678)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
TKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHY
TQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28679)

EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFY
PSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9C

Bottle opener backbone 6

Fab side heavy chain (SEQ ID NO: 28680)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28681)

EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 7

Fab side heavy chain (SEQ ID NO: 28682)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTY
ICNVNHKPSDTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
VDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHN
HYTQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28683)

EPKSSDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 8

Fab side heavy chain (SEQ ID NO: 28684)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT
CNVDHKPSDTKVDKRVESKYGPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQFNWYVD
GVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT
KNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEGDVFSCSVMHEALHNHYT
QKSLSLSLGK

scFv heavy chain (SEQ ID NO: 28685)

ESKYGPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKQEDPEVQFNWYVDGVEVHNAKTKPREEQF
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Figure 9D

Bottle opener backbone 9

Fab side heavy chain (SEQ ID NO: 28686)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTY
TCNVDHKPSDTKVDKTVKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVD
GVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMT
KNQVSLTCDVSGFYPSDIAVEWESDQGPNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHY
TQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28687)

ERKCSVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN
STFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Bottle opener backbone 10

Fab side heavy chain (SEQ ID NO: 28688)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTY
TCNVDHKPSDTKVDKTVKCCVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVD
GVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMT
KNQVSLTCDVSGFYPSDIAVEWESDQGPNYKTTTPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHY
TQKSLSLSPGK

scFv heavy chain (SEQ ID NO: 28689)

ERKCSVECPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQFN
STFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPNYKTTTPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 10A

XENP016432 Nivolumab_H0LO_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVWQPGRSLRLDCKASGITFSNSGMHWWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSL RAEDTAVYYCATNDDYWGQGLTVVSS	28691
vhCDR1	<u>NSGMH</u>	28692
vhCDR2	<u>VIWIYDGSKRYYADSVKG</u>	28693
vhCDR3	<u>NDDY</u>	28694
Full length HC	QVQLVESGGGVWQPGRSLRLDCKASGITFSNSGMHWWVRQAPGKGLEWVAVIWIYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSL RAEDTAVYYCATNDDYWGQGLTVVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSWVTVPSSSLGTQYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPCPAPPVAGPSVFLPPKPKD TLMISRTPEVTCVVVDVVKH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSL SPGK	28690
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATIGIPARFSGSGSGTDFTLTISILEPEDFAVYYCQQSS NWPRTFGQGTKVEIK	28696
vlCDR1	<u>RASQSVSSYLA</u>	28697
vlCDR2	<u>DASNRAT</u>	28698
vlCDR3	<u>QQSSNWPRT</u>	28699
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATIGIPARFSGSGSGTDFTLTISILEPEDFAVYYCQQSS NWPRTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLTIT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28695

Figure 10B

XENP024120 LOPD180[PD-1]_H1L1_IgG1_PVA_/S267K

What	Sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYW ⁵ SWIRQHPGKGLEWIGYIYNGNTYYNP ⁶ SLRSRV ⁷ TISVDTSKNQFSLKLS ⁸ SVTAA DTAVYVCVRASDYVWGGYHYFDAFDLWGRGTLTVSS	28701
vhCDR1	<u>SGAYYWS</u>	28702
vhCDR2	<u>YIYNGNTYYNP⁶SLRS</u>	28703
vhCDR3	<u>ASDYVWGGYHYFDAFDL</u>	28704
Full length HC	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYW ⁵ SWIRQHPGKGLEWIGYIYNGNTYYNP ⁶ SLRSRV ⁷ TISVDTSKNQFSLKLS ⁸ SVTAA DTAVYVCVRASDYVWGGYHYFDAFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTCTCPPCAPPVAGPSVFLFPPKPKD ¹ TL ² MISRTPEV TCVVDV ³ VKHEDPEV ⁴ KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFLYSLKLTVDKSRWQQGNV ⁵ FSCSV ⁶ MHEALH NHYTQKSLSPGK	28700
Variable light (vl) domain	QSVLTQPPSASGTPGQQRVTISC ¹ SGSNSNIGSNSV ² NWYQQLPGTAPKLLIYGNNQRP ³ SGVPDRFSGSKSGTSASLAI ⁴ SLQSEDEADYYC AAWDDSLNGPVFEGGGTKVTVL	28706
vlCDR1	<u>SGSNSNIGSNSV²N</u>	28707
vlCDR2	<u>GNNQRP³S</u>	28708
vlCDR3	<u>AAWDDSLNGPV</u>	28709
Full length light chain	QSVLTQPPSASGTPGQQRVTISC ¹ SGSNSNIGSNSV ² NWYQQLPGTAPKLLIYGNNQRP ³ SGVPDRFSGSKSGTSASLAI ⁴ SLQSEDEADYYC AAWDDSLNGPVFEGGGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKY AASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS	28705

Figure 10C

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY ^Y YGTSLAWFDYWGQGTLVTVST	28711
vhCDR1	<u>TYWMH</u>	28712
vhCDR2	<u>EIDPSDSVNYNQNFKG</u>	28713
vhCDR3	<u>SPDY^YGTSLAWFDY</u>	28714
Full length HC	QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY ^Y YGTSLAWFDYWGQGTLVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT FPAYLQSSGLYSLSSVTV ^P SSSLGTQYICNVN ^H KPSDTKVDKKEPKSCDKHT ^C PCPAPPVAGPSVFLPPKPKDTLMISRTPEVTC VVVDVKHEDPEVKFNWYVDGVEVHNA ^K TKPREEEYNSTYRVSVLT ^V LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCDVS ^G FGFYPSPDIAVEWESDGGQPENNYK ^T TPPVLDSDGSFFLYSKLTVDKSRWEEQGDVFSCSVMEALHNHYT QKSLSLSPGK	28710
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRA ^S ESVDNYGMSFMINWFQQKPGQPKLLIHAASNQGS ^G VP ^S RFSGSGGTDFLT ^L TISSLEPEDFAVY FCQQSKEV ^P YTFGGGTKEIK	28716
vlCDR1	<u>RASEVDNYGMSFMIN</u>	28717
vlCDR2	<u>AASNQGS</u>	28718
vlCDR3	<u>QQSKEV^PYT</u>	28719
Full length light chain	EIVLTQSPATLSLSPGERATLSCRA ^S ESVDNYGMSFMINWFQQKPGQPKLLIHAASNQGS ^G VP ^S RFSGSGGTDFLT ^L TISSLEPEDFAVY FCQQSKEV ^P YTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASV ^V CLLNNFYPREAKVQW ^K VDNALQSGNSQESVTEQDSKDS ^T YS LSSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC	28715

Figure 10D

XENP019686 1G6_H1.279_L1.194_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLV ^K PGGSLRLSC ^V ASGFTFS ^N YWMN ^W VRQAPGKGL ^E WVAEIRLYSN ^N YATHYAESV ^K GRFTISRDDSKSTLYLQM ^N LN LKTEDTG ^V YCTRY ^Y GN ^Y GGYFDV ^V WGRGTLVT ^V SS	28721
vhCDR1	<u>NYWMN</u>	28722
vhCDR2	<u>EIRLYSN^NYATHYAESV^KG</u>	28723
vhCDR3	<u>YYGN^YGGYFDV</u>	28724
Full length HC	EVQLVESGGGLV ^K PGGSLRLSC ^V ASGFTFS ^N YWMN ^W VRQAPGKGL ^E WVAEIRLYSN ^N YATHYAESV ^K GRFTISRDDSKSTLYLQM ^N LN LKTEDTG ^V YCTRY ^Y GN ^Y GGYFDV ^V WGRGTLVT ^V SS/ASTKGP ^S VFPLAPSSKSTSGGTAALGCLVKDYFPEPTV ^S WNSGALTSGVHTF PAVLQSSGLYSLSSV ^T VPSSSLGTQ ^T YICNVN ^H KPSNTK ^V DKKVEPKSCDKTHTCP ^P CPAPPVAGPSV ^F LP ^P KPKDTLMISRTPEV ^T CV VVDVKHEDPEVKFNW ^V YDGV ^E VHNAK ^T KPREEQYNSTYRV ^S VLTVLHQDWLNGKEYKCKV ^S NKALPAPIEK ^T ISKAKGQPREPQ ^V Y TLPPSR ^E EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK ^T TPPVLDSDGSFFLYSKLTVD ^K SRWQQGNV ^F SCSV ^M HEALHNHY TQKSLSPGK	28720
Variable light (vl) domain	EIVLTQSPATLSASPGERVTL ^T CRASQSV ^G NDVAWYQQKPGQAPRLIN ^Y ASHRYT ^G VPDRFTGSGYGTEFTLTIS ^S VQSEDFGVVY ^C Q <u>QDFSSPRTFGGGTKVEIK</u>	28726
vlCDR1	<u>RASQSVGNDVA</u>	28727
vlCDR2	<u>YASHRYT</u>	28728
vlCDR3	<u>QQDFSSPRT</u>	28729
Full length light chain	EIVLTQSPATLSASPGERVTL ^T CRASQSV ^G NDVAWYQQKPGQAPRLIN ^Y ASHRYT ^G VPDRFTGSGYGTEFTLTIS ^S VQSEDFGVVY ^C Q <u>QDFSSPRTFGGGTKVEIK</u> /RTVAAPS ^V FIFPPSDEQLKSGTASV ^V CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK ^D STYSLS ^S T LTLSKADYEKHK ^V YACEVTHQGLSSPV ^T KSFNRGEC	28725

Figure 10E

XENP020156 2E9_H1L1_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGVAFTNYWLGWVRQAPGQGLEWMGNFYPGSSNTYYNEKFQGRVTMTADKSISTAYMELSR LRSDDTAVYFCARHYGTNRYFDVWVGAGTLVTSS	28731
vhCDR1	<u>NYWLG</u>	28732
vhCDR2	<u>NFYPGSSNTYYNEKFQG</u>	28733
vhCDR3	<u>HYGTNRYFDV</u>	28734
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGVAFTNYWLGWVRQAPGQGLEWMGNFYPGSSNTYYNEKFQGRVTMTADKSISTAYMELSR LRSDDTAVYFCARHYGTNRYFDVWVGAGTLVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSWTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI ^S RTPEVTCV VVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCSV ^M HEALHNHY TQKLSLSPGK	28730
Variable light (vl) domain	DIVLTQSPGTLSLSPGERATLSCRASQSVSNDVAWYQQKPGQSPRLLIYYASNRYTGV ^P DRFTGSGYGTDFLTISRLEPEDFAVYFCQQ <u>DYSSPYTFGGG</u> TKVEIK	28736
vlCDR1	<u>RASQSVSNDVA</u>	28737
vlCDR2	<u>YASNRYT</u>	28738
vlCDR3	<u>QQDYSSPYT</u>	28739
Full length light chain	DIVLTQSPGTLSLSPGERATLSCRASQSVSNDVAWYQQKPGQSPRLLIYYASNRYTGV ^P DRFTGSGYGTDFLTISRLEPEDFAVYFCQQ <u>DYSSPYTFGGG</u> TKVEIK/RTVAAPSVFIFPPSDEQLKSGTASV ^V CLLNNFY ^P PREAKVQW ^K VDNALQSGNSQESVTEQDSK ^D STYS ^L SSLT TLISKADY ^E KHKVYACEVTHQGLSSPVTKSFNRGEC	28735

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

What	sequence	SEQ ID NO:
Vh domain	EVQLVESGGGLVKPGGSLRLSCVSGFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAE SVKGRFTISRDDSKSTLYLQMN NLKTEDTGYYCTRIYGNIGGYFDVWGRGTLVTSS	29362
vhCDR1	<u>NYWMN</u>	29363
vhCDR2	<u>EIRLYSNNYATHYAESVKG</u>	29364
vhCDR3	<u>YYGNYGGYFDV</u>	29365
scFv linker	GKPGSGKPGSGKPGSGKPGS	29366
VL domain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLILINASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKVEIK	29367
vICDR1	<u>RASQSVGNDVA</u>	29368
vICDR2	<u>YASHRYT</u>	29369
vICDR3	<u>QQDFSSPRT</u>	29370
scFv	EVQLVESGGGLVKPGGSLRLSCVSGFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAE SVKGRFTISRDDSKSTLYLQMN NLKTEDTGYYCTRIYGNIGGYFDVWGRGTLVTSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSASPGERVTLTCRASQS VGNDVAWYQQKPGQAPRLILINASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVY CQQDFSSPRTFGGKVEIK /	29371

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLTCVASGFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAE SVKGRFTISRDDSKSTLYLQMN NLKTEDTGYYCTRIYGNIGGYFDVWGRGTLVTSS	29372
vhCDR1	<u>NYWMN</u>	29373
vhCDR2	<u>EIRLYSNNYATHYAESVKG</u>	29374
vhCDR3	<u>YYGNYGGYFDV</u>	29375
scFv linker	GKPGSGKPGSGKPGSGKPGS	29376
Variable light (vl) domain	EIVLTQSPATLSVSPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLILINASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFAVY YCQQDWSSPRTFGGKVEIK	29377
vICDR1	<u>RASQSVGNDVA</u>	29378
vICDR2	<u>YASHRYT</u>	29379
vICDR3	<u>QQDWSSPRT</u>	29380
scFv	EVQLVESGGGLVKPGGSLRLTCVASGFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAE SVKGRFTISRDDSKSTLYLQMN NLKTEDTGYYCTRIYGNIGGYFDVWGRGTLVTSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPGERVTLTCRASQS VGNDVAWYQQKPGQAPRLILINASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFAVY CQQDWSSPRTFGGKVEIK	29381

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLIN YASHRYT GVDPDRFTGSGYGTEFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKKEIK	29382
vhCDR1	RASQSVGNDVA	29383
vhCDR2	YASHRYT	29384
vhCDR3	QQDFSSPRT	29385
scFv linker	GKPGSGKPGSGKPGSGKPGS	29386
Variable light (vl) domain	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWVRQAPGKGLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMN NLKTEDTGVYYCTRYYGNYGGYFDVWGRGTLVTVSS	29387
vlCDR1	NYWMN	29388
vlCDR2	EIRLYSNNYATHYAESVKG	29389
vlCDR3	YYGNYGGYFDV	29390
scFv	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLIN YASHRYT GVDPDRFTGSGYGTEFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKKEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWVRQAPGK GLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMN NLKTEDTGVYYCTRYYGNYGGYFDVWGRGTLVTVSS	29391

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLIN YASHRYT GVDPDRFTGSGYGTEFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKKEIK	29392
vhCDR1	RASQSVGNDVA	29393
vhCDR2	YASHRYT	29394
vhCDR3	QQDFSSPRT	29395
scFv linker	GKPGSGKPGSGKPGSGKPGS	29396
Variable light (vl) domain	EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWVRQAPGKCLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMN NLKTEDTGVYYCTRYYGNYGGYFDVWGRGTLVTVSS	29397
vlCDR1	NYWMN	29398
vlCDR2	EIRLYSNNYATHYAESVKG	29399
vlCDR3	YYGNYGGYFDV	29400
scFv	EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLIN YASHRYT GVDPDRFTGSGYGTEFTLTISSVQSEDFGVY YCQQDFSSPRTFGGKKEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMNWVRQAPGK CLEWVAEIRLYSN NYATHYAESVKGRFTISR DDSKSTLYLQMN NLKTEDTGVYYCTRYYGNYGGYFDVWGRGTLVTVSS	29401

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYAF ^T NIYWLGWVRQAAPGQGLEWMGNFY ^Y PGSSNTYYNEK <u>FQGRVTMTADKSI</u> STAYMELSLRLRSDDTAVYFCARHYG ^T NIYRYFDVWGAGTILVTVSS	29402
vhCDR1	NIWL <u>G</u>	29403
vhCDR2	<u>NFY</u> PGSSNTYYNEK <u>FQGRVTMTADKSI</u>	29404
vhCDR3	<u>HYG</u> TNIYRYFDV	29405
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29406
Variable light (vl) domain	DIVLTQSPGTLSLSPGERATLSCRASQSVSNDAWYQOKPGQSPRLLIYYASNRYTGVPDRFTGSGYGTDFTLTIS RLEPEDFAVYFCQDDYSSPYTFGGGKVEIK	29407
vlCDR1	RASQSVSNDAWY	29408
vlCDR2	<u>YASNRYT</u>	29409
vlCDR3	<u>QQDYSSPYT</u>	29410
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYAF ^T NIYWLGWVRQAAPGQGLEWMGNFY ^Y PGSSNTYYNEK <u>FQGRVTMTADKSI</u> STAYMELSLRLRSDDTAVYFCARHYG ^T NIYRYFDVWGAGTILVTVSS / <u>GKPGSGKPGSGKPGSGKPGS</u> / DIVLTQSPGT LSLSPGERATLSCRASQSVSNDAWYQOKPGQSPRLLIYYASNRYTGVPDRFTGSGYGTDFTLTISRLEPEDFAVY FCQDDYSSPYTFGGGKVEIK	29411

Figure 12A [CTLA-4]_H0.25_L0 Anti-CTLA-4 Fv sequences (XENP19235 Fab, XENP19769 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYCCARTGWLGPFDYWGQGTLLTVSS	29412
vhCDR1	<u>SYAMH</u>	29413
vhCDR2	<u>FISYDGNKYYADSVKG</u>	29414
vhCDR3	<u>TGWLGPFDY</u>	29415
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29416
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPW	29417
vlCDR1	<u>RASQSVGSSYLA</u>	29418
vlCDR2	<u>GAFSRAT</u>	29419
vlCDR3	<u>QQYGSSPWT</u>	29420
scFv	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYCCARTGWLGPFDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKEIK/	29421

Figure 12B [CTLA-4]_H0.26_L0 Anti-CTLA-4 Fv sequences (XENP19236 Fab, XENP19770 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYCCARTGWLGPFDYWGQGTLLTVSS	29422
vhCDR1	<u>SYGMH</u>	29423
vhCDR2	<u>FISYDGNKYYADSVKG</u>	29424
vhCDR3	<u>TGWLGPFDY</u>	29425
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29426
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPW	29427
vlCDR1	<u>RASQSVGSSYLA</u>	29428
vlCDR2	<u>GAFSRAT</u>	29429
vlCDR3	<u>QQYGSSPWT</u>	29430
scFv	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYCCARTGWLGPFDYWGQGTLLTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKEIK	29431

Figure 12C [CTLA-4]_H0.27_I0 Anti-CTLA-4 Fv sequences (XENP19237 Fab, XENP19771 scFv)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYSMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS	29432
vhCDR1	<u>SYSMH</u>	29433
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	29434
vhCDR3	<u>TGWLGPFDY</u>	29435
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29436
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGGSSPWTFGQTKVEIK	29437
vlCDR1	<u>RASQSVGSSYLA</u>	29438
vlCDR2	<u>GAFSRAT</u>	29439
vlCDR3	<u>QQYGSSPWT</u>	29440
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYSMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQTKVEIK	29441

Figure 12D [CTLA-4]_H0.29_I0 Fab XENP19773, scFv XENP19239

What	sequence	SEQ ID NO:
Variable heavy (vh) domain		
vhCDR1		
vhCDR2		
vhCDR3		
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29442
Variable light (vl) domain		
vlCDR1		
vlCDR2		
vlCDR3		
scFv	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYSMHVVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQTKVEIK	29443

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS	29444
vhCDR1	<u>SYTMH</u>	29445
vhCDR2	<u>FISYDGNKYYADSVKG</u>	29446
vhCDR3	<u>TGWLGPFDY</u>	29447
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29448
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPW	29449
vlCDR1	<u>RASQSVGSSYLA</u>	29450
vlCDR2	<u>GAFSRAT</u>	29451
vlCDR3	<u>QQYGSSPWT</u>	29452
scFv	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVAFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK/	29453

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS	29454
vhCDR1	<u>SYTMH</u>	29455
vhCDR2	<u>FISYDGNKYYADSVKG</u>	29456
vhCDR3	<u>TGWLGPFDY</u>	29457
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29458
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPW	29459
vlCDR1	<u>RASQSVGSSYLA</u>	29460
vlCDR2	<u>GAFSRAT</u>	29461
vlCDR3	<u>QQYGSSPWT</u>	29462
scFv	QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVGFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29463

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS	29464
vhCDR1	<u>SYTMH</u>	29465
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	29466
vhCDR3	<u>TGWLGPFDY</u>	29467
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29468
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29469
vlCDR1	<u>RASQSVGSSYLA</u>	29470
vlCDR2	<u>GAFSRAT</u>	29471
vlCDR3	<u>QQYGSSPWT</u>	29472
scFv	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29473

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGSNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS	29474
vhCDR1	<u>SYTMH</u>	29475
vhCDR2	<u>FISYDGSNKKYYADSVKG</u>	29476
vhCDR3	<u>TGWLGPFDY</u>	29477
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29478
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29479
vlCDR1	<u>RASQSVGSSYLA</u>	29480
vlCDR2	<u>GAFSRAT</u>	29481
vlCDR3	<u>QQYGSSPWT</u>	29482
scFv	QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGSNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29483

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVESGGGVVQPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYCAQTGWLGPFDYWGQGTLLVTVSS	29484
vhCDR1	<u>SYTMH</u>	29485
vhCDR2	<u>FISYDGNKKYYADSVKG</u>	29486
vhCDR3	<u>TGWLGPFDY</u>	29487
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29488
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGA} FSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29489
vlCDR1	<u>RASQSVSSSYLA</u>	29490
vlCDR2	<u>GAFSRAT</u>	29491
vlCDR3	<u>QQYGSSPWT</u>	29492
scFv	QVQLVESGGGVVQPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAIYCAQTGWLGPFDYWGQGTLLVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGA} FSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29493

Figure 12J [CTLA-4]_H2_L0 (Fab XENP,19545 scFv XENP19552)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYPGSVKGRFTISR ENAKNS LYLQMNSLRAGDTAVYICARTGWLGPFDYWGQGTLLVTVSS	29494
vhCDR1	<u>SYTMH</u>	29495
vhCDR2	<u>FISYDGNKKYYPGSVKG</u>	29496
vhCDR3	<u>TGWLGPFDY</u>	29497
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29498
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGA} FSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29499
vlCDR1	<u>RASQSVGSSSYLA</u>	29500
vlCDR2	<u>GAFSRAT</u>	29501
vlCDR3	<u>QQYGSSPWT</u>	29502
scFv	EVQLVESGGGLVQPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYPGSVKGRFTISR ENAKNS LYLQMNSLRAGDTAVYICARTGWLGPFDYWGQGTLLVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPGTLSLSPG ERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGA} FSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29503

Figure 12K [CTLA-4]_H3.21_L0.124 (Fab XENP20422, scFv XENP20431)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGN TKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGG LLGPFDLWGQGTMTVTVSS	29504
vhCDR1	<u>SYTMH</u>	29505
vhCDR2	<u>FISYDGN TKYYADSVKG</u>	29506
vhCDR3	<u>GGLLGPFDL</u>	29507
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29508
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29509
vlCDR1	<u>RASQSVGSSYLA</u>	29510
vlCDR2	<u>GASSRAT</u>	29511
vlCDR3	<u>QQYGSSPWT</u>	29512
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGN TKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGG LLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29513

Figure 12L [CTLA-4]_H3.21_L0.129 (Fab XENP20423, scFv XENP20432)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGN TKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGG LLGPFDLWGQGTMTVTVSS	29514
vhCDR1	<u>SYTMH</u>	29515
vhCDR2	<u>FISYDGN TKYYADSVKG</u>	29516
vhCDR3	<u>GGLLGPFDL</u>	29517
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29518
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29519
vlCDR1	<u>RASQSVGSSYLA</u>	29520
vlCDR2	<u>GASSRAT</u>	29521
vlCDR3	<u>QQYGSSPWT</u>	29522
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGN TKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGG LLGPFDLWGQGTMTVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29523

Figure 12M [CTLA-4]_H3.21_L0.132 (Fab XENP20424, scFv XENP20433)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVSS	29524
vhCDR1	<u>SYTMH</u>	29525
vhCDR2	<u>FISYDGNTKYYADSVKG</u>	29526
vhCDR3	<u>GLLGPFDL</u>	29527
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29528
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGS SPWTFGQGTKEIK	29529
vlCDR1	<u>RASQSVSSSYLA</u>	29530
vlCDR2	<u>GASSRAT</u>	29531
vlCDR3	<u>QQYGSSPWT</u>	29532
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKEIK	29533

Figure 12N [CTLA-4]_H3.23_L0.124 (Fab XENP20425, scFv XENP20434)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPFDLWGQGTMTVSS	29534
vhCDR1	<u>SYTMH</u>	29535
vhCDR2	<u>FISYDGNKYKYYADSVKG</u>	29536
vhCDR3	<u>GHLGPFDL</u>	29537
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29538
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGS SPWTFGQGTKEIK	29539
vlCDR1	<u>RASQSVGSSSYLA</u>	29540
vlCDR2	<u>GASSRAT</u>	29541
vlCDR3	<u>QQYGSSPWT</u>	29542
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKEIK	29543

Figure 120 [CTLA-4]_H3.23_L0.129 (Fab XENP20426, scFv XENP20435)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPF FDLWGQGTMTVTVSS	29544
vhCDR1	<u>SYTMH</u>	29545
vhCDR2	<u>FISYDGNKYKYADSVKG</u>	29546
vhCDR3	<u>GGHLGPFDL</u>	29547
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29548
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYCCQYGGSPWTFGQGTKVEIK	29549
vlCDR1	<u>RASQSVGSSYLA</u>	29550
vlCDR2	<u>GASSRAT</u>	29551
vlCDR3	<u>QQYGSSPWT</u>	29552
scFv	EVQLVESGGGLVKPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPF FDLWGQGTMTVTVSS /GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPG ERATLSCRASQSVGSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGS SPWTFGQGTKVEIK	29553

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPF FDLWGQGTMTVTVSS	29554
vhCDR1	<u>SYTMH</u>	29555
vhCDR2	<u>FISYDGNKYKYADSVKG</u>	29556
vhCDR3	<u>GGHLGPFDL</u>	29557
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29558
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYCCQYGGSPWTFGQGTKVEIK	29559
vlCDR1	<u>RASQSVSSSYLA</u>	29560
vlCDR2	<u>GASSRAT</u>	29561
vlCDR3	<u>QQYGSSPWT</u>	29562
scFv	EVQLVESGGGLVKPGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGHLGPF FDLWGQGTMTVTVSS /GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYCCQYGS SPWTFGQGTKVEIK	29563

Figure 12Q [CTLA-4]_H3.25_L0.124 (Fab XENP20428, scFv XENP20437)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVTVSS	29564
vhCDR1	<u>SYTMH</u>	29565
vhCDR2	<u>FISYDGNKYKYADSVKG</u>	29566
vhCDR3	<u>GGLLGPFDL</u>	29567
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29568
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29569
vlCDR1	<u>RASQSVGSSYLA</u>	29570
vlCDR2	<u>GASSRAT</u>	29571
vlCDR3	<u>QQYGSSPWT</u>	29572
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29573

Figure 12R [CTLA-4]_H3.25_L0.129 (Fab XENP20429, scFv XENP20438)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVTVSS	29574
vhCDR1	<u>SYTMH</u>	29575
vhCDR2	<u>FISYDGNKYKYADSVKG</u>	29576
vhCDR3	<u>GGLLGPFDL</u>	29577
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29578
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29579
vlCDR1	<u>RASQSVGSSYLA</u>	29580
vlCDR2	<u>GASSRAT</u>	29581
vlCDR3	<u>QQYGSSPWT</u>	29582
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYICARGGLLGPFDLWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSVSPG ERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQYGS SPWTFGQGTKVEIK	29583

Figure 12S [CTLA-4]_H3.25_L0.132 (Fab XENP20430, scFv XENP20439)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYYCARGGLLGPFDLWGQGTMTVTVSS	29584
vhCDR1	<u>SYTMH</u>	29585
vhCDR2	<u>FISYDGNKYKYADSVKG</u>	29586
vhCDR3	<u>GGLLGPFDL</u>	29587
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29588
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYG} ASSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQYGGSPWTFGGTKVEIK	29589
vlCDR1	<u>RASQSVSSSYLA</u>	29590
vlCDR2	<u>GASSRAT</u>	29591
vlCDR3	<u>QQYGSSPWT</u>	29592
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNKYKYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYYCARGGLLGPFDLWGQGTMTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPATLSLSPG ERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYG} ASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGG SPWTFGGTKVEIK	29593

Figure 12T [CTLA-4]_H3.4_L0.118 (Fab XENP20341, scFv XENP20378)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNHKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS	29594
vhCDR1	<u>SSYTMH</u>	29595
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29596
vhCDR3	<u>TGHLGPFDL</u>	29597
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29598
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYG} AFSRATGIPDRFSGSGGTDFLTISR LEPEDFAVYYCQYGGSPWTFGGTKVEIK	29599
vlCDR1	<u>RASQSVGSSSYLA</u>	29600
vlCDR2	<u>GAFSRAT</u>	29601
vlCDR3	<u>QQYGSSPWT</u>	29602
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI SYDGNHKYYADSVKGRFTISRDNAKNS LYLQMNSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> /EIVLTQSPATLSVSPG ERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYG} AFSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYGG SPWTFGGTKVEIK	29603

Figure 12U [CTLA-4] H3.4_I0.119 (Fab XENP20342, scFv XENP20379)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29604
vhCDR1	<u>SYTMH</u>	29605
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29606
vhCDR3	<u>TGHLGPFDL</u>	29607
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29608
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQQYGGSPWTFGQGTKVEIK	29609
vlCDR1	<u>RASQSVGSSYLA</u>	29610
vlCDR2	<u>GAFSRAT</u>	29611
vlCDR3	<u>QQYGSSPWT</u>	29612
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSLSPGERATLSCRASQS VGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGGSPWTFGQGTKVEIK	29613

Figure 12V [CTLA-4] H3.4_I0.12 (Fab XENP20071, scFv XENP20078)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29614
vhCDR1	<u>SYTMH</u>	29615
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29616
vhCDR3	<u>TGHLGPFDL</u>	29617
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29618
Variable light (vl) domain	EIVLTQSPGTLSVSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQQYGGSPWTFGQGTKVEIK	29619
vlCDR1	<u>RASQSVGSSYLA</u>	29620
vlCDR2	<u>GAFSRAT</u>	29621
vlCDR3	<u>QQYGSSPWT</u>	29622
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSVSPGERATLSCRASQS VGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGGSPWTFGQGTKVEIK	29623

Figure 12W [CTLA-4] H3.4_L0.121 (Fab XENP20344, scFv XENP20381)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29624
vhCDR1	<u>SYTMH</u>	29625
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29626
vhCDR3	<u>TGHLGPFDL</u>	29627
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29628
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQQYGGSSPWTFGQGTKVEIK	29629
vlCDR1	<u>RASQSVGSSYLA</u>	29630
vlCDR2	<u>GASSRAT</u>	29631
vlCDR3	<u>QQYGGSSPWT</u>	29632
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSPGERATLSCRASQS VGSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGGSSPWTFGQGTKVEIK	29633

Figure 12X [CTLA-4] H3.4_L0.122 (Fab XENP20345, scFv XENP20382)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29634
vhCDR1	<u>SYTMH</u>	29635
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29636
vhCDR3	<u>TGHLGPFDL</u>	29637
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29638
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDF AVYYCQQYGGSSPWTFGQGTKVEIK	29639
vlCDR1	<u>RASQSVGSSYLA</u>	29640
vlCDR2	<u>GAFSRAT</u>	29641
vlCDR3	<u>QQYGGSSPWT</u>	29642
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCRASQS VGSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGGSSPWTFGQGTKVEIK	29643

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29644
vhCDR1	<u>SYTMH</u>	29645
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29646
vhCDR3	<u>TGHLGPFDL</u>	29647
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29648
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKVEIK	29649
vlCDR1	<u>RASQSVSSSYLA</u>	29650
vlCDR2	<u>GAFSRAT</u>	29651
vlCDR3	<u>QQYGSSPWT</u>	29652
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29653

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29654
vhCDR1	<u>SYTMH</u>	29655
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29656
vhCDR3	<u>TGHLGPFDL</u>	29657
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29658
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKVEIK	29659
vlCDR1	<u>RASQSVSSSYLA</u>	29660
vlCDR2	<u>GASSRAT</u>	29661
vlCDR3	<u>QQYGSSPWT</u>	29662
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29663

Figure 12AA [CTLA-4] H3.4_I0.125 (Fab XENP20348, scFv XENP20385)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29664
vhCDR1	<u>SYTMH</u>	29665
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29666
vhCDR3	<u>TGHLGPFDL</u>	29667
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29668
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKVEIK	29669
vlCDR1	<u>RASQSVSSSYLA</u>	29670
vlCDR2	<u>GAFSRAT</u>	29671
vlCDR3	<u>QQYGSSPWT</u>	29672
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQS VSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29673

Figure 12BB [CTLA-4] H3.4_I0.126 (Fab XENP20349, scFv XENP20386)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29674
vhCDR1	<u>SYTMH</u>	29675
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29676
vhCDR3	<u>TGHLGPFDL</u>	29677
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29678
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKVEIK	29679
vlCDR1	<u>RASQSVSSSYLA</u>	29680
vlCDR2	<u>GASSRAT</u>	29681
vlCDR3	<u>QQYGSSPWT</u>	29682
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSLSPGERATLSCRASQS VSSSYLAWYQQKPGQAPRLIIYGASRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29683

Figure 12CC [CTLA-4] H3.4_L0.127 (Fab XENP20350, scFv XENP20387)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29684
vhCDR1	<u>SYTMH</u>	29685
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29686
vhCDR3	<u>TGHLGPFDL</u>	29687
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29688
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKEIK	29689
vlCDR1	<u>RASQSVSSSYLA</u>	29690
vlCDR2	<u>GASSRAT</u>	29691
vlCDR3	<u>QQYGSSPWT</u>	29692
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLSPGERATLSCRASQS VSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKEIK	29693

Figure 12DD [CTLA-4] H3.4_L0.128 (Fab XENP20351, scFv XENP20388)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29694
vhCDR1	<u>SYTMH</u>	29695
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29696
vhCDR3	<u>TGHLGPFDL</u>	29697
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29698
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDF AVYYCQQYGSSPWTFGQGTKEIK	29699
vlCDR1	<u>RASQSVSSSYLA</u>	29700
vlCDR2	<u>GAFSRAT</u>	29701
vlCDR3	<u>QQYGSSPWT</u>	29702
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQMN SLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCRASQS VSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKEIK	29703

What	sequence	SEQ ID NO:
Variable heavy (vh) domain		
vhCDR1		
vhCDR2		
vhCDR3		
scFv linker	<u>GKPGSGKPGSGKPGKS</u>	29704
Variable light (vl) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI <u>SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM</u> NSLRAREDIAVYYCARTGHLGPFDLWGQGTMVTVSS	29705
vLCDR1	<u>SYTMH</u>	29706
vLCDR2	<u>FISYDGNHKYYADSVKG</u>	29707
vLCDR3	<u>TGHLGPFDDL</u>	29708
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFI <u>SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM</u> NSLRAREDIAVYYCARTGHLGPFDLWGQGTMVTVSS / GKPGSGKPGSGKPGKS / EVILTQSPATLSLSPGERATLSCRAS QSVGSSYLAWYQQKPGQAPRLIIYGASSRATGIPIPRFSGSGSGTDFTLTISRLEPEDEFAVIYCCOYGSSPMTFGQGTKEIK	29709

Figure 12FF [CTLA-4] H3.4 L0.130 (Fab XENP20353, scFv XENP20390)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVPGGSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVSFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPF DL WGQGTMTVSS	29710
vhCDR1	<u>SYTMH</u>	29711
vhCDR2	FISYDGNHKYYADSVKG	29712
vhCDR3	<u>TGHLGPFDL</u>	29713
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29714
Variable light (vl) domain	EIVLTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTFTLTISRLEPED FAVYYCQYQYSSPWTFCQGTKEIK	29715
vlCDR1	<u>RASQSVSSSYLA</u>	29716
vlCDR2	<u>GASSRAT</u>	29717
vlCDR3	<u>QQYGSSPWT</u>	29718
scFv	EVQLVESGGGLVPGGSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVSFI SYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPF DL WGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSVSPGERATLSCRAS QSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPDRFSGSGSGTFTLTISRLEPEDFAVYYCQYQYSSPWTFCQGTKEIK	29719

Figure 12GG [CTLA-4]_H3.4_L0.131 (Fab XENP20354, scFv XENP20391)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29720
vhCDR1	<u>SYTMH</u>	29721
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29722
vhCDR3	<u>TGHLGPFDL</u>	29723
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29724
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPED} FAVYYCQQYGS ^{SPWTFGQGTKVEIK}	29725
vlCDR1	<u>RASQSVSSSYLA</u>	29726
vlCDR2	<u>GASSRAT</u>	29727
vlCDR3	<u>QQYGSSPWT</u>	29728
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLSPGERATLSCRAS QSVSSSYLA ^{WYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGS} ^{SPWTFGQGTKVEIK}	29729

Figure 12HH [CTLA-4]_H3.4_L0.132 (Fab XENP20355, scFv XENP20392)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29730
vhCDR1	<u>SYTMH</u>	29731
vhCDR2	<u>FISYDGNHKYYADSVKG</u>	29732
vhCDR3	<u>TGHLGPFDL</u>	29733
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29734
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPED} FAVYYCQQYGS ^{SPWTFGQGTKVEIK}	29735
vlCDR1	<u>RASQSVSSSYLA</u>	29736
vlCDR2	<u>GASSRAT</u>	29737
vlCDR3	<u>QQYGSSPWT</u>	29738
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNHKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPATLSLSPGERATLSCRAS QSVSSSYLA ^{WYQQKPGQAPRLIIYGASSRATGIPDRFSGSGGTDTLTISRLEPEDFAVYYCQQYGS} ^{SPWTFGQGTKVEIK}	29739

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29740
vhCDR1	<u>SYTMH</u>	29741
vhCDR2	<u>FISYDGNTKYYADSVKG</u>	29742
vhCDR3	<u>TGHLGPFDL</u>	29743
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29744
Variable light (vl) domain	EIVMTQSPATLSVSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGAFSRATGIPARFSGSGGTEFTLTIS} SLQSED FAVYYCQQYGSFPWTFGQGTKVEIK	29745
vlCDR1	<u>RASQSVSSSYLA</u>	29746
vlCDR2	<u>GAFSRAT</u>	29747
vlCDR3	<u>QQYGSSPWT</u>	29748
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVMTQSPATLSVSPGERATLSCRAS QSVSSSYLA ^{WYQQKPGQAPRLLIYGAFSRATGIPARFSGSGGTEFTLTIS} SLQSEDFAVYYCQQYGSFPWTFGQGTKVEIK	29749

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS	29750
vhCDR1	<u>SYTMH</u>	29751
vhCDR2	<u>FISYDGNTKYYADSVKG</u>	29752
vhCDR3	<u>TGHLGPFDL</u>	29753
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29754
Variable light (vl) domain	EIVMTQSPATLSVSPGERATLSCRASQSVSSSYLA ^{WYQQKPGQAPRLLIYGASSRATGIPARFSGSGGTEFTLTIS} SLQSED FAVYYCQQYGSFPWTFGQGTKVEIK	29755
vlCDR1	<u>RASQSVSSSYLA</u>	29756
vlCDR2	<u>GASSRAT</u>	29757
vlCDR3	<u>QQYGSSPWT</u>	29758
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGTMTVSS / GKPGSGKPGSGKPGSGKPGS / EIVMTQSPATLSVSPGERATLSCRAS QSVSSSYLA ^{WYQQKPGQAPRLLIYGASSRATGIPARFSGSGGTEFTLTIS} SLQSEDFAVYYCQQYGSFPWTFGQGTKVEIK	29759

Figure 12KK [CTLA-4] H3.5_L2.3 (Fab XENP20359, scFv XENP20396)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGMVTVSS	29760
vhCDR1	<u>SYTMH</u>	29761
vhCDR2	<u>FISYDGNNTKYYADSVKG</u>	29762
vhCDR3	<u>TGHLGPFDL</u>	29763
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29764
Variable light (vl) domain	EIVMTQSPATLSVSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPARFSGSGSGTEFTLTISSLQSED FAVYYCQQYGSSPWTFGQGTKVEIK	29765
vlCDR1	<u>RASQSVSSSYLA</u>	29766
vlCDR2	<u>GASSRAT</u>	29767
vlCDR3	<u>QQYGSSPWT</u>	29768
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGHLGPFDLWGQGMVTVSS / GKPGSGKPGSGKPGSGKPGS / EIVMTQSPATLSVSPGERATLSCRAS QSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYGSSPWTFGQGTKVEIK	29769

Figure 12LL [CTLA-4] H3_L0 (Fab XENP19546, scFv XENP19553)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGWLGPFDYWGQGTLLTVSS	29770
vhCDR1	<u>SYTMH</u>	29771
vhCDR2	<u>FISYDGNNTKYYADSVKG</u>	29772
vhCDR3	<u>TGWLGPFDY</u>	29773
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	29774
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTEFTLTISRLEPED FAVYYCQQYGSSPWTFGQGTKVEIK	29775
vlCDR1	<u>RASQSVSSSYLA</u>	29776
vlCDR2	<u>GAFSRAT</u>	29777
vlCDR3	<u>QQYGSSPWT</u>	29778
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNNTKYYADSVKGRFTISRDNAKNSLYLQM NSLRAEDTAVYYCARTGWLGPFDYWGQGTLLTVSS / GKPGSGKPGSGKPGSGKPGS / EIVLTQSPGTLISLSPGERATLSCRAS QSVSSSYLAWYQQKPGQAPRLIIYGAFSRATGIPDRFSGSGSGTEFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29779

Figure 12MM [CTLA-4]_H3_L0.22 (Fab XENP20011)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS	29780
vhCDR1	SYTMH	29781
vhCDR2	FISYDGNKYYADSVKG	29782
vhCDR3	TGWLGPFDY	29783
scFv linker	GKPGSGKPGSGKPGSGKPGS	29784
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29785
vlCDR1	RASQSVSSSYLA	29786
vlCDR2	GAFSRAT	29787
vlCDR3	QQYGSSPWT	29788
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS/ GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29789

Figure 12NN [CTLA-4]_H3_L0.44 (Fab XENP20052)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS	29790
vhCDR1	SYTMH	29791
vhCDR2	FISYDGNKYYADSVKG	29792
vhCDR3	TGWLGPFDY	29793
scFv linker	GKPGSGKPGSGKPGSGKPGS	29794
Variable light (vl) domain	EIVLTQSPGTLISLSPGERATLSCRASQSVGSSSYLSWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29795
vlCDR1	RASQSVGSSSYLS	29796
vlCDR2	GAFSRAT	29797
vlCDR3	QQYGSSPWT	29798
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS/ GKPGSGKPGSGKPGSGKPGS/EIVLTQSPGTLISLSPGERATLSCRASQSVGSSSYLSWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK	29799

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS	29800
vhCDR1	SYTMH	29801
vhCDR2	FISYDGNKYYADSVKG	29802
vhCDR3	TGWLGPFDY	29803
scFv linker	GKPGSGKPGSGKPGSGKPGS	29804
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYDAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQGSSPWFQGQTKVEIK	29805
vlCDR1	RASQSVGSSYLA	29806
vlCDR2	DAFSRAT	29807
vlCDR3	QYQGSSPWT	29808
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/ EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYDAFSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQGSSPWFQGQTKVEIK	29809

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS	29810
vhCDR1	SYTMH	29811
vhCDR2	FISYDGNKYYADSVKG	29812
vhCDR3	TGWLGPFDY	29813
scFv linker	GKPGSGKPGSGKPGSGKPGS	29814
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAYSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQGSSPWFQGQTKVEIK	29815
vlCDR1	RASQSVGSSYLA	29816
vlCDR2	GAYSRA	29817
vlCDR3	QYQGSSPWT	29818
scFv	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFIYDGNKYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARTGWLGPFDYWGQGLVTVSS/GKPGSGKPGSGKPGSGKPGS/ EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAYSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQYQGSSPWFQGQTKVEIK	29819

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTT</u> <u>DDAWMSWVRQAPGKGLEWVAEISTKANNHATYYAESVK</u> <u>GRFTISRDDSKSSVYLQ</u> <u>MNSLRAEDTAVYICTRLATWDWYFDVWGQGITVTVSS</u>	29820
vhCDR1	<u>DAWMS</u>	29821
vhCDR2	<u>EISTKANNHATYYAESVKG</u>	29822
vhCDR3	<u>LATWDWYFDV</u>	29823
Variable light (vl) domain	<u>DIVLTQSPSSLSASVGRVTITCRASQSV</u> <u>DYDGDSYMNWYQQKPKPKLLIYAASELESGIPARFS</u> <u>GGSGTDFTLTISSLPQPEDFATYYCQ</u> <u>SNEDPFTFGSGTKLEIK</u>	29824
vlCDR1	<u>RASQSV</u> <u>DYDGDSYMN</u>	29825
vlCDR2	<u>AASELES</u>	29826
vlCDR3	<u>QQSNEDPFT</u>	29827

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	<u>EVQLVQSGAEVKKPGATVKISCKASGF</u> <u>NIKDYFMHWQQAPGKGLEWMGWIDPELGDTEYAPKFQGR</u> <u>VTITADTSTNTAYMELSSLRSEDTAVY</u> <u>ICYARGVYQALDYWGQGITLVTVSS</u>	29828
vhCDR1	<u>DYFMH</u>	29829
vhCDR2	<u>WIDPELGDTEYAPKFQG</u>	29830
vhCDR3	<u>RGVYQALDY</u>	29831
Variable light (vl) domain	<u>DIQMTQSPAF</u> <u>LSVTPGEKVTITCQASQDIGNYLNWFQQKPGQTVKLLIYFTSYLHSGVPSRFS</u> <u>GSGS</u> <u>GTDYFTTIS</u> <u>LEAEDAATYFCQQGN</u> <u>TLPYTFGGG</u> <u>TKVEIK</u>	29832
vlCDR1	<u>QASQDIGNYLN</u>	29833
vlCDR2	<u>FTSYLHS</u>	29834
vlCDR3	<u>QQGN</u> <u>TLPYT</u>	29835

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	<u>EVQLVESGGGLVQPGGSLRLS</u> <u>CAASGFTT</u> <u>DDAWMDWVRQAPGKGLEWVAE</u> <u>ISTKANNNHATYYAESVK</u> <u>GRFTISRDDSKSSVYLQ</u> <u>MNSLRAEDTAVYYCTRLATWDWYFDV</u> <u>WGQGT</u> <u>TVTVSS</u>	29836
vhCDR1	<u>DAWMD</u>	29837
vhCDR2	<u>EISTKANNNHATYYAESVKG</u>	29838
vhCDR3	<u>LATWDWYFDV</u>	29839
Variable light (vl) domain	<u>DTVLTQSPSSLSASVGRVTITCRASQSV</u> <u>VDYDGDSYMNWYQQKPKGPPKLLIYAASELES</u> <u>GIPARLS</u> <u>GGSGTDF</u> <u>TLTIS</u> <u>LQPEDFATYYCQSNEDPFT</u> <u>FGSGTKLEIK</u>	29840
vlCDR1	<u>PASQSV</u> <u>VDYDGDSYMN</u>	29841
vlCDR2	<u>AASELES</u>	29842
vlCDR3	<u>QQSNEDPFT</u>	29843

Figure 13D
2A11_H0L0 (Fab XENP20930)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	<u>EVKLEESGGGLVQPGGSMKLS</u> <u>CAASGFTT</u> <u>SDAWMDWVRQSPEKGLEWVAE</u> <u>IRTKANNNHATYYAESVK</u> <u>GRFTISRDDSKSSVYLQ</u> <u>MNSLRAEDTGIYYCTRLANWDWYFDV</u> <u>WGAGT</u> <u>TVTVSS</u>	29844
vhCDR1	<u>DAWMD</u>	29845
vhCDR2	<u>EIRTKANNNHATYYAESVKG</u>	29846
vhCDR3	<u>LANWDWYFDV</u>	29847
Variable light (vl) domain	<u>DTVLTQSPASLAVSLGQRATIS</u> <u>CKASQSV</u> <u>VDYDGDSYMNWYQQKPGQPPKLLIYAA</u> <u>SNLESGIPARLS</u> <u>GGSGTDF</u> <u>TLLNIHPVEE</u> <u>DAATYYCQSNEDPFT</u> <u>FGSGTKLEVK</u>	29848
vlCDR1	<u>KASQSV</u> <u>VDYDGDSYMN</u>	29849
vlCDR2	<u>AASNLES</u>	29850
vlCDR3	<u>QQSNEDPFT</u>	29851

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISCKASGFNIKHYFMHWVQQAPGKGLEWMGWIDPYPYLGDTTEYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYCYARGVYQALDYWGQGITLVTVSS	29852
vhCDR1	<u>HYFMH</u>	29853
vhCDR2	<u>WIDPYLGDTTEYAPKFQ</u>	29854
vhCDR3	<u>RGVYQALDY</u>	29855
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPDQTVKLLIYFTSYLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29856
vICDR1	<u>QASQDIGNYLN</u>	29857
vICDR2	<u>FTSYLHS</u>	29858
vICDR3	<u>QQGNTLPYT</u>	29859

Figure 13F
2A11_H1L2 (Fab XENP20847)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISCKASGFNIKDYMHVWVQQAPGKGLEWMGWIDPENGDTTEYAPKFQGR VTITADTSTNTAYMELSSLRSEDTAVYCYARGVRQALDYWGQGITLVTVSS	29860
vhCDR1	<u>DYMH</u>	29861
vhCDR2	<u>WIDPENGDTTEYAPKFQ</u>	29862
vhCDR3	<u>RGVRQALDY</u>	29863
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPDQTVKLLIYYTSRLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29864
vICDR1	<u>QASQDIGNYLN</u>	29865
vICDR2	<u>YTSRLHS</u>	29866
vICDR3	<u>QQGNTLPYT</u>	29867

Figure 13G

2A11_H1_L2.25 (Fab XENP21372)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYIMHWVQQAPGKGLEWMGWIDPENGDT EYAPK FQGR VTITADTSTNTAYMELSSLRSED TAVYCYARGVRQALDYWGQGTLLVTVSS	29868
vhCDR1	<u>DYMH</u>	29869
vhCDR2	<u>WIDPENGDT EYAPK FQG</u>	29870
vhCDR3	<u>RGVRQALDY</u>	29871
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNHLNWFQQKPDQTVKLLIYYTSRLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29872
vICDR1	<u>QASQDIGNHLN</u>	29873
vICDR2	<u>YTSRLHS</u>	29874
vICDR3	<u>QQGNTLPYT</u>	29875

Figure 13H

2A11_H1_L2.47 (Fab XENP21394)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYIMHWVQQAPGKGLEWMGWIDPENGDT EYAPK FQGR VTITADTSTNTAYMELSSLRSED TAVYCYARGVRQALDYWGQGTLLVTVSS	29876
vhCDR1	<u>DYMH</u>	29877
vhCDR2	<u>WIDPENGDT EYAPK FQG</u>	29878
vhCDR3	<u>RGVRQALDY</u>	29879
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPDQTVKLLIYYTSHLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29880
vICDR1	<u>QASQDIGNYLN</u>	29881
vICDR2	<u>YTSRLHS</u>	29882
vICDR3	<u>QQGNTLPYT</u>	29883

Figure 13I

2A11_H1_L2.50 (Fab XENP21401)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYMHVQQAPGKGLEWMGWIDPENGDT ^Y APK ^{FQGR} VTITADTSTNTAYMELSSLRSED ^T AVYCYARGV ^{RQALDY} WGQ ^{GTLVTVSS}	29884
vhCDR1	<u>DYMH</u>	29885
vhCDR2	<u>WIDPENGDT^YAPK^{FQGR}</u>	29886
vhCDR3	<u>RGVRQALDY</u>	29887
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPDQTVKLLIYYTSYLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29888
vICDR1	<u>QASQDIGNYLN</u>	29889
vICDR2	<u>YTSYLHS</u>	29890
vICDR3	<u>QQGNTLPYT</u>	29891

Figure 13J

2A11_H1L2 (Fab XENP20847)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGAEVKKPGATVKISKASGFNIKDYMHVQQAPGKGLEWMGWIDPENGDT ^Y APK ^{FQGR} VTITADTSTNTAYMELSSLRSED ^T AVYCYARGV ^{RQALDY} WGQ ^{GTLVTVSS}	29892
vhCDR1	<u>DYMH</u>	29893
vhCDR2	<u>WIDPENGDT^YAPK^{FQGR}</u>	29894
vhCDR3	<u>RGVRQALDY</u>	29895
Variable light (vl) domain	DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPDQTVKLLIYYTSRLHSGVPSRFSGSGS GTDYFTTISLEAEDAATYFCQQGNTLPYTFGGGKVEIK	29896
vICDR1	<u>QASQDIGNYLN</u>	29897
vICDR2	<u>YTSRLHS</u>	29898
vICDR3	<u>QQGNTLPYT</u>	29899

Figure 13K

7G8_H3.23_L1.11 (fab XENP21670)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMDWVRQAPGKGLEWVAEISTKANNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRAEDTAVYYCTRLATWDWYFDVWGQGITTVTVSS	29900
vhCDR1	<u>DAWMD</u>	29901
vhCDR2	<u>EISTKANNHATYYAESVKG</u>	29902
vhCDR3	<u>LATWDWYFDV</u>	29903
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSVDDYDGDSYMNWYQQKPKPKLLIYAASELESGIPARLS GSGGTDFTLTISSLQPEDFATYYCQQSNEDPFTFGSGTKLEIK	29904
vlCDR1	<u>RASQSVDDYDGDSYMN</u>	29905
vlCDR2	<u>AASELES</u>	29906
vlCDR3	<u>QQSNEDPFT</u>	29907

Figure 13L

7G8_H3.28_L1 (Fab XENP21892)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMDWVRQAPGKGLEWVAEISTKAYNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRAEDTAVYYCTRLATWDWYFDVWGQGITTVTVSS	29908
vhCDR1	<u>DAWMD</u>	29909
vhCDR2	<u>EISTKAYNHATYYAESVKG</u>	29910
vhCDR3	<u>LATWDWYFDV</u>	29911
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSVDDYDGDSYMNWYQQKPKPKLLIYAASNLESGIPARLS GSGGTDFTLTISSLQPEDFATYYCQQSNEDPFTFGSGTKLEIK	29912
vlCDR1	<u>RASQSVDDYDGDSYMN</u>	29913
vlCDR2	<u>AASNLES</u>	29914
vlCDR3	<u>QQSNEDPFT</u>	29915

Figure 13M

7G8_H3.28_L1.11 (Fab XENP21893)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMDWVRQAPGKGLEWVAEISTKAYNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYYCTRLATWDWYFDVWGQGT ^T TVVSS	29916
vhCDR1	<u>DAWMD</u>	29917
vhCDR2	<u>EISTKAYNHATYYAESVKG</u>	29918
vhCDR3	<u>LATWDWYFDV</u>	29919
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSVDDYDGDSYMNWYQQKPKPKLLIYAASELESGIPARLS GSGGTDFTLTITSSLPEDFATYYCQQSNEDPFTFGSGTKLEIK	29920
vlCDR1	<u>RASQSVDDYDGDSYMN</u>	29921
vlCDR2	<u>AASELES</u>	29922
vlCDR3	<u>QQSNEDPFT</u>	29923

Figure 13N

7G8_H3.28_L1.13 (Fab XENP21894)

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMDWVRQAPGKGLEWVAEISTKAYNHATYYAESVK GRFTISRDDSKSSVYLQMNSLRRAEDTAVYYCTRLATWDWYFDVWGQGT ^T TVVSS	29924
vhCDR1	<u>DAWMD</u>	29925
vhCDR2	<u>EISTKAYNHATYYAESVKG</u>	29926
vhCDR3	<u>LATWDWYFDV</u>	29927
Variable light (vl) domain	DTVLTQSPSSLSASVGRVTITCRASQSVDDHDGDSYMNWYQQKPKPKLLIYAASELESGIPARLS GSGGTDFTLTITSSLPEDFATYYCQQSNEDPFTFGSGTKLEIK	29928
vlCDR1	<u>RASQSVDDHDGDSYMN</u>	29929
vlCDR2	<u>AASELES</u>	29930
vlCDR3	<u>QQSNEDPFT</u>	29931

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

What: anti-TIM3 XENP21503 1D10_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLKFSCAASGFAFSSFDMSWVRQTPEKRLEWVAYIISDGGASTFYPDITMKGRFTI SRD NAKNTLYLQ MSSSLKSEDTAMYYCTRLGAYWGQGITLVISA	29932
vhCDR1	SFDM	29933
vhCDR2	YISSDGGASTFYPDITMKG	29934
vhCDR3	LGAY	29935
Variable light (vl) domain	DVMTQTPLTSLVSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGQSPKRLIYLVSKLDSGVDPDRFTGS GSGTDFTLKISRVEAEDLGYYICWQGT HF PYTFGGGTKLEIK	29936
vlCDR1	KSSQSLDSDGKTYLN	29937
vlCDR2	VSKLDS	29938
vlCDR3	WQGT HF PYT	29939

Figure 14B

What: anti-TIM3 XENP21492 1D12_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLKFSCAASGFAFSSFDMSWVRQTPEKRLEWVAYIISDGGASTFYPDITMKGRFTI SRD NAKNTLYLQ MSSSLKSEDTAMYYCTRLGAYWGQGITLVISA	29940
vhCDR1	SFDMS	29941
vhCDR2	YISSDGGASTFYPDITMKG	29942
vhCDR3	LGAY	29943
Variable light (vl) domain	DIVLTQSPASLAVSLGQRATISCRASEVEYYGTSIMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSG SGTDFSLNIHPVEEDDIAMYFCQQSRKVPWT FG GGTKLEIK	29944
vlCDR1	RASEVEYYGTSIQ	29945
vlCDR2	AASNVES	29946
vlCDR3	QQSRKVPWT	29947

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

What: anti-TIM3 XENP21189 3H3_H1L2.1	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPNLVKPTETLLTCTVSGFSLNGYGVNWRQPPGKGLEWLA <u>MIWGDGSTDYNSALKSRLTIS</u> KDNSKSQVVLMTNMDPVDFTATYYCARSYYTSD <u>EDYWGQGLVT</u> VSS	29948
vhCDR1	GYGVN	29949
vhCDR2	MIWGDGSTDYNSALKS	29950
vhCDR3	SYTSD <u>EDY</u>	29951
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSLNSTRKKNYLA <u>WYQQKPGQSPKLLIYWASTRESGVPDRFTG</u> SGSGTDFLTITSSLSQAEDVAVYICKQSYSLRTFGGGTKVEIK	29952
vlCDR1	KSSQSLNSTRKKNYLA	29953
vlCDR2	WASTRES	29954
vlCDR3	KQSYSLRT	29955

Figure 14D

What: anti-TIM3 XENP21493 6C8_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPNLVAPSQSLSTCTVSGFSLNGYGVNWRQPPGKGLEWLG <u>MIWGDGSTDYNSALKSRLSIS</u> KDNSKSQVFLKMNLSLQTDITARYYCARSYYTSD <u>EDYWGQGLVT</u> VSA	29956
vhCDR1	GYGVN	29957
vhCDR2	MIWGDGSTDYNSALKS	29958
vhCDR3	SYTSD <u>EDY</u>	29959
Variable light (vl) domain	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGSNVAWCQKPGQSPKALIIY <u>SASFRTSGVPDRFTGSGSGTD</u> FTLTISNVQSEDLAEYFCQQYNSTPYTFGGGT <u>KLEIK</u>	29960
vlCDR1	KASQNVGSNVVA	29961
vlCDR2	SASFRTS	29962
vlCDR3	QQYNSTPYT	29963

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	QVQLKQSGPGLVQPSQSLSTCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGSTEYNAAFI ¹ SRLSIS KDNSKSQVFFKMNSLQADDTAIYYCARGGLLSPFDYWGQGTTLTVSS	29964
vhCDR1	SYGVH	29965
vhCDR2	VIWSGGSTEYNAAFIS	29966
vhCDR3	GGLLSPFDY	29967
Variable light (vl) domain	DIVLTQSPASLAVSLGQRATISCRASESVEYYGTSLSLMQWYQQKPGQPPKLLIYAASNVESGVPARFSGSG SGTDFSLNIHPVEEDDIAMYFCQQSRKVPWTFGGGTKLEIK	29968
vlCDR1	RASESVEYYGTSLMQ	29969
vlCDR2	AASNVES	29970
vlCDR3	QQSRKVPWT	29971

Figure 14F

What: anti-TIM3 XENP21495 7A9_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLLLES ¹ GGGLVQPGGSLKLSCAASGDFDSRYWMSWVRQAPGKGLEWIGEINPDSS ² TINYTPSLKDKFLI SRD ³ NAKNTLYLQMSKVRSEDTALYYCARPN ⁴ GY ⁵ YVGTIFPFAYWGQGT ⁶ LVTVSA	29972
vhCDR1	RYWMS	29973
vhCDR2	EINPDSS ² TINYTPSLKD	29974
vhCDR3	PNGY ⁵ YVGTIFPFAY	29975
Variable light (vl) domain	QAVVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQEKPDHLFTGLIGTNNRAPGVPARFSGSLIG DKAALTITGAQTEDEAIYFCALWYSNHWVFGG ⁶ GTKLT ⁷ VLG	29976
vlCDR1	RSSTGAVTTSNYAN	29977
vlCDR2	GTNNRAP	29978
vlCDR3	ALWYSNHWV	29979

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

What: anti-TIM3 XENP21496 7B11_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPQSLSITCTVSGFSLTSYAVNWVRQSPGKGLEWLGVIWGGSTDYNAAFISRLSIS KDNSKSQVFFKMNSLQANDTAIYYCVSLYYRYDGEDYWGQGLVTVSA	29980
vhCDR1	SYAVN	29981
vhCDR2	VIWGGSTDYNAAFIS	29982
vhCDR3	LYRYDGFY	29983
Variable light (vl) domain	DIVLTQSQKFLSTSVGDRVSVTCKASQNVGTHVARYQQKPGQSPKALVYSASYRYSGVPDRFTGSGSGTD FTLTISNVQSEDLAEYFCQQYNSYPLTFGGGTKLEIK	29984
vlCDR1	KASQNVGTHVA	29985
vlCDR2	SASYRYS	29986
vlCDR3	QQYNSYPLT	29987

Figure 14H

What: anti-TIM3 XENP21501 B11var_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGPGLVQPQSLSITCTVSGFSLTSYAVNWVRQSPGKGLEWLGVIWGGSTDYNAAFISRLSIS KDNSKSQVFFKMNSLQADDTAIYYCVSLYYRYDGEDYWGQGLVTVSA	29988
vhCDR1	SYAVN	29989
vhCDR2	VIWGGSTDYNAAFIS	29990
vhCDR3	LYRYDGFY	29991
Variable light (vl) domain	DIVLTQSQKFLSTSVGDRVSVTCKASQNVGTHVARYQQKPGQSPKALVYSASYRYSGVPDRFTGSGSGTD FTLTISNVQSEDLAEYFCQQYNSYPLTFGGGTKLEIK	29992
vlCDR1	KASQNVGTHVA	29993
vlCDR2	SASYRYS	29994
vlCDR3	QQYNSYPLT	29995

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

What: anti-TIM3 XENP21502 7C2_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKVVESGGGLVKPGGSLKLSCAASGFTTFSRVAMSWVRQTPEKRLEWVASISGGSTYYPPDSVQGRFTTIS RDNARNILYLQMSSLSRSEDITAMYYCARGDYEGYFDYWGQGTSLTVSS	29996
vhCDR1	RYAMS	29997
vhCDR2	SISGGSTYYPPDSVQG	29998
vhCDR3	GDYEGYFDY	29999
Variable light (vl) domain	DIVMTQSPSSLAMSVGQKVTMSCKSSQSLINSLNQKNYLAWYQQKPGQSPKLLVYFASTRESGVPDRFIG SGSGTDFLTITISSVQAEDLADYFCQQHYSTPLTIFGAGTKLELK	30000
vlCDR1	KSSQSLINSLNQKNYLA	30001
vlCDR2	FASTRES	30002
vlCDR3	QQHYSTPLT	30003

Figure 15A

XENP016434 YW243.55.S70[PD-L1]_H0L0_igG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDSWIHVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVVYCARRHWPGGFDYWGQGTLTVTVSS	28741
vhCDR1	<u>DSWIH</u>	28742
vhCDR2	<u>WISPYGGSTYYADSVK</u> G	28743
vhCDR3	<u>RHWPGGFDY</u>	28744
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDSWIHVVRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNSLR AEDTAVVYCARRHWPGGFDYWGQGTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LOSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVWVD VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS LSLSPGK	28740
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIY <u>SASFLY</u> SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQY <u>LYHPATFGQG</u> TKVEIK	28746
vlCDR1	<u>RASQDVSTAVA</u>	28747
vlCDR2	<u>SASFLYS</u>	28748
vlCDR3	<u>QQYLYHPAT</u>	28749
Full length light chain	DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIY <u>SASFLY</u> SGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQY <u>LYHPATFGQG</u> TKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSLT LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28745

Figure 15B

XENP024118 avelumab[PD-L1]_H1L1_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYIMMWVRQAPGKGLEWVSSYPSSGGITFYADTVKGRFTISRDNKNTLYLQMNSLRAE DTAVVYCARIKLGTVTTVDYWGQGTLVTVSS	28751
vhCDR1	<u>SYIMM</u>	28752
vhCDR2	<u>SIYPSGGITFYADTVKG</u>	28753
vhCDR3	<u>IKLGTVTTVDY</u>	28754
Full length HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYIMMWVRQAPGKGLEWVSSYPSSGGITFYADTVKGRFTISRDNKNTLYLQMNSLRAE DTAVVYCARIKLGTVTTVDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL QSSGLYSLSVAVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDV KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSL SLSPGK	28750
Variable light (vl) domain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNVYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY CSSYTSSSTRVFGTGTKVTVL	28756
vlCDR1	<u>IGTSSDVGGYNVVS</u>	28757
vlCDR2	<u>DVSNRPS</u>	28758
vlCDR3	<u>SSYTSSSTRV</u>	28759
Full length light chain	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNVYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYY CSSYTSSSTRVFGTGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTTPSKQSNNKYAA SSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS	28755

Figure 15C

XENP0241119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYVCAREGGWFGELAFDYWGQGLTVTVSS	28761
vhCDR1	<u>RYWMS</u>	28762
vhCDR2	<u>NIKQDGSEKYYVDSVKG</u>	28763
vhCDR3	<u>EGGWFGELAFDY</u>	28764
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYVCAREGGWFGELAFDYWGQGLTVTVSS/ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTV LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRHEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	28760
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSLPWTFGQGTKEIK	28766
vlCDR1	<u>RASQRVSSSYLA</u>	28767
vlCDR2	<u>DASSRAT</u>	28768
vlCDR3	<u>QQYGSLPWT</u>	28769
Full length light chain	EIVLTQSPGTLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSLPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	28765

Figure 16

XENP014410 20H4.9[4-1BB]_H0L0_1gG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQWAGALLKPSETLSLTCAVYGGSGYYSWIRQSPKGLWIGEINHGYYVTYNPSLESRVTISVDTSKNQFSKLKSSVTAAD TAVVYCARDYGPGNYDWYFDLWGRGTLVTSS	26263
vhCDR1	<u>GYYS</u>	26264
vhCDR2	<u>EINHGYYVTYNPSLES</u>	26265
vhCDR3	<u>DYGPNGYDWYFDL</u>	26266
Full length HC	QVQLQQWAGALLKPSETLSLTCAVYGGSGYYSWIRQSPKGLWIGEINHGYYVTYNPSLESRVTISVDTSKNQFSKLKSSVTAAD TAVVYCARDYGPGNYDWYFDLWGRGTLVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLOSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV DVKHEDEPKFKNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLIHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQK SLSLSPGK	26262
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRAIGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQQRS NWPPALTFGGGTKVEIK	26268
vlCDR1	<u>RASQSVSSYLA</u>	26269
vlCDR2	<u>DASNRAT</u>	26270
vlCDR3	<u>QQRSNWPPALT</u>	26271
Full length light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRAIGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQQRS NWPPALTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVWCCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	26267

Figure 17

XENP016437 11D4[OX40]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMINWVRQAPGKGLEWVSYISSSSTIDYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVVYCARESGWYLF ² DYWGQGTLVTVSS	26273
vhCDR1	<u>SYSMN</u>	26274
vhCDR2	<u>YISSSSTIDYADSVK</u> G	26275
vhCDR3	<u>ESGWYLF</u> DY	26276
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSMINWVRQAPGKGLEWVSYISSSSTIDYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVVYCARESGWYLF ² DYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHHKPSNTKVDKKVEPKSCDKTHCTPCPAPPVAGPSVFLFPPKPKD ² TL ² MISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVSVLT ² VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY ² TLPPSREEMITKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK ² TPPVLDSDGSFFLYSKLTVDKSRWQQGNV ² FSCSV ² MHEALHNHYTQKSLSLSPGK	26272
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLA ² WYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGTDF ² FTLT ² ISSLPEDFATYYCQQYNSYPPTFGGGTKVEIK	26278
vlCDR1	<u>RASQGISSW</u> LA	26279
vlCDR2	<u>AASSLQ</u> S	26280
vlCDR3	<u>QQYNSYP</u> PT	26281
Full length light chain	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLA ² WYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGTDF ² FTLT ² ISSLPEDFATYYCQQYNSYPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK ² DSTYSLSSLT ² LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	26277

Figure 18

XENP016438 1D8[GITR]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVTLKESGPGILKPSQTLSTCSFSGFSLSTSGMGVGVGWIQPSGKGLEWLAHIWWDKYYSPSLKSQLTISKDTSRNQVFLKITSLDTA DTATYYCVRSYYYGSSGAMDIYWGGGTSVTVSS	26283
vhCDR1	<u>TS</u> GMGVG	26284
vhCDR2	<u>HI</u> WWDKYYSPSLKS	26285
vhCDR3	<u>SY</u> YGSSGAMDIY	26286
Full length HC	QVTLKESGPGILKPSQTLSTCSFSGFSLSTSGMGVGVGWIQPSGKGLEWLAHIWWDKYYSPSLKSQLTISKDTSRNQVFLKITSLDTA DTATYYCVRSYYYGSSGAMDIYWGGGTSVTVSS/ASTKGP ^{SV} FLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA VLOSSGLYSLSSVTV ^{PS} SSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV DVKHEDEPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQGNV ^F SCSMHEALHNHYTQK SLSLSPGK	26282
Variable light (vl) domain	DIVMTQTPLSLPVSLGDQASISCRSSQSLVHSDGNTY ^L HWY ^L LQKPGQSPKLLIY ^{KV} SKRFSGVPDRFSGSGGTDFTLKISRVEAEDLGVIY FCSQSTHVPPTFGGGTKLEIK	26288
vlCDR1	<u>R</u> SSQSLVHSDGNTY ^L H	26289
vlCDR2	<u>KV</u> SKRF ^S	26290
vlCDR3	<u>SQ</u> STHVPPT	26291
Full length light chain	DIVMTQTPLSLPVSLGDQASISCRSSQSLVHSDGNTY ^L HWY ^L LQKPGQSPKLLIY ^{KV} SKRFSGVPDRFSGSGGTDFTLKISRVEAEDLGVIY FCSQSTHVPPTFGGGTKLEIK/RTVAAPS ^{VF} IFPPSDEQLKSGTASVCLLNNFY ^P REAKVQWKVDNALQSGNSQESVTEQDSKDS ^T YSL SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	26287

Figure 19A

XENP016435 [anti-ICOS]_{H0L0}_IgG1_PVA_5267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVSS	26293
vhCDR1	<u>GYMH</u>	26294
vhCDR2	<u>WINPHSGGTNYAQKFGQ</u>	26295
vhCDR3	<u>TYDSSGGYHDAFDI</u>	26296
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFGQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVSS/ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKD ^{TL} MI ^{SRT} PEVTCVVDVVKHEDPEVKFNWVVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^{FSC} VM ^{IHE} ALHNHYTQKSLSLSPGK	26292
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLA ^{WY} QQKPGKAPKLLIYVASSLQSGVPSRFSGSGGTDFLT ^{TI} SSLQPEDFATYYCQQA ^{NSFPWTFGQGT} KVEIK	26298
vlCDR1	<u>RASQGISRLLA</u>	26299
vlCDR2	<u>VASSLQS</u>	26300
vlCDR3	<u>QQANSFPWT</u>	26301
Full length light chain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLA ^{WY} QQKPGKAPKLLIYVASSLQSGVPSRFSGSGGTDFLT ^{TI} SSLQPEDFATYYCQQA ^{NSFPWTFGQGT} KVEIK/RTVAAPSVFIFPPSDEQLKSGTASV ^W CLIN ^{FN} FYPREAKVQWKVDNALQSGNSQESVTEQDSK ^D STYS ^{LS} STL ^{TL} KADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC	26297

Figure 19B

XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY ^Y YGTSLAWFDYWGQGTLVTVST	26303
vhCDR1	<u>TYWMH</u>	26304
vhCDR2	<u>EIDPSDSVNYNQNFKG</u>	26305
vhCDR3	<u>SPDY^YGTSLAWFDY</u>	26306
Full length HC	QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQLSSLT SEDSAVYFCARSPDY ^Y YGTSLAWFDYWGQGTLVTVST/ASTKGPVFP/APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAYLQSSGLYS ^L SSVTV ^P SSSLGTQYICNVN ^H KPSNTKVDKKEPKSCDKTHTCPPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTC VVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLT ^V LHQDWLNGKEYCKV ^S NKALPAPIEKTISKAKGQPREPQV YTLPPSRHEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV ^F SCVMHEALHNH YTQKSLSPGK	26302
Variable light (vl) domain	DIVMTQAAAPSVPTPGESVSISCRSSKSP ^L HSNGNIYLYWFLQRPQSPQLLIYRMSNLASGV ^P DRFSGSGGTTFTLKISRVEAEDVGV YYCMQHLEY ^P YTFGGG ^T TKLEIK	26308
vlCDR1	<u>RSSKSP^LHSNGNIYLY</u>	26309
vlCDR2	<u>RMSNLAS</u>	26210
vlCDR3	<u>MQHLEY^PY^T</u>	26211
Full length light chain	DIVMTQAAAPSVPTPGESVSISCRSSKSP ^L HSNGNIYLYWFLQRPQSPQLLIYRMSNLASGV ^P DRFSGSGGTTFTLKISRVEAEDVGV YYCMQHLEY ^P YTFGGG ^T TKLEIK/RTVAAPSVFIFPPSDEQLKSGTASV ^V CLLNFPY ^E REAKVQWKVDNALQSGNSQESVTEQDSKDS ^T Y SLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	26307

Figure 19C

XENP021821 GSK_88.2[ICOS]_HOL0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQPGAELVRPGASVKLSCKASGYFTSYWINWVKQRPQGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSNTAYMQLTSP TSEDSAVYVCTRWNL ^{SYFDN} NYYLDYWGGQTTLTVSS	26313
vhCDR1	<u>SYWIN</u>	26314
vhCDR2	<u>NIYPSDSYTNYNQMFKD</u>	26315
vhCDR3	<u>WNL^{SYFDN}NYYLDY</u>	26316
Full length HC	QVQLQQPGAELVRPGASVKLSCKASGYFTSYWINWVKQRPQGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSNTAYMQLTSP TSEDSAVYVCTRWNL ^{SYFDN} NYYLDYWGGQTTLTVSS/ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGV HTFP ^{AVL} QSSGLYSLSVTV ^{PS} SSLTGTQYICNVN ^{HK} PSNTKVDKKVEPKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEV TCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLT ^{VL} HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQQGNV ^F SCSV ^M HEALH NHYTQKSLSPGK	26312
Variable light (vl) domain	DIVMTQAAPSVPTPGESVSISCRSSK ^{LL} HSNGNTLYYWF ^L QRPQSPQLLIYRMSN ^{LA} SGVPDRFSGSGGTFTLRISRVEAEDVGV YYCMQHLEY ^{PWT} FGGGTKLEIK	26318
vlCDR1	<u>RSSK^{LL}HSNGNTLY</u>	26319
vlCDR2	<u>RMSN^{LA}</u>	26320
vlCDR3	<u>MQHLEY^{PWT}</u>	26321
Full length light chain	DIVMTQAAPSVPTPGESVSISCRSSK ^{LL} HSNGNTLYYWF ^L QRPQSPQLLIYRMSN ^{LA} SGVPDRFSGSGGTFTLRISRVEAEDVGV YYCMQHLEY ^{PWT} FGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYFREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	26317

Figure 19D

XENP021822 jMab-138[ICOS]_HOL0_igG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWHVVRQATGKGLEWVSAIGTAGDTYYPGSVKGRTISRENAKNSLYLQMNSLRA GDTAVVYCVRDNRKVTHEHYHYYGMDVWGQGTTVTVSS	26323
vhCDR1	<u>SYDMH</u>	26324
vhCDR2	<u>AIGTAGDTYYPGSVKG</u>	26325
vhCDR3	<u>DNRKVTHEHYHYYGMDV</u>	16326
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWHVVRQATGKGLEWVSAIGTAGDTYYPGSVKGRTISRENAKNSLYLQMNSLRA GDTAVVYCVRDNRKVTHEHYHYYGMDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLVSTVPSSSLGTQYICNVNHHKPSNTKVDKKEPKSCDKTHCTCPAPPVAGPSVFLFPPKPKDITLMISRTIP EVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVMEAL HNHYTQKSLSLSPGK	26322
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQNIIRSSYLAWYQQKPGQAPGGLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQF <u>GSSPMCSFGQGTKLEIK</u>	26328
vlCDR1	<u>RASQNIIRSSYLA</u>	26329
vlCDR2	<u>GASSRAT</u>	26330
vlCDR3	<u>QQFGSSPMCS</u>	26331
Full length light chain	EIVLTQSPGTLSPGERATLSCRASQNIIRSSYLAWYQQKPGQAPGGLLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQF <u>GSSPMCSFGQGTKLEIK</u> /RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	26327

Figure 19E

XENP021823 jMab-139[ICOS]_H0L0_igG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYPGSKGRTISRENAKNSLYLQMNSLRA GDTAVVYCVRDKRTVTHEHYHYGMDVWVGQGTTVTVSS	26333
vhCDR1	<u>SYDMH</u>	26334
vhCDR2	<u>AIGTAGDTYPGSKG</u>	26335
vhCDR3	<u>DKRTVTHEHYHYGMDV</u>	26336
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYPGSKGRTISRENAKNSLYLQMNSLRA GDTAVVYCVRDKRTVTHEHYHYGMDVWVGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPE VTCWVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEAL HNHYTQKSLSLSPGK	26332
Variable light (vl) domain	EIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQKPGQAPGGLLIIFGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQE GSSPMCSFGQGTKLEIK	26338
vlCDR1	<u>RASQSISSSLA</u>	26339
vlCDR2	<u>GASSRAT</u>	26340
vlCDR3	<u>QQFGSSPMCS</u>	26341
Full length light chain	EIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQKPGQAPGGLLIIFGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQQE GSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL TLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	26337

Figure 19F

XENP022346 WO2016059602_GSK[ICOS]_HOL0_igG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGSSVKVCKASGYTFD <u>YAMHWVRQAPGQGLEWMGLISYSDHTN</u> <u>NQKFQGRVTITADKSTSTAYMELSSLR</u> SED <u>TA</u> VYCGR <u>IN</u> NYGNYGWYFDV <u>W</u> GQGT <u>TV</u> VSS	26343
vhCDR1	<u>DYAMH</u>	26344
vhCDR2	<u>LISYSDHTN</u> <u>NQKFQGR</u>	26345
vhCDR3	<u>NNYGN</u> YGWYFDV	26346
Full length HC	QVQLVQSGAEVKKPGSSVKVCKASGYTFD <u>YAMHWVRQAPGQGLEWMGLISYSDHTN</u> <u>NQKFQGRVTITADKSTSTAYMELSSLR</u> SED <u>TA</u> VYCGR <u>IN</u> NYGNYGWYFDV <u>W</u> GQGT <u>TV</u> VSS/ASTKGPSVFPLAPSSKSTSGGTAA <u>LGCLVKDYFPEPVTVSWNSGALTSGVHT</u> FP <u>AV</u> LQSSGLYSLSSV <u>TV</u> PS <u>SLGTQYICNVN</u> HKPSNTKV <u>DK</u> VEPKSCDK <u>TH</u> TCPPCP <u>APPVAGPSVFLPPKPKD</u> TL <u>MISRTPEVTC</u> VVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV <u>SVLT</u> VL <u>HQD</u> WLN <u>GEYKCKV</u> SNKALPAPIEK <u>TI</u> SKAKGQGP <u>REPQV</u> YTLPPSRHEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK <u>TT</u> PPVLDS <u>DSGFFLYSKLTVD</u> KSRWQQGNV <u>FSC</u> VMHEAL <u>HNH</u> YTQKSLSPGK	26342
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSC <u>SASSSVSYMH</u> WYQQKPGQAP <u>RLIYDTSKL</u> ASGIPARFSGSGGT <u>DTYLT</u> TISSLEPEDFAVY <u>YCFQGS</u> GSGYPYTFGGQGTKLEIK	26348
vlCDR1	<u>SASSSVSYMH</u>	26349
vlCDR2	<u>DTSKLAS</u>	26350
vlCDR3	<u>FQGS</u> GYPT	26351
Full length light chain	EIVLTQSPATLSLSPGERATLSC <u>SASSSVSYMH</u> WYQQKPGQAP <u>RLIYDTSKL</u> ASGIPARFSGSGGT <u>DTYLT</u> TISSLEPEDFAVY <u>YCFQGS</u> GSGYPYTFGGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSPVTKSNRGEC	26347

Figure 19G

XENP023057 Jounce_37A10S713[ICOS]_H0L0_IgG1_PVA_/S267K

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYWMIDWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDNAKNTLYLQMNSLR AEDTAVYYCTRWGRFGFDSWGQGLTVTVSS	26353
vhCDR1	<u>DYWMID</u>	26354
vhCDR2	<u>NIDEDGSITEYSPFVKG</u>	26355
vhCDR3	<u>WGRFGFDS</u>	26356
Full length HC	EVQLVESGGGLVQPGGSLRLSCAASGFTTFSDYWMIDWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDNAKNTLYLQMNSLR AEDTAVYYCTRWGRFGFDSWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVAVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVWVDV KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVLHQDWLNGKEYCKVSNKALPAIEKTIKAKGQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSL SLSPGK	26352
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLSGSFNYLTWYQQKPGQPPKLLIFYASTRHTGVPDRFSGSGGTDFTLTISSLQAEDVAVYY CHHHYNAPPTFGPGTKVDIK	26358
vlCDR1	<u>KSSQSLLSGSFNYLT</u>	26359
vlCDR2	<u>YASTRHT</u>	26360
vlCDR3	<u>HHHYNAPPT</u>	26361
Full length light chain	DIVMTQSPDSLAVSLGERATINCKSSQSLLSGSFNYLTWYQQKPGQPPKLLIFYASTRHTGVPDRFSGSGGTDFTLTISSLQAEDVAVYY CHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL SSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC	26357

Figure 20A

XENP022091 [ICOS]_H0_L0.7_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELS RLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGMVTVSS	28771
vhCDR1	<u>GYMH</u>	28772
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28773
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28774
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELS RLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGS	28770
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQGISSYLAWYQQKPKGKAPKLLIYVASSLQSGVPSRFSGSGGTDFLTITSLQPEDFATYYCQQA NSFPWTFGQGTKEIK	28776
vlCDR1	<u>RASQGISSYLA</u>	28777
vlCDR2	<u>VASSLQS</u>	28778
vlCDR3	<u>QQANFPWT</u>	28779
Full length light chain	DIQMTQSPSSVSASVGDRVTITCRASQGISSYLAWYQQKPKGKAPKLLIYVASSLQSGVPSRFSGSGGTDFLTITSLQPEDFATYYCQQA NSFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTL TLISKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	28775

Figure 20B

XENP022780 [ICOS]_H0_L0.34_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYVCARTYYDSSGGYHDAFDIWGQGTMTVSS	28781
vhCDR1	<u>GYMH</u>	28782
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28783
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28784
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYVCARTYYDSSGGYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGS	28780
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAESEFPWTFGGGTKVEIK	28786
vlCDR1	<u>QASQDISRLLA</u>	28787
vlCDR2	<u>VASSLQS</u>	28788
vlCDR3	<u>QQAESFPWT</u>	28789
Full length light chain	DIQMTQSPSSVSASVGDRVTITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAESEFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28785

Figure 20C

XENP022782 [ICOS]_H0_L0.36_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVSS	28791
vhCDR1	<u>GYMH</u>	28792
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28793
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28794
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGS	28790
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCQASQDISSLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFLTITSLQPEDFATYYCQQAESFPWTFGQGTKEIK	28796
vlCDR1	<u>QASQDISSLLA</u>	28797
vlCDR2	<u>VASSLQS</u>	28798
vlCDR3	<u>QQAESFPWT</u>	28799
Full length light chain	DIQMTQSPSSVSASVGDRTITTCQASQDISSLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFLTITSLQPEDFATYYCQQAESFPWTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	28795

Figure 20D

XENP022783 [ICOS]_H0_L0.37_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDI <u>WGQGTMTVSS</u>	28801
vhCDR1	<u>GYMH</u>	28802
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28803
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28804
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDI <u>WGQGTMTVSS</u> /ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGS	28800
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCQASQDISRLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAESEFPWTFGGQTKVEIK	28806
vlCDR1	<u>QASQDISRLLA</u>	28807
vlCDR2	<u>AASSLQS</u>	28808
vlCDR3	<u>QQAESFPWT</u>	28809
Full length light chain	DIQMTQSPSSVSASVGDRTITTCQASQDISRLLAWYQQKPGKAPKLLIYAASLSQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAESEFPWTFGGQTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28805

Figure 20E

XENP022784 [ICOS]_H0_L0.38_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELS RLRSDDTAVYVCARTYYDSSGGYHDAFDIWGQGTMTVSS	28811
vhCDR1	<u>GYMH</u>	28812
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28813
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28814
Full length HC	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELS RLRSDDTAVYVCARTYYDSSGGYHDAFDIWGQGTMTVSS/ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCGS	28810
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCQASQDISSLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFLTITSSLPEDFATYYCQQ <u>AESFPWT</u> FGQGTKVEIK	28816
vlCDR1	<u>QASQDISSLLA</u>	28817
vlCDR2	<u>AASSLQS</u>	28818
vlCDR3	<u>QQAESFPWT</u>	28819
Full length light chain	DIQMTQSPSSVSASVGDRVTITCQASQDISSLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFGSGSGTDFLTITSSLPEDFATYYCQQ <u>AESFPWT</u> FGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28815

Figure 20F

XENP023088 [ICOS]_H0.66_LO_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS	28821
vhCDR1	<u>GYMH</u>	28822
vhCDR2	<u>WINPHSGETIYAQKFQ</u>	28823
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28824
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCGS	28820
Variable light (vl) domain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLQSGVPSRFSGSGGTDFLTITSLQPEDFATYYCQQA NSFPWTFGQGTKVEIK	28826
vlCDR1	<u>RASQGISRLLA</u>	28827
vlCDR2	<u>VASSLQS</u>	28828
vlCDR3	<u>QQANSPFWT</u>	28829
Full length light chain	DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLQSGVPSRFSGSGGTDFLTITSLQPEDFATYYCQQA NSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYISLSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28825

Figure 20G

XENP023409 [ICOS]_H0.66_L0.34_Fab

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS	28831
vhCDR1	<u>GYMH</u>	28832
vhCDR2	<u>WINPHSGETIYAQKFQ</u>	28833
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28834
Full length HC	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHHKPSNTKVDKKEPKSCGS	28830
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ <u>AESEFPWTFGQGT</u> KVEIK	28836
vlCDR1	<u>QASQDISRLLA</u>	28837
vlCDR2	<u>VASSLQS</u>	28838
vlCDR3	<u>QQAESFPWT</u>	28839
Full length light chain	DIQMTQSPSSVSASVGDRTITTCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ <u>AESEFPWTFGQGT</u> KVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	28835

Figure 21A

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

Figure 22C

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

Figure 23

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	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELS RLRSDDTAVYYCARTYYDSSGGYHDAFDI <u>WGQGTMTVSS</u>	28840
vhCDR1	<u>GYMH</u>	28841
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28842
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28843
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28849
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPKGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQA <u>NSFPWTFGQGTKEIK</u>	28844
vlCDR1	<u>RASQGISRLLA</u>	28845
vlCDR2	<u>VASSLQS</u>	28846
vlCDR3	<u>QQANSFPWT</u>	28847
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELS RLRSDDTAVYYCARTYYDSSGGYHDAFDI <u>WGQGTMTVSS/GKPGSGKPGSGKPGS/DIQMTQSPSSVSASVGDRTTICRA</u> <u>SQGISRLLAWYQQKPKGKAPKLLIYVASSLSQSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQA</u> <u>NSFPWTFGQGTKEIK/GS</u>	28848

Figure 24B

XENP024353 [anti-ICOS]_{L0H0}_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGMVTVSS	28850
vhCDR1	<u>GYMH</u>	28851
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28852
vhCDR3	<u>TYDSSGGYHDAFDI</u>	28853
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28859
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQA NSFPWTFGQGTKEIK	28854
vlCDR1	<u>RASQGISRLLA</u>	28855
vlCDR2	<u>VASSLQS</u>	28856
vlCDR3	<u>QQANSFPWT</u>	28857
scFv	DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQA NSFPWTFGQGTKEIK/GKPGSGKPGSGKPGSG/ QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDSSGGYHDAFDIWGGQGMVTVSS/GS	28858

Figure 24C

XENP024354 [anti-ICOS]_H0.40_L0.22_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVY CARTYYDTSGYYHDAFDVWGQGTMTVTVSS	28860
vhCDR1	<u>GYMH</u>	28861
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28862
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28863
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28869
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPKGAPKAPKLLIYAASSLQSGVPSRFS GGSGTDFLT TISS LQPEDFATYYCQQA <u>NSFPWT</u> FGQGTKVEIK	28864
vlCDR1	<u>RASQDISRLLA</u>	28865
vlCDR2	<u>AASSLQS</u>	28866
vlCDR3	<u>QQANSFPWT</u>	28867
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVY CARTYYDTSGYYHDAFDVWGQGTMTVTVSS/ <u>GKPGSGKPGSGKPGS</u> /DIQMTQSPSSVSASVGDRTTITCRA <u>SQDISRLLA</u> WYQQKPKGAPKLLIYAASSLQSGVPSRFSGGSGTDFLT TISS LQPEDFATYYCQQA NSFPWT FGQGTKVEIK/GS	28868

Figure 24D

XENP024355 [anti-ICOS]_{H0.40_L0.45_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED ^T AVYVCARTYYDTS ^{GYHDAFDV} WGQGTMTVSS	28870
vhCDR1	<u>GYMH</u>	28871
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28872
vhCDR3	<u>TYDTS^{GYHDAFDV}</u>	28873
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28879
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA ^{WYQQKPKGAPKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQA} <u>QSFPWTFGQGTKEIK</u>	28874
vlCDR1	<u>RASQDISRLLA</u>	28875
vlCDR2	<u>AASSLQ</u>	28876
vlCDR3	<u>QQAQSF^{WT}</u>	28877
scFv	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED ^T AVYVCARTYYDTS ^{GYHDAFDV} WGQGTMTVSS/ <u>GKPGSGKPGSGKPGS</u> / <u>DIQMTQSPSSVSASVGDRTTITCRA</u> <u>SQDISRLLA^{WYQQKPKGAPKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQAQSF^{WT}FGQGTKEIK}/GS</u>	28878

Figure 24E

XENP024356 [anti-ICOS]_{H0.66_L0.22_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTVSS	28880
vhCDR1	<u>GYMH</u>	28881
vhCDR2	<u>WINPHSGETIYAQKFQ</u>	28882
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28883
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28889
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA ^{WYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLT} TISSLQPEDFATYYCQQA NSFPWTIFGQGTKVEIK	28884
vlCDR1	<u>RASQDISRLLA</u>	28885
vlCDR2	<u>AASSLQS</u>	28886
vlCDR3	<u>QQANSFPWT</u>	28887
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTVSS/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>DIQMTQSPSSVSASVGDRTTITCRAS</u> <u>QDISRLLA</u> ^{WYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLT} TISSLQPEDFATYYCQQA ^{NSFPWTIFGQGTKVEIK} /GS	28888

Figure 24F

XENP024357 [anti-ICOS]_{H0.66_L0.45_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS	28890
vhCDR1	<u>GYMH</u>	28891
vhCDR2	<u>WINPHSGETIYAQKFQ</u>	28892
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28893
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28899
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA ^{WYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQA} <u>QSFPWTFGQGTKVEIK</u>	28894
vlCDR1	<u>RASQDISRLLA</u>	28895
vlCDR2	<u>AASSLQS</u>	28896
vlCDR3	<u>QQAQSF^{WT}</u>	28897
scFv	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTTRDTSISTAYMELSS LRSEDTAVVYCARTYYDTSGYYHDAFDVWGQGTMTVTSS/ <u>GKPGSGKPGSGKPGS</u> / <u>DIQMTQSPSSVSASVGDRTTITCRAS</u> <u>QDISRLLA</u> <u>WYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISSLPEDFATYYCQQAQSF^{WT}FGQGTKVEIK/GS</u>	28898

Figure 24G

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVVYCAR <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS	28900
vhCDR1	<u>GYMH</u>	28901
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28902
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28903
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28909
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPKGKAPKLLIYAASSLQSGVPSRFS SGSGTDFTLTISSLPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK	28904
vlCDR1	<u>RASQDISRLLA</u>	28905
vlCDR2	<u>AASSLQS</u>	28906
vlCDR3	<u>QQAQSF</u> <u>FWT</u>	28907
scFv	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPKGKAPKLLIYAASSLQSGVPSRFS SGSGTDFTLTISSLPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEW</u> <u>MGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSLRSED</u> <u>TAVVYCAR</u> <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS/GS	28908

Figure 24H

XENP024689 [anti-ICOS]_{L0.45_H0.37_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKSCASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVVYCAR <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS	28910
vhCDR1	<u>GYMH</u>	28911
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28912
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28913
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28919
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPKGAPKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK	28914
vlCDR1	<u>RASQDISRLLA</u>	28915
vlCDR2	<u>AASSLQS</u>	28916
vlCDR3	<u>QQAQSFPWT</u>	28917
scFv	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPKGAPKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QVQLVQSGAEVKKPGASVKSCASGYTFTGYMHVVRQAPGQGLEW</u> <u>MGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSLRSED</u> <u>TAVVYCAR</u> <u>TYYYDTSGYYHDAFDV</u> <u>WGQGTMTVTVSS</u> /GS	28918

Figure 24I

XENP024690 [anti-ICOS]_{L0.45_H0.68_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVTVSS	28920
vhCDR1	<u>GYMH</u>	28921
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28922
vhCDR3	<u>TYDDTSYYHDAFDV</u>	28923
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28929
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK	28924
vlCDR1	<u>RASQDISRLLA</u>	28925
vlCDR2	<u>AASSLQS</u>	28926
vlCDR3	<u>QQAQSFPT</u>	28927
scFv	DIQMTQSPSSVSASVGDRTITTCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVTVSS/GS	28928

Figure 24J

XENP024691 [anti-ICOS]_{L0.45_H0.35_scFv}

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVTVSS	28930
vhCDR1	<u>GYMH</u>	28931
vhCDR2	<u>WINPHSGGTNYAQKFQ</u>	28932
vhCDR3	<u>TYDDTSYYHDAFDV</u>	28933
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28939
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTITTCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK	28934
vlCDR1	<u>RASQDISRLLA</u>	28935
vlCDR2	<u>AASSLQS</u>	28936
vlCDR3	<u>QQAQSFPT</u>	28937
scFv	DIQMTQSPSSVSASVGDRTITTCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYYCARTYYDDTSYYHDAFDVWGQGTMTVTVSS/GS	28938

Figure 24K

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYVCARTYYDSSGGYHDAFDVWGQGTMTVTSS	28940
vhCDR1	<u>GYMH</u>	28941
vhCDR2	<u>WINPHSGGTNYAQKFQG</u>	28942
vhCDR3	<u>TYDSSGGYHDAFDV</u>	28943
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28949
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK	28944
vlCDR1	<u>RASQDISRLLA</u>	28945
vlCDR2	<u>AASSLQS</u>	28946
vlCDR3	<u>QQAQSFPT</u>	28947
scFv	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLAWYQQKPKGKAPKLLIYAASSLQSGVPSRFSGSGGTDFLTISLQPEDFATYYCQQAQSFPTFTFGQGTKEIK/GKPGSGKPGSGKPGSGKPGS/QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLRSDDTAVYVCARTYYDSSGGYHDAFDVWGQGTMTVTSS/GS	28948

Figure 24L

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

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVVYCAR <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS	28950
vhCDR1	<u>GYMH</u>	28951
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28952
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28953
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28959
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQISIRLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGGTDFTLTISSLQPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK	28954
vlCDR1	<u>RASQISIRLLA</u>	28955
vlCDR2	<u>AASSLQS</u>	28956
vlCDR3	<u>QQAQSF</u> <u>FWT</u>	28957
scFv	DIQMTQSPSSVSASVGDRTTITCRASQISIRLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGGTDFTLTISSLQPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGQGLEW</u> <u>MGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSSLRSED</u> <u>TAVVYCAR</u> <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS/GS	28958

Figure 24M

XENP024694 [anti-ICOS]_L0.47_H0.40_scFv

What	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGGQGLEWMGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELS SLRSED TAVVYCAR <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS	28960
vhCDR1	<u>GYMH</u>	28961
vhCDR2	<u>WINPHSGETNYAQKFQ</u>	28962
vhCDR3	<u>TYYYDTSGYYHDAFDV</u>	28963
scFv linker	<u>GKPGSGKPGSGKPGSGKPGS</u>	28969
Variable light (vl) domain	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPGKAPKAPKLLIY <u>SASSLQSGVPSRFSGSGGTDFTLTIS</u> LQPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK	28964
vlCDR1	<u>RASQDISRLLA</u>	28965
vlCDR2	<u>SASSLQ</u>	28966
vlCDR3	<u>QQAQSF</u> <u>FWT</u>	28967
scFv	DIQMTQSPSSVSASVGDRTTITCRASQDISRLLA WYQQKPGKAPKAPKLLIY <u>SASSLQSGVPSRFSGSGGTDFTLTIS</u> LQPEDFATYYCQQA <u>QSFPWT</u> FGQGTKVEIK/ <u>GKPGSGKPGSGKPGSGKPGS</u> / <u>QVQLVQSGAEVKKPGASVKVCKASGYTFTGYMHVVRQAPGGQGLEW</u> <u>MGWINPHSGETNYAQKFQGRVTMTTRDTSISTAYMELSLRSED</u> <u>TAVVYCAR</u> <u>TYYYDTSGYYHDAFDV</u> WGQGTMTVTVSS/GS	28968

Figure 25

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 (SEQ ID NOS 26362-26366)
 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGGQGLEWMGMWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELSRRLSRDSDTAVYYCARTYYVDSSG
YYHDAFEDIWGGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSDT
 KVDKKVEPKSCDKTHCTCPCPAPPVAGPSVFLFPPKPKDGLMISRTPEVTCVVDVKHEDPEVKFNWVVDGVEVHNAKTKPREEEYNSTYRVSVLTVLHQDWLNGKEYK
 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSPDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQQGDVFCSCVLHEAL
 HSHYTKQSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26367-26376)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPKGQAPRLLINYYASHRYTGVDPDRFTGSGYGTFTLTISVQSEDFGVVYCCQDFFSPRTFGGGTKVEIK/GKPG
 SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYYWMNWWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMINNLKTED
 TGVVYCTRYGNYGGYFDVWGRGTLTVSS/EPKSSDKTHCTCPCPAPPVAGPSVFLFPPKPKDGLMISRTPEVTCVVDVKHEDPEVKFNWVVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTKLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFCSCVLHEALHSHYTKQSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26377-26381)
 DIQMTQSPSSVSASVGDRTVITCRASQGISRLLAWYQQKPKGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGGQTKVEIK/RTVAA
 PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEHKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 26B**XENP23377**

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26382-26386)
 EVQLVESGGGLVQPGGSLRLSCAASGFTSSVSMNWVRQAPGKGLEWVSYISSSSTIDYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVVYCARESGWYLFDYWGQ
 GTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHHKPSDTKVDKKVEPKSCDK
 THTCPCPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVCKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEK
 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSFGFYPSDIAVEWESDGGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSP
 GK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26387-26396)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPKGQAPRLLIN^YASHRYTGV^PDRFTGSGYGTEFTLTIS^SVQSEDFGVVYCQ^QQDFSSPRTFGGGTKVEIK/GKPG
SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSN^YWMNWVRQAPGKGLEWVAE^IRLYSNNYATHYAESVKG^RFTISRDDSKSTLYLQMNNLKTED
 TGVVYCTRYGNYGGYFDVWGRGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVCKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQV^KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26397-26401)
 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLA^WYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFLT^ISSLPEDFATY^CQQYN^SYPPTFGGGTKVEIK/RTVAA
 PSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS^TYSLS^TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 26C**XENP23378**

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26402-26406)
 QVTLKESGPGILKPSQTLSTCSFSGFSLSTSGMGV/GWIRQPSGKGLEWLAHIW/DDDDKY^{SP}SLKSQLTISKDTSRNQVFLKITS^{LD}TADTATYYC^{VR}SYYYGSSGAMDY^W
 GQGTSVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSDTKVDKKVEPKS
 CDKTHTCPPCPAPPVAGPSVFLFPPKPKD^{TL}MISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAA
 PIEKTSKAKGQPREPQVY^{TL}PPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYK^{TT}PPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNH^{YT}QKSL
 SLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26407-26416)
 EIVLTQSPATLSASPGERV^{TL}TCRASQSVGNDVAWYQQKPKGQAPRLLIN^YASHRY^{TG}VPDRFTGSGYGTEFTLTIS^{SV}QSEDFGVY^{CQ}QDFSSPRTFGGGTKVEIK/GKPG
SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSN^YWMNWVRQAPGKGLEWVAEIRLYSN^{NY}ATHYAESVKG^{RFT}ISRDDSKSTLYLQMN^NLKTED
 TGVYCYTRYGN^YGGYFDVWGRGTLVTVSS/EPKSSDKTH^{TC}PPCPAPPVAGPSVFLFPPKPKD^{TL}MISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTSKAKGQPREPQVY^{TL}PPSREQMTKNQV^{KL}TCLVKGFYPSDIAVEWESNGQPENNYK^{TT}PPVLDSDGSFFL
 YSKLTVDKSRWQQGNV^FSCVMHEALHNH^{YT}QKSLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26417-26421)
 DIVMTQTPLSLPVSLGDQASISCRSSQSLVHSDGNTY^LHWY^LQKPGQSPKLL^{NY}KVSKRFS^{GV}PDRFSGSGGTDF^{TL}LKISRVEAEDLG^VYFCSQSTHVPPTFGGGTKLEIK/R
 TVAAPS^VFIFPPSDEQLKSGTASV^VCLLNNFY^PREAKVQWKVDNALQSGNSQESVTEQDSKDS^{TS}LSSTLSKADYEKHK^VYACEVTHQGLSSP^VTKSFNRGEC

Figure 26D**XENP23379**

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26422-26426)
 QVQLQQWGAGLLKPSETLSLTCAVYGGFSFGYYWSWIROSPEKGLEWIGEINHGYYVTYNPSLESRVTISVDTSKNQFSLKSSVTAADTAVYYCARDYGPNGYDWYFDL
 WGRGTLTVTSS/ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSDTKVDKKVEPK
 SCDKTHTCPAPPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALP
 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHHTQKS
 LSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26427-26436)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPKGQAPRLLINYYASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVVYCCQQDFSSPRTFGGGTKVEIK/GKPG
SGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYYWMNWWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTED
 TGVYCYTRYGNYGGYFDVWGRGTLTVTSS/EPKSSDKTHTCPAPPVAGPSVFLFPKPDKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL
 YSKLTVDKSRWQQGNVFCFSVMHEALHNHHTQKSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26437-26441)
 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPKGQAPRLLIYDASNRAITGIPARFSGSGGTDFLTITSSLEPEDFAVYYCQQQRSNWPPALTFGGGTKVEIK/RTVA
 APSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSLSPVTKSFNRGEC

Figure 27

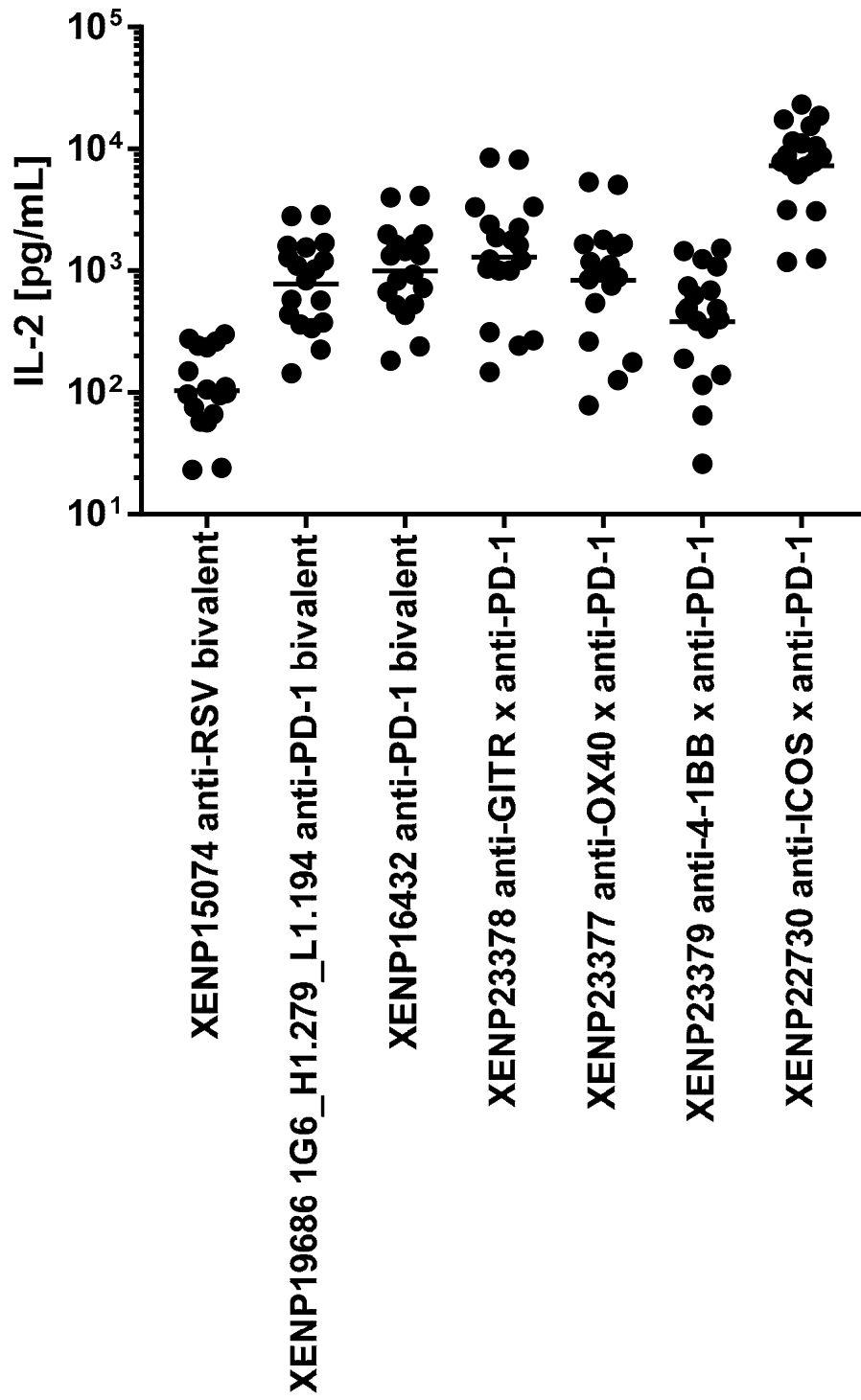


Figure 28

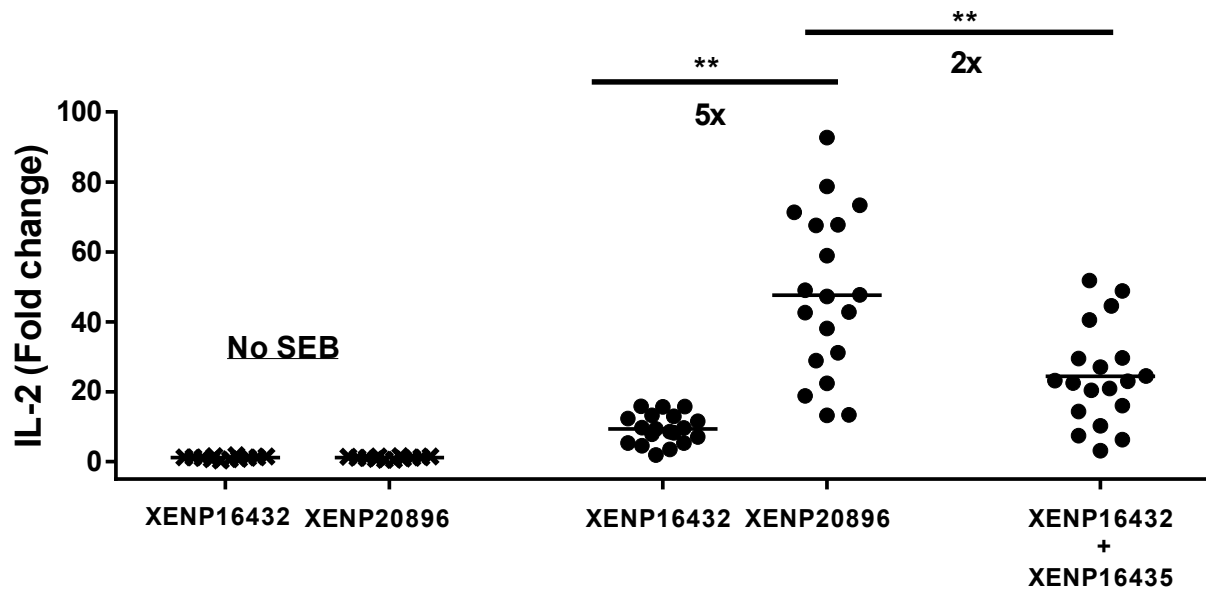


Figure 29

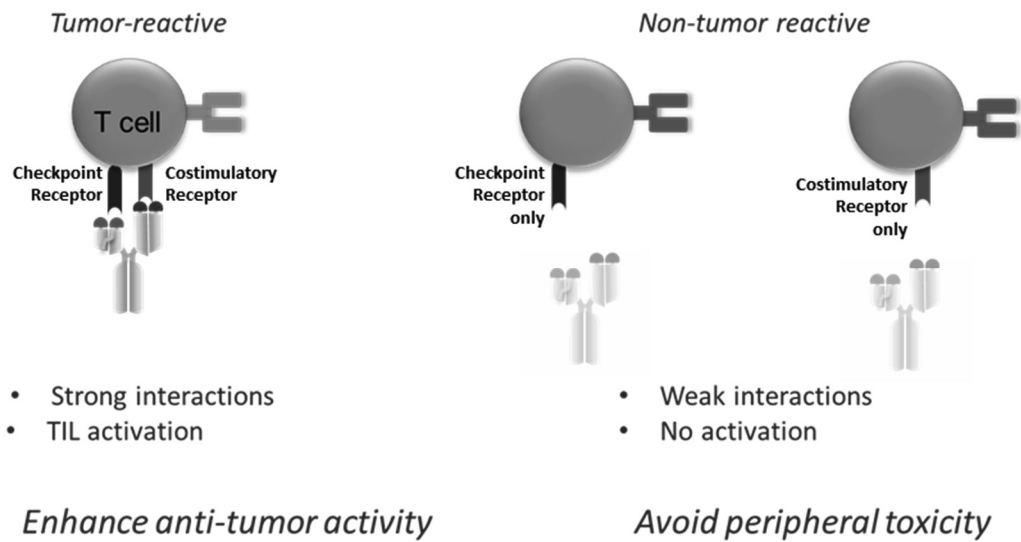


Figure 30

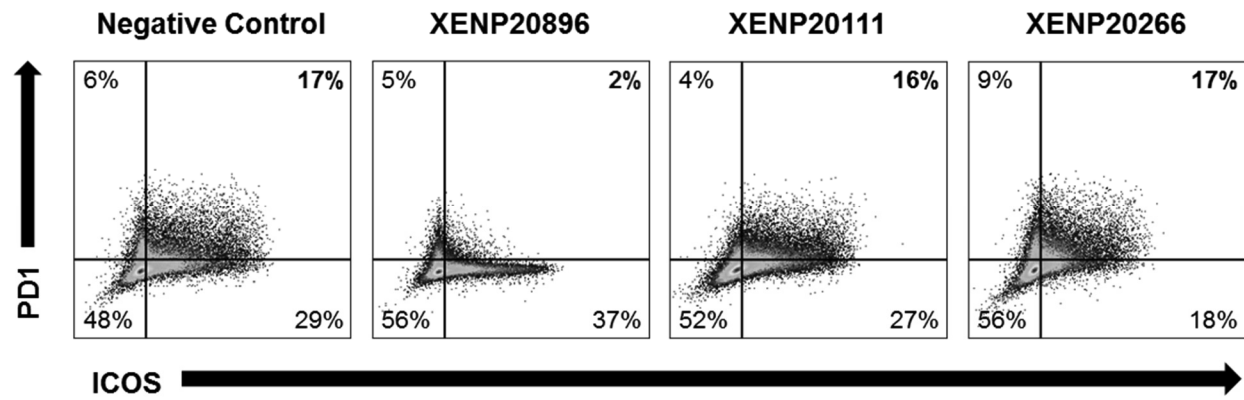


Figure 31A

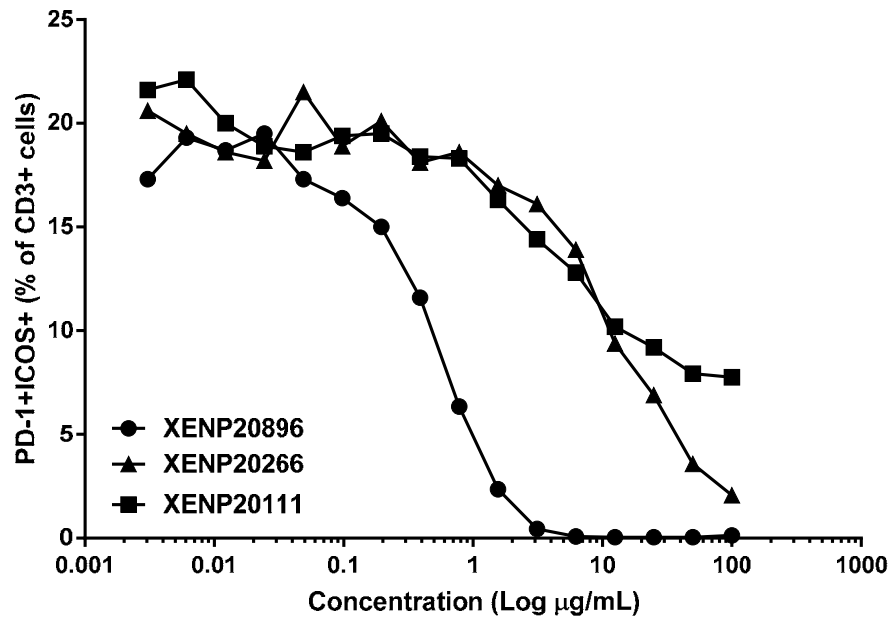


Figure 31B

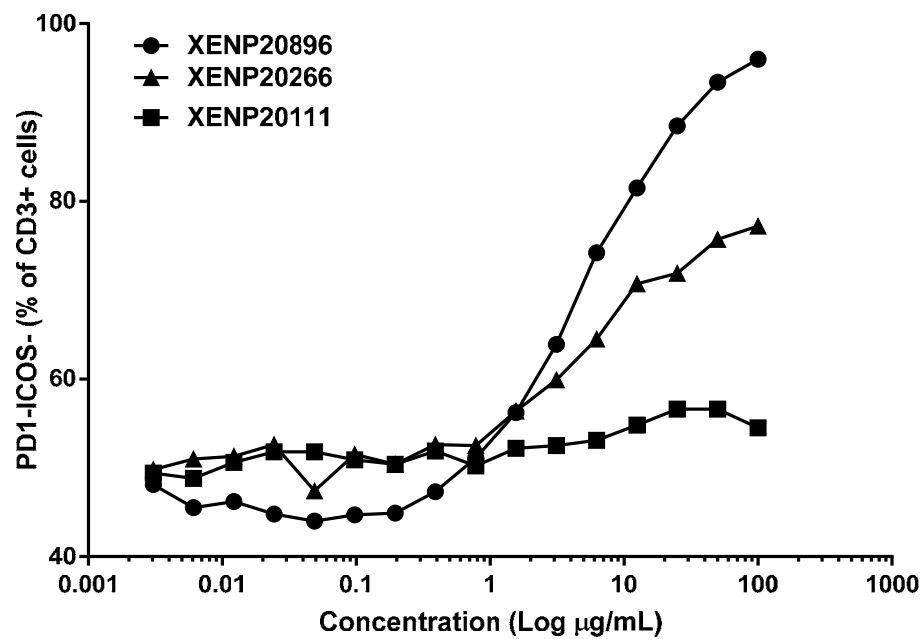


Figure 32A**XENP20896**

>XENP020896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26442-26446)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYIDSSGYHDAFDIWGQGTMTVTS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSG
SFFLYSKLTVDKSRWEQGDVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP020896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26447-26456)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCYTRYGNYYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTKLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP020896 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26457-26461)
DIQMTQSPSSVSASVGDRVTTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKSDSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22433

>XENP022433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26462-26466)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYIDSSGYHDAFDIWGQGTMTVTS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSG
SFFLYSKLTVDKSRWEQGDVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP022433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26467-26476)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCYTRYGNYYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTKLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP022433 [ICOS]_H0_L0.7_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26477-26481)

DIQMTQSPSSVSASVGDRVTTITCRASQGISSYLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKSDSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32B**XENP22744**

>XENP022744 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26482-26486)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022744 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26487-26496)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022744 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26497-26501)

DIQMTQSPSSVSASVGDRTITCQASQDISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22746

>XENP022746 [ICOS]_H0_L0.36_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26502-26506)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022746 [ICOS]_H0_L0.36_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26507-26516)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022746 [ICOS]_H0_L0.36_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26517-26521)

DIQMTQSPSSVSASVGDRTITCQASQDISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32C**XENP22747**

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26522-26526)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26527-26536)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCYTRYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022747 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26537-26541)

DIQMTQSPSSVSASVGDRTITCQASQDISRLRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22748

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26542-26546)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26547-26556)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCYTRYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022748 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26557-26561)

DIQMTQSPSSVSASVGDRTITCQASQDISRLRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 32D**XENP23092**

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26562-26566)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSISTAYME
LSSLRSED^TAVYYCARTYYYDTS^GYYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26567-26576)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSN^NYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG^VYYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQV^KLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP023092 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26577-26581)

DIQMTQSPSSVSASVGDRTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQANSFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDS^TYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23410

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26582-26586)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSISTAYME
LSSLRSED^TAVYYCARTYYYDTS^GYYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26587-26596)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSN^NYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG^VYYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQV^KLTCLVKGFYP
SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP023410 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26597-26601)

DIQMTQSPSSVSASVGDRTITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDS^TYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 33A**XENP22730**

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26602-26606)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWQGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26607-26616)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVDFSC
VLHEALHSHYTQKSLSLSPGK

>XENP022730 [ICOS]_H0L0_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26617-26621)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP22974

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26622-26626)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWQGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26627-26636)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRY
GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREMQTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVDFSC
VLHEALHSHYTQKSLSLSPGK

Figure 33B

>XENP022974 [ICOS]_H0_L0.34_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26637-26641)

DIQMTQSPSSVSASVGDRVITITCQASQDISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQAESFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP23104

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26642-26646)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYYDTSGLYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCSVLHEALHSHYTQKSLSLSPGK

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26647-26656)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVTSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSC
VLHEALHSHYTQKSLSLSPGK

>XENP023104 [ICOS]_H0.66_L0_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26657-26661)

DIQMTQSPSSVSASVGDRVITITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP23411

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NOS 26662-26666)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSIS
TAYMELSSLRSEDTAVYYCARTYYYDTSGLYHDAFDVWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCSVLHEALHSHYTQKSLSLSPGK

Figure 33C

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NOS 26667-26676)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTISS
 VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
 GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
 GNYGGYFDVWGRGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREQMTKNQVKLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 CS
 VLHEALHSHYTQKSLSLSPGK

>XENP023411 [ICOS]_H0.66_L0.34_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NOS 26677-26681)

DIQMTQSPSSVSASVGDRVTITCQASQDISRLLEAWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTDFTLT
 ISS
 LQPEDFATYYCQQAESFPWTFGQGTKVEIK/RTVAAPSVPFIAPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 34A

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

Figure 34B

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

Figure 34C

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

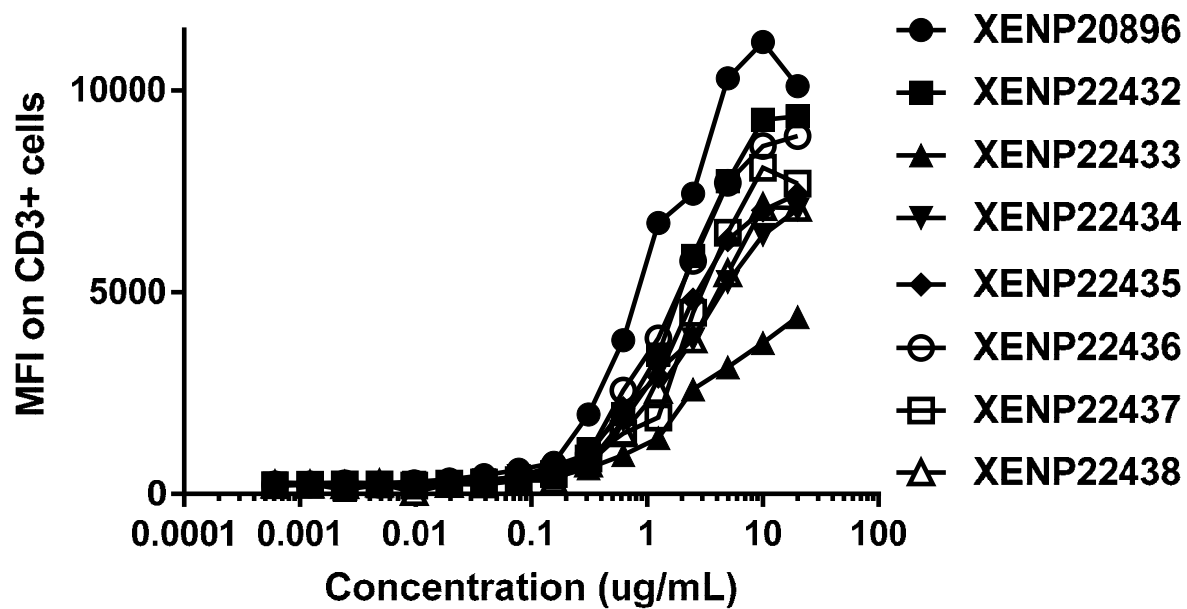


Figure 36B

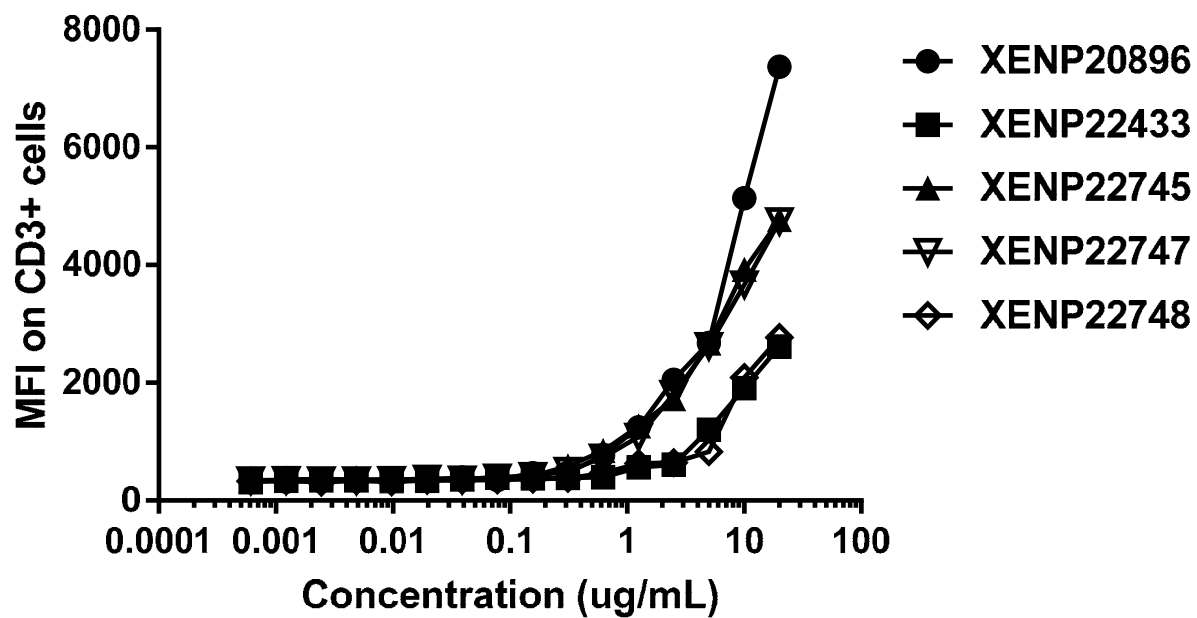


Figure 37

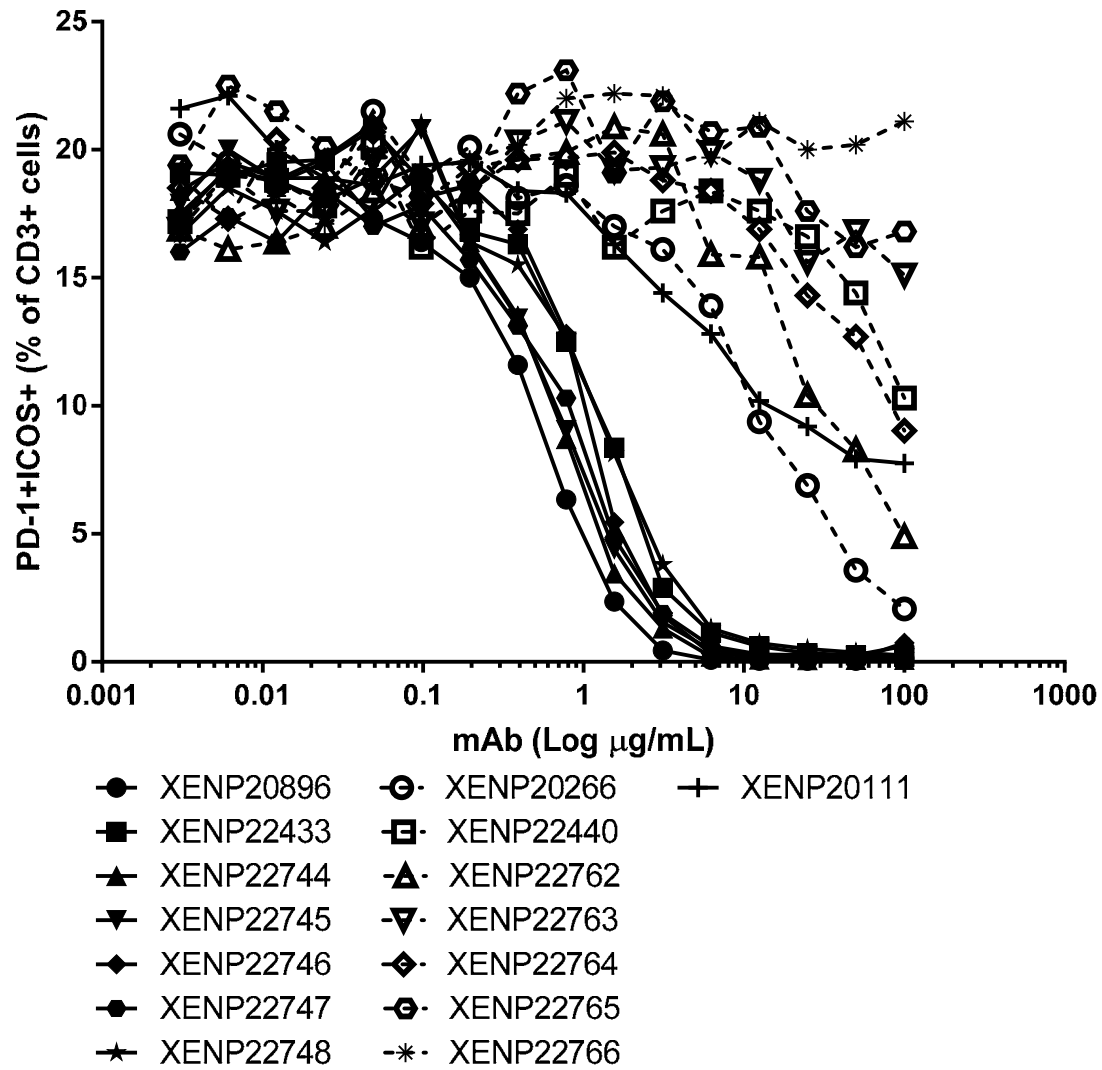


Figure 38A

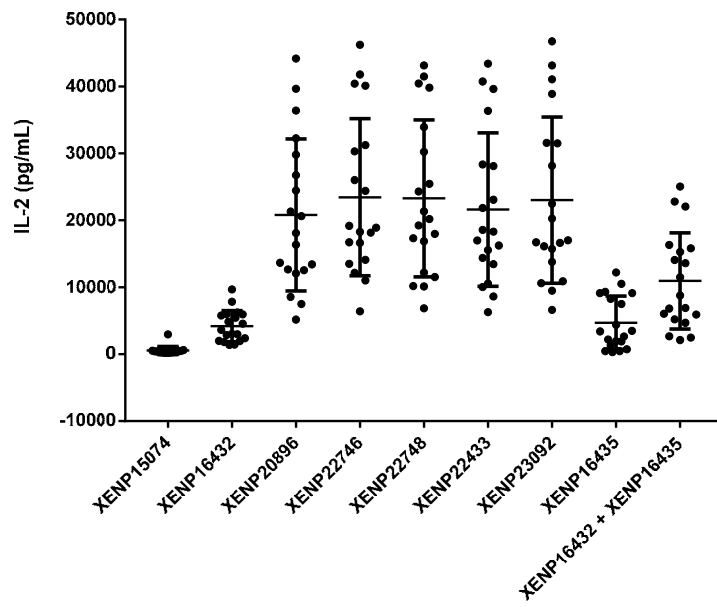


Figure 38B

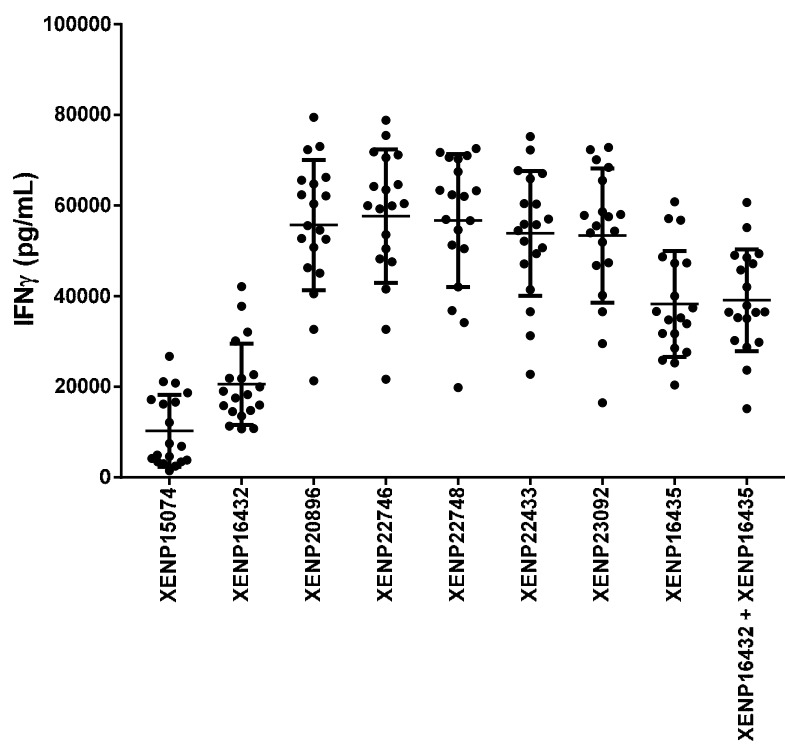


Figure 39A

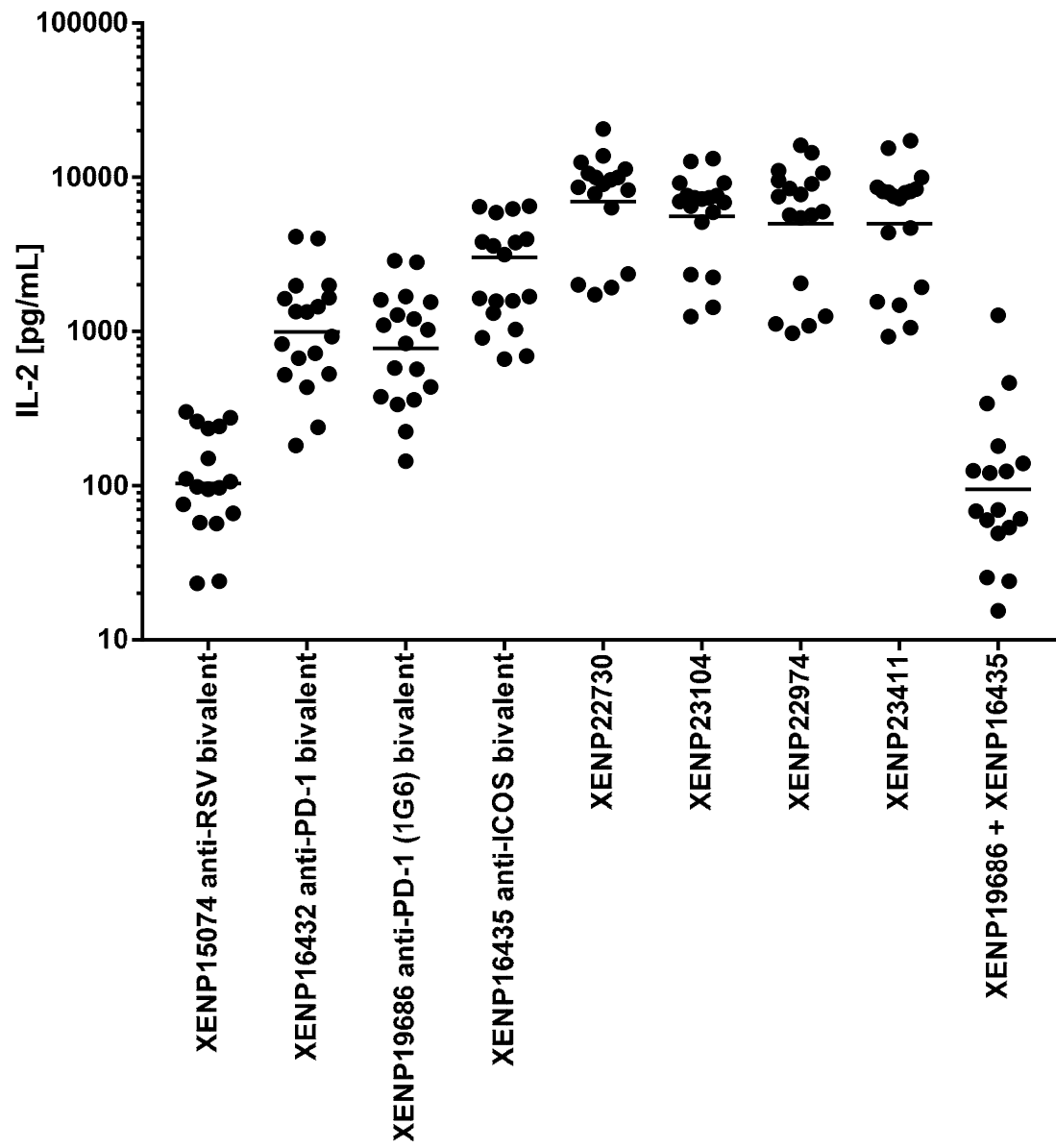


Figure 39B

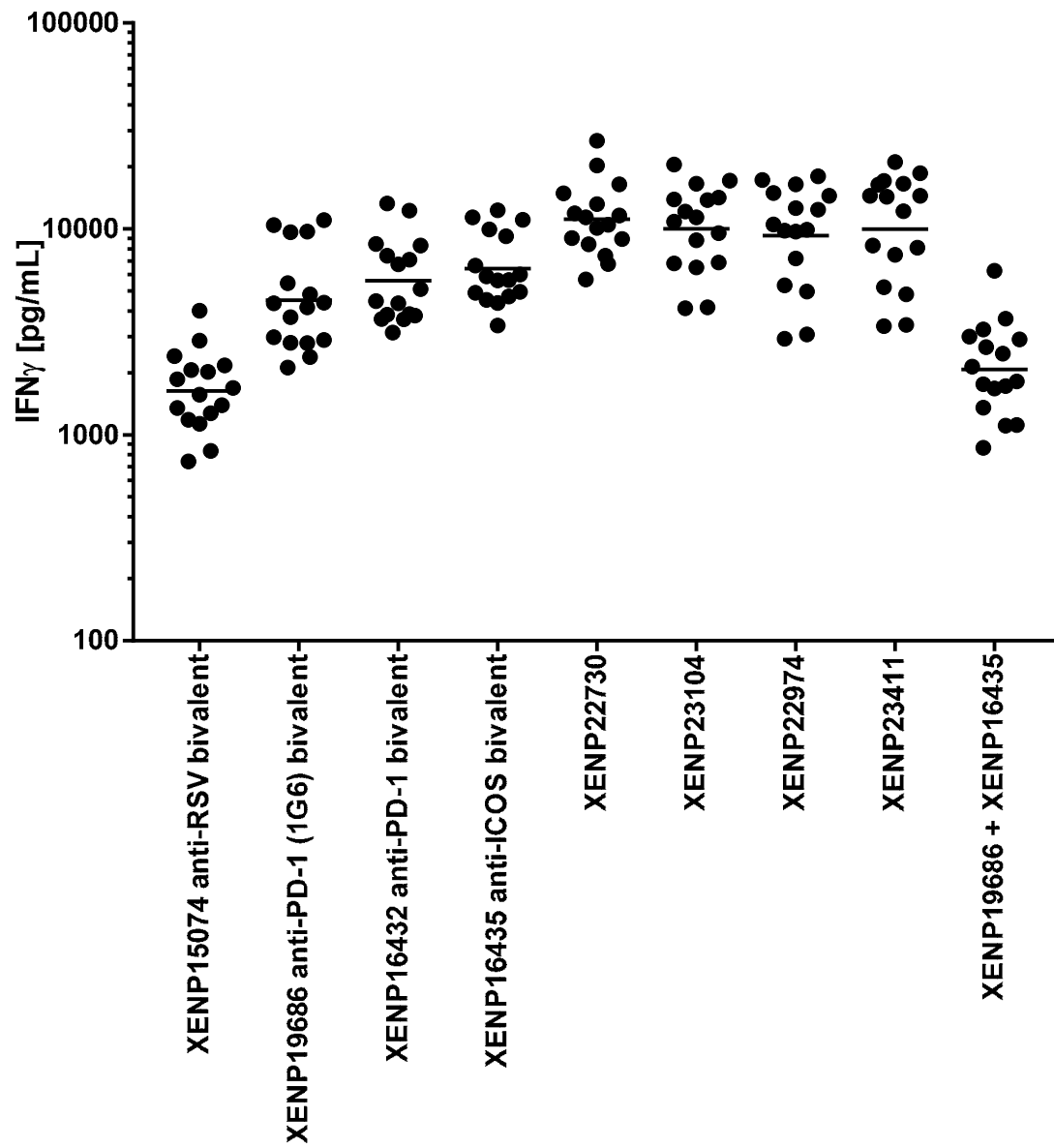


Figure 40A

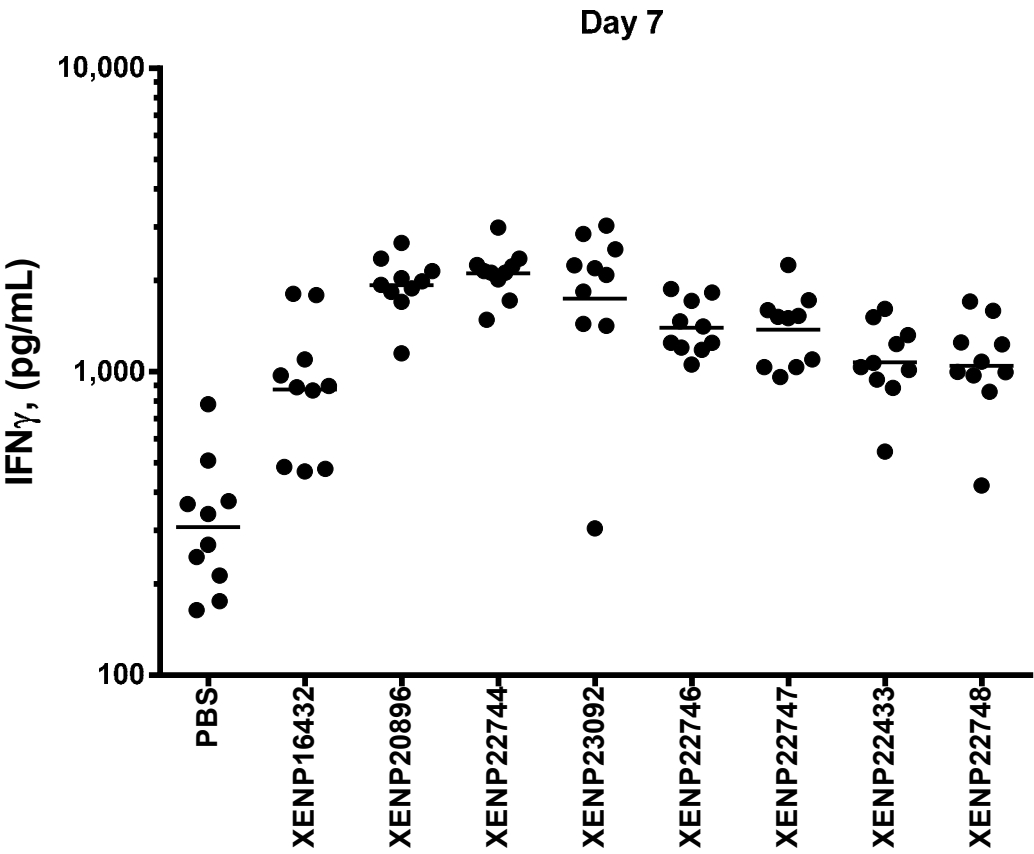


Figure 40B

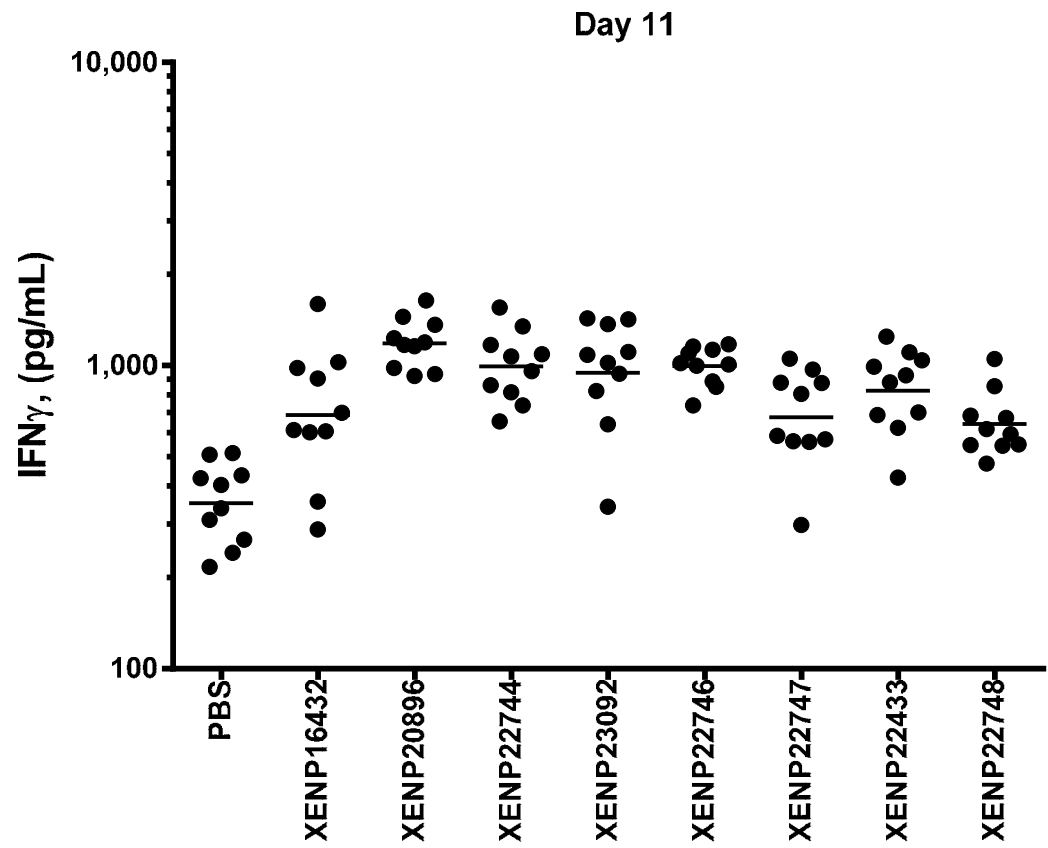


Figure 41A

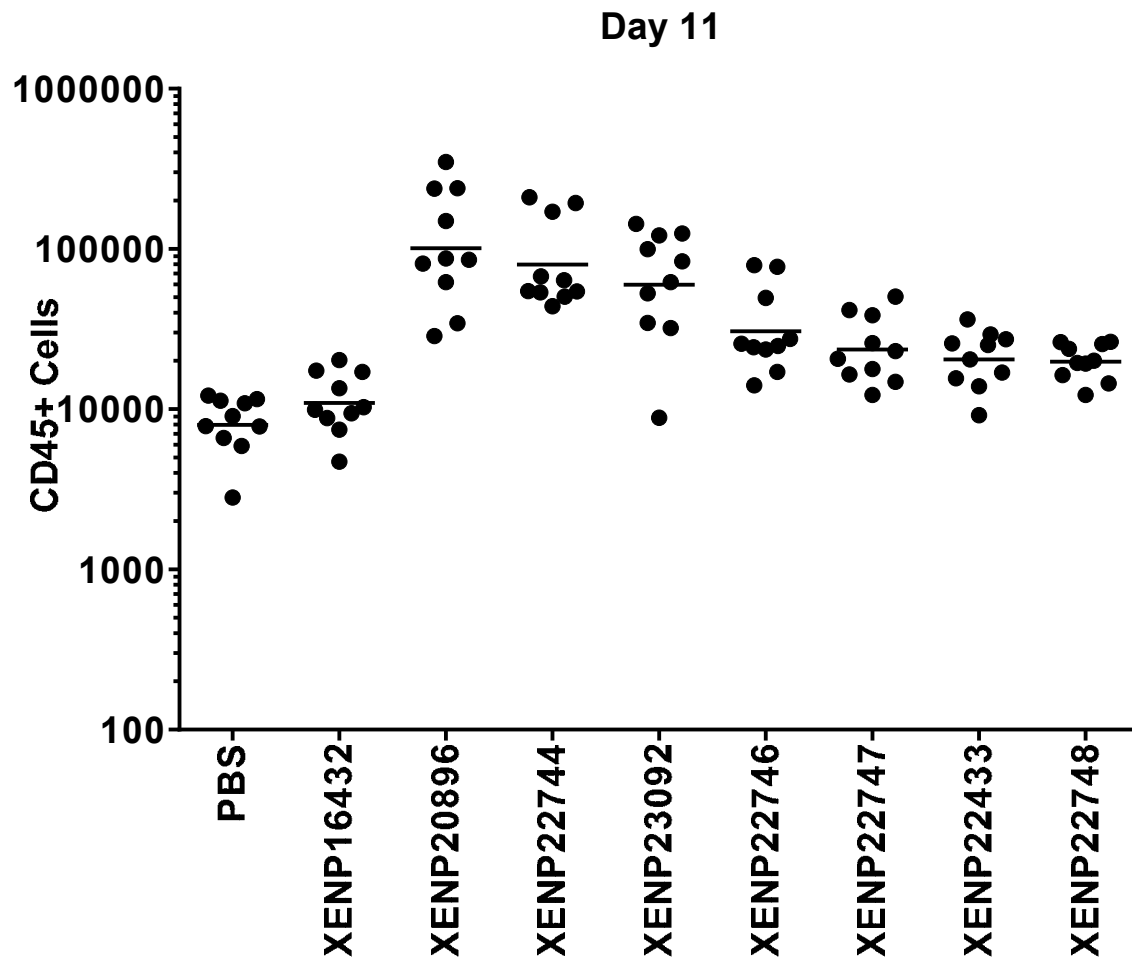


Figure 42A

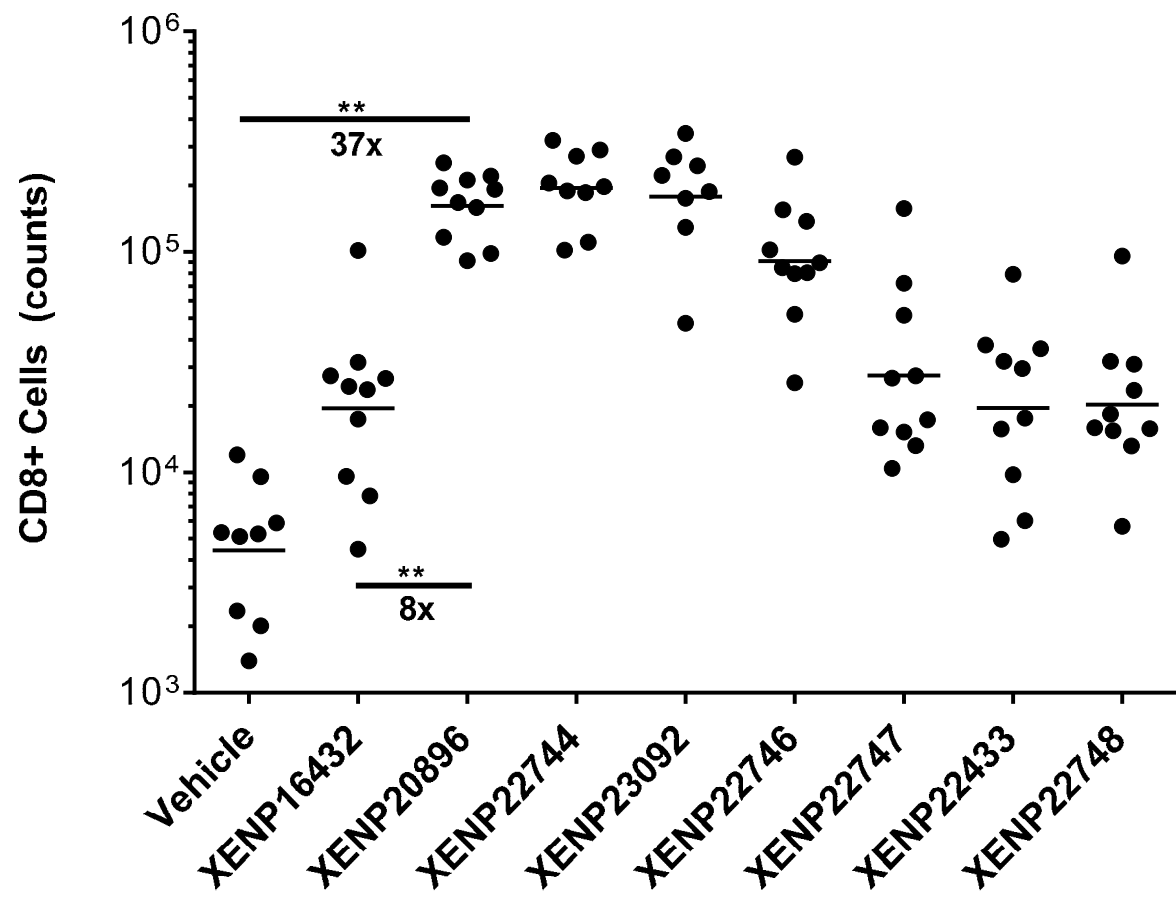


Figure 42B

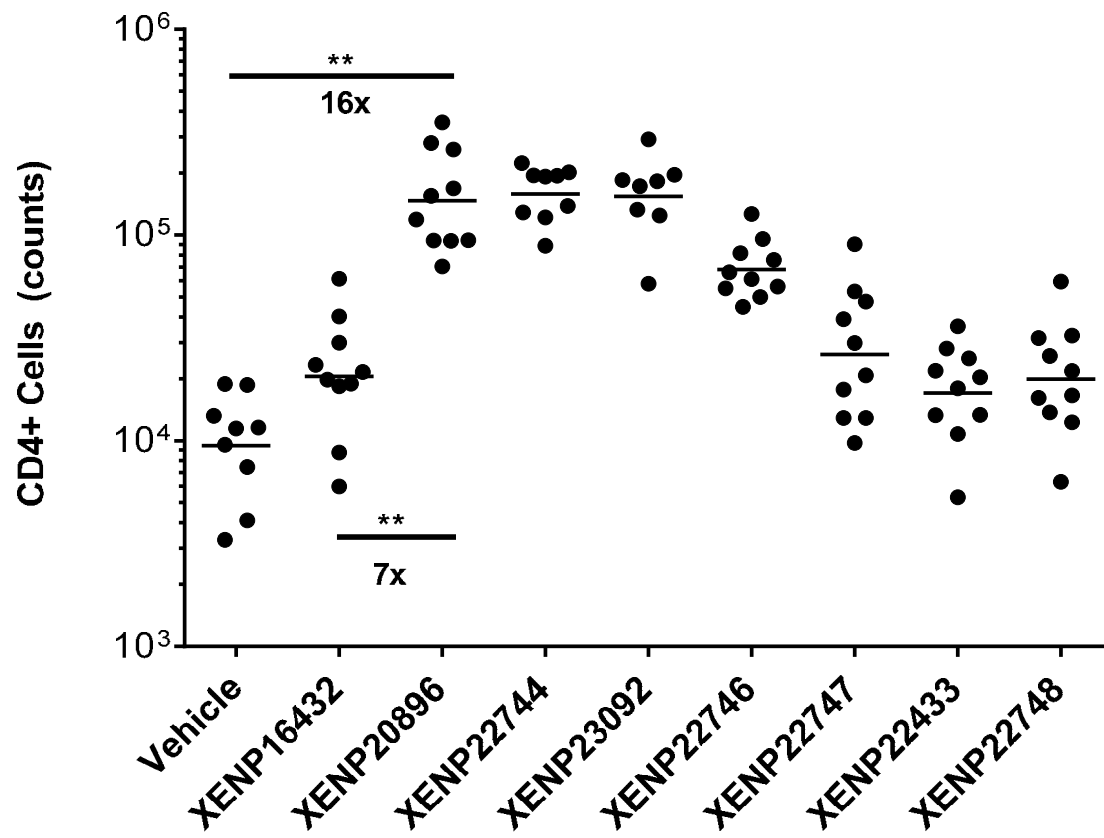


Figure 43

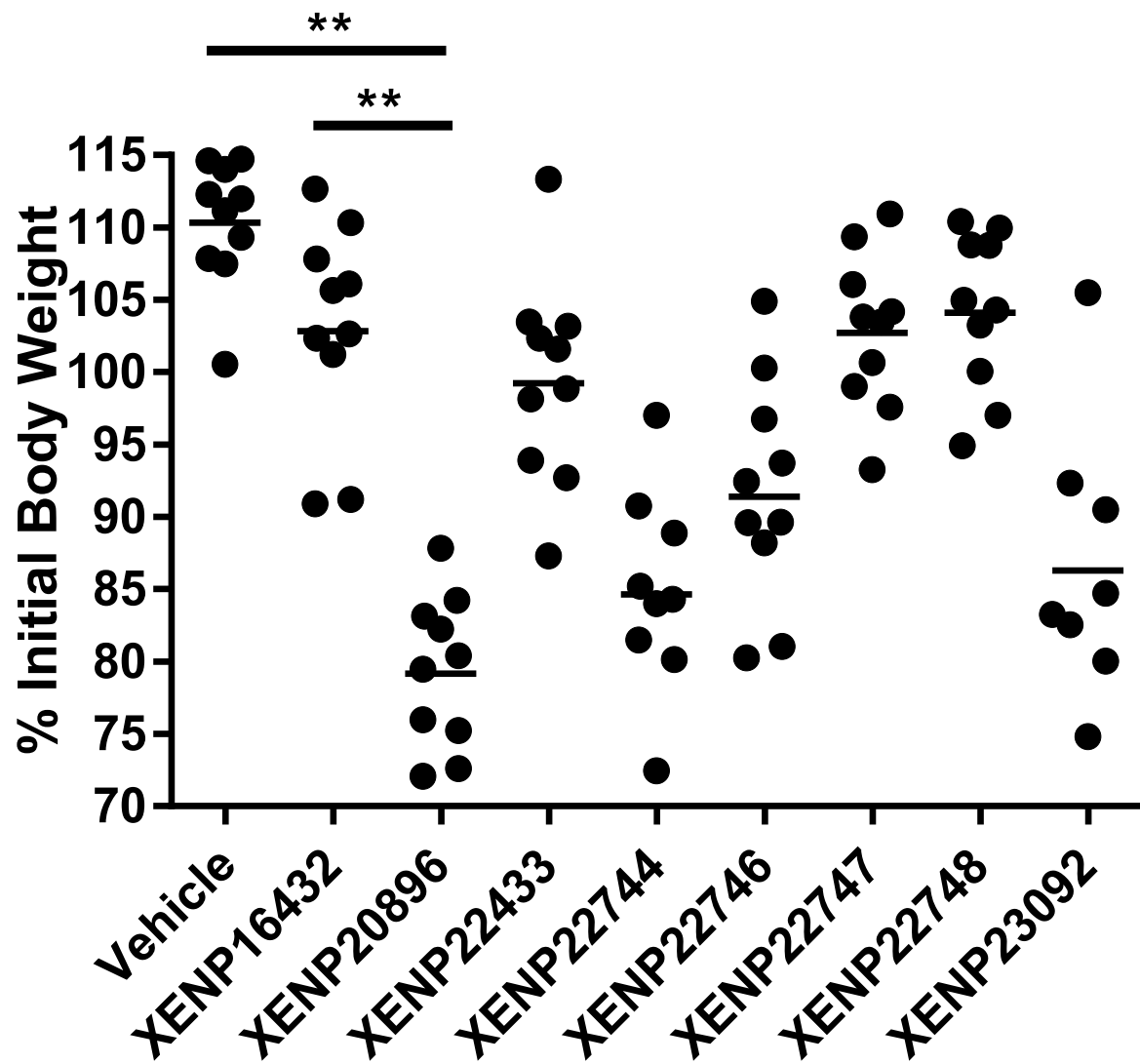


Figure 44A

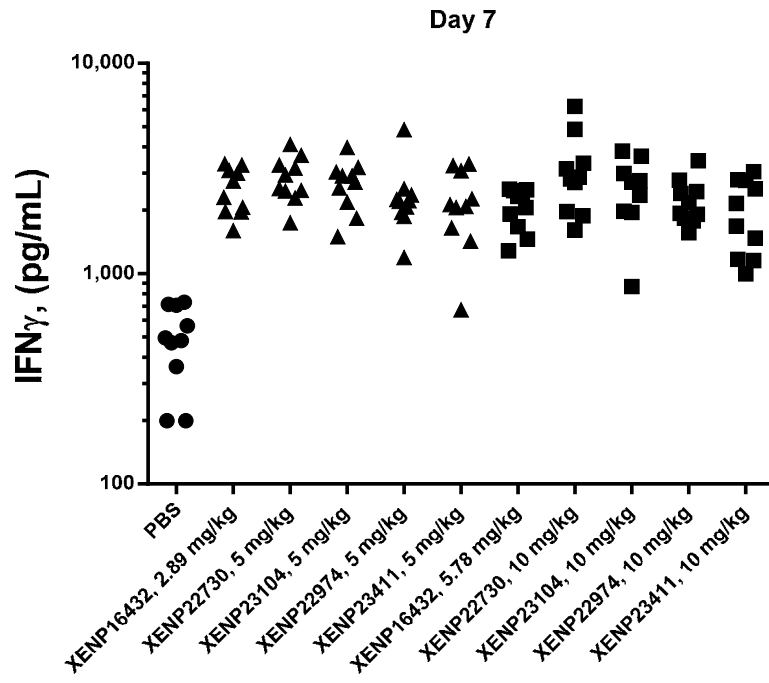


Figure 44B

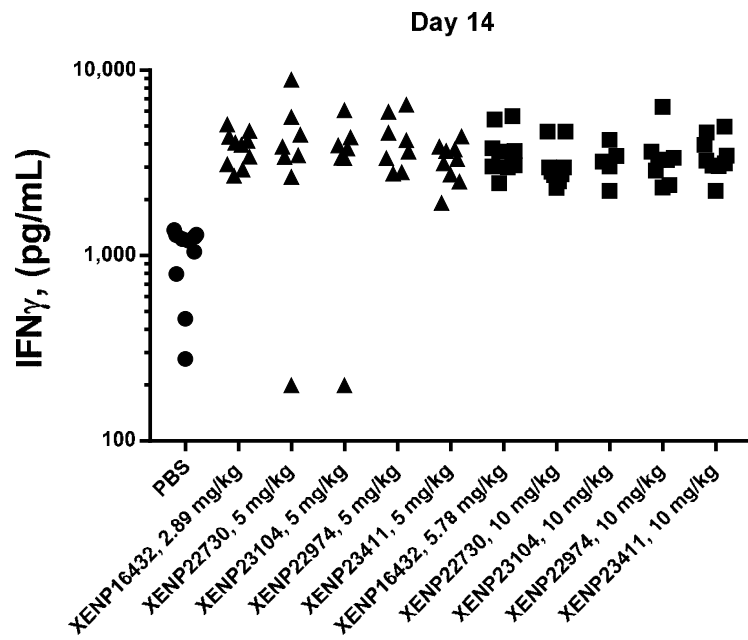


Figure 45

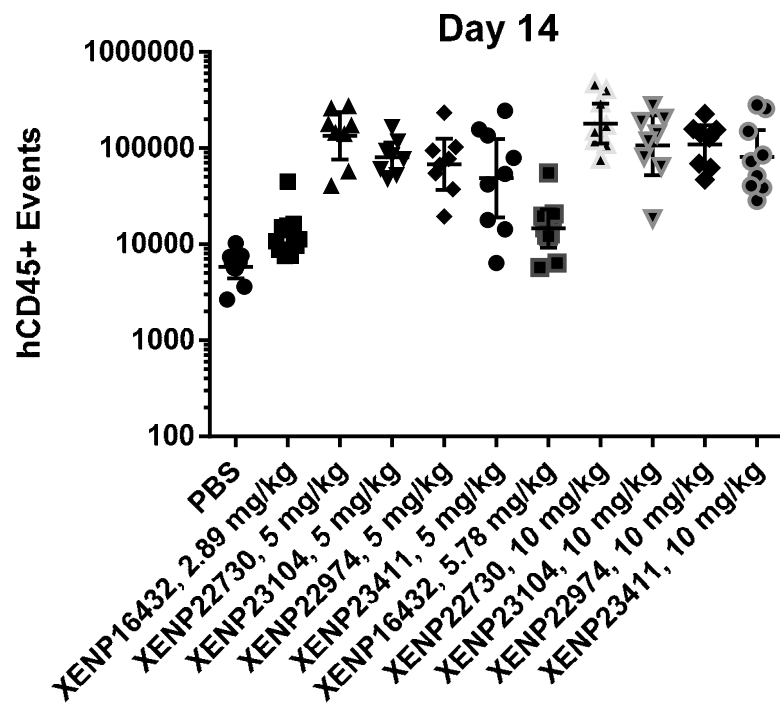


Figure 46A

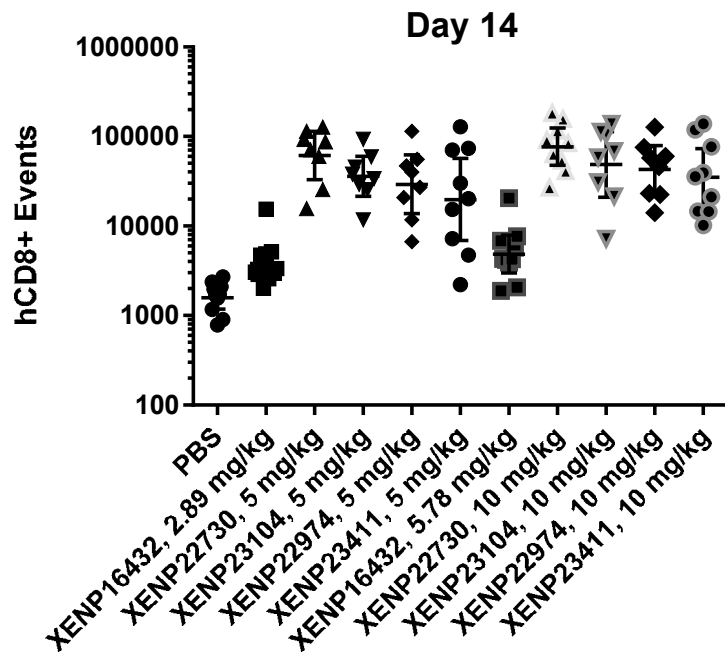


Figure 46B

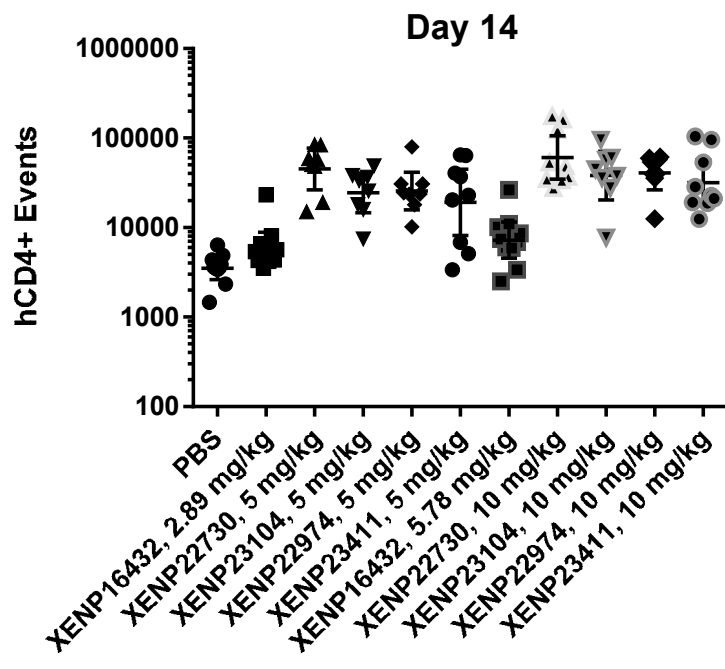


Figure 46C

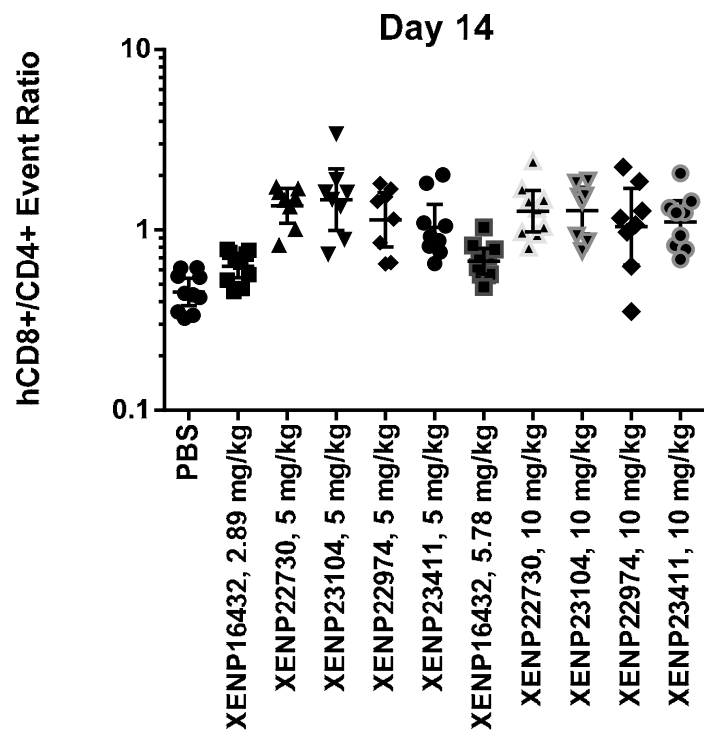


Figure 47A

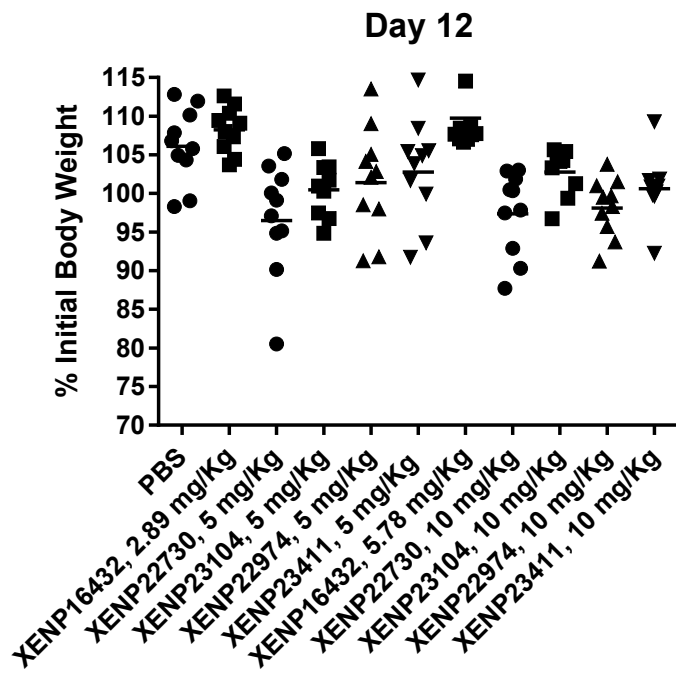


Figure 47B

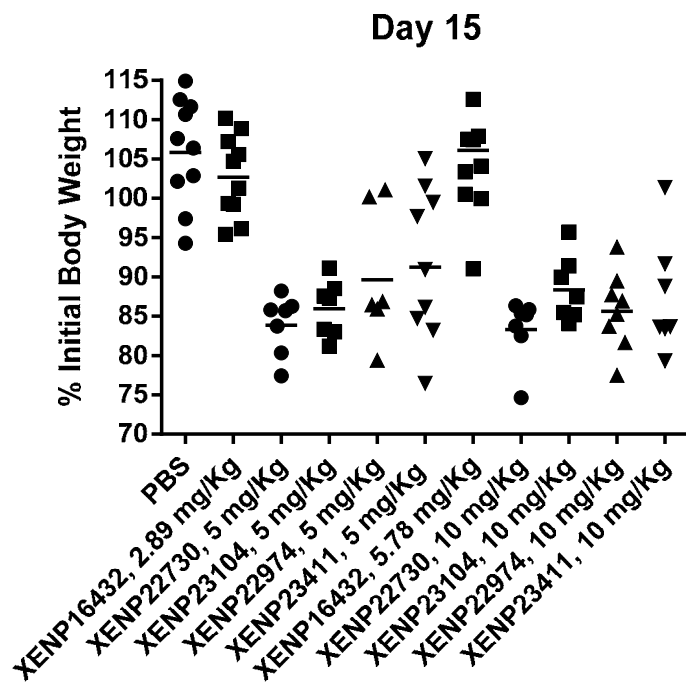


Figure 48A

XENP21828

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
(SEQ ID NOS 26682-26686)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQ
LSSLTSEDSAVYFCARSPDIYGTSLAWFDYWGQGTTLVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPPENNYKTTTPVLDSDGSF
FLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
(SEQ ID NOS 26687-26696)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID
NOS 26697-26701)

DIVMTQAAPSVPTPGESVVISCRSSKSPHLSNGNIYLYWFLQRPGQSPQLLIYRMSNLASGVPDRFSGSGSGTTFTLKISR
VEAEDGVGYCMQHLEYPYTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21829

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ
ID NOS 26702-26706)

QVQLQQPGAELVRPGASVKLSCKASGYSTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKD KATLTVDKSSNTAYMQ
LTSPSEDSAVYYCTRWNLSTYFDNNYYLDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDQGPPENNYKTTTPVLDSDGS
FFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
(SEQ ID NOS 26707-26716)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYNASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVCLTCLVKGFYP
SDIAVEWESNGQPPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

Figure 48B

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26717-26721)

DIVMTQAAPSVPTPGESVSISCRSSKSLLSNGNTYLYWFLQRPQGSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRISRVEAEDVGYYCMQHLEYPWTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21830

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26722-26726)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26727-26736)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTISLVQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAPGKLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCYTRYGNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26737-26741)

EIVLTQSPGTLSLSPGERATLSCRASQNISSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21831

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26742-26746)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 48C

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26747-26756)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26757-26761)

EIVLTQSPGTLISLSPGERATLSCRASQSISSSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22348

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26762-26766)

QVQLVQSGAEVKKPGSSVKVSKASGYTFTDYAMHWVRQAPGQGLEWMGLISIIYSDHTNYNQKFQGRVTITADKSTS
TAYMELSSLRSEDTAVYYCGRNNGNYGWYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDQGQENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26767-26776)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTIS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVAS
GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
GNYGGYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26777-26781)

EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISL
EPEDFAVYYCFQGSGLPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48D**XENP23059**

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
Fab-Fc Heavy Chain (SEQ ID NOS 26782-26786)

EVQLVESGGGLVQPGGSLRLSCAASGFTFS¹SDYWMDWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDNAKN
TLYLQMNSLRAEDTAVYYCTRWGRFGFDSWGQGT²LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSPGK

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
scFv-Fc Heavy Chain (SEQ ID NOS 26787-26796)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN¹YASHRYTGVPDRFTGSGYGTEFTLTISS
VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAS
GFTFS²SNYWMNWVRQAPGKGLEWVAEIRLYSN³NYATHYAESVKGRFTISRDDSKSTLYLQMN⁴NLKTEDTG⁵VYYCTRY⁶
GNYG⁷GYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQV⁸KLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP023059 Jounce_37A10S713[ICOS]_H0L0_Fab-1G6_[PD-1]_L1.194_H1.279_scFv
Light Chain (SEQ ID NOS 26797-26801)

DIVMTQSPDLSAVSLGERATINCKSSQSL¹LSGSFN²YLTWYQQKPGQP³PKLLIFYASTRHTGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY⁴PREAKVQWK
VDNALQSGNSQESVTEQDSK⁵DSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49

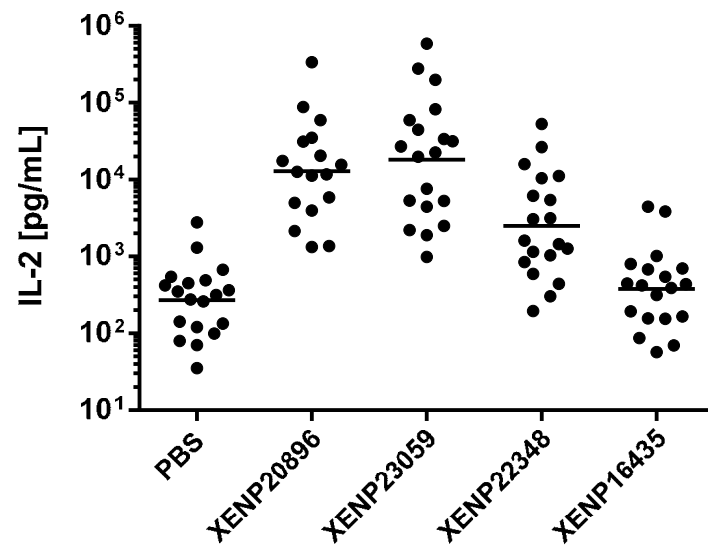


Figure 50

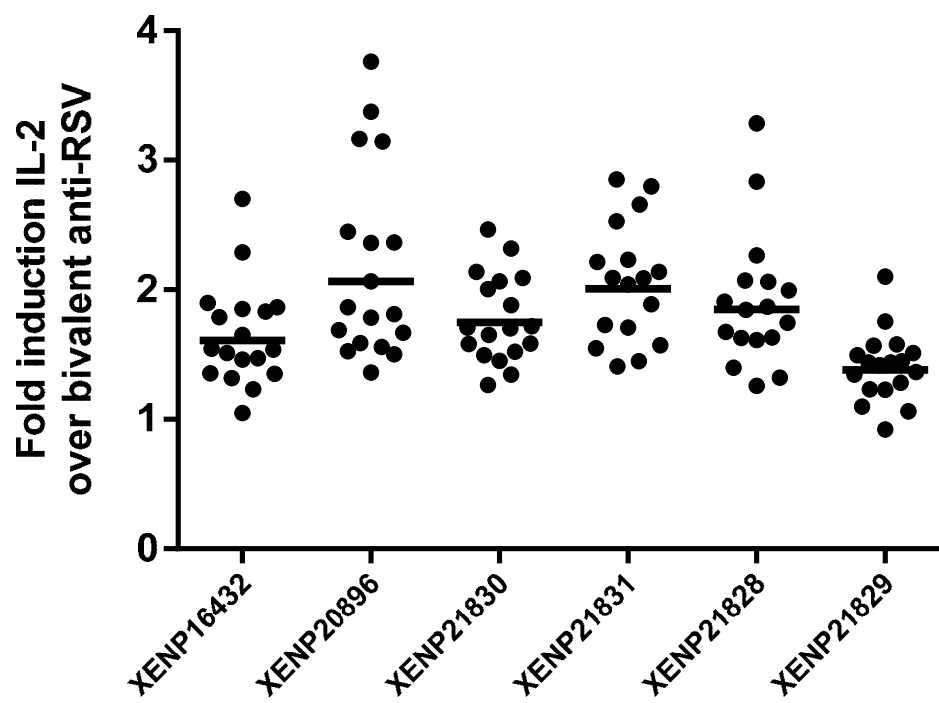


Figure 51

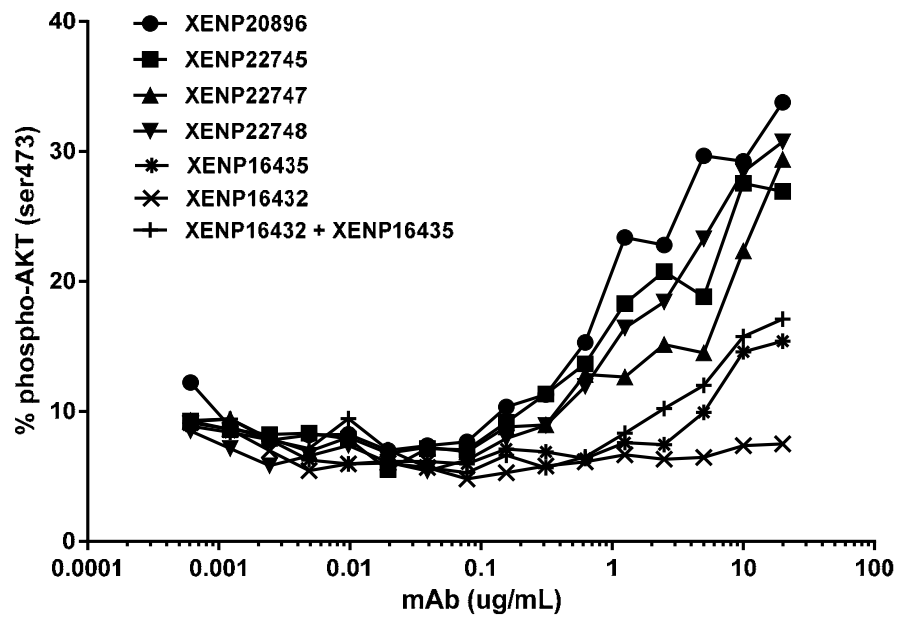


Figure 52

		XENP16435 +			
		XENP23104	XENP16435	XENP19686	XENP19686
Th17	IL17A	14.6	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

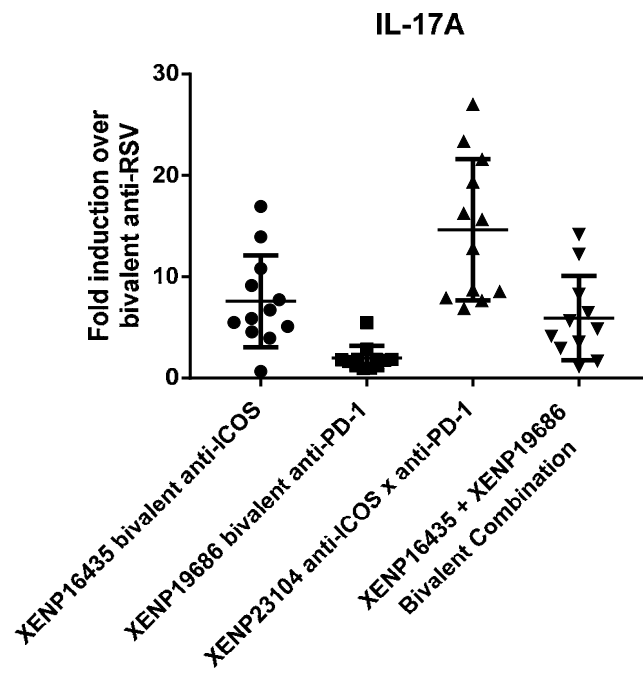


Figure 53B

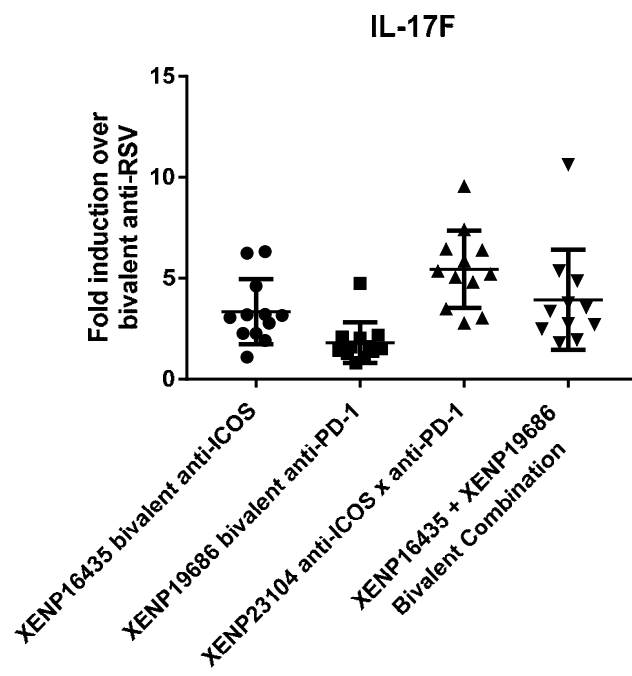


Figure 53C

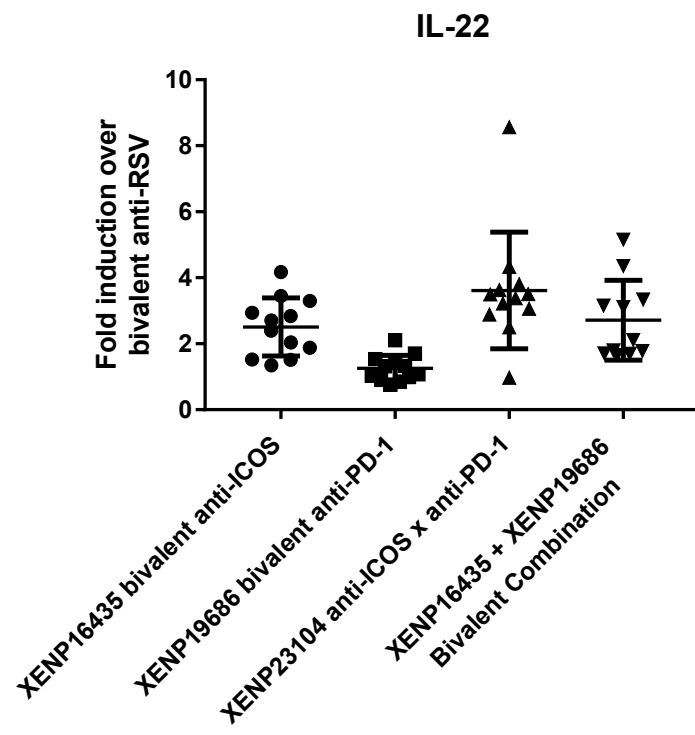


Figure 53D

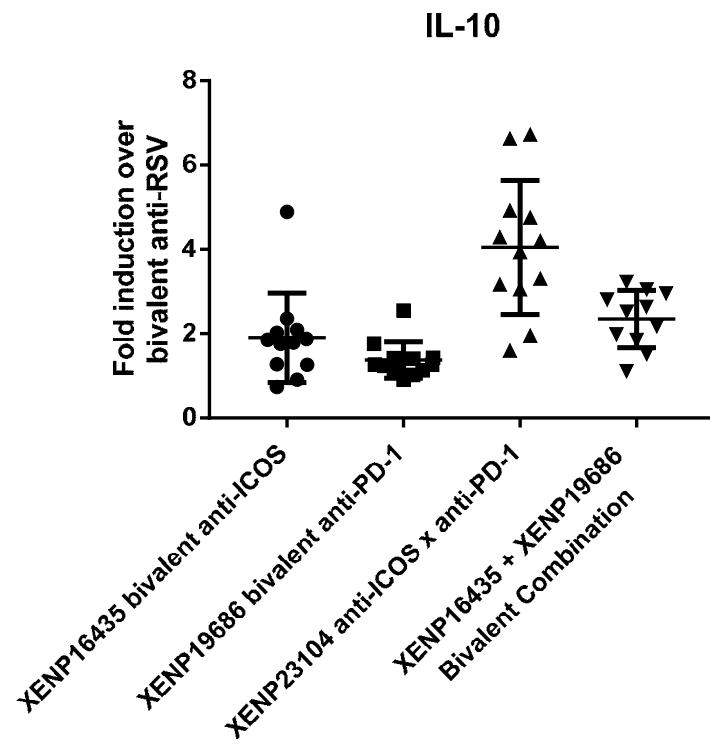


Figure 53E

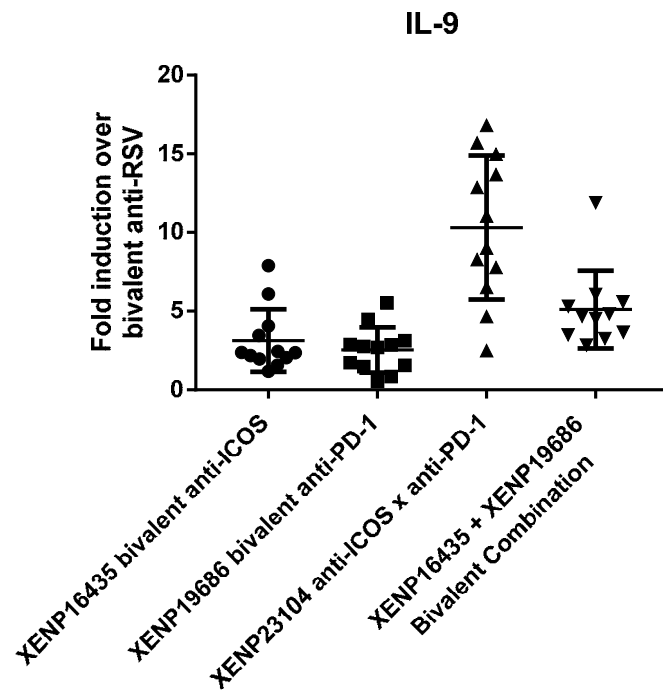


Figure 53F

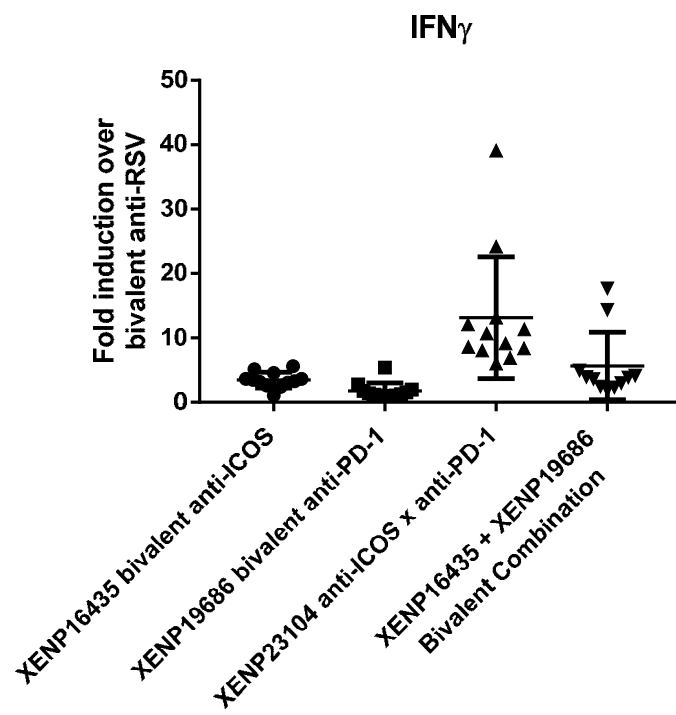


Figure 54

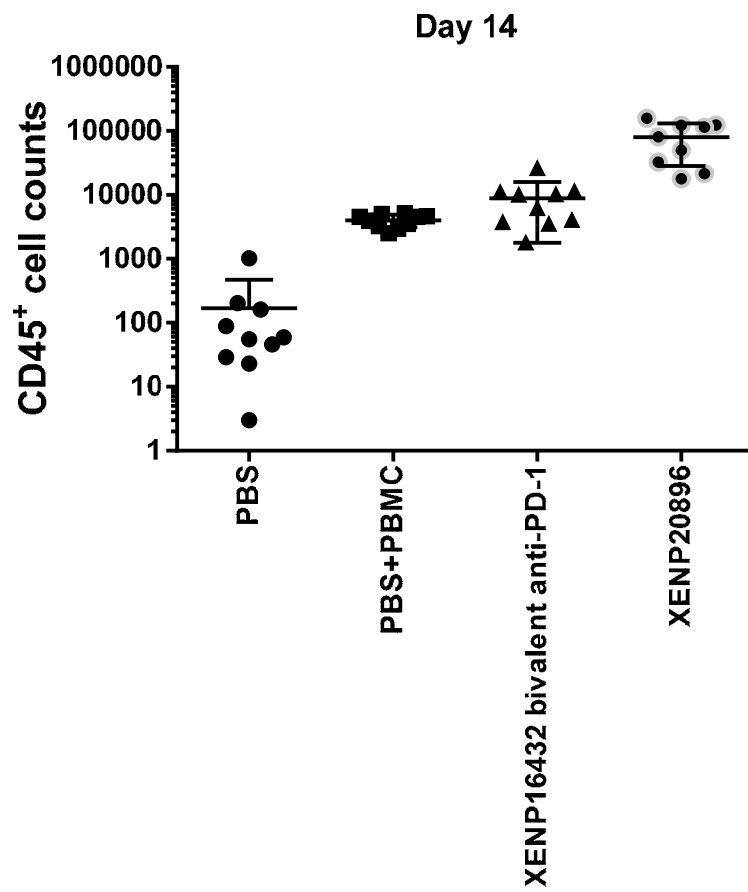


Figure 55A

Central scFv

Fab-Fc Heavy Chain (SEQ ID NO: 28970)

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVD
KKVEPKSCDKTHTCTCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQD
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPPVLDSDGGSFFLYSKLT
VDKSRWEQGDVFSCVMHEALHNHYTQKSLSLSPGK

Fab-scFv-Fc Heavy Chain (SEQ ID NOS 28971-28972)

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCGKPGSGKPGS /**VH2-scFv linker**-
VL2 /GGGSGGGGSKTHTCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFL
YSKLTVDKSRWQQGNVFCFSCVMHEALHNHYTQKSLSLSPGK

Light Chain (SEQ ID NO: 28973)

VL1 /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Central scFv2

Heavy Chain (SEQ ID NOS 28974-28975)

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVD
KKVEPKSCGGGGGGGGGS /**VH2-scFv linker**-
VL2 /GGGSGGGGSKTHTCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFL
YSKLTVDKSRWQQGNVFCFSCVMHEALHNHYTQKSLSLSPGK

Figure 55B*Light Chain (SEQ ID NO: 28976)*

VL1 /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Bispecific mAb*Heavy Chain 1 (SEQ ID NO: 28977)*

VH1 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVD
KKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSGFFLYSKLT
VDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Heavy Chain 2 (SEQ ID NO: 28978)

VH2 /ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
KKVERKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT
VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Light Chain 1 (SEQ ID NO: 28979)

VL1 /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Light Chain 2 (SEQ ID NO: 28980)

VL2 /RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Figure 55C

DVD-Ig

Heavy Chain (SEQ ID NOS 28981-28982)

VH1 / ASTKGPSVFPLAP / **VH2** / ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLG
TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFFLYSKLTVDKSRWQQGNVVFSCSVMHREALHNHYTQKSLSLSPGK

Light Chain (SEQ ID NOS 28983-28984)

VL1 / RTVAAPSVFIFPP / **VL2** / RTVAAPSVFIFPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Trident

Heavy Chain 1 (SEQ ID NOS 28985-28986)

VL1 / GGGSGGGG / **VH1** / GCGGGGEVAAACEKEVAALEKEVAALEKEPKSSDKTHTCTPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQV
SLTCDVSGFYPSDIAVEWESDGPENNYKTTPPVLDSDGSFFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Heavy Chain 2 (SEQ ID NO: 28987)

VH2 / ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTKTYTCNVNHNKPSNTKVD
KKVERKSCDKTHTCTPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYSKLT
VDKSRWQQGNVVFSCSVMHREALHNHYTQKSLSLSPGK

Light Chain 1 (SEQ ID NOS 28988-28989)

VL1 / GGGSGGGG / **VH1** / GCGGGKVAACEKEKVAALKEKVAALKEKVAALKE

Figure 55D

Light Chain 2 (SEQ ID NO: 28990)

VL2 /RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Figure 56A

XENP18920

>XENP018920 nivolumab [PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26802-26806)

QVQLVESGGGVVQPGRLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCATND¹YWGQGTILV
TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSDTKVKDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTILMTSRTPETVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
TEKTTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWEQGVFSCSVMH²EALHNH³Y⁴TQKS
LSLSPGK

>XENP018920 nivolumab [PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26807-26816)

QVQLVESGGGVVQPGRLRLSCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCATND¹YWGQGTILV
TVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIIYDASNRA²TGIPARFSGSGSGTDFTLT³ISSLEPEDE
AVYYCQQSSNWPRTFGGGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTILMTSRTPETVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTTISKAKGQPREPQVYITLPPSREQMTKNQVKLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCSCVMHEALHNH⁴Y⁵TQKSLSPGK

>XENP018920 nivolumab [PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 26817-26821)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIIYDASNRA¹TGIPARFSGSGSGTDFTLT²ISSLEPEDEFAVYYCQQSSNWPRTFGGGTKVEIK/R
TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS³TYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 56B

XENP24130

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26822-26826)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGIYYNGNTYYNPISLRSRVTTISVDTSKNQFSLKLSSTAAADTAVVYCVRASDIYVWGGYH
YFDADFLLWGRGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTIVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPS
DTKVDKVEPKSCDKTHTCPPCPAPPVAGPSVFLPPPKPKDTLMTSRTPETVCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 26827-26836)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYNHWVRQAPGQGQGLEWMGMWINPHSGGTNVAQKFOGRVTMTTRDTSISTAYMELSLRLSRDSDTAVVYCARTTYDSSGYYH
DAFDIWGGQTMVTVSS/GKPGSGKPGSGKPGSG/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLSQSGVPSRFSRFGSGSGTDF
TLTISSLQPEDFATYYCQANSFPWTFGGTKVEIK/EPKSSDKTHTCCPPCPAPPVAGPSVFLPPPKPKDTLMTSRTPETVCVVVDVKHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVCLTCLVKGIFYPSDIAVEWESNGQPENNYKTTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 26837-26841)

QSVLTQPPSASGTPGQRVTTISCGSNSNIGSNSVNWYQQLPGTAPKLLIYGNNQRPSPGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGPVGFGGTKVTV
L/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAMKADSSPVKAGVETTTTPSKQNNKYYAASSYLSLTPEQWKSHRSYSQCQVTHEGSTVEKTVAPTECS

Figure 57A

XENP23406

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26842-26846)

QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYMHVWRQAPCGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRRLSRDSDTAVYYCARTYYVYDSSGYHDAFDIW
GQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHCTPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
KAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-scFv-Fc Heavy Chain (SEQ ID NOS 26847-26857)

QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYMHVWRQAPCGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRRLSRDSDTAVYYCARTYYVYDSSGYHDAFDIW
GQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCG
KPGSGKPGS/EIVLTQSPATLSAEPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYNASHRYTGVDPDRFTGSGYGTEFTLTISVQSEDFGVYYCQQDFSSPRTFGGGTKVE
IK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTE
DTGVYCYTRYIGNYGIFYDVGRTLTVTSS/GGGSGGGGSKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREMQTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLK
TVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP023406 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26858-26862)

DIQMTQSPSSVSASVGDRTVITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLQSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCQANSFPWTFGQGTKEIK/RTVAAPS
VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP23407

>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26863-26867)

QVQLVQSGAEVKKPGASVKVSKKASGYTFTGYYMHVWRQAPCGQGLEWMGWINPHSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRRLSRDSDTAVYYCARTYYVYDSSGYHDAFDIW
GQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHCTPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWEGQDVFSCSVMEALHNHYTQKSLSLSPGK

Figure 57B

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>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Fab-scFv-Fc Heavy Chain (SEQ ID NOS
26868-26878)

QVLVQSGAEVKKPGASVKVSCKASGYTFFTGYMHVWRQAPQGLEWMMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDDTAVYYCARTYYYDSSGYHDAFDIW
GGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCG
KPGSGKPGS/EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRTFTSGYGTEFTLTISSVQSEDFGVYYCCQDFSSPRTFGGGTKE
IK/GKPGSGKPGSGKPGS/EVQLVESGGGLVKPGSLRLSCVASGFTFSNYMMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTE
DTGVYICTRYYGNGGYFDVWGRGTLTVVSS/GGGGSGGGGSKTHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYITLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSK
LTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023407 [anti-ICOS]_H0L0_Fab-[anti-ICOS]_H0L0_Fab_1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 26879-26883)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSSGSGTDFTLTTISSLPEDFATYYCQANSPFWTFGQGTKEIK/RTVAAPS
VFIFPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24128

>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 26884-
26888)

EVQLVESGGGLVKPGSLRLSCVASGFTFSNYMMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRYYGNGGYFDVWGRG
TLTVVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYITLPPSREQMTKNQVSLTCDVSGFYPSDIAVEWESDGQGPENNYKTTPVLDSDGSFFLYSKLTVDKSRWEQGVFSCSCVMHEALHNHYTQKSLSLSPGK

>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_H0L0_scFv Fab-scFv-Fc Heavy Chain (SEQ ID NOS
26889-26899)

EVQLVESGGGLVKPGSLRLSCVASGFTFSNYMMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRYYGNGGYFDVWGRG
TLTVVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGKPG
SGKPGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDDTAVYYCARTYYYDSSGY
HDAFDIWGGQTMVTVSS/GKPGSGKPGSGKPGS/DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSSGSGTDFTLTIS
SLQPEDFATYYCQANSPFWTFGQGTKEIK/GGGGSGGGGSKTHTCPCPAPPVAGPSVFLFPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREQMTKNQVSLTCDVSGFYPSDIAVEWESDGQGPENNYKTTPVLDSDGSFFLYSKL
TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

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Figure 57C

>XENP024128 1G6_L1.194_H1.279_Fab-1G6_L1.194_H1.279_Fab_[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 26900-26904)

EIVLTQSPATLSA^{SPGERVITL}TCRASQ^{SVGNDVAMV}QQKPGQAP^{RL}LLIN^{YAS}HR^{YT}GV^{PD}RFTGSGYGTEFTLT^{IS}SVQSEDFGVY^CQQD^{FSS}PR^TFGGGTK^{VE}IK/R
TVAAPSVFIFPPSDEQLKSGTASV^VCLLNNFY^PPREAKVQWKVDNALQSGNSQ^{ES}VT^EQDSKDS^TYLS^SLT^LLSKADY^EKKH^KVYACEV^THQGLSPV^TKSFNRGEC

Figure 58

XENP24123

>XENP024123 1G6_H1.279_L1.194_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Heavy Chain (SEQ ID NOS 26905-26915)
EVQLVESGGGLVPGGSLRLSCVASFSTFSNYMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNILKTEDTGVIYCTRYGYGDFDVWGRG
TLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGG
SGGGGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHVWRQAPGQGLEGWMGWINPHSGGTNYAQKFQGRVTMTDRDTSISTAYMELSRLLSRDSDTAVYICARTYYIDSSGYI
HDAFDIWGQGTMTVSS/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDFTLTIS
SLQPEDFATYYCQANSPFWTFGGGTKEIK/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDFTLTIS
YNSTRVWSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKL
TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024123 1G6_H1.279_L1.194_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Light Chain (SEQ ID NOS 26916-26920)
EIVLTQSPATLSASGERVTLTCRASQSVGNDAWYQQKPGQAPRLINYASHRYTGVDPDRFTGSGYGTEFTLTISSVQSEDFGVYCYQQDFSSPRTFGGGTKVEIK/RTVAAPS
VFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24125

>XENP024125 LOPD180[PD-1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Heavy Chain (SEQ ID NOS 26921-26931)
QVQLQESGPGLVKPQTLSTLTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGIYYNGNTYYNPSLRSRVTISVDTSKNQFSLKSSVTAADTAVYYCVRASDYVWGGYHYFDAFD
LWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKS
CGGGSGGGGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFGTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTDRDTSISTAYMELSRLLSRDSDTAVYICARTYYID
SSGYIHDAFDIWGQGTMTVSS/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF
TLTISLQPEDFATYYCQANSPFWTFGGGTKEIK/SGGGSGGGSGGGSGGGGS/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGTDF
PREEQYNSTRVWSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFF
LYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024125 LOPD180[PD-1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1 Light Chain (SEQ ID NOS 26932-26936)
QSVLTQPPSASGTPGQRVTTISCSGSNSNIGSNSVNWYQQLPCTAPKLLIYGNNQRPSPGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGPVFGGGTKVTVL/GQPK
AAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNKNKYAASSYLSTLTPSEQWKSHRYSQCQVTHEGSTVEKTVAPT ECS

Figure 59

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>XENP024134 1G6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Heavy Chain 1 (SEQ ID NOS 26937-26941)

EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYMNWVRQAPGKGLEWVAELRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRIYGNIGGYF
DVGGRGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNHHKPSDTKVD
KKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCK
VSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNNYKTTPPVLDSDGSEFFLYSKLTVDKSRWEQGDVFSCSVMHEA
LHNHYTQKSLSLSPGK

>XENP024134 1G6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Heavy Chain 2 (SEQ ID NOS 26942-26946)

QVQLVQSGAEVKKPGASVKVSCKASGYFTFTGYVMHWVRQAPGQGLEWMGWINPHSGGTNYYAQKFQGRVTMTTRDTSISTAYMELSLRLSRDSDTAIVYCARITYYDSSGGYIH
DAFDIWGGQTMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYTCNVNHHKPSNT
KVDKKVERKSCDKTHTCPRCAPPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQOQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>XENP024134 1G6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Light Chain 1 (SEQ ID NOS 26947-26951)

ELVLTQSPATLSASPERVTLTCRASQSVGNDVAVYQQKPGQAPRLLINVASHRVYTGVPDRFTGSGYGTEFTLTITSSVQSEDFGVYCCQDFSSPRTFGGKVEIK/R
TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024134 1G6_H1.279_L1.194_Fab-[anti-ICOS]_H0L0_Fab-IgG1 Light Chain 2 (SEQ ID NOS 26952-26956)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSFGSGSGTDFTLTITSSLPQPEDFATYYCQQQANSFPWTFGQGTKVEIK/R
TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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Figure 60

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>XENP024122 1G6_H1.279_L1.194_[anti-ICOS]_H0L0_IgG1_Heavy_Chain (SEQ ID NOS 26957-26966)
EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYYMNWVRQAPGKGLEWVAEIRLYSNNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYICTRYIGNYGGYF
DVGWGRGTLVTSS/ASTKGPSVFPLAP/QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYNMHWVRQAPGQGLEWMGMWINPHSGGTNYAQKFQGRVTMTTRDTSISSTAYM
ELSLRLSDDTAVYYCARTYYDSSGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDILMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTISKAKGQPREPQVYITLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSP
DGSFFLYSKLTVDKSRWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK

>XENP024122 1G6_H1.279_L1.194_[anti-ICOS]_H0L0_IgG1_Light_Chain (SEQ ID NOS 26967-26976)
EIVLTQSPATLSASPGERVTLTTCRASQSVGNDVAVWYQQKPKGQAPRLLINVAASHRYTGVDPDRFTGSGYGTETFTLTISSVQSEDFGVYVCOQDFSSPRTFGGGKVEIK/R
TVAAPSVFIFFP/DIQMTQSPSSVSASVGDRTTITCRASQGISRLLAWYQQKPKGAPKLLIYVASSLSQSGVPSRFRSGSGGTDFLTITSSLPQPEDEATYYCQQANSFPW
TFGQGTKEIK/RTVAAPSVFIFFPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISSTLTLSKADYEKHKVYACEVTHQGLSSP
VTKSFNRGEC

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Figure 61A

XENP24132

>XENP024132 1G6_L1.194_1G6_H1.279_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1_Heavy Chain 1 (SEQ ID NOS 26977-26986)
 EIVLTQSPATLSASPGERVLTTCRASQSGVNDVAVYQQKPGQAPRLINVAASHRYTGVPDRFTGSGYGTEFTLTISVQSEDFGVYCCQDFSSPRTFGGGTKVEIK/G
 GSGGGG/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNVMNWRQAPGKGLEWVAEIRLYSNVYATHVAESVKGRTTISRDDSKSTLYLQMNLLKTEDTGYYICTRY
 YGNYGGYFDVWGRGTLVTSS/GGCGGGEVAAACEKEVAALEKEVALEKEPKSSDKTHTCCPPCAPPVAGPSVFLFPKPKDTILMISRTPEVTICVVVDVKHE
 DPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDIA
 VEWESDGPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWEQGVFSCVMHEALHNHYTQKSLSLSPGK

>XENP024132 1G6_L1.194_1G6_H1.279_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1_Heavy Chain 2 (SEQ ID NOS 26987-26991)
 QVQLVQSGAEVKPGASVKSCASGYTFTGYXMHVWRQAPGQGLEWMGWINPHSGGTNVAQKFGQGRVTMTRDTSISIAVMELSLRSLRSDDTAVYYCARITYYDSSGYYH
 DAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTKYTCNVNHHKPSNT
 KVDKVERKSCDKTHTCCPPCAPPVAGPSVFLFPKPKDTILMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
 KCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSV
 MHEALHNHYTQKSLSLSPGK

>XENP024132 1G6_L1.194_1G6_H1.279_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1_Light Chain 1 (SEQ ID NOS 26992-27001)
 EIVLTQSPATLSASPGERVLTTCRASQSGVNDVAVYQQKPGQAPRLINVAASHRYTGVPDRFTGSGYGTEFTLTISVQSEDFGVYCCQDFSSPRTFGGGTKVEIK/G
 GSGGGG/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNVMNWRQAPGKGLEWVAEIRLYSNVYATHVAESVKGRTTISRDDSKSTLYLQMNLLKTE
 DTGVYICTRYIGNYGGYFDVWGRGTLVTSS/GGCGGGEVAAACEKEVAALEKEVALEKEPKSSDKTHTCCPPCAPPVAGPSVFLFPKPKDTILMISRTPEVTICVVVDVKH
 EDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDI
 AVEWESDGPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWEQGVFSCVMHEALHNHYTQKSLSLSPGK

>XENP024132 1G6_L1.194_1G6_H1.279_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1_Light Chain 2 (SEQ ID NOS 27002-27006)
 DIQMTQSPSSVSASVGRVTTTCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAFYCCQANSPFWTFGGGTKVEIK/R
 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTISLSTLTKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24133

>XENP024133 mAb7 (1.2) [PD-1]_L1_mAb7 (1.2) [PD-1]_H1_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1_Heavy Chain 1 (SEQ ID NOS 27007-27016)
 EIVLTQSPATLSLSPGERATLSCRASESDVDNYGMSFMNWFQQKPGQPPKLLIHAASNQSGVPSRFSGSGSGTDFTLTISLLEPEDFAVYFCQQSKEVPYTFGGGKVE
 IK/GGSGGGG/QVQLVQSGAEVKKPGASVKVSCKASGYSTSYVMNWRQAPGQGLEWIGVTHPSDSETWLDDQKFKDRVTITVDKSTSTAYMELSSLSRSEDFAVYYCA
 REHYGTSPPFAYWGQGTLLVTSS/GGCGGGEVAAACEKEVAALEKEVALEKEPKSSDKTHTCCPPCAPPVAGPSVFLFPKPKDTILMISRTPEVTICVVVDVKH
 EDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCDVSGFYPSDI
 AVEWESDGPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWEQGVFSCVMHEALHNHYTQKSLSLSPGK

Figure 61B

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>XENP024133 mAb7 (1.2) [PD-1]_L1_mAb7 (1.2) [PD-1]_H1_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1 Heavy Chain 2 (SEQ ID NOS
27017-27021)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYNHMWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYMELSLRSRDDTAVYYCARTYYDSSGYIH
DAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYTTCNVNHKPSNT
KVDKKVERKSCDKTHTCPRCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVYDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>XENP024133 mAb7 (1.2) [PD-1]_L1_mAb7 (1.2) [PD-1]_H1_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1 Light Chain 1 (SEQ ID NOS
27022-27031)
EIVLTQSPATLSLSPGERATLSCRASESVDNYGMSFMNWFQOKPGPQPPKLLIHAASNQGSGVPSRFSGSGSGTDFTLTISSLEPEDEFAVYFCQQSKEVPYTFGGGTKVE
IK/GGGSGGGG/QVQLVQSGAEVKKPGASVKVSCKASGYSTSYMNNWVRQAPGQGLEWIGVIHPSDSETWLDQKFKDRVTTITVDKSTSTAYMELSSLR
SEDTAVYYCAREHYGTSPFAYWGQGTLVTVSS/GGCGGGKVAACKEKVAALKEKVAALKE

>XENP024133 mAb7 (1.2) [PD-1]_L1_mAb7 (1.2) [PD-1]_H1_DART-[anti-ICOS]_HOL0_Fab-Fc_IgG1 Light Chain 2 (SEQ ID NOS
27032-27036)
DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIVYASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSPFWTFGQGTKVEIK/R
TVAAPSVFTIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC
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Figure 62

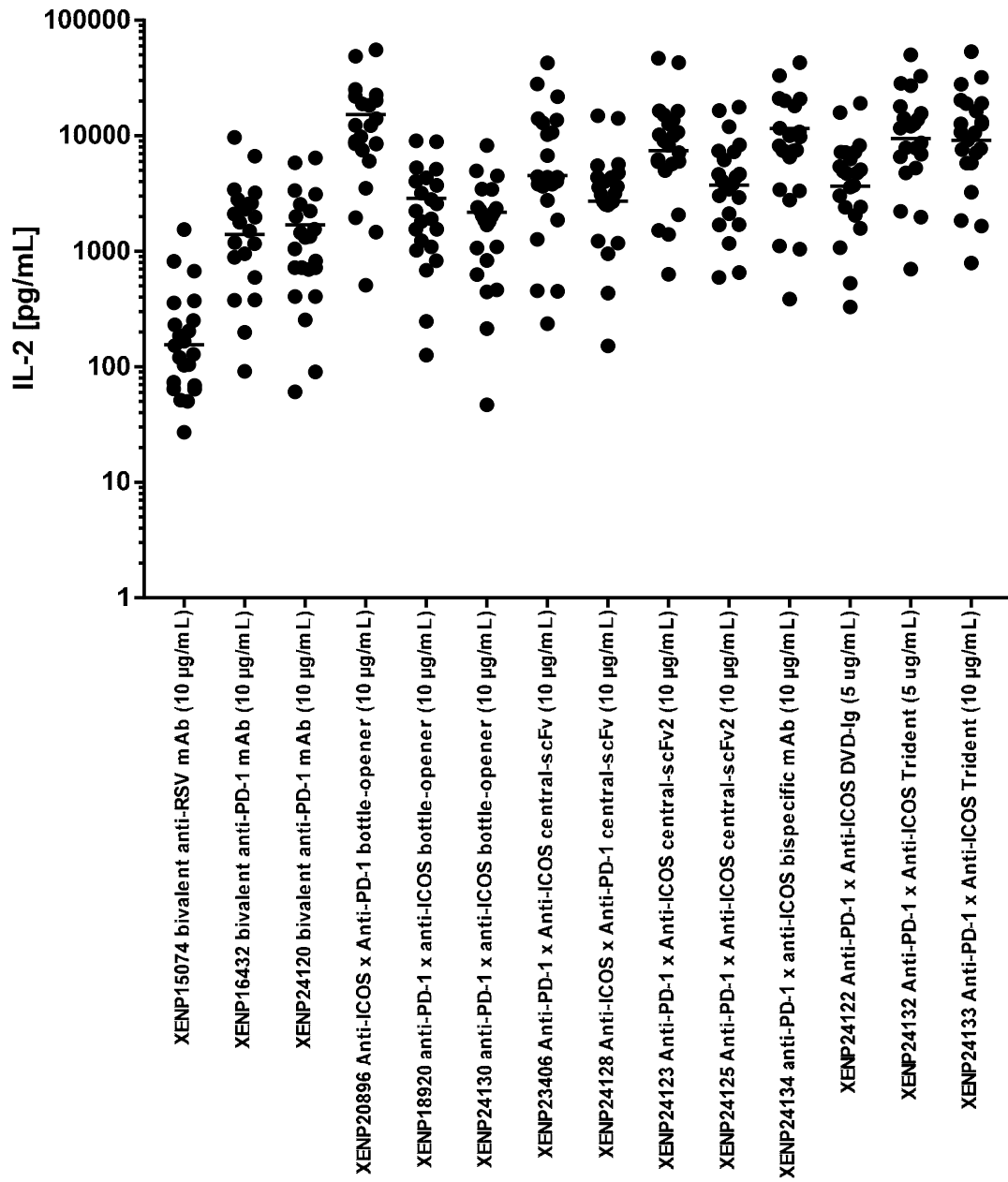


Figure 63

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27037-27041)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYDSSGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDQGPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMEALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27042-27051)

EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNKN
SLYLQMNSLRRAEDTAVYYCARGGHLGPFDLWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLS
PGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ
YGSSPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMH
EALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Light Chain (SEQ ID NOS 27052-27056)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSFGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 64A**XENP24359**

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1 (SEQ ID NOS 27057-27061)

EVQLVESGGGLVQPGGSLRLSCAASGFTFDDAWMSWVRQAPGKGLEWVAEISTKANNHATYYAESVKGRFTISRDDS
KSSVYLQMNSLRAEDTAVYYCTRLATWDWYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2 (SEQ ID NOS 27062-27066)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSLRSDDTAVYYCARTYYIDSSGYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYTCNVNHKPSNTKVDKKVERKSCDK
THTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1 (SEQ ID NOS 27067-27071)

DIVLTQSPSSLSASVGDRVTITCRASQSVDDYDGDSYMNWYQQKPKGPKLLIYAASELESGIPARFSGSGSGTDFTL
TISSLQPEDFATYYCQQSNEDPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>XENP024359 7G8_H3.30_L1.34_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2 (SEQ ID NOS 27072-27076)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSFGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP24360

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1 (SEQ ID NOS 27077-27081)

EVQLVQSGAEVKKPGATVKISCKASGFNIKDYFMHWVQAPGKGLEWMGWIDPELGDTEYAPKFQGRVTITADTSTN
TAYMELSSLRSEDTAVYYCYARGVYQALDYWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPCP
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 64B

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2 (SEQ ID NOS 27082-27086)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTCNVNHKPSNTKVDKKVERKSCDK
THTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1 (SEQ ID NOS 27087-27091)

DIQMTQSPAFLSVTPGEKVTITCQASQDIGNYLNWFQQKPGQTVKLLIYFTSYLHSGVPSRFSGSGSGTDYFTISS
LEAEDAATYFCQQGNTLPYTFGGGKVEIK/RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024360 2A11_H1.144_L2.142_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2 (SEQ ID NOS 27092-27096)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQANSFPWTFGGGKVEIK/RTVAAPSVEFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 65

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 1 (SEQ ID NOS 27097-27101)

QVTLKESGPVLVKPTETLTCTVSGFSLNGYGVNWVRQPPGKGLEWLAMIWGDGSTDYNSALKSRLTISKDNSKSQ
VVLTMNTMDPVDTATYYCARSYYTSD~~EDYWGQ~~TLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Heavy Chain 2 (SEQ ID NOS 27102-27106)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSR~~LRSD~~TAVYYCARTYYDSSGGYYHDAFDI~~WGQ~~TMVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKT~~YTCNVNHKPSNTKVDKKVERK~~SCDK
THTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Light Chain 1 (SEQ ID NOS 27107-27111)

DIVMTQSPDSLAVSLGERATINCKSSQSL~~LSNR~~TRK~~NYLAWY~~QKPGQSPKLLIYWASTRESGV~~PDRFTGSGSGTDF~~
TLTISSLQAEDVAVYYCKQSYSLRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024361 3H3_H1_L2.1_Fab-[anti-ICOS]_H0L0_Fab Light Chain 2 (SEQ ID NOS 27112-27116)

DIQMTQSPSSVSASVGDRVTITCRASQGISRL~~LAWY~~QKPGKAPKLLIYVASSLQSGVPSR~~FSGSGTDF~~TLTISS
LQPEDFATYYCQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 66A**XENP21748**

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27117-27121)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPC
PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27122-27131)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRLRSDDTAVYYCARTYYYDSSGYHDAFDIWGQGTMTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSVSASVGDRTTITCRASQGISRL^{LA}WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLT^{IS}SLQPEDFA
TYYCQ^QANSFPWT^{FG}QGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27132-27136)

DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLT^{IS}
LQPEDFATYYCQ^QYLYHPAT^{FG}QGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24129

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27137-27141)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKN
SLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDFVSCSVMHEALHNHYTQKSLSLSPGK

Figure 66B

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27142-27151)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWQGQTMVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSVSASVGDRVTITCRASQGISRL^{LA}WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
TYYCQQA^{NS}FPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQV^{KL}TCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVF
SCSVMEALHNHYTQKSLSLSPGK

>XENP024129 durvalumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27152-27156)

EIVLTQSPGTL^{SL}SPGERATLSCRASQRVSSSYLA^{WY}QQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQA^YSLPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^{LL}NNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP24131

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27157-27161)

EVQLLES^{GG}GLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGT^LLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVT^{SV}SWNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFIYPSDIAVEWE
SDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27162-27171)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWQGQTMVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSVSASVGDRVTITCRASQGISRL^{LA}WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
TYYCQQA^{NS}FPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREQMTKNQV^{KL}TCLVKGFIYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVF
SCSVMEALHNHYTQKSLSLSPGK

>XENP024131 avelumab[PD-L1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27172-27176)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLM^YDVSNRPSGVSNRFSGSGSGNTASLT
ISGLQAEDEADYYC^{SS}YTSSSTRVFGTGKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
ADSSPVKAGVETTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

Figure 66C**XENP24124**

>XENP024124 durvalumab[PD-L1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1
Heavy Chain (SEQ ID NOS 27177-27187)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDN
AKN SLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTR
DTSISTAYMELSRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVTVSS/GGGGSGGGSGGGSGGGGS/DI
QMTQSPSSVSASVGDRVTITCRASQGISRLLAQYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
SLQ PEDFATYYCQQANSFPWTFGQGTKVEIK/GGGSGGGSGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK
SRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024124 durvalumab[PD-L1]_H1L1_Fab_(G4S)2_[anti-ICOS]_H0L0_scFv20_Fc_IgG1
Light Chain (SEQ ID NOS 27188-27192)

EIVLTQSPGTLSLSPGERATLSCRASQRVSSSYLAQYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQYGSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 67

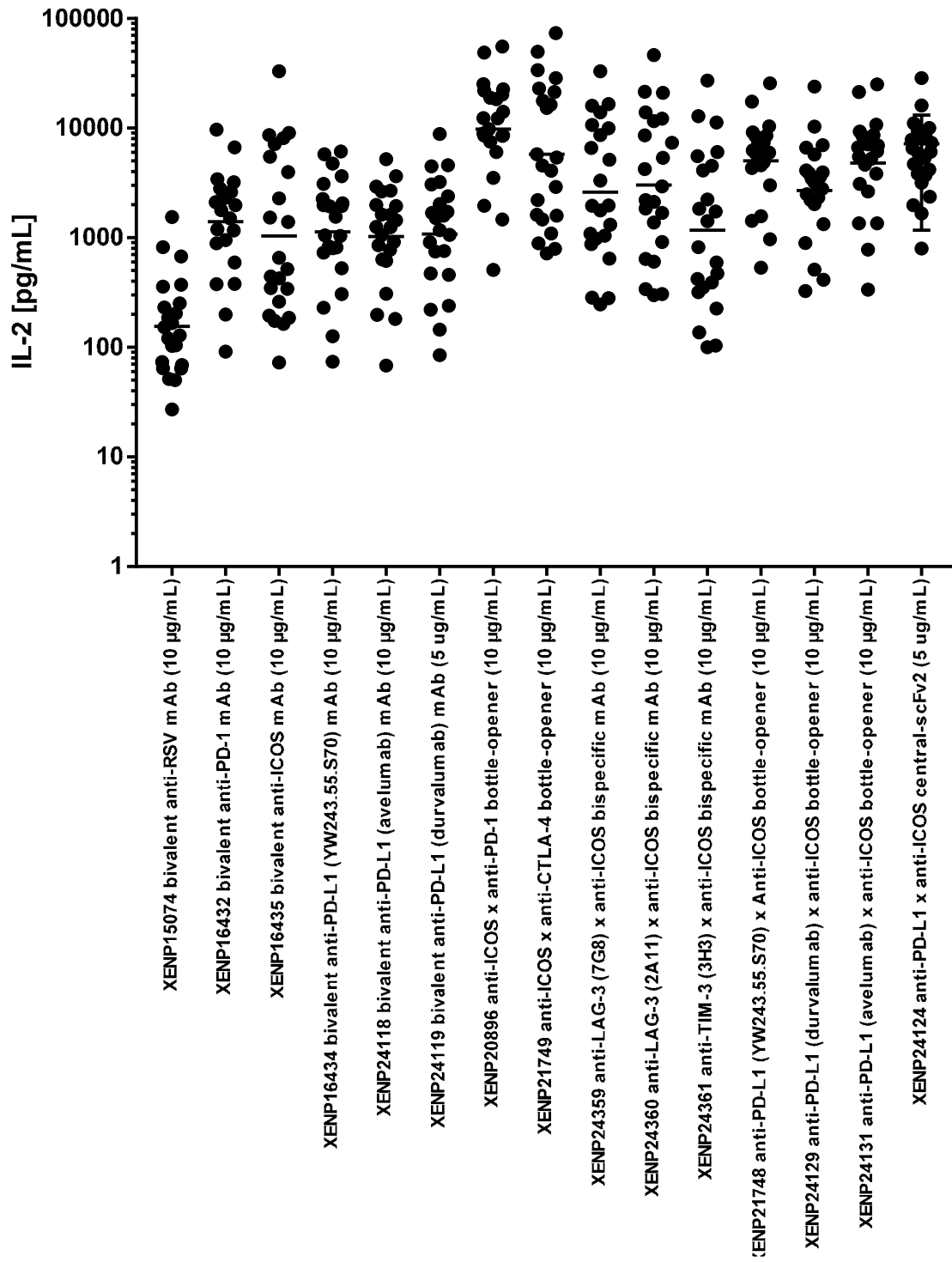


Figure 68A**XENP20266**

>XENP020266 [ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27193-27197)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP020266 [ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27198)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP020266 [ICOS]_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27199-27203)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLLA^{WYQ}KPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQ^{QANS}FPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP21861

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27204-27208)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYYWMHWVKQRPQGLEWIGEIDPSDSYVNYNQNF^{KGK}ATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYYGTSLAWFDYWGQGT^{LVTVST}/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27209)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27210-27214)

DIVMTQAAPSVPTPGESVSISCRSSKSPLHSNGNIYLYWFLQRPQGSPQLLIYRMSNLASGV^{PDR}FSGSGSGTFTT
LKISRVEAEDVGVYYCMQHLEYPYT^{FGGG}TKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW
KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68B**XENP21863**

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27215-27219)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQM
NSLRAGDTAVYYCVRDNRKVTHEHYYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27220)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27221-27225)

EIVLTQSPGTLSLSPGERATLSCRASQNISSYLAWEYQKPKGAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22349

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27226-27230)

QVQLVQSGAEVKKPGSSVKVCKASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNINQKFQGRVTITADKSTSTAYME
LSSLRSEDTAVYYCGRNNGYIGWYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL
FPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFL
YSKLTVDKSRWEQGDVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27231)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCVMHEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27232-27236)

EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQKPKGAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISILEPEDF
AVYYCFQSGGYPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68C**XENP22439**

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27237-27241)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27242)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022439 [ICOS]_H0_L0.5 one-arm mAb Light Chain (SEQ ID NOS 27243-27247)

DIQMTQSPSSVSASVGDRVTITCRASQGISSLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP22440

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27248-27252)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27253)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022440 [ICOS]_H0_L0.7 one-arm mAb Light Chain (SEQ ID NOS 27254-27258)

DIQMTQSPSSVSASVGDRVTITCRASQGISSYLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS
LQPEDFATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 68D**XENP22441**

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27259-27263)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27264)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022441 [ICOS]_H0_L0.9 one-arm mAb Light Chain (SEQ ID NOS 27265-27269)

DIQMTQSPSSVSASVGDRVTTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22442

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27270-27274)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27275)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022442 [ICOS]_H0_L0.10 one-arm mAb Light Chain (SEQ ID NOS 27276-27280)

DIQMTQSPSSVSASVGDRVTTITCRASQGISRLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQANSFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68E**XENP22443**

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27281-27285)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27286)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022443 [ICOS]_H0_L0.14 one-arm mAb Light Chain (SEQ ID NOS 27287-27291)

DIQMTQSPSSVSASVGDRVITITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQSNSFPWTFTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22444

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27292-27296)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHVVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27297)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022444 [ICOS]_H0_L0.15 one-arm mAb Light Chain (SEQ ID NOS 27298-27302)

DIQMTQSPSSVSASVGDRVITITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 68F**XENP22445**

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27303-27307)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27308)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022445 [ICOS]_H0_L0.20 one-arm mAb Light Chain (SEQ ID NOS 27309-27313)

DIQMTQSPSSVSASVGDRVTITCRASQGISRL^{LA}WYQKPGKAPKLLIYVASSLQSGVPSRFS^{GS}SGSGTDFTLTIS
LQPEDFATYYCQ^QANSYPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

XENP22766

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27314-27318)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
TAYMELSRRLRSDDTAVYYCARTYYYDSSGGYYHDAFDIWGQGTMTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27319)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCSVMEALHNHYTQKSLSLSPGK

>XENP022766 [ICOS]_H0_L0.38 one-arm mAb Light Chain (SEQ ID NOS 27320-27324)

DIQMTQSPSSVSASVGDRVTITCQASQDISLLAWYQKPGKAPKLLIYAASSLQSGVPSRFS^{GS}SGSGTDFTLTIS
LQPEDFATYYCQ^QAESFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 68G**XENP23096**

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27325-27329)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGETIYAQKFQGRVTMTRDTSIS
TAYMELSSLRSED~~TAVYYCARTYYYDTSGYYHDAFDVWGQGTMTV~~VSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDI
AVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27330)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP023096 [ICOS]_H0.66_L0 one-arm mAb Light Chain (SEQ ID NOS 27331-27335)

DIQMTQSPSSVSASVGDRVTITCRASQGISRL~~LAWYQQKPGKAPKLLIYVASSLQSGVPSR~~FSGSGSGTDFTLTIS
LQPEDFATYYCQ~~QANSFPWTFGQGTKVEIK~~/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

Figure 69

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

Figure 70

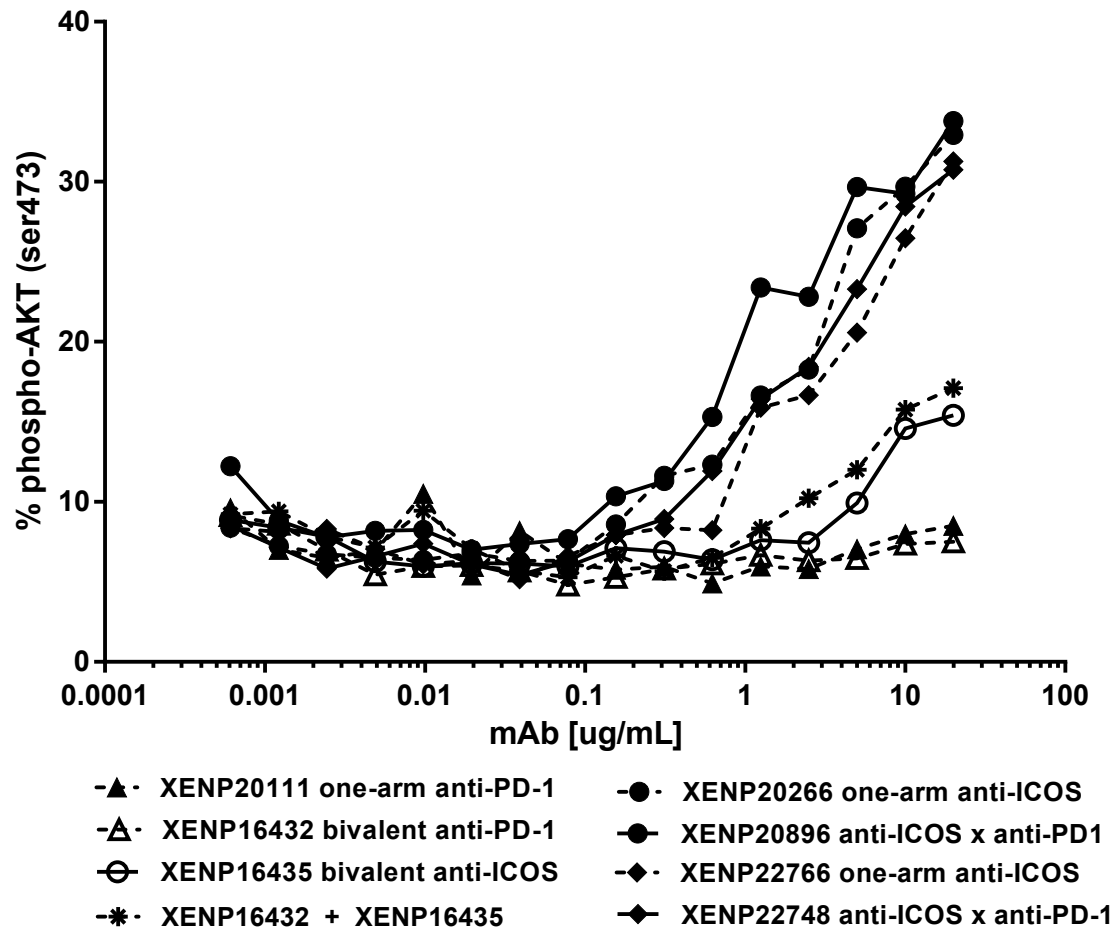


Figure 71

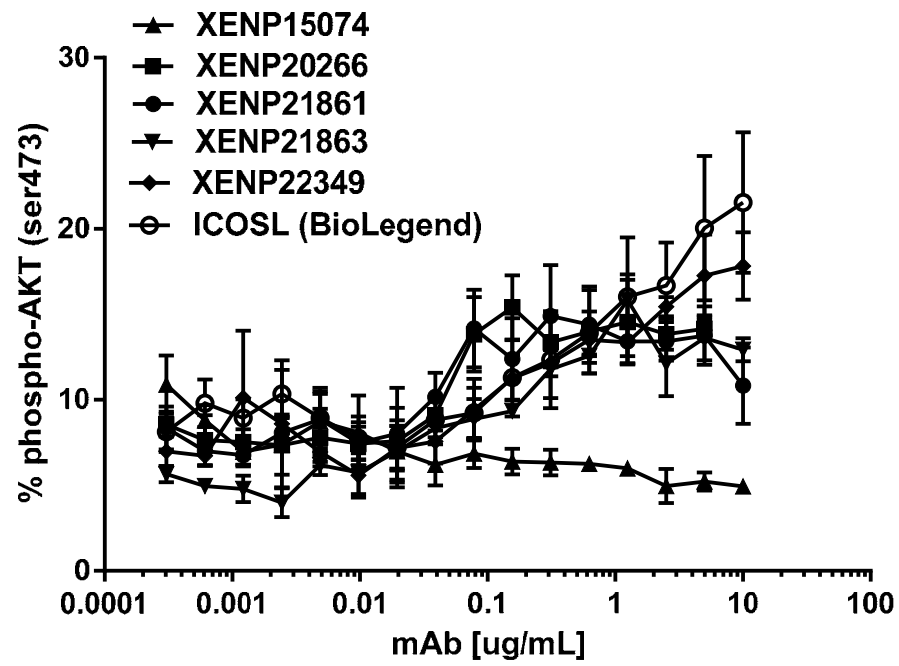


Figure 72A**Prototype Costim x PD-1 Bispecific**

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27336-27340)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSSTIDYADSVKGRFTISRDNAKNSLYLQM
NSLRDEDTAVYYCAREESGWYLFDIYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSR
WEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27341-27350)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSEDFG
VYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYWMNW
VRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYGGGYFDVWGRGTLV
TVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK

>XENP023377 11D4[OX40]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27351-27355)

DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFAT
YYCQYNSYPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27356-27360)

QVTLKESGPGILKPSQTLSTCSFGFSLSTSGMGVGVWIRQPSGKGLEWLAHIWWDDDKYSPSLKSQLTISKDTSRNQVFLKI
TSLDTADTATYYCVRSYYGGSSGAMDYWGQGTSTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPK
KDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSGDSFFLYSKLTV
DKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27361-27370)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSEDFG
VYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVASGFTFSNYWMNW
VRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGYYCTRYYGNYGGGYFDVWGRGTLV
TVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDI
AVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYTQKSLSLSPGK

Figure 72B

>XENP023378 1D8[GITR]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27371-27375)
 DIVMTQTPLSLPVSLGDQASISCRSSQSLVHSDGNTYLHWYQLKPGQSPKLLIYKVSKRFSGVPDRFSGSGSGTDFTLKIS
 RVEAEDLGVIYFCSTHVPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
 SGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27376-27380)
 QVQLQQWAGALLKPSSETLSLCAVYGGSFSGYYWSWIRQSPEKGLEWIGEINHGGYVTYNPSLESRVTISVDTSKNQFS
 LKLSSVTAADTAVYYCARDYGPGRNYDWYFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPP
 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNY
 KTTTPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27381-27390)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQS
 EDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFS
 NYWMNWWVRQAPGKGLEWVAEIRLYSNYYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRYGNYG
 GYFDVWGRGTLTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWY
 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCFSVMHEALHN
 HYTQKSLSLSPGK

>XENP023379 20H4.9[4-1BB]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27391-27395)
 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLEPED
 FAVYYCQQRSNWPPALTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
 NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Additional CTLA-4 x ICOS Bispecific SEQ

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27396-27400)
 QVQLVESGGGVVQGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVA
 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWL
 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKT
 TPPVLDSGDSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 72C

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27401-27410)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRD
TSISTAYMELSRLRSDDTAVYYCARTYYYDSSGYYHDAFDIWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMT
QSPSSVSASVGDRVITITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYY
CQQANSFPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PSREQMTKNQVKLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMH
EALHNHYTQKSLSLSPGK

>XENP019192 ipilimumab[CTLA-4]_H0L0_Fab-[anti-ICOS]-H0L0_scFv Light Chain (SEQ ID NOS 27411-27415)

EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQYGSSPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 73A**Prototype anti-4-1BB mAb**

>XENP014410 20H4.9[4-1BB]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27416-27420)
 QVQLQQWAGAGLLKPSSETLSLTCAVYGGSFSGYYWSWIRQSPEKGLEWIGEINHGGYVTYNPSLESRVTISVDTSKNQFS
 LKLSVTAADTAVYYCARDYGPGNYDWYFDLWGRGTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP014410 20H4.9[4-1BB]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27421-27425)
 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLPEP
 FAVYYCQQRSNWPPALTFGGGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 (LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-OX40 mAb

>XENP016437 11D4[OX40]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27426-27430)
 EVQLVESGGGLVQPGLSLRLSCAASGFTFSSYSMNWVRQAPGKLEWVSYISSSSTIDYADSVKGRFTISRDNAKNSL
 YLQMNSLRDEDTAVYYCARESGWYLFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAG
 PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
 GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP016437 11D4[OX40]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27431-27435)
 DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAAASSLQSGVPSRFSGSGSGTDFTLTISLQPE
 DFATYYCQQYNSYPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
 QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-GITR mAb

>XENP016438 1D8[GITR]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27436-27440)
 QVTLKESGPGILKPSQTLSTCSFSGFSLSTSGMGVGVWIRQPSGKGLEWLAHIWDDDKYYSPSLKSQLTISKDTSRNQ
 VFLKITSLDTATYYCVRSYYYYGSSGAMDYWGQGTSTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
 VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 73B

>XENP016438 1D8[GITR]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27441-27445)

DIVMTQTPLSLPVS LGDQASISCRSSQSLVHSDGNTYLHWYLQKPGQSPKLLIYKVKSRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDLG VYFC SQSTHVPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-ICOS mAbs

>XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27446-27450)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIG EIDPSDSYVNYNQNFKGKATLTVDKSS
STAYIQLSSLTSEDSAVYFCARSPDY YGTSLAWFDYWGQGT LTVTST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

>XENP021820 GSK_314.8[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27451-27455)

DIVMTQAAPSVPTPGESVSISCRSSK SPLHSNGNIYLYWFLQRPGQSPQLLIY RMSNLASGVDPDRFSGSGSGTTFTLKIS
RVEAEDVG VYYCM QHLEYPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021821 GSK_88.2[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27456-27460)

QVQLQQPGAELVRPGASVKLSCKASGYSFTSY WINWVKQRPGQGLEWIG NIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTSSEDSAVYYCTR WNLSYFDNNYYLDYWGQGT LTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

>XENP021821 GSK_88.2[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27461-27465)

DIVMTQAAPSVPTPGESVSISCRSSK SLLHSNGNTYLYWFLQRPGQSPQLLIY RMSNLASGVDPDRFSGSGSGTAFTLRIS
RVEAEDVG VYYCM QHLEYPWTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021822 jMab-138[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27466-27470)

EVQLVESGGGLVQP GGSRLS CAASGFTFSSY DMHWVRQATGKGLEWVSA IGTAGDYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDNRKVT HEHYYYGMDVWGQGT LTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK

Figure 73C

>XENP021822 jMab-138[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27471-27475)
 EIVLTQSPGTLSPGERATLSCRASQNISSYLAWYQQKPGQAPGGLLIYGASSRATGIPDRFSGSGSGTDFLTISRLEPE
 DFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021823 jMab-139[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27476-27480)
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRNAKNSL
 YLQMNSLRAGDTAVYYCVRDRTVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
 PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
 PENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021823 jMab-139[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27481-27485)
 EIVLTQSPGTLSPGERATLSCRASQSISSSLAWYQQKPGQAPGGLIFGASSRATGIPDRFSGSGSGTDFLTISRLEPED
 FAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
 QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP022346 WO2016059602_GSK[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27486-
 27490)
 QVQLVQSGAEVKKPGSSVKVSCASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNYNQKFQGRVTITADKST
 STAYMELSSLRSEDTAVYYCGRNNYGNYGWYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
 FPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
 PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
 HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
 NNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP022346 WO2016059602_GSK[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27491-
 27495)
 EIVLTQSPATLSLSPGERATLSCASSVSVMHWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTISLEPEDF
 AVYYCFQGSGLPYTFGGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
 SVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP023057 Jounce_37A10S713[ICOS]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27496-
 27500)
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDAKN
 TLYLQMNSLRAGDTAVYYCTRWGRFGFDSWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV
 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
 NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 73D

>XENP023057 Jounce_37A10S713[ICOS]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27501-27505)

DIVMTQSPDSLAVSLGERATINCKSSQSLLSGSFNYLTWYQQKPGQPPKLLIFYASTRHTGVPDRFSGSGSGTDFTLTIS
LQAEDVAVYYCHHHYNAPPTFGPGTKVDIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-PD-L1 mAbs

>XENP016434 YW243.55.S70[PD-L1]_H0L0_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27506-27510)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVVWRQAPGKGLEWVAVWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
AGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP016434 YW243.55.S70[PD-L1]_H0L0_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27511-27515)
DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSFGSGSGTDFTLTISLQPE
DFATYYCQYLYHPATFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024118 avelumab[PD-L1]_H1L1_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27516-27520)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPV
GPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP024118 avelumab[PD-L1]_H1L1_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27521-27525)
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISG
LQAEDADYYCSSYTSSTRVFGTGTQVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV
KAGVETTPSKQSNNKYAASSYLSLTPEQWKSRSYSCQVTHEGSTVEKTVAPTECS

>XENP024119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27526-27530)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNK
NSLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 73E

>XENP024119 durvalumab[PD-L1]_H1L1_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27531-27535)
 EIVLTQSPGTLSPGERATLSCRASQRVSSSYLA^{WYQQKPGQAPRLLIY}DASSRATGIPDRFSGSGSGTDFTLTISRLEPE
 DFAVYYCQQYGSLPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
 SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Prototype anti-PD-1 mAbs

>XENP024120 LOPD180[PD-1]_H1L1_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27536-27540)
 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYYNGNTYYNPSLRSRVTISVDTSKNQF
 SLKLSSVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
 YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
 CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
 PENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024120 LOPD180[PD-1]_H1L1_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27541-27545)
 QSVLTQPPSASGTPGQRTVISC^{SGSNSNIGSNSVNWY}QQLPGTAPKLLIYGNNQRPSGV^{PDRFSGSKSGTSASLAISGL}
 QSEDEADYYCAAWDDSLNGPVFGGGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADS
 SPVKAGVETTTPSKQSNKNYAASSYLSLTPEQWKSHRYSYSCQVTHEGSTVEKTVAPTECS

>XENP024121 mAb7(1.2)[PD-1]_H1L1_IgG1_PVA_/S267K Heavy Chain (SEQ ID NOS 27546-27550)
 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYWMNWRQAPGQGLEWIGVIHPSDSETWLDQKFKDRVTITVDKST
 STAYMELSSLRSEDTAVYYCAREHYGTSPFAYWGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPP
 VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
 KTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP024121 mAb7(1.2)[PD-1]_H1L1_IgG1_PVA_/S267K Light Chain (SEQ ID NOS 27551-27555)
 EIVLTQSPATLSLSPGERATLSCRASESDNYGMSFMNWFQQKPGQPPKLLIHAASNQGS^{GVPSRFS}SGSGSGTDFTLTIS
 SLEPEDFAVYFCQQSKEVPYTFGGGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
 SGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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 (SEQ ID NOS 27556-27560)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQLSS
LTSEDSAVYFCARSPDYYGTS~~LA~~WFDYWGGQGLTVTVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWEQGDVFSCSV
MHEALHNHYTQKSLSLSPGK

>XENP021832 GSK_314.8[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27561-27570)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNS
LRAEDTAVYYCARRHWPGGFDYWGGQGLTVTVSS/~~GGGGSGGGSGGGGS~~/DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA
WYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQLYHPATFGQGTKVEIK/EPKSSDKTHTCPPCPA
PPVAGPSVFLFPPKPKDTLMISRTPETCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLSDSGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021832 GSK_314.8[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain (SEQ ID NOS 27571-27575)

DIVMTQAAPSVPTPGESVSISCRSSKSPLHSNGNIYLYWFLQRPQGSPQLLIYRMSNLASGVDPDRFSGSGSGTFTLKISRVEAEDVG
VYYCMQHLEYPYTFGGGTGLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
STYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021833 GSK_88.2[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27576-27580)

QVQLQQPGAELVRPGASVKLSCKASGYSTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSNTAYMQLT
PTSEDSAVYYCTRWNLSYFYDNNYYLDYWGGQGLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLSDSGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

>XENP021833 GSK_88.2[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27581-27590)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHVWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNTAYLQMNS
LRAEDTAVYYCARRHWPGGFDYWGGQGLTVTVSS/~~GGGGSGGGSGGGGS~~/DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVA
WYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQLYHPATFGQGTKVEIK/EPKSSDKTHTCPPCPA
PPVAGPSVFLFPPKPKDTLMISRTPETCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLSDSGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 73G

>XENP021833 GSK_88.2[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain (SEQ ID NOS 27591-27595)

DIVMTQAAPSVPTPGESVSISCRSSKSLHNSGNTYLYWFLQRPGQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRIS
RVEAEDVGVIYCMQHLEYPWTFGGGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021834 jMab-138[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27596-27600)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

>XENP021834 jMab-138[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27601-27610)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAVISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAGDTAVYYCARRHWPGGFDYWGQGTITVTVSS/GGGGSGGGGSGGGGS/DIQMTQSPSSLSASVGR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFG
QGTEKVEIK/EPKSSDKHTCPCPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENP021834 jMab-138[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain (SEQ ID NOS 27611-27615)

EIVLTQSPGTLSPGERATLSCRASQNISSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021835 jMab-139[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27616-27620)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKHTCPC
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
VLHQQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK

Figure 73H

>XENP021835 jMab-139[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27621-27630)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGTLTVTVSS/GGGGSGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFG
QGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENP021835 jMab-139[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain (SEQ ID NOS 27631-27635)

EIVLTQSPGTLSLSPGERATLSCRASQSISSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQFGSSPMCSFGQGKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021836 jMab-136[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27636-27640)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRD
TSISTAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVTSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCFSVMHEALHNHYTQKSLSLSPGK

>XENP021836 jMab-136[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27641-27650)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGGTLTVTVSS/GGGGSGGGSGGGGS/DIQMTQSPSSLSASVGDR
VTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYLYHPATFG
QGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKL
TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSL
SPGK

>XENP021836 jMab-136[ICOS]_H0L0_Fab-YW243.55.S70[PD-L1]_H0L0_scFv Light Chain (SEQ ID NOS 27651-27655)

DIQMTQSPSSVSASVGDRVTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQANSFPWTFGQGKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
SQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74A**Anti-PD-1-Fab x Anti-ICOS-scFv Bottle-openers**

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27656-27660)

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRIYADSVKGRFTISRDN SKN
 TLFLQMNSLRAEDTAVYYCATNDDYWGQGT¹LVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPV
 AGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
 WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
 NYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27661-27670)

QVQLVESGGGVVQPGRSLRLSCKASGITFSNSGMHWVRQAPGKGLEWVAVIWIYDGSKRIYADSVKGRFTISRDN SKN
 TLFLQMNSLRAEDTAVYYCATNDDYWGQGT¹LVTVSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERA
 TLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLT¹TISSLEPEDFAVYYCQSSNWPR
 TFGQGTKEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDG
 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQM
 TKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNH
 YTQKSLSLSPGK

>XENP018920 nivolumab[PD-1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27671-27675)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLT¹ISS
 LEPEDFAVYYCQSSNWPRPTFGQGTKEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
 LQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27676-27680)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYYNGNTYYNP¹SLRSRV¹TISVDTSK
 NQFSLKLSSVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALG
 CLVKDYFPEPVTVS¹WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSC
 DKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNS
 TYRVVSVLTVLHQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
 DIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27681-27690)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
 TAYMELSR¹LRSDDTAVYYCARTYYIDSSGYHDAFDI¹WGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
 PSSVSASVGRV¹TITCRASQGISRL¹LAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLT¹ISSLPEDFA
 TYYCQQA¹NSFPWTFGQGTKEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHE
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREP
 QVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMEALHNHYTQKSLSLSPGK

>XENP024130 LOPD180[PD-1]_H1L1_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27691-27695)

QSVLTQPPSASGTPGQRTVISC¹SGSNSNIGSNSVNWYQQLPGTAPKLLIYGN¹QRPSGVPDRFSGSKSGTSASLAIS
 GLQSEDEADYYCAAWDDSLNGPVFGGGTKVTVL/GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWK
 ADSSPVKAGVETTPSKQSN¹NKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

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 (SEQ ID NOS 27696-27700)
 QVQLQQPGTELMKPGASVKLSCKASGYTFTTYYWMHWVKQRPQGQLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
 TAYIQLSSLTSEDSAVYFCARSPDYTGTS~~LA~~WFDYWGQGT~~LV~~TVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVK
 DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH
 TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV
 VSVLT~~TV~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
 EWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGQDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27701-27710)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN~~Y~~ASHRYTGVPDRFTGSGYGTEFTLT~~IS~~
 VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVKPGGSLRLSCVAS
 GFTFSNYWMNWVRQAPGKLEWVAEIRLYSN~~NY~~ATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG~~V~~YYCTRY
 GNYGGYFDVWGRGTLTVTSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~TV~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREQMTKNQV~~KL~~TCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
 VMHEALHNHYTQKSLSLSPGK

>XENP021828 GSK_314.8[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27711-27715)
 DIVMTQAAPSVPTPGESVSI~~SCR~~SSKSP~~L~~HSNGNIYLYWFLQRPQGSPQLLIYRMSN~~LA~~SGVPDRFSGSGSGTTFT
 LKISRVEAEDGVYYCMQHLEYPYTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC~~LL~~NNFYPREAKVQW
 KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27716-27720)
 QVQLQQPGAELVRPGASVKLSCKASGYSTSYWINWVKQRPQGQLEWIGNIYPSDSYTNYNQMF~~K~~DKATLTVDKSSN
 TAYMQLTSPTSEDSAVYYCTRWNL~~SY~~FDNNYYLDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
 KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
 HTCPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
 VVSVLT~~TV~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
 VEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGQDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27721-27730)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLIN~~Y~~ASHRYTGVPDRFTGSGYGTEFTLT~~IS~~
 VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/~~GKPGSGKPGSGKPGSGKPGS~~/EVQLVESGGGLVKPGGSLRLSCVAS
 GFTFSNYWMNWVRQAPGKLEWVAEIRLYSN~~NY~~ATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTG~~V~~YYCTRY
 GNYGGYFDVWGRGTLTVTSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~TV~~LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREQMTKNQV~~KL~~TCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
 VMHEALHNHYTQKSLSLSPGK

>XENP021829 GSK_88.2[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27731-27735)
 DIVMTQAAPSVPTPGESVSI~~SCR~~SSKSL~~L~~HSNGNTYLYWFLQRPQGSPQLLIYRMSN~~LA~~SGVPDRFSGSGSGTAFT
 LRISRVEAEDGVYYCMQHLEYPWT~~F~~GGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC~~LL~~NNFYPREAKVQW
 KVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74C

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>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ
ID NOS 27736-27740)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQM
NSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
(SEQ ID NOS 27741-27750)
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYASHRYTGVPDRFTGSGYGTEFTLTISSVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021830 jMab-138[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS
27751-27755)
EIVLTQSPGTLSLSPGERATLSCRASQNIRSSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain (SEQ
ID NOS 27756-27760)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQM
NSLRAGDTAVYYCVRDKRTVTHEHYYYGMDVWGQGTTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain
(SEQ ID NOS 27761-27770)
EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLINYASHRYTGVPDRFTGSGYGTEFTLTISSVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVYYCTRYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVMEALHNHYTQKSLSLSPGK

>XENP021831 jMab-139[ICOS]_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS
27771-27775)
EIVLTQSPGTLSLSPGERATLSCRASQSISSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
SVTEQDSKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Fab-Fc Heavy Chain
(SEQ ID NOS 27776-27780)
QVQLVQSGAEVKKPGSSVKVCSKASGYTFTDYAMHWVRQAPGQGLEWMGLISIYSDHTNYNQKFQGRVTITADKSTSTAYME
LSSLRSEDTAVYYCGRNNYGNYGWYFDVWGQGTTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFL
FPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWEQGDVDFSCSVMEALHNHYTQKSLSLSPGK

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Figure 74D

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27781-27790)
 EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYNASHRYTGVPDRFTGSGYGTEFTLTISS
 VQSEDFGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCVAS
 GFTFSNYWMNWVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNNLKTEDTGVIYCTRY
 GNYGGYFDVWGRGTLTVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSREQMKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 VMHEALHNHYTQKSLSLSPGK

>XENP022348 WO2016059602_GSK_H0L0_Fab-1G6_L1.194_H1.279_scFv Light Chain (SEQ ID NOS 27791-27795)
 EIVLTQSPATLSLSPGERATLSCSASSSVSYMHYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDYTLTIS
 EPEDFAVYYCFQGSYGYPTFGGQTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNAL
 QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Anti-PD-L1 x anti-ICOS Antibodies

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Fab-Fc Heavy Chain (SEQ ID NOS 27796-27800)
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKN
 TAYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
 PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPC
 PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLT
 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
 GPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27801-27810)
 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
 TAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIHWGQGTMTVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
 PSSVSASVGDRTITCRASQGISRLRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFA
 TYYCQQAANSFPWTFGQGTKVEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHE
 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
 QVYTLPPSREQMKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCVMHEALHNHYTQKSLSLSPGK

>XENP021748 YW243.55.S70[PD-L1]_H0L0_Fab-[anti-ICOS]_H0L0_scFv Light Chain (SEQ ID NOS 27811-27815)
 DIQMTQSPSSLSASVGRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTIS
 LQPEDFATYYCQYLYHPATFGGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNA
 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 (SEQ ID NOS 27816-27820)
 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHWRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSIS
 TAYMELSRRLSDDTAVYYCARTYYDSSGYHDAFDIHWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCL
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDK
 THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
 VEFWESDGPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK

Figure 74E

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv scFv-Fc Heavy Chain (SEQ ID NOS 27821-27830)
 EVQLVESGGGLVKPGGSLRLSCAASGFTFSYTMHWVRQAPGKGLEWVSFISYDGNKYKYADSVKGRFTISRDNAKNSLYLQ
 MNSLRAEDTAVYYCARGGHLGPFDLWGQGTMTVTSS/GKPGSGKPGSGKPGSGKPGS/EIVLTQSPATLSLSPGERATLSCR
ASQSVGSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVE
 IK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDI
 AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021749 [anti-ICOS]_H0L0_Fab-[anti-CTLA-4]_H3.23_L0.129_scFv Light Chain (SEQ ID NOS 27831-27835)
 DIQMTQSPSSVSASVGDRTITCRASQGISRL^{LA}WYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTIS^{SL}QPED
 FATYYCQQANSF^{FW}TFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^{LL}NNFYPREAKVQWKVDNALQSGNSQESV
 TEQDSKDS^{TY}SLSS^{TL}TL^{TS}SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

ICOS one-arm from alternative ICOS ABDs

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27836-27840)
 QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPGQGLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSSTAYIQ
 LSSLTSEDSAVYFCARSPDYYGTS^{LA}WFDYWGQGT^{LV}TVST/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
 WNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSV
 FLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCK
 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDGSF
 FLYSKLTVDKSRWEQGDV^FSCSVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27841)
 ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVE
 WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021861 GSK_314.8[ICOS]_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27842-27846)
 DIVMTQAAPSVPVTPGESVSISCRSSKSP^{LH}SNGNIYLYWFLQRPQGSPQLLIYRMSNLASGV^{PD}RFSGSGSGTTFTLKISR
 VEAEDVGYYCMQHLEYPYTFGGG^TKTLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^{LL}NNFYPREAKVQWKVDNALQSGN
 SQESVTEQDSKDS^{TY}SLSS^{TL}TL^{TS}SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ ID NOS 27847-27851)
 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISR^{EN}AKNSLYLQM
 NSLRAGDTAVYYCVRDNRKVT^{HE}HY^{YY}YGM^{DV}WGQGT^{TV}TVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV^{PS}SSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
 SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPVLDSDG
 SFFLYSKLTVDKSRWEQGDV^FSCSVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ ID NO: 27852)
 ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNS
 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVE
 WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021863 jMab-138[ICOS]_H0L0 one-arm mAb Light Chain (SEQ ID NOS 27853-27857)
 EIVLTQSPGTLSLSPGERATLSCRASQNI^{RS}SYLAWYQQKPGQAPGLLIY^GASSRATGIPDRFSGSGSGTDFTLTISRLEPE
 DFAVYYCQQ^FGSSPMCSFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVC^{LL}NNFYPREAKVQWKVDNALQSGNSQE
 SVTEQDSKDS^{TY}SLSS^{TL}TL^{TS}SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 74F

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>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fab-Fc Heavy Chain (SEQ
ID NOS 27858-27862)
QVQLVQSGAEVKKPGSSVKVSCASGYTFTDYAMHWVRQAPGQGLEWMGLISIIYSDHTNYNQKFQGRVTITADKSTS
TAYMELSSLRSEDTAVYYCGRNNYGNYGWYFDVWGQGTITVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Fc-only Heavy Chain (SEQ
ID NO: 27863)
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFKWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVK
GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK

>XENP022349 WO2016059602[ICOS]_GSK_H0L0 one-arm mAb Light Chain (SEQ ID NOS
27864-27868)
EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRLLIYDTSKLGIPARFSGSGSGTDYTLTISSL
EPEDFAVYYCFQGSQPYTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

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Figure 75A

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

monomer 1 (Fab-scFv side) (SEQ ID NO:28991)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

monomer 2 (Fab side) (SEQ ID NO:28992)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

constant light chain (SEQ ID NO:28993)

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 75B**mAb-scFv backbone 2**

Fab-scFv-Hc - 356D/358L allotype (SEQ ID NO:28994)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - 356D/358L allotype (SEQ ID NO:28995)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDQLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

mAb-scFv backbone 3

>mAb-scFv Fab-scFv-Hc - N297A (SEQ ID NO:28996)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCS
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - N297A (SEQ ID NO:28997)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK

Figure 75C

mAb-scFv backbone 4

>mAb-scFv Fab-scFv-Hc - N297S (SEQ ID NO:28998)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVDFSCS
VMHEALHNHYTQKSLSLSPGK

>mAb-scFv Fab-Hc - N297S (SEQ ID NO:28999)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKVEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPE
VKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCS
VMHEALHNHYTQKSLSLSPGK

mAb-scFv backbone 5

mAb-scFv Fab-scFv-IgG4-Hc (SEQ ID NO:29000)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVNHHKPSDTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVKQEDPEVQ
FNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEEGDVDFSCSVM
HEALHNHYTQKSLSLGLGK

>mAb-scFv Fab-IgG4-Hc (SEQ ID NO:29001)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVNHHKPSDTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVKQEDPEVQ
FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
PPSQEQMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQEGNVDFSCSVM
HEALHNHYTQKSLSLGLGK

Figure 75D

mAb-scFv backbone 6

>mAb-scFv Fab-scFv-IgG2-Hc - without S267K (SEQ ID NO:29002)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPMLDSGSSFFLYSKLTVDKSRWEQGDVFSCSVMH
EALHNHYTQKSLSLSPGK

>mAb-scFv Fab-IgG2-Hc - without S267K (SEQ ID NO:29003)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVKCSVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREQMTKNQVSLTCLVKGFIYPSDIAVEWESNGQENNYKTTTPMLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

mAb-scFv backbone 7

>mAb-scFv Fab-scFv-IgG2-Hc - with S267K (SEQ ID NO:29004)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEEFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTTTPMLDSGSSFFLYSKLTVDKSRWEQGDVFSCSVMH
EALHNHYTQKSLSLSPGK

>mAb-scFv Fab-IgG2-Hc - with S267K (SEQ ID NO:29005)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTVKCSVECPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF
PSREQMTKNQVSLTCLVKGFIYPSDIAVEWESNGQENNYKTTTPMLDSGSSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

Figure 76A additional anti-PD-1 sequences

Merck Pembrolizumab VH (SEQ ID NO: 29006)

QVQLVQSGVEVKKPGASVKVSKKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNFNEKFKNRVTLTDSST
TTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTTVTVSS

Merck Pembrolizumab VL (SEQ ID NO: 29007)

EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLAstyleSGVparfsgsgsgtdftltiss
LEPEDFAVYYCQHSRDLPLTFGGGTKVEIK

BMS nivolumab VH (SEQ ID NO: 29008)

QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWDGSKRYYADSVKGRFTISRDN SKN
TLFLQMNSLRAEDTAVYYCATNDDYWGQGTTLTVTVSS

BMS nivolumab VL (SEQ ID NO: 29009)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSEPED
FAVYYCQSSNWPRTFGQGTKVEIK

Teva pidilizumab VH (SEQ ID NO: 29010)

QVQLVQSGSELKKPGASVKISKASGYTFTNYGMNWVRQAPGQLQWMGWINTDSGESTYAEFEKGRFVFSLDTSVN
TAYLQITSLTAEDTGMVFCVRVGYDALDYWGQGTTLTVTVSS

Teva pidilizumab VL (SEQ ID NO: 29011)

EIVLTQSPSSLSASVGRVTITCSARSSVSYMHWFQQKPGKAPKLWIYRTSNLASGVPSRFSGSGSGTSYCLTINSLQPED
FATYYCQQRSSFPLTFGGGTKLEIK

Pfizer MK-3475 VH (SEQ ID NO: 29012)

QVQLVQSGVEVKKPGASVKVSKKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNFNEKFKNRVTLTDSST
TTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTTVTVSS

Pfizer MK-3475 VL (SEQ ID NO: 29013)

EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLAstyleSGVparfsgsgsgtdftltiss
LEPEDFAVYYCQHSRDLPLTFGGGTKVEIK

Novartis/Dana Farber BAP049 clone E VH (SEQ ID NO: 29014)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKNRVTITADKSTS
TAYMELSSLRSEDTAVYYCTRWTGTGAYWGQGTTVTVSS

Novartis/Dana Farber BAP049 clone E VL (SEQ ID NO: 29015)

EIVLTQSPATLSLSPGERATLSCKSSQSLDsgnqknfltwyqqkpgqaprllywastresgvpsrfsgsgsgtdftfti
SSLEAEDAATYYCQNDYSYPYTFGQGTKVEIK

Novartis/Dana Farber BAP049 clone B VH (SEQ ID NO: 29016)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTTYWMHWVRQATGQGLEWMGNIYPGTGGSNFDEKFKNRVTITADKSTS
TAYMELSSLRSEDTAVYYCTRWTGTGAYWGQGTTVTVSS

Novartis/Dana Farber BAP049 clone B VL (SEQ ID NO: 29017)

EIVLTQSPATLSLSPGERATLSCKSSQSLDsgnqknfltwyqqkpgkpklliywastresgvpsrfsgsgsgtdftfti
SSLQPEDATYYCQNDYSYPYTFGQGTKVEIK

Figure 76B

Regeneron H7798N VH (SEQ ID NO: 29018)

EVQLLESGGVLVQPGGSLRLSCAASGFTFSNFGMTWVRQAPGKGLEWVSGISGGGRDITYFADSVKGRFTISRDN SKNT
LYLQMNSLKGEDTAVYYCVKWGNIYFDYWGGQTLTVSS

Regeneron H7798N VH (SEQ ID NO: 29019)

DIQMTQSPSSLSASVGD SITITCRASLSINTFLN WYQQKPGKAPNLLIYAASSLHGGVPSRFSGSGSGTDFTLTIRTLQPED
FATYYCQSSNTPFTFGPGTVVDFR

Medimmune h1H3 Var 6 VH (SEQ ID NO: 29020)

EVQLVESGGGLVQPGGSLRLSCAASGFTFS DYGMHWVRQAPGKGLEWVAYISSGSYTIYYADSVKGRFTISRDN AKNT
LYLQMSSLRAEDTAVYYCARRGYGSFYEYFFDYWGQGTTTVTVSS

Medimmune h1H3 Var 6 VL (SEQ ID NO: 29021)

QIVLTQSPATLSLSPGERATLSCSASSSVSYMYWYQQKPGQAPRLLIYLT SNRATGIPARFSGSGSGTDYTLTISSLEPEDF
AVYYCQQWSSNPFTFGQGTKLEIK

Tesaro TSR-042/APE2058 VH (SEQ ID NO: 29022)

EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYDMSWVRQAPGKGLEWVSTISGGGSYTTYQDSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCASPYYAMDYWGQGTTTVTVSS

Tesaro TSR-042/APE2058 VL (SEQ ID NO: 29023)

DIQLTQSPSFLSAYVGDRVTITCKASQDVGTAVAWYQQKPGKAPKLLIYWASTLHTGVPSRFSGSGSGTEFTLTISSLQP
EDFATYYCQHYSSYPWTFGQGTKLEIK

Incyte Camrelizumab VH (SEQ ID NO: 29024)

EVQLVESGGGLVQPGGSLRLSCAASGFTFS SYMMSWVRQAPGKGLEWVATISGGGANTYYPDSVKGRFTISRDN AKNS
LYLQMNSLRAEDTAVYYCARQLYYFDYWGGQTTTVTVSS

Incyte Camrelizumab VL (SEQ ID NO: 29025)

DIQMTQSPSSLSASVGD RVTITCLASQTIGTWLTWYQQKPGKAPKLLIYTATSLADGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQVYSIPWTFGGGTKVEIK

Beigene 317-4B6 VH (SEQ ID NO: 29026)

QVQLQESGPGLVKPSETLSLTCTVSGFSLTSYGVHWIRQPPGKGLEWIGVIYADGSTNYPNPSLKS RVTISKDTSKNQVSL
KLSSVTAADTAVYYCARAYGNYWYIDVWGQGTTTVTVSS

Beigene 317-4B6 VL (SEQ ID NO: 29027)

DIVMTQSPDSLAVSLGERATINCKSSESVDNAWYQQKPGQPPKLLINYAFHRFTGV PDRFSGSGYGTDFTLTISSLQA
EDVAVYYCHQAYSSPYTFGQGTKLEIK

Beigene 326-4A3 VH (SEQ ID NO: 29028)

QVQLVQSGSELKKPGASVKVSKASGYTFTNYGMNWVRQAPGQGLKWMGWINNNAEPTYAQDFRGRFVFSLD TSA
STAYLQISSLKTEDTAVYYCARDVMDYWGQGTLTVTVSS

Beigene 326-4A3 VL (SEQ ID NO: 29029)

DIVLTQSPASLAVSPGQRATITCRASESVDNYGYSFMHWYQQKPGQPPKLLIYRASNLES GVPARFSGSGSGTDFTLTIN
PVEAEDTANYYCQSKSEYPTFGGGTKVEIK

Figure 76C

Macrogenics mAb 7 (1.2) VH (SEQ ID NO: 29030)

QVQLVQSGAEVKKPGASVKVSCKASGYSTSYWMNWVRQAPGQGLEWIGVIHPDSETWLDQKFKDRVITITVDKSTS
TAYMELSSLRSEDTAVYYCAREHYGTSPFAYWGQGLTVTVSS

Macrogenics mAb 7 (1.2) VL (SEQ ID NO: 29031)

EIVLTQSPATLSLSPGERATLSCRASESVSDNYGMSFMNWFQKPGQPPKLLIHAASNQGSVPSRFSGSGSGTDFTLTSS
LEPEDFAVYFCQQSKEVPYTFGGGTKVEIK

Junmeng Clone 38 VH (SEQ ID NO: 29032)

QGQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPIHGLEWIGVIESETGGTAYNQKFKGRVTITADKSTST
AYMELSSLRSEDTAVYYCAREGITTVATTYYWYFDVWGQGTTVTVSS

Junmeng Clone 38 VL (SEQ ID NO: 29033)

DVVMTQSPSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHVPLTFGQGTKLEIK

Junmeng Clone 39 VH (SEQ ID NO: 29034)

QGQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWMGVIESETGGTAYNQKFKGRAKITADKST
STAYMELSSLRSEDTAVYYCTREGITTVATTYYWYFDVWGQGTTVTVSS

Junmeng Clone 39 VL (SEQ ID NO: 29035)

DVVMTQSPSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHVPLTFGQGTKLEIK

Junmeng Clone 41 VH (SEQ ID NO: 29036)

QGQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWMGVIESETGGTAYNQKFQGRVTLTADKSS
STAYMELSSLRSEDTAVYYCTREGITTVATTYYWYFDVWGQGLTVTVSS

Junmeng Clone 41 VL (SEQ ID NO: 29037)

DVVMTQSPSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHVPLTFGQGTKLEIK

Junmeng Clone 48 VH (SEQ ID NO: 29038)

QGQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWMGVIESETGGTAYNQKFKGRAKITADKST
STAYMELSSLRSEDTAVYYCTREGITTVATTYYWYFDVWGQGTTVTVSS

Junmeng Clone 48 VL (SEQ ID NO: 29039)

DVVMTQSPSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPRLLIYKVSNRFSGVPDRFSGSGSGTDFTLKIS
RVEAEDVGYYCFQGSHVPLTFGQGTKLEIK

Wyeth PD1-17 VH (SEQ ID NO: 29040)

QVQLQESGPGVVKPSGTLSTCAISGSGISGGSIRSTRWWSWVRQSPGKGLEWIGEYHSGSTNYPNPSLKSRTISLDKS
RNHFSRLNSVTAADTAVYYCARQDYGDSGDWYFDLWGKGTMVTVSS

Wyeth PD1-17 VL (SEQ ID NO: 29041)

NFMLTQPHSVSESPGKTVTISCTRSSGSIASNSVQWYQQRPGSSPTTVIYEDNQRPSPGVPDRFSGSIDSSSNSASLTVSGLK
TEDEADYYCQSSDSSAVVFGSGTKLTVL

Figure 76D

Wyeth PD1-28 VH (SEQ ID NO: 29042)

EVQLVQSGAEVKKPGASVKVSCKASGYRFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTST
NTAYMELRSLRSDDTAVYYCARDADYSSSGSYWGQGLTVTVSS

Wyeth PD1-28 VL (SEQ ID NO: 29043)

SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVMVIYKDTERPSGIPERFSGSSSGTKVTLTISGVQAE
DEADYYCQSADNSITYRVFGGGKVTVL

Wyeth PD1-33 VH (SEQ ID NO: 29044)

QVQLVQSGAEVKKPGASVRVSCKASGYTLTSYYIHWVRQAPGQGLEWMGIINPRGATISYAQKFQGRVTMTRDTSTST
VYMELRNKSEDALYYCATAGIYGDFDYWGRGTLTVTVSS

Wyeth PD1-33 VL (SEQ ID NO: 29045)

QSALTQPASVSGSPGQSITISCTGTSNDVGGYNYVSWYQHHPGKAPKLIYDVTNRPSGVSDRFGSGSKSGNTASLTISGLL
AEDEGDYYCSSYTIVTNFEVLFGGGTKLTV

Wyeth PD1-35 VH (SEQ ID NO: 29046)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYNGNTYYNPSLRSLVTISVDASKNQF
SLKLSSVTAADTAVYYCARASDYVWGGYRYMDAFDIWGRGTLITVSS

Wyeth PD1-35 VL (SEQ ID NO: 29047)

QSVLTQPPSASGTPGQRVTISCSGSNSNIGSNSNVNWWYQQLPGTAPKLLIYGNNQRPSGVPDRFGSGSKSGTSASLAISGLQS
ENEADYYCAAWDSDLNGPVFGRGTKVTVL

Wyeth LOPD180 VH (SEQ ID NO: 29048)

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGAYYWSWIRQHPGKGLEWIGYIYNGNTYYNPSLRSRVTISVDTSKNQF
SLKLSSVTAADTAVYYCVRASDYVWGGYHYFDAFDLWGRGTLTVTVSS

Wyeth LOPD180 VL (SEQ ID NO: 29049)

QSVLTQPPSASGTPGQRVTISCSGSNSNIGSNSNVNWWYQQLPGTAPKLLIYGNNQRPSGVPDRFGSGSKSGTSASLAISGLQS
EDEADYYCAAWDSDLNGPVFGGGKVTVL

UCB Ab948 VH (SEQ ID NO: 29050)

EVQLQESGPGLVKPSQTLSTCTVTGYSITSDYAWNWRQPPGKKLEWMGYINYSGSTSYNPSLKSRTISRDTSKNQFS
LKLSSVTAADTAVYYCARWIGSSAWYFDVWGQGLTVTVSS

UCB Ab948 VL (SEQ ID NO: 29051)

DVLMTQTPLSLSVTPGQPASISCRSGQNIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFFGVDPDRISGSGSGTDFTLKIS
RVEAEDVGIFYFCFGSHVPFTFGQGKLEIK

Dana-Farber EH-12.2h7 VH (SEQ ID NO: 29052)

QVQLVQSGHEVKQPGASVKMSCKASGYSTSSWIHWVRQAPGQGLEWIGYIYPSTGFTEYNQKFKDRATLTADKSTST
AYMELSSLRSEDATVYYCARWRDSSGYHAMDYWGQGLTVTVSS

Dana-Farber EH-12.2h7 VL (SEQ ID NO: 29053)

EIVLTQSPATLSLSPGQRLTISCRASQSVSTSGYSYMHWYQQKPDQSPKLLIKFGSNLESGIPARFSGSGSGTDFTLTISSE
PEDFATYYCQHSWEIPYTFGQGKLEIK

Figure 76E

Sorrento RG1H10 VH (SEQ ID NO: 29054)

QVQLVQSGSELKKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKIGNPTYAQGFTGRFVFSLDTSIST
 YLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVSS

Sorrento RG1H10 VL (SEQ ID NO: 29055)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-H2A-22-1S VH (SEQ ID NO: 29056)

QVQLVQSGSELKKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
 TYLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVSS

Sorrento RG1H10-H2A-22-1S VL (SEQ ID NO: 29057)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-H2A-27-2S VH (SEQ ID NO: 29058)

QVQLVQSGSELKKPGASVKISCKASGYIFSDNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
 TYLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVSS

Sorrento RG1H10-H2A-27-2S VL (SEQ ID NO: 29059)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-3C VH (SEQ ID NO: 29060)

QVQLVQSGSELKKPGASVKISCKASGYTFSDNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
 TYLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVSS

Sorrento RG1H10-3C VL (SEQ ID NO: 29061)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-16C VH (SEQ ID NO: 29062)

QVQLVQSGSELKKPGASVKISCKASGYTFSDNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
 TYLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVS

Sorrento RG1H10-16C VL (SEQ ID NO: 29063)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-17C VH (SEQ ID NO: 29064)

QVQLVQSGSELKKPGASVKISCKASGYKFSNGVNWVRQAPGQGLEWMGWINTKSGNPTYAQGFTGRFVFSLDTSIST
 TYLQISSQLAGDTAVYYCAREHDYYYGMDVWGQGTTVTVSS

Sorrento RG1H10-17C VL (SEQ ID NO: 29065)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
 TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Figure 76F

Sorrento RG1H10-19C VH (SEQ ID NO: 29066)

QVQLVQSGSELKKPGASVKISCKASGYKFS DNGVNWVRQAPGQGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTTTVTVSS

Sorrento RG1H10-19C VL (SEQ ID NO: 29067)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-21C VH (SEQ ID NO: 29068)

QVQLVQSGSELKKPGASVKISCKASGYTFSDNGVNWVRQAPGQGLEWMGWINTKSGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTTTVTVSS

Sorrento RG1H10-21C VL (SEQ ID NO: 29069)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Sorrento RG1H10-23C2 VH (SEQ ID NO: 29070)

QVQLVQSGSELKKPGASVKISCKASGYKFS DNGVNWVRQAPGQGLEWMGWINTKDGNPTYAQGFTGRFVFSLDTSIST
TYLQISSLQAGDTAVYYCAREHDYYYGMDVWGQGTTTVTVSS

Sorrento RG1H10-23C2 VL (SEQ ID NO: 29071)

QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQHHPGKAPKLMIEVSKRPSGVPDRFSGSKSAITASLTISGLL
TEDEADYYCSAWDDSLNADVFGGGTKVTVL

Rinat mAb 7 VH (SEQ ID NO: 29072)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWINWVRQAPGQGLEWMGNIYPGSSLTNYNEKFKNRVTMTRDTSTS
TVYMELSSLRSEDTAVYYCARLSTGTFAYWGQGTLLTVTVSS

Rinat mAb 7 VL (SEQ ID NO: 29073)

DIVMTQSPDSLAVSLGERATINCKSSQSLWDSGNQKNFLTWYQQKPGQPPKLLIYWTSYRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQNDYFYPHTFGGGTKVEIK

Celgene PD1AB-6 VH (SEQ ID NO: 29074)

EVQLVQSGAEVKKPGATVKISCKASGFNIKDTYMHVWVQAPGKGLEWMGRIDPANGDRKYDPKFQGRVTITADTSTD
TAYMELSSLRSEDTAVYYCARSGPVYYYGSSYVMDYWGQGTTTVTVSS

Celgene PD1AB-6 VL (SEQ ID NO: 29075)

DIVMTQSPDSLAVSLGERATINCKSGQSVLYSSNQKNFLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCHQYLYSWTFQGQGTKLEIK

Figure 77A additional ICOS sequences

GSK 88.2 VH (SEQ ID NO: 29076)

QVQLQQPGAELVRPGASVKLSCKASGYSTSYWINWVKQRPQGQLEWIGNIYPSDSYTNYNQMFKDKATLTVDKSSN
TAYMQLTSPTSEDSAVYYCTRWNLSSYFDNNYLDYWGQGTTLTVSS

GSK 88.2 VL (SEQ ID NO: 29077)

DIVMTQAAPSPVPTPGESVSISCRSSKSLLSHNGNTYLYWFLQRPQGQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRIS
RVEAEDVGVYYCMQHLEYPWTFGGGKLEIK

GSK 314.8 VH (SEQ ID NO: 29078)

QVQLQQPGTELMKPGASVKLSCKASGYTFTTYWMHWVKQRPQGQLEWIGEIDPSDSYVNYNQNFKGKATLTVDKSSS
TAYIQLSSLTSEDSAVYFCARSPDYGTSLAWFDYWGQGTTLTVST

GSK 314.8 VL (SEQ ID NO: 29079)

DIVMTQAAPSPVPTPGESVSISCRSSKSPLSHNGNIYLYWFLQRPQGQSPQLLIYRMSNLASGVPDRFSGSGSGTFTLKISR
VEAEDVGVYYCMQHLEYPYTFGGGKLEIK

GSK H2L5 VH (SEQ ID NO: 29080)

QVQLVQSGAEVKKPGSSVKVSCASGYTFTDYAMHWVRQAPGQGLEWMGLISYSDHTNYNQKFQGRVTITADKSTS
TAYMELSSLRSEDAVYYCGRNNYGNYGWYFDVWGQGTTLTVSS

GSK H2L5 VL (SEQ ID NO: 29081)

EIVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRLIYDTSKLASGIPARFSGSGSGTDYTLTISSLEPEDF
AVYYCFQGSQGYPTFGGQTKLEIK

Jounce 37A10S713 VH (SEQ ID NO: 29082)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYWMDWVRQAPGKGLVWVSNIDEDGSITEYSPFVKGRFTISRDNKNT
LYLQMNSLRSEDVAVYYCTRWGRFGFDSWGQGTTLTVSS

Jounce 37A10S713 VL (SEQ ID NO: 29083)

DIVMTQSPDSLAVSLGERATINCKSSQSLLSGSFNYLTWYQQKPGQPPKLLIFYASTRHTGVPDRFSGSGSGTDFTLTISS
LQAEDVAVYYCHHHYNAPPTFGPGTKVDIK

Japan Tobacco Jmab-136 VH (SEQ ID NO: 29084)

QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHWVRQAPGQGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTS
ISTAYMELSLRSDDTAVYYCARTYYDSSGYHDAFDIWGQGTMTVTVSS

Japan Tobacco Jmab-136 VL (SEQ ID NO: 29085)

DIQMTQSPSSVSASVGDRTITCRASQGISRLAWYQQKPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQANSFPWTFGQGTKVEIK

Japan Tobacco Jmab-138 VH (SEQ ID NO: 29086)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDNRKVTHEHYYYGMDVWGQGTTLTVSS

Japan Tobacco Jmab-138 VL (SEQ ID NO: 29087)

EIVLTQSPGTLSLSPGERATLSCRASQNISSYLAWYQQKPGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQFGSSPMCSFGQGTKLEIK

Figure 77B

Japan Tobacco Jmab-139 VH (SEQ ID NO: 29088)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSAIGTAGDTYYPGSVKGRFTISRENAKNSL
YLQMNSLRAGDTAVYYCVRDKRTVTHEHYYYYGMDVWGQGTTVTVSS

Japan Tobacco Jmab-139 VL (SEQ ID NO: 29089)

EIVLTQSPGTLSPGERATLSCRASQSISSSSLAWYQQKPGQAPGLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPED
FAVYYCQQFGSSPMCSFGQGTKLEIK

Figure 78A additional PD-L1 sequences

AstraZeneca/Celgene/MedImmune 2.14H9 OPT VH (SEQ ID NO: 29090)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNANKN
SLYLQMNSLRAEDTAVYYCAREGGWFGELAFDYWGQGTLLTVSS

AstraZeneca/Celgene/MedImmune 2.14H9 OPT VL (SEQ ID NO: 29091)

EIVLTQSPGTLSPGERATLSCRASQRVSSSYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQYGSLLPWTFGQGTKVEIK

Genentech atezolizumab VH (SEQ ID NO: 29092)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDSWIHWVRQAPGKGLEWVAWISPYGGSTYYADSVKGRFTISADTSKNT
AYLQMNSLRAEDTAVYYCARRHWPGGFDYWGQGTLLTVSA

Genentech atezolizumab VL (SEQ ID NO: 29093)

DIQMTQSPSSLSASVGDRTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQYLYHPATFGQGTKVEIKR

Merck/Pfizer avelumab VH (SEQ ID NO: 29094)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYIMMWVRQAPGKGLEWVSSIYPSGGITFYADTVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCARIKLGTVTTVDYWGQGTLLTVSS

Merck/Pfizer avelumab VL (SEQ ID NO: 29095)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEADYYCSSYTSSSTRVFGTGTKVTVL

Medarex 12A4 VH (SEQ ID NO: 29096)

QVQLVQSGAEVKKPGSSVKVSKCTSGDTFSTYAIWVRQAPGQGLEWMGGIPIFGKAHYAQKFQGRVTITADESTSTA
YMESSLRSEDYAVYYFCARKFHFVSGSPFGMDVWGQGTITVTVSS

Medarex 12A4 VL (SEQ ID NO: 29097)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLPEP
FAVYYCQQRSNWPTFGQGTKVEIK

Medarex 3G10 VH (SEQ ID NO: 29098)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYGFSWVRQAPGQGLEWMGWITAYNGNTNYAQKLQGRVTMTTDT
TSTVYMESSLRSDDTAVYYCARDYFYGMDVWGQGTITVTVSS

Medarex 3G10 VL (SEQ ID NO: 29099)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLVWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLPEP
FAVYYCQQRSNWPTFGQGTKVEIK

Medarex 10A5 VH (SEQ ID NO: 29100)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDVHWVRQAPGQRLEWMGWLHADTGITKFSQKFQGRVTITRDT
TAS TAYMESSLRSEDYAVYYCARERIQWFDYWGQGTLLTVSS

Medarex 10A5 VL (SEQ ID NO: 29101)

DIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQYNSYPYTFGQGTKLEIK

Figure 78B

Amplimmune/GSK/MedImmune h3D10 Var1 VH (SEQ ID NO: 29102)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQGLEWMGDIDPNYGGTNYAQKFQGRVTMTRDTSI
STAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var1 VL (SEQ ID NO: 29103)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQAPRLLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var2 VH (SEQ ID NO: 29104)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTRDTSI
STAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var2 VL (SEQ ID NO: 29105)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQSPRPLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var3 VH (SEQ ID NO: 29106)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTRDTSI
STAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var3 VL (SEQ ID NO: 29107)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var4 VH (SEQ ID NO: 29108)

EVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQSLEWMGDIDPNYGGTNYNQKFQGRVTMTVDRS
SSTAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var4 VL (SEQ ID NO: 29109)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQSPRPLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var5 VH (SEQ ID NO: 29110)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var5 VL (SEQ ID NO: 29111)

DIQLTQSPSILSASVGDRTITCRASSSVSYIYWFQQKPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var6 VH (SEQ ID NO: 29112)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYAASVKGRFTISVDRSKSI
AYLQMSSSLKTEDTAVYYCTRGAALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var6 VL (SEQ ID NO: 29113)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQAPRLLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Figure 78C

Amplimmune/GSK/MedImmune h3D10 Var7 VH (SEQ ID NO: 29114)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQGLEWMGDIDPNYGGTNYAQKFQGRVTMTRDTS
ISTAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var7 VL (SEQ ID NO: 29115)

DIQLTQSPSSLSASVGDRVITITCRASSGVSYIYWFQKPGKAPKLLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var8 VH (SEQ ID NO: 29116)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var8 VL (SEQ ID NO: 29117)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var9 VH (SEQ ID NO: 29118)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var9 VL (SEQ ID NO: 29119)

DIQLTQSPSSLSASVGDRVITITCRASSGVSYIYWFQKPGKAPKPLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var10 VH (SEQ ID NO: 29120)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var10 VL (SEQ ID NO: 29121)

DIQLTQSPSILSASVGDRVITITCRASSSVSYIYWFQKPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var11 VH (SEQ ID NO: 29122)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYAASVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCTRGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var11 VL (SEQ ID NO: 29123)

EIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQKPGQAPRLLIYAAFNRATGIPARFSGSGSGTDYTLTISSLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var12 VH (SEQ ID NO: 29124)

QVQLVQSGAEVKKPGASVKVSCKASGYTFPDYYMNWVRQAPGQGLEWMGDIDPNYGGTNYAQKFQGRVTMTRDTS
ISTAYMELSRLRSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var12 VL (SEQ ID NO: 29125)

DIQLTQSPSSLSASVGDRVITITCRASSGVSYIYWFQKPGKAPKLLIYAAFNLASGVPSRFSGSGSGTEYTLTISSLQPEDF
ATYYCQQWSNNPLTFGQGTKVEIK

Figure 78D

Amplimmune/GSK/MedImmune h3D10 Var13 VH (SEQ ID NO: 29126)

EVQLVESGGGLVQPGRSLRLSCTASGYTFPDYYMNWVRQAPGKGLEWVGIDIDPNYGGTTYNQSVKGRFTISVDRSKSI
AYLQMSSLKTEDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var13 VL (SEQ ID NO: 29127)

QIVLTQSPATLSLSPGERATLSCRASSSVSYIYWFQQKPGQSPRPLIYATFNLASGIPARFSGSGSGTSYTLTISRLEPEDFA
VYYCQQWSNNPLTFGQGTKVEIK

Amplimmune/GSK/MedImmune h3D10 Var14 VH (SEQ ID NO: 29128)

EVQLVQSGAEVKKPGASVKVSKASGYTFPDYYMNWVRQAPGQSLEWMDIDIDPNYGGTNYNQKFQGRVTMTVDRS
SSTAYMELSRLSDDTAVYYCARGALTDWGQGTMTVTVSS

Amplimmune/GSK/MedImmune h3D10 Var14 VL (SEQ ID NO: 29129)

DIQLTQSPSILSASVGDRVITICRASSSVSYIYWFQQKPGKAPKPLIYATFNLASGVPSRFSGSGSGTSYTLTISSLQPEDFA
TYYCQQWSNNPLTFGQGTKVEIK

Eli Lily Antibody A VH (SEQ ID NO: 29130)

QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTA
YMELSSLRSEDTAVYYCARSPDYSPYGYGMDVWGQGTITVTVSS

Eli Lily Antibody A VL (SEQ ID NO: 29131)

QSVLTQPPSASGTPGQRTISCSGSSNIGSNTVNWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAISGLQSE
DEADYYCQSYDSSLSGSVFGGKILTVLG

Cytomyx C5H9v2 VH (SEQ ID NO: 29132)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSSIWRNGIVTVYADSVKGRFTISRDNKNT
LYLQMNSLRAEDTAVYYCAKWSAAFDYWGQGTILVTVSS

Cytomyx C5H9v2 VL (SEQ ID NO: 29133)

DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQDNGYPSTFGGGTKVEIKR

Dana-Farber/Novartis Humanized 29E.2A3 VH (SEQ ID NO: 29134)

CKASGYTFTSYVMHWVKAPGQRLEWIGYVNPFDGTYNEMFKGRATLTSDKSTSTAYMELSSLRSEDTAVYYCAR
QAWGYPWGQGTILVTVSS

Dana-Farber/Novartis Humanized 29E.2A3 VL (SEQ ID NO: 29135)

DIVLTQSPATLSLSPGERATLSCRATESVEYYGTSVLVQWYQKPGQPPKLLIYAASSVDSGVPSRFSGSGSGTDFTLTINS
LEAEDAATYFCQSRVPYTFGQGTKLEIK

Dana-Farber/Novartis 1B9 VH (SEQ ID NO: 29136)

DVQLQESGPGLVKPSQSLTCTVTGYSITSDHAWNWRQVPGNKLEWMGYITYRGSTTYSPLKSRISITRDTSKNQFF
LQLNSVTTEDTATYYCARSMITGYYVMDYWGQGTSTVTVSS

Dana-Farber/Novartis 1B9 VL (SEQ ID NO: 29137)

DIVMTQSHKFMSTSLGDRVITICKASQDVGISVVWYQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTINNVO
SEDLADYFCQYSSYPLTVGAGTKLELK

Figure 78E

Dana-Farber/Novartis 4H1 VH (SEQ ID NO: 29138)

DVQLQESGPGLVKPSQSLSLTCTVTDYSITSIDYAWTWIRQFPGNKLEWMGYITYRGTTTRYNPSTSRISFTRDTSKNQLF
LQLNSVTTEDTGTYCCARSMITGYYAMDYWGQTSVTVSS

Dana-Farber/Novartis 4H1 VL (SEQ ID NO: 29139)

DIVMTQSHKFMSTSVGDRVSISCKASQDVGISVAWYQQKPGQSPKLLIYWASTRHTGVPVRFTGSGSGTDFTLTISNVQ
SEDLADYFCQQYSSYPPTFGAGTKLELK

Dana-Farber/Novartis mAb-42 VH (SEQ ID NO: 29140)

QVQLVQSGAEVKKPGSSVKVSCASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTA
YMESSLRSEDTAVYYCARGRMFGAGIDFWGPGTLVTVSS

Dana-Farber/Novartis mAb-42 VL (SEQ ID NO: 29141)

NFMLTQPHSVSESPGKTVTISCTRSSGIDSNIYVQWYQQRPGSAPTTVIYEDNQRPSGVPDRFSGSIDSSNSASLTISGLK
TEDEADYYCQSYDSNNRHVIFGGGTKLTVL

Dana-Farber/Novartis BAP058-03 VH (SEQ ID NO: 29142)

EVQLVQSGAEVKKPGATVKISCKVSGYTFTSYWMYWVRQATGQGLEWMGRIDPNSGSTKYNEKFKNRVTITADKSTS
TAYMESSLRSEDTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-03 VL (SEQ ID NO: 29143)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAVAWYLQKPGQSPQLLIYWASTRHTGVPDRFSGSGSGTDFTLKISRVEA
EDVGYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-04 VH (SEQ ID NO: 29144)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMYWVRQAPGQGLEWMGRIDPNSGSTKYNEKFKNRVTISVDTSKN
QFSLKLSVTAADTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-04 VL (SEQ ID NO: 29145)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAVAWYLQKPGQSPQLLIYWASTRHTGVPSRFSGSGSGTDFTTISLQPE
DIATYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-06 VH (SEQ ID NO: 29146)

EVQLVQSGAEVKKPGESLRISCKGSGYTFTSYWMYWIRQPPGKGLEWIGRIDPNSGSTKYNEKFKNRVTITADKSTSTA
YMESSLRSEDTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-06 VL (SEQ ID NO: 29147)

EIVLTQSPDFQSVTPKEKVTITCKASQDVGTAVAWYLQKPGQSPQLLIYWASTRHTGVPSRFSGSGSGTDFTTISLQPE
DIATYYCQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-07 VH (SEQ ID NO: 29148)

QVQLVQSGAEVKKPGASVKVSCASGYTFTSYWMYWIRQSPSRGLEWLGRIDPNSGSTKYNEKFKNRFTISRDDSKNT
AYLQMNSLKTEDTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-07 VL (SEQ ID NO: 29149)

EIVLTQSPATLSLSPGERATLSCKASQDVGTAVAWYLQKPGQSPQLLIYWASTRHTGIPPRFSGSGYGTDFTLINNIESE
DAAYYFCQYNSYPLTFGQGTKVEIK

Figure 78F

Dana-Farber/Novartis BAP058-11 VH (SEQ ID NO: 29150)

EVQLVQSGAEVKKPGATVKISCKVSGYTFTSYWMYWVRQATGQGLEWMGRIDPNSGSTKYNEKFKNRVTITADKSTS
TAYMELSSLRSEDTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-11 VL (SEQ ID NO: 29151)

DVVMTQSPSLPVTLGQPASISCKASQDVGTAVAWYQQKPGQAPRLLIYWASTRHTGVPSRFSGSGSGTEFTLTISLQP
DDFATYYCQQYNSYPLTFGQGTKVEIK

Dana-Farber/Novartis BAP058-13 VH (SEQ ID NO: 29152)

EVQLVQSGAEVKKPGATVKISCKVSGYTFTSYWMYWVRQARGQRLEWIGRIDPNSGSTKYNEKFKNRFTISRDNKNT
LYLQMNSLRAEDTAVYYCARDYRKGLYAMDYWGQGTTVTVSS

Dana-Farber/Novartis BAP058-13 VL (SEQ ID NO: 29153)

AIQLTQSPSSLSASVGDRVITITCKASQDVGTAVAWYLQKPGQSPQLLIYWASTRHTGVPSRFSGSGSGTDFTFTISLEAE
DAATYYCQQYNSYPLTFGQGTKVEIK

Sorrento H6 VH (SEQ ID NO: 29154)

QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAIWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTA
YMELSSLRSEDTAVYYCARGNIVATITPLDYWGQGTTLTVSS

Sorrento H6 VL (SEQ ID NO: 29155)

SYELMQPPSVSVAPGKTATACGGENIGRKTVHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
DEADYYCQVWDSSDHRIFGGGTKLTVL

Sorrento RC5 VH (SEQ ID NO: 29156)

EVQLLESGGGVVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNT
TVSLQMNSLRAEDTAVYYCAKDRYYNPLGMDVWGQGTTVTVSS

Sorrento RC5 VL (SEQ ID NO: 29157)

AIRMTQSPSSLSASVGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYTTSSLKSGVPSRFSGSGSGTDFTLTISRQPED
FATYYCQSYSSTWTFGRGTKVEIK

Sorrento SH1A1Q VH (SEQ ID NO: 29158)

EVQLVQSGAEVKKPGSSVKVSCASGGTFSSYAIWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADKSTSTA
YMELSSLRSEDTAVYYCAREGTIYDSSGYSFDYWGQGTTLTVSS

Sorrento SH1A1Q VL (SEQ ID NO: 29159)

QSVLTQPPSVSAAPGQKVTISCSGNNSNIANNYVSWYQQLPGTAPKLLIYDNNYRPSGIPDRFSGSKSGTSATLDITGLQT
GDEADYYCGVWDGSLTTGVFGGGTKLTVL

Sorrento SH1B3 VH (SEQ ID NO: 29160)

QVQLVESGGGVVQPGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDNKNT
LYLQMNSLRTEDTAVYYCARGWLDRLDIDYWGQGTTLTVSS

Sorrento SH1B3 VL (SEQ ID NO: 29161)

LPVLTQPASVSGSPGQSITISCTGTSDIGGYDYVSWYQHPGKAPKLMYDVSKRPSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYTSSSTHVFGTGTKLTVL

Figure 78G

Sorrento SH1D1 VH (SEQ ID NO: 29162)

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLDRDIDYWGQGLTVTVSS

Sorrento SH1D1 VL (SEQ ID NO: 29163)

QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFGSGSKSGNTASLTISGL
QAEDEADYYCSSLRSSTLGPVFGGGTKLTVL

Sorrento SH1D2 VH (SEQ ID NO: 29164)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLDRDIDYWGQGLTVTVSS

Sorrento SH1D2 VL (SEQ ID NO: 29165)

QAGLTQPPSVSEAPRQRTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDDLPSGVSDRFGSGSKSGTSASLAISGLQS
EDEADYYCAAWDSSLNGYVFGTGTCLTVL

Sorrento SH1D12 VH (SEQ ID NO: 29166)

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLDRDIDYWGQGLTVTVSS

Sorrento SH1D12 VL (SEQ ID NO: 29167)

QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSKRPSGVDPDRFGSGSKSGNTASLTISGL
QAEDEADYYCSSLTSSTTHVFGTGTCLTVL

Sorrento SH1E1 VH (SEQ ID NO: 29168)

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLDRDIDYWGQGLTVTVSS

Sorrento SH1E1 VL (SEQ ID NO: 29169)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFGSGSKSGTSATLGITGLQT
GDEADYYCGTWSSLSVWVFGGGTCLTVL

Sorrento SH1G9 VH (SEQ ID NO: 29170)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKNT
LYLQMNSLRTEDTAVYYCARGWLDRDIDYWGQGLTVTVSS

Sorrento SH1G9 VL (SEQ ID NO: 29171)

QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGRAPRLMIYDVSNRPSGVSNRFGSGSKSGNTASLTISGL
QAEDEGDYYCSSLTSGGTLGPVFGGGTKLTVL

Sorrento SH1E6 VH (SEQ ID NO: 29172)

QVQLVQSGAEVKKPGSSVKVSKASGGTFSRYGVHWVRQAPGQGLEWMGRLPIVSMNTYAQKFQDRVSITTDKSTG
TAYMELRSLTSEDALYYCASVGQQLPWVFFAWGQGLTVTVSS

Sorrento SH1E6 VL (SEQ ID NO: 29173)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFGSGSKSGTSATLGITGLQT
GDEADYYCGTWSSLSAVVFGGGTKLTVL

Figure 78H

Sorrento SH1A2 VH (SEQ ID NO: 29174)

QMQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKN
 TLYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGLTVTVSS

Sorrento SH1A2 VL (SEQ ID NO: 29175)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIPDRFSGSNSDTSATLGITGLQT
 GDEADYYCGTWDSSLSAWVFGGGTKLTVL

Sorrento SH1B1 VH (SEQ ID NO: 29176)

QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISFDGSNKYYADSVRGRFTISRDN SKN
 TLYLQMNSLRTEDTAVYYCARGWLD RDIDYWGQGLTVTVSS

Sorrento SH1B1 VL (SEQ ID NO: 29177)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT
 GDEADYYCGTWDSSLSAGSVVFGGGTKLTVL

Sorrento H6B1L VH (SEQ ID NO: 29178)

QMQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAYSWVRQAPGGGLEWMGGIIPSGFTANYAQKFQGRVTITADESTST
 AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGLTVTVSS

Sorrento H6B1L VL (SEQ ID NO: 29179)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
 DEADYYCLVWDSSSDHRIFGGGTKLTVL

Sorrento H6A1 VH (SEQ ID NO: 29180)

QMQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAYSWVRQAPGGGLEWMGGIIPFGTANYAQKFQGRVTITADESTST
 AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGLTVTVSS

Sorrento H6A1 VL (SEQ ID NO: 29181)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
 DEADYYCQVWDSSSDHRIFGGGTKLTVL

Sorrento H6B1 VH (SEQ ID NO: 29182)

QMQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAYSWVRQAPGGGLEWMGGIIPSGFTANYAQKFQGRVTITADESTST
 AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGLTVTVSS

Sorrento H6B1 VL (SEQ ID NO: 29183)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
 DEADYYCQVWDSSSDHRIFGGGTKLTVL

Sorrento H6B2 VH (SEQ ID NO: 29184)

QMQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAPGGGLEWMGGIIPAFGTANYAQKFQGRVTITADESTST
 AYMELSSLRSEDTAVYYCARGPIVATITPLDYWGQGLTVTVSS

Sorrento H6B2 VL (SEQ ID NO: 29185)

SYELMQPPSVSVAPGKTATIACGGENIGRKT VHWYQQKPGQAPVLVIYYDSDRPSGIPERFSGSNSGNTATLTISRVEAG
 DEADYYCQVWDSSSDHRIFGGGTKLTVL

Figure 78I

Sorrento G12 VH (SEQ ID NO: 29186)

EVQLVQSGAEVKKPGASVKVSKASGYTFTGYYMHVVRQAPGQGLEWMGWINPNSDNTGSAQKFQGRVFMKTTS
LNTAYMELSGLRSEDTAIYYCARERSSGYFDFWQGGLTVTVSS

Sorrento G12 VL (SEQ ID NO: 29187)

DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQSYSTPITFGQGTRLEIK

Sorrento RSA1 VH (SEQ ID NO: 29188)

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSTIYYADSVKGRFTISRDNKNSL
YLQMNSLRDEDTAVYYCARGDYYYGMDVWGQGTITVTVSS

Sorrento RSA1 VL (SEQ ID NO: 29189)

NIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFALTISLQPE
DFATYYCQQAQDSFFSITFGQGTRLEIK

Sorrento RA3 VH (SEQ ID NO: 29190)

QMQLVQSGAEVKKPGSSVKVSKASGGTFSRYGVHWVRQAPGQGLEWMGRLPIVSMNTNYAQKFQDRVSITTDKSTG
TAYMELRSLTSEDALYYCASVGQQLPWVFFAWGQGLTVTVSS

Sorrento RA3 VL (SEQ ID NO: 29191)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASTLQSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQSYSSHWTFGQGTKVEIK

Sorrento SH1E2 VH (SEQ ID NO: 29192)

EVQLVESGAEVKKPGSSVKVSKASGGTFSRYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTA
YMELSSLRSEDTAVYYCARAPYYYYYMDVWGQGTITVTVSS

Sorrento SH1E2 VL (SEQ ID NO: 29193)

QSALTQPASVSGSLGQSVTISCTGSSSDVGSYNLWSWYQQHPGKAPNLMYDVSKRSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYTGSTVVFVGGGKLTVL

Sorrento SH1E4 VH (SEQ ID NO: 29194)

QVQLVQSGAEVKKPGSSVKVSKASGGTFSRYGVHWVRQAPGQGLEWMGRLPIVSMNTNYAQKFQDRVSITTDKSTG
TAYMELRSLTSEDALYYCASVGQQLPWVFFAWGQGLTVTVSS

Sorrento SH1E4 VL (SEQ ID NO: 29195)

QSVLTQPPSASGSPGQSVTISCTGTSSDIGGYDSVSWYQQHPGKAPKLMYDVSKRPSGVSNRFSGSKSGNTASLTISGLQ
AEDEADYYCSSYTSSSIFVYVFGTGTKVTVL

Sorrento SH1B11 VH (SEQ ID NO: 29196)

QVQLVQSGSELKKPGSSVKVSKASGYFSFGYYIHWVRQAPGQGLEWMGWIDPNSGVTNYVRRFQGRVTMTRDTSLS
TAYMELSGLTADDTAVYYCARDENLWQFGYLDYWGQGLTVTVSS

Sorrento SH1B11 VL (SEQ ID NO: 29197)

DIVMTQSPSSLSASIGDRVTITCRASQRISAYVNWYQQKPGKAPKVLIIYAASSLRSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQTYSPPWTFGQGTKVEIK

Figure 78J

Sorrento SH1C8 VH (SEQ ID NO: 29198)

EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAVYYCARGQWLVTEDYWGQGTLLTVSS

Sorrento SH1C8 VL (SEQ ID NO: 29199)

QSVVTQPPSVSAAPGQKVTISCSGSSSDIGNHYVSWYQQLPGTAPKLLIYDNNQRPSGIPDRFSGSGSKSGTSATLAI TGLQT
 GDEADYYCGTWDNSLSPHLLFGGGTKLTVL

Regeneron H1H9364P2 VH (SEQ ID NO: 29200)

EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYALHWVRQAPGKGLEWVSGISWTGGTIDYADSVKGRFTISRDN AKNS
 LYLQMSSLRTEDTAIYYCTRDIRGNWKYGGWFDPPWGQGTLLTVSS

Regeneron H1H9364P2 VL (SEQ ID NO: 29201)

DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGSGTDFTL TISSLQPED
 FATYYCQQSYSTPPITFGQGTRLEIK

Regeneron H1H9373P2 VH (SEQ ID NO: 29202)

QVQLVQSGTEVKKPGASVKVSCKASGYTFTAYYMHWVRQAPGQGLDWMGWISPN SGFTNYAQKFQGRVTMTRDTSI
 NTFYMELSGLRSDDTAVYYCAREGSTHHNSFDPWGQGTLLTVSS

Regeneron H1H9373P2 VL (SEQ ID NO: 29203)

DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFRSGSGSGTDFTL TISSLQPED
 FATYYCQQSYSTPPITFGQGTRLEIK

Regeneron H1H8314N VH (SEQ ID NO: 29204)

EVQLVESGGGVVVRPGGSLRLSCAASGFTFDDYGMTWVRQAPGRGLEWVSGIHWGKRTGYADSVKGRFTISRDN AK
 KSLYLQMNSLKGEDTALYHCVRGGMSTGDWFDPPWGQGTLLVIVSS

Regeneron H1H8314N VL (SEQ ID NO: 29205)

DIQMTQSPSSLSASLGDRTITCRASQSINSYLNWYQQKPGKAPKLLIYVASSLQSGVPSRFRSGSGSGTEFTL TISNLQPED
 FATYYCQQSYSTPPITFGQGTRLEIK

Inserm PDL1.3.1 VH (SEQ ID NO: 29206)

EVQLQQSGTELVKPGASVKLSCTTSGFNIQDTYMHWVKQRPEQGLEWIGWIDPANGNTKYDPKFQ GKATIIADTSNT
 AYLQLRGLTSED TAVYYCARSGVSTA HFDYWGQGTLLTVSS

Inserm PDL1.3.1 VL (SEQ ID NO: 29207)

QIVLSQSPAILSASPGEKVTMTCRASSSVFMHWYQQKPGSSPKPWYATSNLASGVPTRFSGSGSGTSYSLT LSRVEAE
 DAATYYCQQWSSYPRTFGGGTKLEIK

Figure 79A additional CTLA-4 sequences

Medarex Ipilimumab VH (SEQ ID NO: 29208)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNT
 LYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLTVSS

Medarex Ipilimumab VL (SEQ ID NO: 29209)

EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPE
 DFAVYYCQQYGSSPWTFGQGTKVEIK

Amgen/MedImmune/Pfizer Tremelimumab VH (SEQ ID NO: 29210)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDGSKNYYADSVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAVYYCARDPRGATLYYYYYGMDVWGQGTLLTVSS

Amgen/MedImmune/Pfizer Tremelimumab VL (SEQ ID NO: 29211)

DIQMTQSPSSLSASVGDRTITCRASQSINSYLDWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
 FATYYCQQYYSTPFTFGPGTKVEIK

Agenus AGEN1884 VH (SEQ ID NO: 29212)

EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYYADSVKGRFTISRDN AKNSL
 YLQMNSLRAEDTAVYYCARVGLMGPFDIWGQGTMTVTVSS

Agenus AGEN1884 VL (SEQ ID NO: 29213)

EIVLTQSPGTLSLSPGERATLSCRASQSVSRYLGWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTITRLEPED
 FAVYYCQQYGSSPWTFGQGTKVEIK

Tegenero 4.3F6B5 VH (SEQ ID NO: 29214)

EVQLQPSGPVLVKPGASVKISKASGYTFTDYKIHVWKQSHGKSLEWIGYIYPYSGSSDYNQKFKSKATLTVDNSSTTA
 YMELRSLTSEDSAVYYCARGGDAMDYWGQGTAVTVSS

Tegenero 4.3F6B5 VL (SEQ ID NO: 29215)

DILMTQSPASLSASVGETVTITCGASENIYGALNWKYQKQKSPQLLIYGATNLADGMSSRFSGSGGLGRQYYLKISLHP
 DDVATYFCQNILGTWTFGGGTKLEIKR

Tegenero 4.8H10H5 VH (SEQ ID NO: 29216)

DVKLVESGGGLVKLGSLKLSCAASGFTFNIIYMSWVRQTPEKRLELVAAINPDGGNTYYPDTVKGRFTISRDN AKNT
 LYLQMSSSLKSEDSALYYCARYGGPGFDSWGQGTLLTVSS

Tegenero 4.8H10H5 VL (SEQ ID NO: 29217)

ENVLTQSPAISASPGERVTMTCSASSSVSYMHWYQQKSNTPKLIWYDTSKLASGVPGRFSGSGSRNSYSLTISSMEAE
 DVATYYCFPGSGFPFMYTFGGGTKLEIKR

Tegenero TGN2122.C VH (SEQ ID NO: 29218)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYKIHVVRQAPGQGLEWIGYIYPYSGSSDYNQKFKSRATLTVDNSIST
 AYMELSRRLRSDDTAVYYCARGGDAMDYWGQGTLLTVSS

Tegenero TGN2122.C VL (SEQ ID NO: 29219)

DIQMTQSPSSLSASVGDRTITCGASENIYGALNWKYQKPGKAPKLLIYGATNLADGVPSRFSGSGSGRDTLTISLQPED
 FATYYCQNILGTWTFGGGTKVEIK

Figure 79B

Tegenero TGN2122.H VH (SEQ ID NO: 29220)

EVQLVESGGGLVQPGGSLRLSCAASGFTFNIIYMSWVRQAPGKGLELVAAINPDGGNTYYPDTVKGRTISRDNKNS
LYLQMNSLRAEDTAVYYCARYGGPGFDSWGQGLVTVSS

Tegenero TGN2122.H VL (SEQ ID NO: 29221)

ENVLTQSPATLSLSPGERATLSCSASSSVSYMHWYQQKPGQAPRLWIYDTSKLASGIPARFSGSGSRNDYTLTISSLEPED
FAVYYCFPGSGFPFMYTFGGGTKVEIK

Sorrento F7 VH (SEQ ID NO: 29222)

QVQLVQSGAEVKKPGASVKVSCKASGYAFDGHYMHWVRQAPGQRLEWMGWVDPHSGATNYAQNFQGGVTMTRDT
SINTVYMELSSLKSDDTAVYYCARDFYDTSKSGAFDIWGQGTMTVTVSS

Sorrento F7 VL (SEQ ID NO: 29223)

AIQLTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQVNSFPWAFGQGTKVEIK

Sorrento E8 VH (SEQ ID NO: 29224)

QVQLVQSGAEVKKPGASVKVSCEASGYTFTNYYIHWLRQAPQGQLEWMGIINPSGGSTTYAQKFQGRITMTRDTSTNT
LYMELSSLRSEDTAIYYCARRDCRGPSYFAYWGQGTITVTVSS

Sorrento E8 VL (SEQ ID NO: 29225)

DIVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPPRFSGSGSGTEFTLTISLQPED
FATYYCQQANSFPPTFGQGTKVDIK

Sorrento CT1E1 VH (SEQ ID NO: 29226)

EVQLVESGGGLVQPGSLRLSCRGSNFNFDLAISWVRQAPGKGLEWLGFVRSKAYGETTDYVASVKGRFTISRDDSK
FIAWLQMDSLKTDDTAVYYCTTFNYWGQGLVTVSS

Sorrento CT1E1 VL (SEQ ID NO: 29227)

QPVLTPPSVSVAPGKTARISCGGNNIASEAVHWYQKKPGQAPVLVIYYDSRPSGIPERFSGSNSGNTATLRISRVDAG
DEADYYCQVWDRTTDQPVFGGGTKLTVL

Figure 80A additional LAG-3 sequences

Medarex BMS-986016 VH (SEQ ID NO: 29228)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSDYYWNWIRQPPGKGLEWIGEINHRGSTNSNPSLKSRVTLSDTSKNQFS
LKLRSVTAADTAVYYCAFGYSDYEYNWFDPWGQGTLTVSS

Medarex BMS-986016 VL (SEQ ID NO: 29229)

EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSELPEDF
AVYYCQQRSNWPLTFGQGTNLEIK

Immutep/INSERM/Novartis IMP731 VH (SEQ ID NO: 29230)

QVQLKESGPGLVAPSQSLSTCTVSGFSLTAYGVNWVRQPPGKGLEWLGMWDDGSTDYNSALKSRLSISKDNSKSQVF
LKMNSLQTDATARYYCAREGDVAFDYWGQGTTLTVSS

Immutep/INSERM/Novartis IMP731 VH (SEQ ID NO: 29231)

DIVMTQSPSSLAVSVGQKVTMSCKSSQSLNNGSNQKNYLAWYQQKPGQSPKLLVYFASTRDSGVPDRFIGSGSGTDFTL
TISSVQAEDLADYFCLQHFGTPTFGGGTKLEIK

Immutep/INSERM/Novartis 13E2 VH (SEQ ID NO: 29232)

QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGLGWIRQPSGKGLEWLTHIWDDIKRYNPDLRSRLTISKDTSSSQIFL
KIASVDATATYYCARIVEGSYSSSYFDVWGAGTTTVSS

Immutep/INSERM/Novartis 13E2 VH (SEQ ID NO: 29233)

DIVMTQPHKFMSTSVEDRVITCKASQDVIFDVAWYQQKPGQSPKLLIYSASSRVSGVPDRFTGSGSGTDFTFTISSVQA
EDLAVYYCQQHSTPYTFGGGTLEIK

Immutep/INSERM/Novartis 34F4 VH (SEQ ID NO: 29234)

QVTLKESGPGILQPSQTLSTCSFSGFSLNTSGMGVGVIRQPSGKGLEWLTHIWDDVKRYNPALKSRLTISKDTSSSQV
FLKIASVDATATYYCARIEGDTYYDYFDYWGQGVTLTVSS

Immutep/INSERM/Novartis 34F4 VH (SEQ ID NO: 29235)

DIVMTQSHKLMSTSVGDGLSITCKASQDVSIADVWYQQKPGQSPKLLIYSASFRYTGVPDRFTGSGSGTDFTFTISSVQA
EDLAVYYCQQHYSIPWTFGGGTLEIK

Immutep/INSERM/Novartis IMP761 VH (SEQ ID NO: 29236)

QITLKESGPTLVKPTQTLTLCTFSGFSLSTSGMGLGWIRQPPGKLEWLTHIWDDIKRYNPDLRSRLSITKDTSKNQV
VLTMTNMDPLDTGYTCARIVEGSYSSSYFDVWGQGTTLTVSS

Immutep/INSERM/Novartis IMP761 VH (SEQ ID NO: 29237)

DIVMTQTPSSLSASVGDRTITCKASQDVIFDVAWYQQRPGQAPKLLIYSASSRVSGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQQHSTPYTFGQGTSLDIK

GSK H5L7 VH (SEQ ID NO: 29238)

QVQLQESGPGLVKPSSETLSLTCTVSGFSLTAYGVNWIRQPPGKGLEWIGMIWDDGSTDYDSALKSRVTISVDTSKNQFS
LKLSSVTAADTAVYYCAREGDVAFDYWGQGTTLTVSS

GSK H5L7 VL (SEQ ID NO: 29239)

DIQMTQSPSSLSASVGDRTITCKSSQSLNPSNQKNYLAWYQQKPGKAPKLLVYFASTRDSGVPSPRFSGSGSGTDFTLT
ISSLPEDFATYYCLQHFGTPTFGQGTLEIKR

Figure 80B

Merck hu22D2 VH (SEQ ID NO: 29240)

QMQLVQSGPEVKKPGTSVKVSKASGYTFTDYNVDWVRQARGQRLEWIGDINPNNGGTIYAQKFQERVITITVDKSTST
AYMELSSLRSEDТАVYYCARNYRWFGAMDHWGQGTTTVTVSS

Merck hu22D2 VL (SEQ ID NO: 29241)

DIVMTQTPLSLSVTPGQPASISCKASQSLDYEGSDMNWYLQKPGQPPQLLIYGASNLESGVPDRFSGSGSGTDFTLKIS
RVEAEDVGYYCQQSTEDPRTFGGGTKVEIK

Regeneron H4sH15482P VH (SEQ ID NO: 29242)

QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAIIWYDGSNKYYADSVKGRFTISRDN SKN
TQYLMNSLRAEDТАVYYCASVATSGDFDYGM DVWGQGTTTVTVSS

Regeneron H4sH15482P VH (SEQ ID NO: 29243)

EIVLTQSPATLSLSPGERTTLSCRASQRISTYLA WYQKPGQAPRLLIYDASKRATGIPARFSGSGSGTGFTLTISSEPEDF
AVYYCQQRSNWPLTFGGG TKVEIK

Sorrento L35D4 VH (SEQ ID NO: 29244)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDТАVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L35D4 VL (SEQ ID NO: 29245)

QSVLTQPPSASGSPGQSITISCTGTSSDVGGYNYVSWYQQYPGKAPRLMIFEVTERASGVPDRFSGSKSGNTASLTVSGL
QTEDEAVYFCSSYSGSNPGAMFGGGTKLTVL

Sorrento L35G6 VH (SEQ ID NO: 29246)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDТАVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L35G6 VL (SEQ ID NO: 29247)

QAGLTQPASVSGSPGQSITISCTGSSSDVGGYSYVSWYQKHPGKAPKLMYDVTNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEADYYCSTYTRSNTLVFGPGTKVTVL

Sorrento L33H11 VH (SEQ ID NO: 29248)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDТАVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L33H11 VL (SEQ ID NO: 29249)

LPVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVTNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEADYYCSTYSSNTLLFGGGTQLTVL

Sorrento L32A9 VH (SEQ ID NO: 29250)

QVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMELSSLRSEDТАVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L32A9 VL (SEQ ID NO: 29251)

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRHSGIPDRFSGSTSDTSATLGITRLQT
GDEADYYCGTWDSSLSAYVFGTGKTVL

Figure 80C

Sorrento L32D10 VH (SEQ ID NO: 29252)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMESSLRSEDTAVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L32D10 VL (SEQ ID NO: 29253)

QSVLTQPPSASGSPGQSVTISCTGTSSDVGGYDYVSWYQQHQGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEADYYCSSYTSSTLVFGGGTKLTVL

Sorrento L32A4 VH (SEQ ID NO: 29254)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMESSLRSEDTAVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L32A4 VL (SEQ ID NO: 29255)

QSVLTQPASVSGSPGQSITISCTGTSSDIGAYNFVSWYQQHPGKAPKLMYGVSNRPSGVSSRFSGSKSGSTASLTISGLQ
AEDEADYYCSSYTTSGSAVFGTGTKLTVL

Sorrento L3A1 VH (SEQ ID NO: 29256)

EVQLLESGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMESSLRSEDTAVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L3A1 VL (SEQ ID NO: 29257)

QSVLTQPASVSGSPGQSITISCTGTSSDIGAYNFVSWYQQHPGKAPKLMYGVSNRPSGVSSRFSGSKSGSTASLTITGLQ
AEDEADYYCSSYTTSGSAVFGTGTKLTVL

Sorrento L3A10 VH (SEQ ID NO: 29258)

EVQLLESGGGVVPGRSLRVSCAASGFTFSNHAMHVVRQAPGKGLEWVAVISYDGSKKFYSDSVRGRFTISRDNKNT
LYLQMNSLRPEDTAVYYCAKGAHGYTSGWHDYWGQGLTVTVSS

Sorrento L3A10 VL (SEQ ID NO: 29259)

DVVMTQSPSSLSASVGDRVSITCRASQNIGRYLNWYQQKPGKAPKLLVSAASSLQGGVPSRFSGSGSGTDFTLISRQLP
EDFATYFCQQTYSPPQCTFGQGTKVDIK

Sorrento L3C5 VH (SEQ ID NO: 29260)

QVQLVQSGSELKKPGASVKVSCKASGYTFTNYYMHVVRQAPGGLEWMGIINPSGGATNYAQKFQGRVTMTRDTST
STVYMESSLRSEDTAVYYCARDSGYDLGYGMDVWGQGLTVTVSS

Sorrento L3C5 VL (SEQ ID NO: 29261)

QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGASNRFSGSKSGNTASLTISGL
QAEDEADYYCSSYTNRNTLLFGGGTKLTVL

Sorrento L3E3 VH (SEQ ID NO: 29262)

EVQLLESGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGGLEWMGIINPSAGSTSYAQKFQGRVTMTRDTSTS
TVYMESSLRSEDTAVYYCARELMATGGFDYWGQGLTVTVSS

Sorrento L3E3 VL (SEQ ID NO: 29263)

QSVLTQPASASGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMYDVSNRPSGVSNRFSGSKSGNTASLTISGL
QAEDEANYCASYTSSSTNVFGTGTKVTVL

Figure 81A additional TIM-3 sequences

AnaptysBio/Tesaro APE5137 VH (SEQ ID NO: 29264)

EVQLLESGGGLVQPGGSLRLSCAAASGFTFSYDMSWVRQAPGKGLDWVSTISGGGTYTYYQDSVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAVYYCASMDYWGQGT TVTVSSA

AnaptysBio/Tesaro APE5137 VL (SEQ ID NO: 29265)

DIQMTQSPSSLSASVGDRTITCRASQSIRRYLNWYHQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTIS SLQPE
 DFAVYYCQQSHSAPLTFGGG TKVEIKR

AnaptysBio/Tesaro APE5121 VH (SEQ ID NO: 29266)

EVQVLESGGGLVQPGGSLRLYCVASGFTFSGSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISR DN SKN
 TLYLQMNSLRAEDTAVYYCAKKYYVGPADYWGQGT LTVTVSSG

AnaptysBio/Tesaro APE5121 VL (SEQ ID NO: 29267)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQHKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFT L
 TISSLQAEDVAVYYCQQYYSSPLTFGGG TKIEVK

Dana-Farber/Novartis ABTIM3-hum03 VH (SEQ ID NO: 29268)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWIGDIYPGQGDTSYNQKFKGRATMTADK ST
 STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGT LTVTVSS

Dana-Farber/Novartis ABTIM3-hum03 VL (SEQ ID NO: 29269)

DIVLTQSPDSLAVSLGERATINCRASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVESGVPDRFSGSGSGTDFT LTISS
 LQAEDVAVYYCQQSRKDPSTFGGG TKVEIK

Dana-Farber/Novartis ABTIM3-hum11 VH (SEQ ID NO: 29270)

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGDIYPGNGDTSYNQKFKGRVTITADK ST
 STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGT TTVTVSS

Dana-Farber/Novartis ABTIM3-hum11 VL (SEQ ID NO: 29271)

AIQLTQSPSSLSASVGDRTITCRASESVEYYGTSLMQWYQQKPGKAPKLLIYAASNVESGVPDRFSGSGSGTDFTLT ISS
 LQPEDFATYFCQQSRKDPSTFGGG TKVEIK

Dana-Farber/Novartis ABTIM3-hum21 VH (SEQ ID NO: 29272)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWIGDIYPGQGDTSYNQKFKGRATMTADK ST
 STVYMELSSLRSEDTAVYYCARVGGAFPM DYWGQGT LTVTVSS

Dana-Farber/Novartis ABTIM3-hum21 VL (SEQ ID NO: 29273)

DIVLTQSPDSLAVSLGERATINCRASESVEYYGTSLMQWYQQKPGQPPKLLIYAASNVESGVPDRFSGSGSGTDFTLT ISS
 LQAEDVAVYYCQQSRKDPSTFGGG TKVEIK

KHK 4177 VH (SEQ ID NO: 29274)

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIFHSGSTNYPNPSLKSRVTISVDTSKNQFSL K
 LSSVTAADTAVYYCARDGEYFDMLTGFDYWGQGT LTVTVSS

KHK 4177 VL (SEQ ID NO: 29275)

RCDIQMTQSPSSLSASVGDRTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQP
 EDFATYYCQQYNSYPRTFGGQ TKVEIK

Figure 81B

KHK 4545 VH (SEQ ID NO: 29276)

QVQLQESGPGLVKPSSETLSLTCTVSGGSFSRGGYYWNWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRTISLDTSKNQF
SLKLSSVTAADTAVYYCARDHYSSSWTFDYWGQGTLLTVSS

KHK 4545 VL (SEQ ID NO: 29277)

EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLLEPED
FAVYYCQQRSNWPPTFGQGTKLEIK

KHK 8123 VH (SEQ ID NO: 29278)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVRQAPGQGLEWMGEINPSNGRTNYNEKFKTRVTITADTSTS
TAYMELSSLRSEDTAVYYCARGYYLYFDYWGQGTLLTVSS

KHK 8123 VL (SEQ ID NO: 29279)

DIQMTQSPSSLSASVGDRTITCHASQGIRINIGWYQQKPGKAPKLLIYHGTNLEDGVPSRFSGSGSGTDFTLTISLQPED
FATYYCVQYGGFPWTFGQGTKLEIK

Jounce mAb15 VH (SEQ ID NO: 29280)

QVQLKESGPGLVAPSQSLTCTVSGFSLTGYGVTWVRQPPGKGLEWLGMWGDGNTDYNGLKSRNLNISKDNKSQV
FLKMNSLQTDATARYYCARSYYYGPPDYWGQGTLLTVSS

Jounce mAb15 VL (SEQ ID NO: 29281)

DIVMTQSPSSLAMSVGQKVTMSCKSSQSLNRSQKNYLAWYQRKPGQSPKLLYFASTRESGVPDRFIGSGSGTDFTL
TISSVQAEDLADYFCHQHYNTPTFTFGGGTKLEIK

Jounce mAb58 VH (SEQ ID NO: 29282)

QIQLVQSGPELKKPGETVKISCKASGYTFTTYGMSWVKQAPGKGLKLMGWINTYSGPTYADDFKGRFAFSLETSASA
AYLQINNLKNEDTATYFCARKPPHYVNSFDYWGQGTLLTVSS

Jounce mAb58 VL (SEQ ID NO: 29283)

DIVMTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGSDFTLSINSVEPEDV
GVYYCQNGHSFPYTFGGGTKLEIK

Roche TIM3-0433 VH (SEQ ID NO: 29284)

QITLKESGPTLVKPTQTLTLCTFSGFSLSTSGMSVGWIRQPPGKGLEWLAHIWLNDDVFFNPALKSRLTITKDTSKNQV
VLTMTNMDPVDATYYCVRANGYLYALDYWGQGTLLTVSS

Roche TIM3-0433 VH (SEQ ID NO: 29285)

ETTLTQSPAFMSATPGDKVNIACSSSVSYTQWYQQKPGEAPKLWIYDAFKLAPGIPPRFSGSGYGTDFTLTINNIESED
AAYYFCHQWSSYPWTFGQGTKLEIK

Roche TIM3-0434 VH (SEQ ID NO: 29286)

QITLKESGPTLVKPTQTLTLCTFSGFSLSTSGMSVGWIRQPPGKGLEWLAHIWLNDDVFFNPALKSRLTITKDTSKNQV
VLTMTNMDPVDATYYCVRANGYLYALDYWGQGTLLTVSS

Roche TIM3-0434 VH (SEQ ID NO: 29287)

DIQLTQSPSFLSASVGDRTITCSASSSVSYTQWYQQKPGKAPKLWIYDAFKLAPGVPSRFSGSGSGTEFTLTISLQPEDF
ATYFCHQWSSYPWTFGQGTKLEIK

Figure 81C

Roche TIM3-0438 VH (SEQ ID NO: 29288)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKTTYMHWVRQAPGKGLEWVGRIDPADDNTKYAPKFQGKATISADTSKN
TAYLQMNSLRAEDTAVYYCVRDFGYVAWFAYWGQGLTVTVSS

Roche TIM3-0438 VH (SEQ ID NO: 29289)

DIVMTQSPLSLPVTPGEPASISCRASQSVDNVVAWYLQKPGQSPQLLIYYASNRYIGVPDRFSGSGSGTDFTLKISRVEAE
DVGVYYCQQHYSSPYTFGQGTKVEIK

Roche TIM3-0443 VH (SEQ ID NO: 29290)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKTTYMHWVRQAPGKGLEWVGRIDPADDNTKYAPKFQGKATISADTSKN
TAYLQMNSLRAEDTAVYYCVRDFGYVAWFAYWGQGLVTFSS

Roche TIM3-0443 VH (SEQ ID NO: 29291)

DIVMTQSPLSLPVTPGEPASISCRASQSVDNVVAWYLQKPGQSPQLLIYYASNRYIGVPDRFSGSGSGTDFTLKISRVEAE
DVGVYYCQQHYSSPYTFGQGTKVEIK

Figure 82 additional BTLA sequences

Medarex 3C2 VH (SEQ ID NO: 29292)

QVQLQESGPGLVKPSETLSLTCTISGGSISNYYWNWIRQPPGKGLEWIGYIYYSTSTKYNPSLKSRTMSVETSKNQFSL
KLSSVTAADTAVYYCARVKVYSTGWFFDYWGQGLTVTVSS

Medarex 3C2 VL (SEQ ID NO: 29293)

AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQFNSYPLTFGGGTKVEIK

Medarex 11E2 VH (SEQ ID NO: 29294)

EVQLVESGGGVIRPGGSLRLSCAASGFTFDDYGMSSWRQAPGKGLEWVSGINWNGGSTGYAASVKGRFTISRDNANK
SLYLQMNSLRAGDSALYYCARDYYYGPGSPNYFYAMDVWGQGTITVTVSS

Medarex 11E2 VL (SEQ ID NO: 29295)

DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQYNSYPRTFGGQGTKVEIK

Medarex 4C7 VH (SEQ ID NO: 29296)

QVQLQESGPGLVKPSETLSLTCTVHGGSSINHYWWSWIRQPPGKGLEWIGYIYSGSTKYNPSLKSRSISVDTSKNQFSL
KLTSVTAADTAVYYCAREWPYYYEMDVWGQGTITVTVSS

Medarex 4C7 VL (SEQ ID NO: 29297)

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQYGSSFRFTFGGQGTKVEIK

Medarex 8D5 VH (SEQ ID NO: 29298)

EVQLVESGGGLVQPGGSLRLSCAASGFTISSYDMHWVRQATGKGLEWVSVIGPAGDTYYPGSVKGRFTISRDNANKSL
LYLQMNSLRAGDTAVYYCAREGMAAHNYYGMDVWGQGTITVTVSS

Medarex 8D5 VL (SEQ ID NO: 29299)

EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISLQPED
FAVYYCQQRSNWPPITFGQGTREIK

Figure 83A additional TIGIT sequences

Genentech 10A7 VH (SEQ ID NO: 29300)

EVQLVESGGGLTQPGKSLKLSCEASGFTFSSFTMHWVRQSPGKGLEWVAFIRSGSGIVFYADAVRGRFTISRDNKNLL
FLQMNDLKSEDTAMYYCARRPLGHNTFDSWGQGLTVTVSS

Genentech 10A7 VL (SEQ ID NO: 29301)

DIVMTQSPSSLAIVSPGEKVTMTCKSSQSLYYSGVKENLLAWYQQKPGQSPKLLIYYASIRFTGVPDRFTGSGSGTDYTLT
ITSVQAEDMGQYFCQQGINNPLTFGDGKLEIK

Genentech 1F4 VH (SEQ ID NO: 29302)

EVQLQQSGPELVKPGTSMKISCKASGYSTGHLMNWVKQSHGKNLEWIGLIIPYNGGTSYNQKFKGKATLTVDKSSST
AYMELLSLTSDSAVYFCRGLRGFYAMDYWGQGTSTVTVSS

Genentech 1F4 VL (SEQ ID NO: 29303)

DVVLVTQTPSLSVSFGDQVSISCRSSQSLVNSYGNFTLSWYLHKPGQSPQLLIFGISNRFSGVPDRFSGSGSGTDFTLKISTI
KPEDLGMYCYCLQGTHQPPTFGPGTKLEVK

Genentech 4.1D3 VH (SEQ ID NO: 29304)

QVQLQQSGPGLVKPSQTLSTCAISGDSVSSNSAAWNWIRQSPSRGLEWLKGTYYRFBKWDYAVSVKGRITINPDTSK
NQFSLQLNSVTPEDTAVFYCTRESTTYDLLAGPFDYWGQGLTVTVSS

Genentech 4.1D3 VL (SEQ ID NO: 29305)

DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSNNKKYLAWYQQKPGQPPNLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQQYYSTPFTFGPGTKVEIK

Genentech 4.1D3.Q1E VH (SEQ ID NO: 29306)

EVQLQQSGPGLVKPSQTLSTCAISGDSVSSNSAAWNWIRQSPSRGLEWLKGTYYRFBKWDYAVSVKGRITINPDTSK
NQFSLQLNSVTPEDTAVFYCTRESTTYDLLAGPFDYWGQGLTVTVSS

Genentech 4.1D3.Q1E VL (SEQ ID NO: 29307)

DIVMTQSPDSLAVSLGERATINCKSSQTVLYSSNNKKYLAWYQQKPGQPPNLLIYWASTRESGVPDRFSGSGSGTDFTL
TISSLQAEDVAVYYCQQYYSTPFTFGPGTKVEIK

Merck MEB125.31C6.A1.205 VH4/VL1 VH (SEQ ID NO: 29308)

EVQLVQSGAEVKKPGASVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQKFQGRVTLTSDKSTS
TVYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH4/VL1 VL (SEQ ID NO: 29309)

DIQMTQSPSSLSASVGDRTVITCRASEHIYSYLSWYQQKPGKAPKLLIYNAKTLAEGVPSRFSGSGSGTDFTLTISLQPE
DFATYYCQHHFGSPLTFGQGTREIK

Merck MEB125.31C6.A1.205 VH5/VL4 VH (SEQ ID NO: 29310)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFSSYVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQKFQGRVTLTSDKSTS
TAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH5/VL4 VL (SEQ ID NO: 29311)

DIQMTQSPSSLSASVGDRTVITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSGSGSGTQFTLTISLQPE
DVATYYCQHHFGSPLTFGQGTREIK

Figure 83B

Merck MEB125.31C6.A1.205 VH5/VL3 VH (SEQ ID NO: 29312)

EVQLVQSGAEVKKPGSSVKVSKASGYTFSSVMHWVRQAPGQGLEWIGYIDPYNDGAKYAQKFQGRVTLTSDKSTS
TAYMELSSLRSEDTAVYYCARGGPYGWYFDVWGQGTITVTVSS

Merck MEB125.31C6.A1.205 VH5/VL3 VL (SEQ ID NO: 29313)

DIQMTQSPSSLSASVGRVTITCRASEHIYSYLSWYQQKPGKVPKLLIYNAKTLAEGVPSRFSGSGSGTDFTLTISLQPE
DVATYYCQHHFGSPLTFGQGTREIK

Merck Hu14D7 VH1 (SEQ ID NO: 29314)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KSTVYLMNSLRSEDVAVYYCRGALYDGFYFDYWGQGTITVTVSS

Merck Hu14D7 VH2 (SEQ ID NO: 29315)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KSSVYLMNSLRSEDVAVYYCRGALYDGFYFDYWGQGTITVTVSS

Merck Hu14D7 VH3 (SEQ ID NO: 29316)

EVQLVESGGGLVQPGGSLKLSAASGFTFSGAWMDWVRQAPGKGLEWVAEIRTKVNNHATNYGESVKGRFTISRDDS
KNTVYLMNSLRSEDVAVYYCRGALYDGFYFDYWGQGTITVTVSS

Merck Hu14D7 VL1 (SEQ ID NO: 29317)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQQKPGQAPKLWIYGTSTLASGVPARFSGSGSGTDYTLTISLPEP
EDFAVYYCHQWSSFPYTFGQGTREIK

Merck Hu14D7 VL2 (SEQ ID NO: 29318)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQQKPGQAPRLWIYGTSTLASGVPARFSGSGSGTDYTLTISLPEP
DFAVYYCHQWSSFPYTFGQGTREIK

Merck Hu14D7 VL3 (SEQ ID NO: 29319)

EIVLTQSPATLSLSPGERATLSCSASSSVSSGYLYWYQQKPGQAPRLWIYGTSTLASGIPARFSGSGSGTDYTLTISLPEP
DFAVYYCHQWSSFPYTFGQGTREIK

Merck Hu26B10 VH1 (SEQ ID NO: 29320)

EVQLVQSGAEVKKPGASVKISCKTSGYTFTEFTMHWVKQAPGKGLEWIGGLKPDNNGGISYNQKFGRATLTVDKSTNT
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTITVTVSS

Merck Hu26B10 VH2 (SEQ ID NO: 29321)

EVQLVQSGAEVKKPGASVKISCKTSGYTFTEFTMHWVRQAPGKGLEWIGGLKPDNNGGISYNQKFGRATLTVDKSTST
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTITVTVSS

Merck Hu26B10 VH3 (SEQ ID NO: 29322)

EVQLVQSGAEVKKPGASVKISCKVSGYTFTEFTMHWVRQAPGKGLEWIGGLKPDNNGGISYNQKFGRATLTVDTSTST
AYMELSSLRSEDTAVYYCARGAYRYDADYWGQGTITVTVSS

Merck Hu26B10 VL1 (SEQ ID NO: 29323)

DIQLTQSPSSLSASVGRVTITCKASQDVKTAVAWYQQKPGKAPKLLIYSASYRNTGVPDRFSGSGSGTDFTFTISLQPE
DFATYYCQHHYSTPFTFGQGTREIK

Figure 83C

Merck Hu26B10 VL2 (SEQ ID NO: 29324)

DIQLTQSPSSLSASVGDRVTITCKASQDVKTAVAWYQQKPGKAPKLLIYSASYRNTGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQHYSTPFTFGQGTKLEIK

Merck Hu26B10 VL3 (SEQ ID NO: 29325)

DIQLTQSPSSLSASVGDRVTITCKASQDVKTAVAWYQQKPGKAPKLLIYSASYRNTGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQHYSTPFTFGQGTKLEIK

BMS 15A6 VH (SEQ ID NO: 29326)

QLQLQESGPGLVKPSETLSLTCTVSGGSISSRYFWGWIRQPPGKGLEWIGYIYYRGSTYYNPSLKSRTIAVDTSKNQFS
LKLSSVTAADTAVYYCASSAWYFDYWGQGNLTVTVSS

BMS 15A6 VL (SEQ ID NO: 29327)

EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPE
DFAVYYCQQYGSlyTFGQGTKLEIK

BMS 22G2 VH (SEQ ID NO: 29328)

QVHLQESGPGLVKPSETLSLTCTVSGGSVSSGIYYWSWIRQPPGKGLEWIGYIYYSGSTNYPNPSLKSRTISVDTSKNQFS
LKLSSVTAADTAVYYCARDYYVSGNYNVDYFFGVDVWGQGTTVTVSS

BMS 22G2 VL (SEQ ID NO: 29329)

EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED
FAVYYCQQRSNWPLFTFGPGTKVDIK

BMS 11G11 VH (SEQ ID NO: 29330)

QLQLQESGPGLVKPSETLSLTCTVSGGSISSSHYWGWRQPPGKGLEWIGNIFYSGHTYYNPSLKSRTISVDTSKNQFS
LKLSSVTAADTAVYYCARQGLLWFGGLSPYYFDYWGQGTTLTVTVSS

BMS 11G11 VL (SEQ ID NO: 29331)

EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED
FAVYYCQQRSNWPTFGQGTKLEIK

BMS 10D7 VH (SEQ ID NO: 29332)

QGQLVQSGAEVKKPGSSVKVSCASGGIFRNYAISWVRQAPGQGLEWMGGIIPFFGTANYAQKFQGRVTITADESTSTA
YMESSLRSEDTAVYYCARGGAAAGTTRYGYYYYGMDVWGQGTTLTVTVSS

BMS 10D7 VL (SEQ ID NO: 29333)

DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQYNSYPITFGQGTRLEIK

Oncomed 313R19 VH (SEQ ID NO: 29334)

QVQLQESGPGLVKPSETLSLTCTVSGFSLSSSYMSWIRQPPGKGLEWIGIIGSNGNTYYANWAKGRVTISKSSNQVSLKL
SSVTAADTAVYYCARGGYRTSGMDPWGQGTTLTVTVSS

Oncomed 313R19 VL (SEQ ID NO: 29335)

DIQMTQSPSSLSASVGDRVTITCQASQNIYSDLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQEHLVAWIYNVFGQGTKVEIKR

Figure 83D

Oncomed 313M32 VH (SEQ ID NO: 29336)

QVQLQESGPGLVKPSSETLSLTCAVSGYSITSDYAWNWIRQPPGKGLEWIGYISYSGSTSYNPSLRSRVTISRDTSKNQFFL
KLSSVTAADTAVYYCARRQVGLGFAYWGQGLTVTVSS

Oncomed 313M32 VL (SEQ ID NO: 29337)

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSTRFSGSGSGTDFTFTISLQPE
DIATYYCQGHYSTPWTFG

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

What: anti-BTLA XENP20269 9C6_H0L0	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGPGLVAPQSLSITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWIDGSTDYNSALKSRLSIN KDNSKSQVFLKMNLSLTQDDTARYYCARDRDPDGRAMDYWGQGTSTVTVSS	29338
vhCDR1	GYGVN	29339
vhCDR2	MIWIDGSTDYNSALKS	29340
vhCDR3	DRPDGRAMDY	29341
Variable light (vl) domain	SIVMTQTPKFLVLSAGDRVTTTCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD FTFTISTVQAEIDLAVYFCQQDYSSPTFGGGTKLEIK	29342
vlCDR1	KASQSVSNDVA	29343
vlCDR2	YASNRYT	29344
vlCDR3	QQDYSSPT	29345

Figure 84B

What: anti-BTLA XENP20872 9C6_H1.1L1	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKESGAEVKKPGASVKVSCKVSGFSLTGYGVNWVRQAPGQGLEWMGMIMWIDGSTDYNSKFQGRVTMT KDNSKSTVYMELSSLRSEDTAVYYCARDRDPDGRAMDYWGQGTMTVTVSS	29346
vhCDR1	GYGVN	29347
vhCDR2	MIWIDGSTDYNSKFQ	29348
vhCDR3	DRPDGRAMDY	29349
Variable light (vl) domain	SIVMTQSPDLSAVSLGERATINCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD FTLTISLQAEDVAVYFCQQDYSSPTFGGGTKLEIK	29350
vlCDR1	KASQSVSNDVA	29351
vlCDR2	YASNRYT	29352
vlCDR3	QQDYSSPT	29353

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	QVQLVQSGAEVKKPGASVKVSCKVSGFSLTGYGVNWVRQAPGQGLEWMGMIWIDGSTDYNSKFQGRLSIN KDNSKSTVYMELSSLRSEDIAVYYCARDRPDGRAMDYWGQGTMTVTVSS	29354
vhCDR1	GYGVN	29355
vhCDR2	MIWIDGSTDYNSKFQG	29356
vhCDR3	DRPDGRAMDY	29357
Variable light (vl) domain	SIVMTQSPDLSAVSLGERATINCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD FTLTISLQAEDEVAVYFCQQDYSSPTFGGGTKLEIK	29358
vlCDR1	KASQSVSNDVA	29359
vlCDR2	YASNRYT	29360
vlCDR3	QQDYSSPT	29361

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
GTR	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 86**XENP22917**

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NO: 28468)

QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGGGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NO: 28469)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGVIYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYP
SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022917 [ICOS]_H0_L0.38_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NO: 28470)
DIQMTQSPSSVSASVGDRTITCQASQDISLLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSITYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP22977

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Fab-Fc Heavy Chain (SEQ ID NO: 28522)

QVQLVQSGAEVKKPGASVKVSKASGYTFTGYMHVWRQAPGGGLEWMGWINPHSGGTNYAQKFQGRVTMTRDTSISTAYME
LSRLRSDDTAVYYCARTYYDSSGGYYHDAFDIWGQGTMTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDG
SFFLYSKLTVDKSRWEQGDVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 scFv-Fc Heavy Chain (SEQ ID NO: 28523)

EIVLTQSPATLSASPGERVTLTCRASQSVGNDVAWYQQKPGQAPRLLINYASHRYTGVPDRFTGSGYGTEFTLTISVQSED
FGVYYCQQDFSSPRTFGGGTKVEIK/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVKPGGSLRLSCVASGFTFSNYWMN
WVRQAPGKGLEWVAEIRLYSNNYATHYAESVKGRFTISRDDSKSTLYLQMNLLKTEDTGVIYCTRYYGNYGGYFDVWGRGTL
VTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYP
SDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVDFSCSVLHEALHSHYTQKSLSLSPGK

>XENP022977 [ICOS]_H0_L0.37_Fab-1G6_L1.194_H1.279 Light Chain (SEQ ID NO: 28524)
DIQMTQSPSSVSASVGDRTITCQASQDISRLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED
FATYYCQQAESFPWTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSITYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC