Figure 1

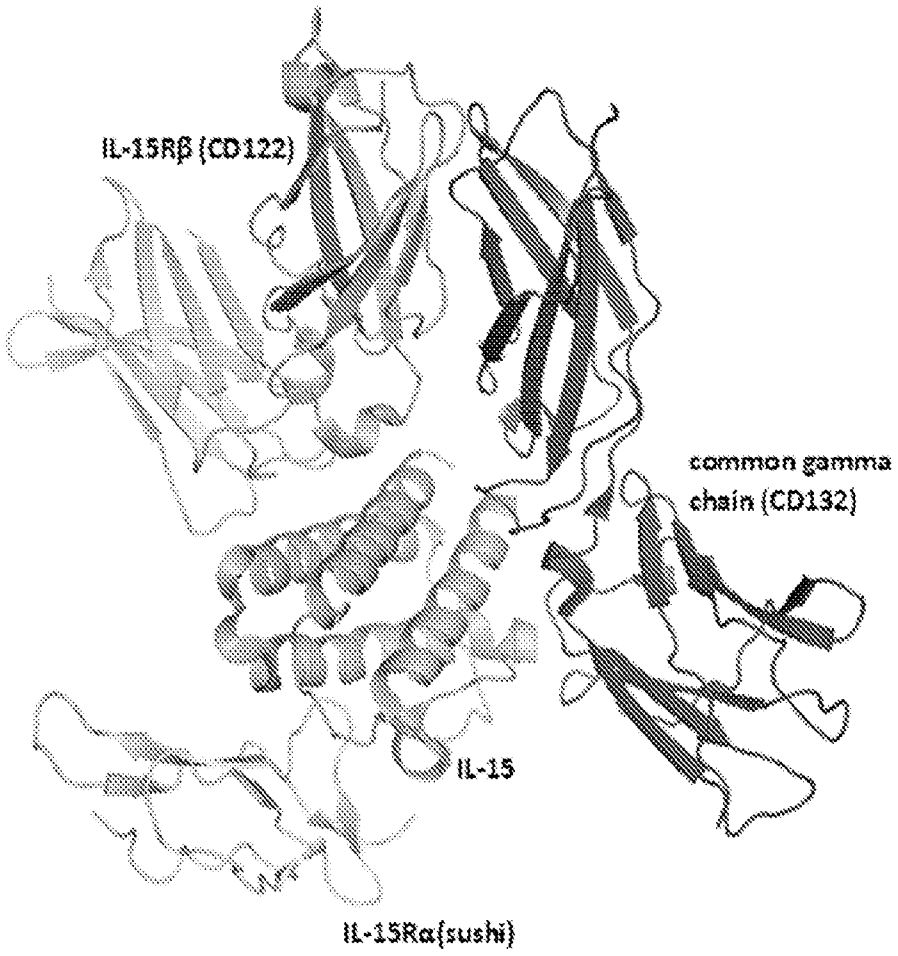


Figure 2A

Human IL-15 precursor sequence (SEQ ID NO: 5)

>sp|P40933
MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYT
ESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQS
FVHIVQMFINTS

Human IL-15 mature form sequence (SEQ ID NO: 6)

>sp|P40933|49-162
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Human IL-15Rα sequence (SEQ ID NO: 7)

>sp|Q13261
MAPRRARGCRTLGLPALLLLLLLRPPATRGITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTEC
VLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGS
QLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLA
CYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENCSHHL

Human IL-15Rα, extracellular domain (SEQ ID NO: 8)

>sp|Q13261|31-205
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPA
PPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTA
KNWELTASASHQPPGVYPQGHSDTT

Human IL-15Rα, sushi domain (SEQ ID NO: 9)

>sp|Q13261|31-95
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Human IL-15Rß sequence (SEQ ID NO: 10)

>sp|P14784
MAAPALSWRLPLLILLLPLATSWASAAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE
LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNI
SWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQ
PLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGPWLKKVLKCNTPDPSKFFSQLSSEHGGDV
QKWLSSPFPSSSFSPGGLAPEISPLEVLERDKVTQLLLQQDKVPEPASLSSNHSLTSCFTNQGYFFFHLPDALEI
EACQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSGEDDAYCTFPSRDDLLLFSPSLLGGPSPPSTAPGGSGA
GEERMPPSLQERVPRDWDPQPLGPPTPGVPDLVDFQPPPELVLREAGEEVPDAGPREGVSFPWSRPPGQGEFRAL
NARLPLNTDAYLSLQELQGQDPTHLV

Human IL-15Rß, extracellular domain (SEQ ID NO: 11)

>sp|P14784|27-240
AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTV
DIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGH
TWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKDT

Figure 2B

Human common gamma chain sequence (SEQ ID NO: 12)

>sp|P31785
MLKPSLPFTSLLFLQLPLLGVGLNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWN
SSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQN
LVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS
RFNPLCGSAQHWSEWSHPIHWGSNTSKENPFLFALEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLEDLV
TEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

Human common gamma chain, extracellular domain (SEQ ID NO: 13)

>sp|P31785|23-262
LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDND
KVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLEL
NWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWG
SNTSKENPFLFALEA

Figure 3A

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 3B

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 3C

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 3D

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

Figure 3E

Monomer 1	Monomer 2
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	P217R/P228R/N276K
K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	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
K247Q/R355Q/Q419E/K447_	P217R/P228R/N276K
K247Q/R355Q/Q419E/K447_	N276K
K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	
Q295E/N384D/Q418E/N421D	
Q295E/Q418E/N421D	
P217R/P228R/N276K	
N276K	
E269Q/E272Q/E283Q/E357Q	
E269Q/E272Q/E283Q	
E269Q/E272Q	
E269Q/E283Q	
E272Q/E283Q	
E269Q	

Figure 4

Variant constant region	Substitutions
pI_ISO(-)-Fc only	K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_
pI_(-)_isosteric A-Fc only	Q295E/N384D/Q418E/N421D
pI_(-)_isosteric_B-Fc only	Q295E/Q418E/N421D
pI_ISO(+RR)-Fc only	P217R/P228R/N276K
pI_ISO(+)-Fc only	N276K
pI_(+)_isosteric_A	E269Q/E272Q/E283Q/E357Q
pI_(+)_isosteric_B	E269Q/E272Q/E283Q
pI_(+)_isosteric_E269Q/E272Q	E269Q/E272Q
pI_(+)_isosteric_E269Q/E283Q	E269Q/E283Q
pI_(+)_isosteric_E272Q/E283Q	E272Q/E283Q
pI_(+)_isosteric_E269Q	E269Q

Figure 5

Ablation Variants

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

Figures 6A-6E

Figure **s 6**A	
IL-15-Fc monomer (-)	**IL-15Rα(sushi)-Fc monomer (+)**
C220S	C220S
Heterodimer pI variants L368D/K370S	Heterodimer pI variants S364K/E357Q
Isosteric pI substitutions Q295E/N384D/Q418E/N421D	
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure **s 6**B	
scIL-15/Rα-Fc monomer (-)	**empty-Fc monomer (+)**
C220S	C220S
Heterodimer pI variants L368D/K370S	Heterodimer pI variants S364K/E357Q
Isosteric pI substitutions Q295E/N384D/Q418E/N421D	
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure **s 6**C	
empty-Fc monomer (-)	**IL-15Rα(sushi)-Fc monomer (+)**
C220S	C220S
Heterodimer pI variants L368D/K370S	Heterodimer pI variants S364K/E357Q
Isosteric pI substitutions Q295E/N384D/Q418E/N421D	
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure **s 6**D	
IL-15Rα(sushi)-Fc Chain 1	**IL-15Rα(sushi)-Fc Chain 2**
C220S	C220S
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure **s 6**E	
Fc-IL-15Rα(sushi) (-)	**empty-Fc monomer (+)**
C220S	C220S
Heterodimer pI variants L368D/K370S	Heterodimer pI variants S364K/E357Q
	Isosteric pI substitutions P217R/P228R/N276K
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S	±M428L/N434S

Figure 7

Name	Sequence	SEQ ID NO:
$(GGGGS)_1$ or GGGGS	GGGGS	14
$(GGGGS)_2$	GGGGSGGGGS	15
$(GGGGS)_3$	GGGGSGGGGSGGGGS	16
$(GGGGS)_4$	GGGGSGGGGSGGGGSGGGGS	17
$(GGGGS)_5$	GGGGSGGGGSGGGGSGGGGSGGGGS	18
$(GGGGS)_6$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	19
$(GGGGS)_7$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	20
30AA-linker	DPALVHQRPAPPGGGGSGGGGSGGGGSGGG	21
$(GKPGS)_1$ or GKPGS	GKPGS	22
$(GKPGS)_5$	GKPGSGKPGSGKPGSGKPGSGKPGS	23
$(GKPGS)_6$	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	24
$(GGGES)_1$ or GGGES	GGGES	25

Figure 8A

IL-15/Rα-Fc Backbone 1

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 26)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 27)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 2

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 28)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 29)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 3

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 30)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 31)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 8B

IL-15/Rα-Fc Backbone 4

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 32)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSKGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 33)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTENEVSLTCLVKGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLEVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 5

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 34)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 35)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 6

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 36)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 37)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 8C

IL-15/Rα-Fc Backbone 7

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 38)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 39)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 8

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 40)
ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHN
AKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPS
QEQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNV
FSCSVMHEALHNHYTQKSLSLSLGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 41)
ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHN
AKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPS
QEEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWEEGDV
FSCSVMHEALHNHYTQKSLSLSLGK

IL-15/Rα-Fc Backbone 9

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 42)
ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA
KTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 43)
ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA
KTKPREEEFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVF
SCSVMHEALHNHYTQKSLSLSPGK

Figure 8D

IL-15/Rα-Fc Backbone 10

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 44)
ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNA
KTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 45)
ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNA
KTKPREEEFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVF
SCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 11

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 46)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVLHEALHSHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 47)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVLHEALHSHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 12

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 48)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 49)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

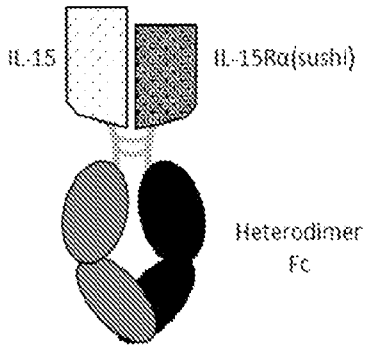
Figure 8E

IL-15/Rα-Fc Backbone 13

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 50)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

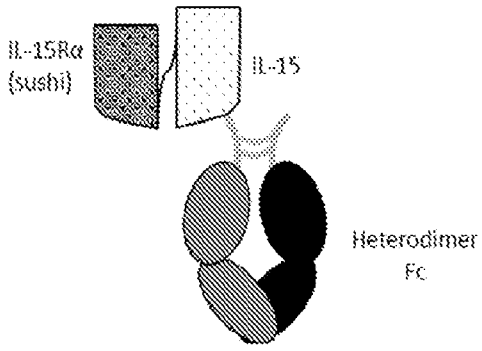
>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 51)
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 9A



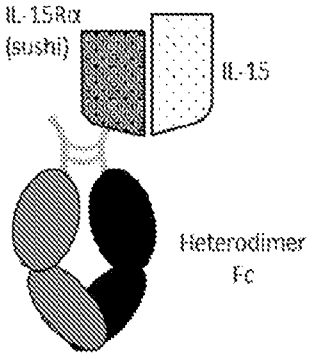
IL-15/Rα-heteroFc
Example: XENP20818

FIGURE 9B



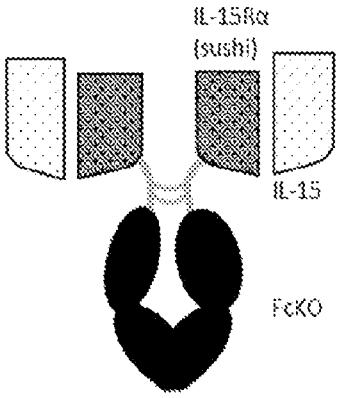
scIL-15/Rα-Fc
Example: XENP21478

FIGURE 9C



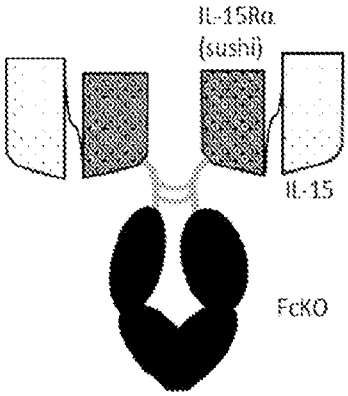
ncIL-15/Rα-Fc
Example: XENP21479

FIGURE 9D



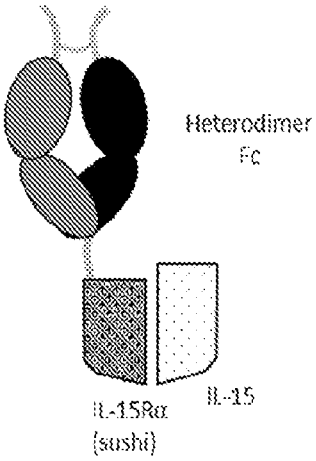
Bivalent ncIL-15/Rα-Fc
Example: XENP21978

FIGURE 9E



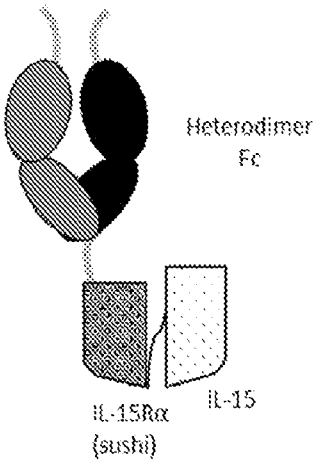
Bivalent scIL-15/Rα-Fc

FIGURE 9F



Fc-ncIL-15/Rα
Example: XENP22637

FIGURE 9G



Fc-scIL-15/Rα

Figure 10

>XENP20818 – human IL15-(GGGGS)$_1$ x human IL15Rα(Sushi)-(GGGGS)$_1$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (15902) (SEQ ID NOS 52-54)

NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 55-57)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP21475 – human IL15 x human IL15Rα(Sushi) Fc heterodimer

Chain 1 - human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16479) (SEQ ID NOS 58-60)

NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDW_NGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 61-63)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHED?EVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE?QVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 11

>XENP21478 – human IL15Rα(Sushi)-(GGGGS)$_6$-human IL15(single-chain) Fc heterodimer

Chain 1 - human_IL15Rα(sushi)_(GGGGS)$_6$-human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16478) (SEQ ID NOS 64-67)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE
SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - empty-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (8924) (SEQ ID NO: 68)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 12A

>XENP21479 – empty-Fc-IL15(non-covalent)-human_IL15Rα(Sushi) Fc heterodimer

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 69)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 70)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Rα(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 71-73)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHED?EVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE?QVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022366 – empty-Fc-IL15(non-covalent)-human_IL15Ra(sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 74)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 75)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 76-78)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

Figure 12B

>XENP024348 IL15(non-covalent)-human_IL15Ra(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – IL15 WT (SEQ ID NO: 79)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 – human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 80-82)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 83)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 13

>XENP021978 – human_IL15(non-covalent)-human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K (17023) (SEQ ID NOS 84-86)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_no_tag (16484) (SEQ ID NO: 87)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 14

human_IL15Ra(sushi)(single-chain)-human_IL15_Fc(216)_IgG1_C220S/PVA_/S267K (SEQ ID NOS 88-91)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/NWV
NVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNG
NVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 15

>XENP022637 – empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(non-covalent)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - empty- Figure 15

Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi) (17603) (SEQ ID NOS 92-94)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIR

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 95)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15_no_tag (16484) (SEQ ID NO: 96)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 16

empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(single-chain)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q

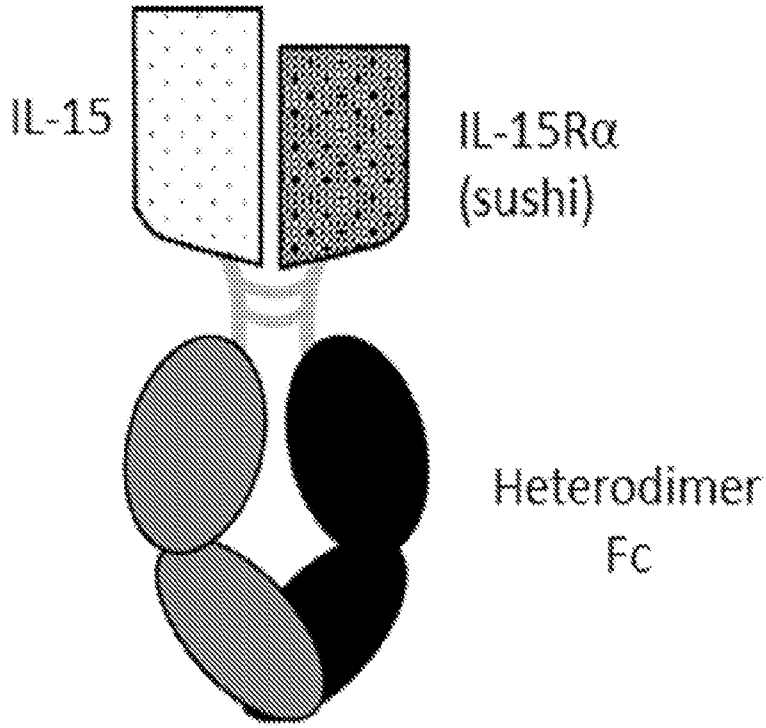
Chain 1 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(single-chain) (SEQ ID NOS 97-100)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIR/GGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIH
DTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 101)

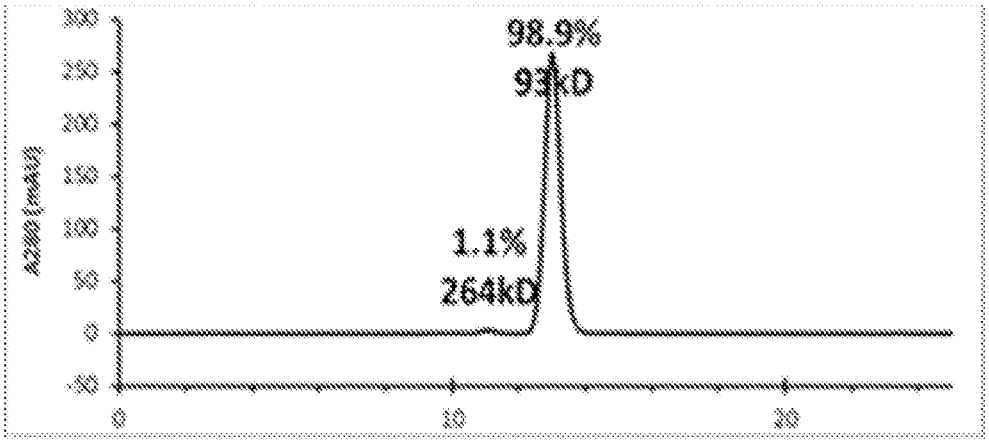
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 17A



XENP20818

Figure 17B



pI(MW) = 6.41 (72.7 kDa)
Protein A yield = 25.7 mg/L

Figure 17C

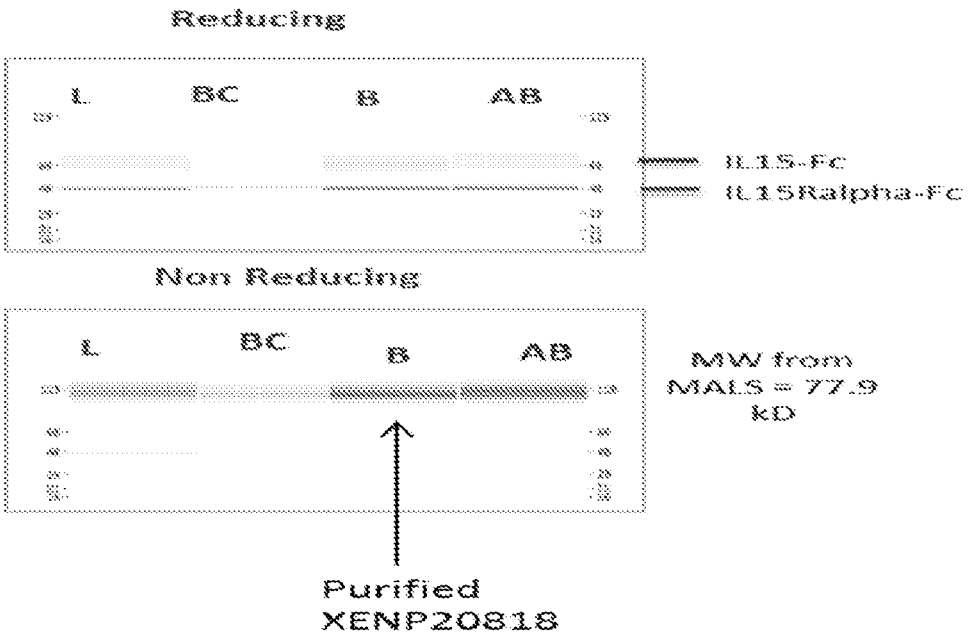
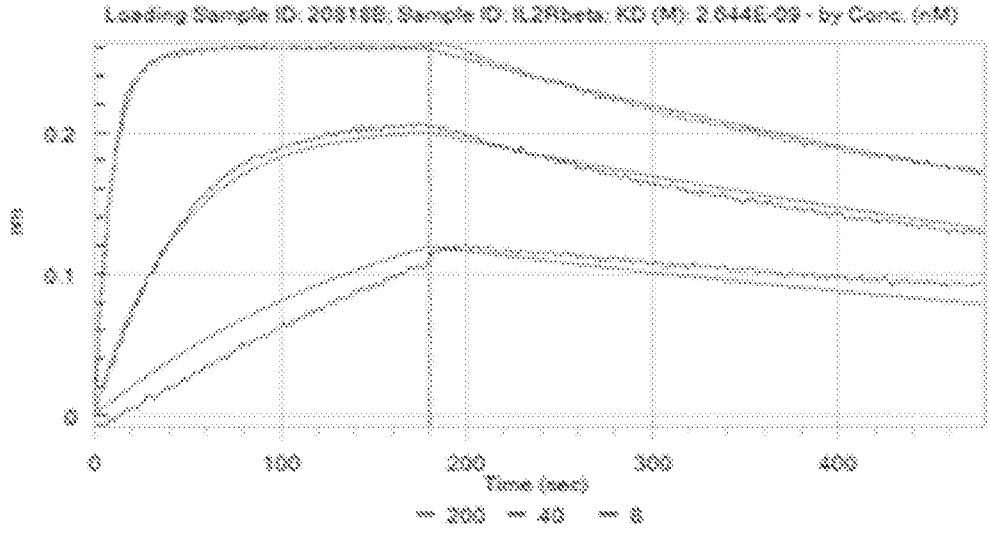


Figure 17D



Octet Red 96 – AHC capture of XENP20818; dip in 200 nM, 40 nM, or 8 nM IL2-Rβ (R&D systems); KD ~ 3 nM

Figure 17E

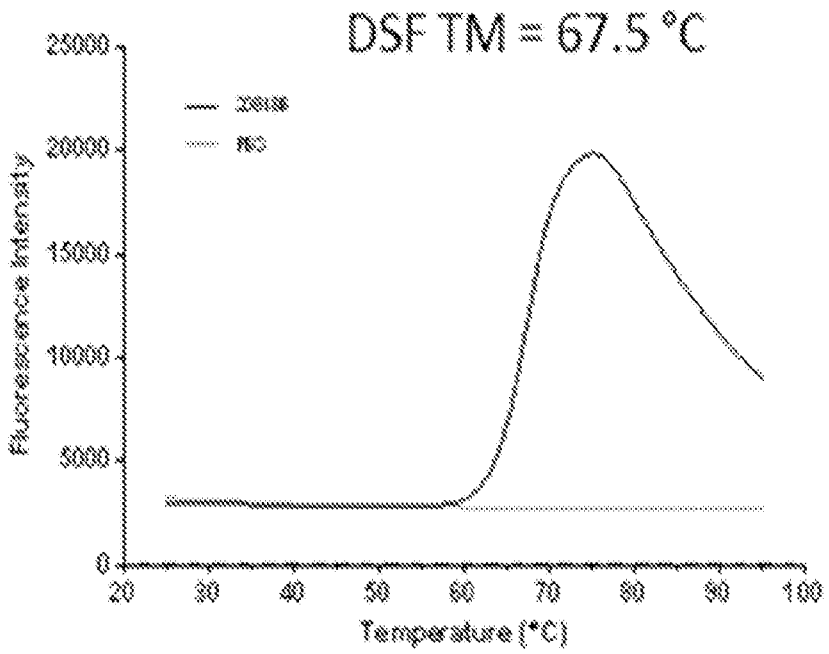
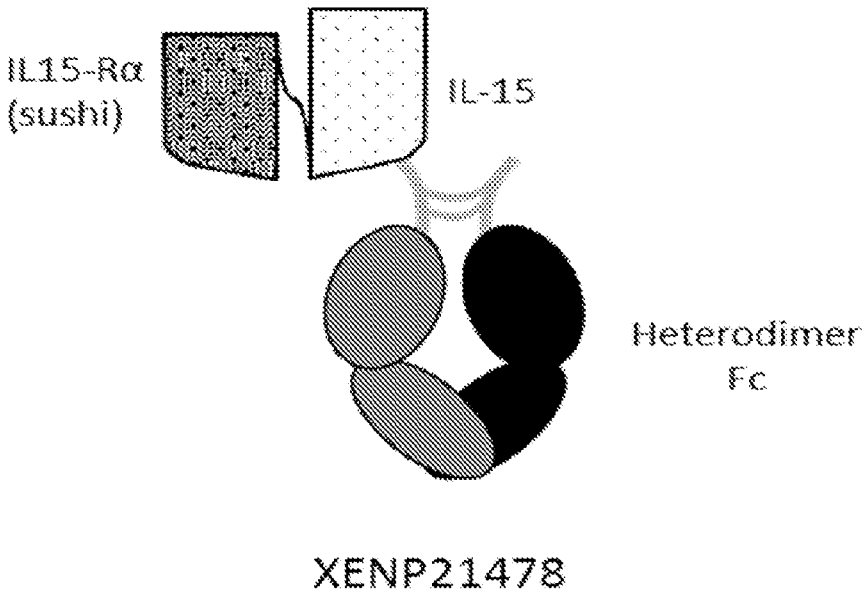
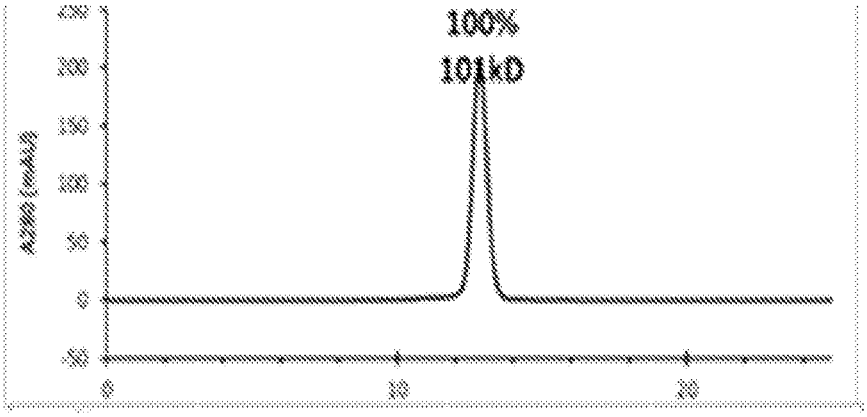


Figure 18A



XENP21478

Figure 18B



pI(MW) = 6.41 (74.0 kDa)
Protein A yield = 68.1 mg/L

Figure 18C

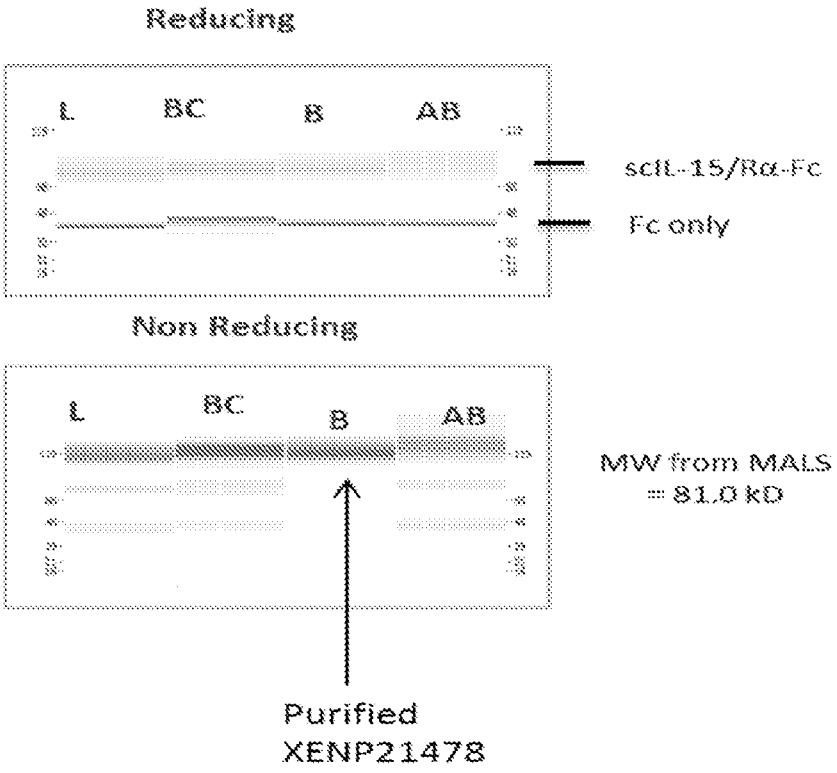
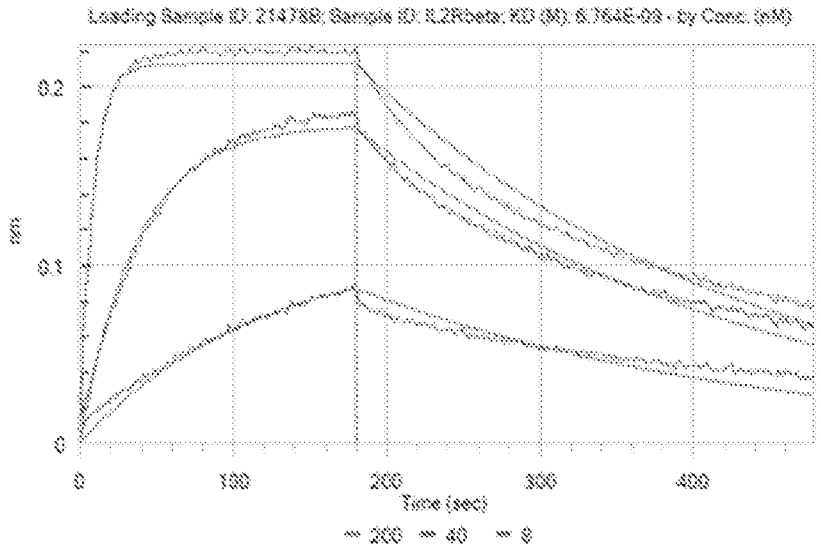


Figure 18D



Octet Red 96 – AHC capture of XENP21478; dip in 200 nM, 40 nM, or 8 nM IL2Rβ (R&D systems); KD ~ 3 nM

Figure 18E

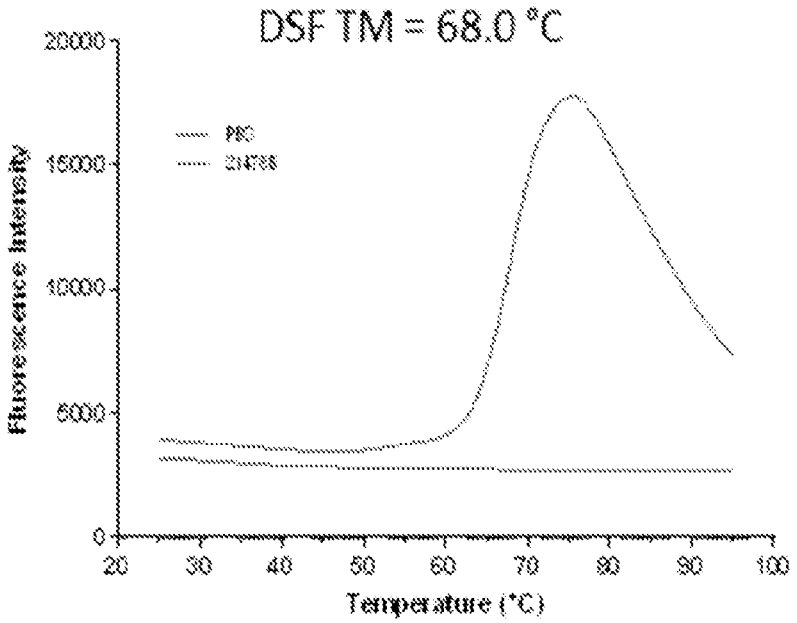


Figure 19A

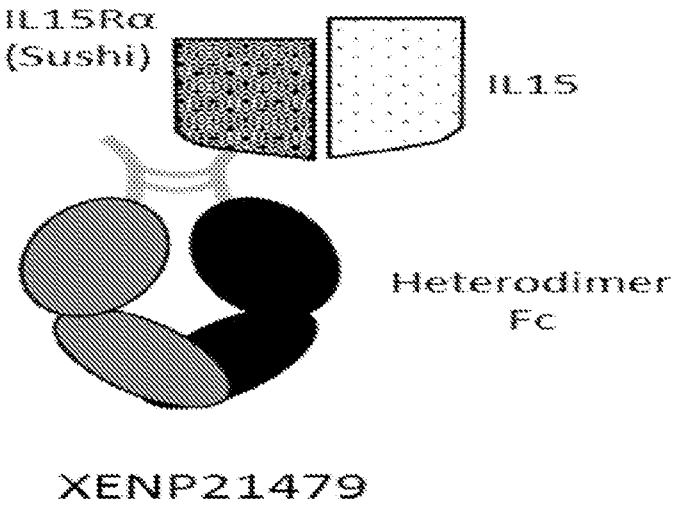
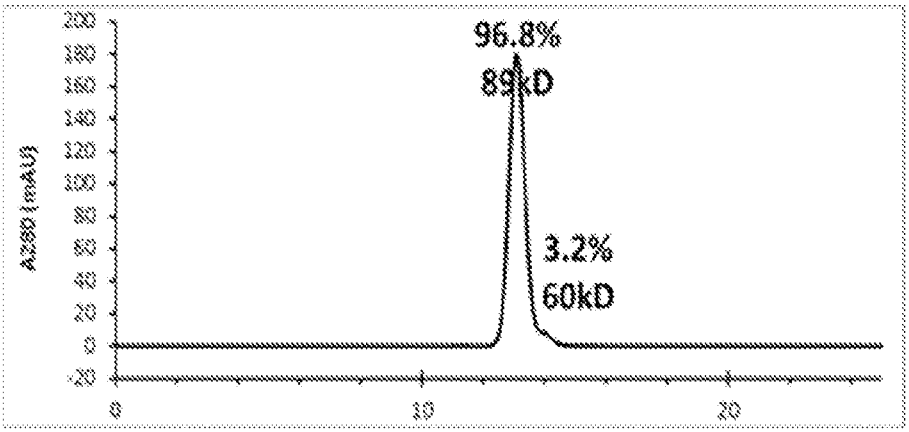


Figure 19B



pI(MW) = 6.41 (72.1 kDa)
Protein A yield = 57.1 mg/L

Figure 19C

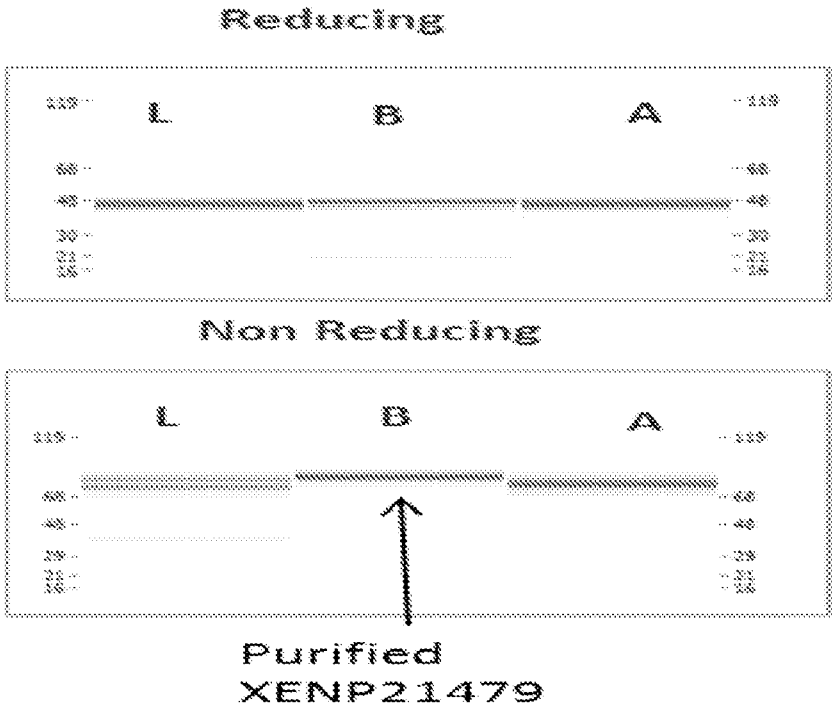
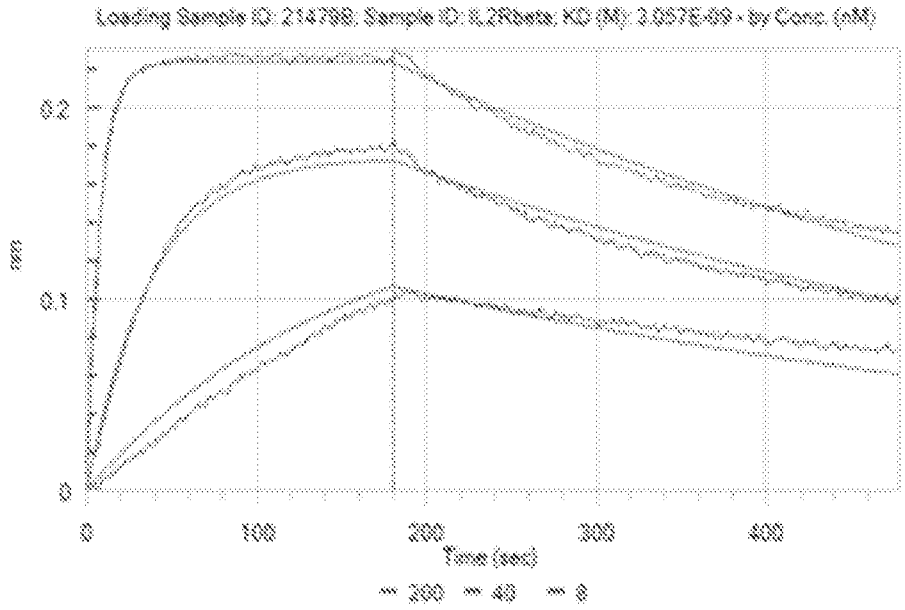


Figure 19D



Octet Red 96 – AHC capture of XENP21479; dip in 200 nM, 40 nM, or 8 nM IL2Rβ (R&D systems); KD ~ 3 nM

Figure 19E

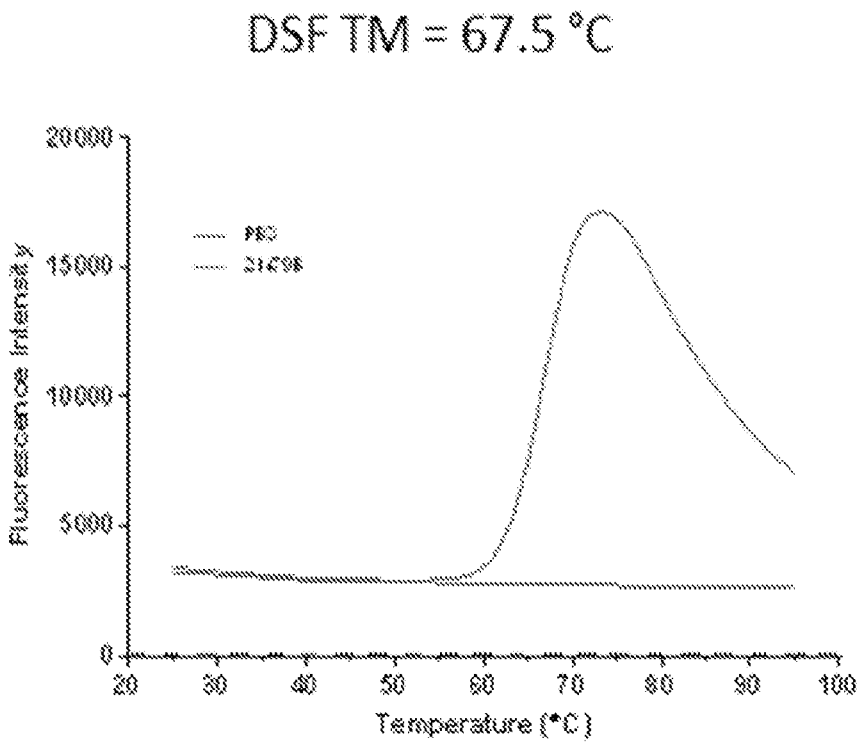


Figure 20A

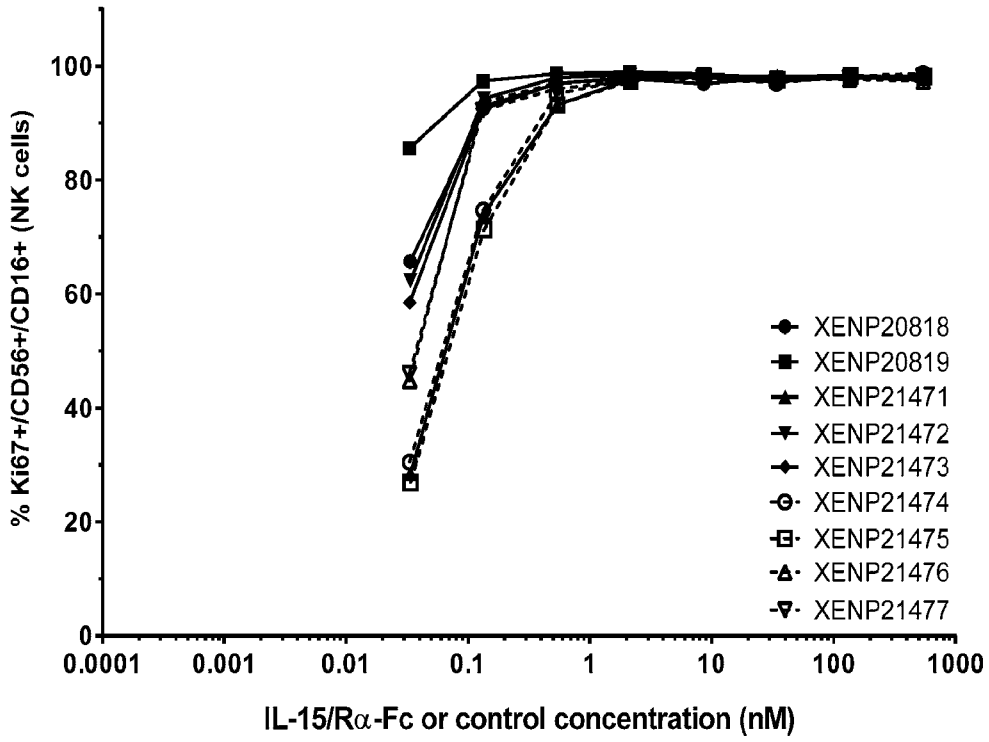


Figure 20B

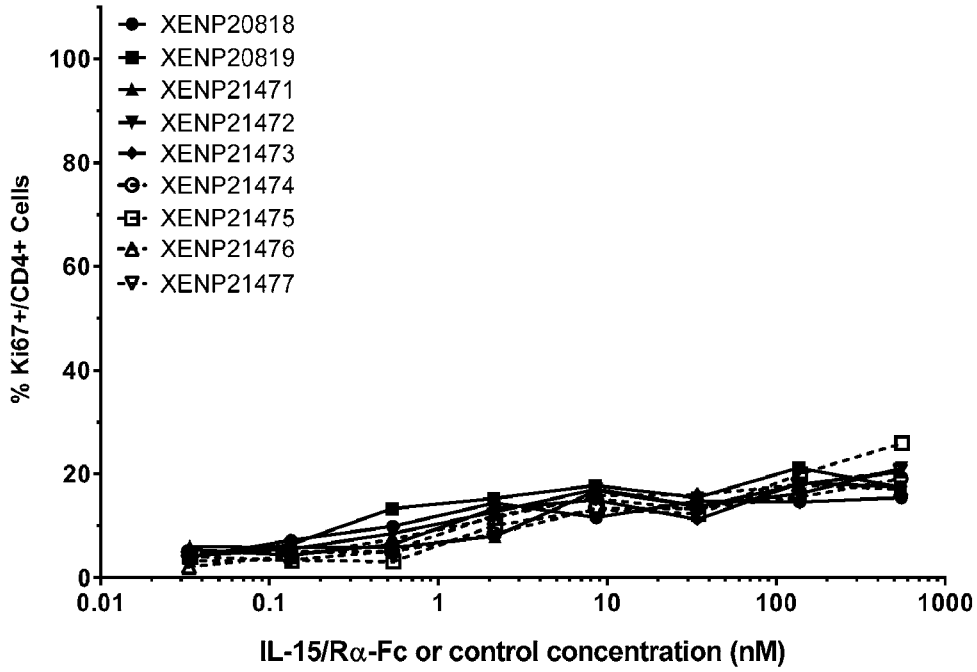


Figure 20C

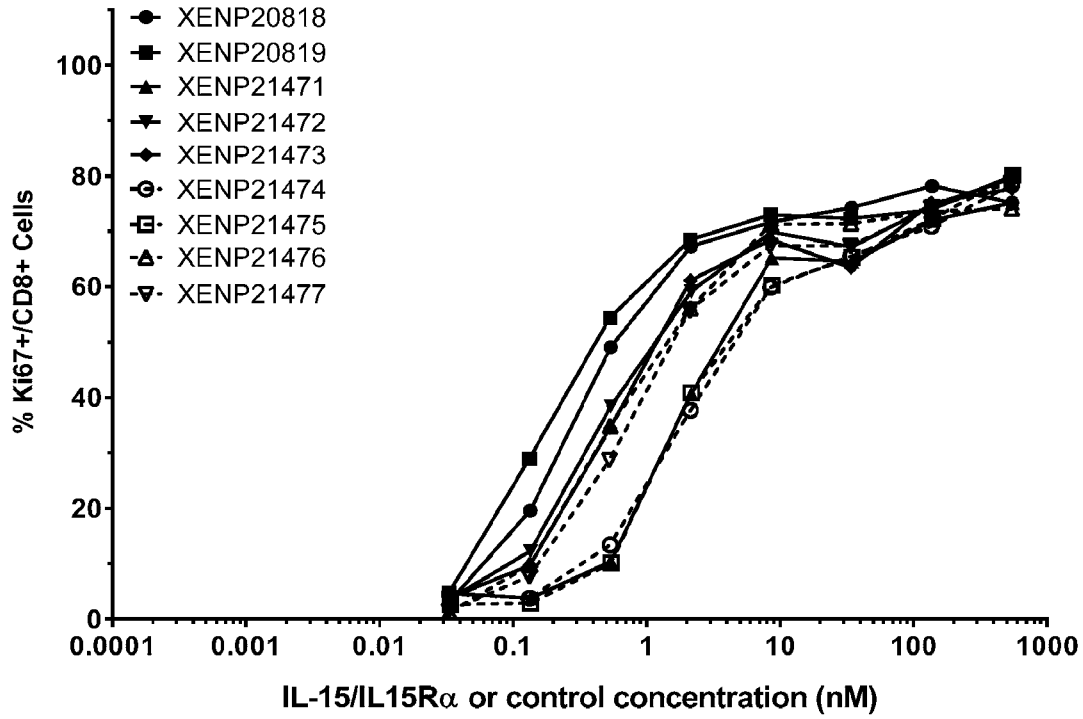


Figure 21A

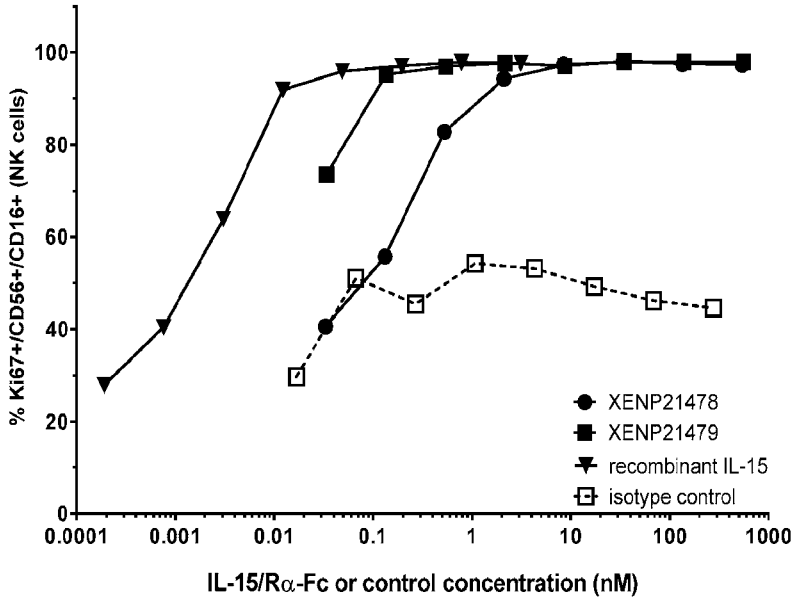


Figure 21B

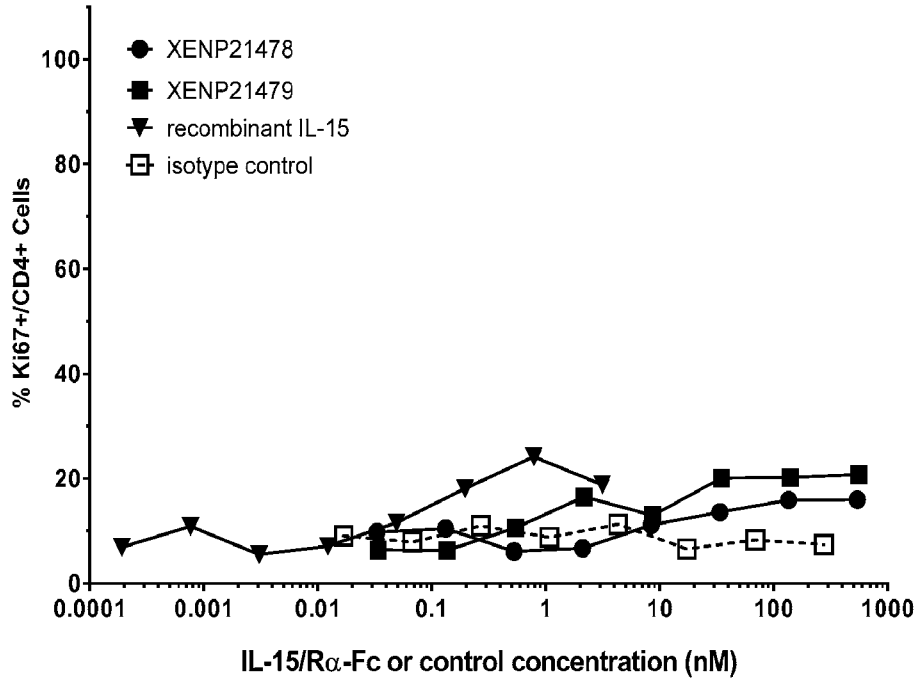


Figure 21C

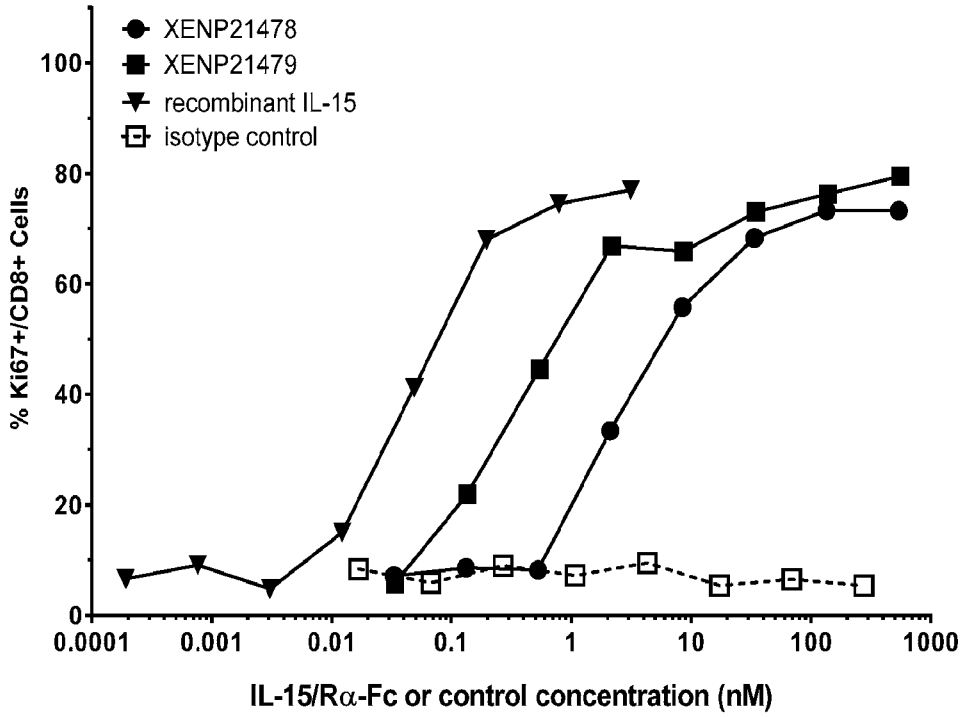


Figure 22

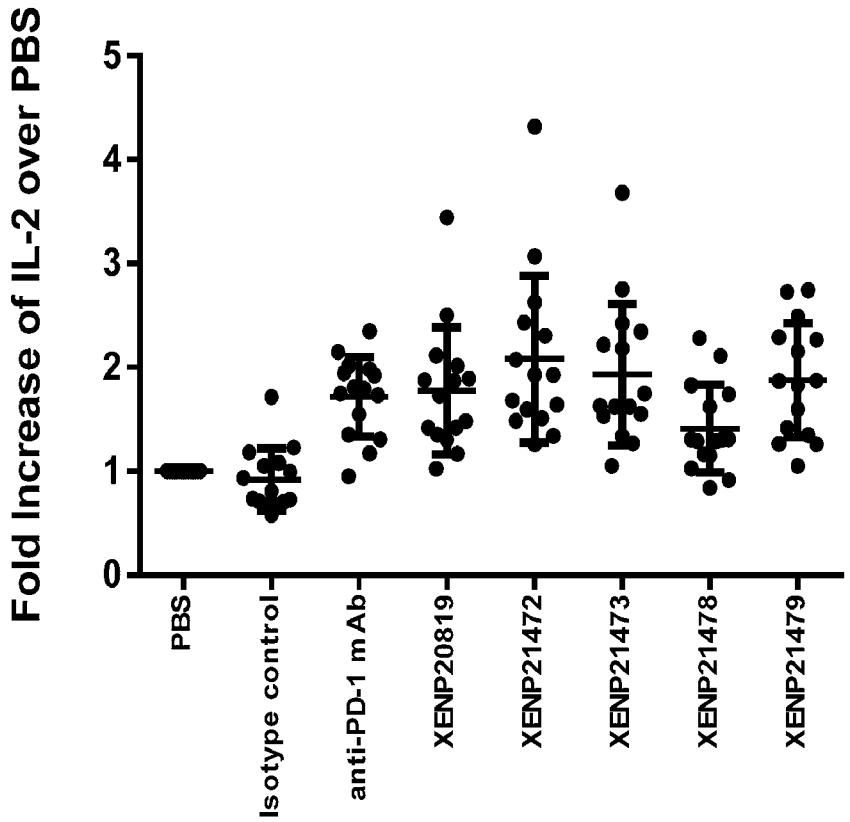


Figure 23

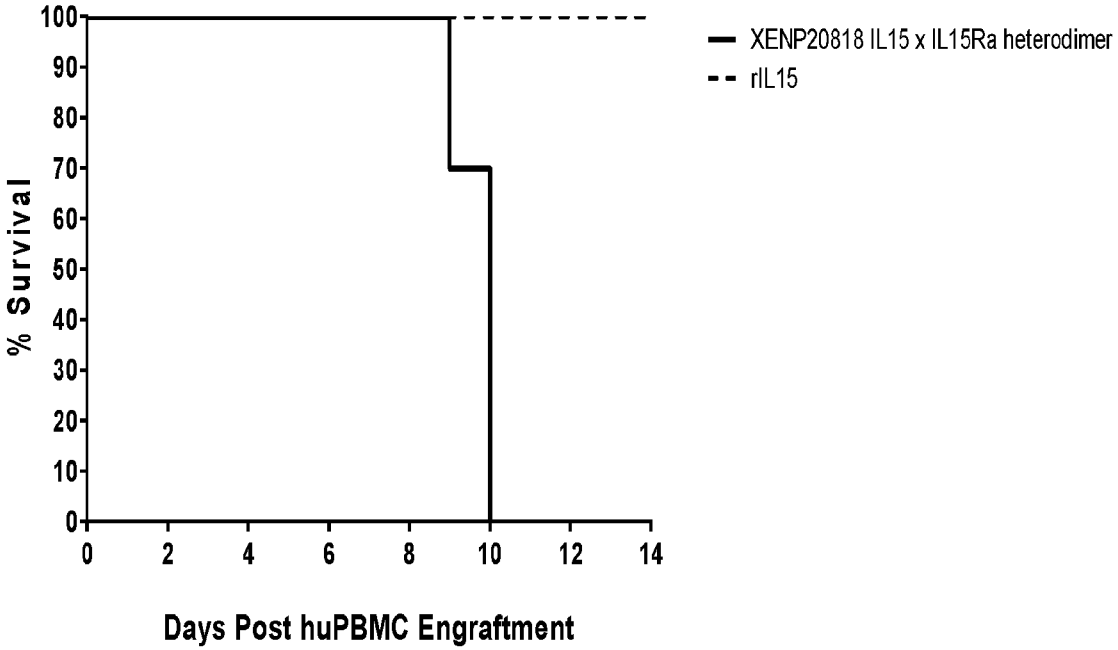


Figure 24

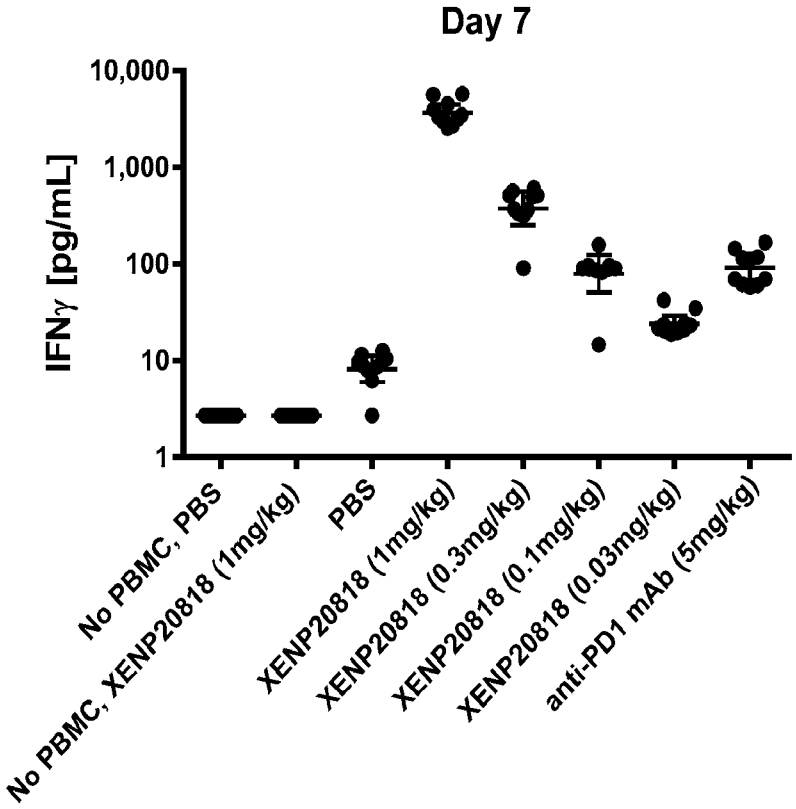


Figure 25A

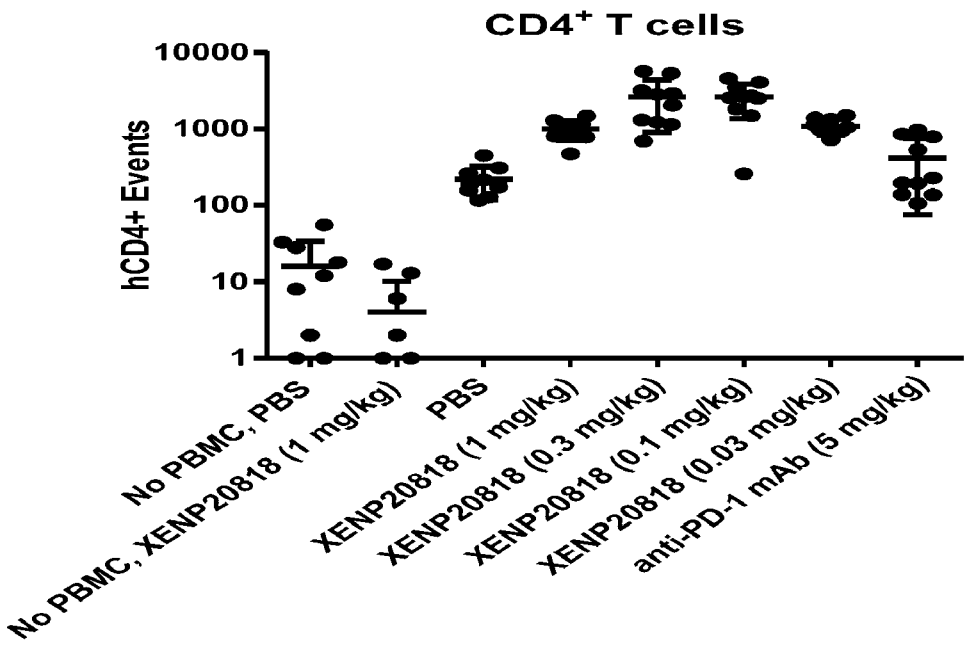


Figure 25B

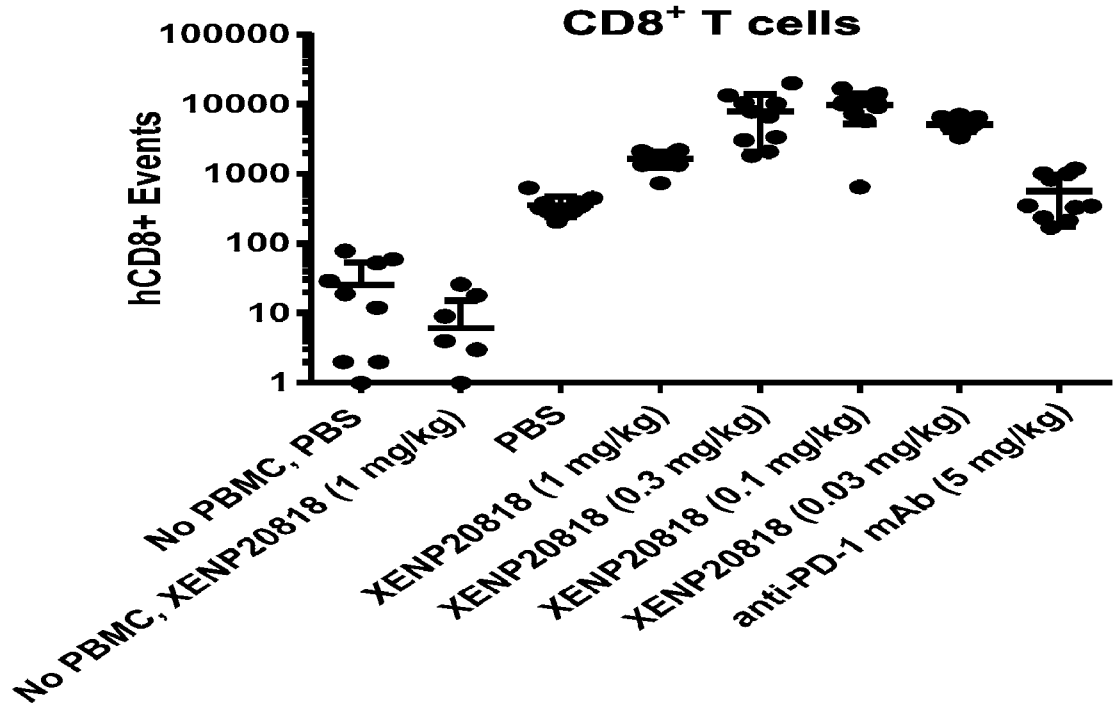


Figure 25C

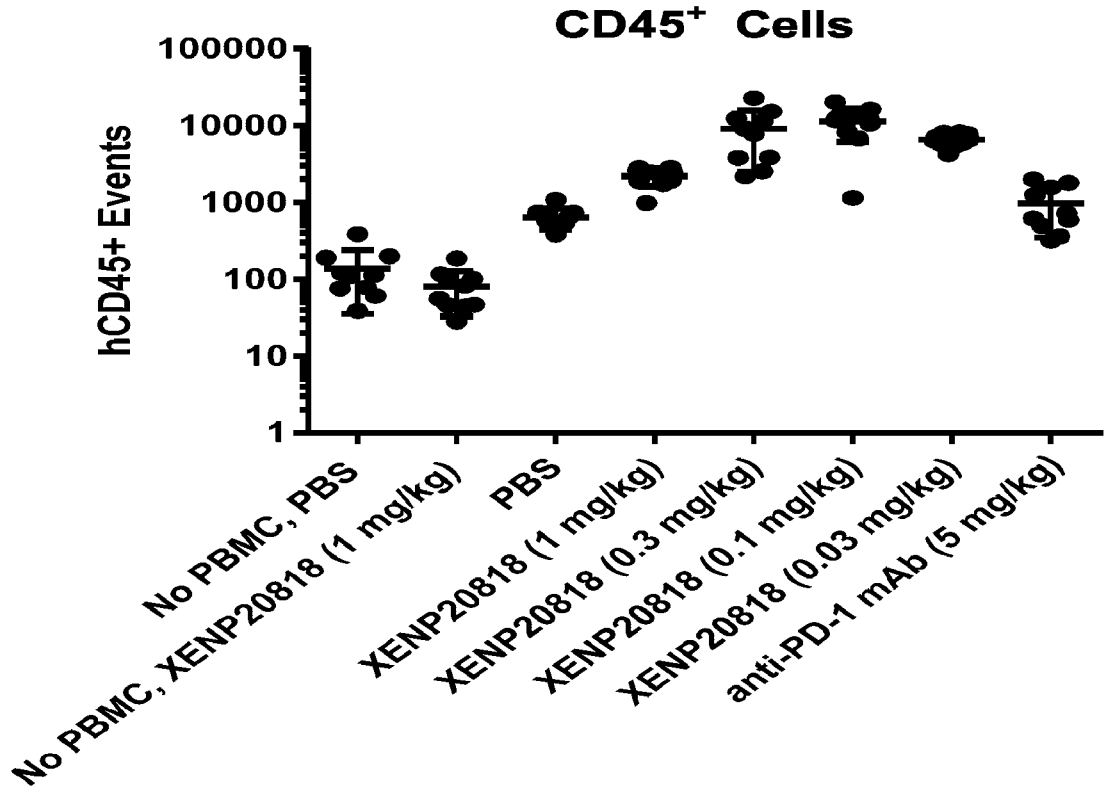

CD45+ Cells
hCD45+ Events
100000
10000
1000
100
10
1
No PBMC, PBS
No PBMC, XENP20818 (1 mg/kg)
PBS
XENP20818 (1 mg/kg)
XENP20818 (0.3 mg/kg)
XENP20818 (0.1 mg/kg)
XENP20818 (0.03 mg/kg)
anti-PD-1 mAb (5 mg/kg)

Figure 26

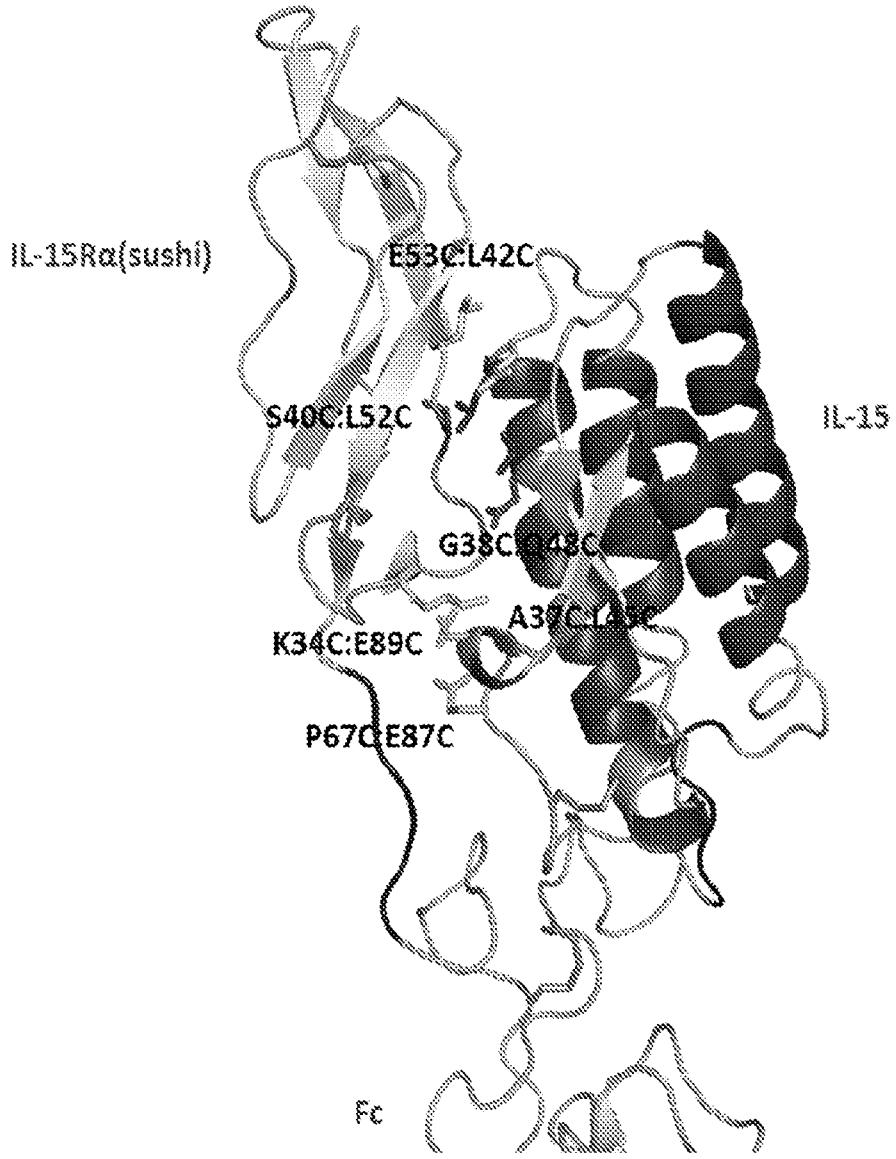

IL-15Rα(sushi)
E53C:L42C
S40C:L52C
IL-15
G38C:Q48C
A39C:L45C
K34C:E89C
P67C:E87C
Fc

Figure 27

IL-15Rα(sushi-D96) (SEQ ID NO: 102)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD

IL-15Rα(sushi-D96/P97) (SEQ ID NO: 103)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDP

IL-15Rα(sushi-D96/P97/A98) (SEQ ID NO: 104)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA

Figure 28

IL-15(E87C) (SEQ ID NO: 105)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(V49C) (SEQ ID NO: 106)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQCISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(L52C) (SEQ ID NO: 107)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(E89C) (SEQ ID NO: 108)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECCELEEKNIKEFLQSFVHIVQMFINTS

IL-15(Q48C) (SEQ ID NO: 109)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELCVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(E53C) (SEQ ID NO: 110)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLCSGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(C42S) (SEQ ID NO: 111)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKSFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(L45C) (SEQ ID NO: 112)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLCELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 29

IL-15Rα(sushi-D96/C97) (SEQ ID NO: 113)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC

IL-15Rα(sushi-D96/P97/C98) (SEQ ID NO: 114)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC

IL-15Rα(sushi-D96/C97/A98) (SEQ ID NO: 115)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA

IL-15Rα(sushi-S40C) (SEQ ID NO: 116)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR

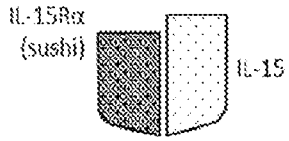
IL-15Rα(sushi-K34C) (SEQ ID NO: 117)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFCRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-G38C) (SEQ ID NO: 118)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKACTSSLTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-L42C) (SEQ ID NO: 119)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSCTECVLNKATNVAHWTTPSLKCIR

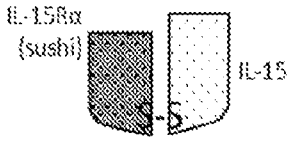
IL-15Rα(sushi-A37C) (SEQ ID NO: 120)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 30A



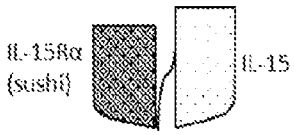
ncIL-15/Rα Heterodimer
Example: XENP21996

Figure 30B



dsIL-15/Rα Heterodimer
Example: XENP22004

Figure 30C



scIL-15/Rα Heterodimer
Example: XENP22049

Figure 31

>XENP021996 - human_IL15(non-covalent)-human_IL15Ra(Sushi)

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 121)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi) (17033) (SEQ ID NO: 122)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 32

>XENP022004 - human_IL15_E87C-human_IL15Ra(Sushi-D96/C97)

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 123)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/C97) (17051) (SEQ ID NO: 124)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC

>XENP022005 - human_IL15_E87C-human_IL15Ra(Sushi-D96/P97/C98)

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 125)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/P97/C98) (17052) (SEQ ID NO: 126)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC

>XENP022006 - human_IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 127)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/C97/A98) (17053) (SEQ ID NO: 128)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA

>XENP022008 - human_IL15_L52C-human_IL15Ra(Sushi-S40C)

Chain 1 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 129)NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANN
SLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-S40C) (17057) (SEQ ID NO: 130)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR

>XENP022494 – human_IL15_L45C-human_IL15Ra(Sushi-A37C)

Chain 1 - human_IL15_L45C_no_tag (17069) (SEQ ID NO: 131)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLCELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-A37C) (17055) (SEQ ID NO: 132)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 33

>XENP022049 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15-sc (SEQ ID NOS 133-135)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE
SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 34

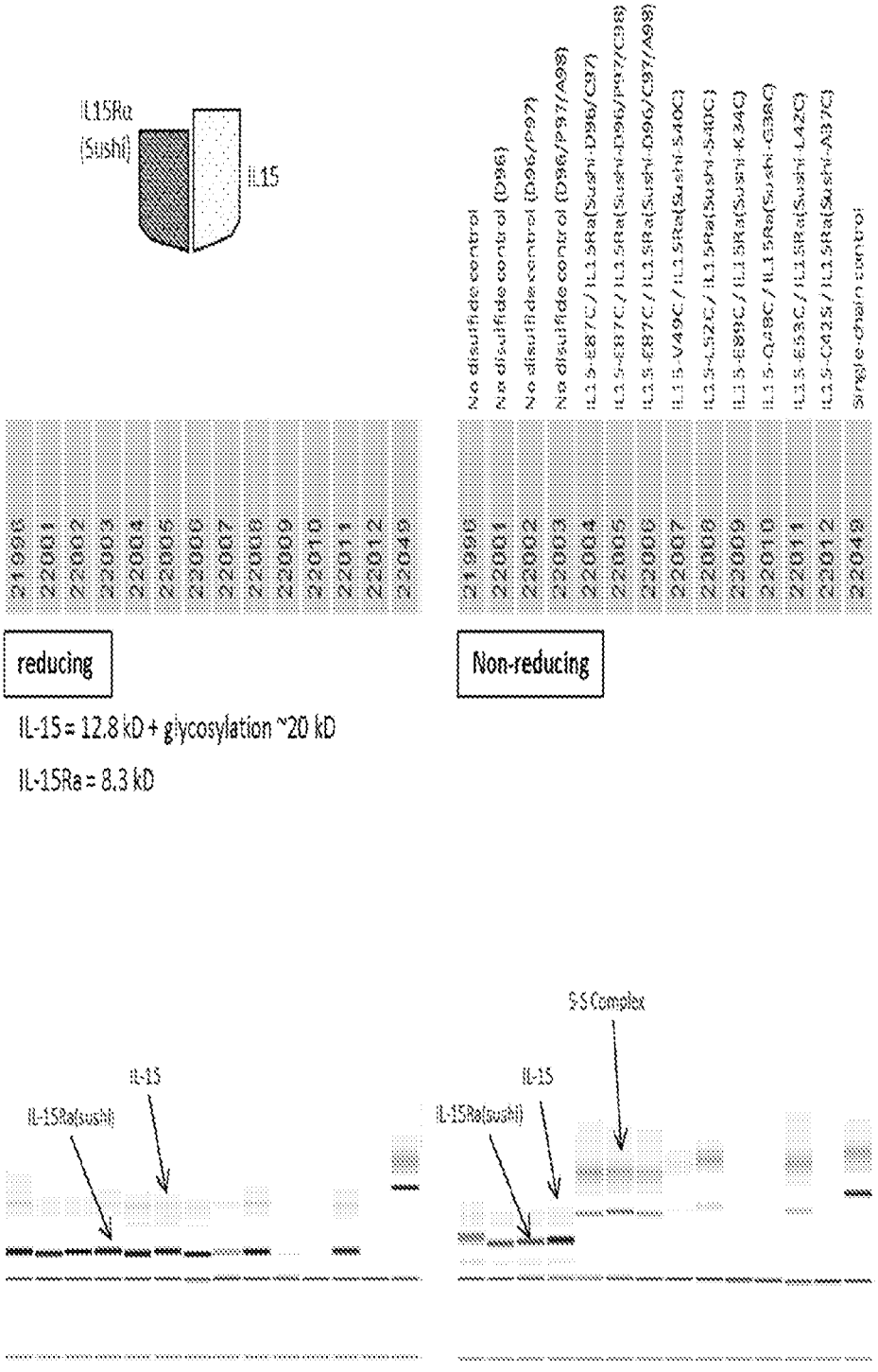
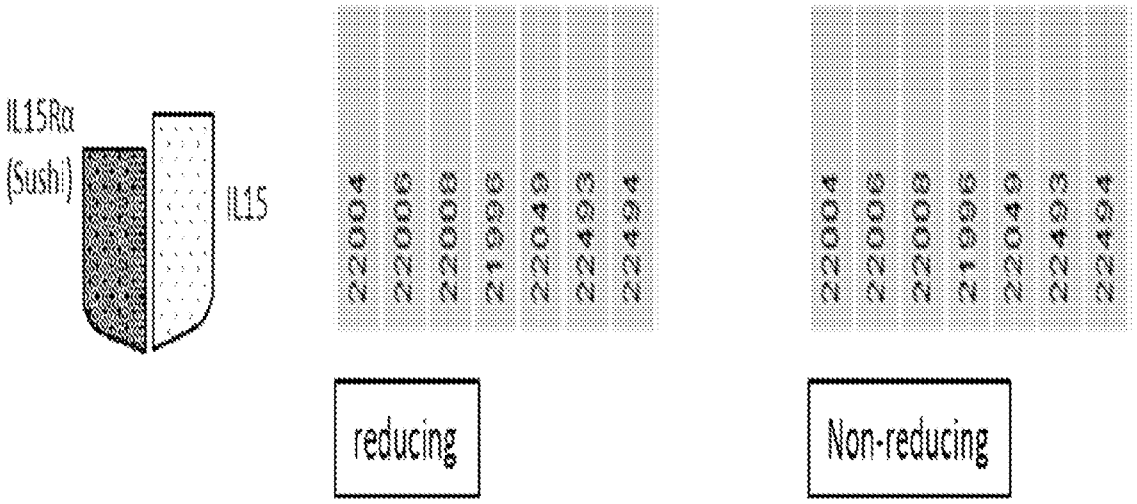

IL15Ra
(Sushi)
IL15
No disulfide control
No disulfide control (D96)
No disulfide control (D96/P97/A98)
No disulfide control (D96/P97/C98)
IL15-E87C / IL15Ra(Sushi-D96/C97)
IL15-E87C / IL15Ra(Sushi-D96/P97/C98)
IL15-E87C / IL15Ra(Sushi-D96/C97/A98)
IL15-V49C / IL15Ra(Sushi-S40C)
IL15-L52C / IL15Ra(Sushi-S40C)
IL15-E89C / IL15Ra(Sushi-K34C)
IL15-Q28C / IL15Ra(Sushi-G38C)
IL15-E53C / IL15Ra(Sushi-L42C)
IL15-C42S / IL15Ra(Sushi-A37C)
Single chain control
21908
22001
22002
22003
22004
22006
22008
22007
22010
22009
22011
22012
22049
reducing
Non-reducing
IL-15 = 12.8 kD + glycosylation ~20 kD
IL-15Ra = 8.3 kD
IL-15Ra(sushi)
IL-15
9:5 Complex

Figure 35


IL15Rα
(Sushi)
IL15
22004
22006
22008
21696
22049
22493
22494
reducing
Non-reducing

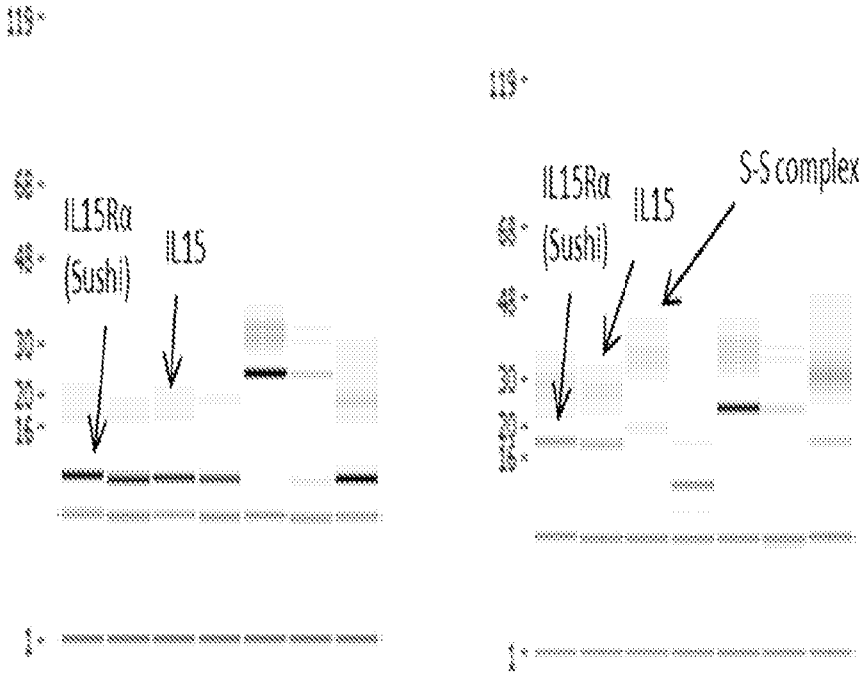

IL15Rα
(Sushi)
IL15
S-S complex

Figure 36

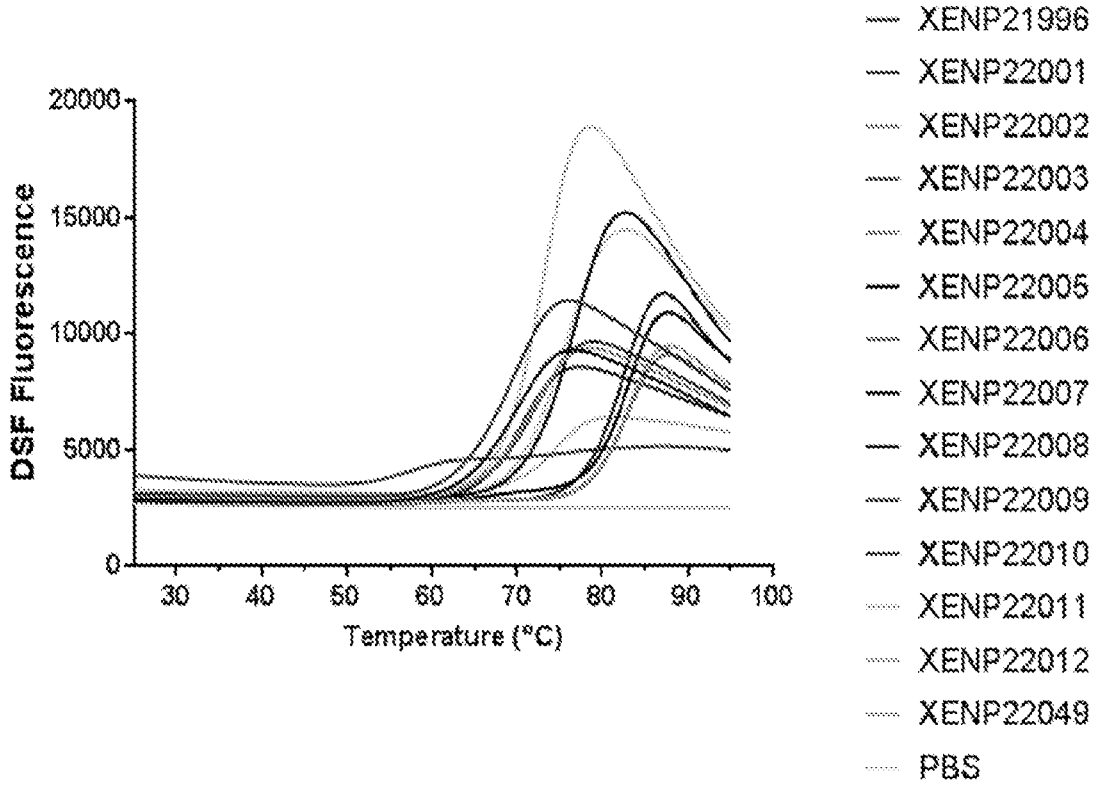

DSF Fluorescence
20000
15000
10000
5000
0
30
40
50
60
70
80
90
100
Temperature (°C)
XENP21996
XENP22001
XENP22002
XENP22003
XENP22004
XENP22005
XENP22006
XENP22007
XENP22008
XENP22009
XENP22010
XENP22011
XENP22012
XENP22049
PBS

Figure 37

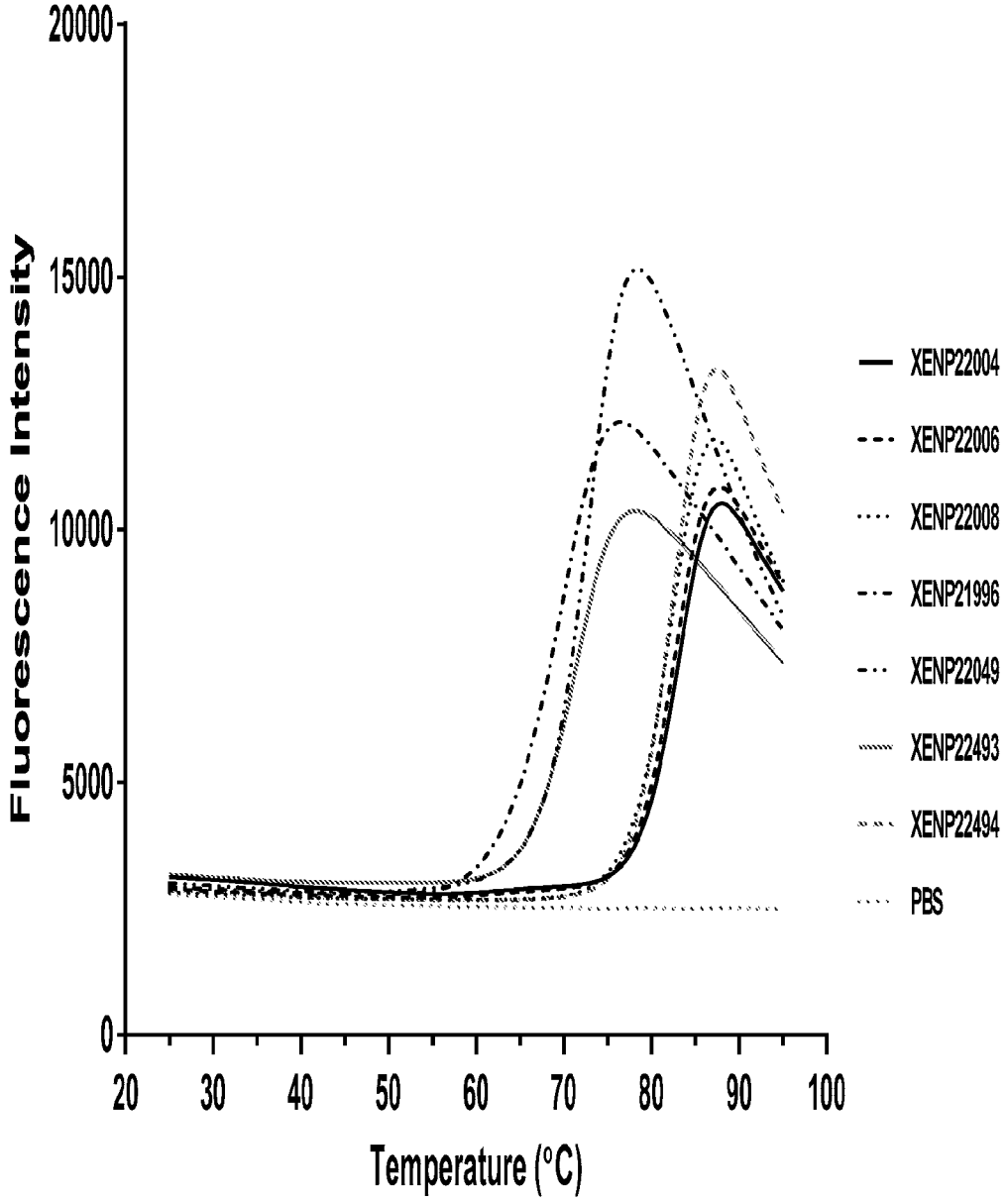
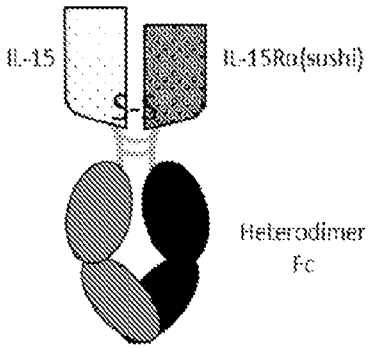

20000
15000
10000
5000
0
Fluorescence Intensity
20
30
40
50
60
70
80
90
100
Temperature (°C)
XENP22004
XENP22006
XENP22008
XENP21996
XENP22049
XENP22493
XENP22494
PBS

Figure 38

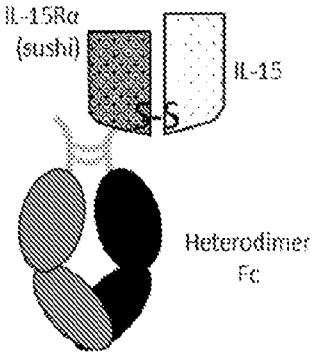
XENP	Variant	Yield (mg/ml)	MW (g/mol)	Calculated ΔAffinity	T_m (°C)	IL2Rß Affinity (~nM K_D)
21996	No Disulfide Control IL-15/Rα	8.04	21079.9	NA	70.0	6.3
22001	No Disulfide Control IL-15/Rα(D96)	2.45	21195.0	NA	70.0	5.2
22002	No Disulfide Control IL-15/Rα(D96/P97)	2.47	21292.1	NA	72.0	7.4
22003	No Disulfide Control IL-15/Rα(D96/P97/A98)	3.48	21363.2	NA	72.5	5.7
22004	IL-15(E87C)/Rα(D96/C97)	4.58	21272.2	-7.61	83.0	4.1
22005	IL-15(E87C)/Rα(D96/C97/A98)	8.4	21369.3	NA	83 (shoulder)	6.1
22006	IL-15(E87C)/Rα(D96/C97/A98)	3.19	21343.2	-7.61	83.0	5.1
22007	IL-15(V49C)/Rα(S40C)	1.58	21100.0	1.22	77.0	11
22008	IL-15(L52C)/Rα(S40C)	4.56	21085.9	-0.97	82.5	17
22009	IL-15(E89C)/Rα(K34C)	0.51	21028.9	-0.33	70.5	7.3
22010	IL-15(Q48C)/Rα(G38C)	0.42	21101.0	0.91	57.5	3.8
22011	IL-15(E53C)/Rα(L42C)	3.72	21043.9	3.73	76.0	17
22012	IL-15(C42S)/Rα(A37C)	0.44	21095.9	NA	75.0	5.3
22049	Single-chain control	5.77	22953.6	NA	73.0	22
22493	IL-15(L45C)/Rα(G38C)	0.40	21116.0	0.77	71.5	NA
22494	IL-15(L45C)/Rα(A37C)	3.63	21101.9	0.63	82.5	NA

Figure 39A



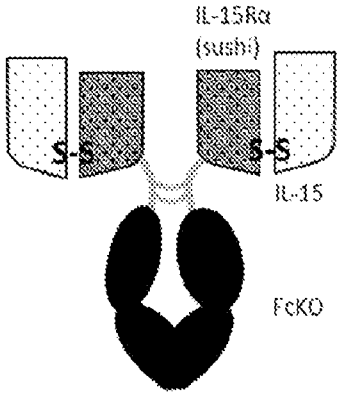
dsIL-15/Rα-heteroFc
Example: XENP22013

Figure 39B



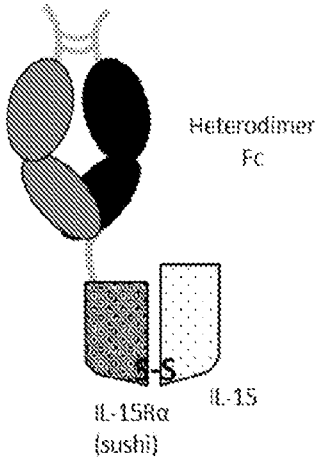
dsIL-15/Rα-Fc
Example: XENP22357

Figure 39C



Bivalent dsIL-15/Rα-Fc
Example: XENP22634

Figure 39D



Fc-dsIL-15/Rα
Example: XENP22639

Figure 40A

>XENP022013 human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 136-138)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 139-141)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/GGGGS/EPKSSDKTHTCPPCPA
PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022014 human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 142-144)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 145-147)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC/GGGGS/EPKSSDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022015 human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 148-150)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 151-153)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/GGGGS/EPKSSDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 40B

>XENP022017 human_IL15_L52C_(GGGGS)1-human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_L52C_(GGGGS)1-_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 154-156)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 157-159)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 41A

>XENP022358 – empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 160)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 161)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17039) (SEQ ID NOS 162-164)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

>XENP022359 – empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 165)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 166)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17040) (SEQ ID NOS 167-169)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 41B

>XENP022361 – empty-Fc-IL15_L52C-human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 170)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 171)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17044) (SEQ ID NOS 172-174)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022684 empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – IL15_E87C (SEQ ID NO: 175)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 176-178)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/EPKSSDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 42

>XENP022634 – human_IL15(E87C)-human_IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-D96/C97)-Fc(216)_IgG1_C220S/PVA_/S267K (17581)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/EPKSSDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NOS 179-181)

Chain 2 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 182)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022635 – human_IL15(E87C)-human_IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-D96/C97/A98)-Fc(216)_IgG1_C220S/PVA_/S267K (17582) (SEQ ID NOS 183-185)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 186)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022636 – human_IL15(L52C)-human_IL15Ra(Sushi-S40C)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-S40C)-Fc(216)_IgG1_C220S/PVA_/S267K (17583) (SEQ ID NOS 187-189)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHED?EVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE?QVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 190)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 43

>XENP022639 – empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi-D96/C97)_IL15(E87C)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi-D96/C97) (17605) (SEQ ID NOS 191-193)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIRDC

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 194)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 195)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022640 empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q_(GGGGS)2_IL15Ra(Sushi-D96/C97)_IL15(E87C)

Chain 1 – IL15 (SEQ ID NO: 196)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 – empty_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 197)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 44

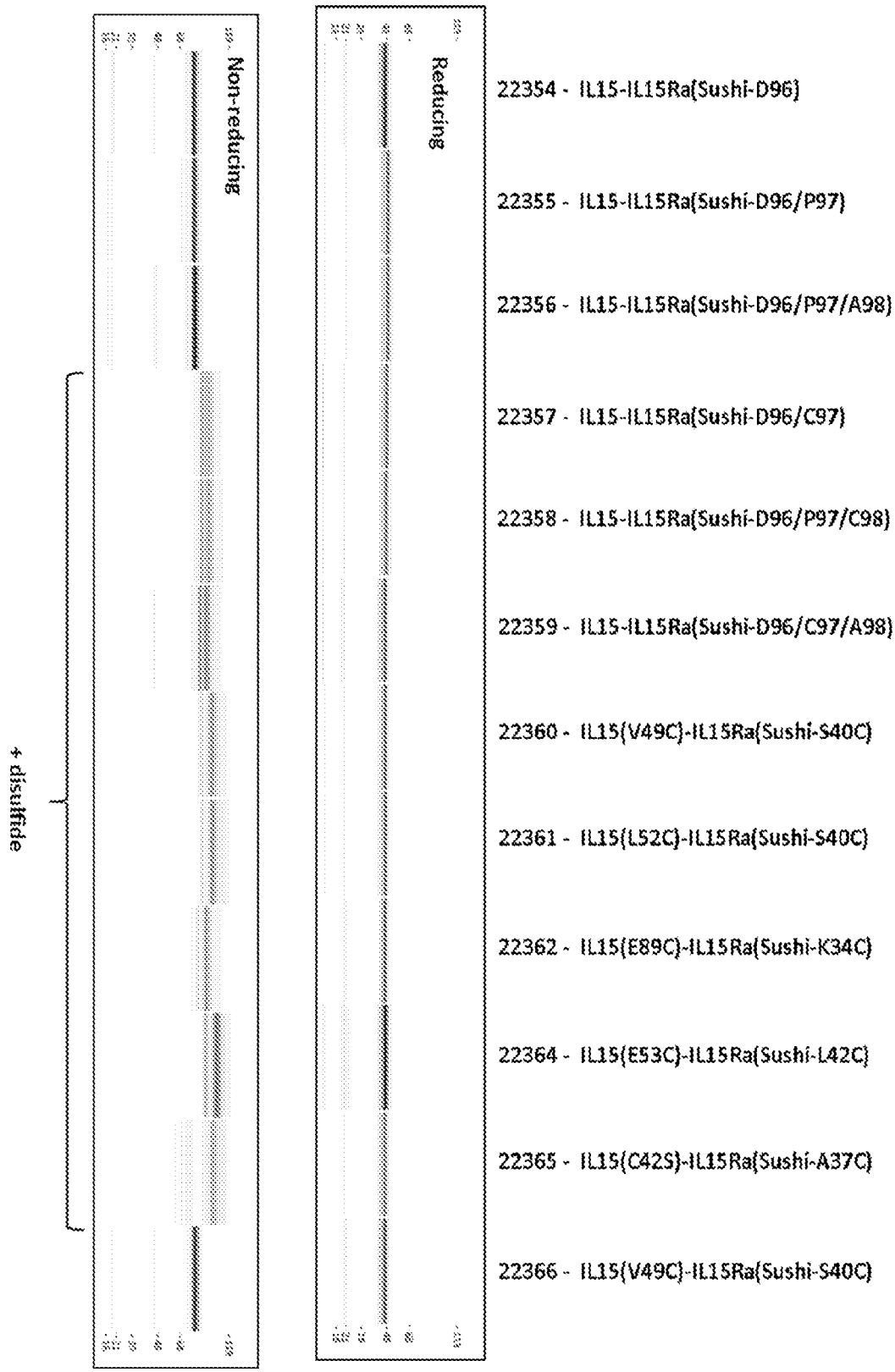

Non-reducing
Reducing
+ disulfide
22354 - IL15-IL15Ra(Sushi-D96)
22355 - IL15-IL15Ra(Sushi-D96/P97)
22356 - IL15-IL15Ra(Sushi-D96/P97/A98)
22357 - IL15-IL15Ra(Sushi-D96/C97)
22358 - IL15-IL15Ra(Sushi-D96/P97/C98)
22359 - IL15-IL15Ra(Sushi-D96/C97/A98)
22360 - IL15(V49C)-IL15Ra(Sushi-S40C)
22361 - IL15(L52C)-IL15Ra(Sushi-S40C)
22362 - IL15(E89C)-IL15Ra(Sushi-K34C)
22364 - IL15(E53C)-IL15Ra(Sushi-L42C)
22365 - IL15(C42S)-IL15Ra(Sushi-A37C)
22366 - IL15(V49C)-IL15Ra(Sushi-S40C)

Figure 45A

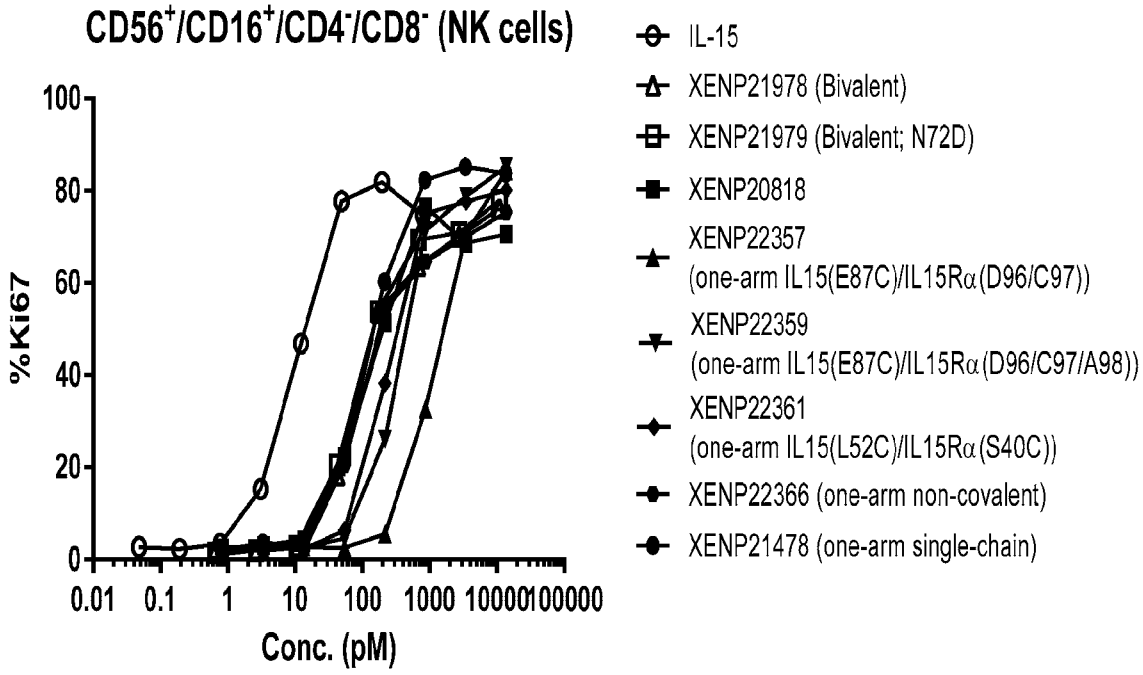


Figure 45B

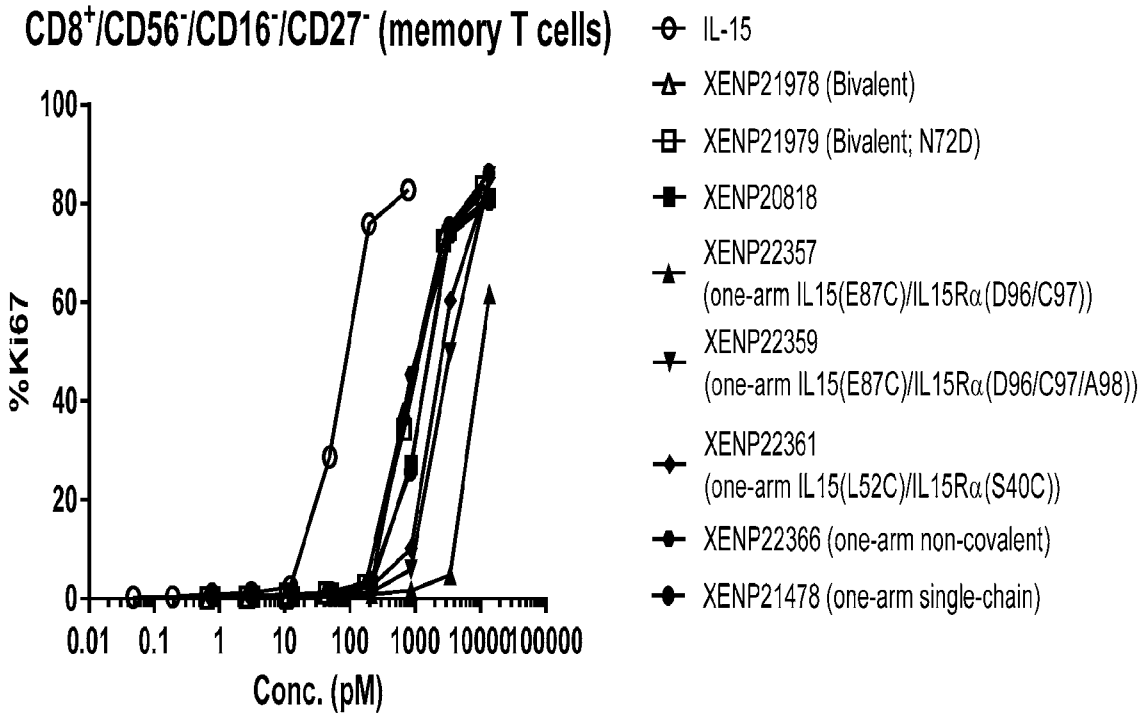


Figure 45C

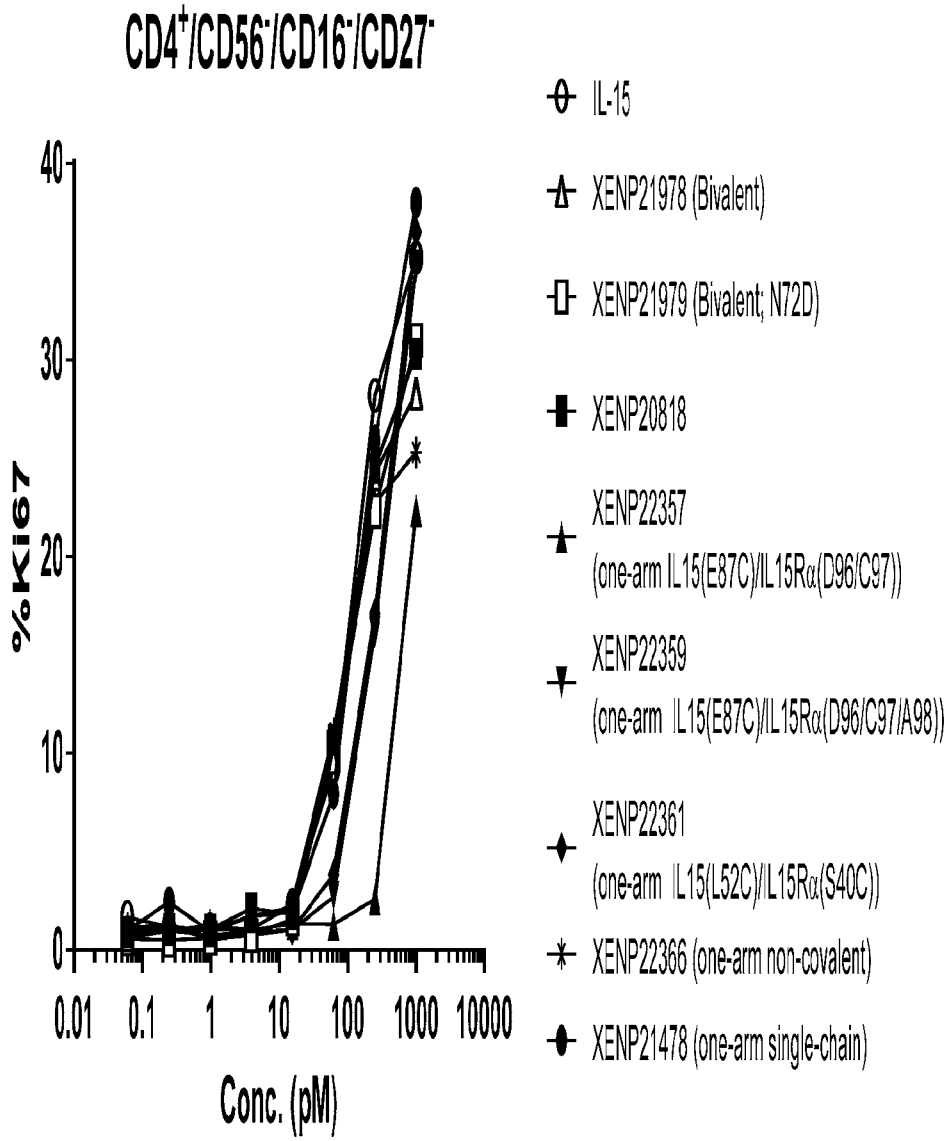

CD4+/CD56-/CD16-/CD27-
%Ki67
40
30
20
10
0
0.01
0.1
1
10
100
1000
10000
Conc. (pM)
IL-15
XENP21978 (Bivalent)
XENP21979 (Bivalent; N72D)
XENP20818
XENP22357
(one-arm IL15(E87C)/IL15Rα(D96/C97))
XENP22359
(one-arm IL15(E87C)/IL15Rα(D96/C97/A98))
XENP22361
(one-arm IL15(L52C)/IL15Rα(S40C))
XENP22366 (one-arm non-covalent)
XENP21478 (one-arm single-chain)

Figure 46

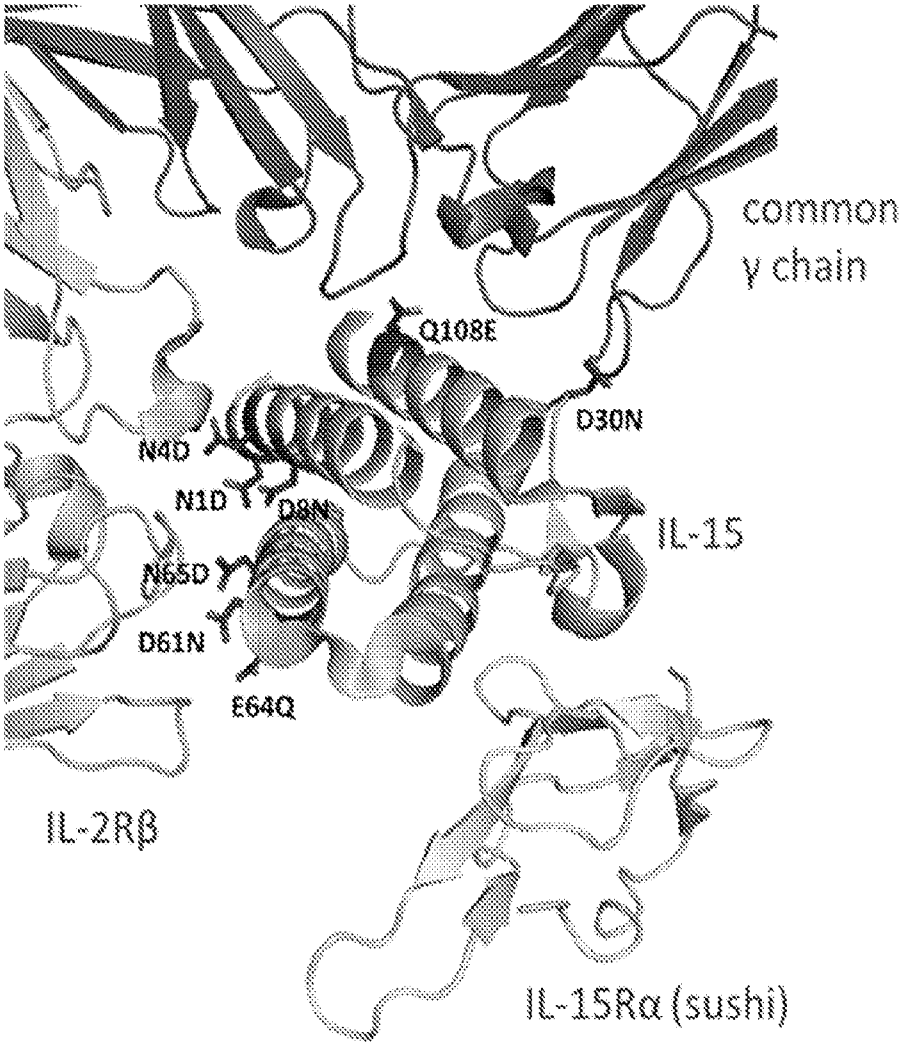

common
γ chain
Q108E
D30N
N4D
N1D
D8N
IL-15
N65D
D61N
E64Q
IL-2Rβ
IL-15Rα (sushi)

Figure 47A

N1D (SEQ ID NO: 198)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D (SEQ ID NO: 199)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D8N (SEQ ID NO: 200)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N (SEQ ID NO: 201)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D61N (SEQ ID NO: 202)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

E64Q (SEQ ID NO: 203)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N65D (SEQ ID NO: 204)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Q108E (SEQ ID NO: 205)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N1D/D61N (SEQ ID NO: 206)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/E64Q (SEQ ID NO: 207)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/D61N (SEQ ID NO: 208)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/E64Q (SEQ ID NO: 209)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Figure 47B

D8N/D61N (SEQ ID NO: 210)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D8N/E64Q (SEQ ID NO: 211)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D61N/E64Q (SEQ ID NO: 212)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

E64Q/Q108E (SEQ ID NO: 213)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N1D/N4D/D8N (SEQ ID NO: 214)
DWVDVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D61N/E64Q/N65D (SEQ ID NO: 215)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/D61N/E64Q/Q108E (SEQ ID NO: 216)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N4D/D61N/E64Q/Q108E (SEQ ID NO: 217)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N1D/N65D (SEQ ID NO: 218)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/Q108E (SEQ ID NO: 219)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N4D/N65D (SEQ ID NO: 220)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/N65D (SEQ ID NO: 221)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/Q108E (SEQ ID NO: 222)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

Figure 47C

N65D/Q108E (SEQ ID NO: 223)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

E64Q/N65D (SEQ ID NO: 224)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/N4D/N65D (SEQ ID NO: 225)
DWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/E64Q/N65D (SEQ ID NO: 226)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/D61N/N65D (SEQ ID NO: 227)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Figure 48A

>XENP022821 - human_IL15_N65D_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N65D_(GGGGS)$_1$ (17692) (SEQ ID NOS 228-230)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 231-233)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP022822 - human_IL15_Q108E_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_Q108E_(GGGGS)$_1$ (17693) (SEQ ID NOS 234-236)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 237-239)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023554 - human_IL15_N1D/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18783) (SEQ ID NOS 240-242)
DWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 243-245)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

Figure 48B

>XENP023557 - human_IL15_N4D/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18786) (SEQ ID NOS 246-248)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 249-251)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023561 human_IL15_N65D/Q108E_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N65D/Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 252-254)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 255-257)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024018 human_IL15(N65D)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 258-260)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 261-263)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 48C

>XENP024019 - human_IL15(Q108E)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(Q108E)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (19242) (SEQ ID NOS 264-266)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDW_NGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 267-269)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024045 human_IL15_D30N/E64Q/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_D30N/E64Q/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 270-272)
NWVNVISDLKKIED_IQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 273-275)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP024051 human_IL15_N1D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N1D/N65D-human_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 276-278)
DWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDW_NGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 279-281)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 48D

>XENP024052 human_IL15_N4D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N4D/N65D-human_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 282-284)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 285-287)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 49A

>XENP024015 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(Q108E;single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(Q108E;single-chain) _Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 288-291)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 292)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024050 human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 293-296)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 297)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 49B

>XENP024475 human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 298-301)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 302)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024476 human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;N4D/N65D)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;N4D/N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 303-306)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 307)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024478 human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 308-311)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 312)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 49C

>XENP024479 human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;N4D/N65D)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;N4D/N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 313-316)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - empty-Fc_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 317)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024481 human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 318-321)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/DPALVHQRPAPPGGGGSGGGGSGGGGSGGG/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 322)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 50A

>XENP024349 IL15_Q108E_(non-covalent)-human_IL15Rα(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15Rα(Sushi)_ Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 323-325)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty- Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 326)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 – IL15_Q108E_(non-covalent) (SEQ ID NO: 327)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

>XENP024890 IL15_N4D/N65D_(non-covalent)-human_IL15Ra(Sushi)-empty-Fc_IgG1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q

Chain 1 – IL-15_N4D/N65D (SEQ ID NOS 328-330)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 331-333)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – empty_Fc(216)_ IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 334)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 50B

>XENP25138 IL15_D30N/E64Q/N65D_(non-covalent)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - IL15_D30N/E64Q/N65D (SEQ ID NO: 335)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 336-338)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - empty_Fc(216)_ IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 339)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 51

>XENP022801 - human_IL15_N65D(non-covalent)-human_IL15Rα(Sushi)

Chain 1 - human_IL15_N65D(non-covalent) (17672) (SEQ ID NO: 340)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi) (17033) (SEQ ID NO: 341)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022802 - human_IL15_Q108E(non-covalent)-human_IL15Rα(Sushi)

Chain 1 - human_IL15_Q108E(non-covalent) (17673) (SEQ ID NO: 342)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Rα(Sushi) (17033) (SEQ ID NO: 343)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 52

>XENP024342 human_IL15(non-covalent; Q108E)-human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 – human_IL15Rα(Sushi) _Fc(216)_IgG1_C220S/PVA_/S267K (SEQ ID NOS 344-346)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 –human_IL15(non-covalent; Q108E) (SEQ ID NO: 347)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Figure 53

>XENP023472 empty-Fc-IL15_N65D/E87C-human_IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – empty_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 348)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 2 - IL15_N65D/E87C (SEQ ID NO: 349)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 3 - IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 350-352)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/EPKSSDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP023473 empty-Fc-IL15_N65D/L52C-human_IL15Ra(Sushi-S40C)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – empty_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 353)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 2 - IL15_N65D/L52C (SEQ ID NO: 354)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 3 - IL15Ra(Sushi-S40C)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 355-357)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 54A

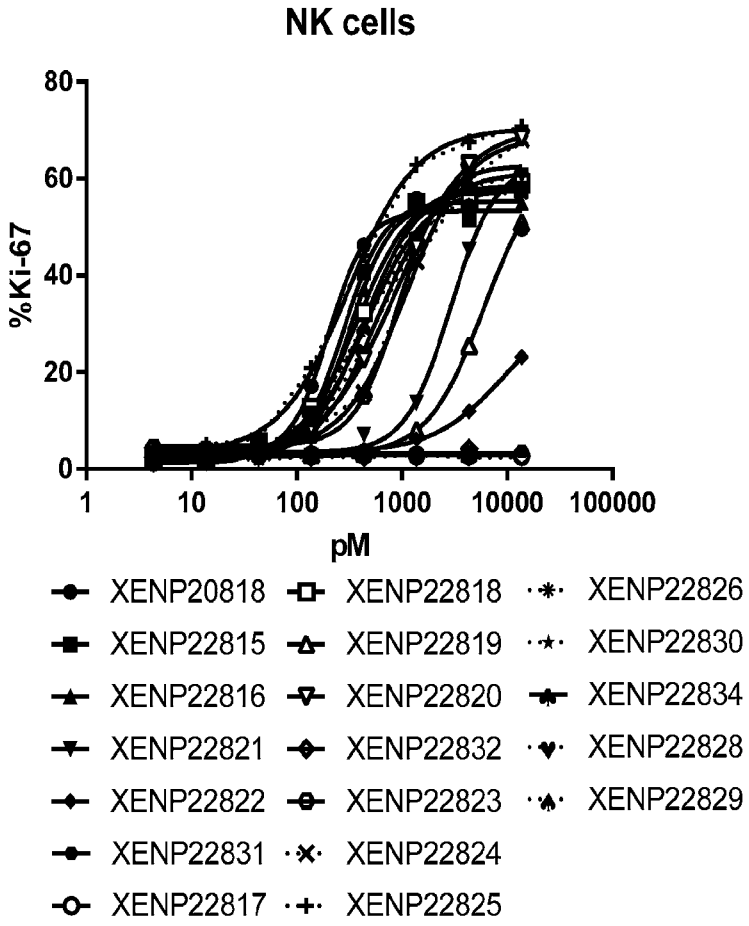

NK cells
%Ki-67
80
60
40
20
0
1
10
100
1000
10000
100000
pM
XENP20818
XENP22818
XENP22826
XENP22815
XENP22819
XENP22830
XENP22816
XENP22820
XENP22834
XENP22821
XENP22832
XENP22828
XENP22822
XENP22823
XENP22829
XENP22831
XENP22824
XENP22817
XENP22825

Figure 54B

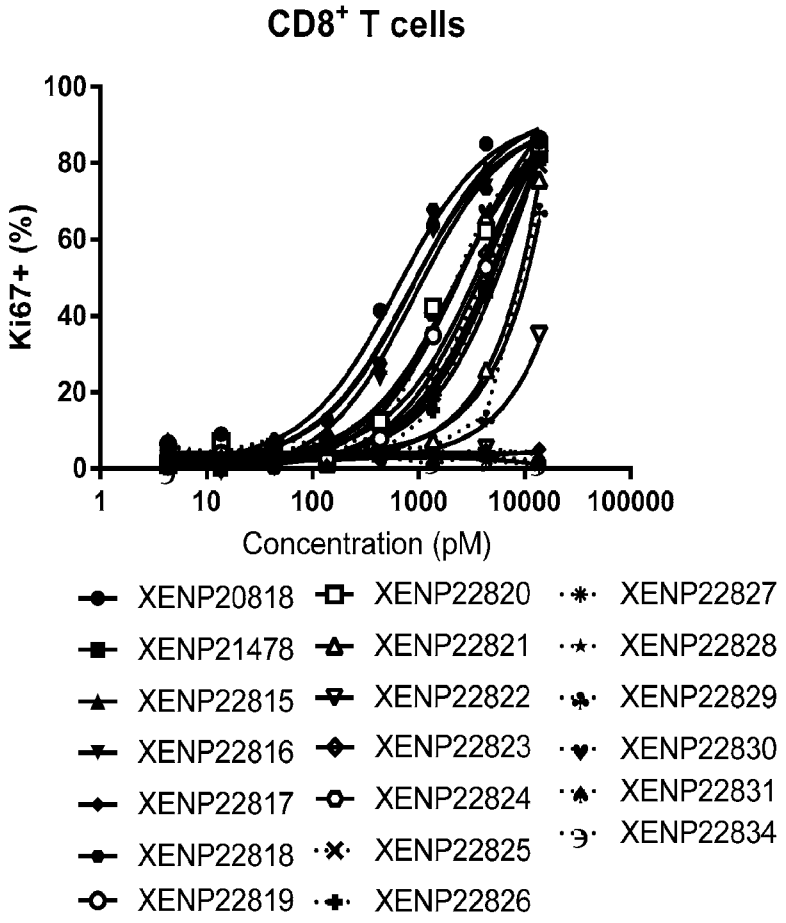

CD8+ T cells
Ki67+ (%)
100
80
60
40
20
0
1
10
100
1000
10000
100000
Concentration (pM)
XENP20818
XENP21478
XENP22815
XENP22816
XENP22817
XENP22818
XENP22819
XENP22820
XENP22821
XENP22822
XENP22823
XENP22824
XENP22825
XENP22826
XENP22827
XENP22828
XENP22829
XENP22830
XENP22831
XENP22834

Figure 54C

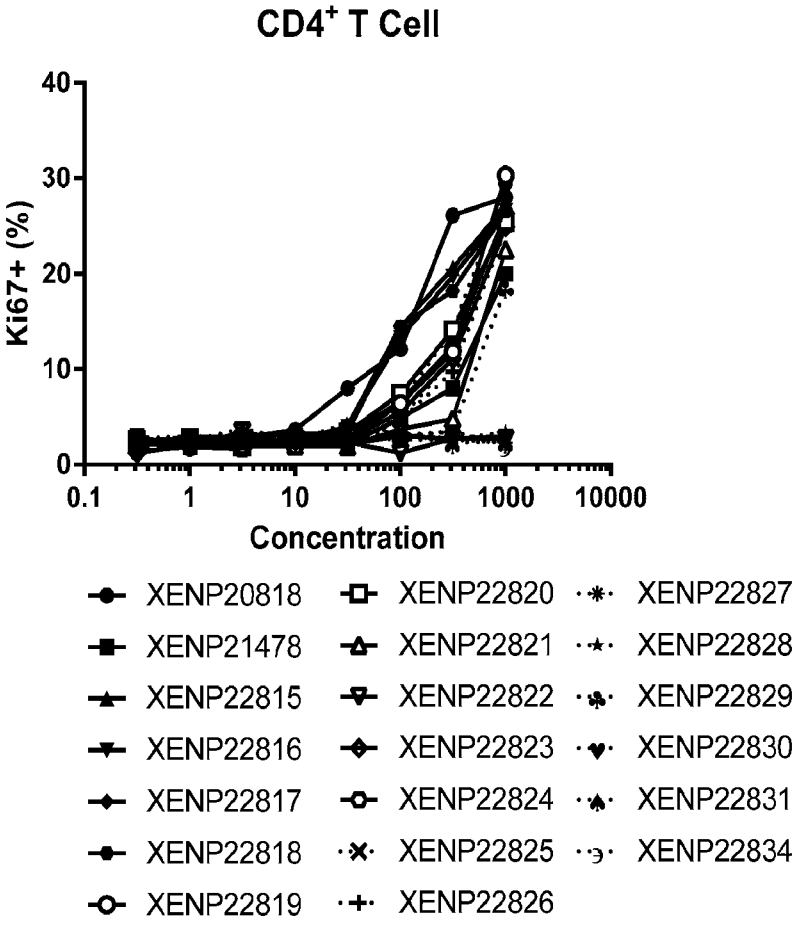

CD4+ T Cell
Ki67+ (%)
40
30
20
10
0
0.1
1
10
100
1000
10000
Concentration
XENP20818
XENP21478
XENP22815
XENP22816
XENP22817
XENP22818
XENP22819
XENP22820
XENP22821
XENP22822
XENP22823
XENP22824
XENP22825
XENP22826
XENP22827
XENP22828
XENP22829
XENP22830
XENP22831
XENP22834

Figure 55

XENP	Variant	EC50 pM (NK cells)	Fold reduced (NK cells)	EC50 pM (CD8 T cells)	Fold reduced (CD8 T cells)
20818	WT	200.6		637.1	
21478	single-chain	848.5	4.2	4982.0	7.8
22815	N1D	281.3	1.4	1051.0	1.6
22816	N4D	321.9	1.6	1190.0	1.9
22817	D8N	very weak	very weak	very weak	very weak
22818	D30N	376.3	1.9	1366.0	2.1
22819	D61N	5934.0	29.6	161937.0	>100
22820	E64Q	877.0	4.4	2858.0	4.5
22821	N65D	2883.0	14.4	6928.0	10.9
22822	Q108E	9777.0	48.7	very weak	>100
22823	N1D/D61N	918.0	4.6	4225.0	6.6
22824	N1D/E64Q	1091.0	5.4	4228.0	6.6
22825	N4D/D61N	309.0	1.5	1070.0	1.7
22826	N4D/E64Q	very weak	very weak	very weak	very weak
22827	D8N/D61N	ND	ND	ND	ND
22828	D8N/E64Q	597.7	3.0	1658.0	2.6
22829	D61N/E64Q	458.2	2.3	2115.0	3.3
22830	E64Q/Q108E	436.6	2.2	1815.0	2.8
22831	N1D/N4D/D8N	very weak	very weak	very weak	very weak
22832	D61N/E64Q/N65D	ND	ND	ND	ND
22833	N1D/D61N/E64Q/Q108E	ND	ND	ND	ND
22834	N4D/D61N/E64Q/Q108E	very weak	very weak	very weak	very weak

Figure 56A

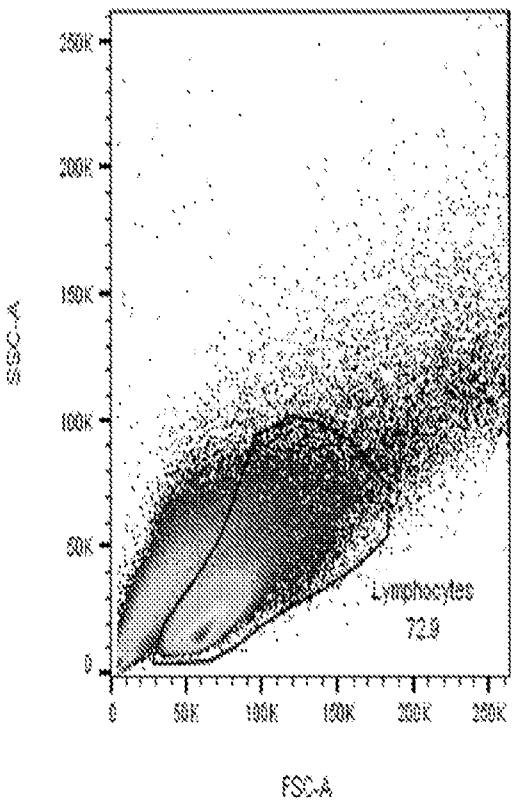


Figure 56B

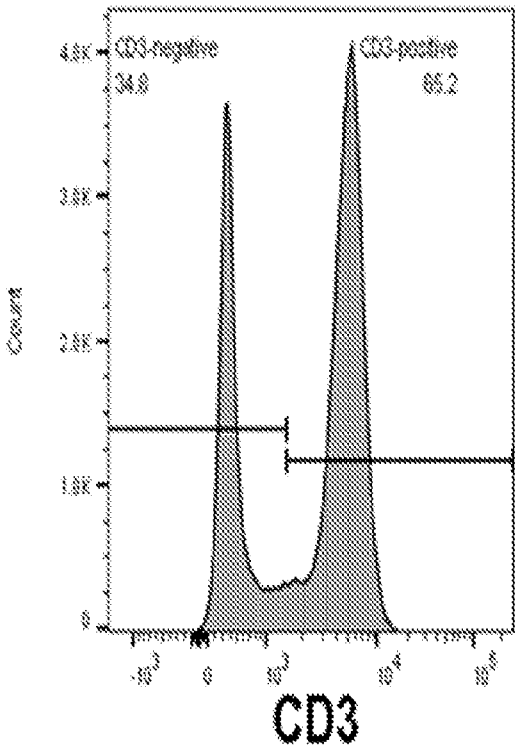


Figure 56C

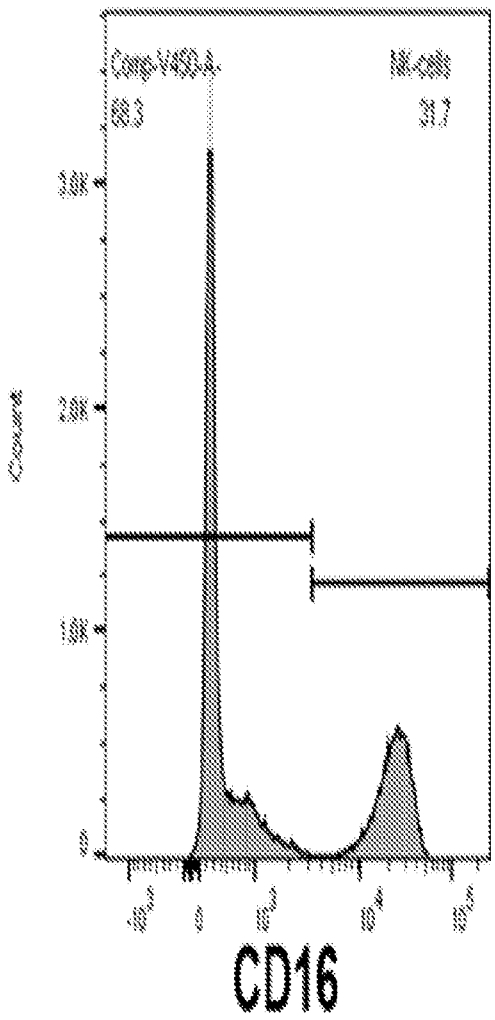


Figure 57A

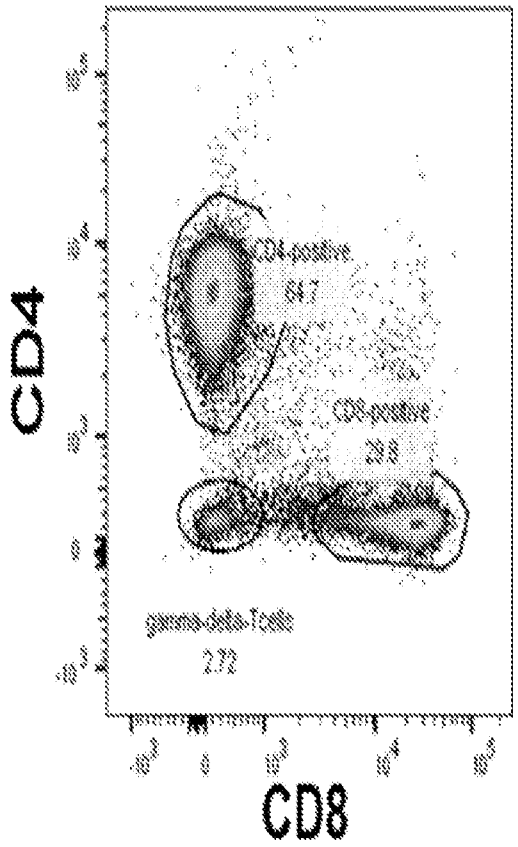


Figure 57B

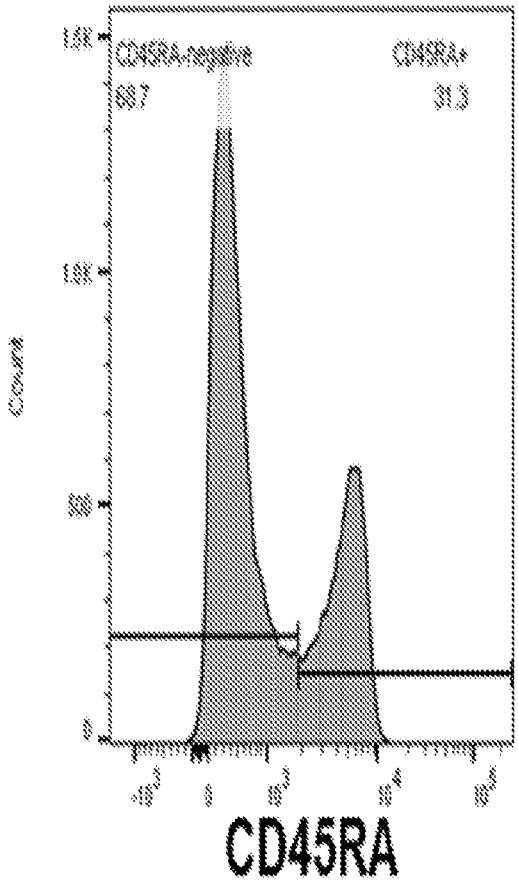


Figure 57C

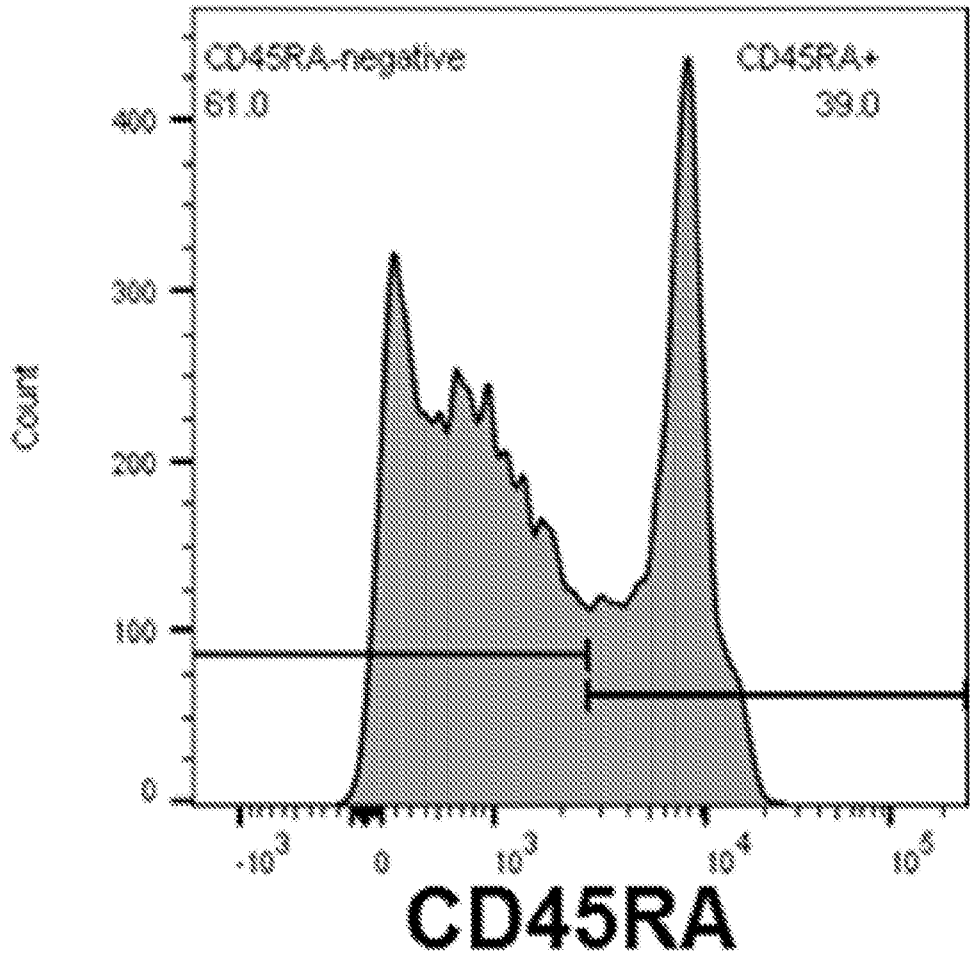

CD45RA-negative
61.0
CD45RA+
39.0
Count
400
300
200
100
0
-10^3
0
10^3
10^4
10^5
CD45RA

Figure 58A

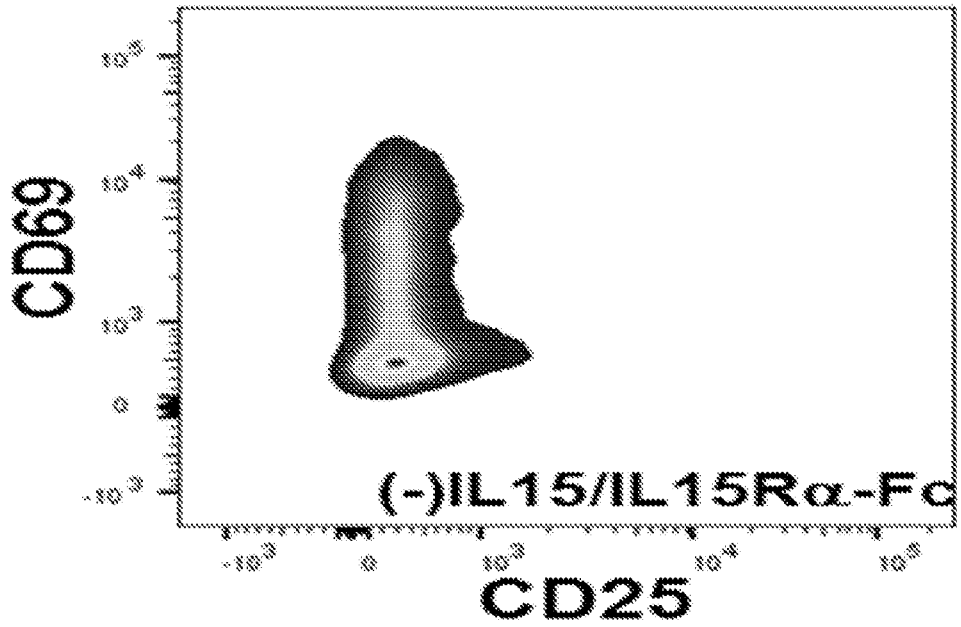


Figure 58B

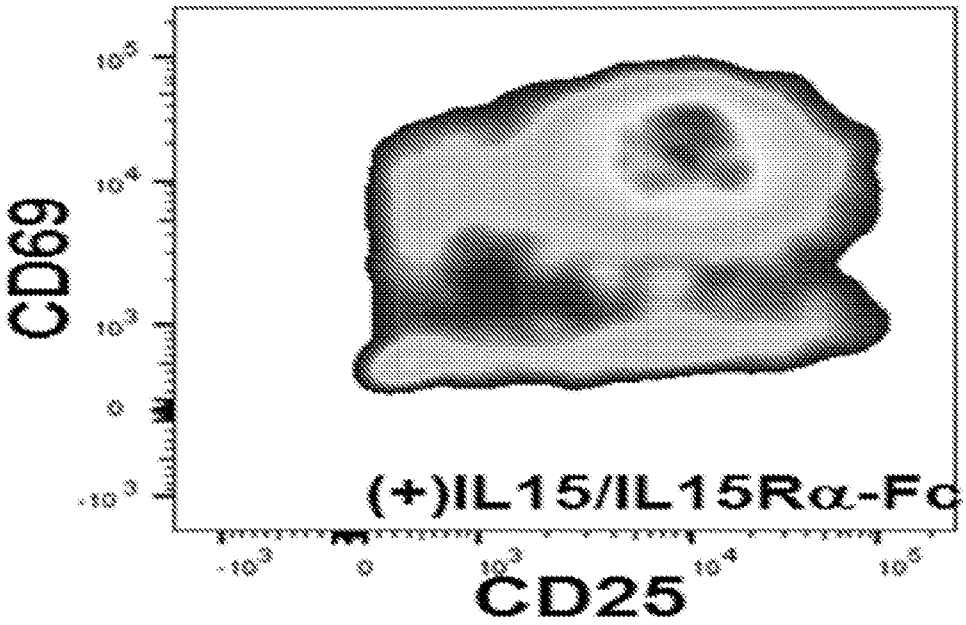


Figure 59A

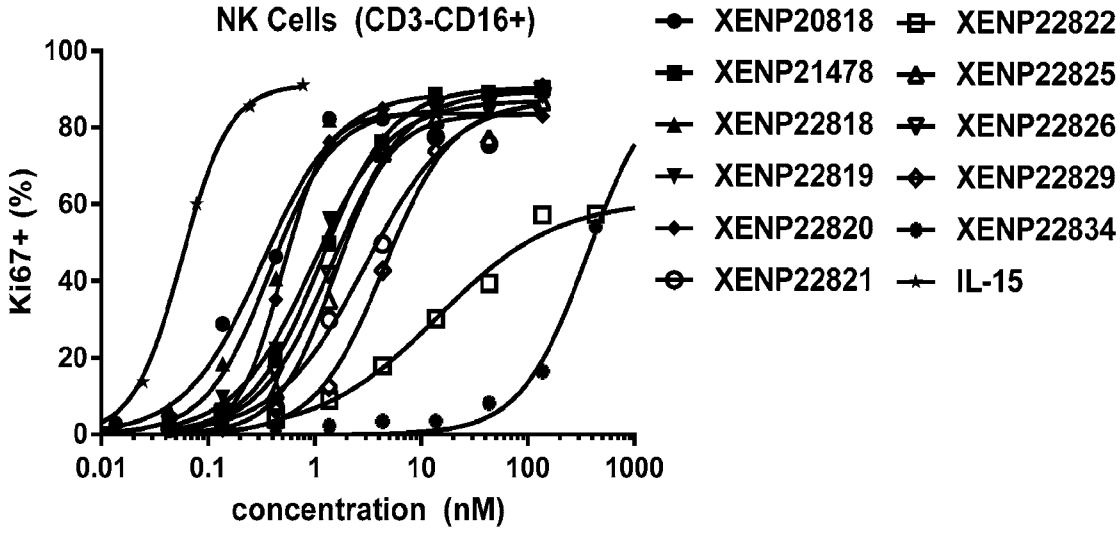


Figure 59B

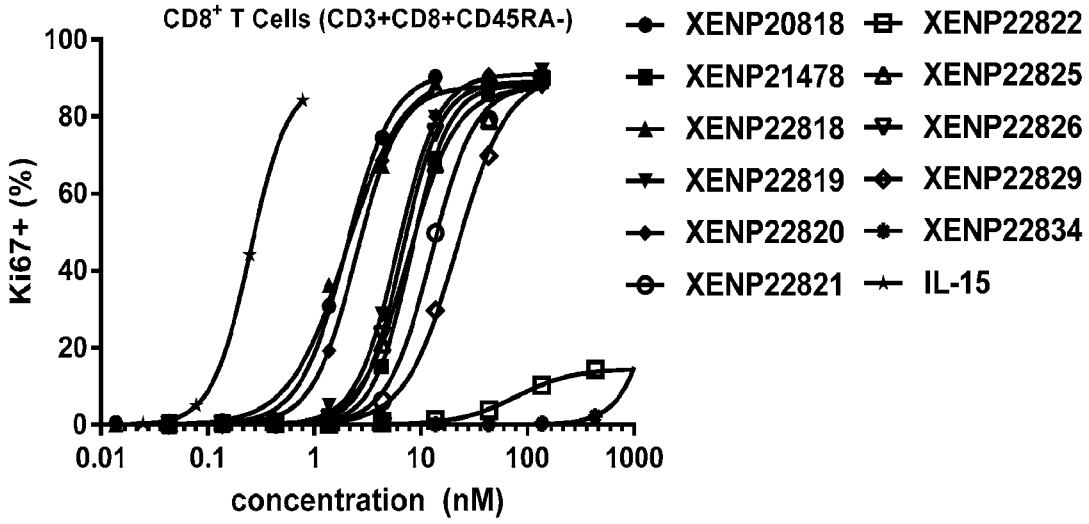


Figure 59C

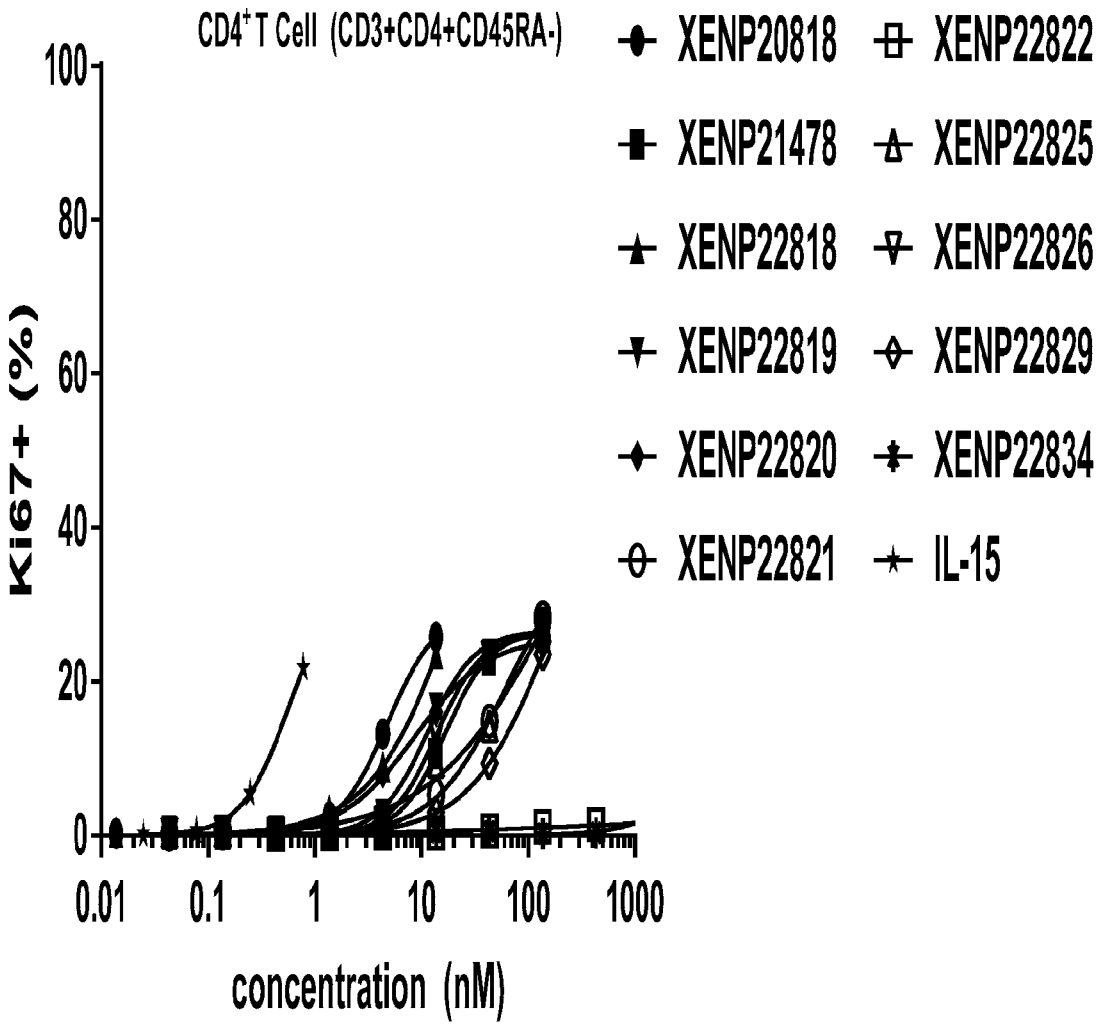

CD4+ T Cell (CD3+CD4+CD45RA-)
Ki67+ (%)
100
80
60
40
20
0
0.01
0.1
1
10
100
1000
concentration (nM)
XENP20818
XENP21478
XENP22818
XENP22819
XENP22820
XENP22821
XENP22822
XENP22825
XENP22826
XENP22829
XENP22834
IL-15

Figure 59D

XENP	EC50 nM (NK cells)	Fold reduced (NK cells)	EC50 nM (CD8 T cells)	Fold reduced (CD8 T cells)	EC50 nM (CD4 T cells)	Fold reduced (CD4 T cells)
20818	0.3223	1.0	2.701	1.0	16.467	1.0
21478	1.116	3.5	11.728	4.3	28.349	1.7
22818	0.4205	1.3	2.829	1.0	40.676	2.5
22819	1.016	3.2	8.254	3.1	18.101	1.1
22820	0.562	1.7	3.918	1.5	10.362	0.6
22821	3.14	9.7	18.706	6.9	112.823	6.9
22822	68.866	213.7	6439.69	2384.2	48.738	3.0
22825	1.769	5.5	12.09	4.5	60.081	3.6
22826	1.448	4.5	9.678	3.6	22.41	1.4
22829	4.839	15.0	29.638	11.0	337.571	20.5
22834	331.293	1027.9	4107.897	1520.9	ND	ND
IL-15	0.05322	0.2	0.3452	0.1	ND	ND

Figure 60A

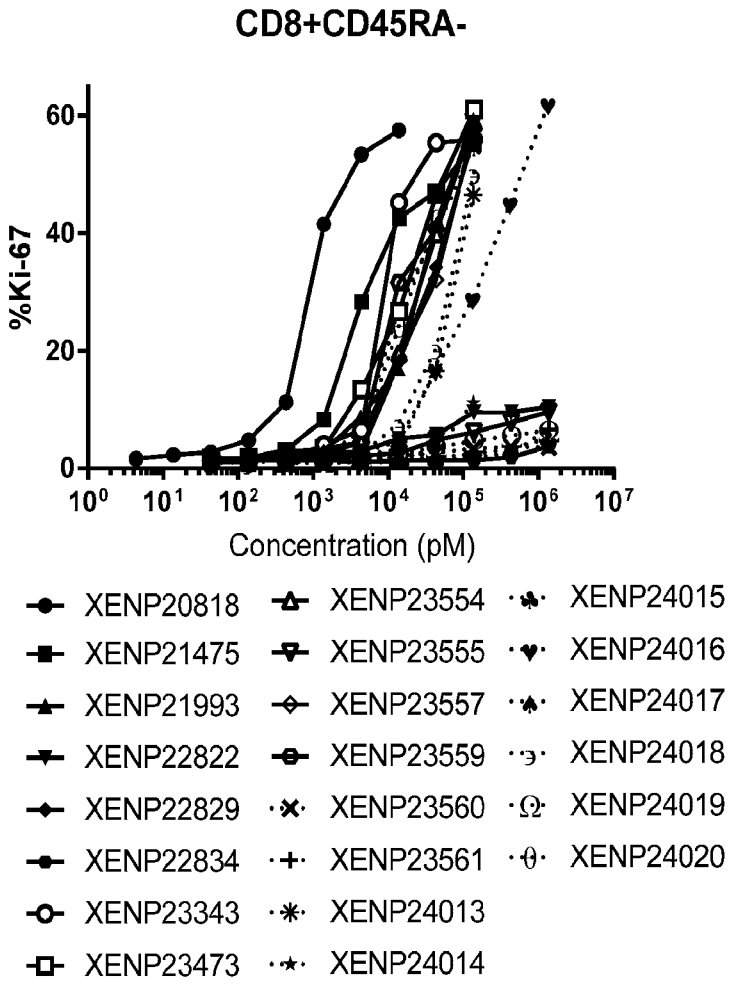

CD8+CD45RA-
%Ki-67
60
40
20
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP21475
XENP21993
XENP22822
XENP22829
XENP22834
XENP23343
XENP23473
XENP23554
XENP23555
XENP23557
XENP23559
XENP23560
XENP23561
XENP24013
XENP24014
XENP24015
XENP24016
XENP24017
XENP24018
XENP24019
XENP24020

Figure 60B

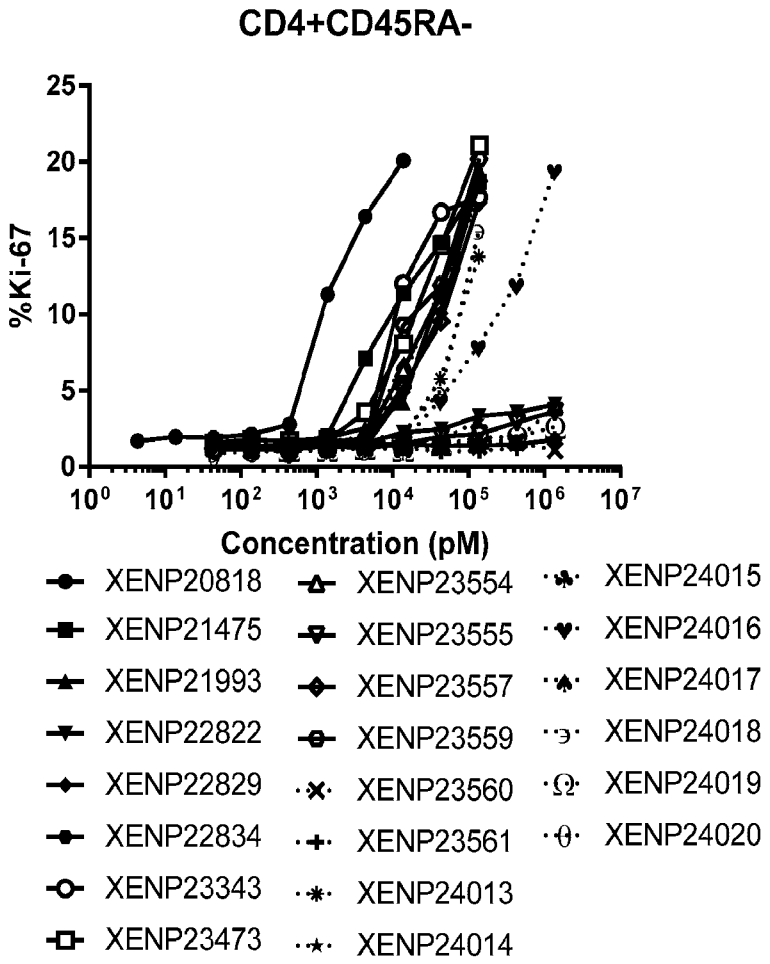

CD4+CD45RA-
%Ki-67
25
20
15
10
5
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP21475
XENP21993
XENP22822
XENP22829
XENP22834
XENP23343
XENP23473
XENP23554
XENP23555
XENP23557
XENP23559
XENP23560
XENP23561
XENP24013
XENP24014
XENP24015
XENP24016
XENP24017
XENP24018
XENP24019
XENP24020

Figure 60C

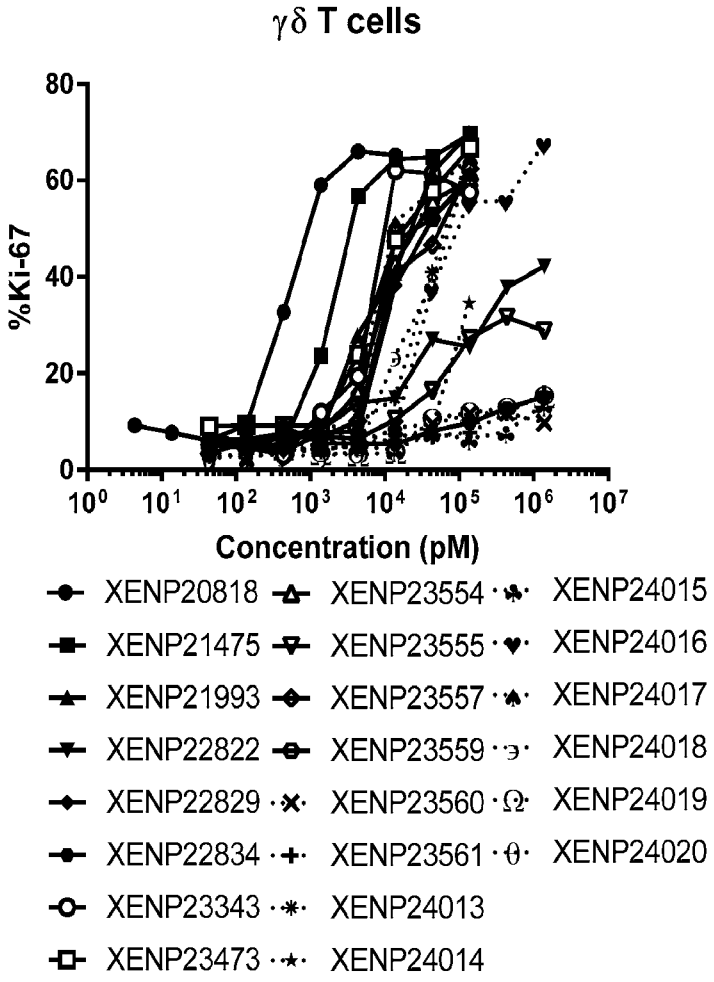

γδ T cells
%Ki-67
80
60
40
20
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP21475
XENP21993
XENP22822
XENP22829
XENP22834
XENP23343
XENP23473
XENP23554
XENP23555
XENP23557
XENP23559
XENP23560
XENP23561
XENP24013
XENP24014
XENP24015
XENP24016
XENP24017
XENP24018
XENP24019
XENP24020

Figure 60D

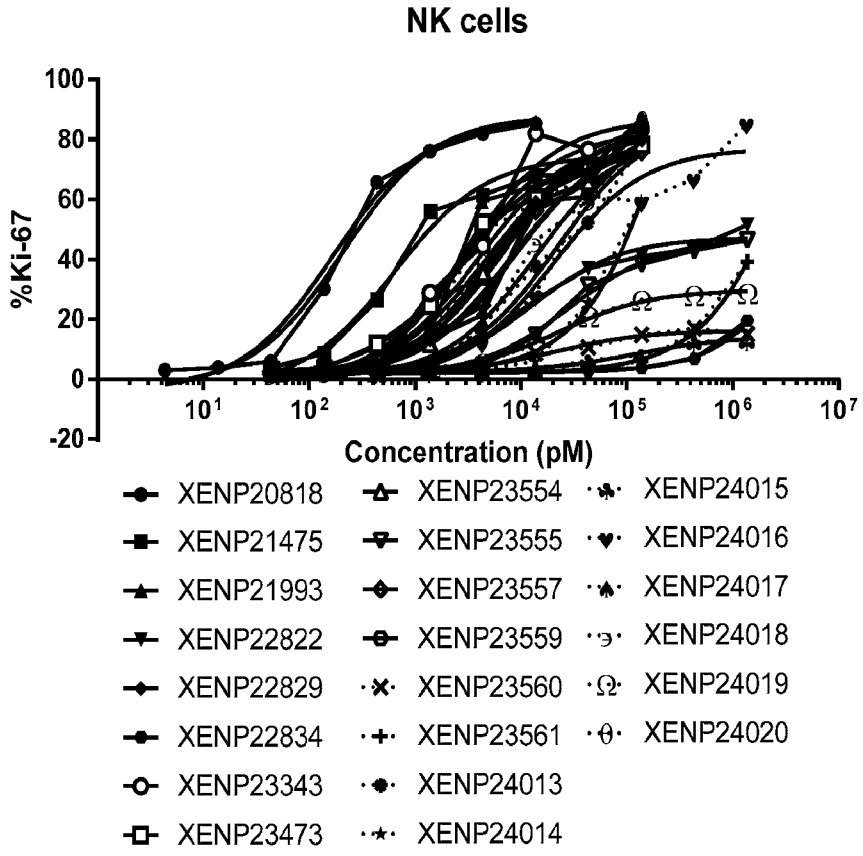

NK cells
%Ki-67
100
80
60
40
20
0
-20
10^1
10^2
10^3
10^4
10^5
10^6
10^7
Concentration (pM)
XENP20818
XENP21475
XENP21993
XENP22822
XENP22829
XENP22834
XENP23343
XENP23473
XENP23554
XENP23555
XENP23557
XENP23559
XENP23560
XENP23561
XENP24013
XENP24014
XENP24015
XENP24016
XENP24017
XENP24018
XENP24019
XENP24020

Figure 61A

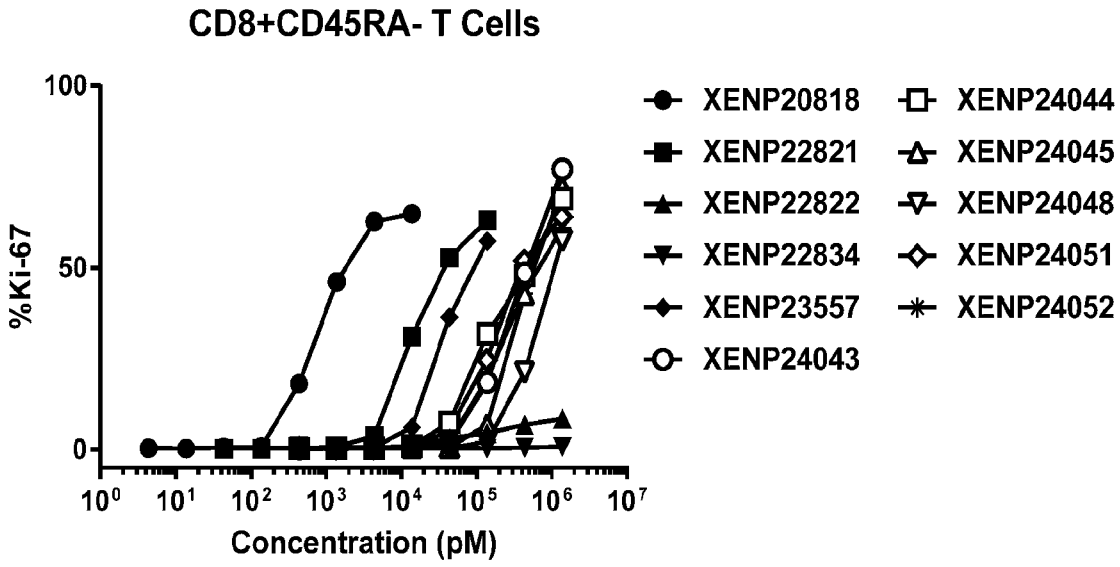


Figure 61B

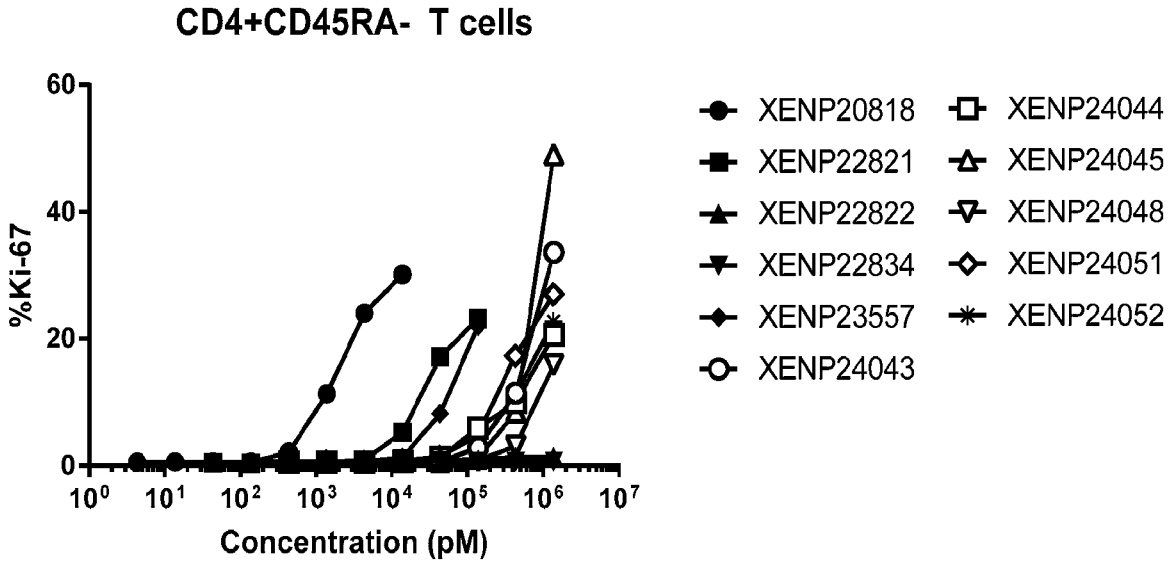


Figure 61C

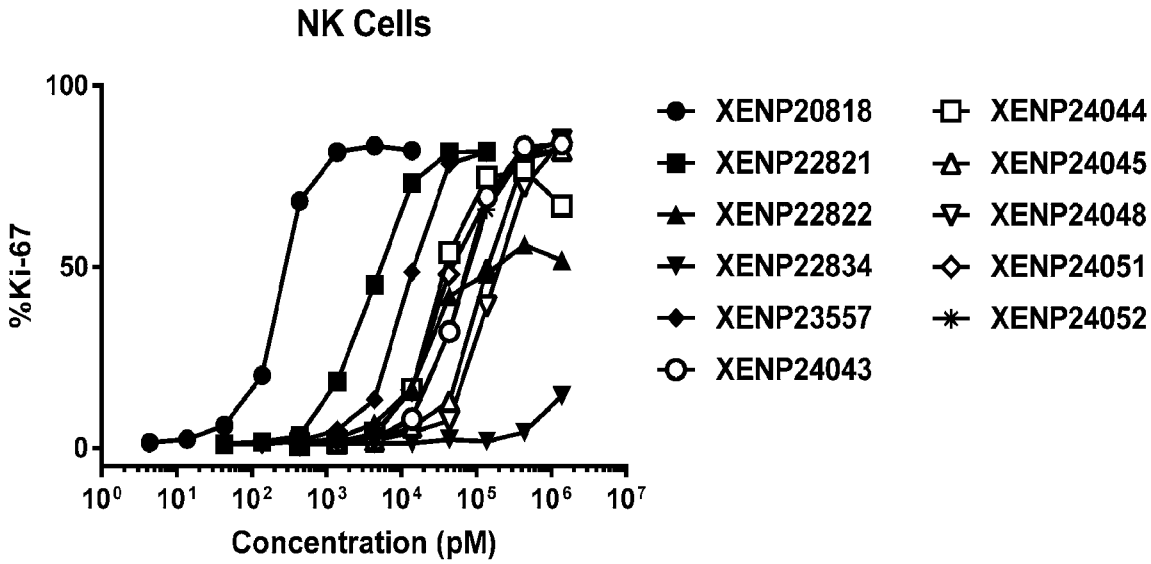

NK Cells
%Ki-67
100
50
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP22821
XENP22822
XENP22834
XENP23557
XENP24043
XENP24044
XENP24045
XENP24048
XENP24051
XENP24052

Figure 62A

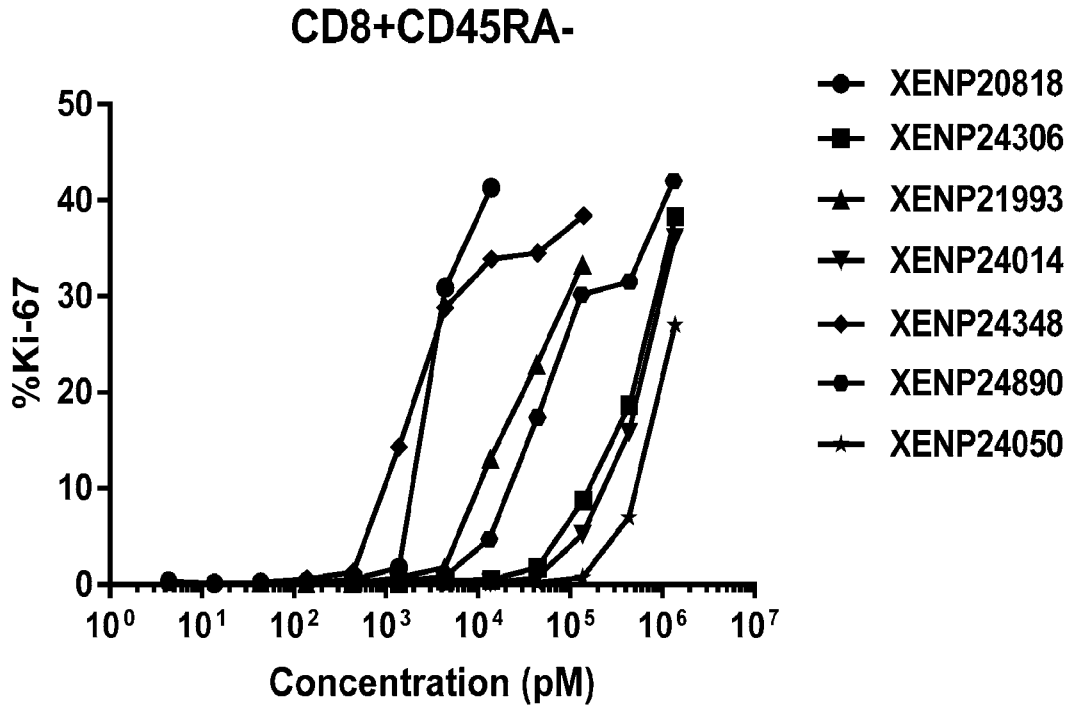


Figure 62B

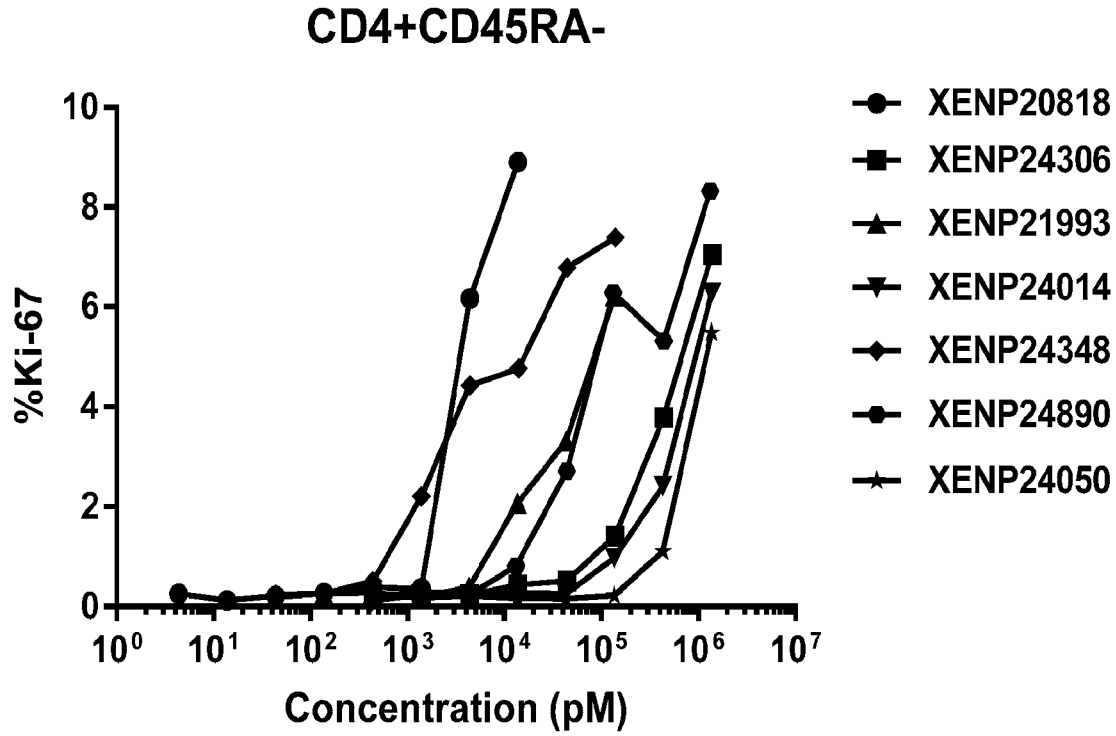


Figure 62C

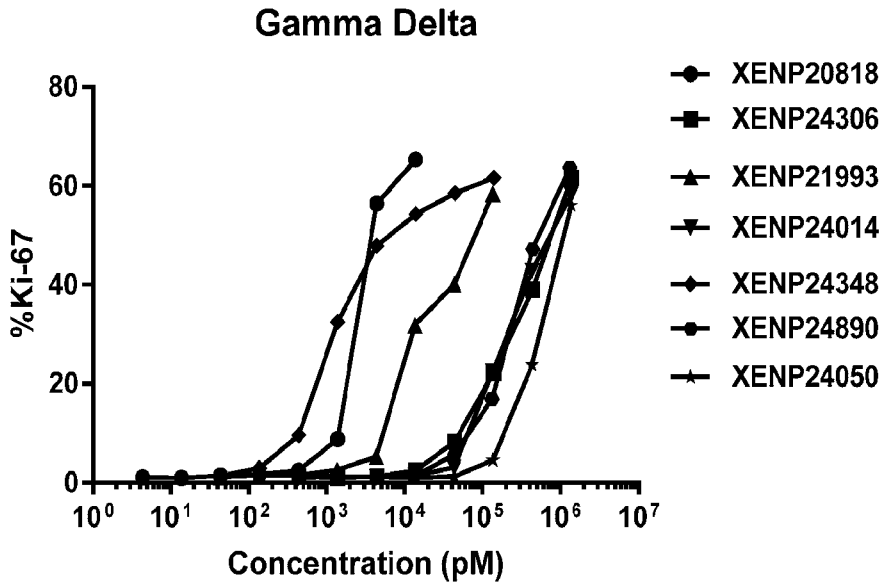


Figure 62D

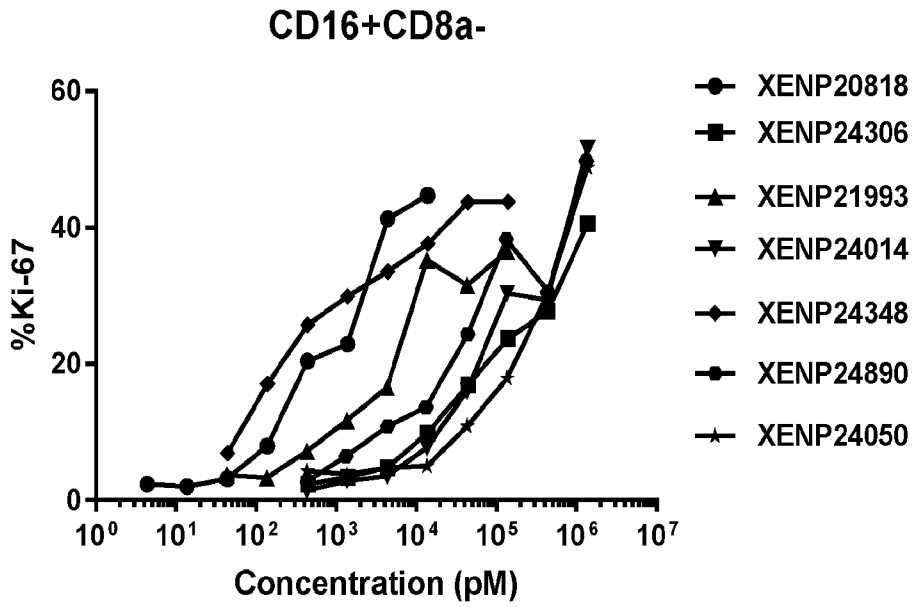


Figure 62E

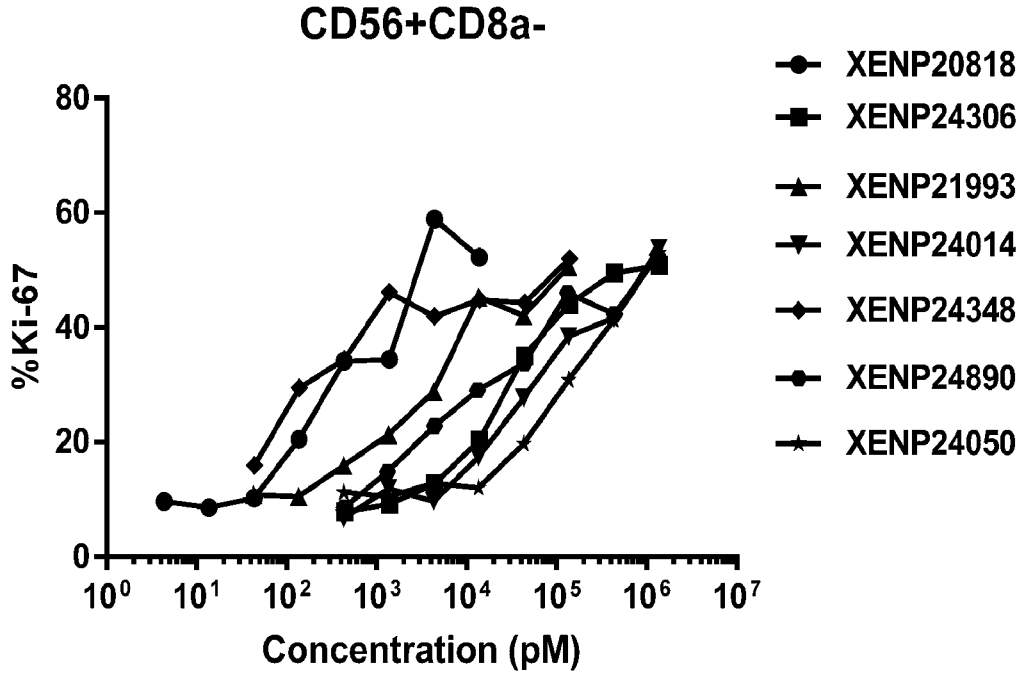

CD56+CD8a-
%Ki-67
80
60
40
20
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP24306
XENP21993
XENP24014
XENP24348
XENP24890
XENP24050

Figure 63A

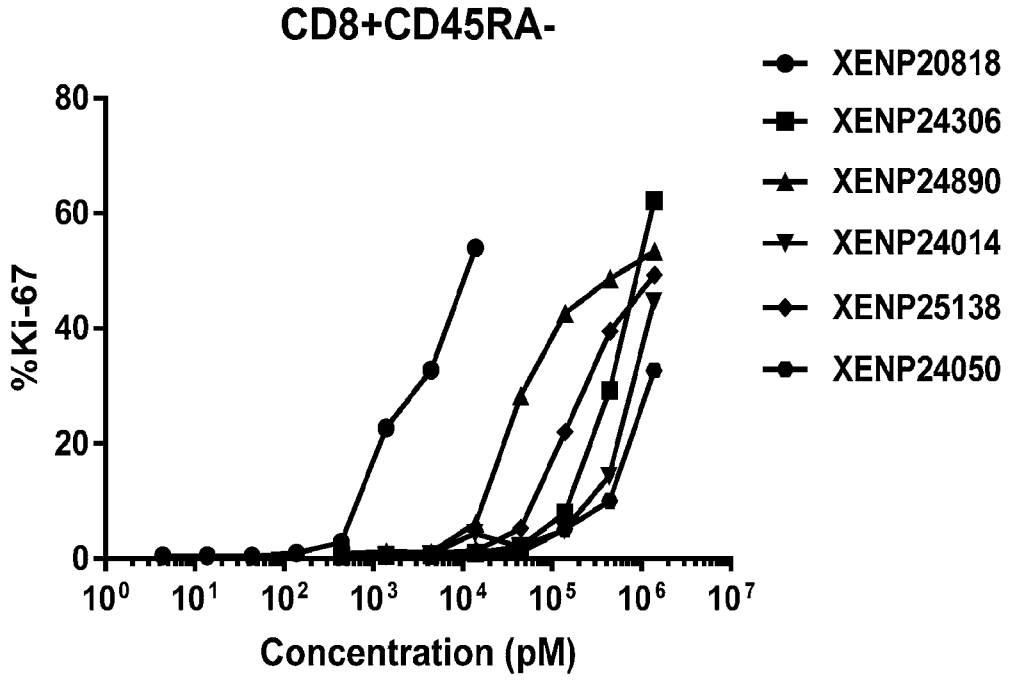


Figure 63B

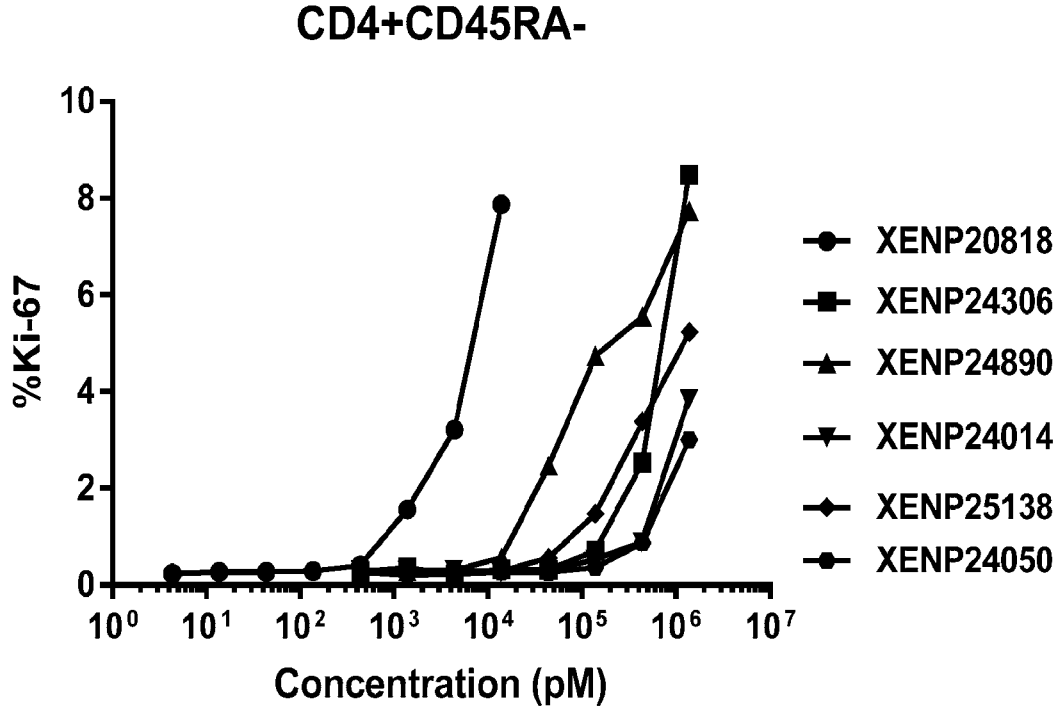


Figure 63C

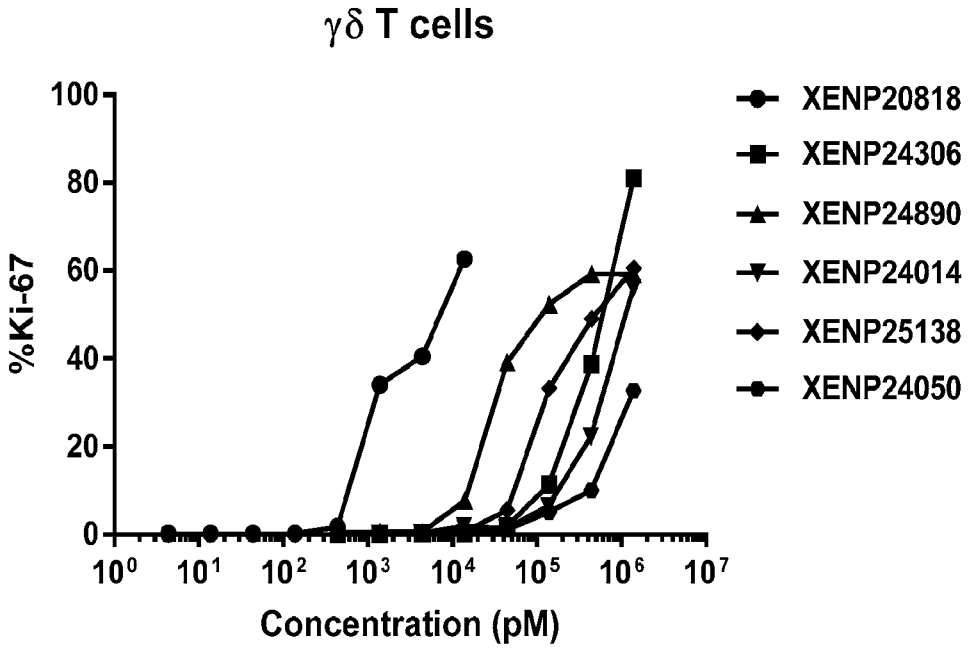


Figure 63D

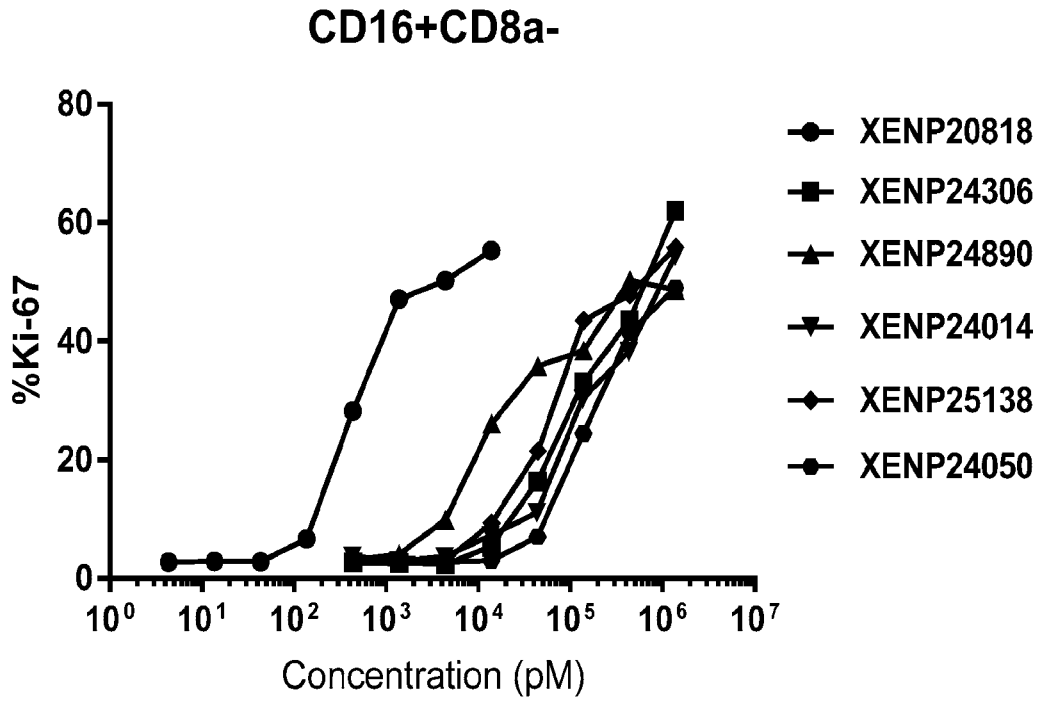


Figure 63E

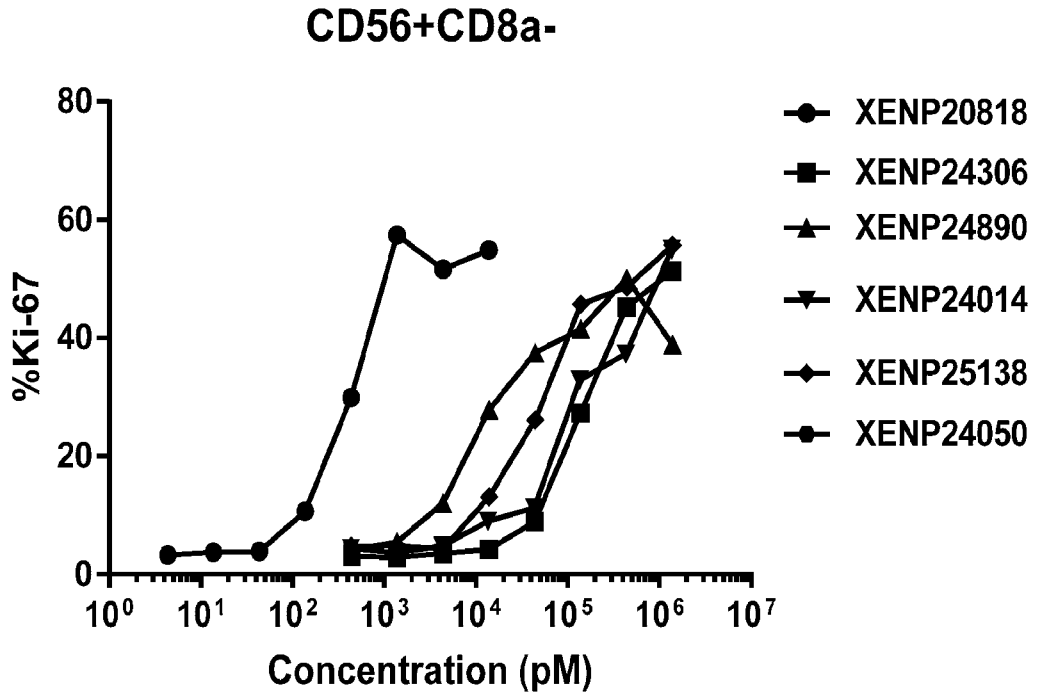

CD56+CD8a-
%Ki-67
80
60
40
20
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP20818
XENP24306
XENP24890
XENP24014
XENP25138
XENP24050

Figure 64A

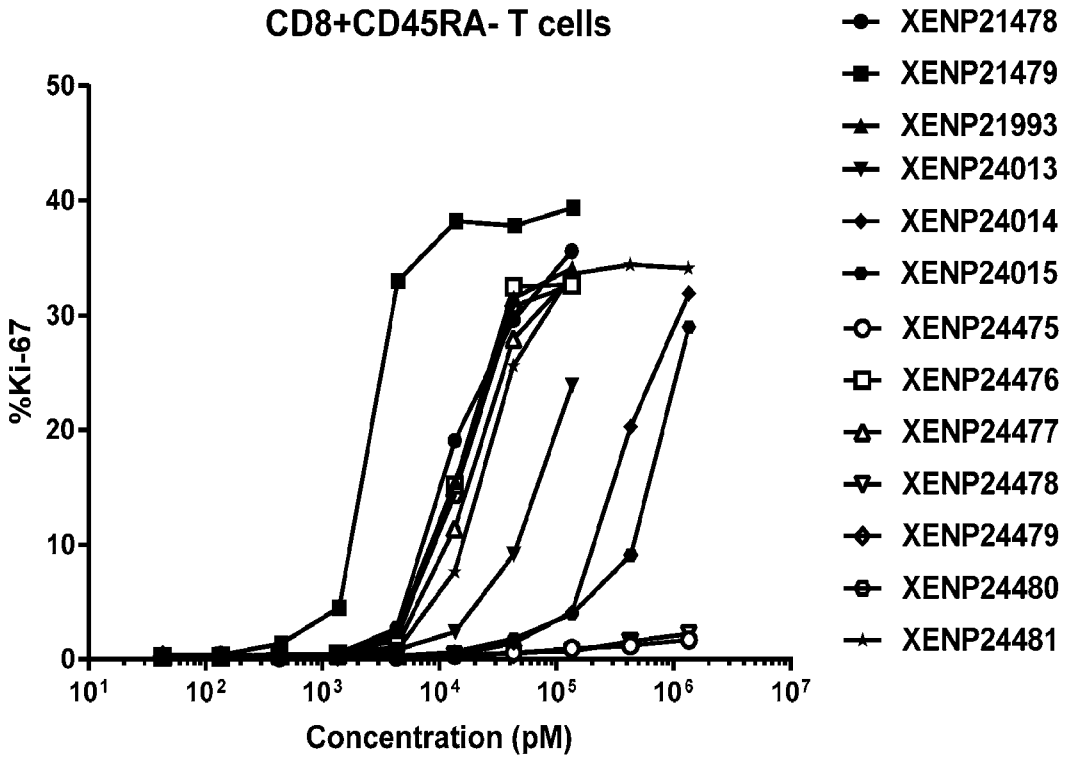

CD8+CD45RA- T cells
%Ki-67
Concentration (pM)
XENP21478
XENP21479
XENP21993
XENP24013
XENP24014
XENP24015
XENP24475
XENP24476
XENP24477
XENP24478
XENP24479
XENP24480
XENP24481

Figure 64B

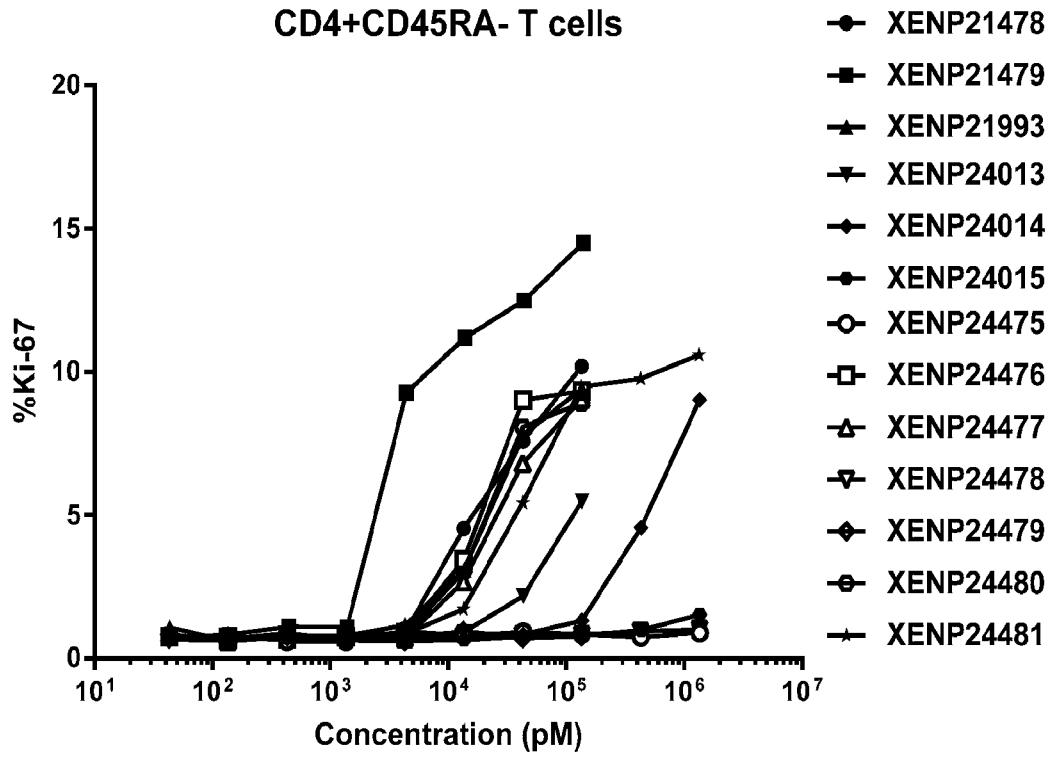

CD4+CD45RA- T cells
%Ki-67
Concentration (pM)
XENP21478
XENP21479
XENP21993
XENP24013
XENP24014
XENP24015
XENP24475
XENP24476
XENP24477
XENP24478
XENP24479
XENP24480
XENP24481

Figure 64C

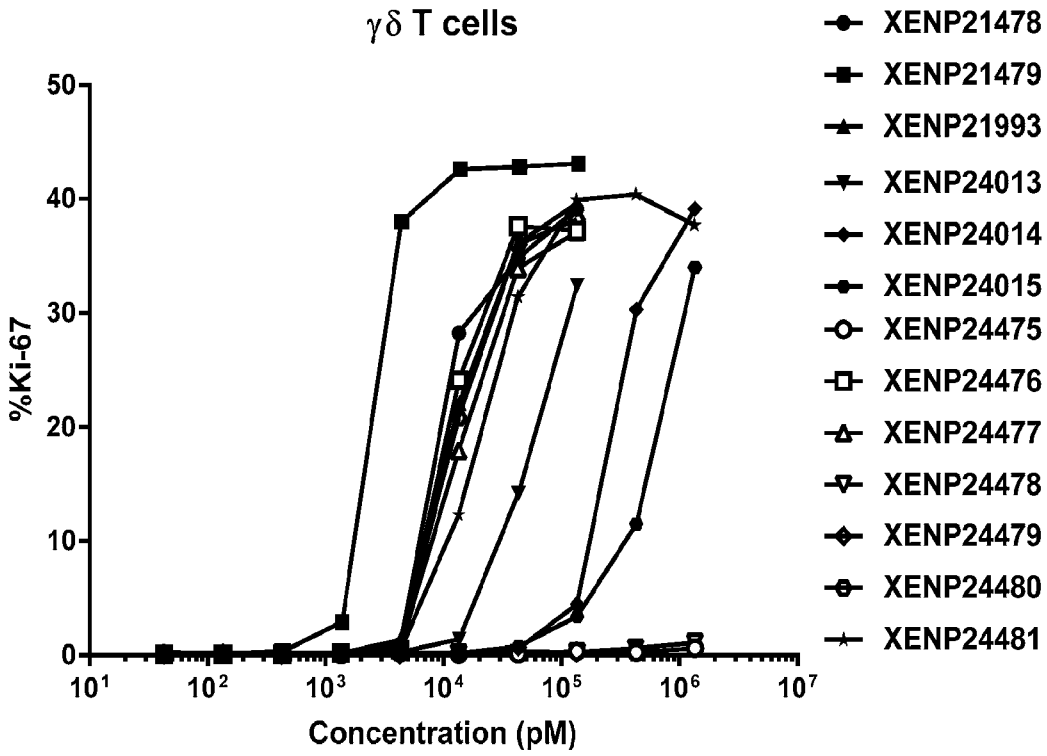

γδ T cells
%Ki-67
Concentration (pM)
XENP21478
XENP21479
XENP21993
XENP24013
XENP24014
XENP24015
XENP24475
XENP24476
XENP24477
XENP24478
XENP24479
XENP24480
XENP24481

Figure 64D

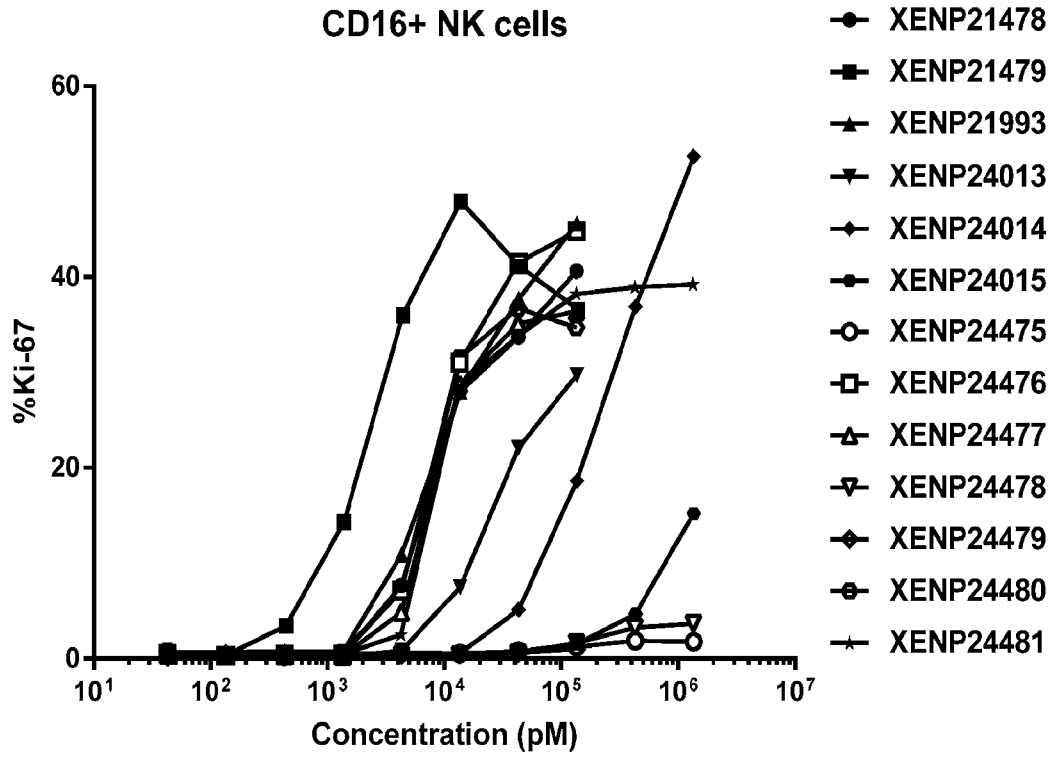

CD16+ NK cells
%Ki-67
60
40
20
0
10^1
10^2
10^3
10^4
10^5
10^6
10^7
Concentration (pM)
XENP21478
XENP21479
XENP21993
XENP24013
XENP24014
XENP24015
XENP24475
XENP24476
XENP24477
XENP24478
XENP24479
XENP24480
XENP24481

Figure 65A

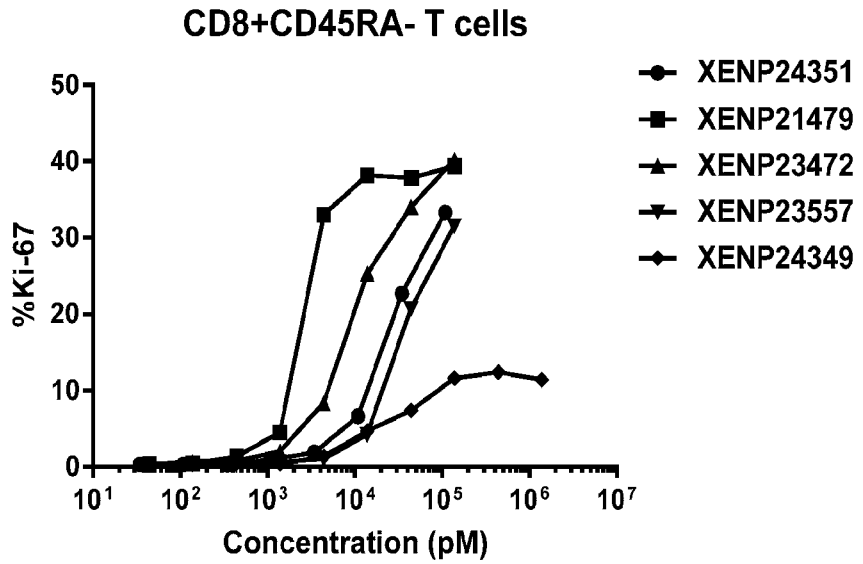


Figure 65B

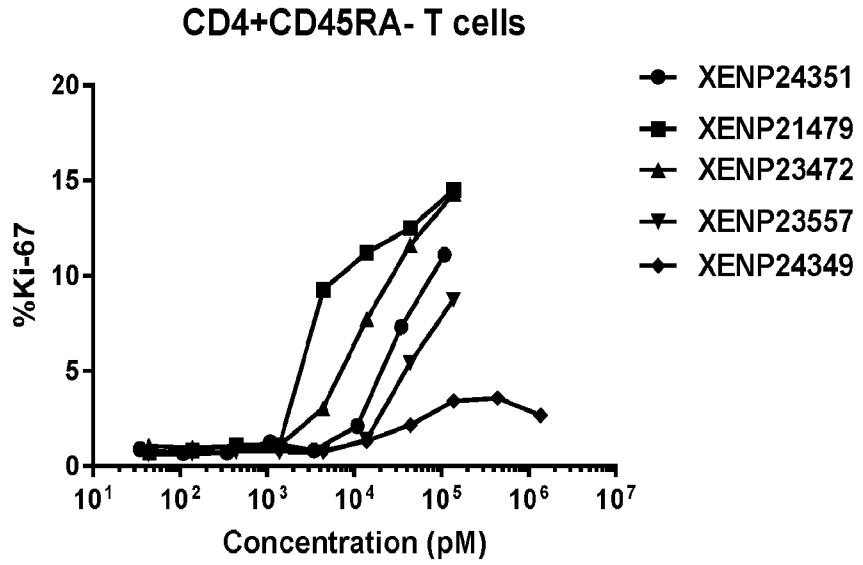


Figure 65C

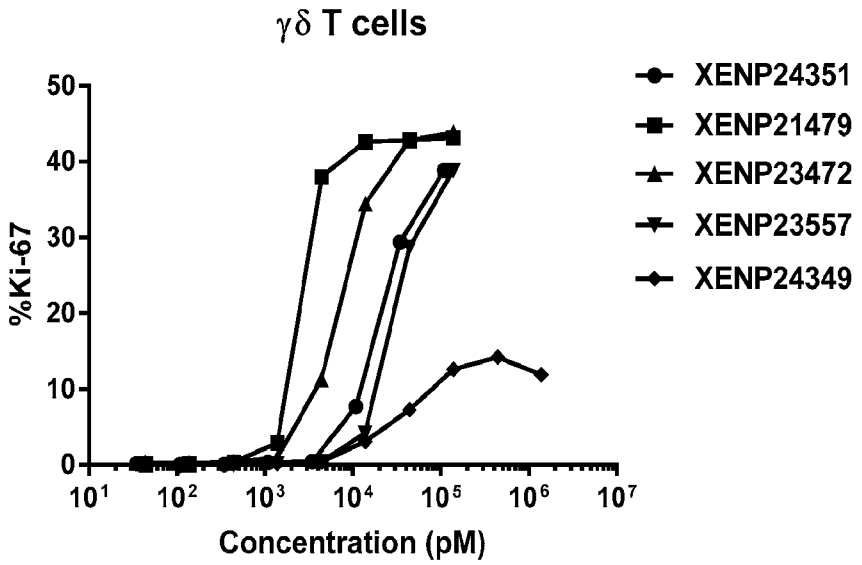


Figure 65D

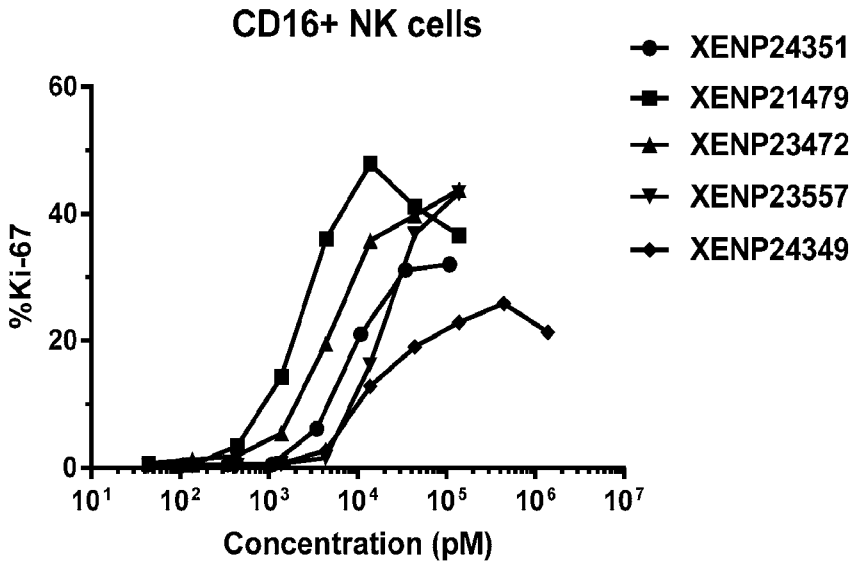


Figure 66A

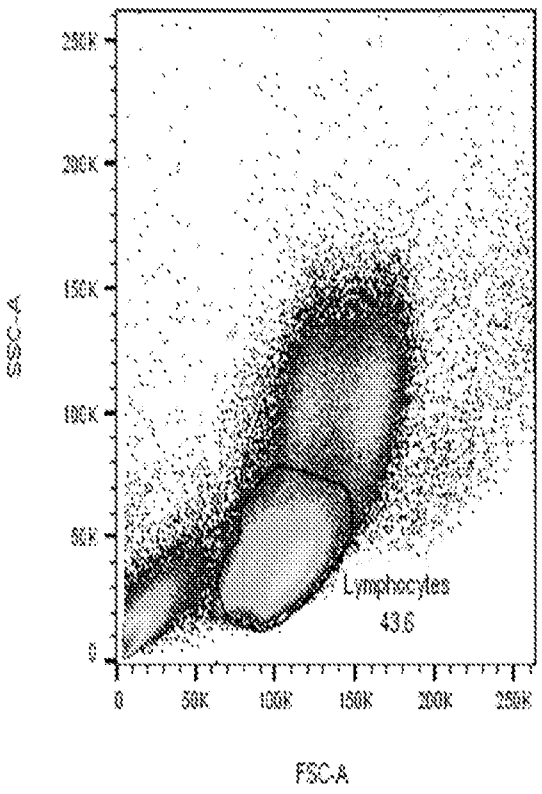


Figure 66B

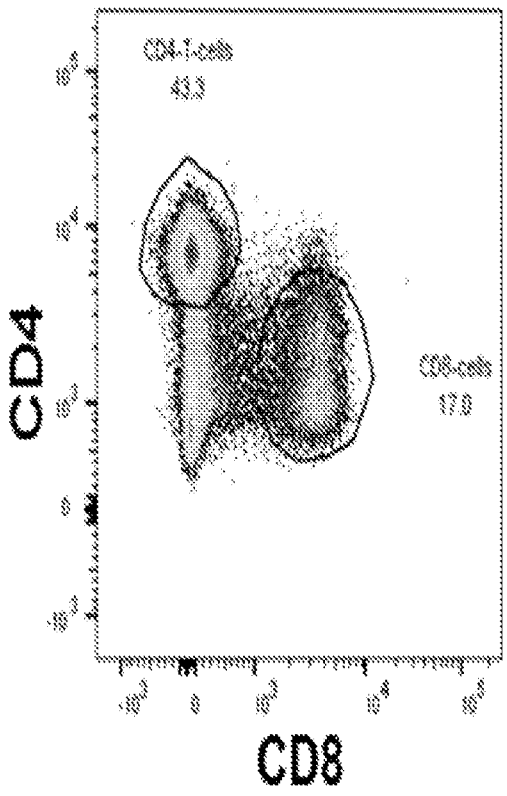


Figure 66C

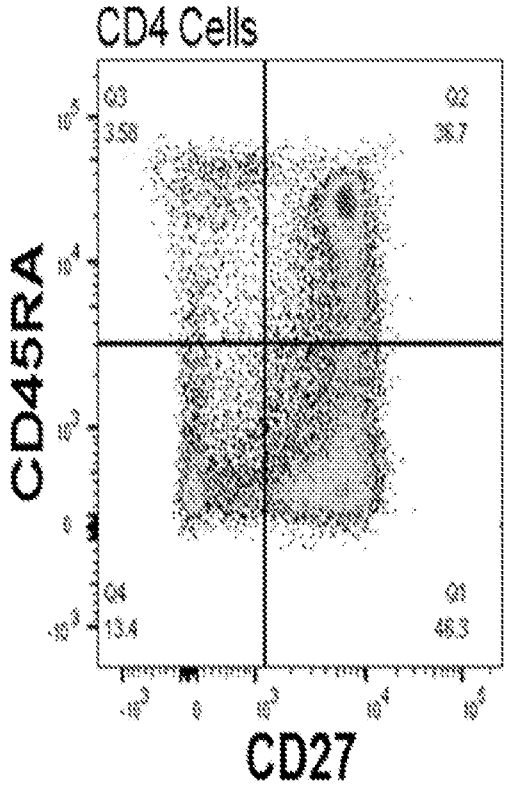


Figure 66D

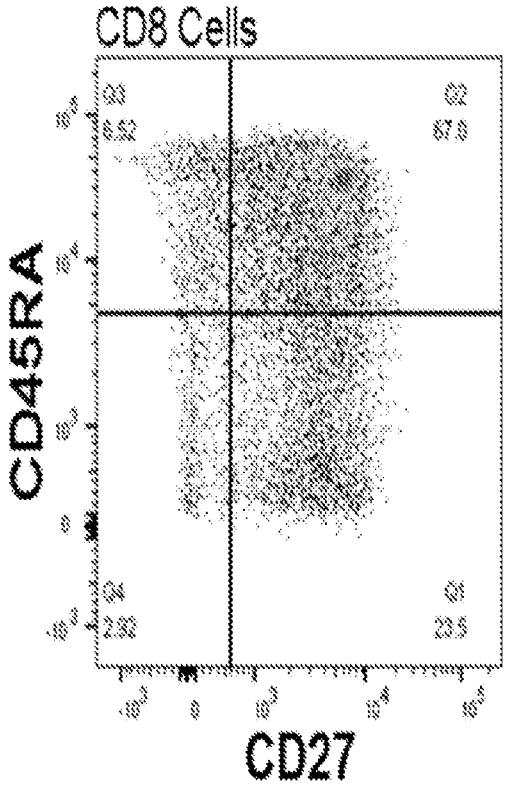


Figure 67A

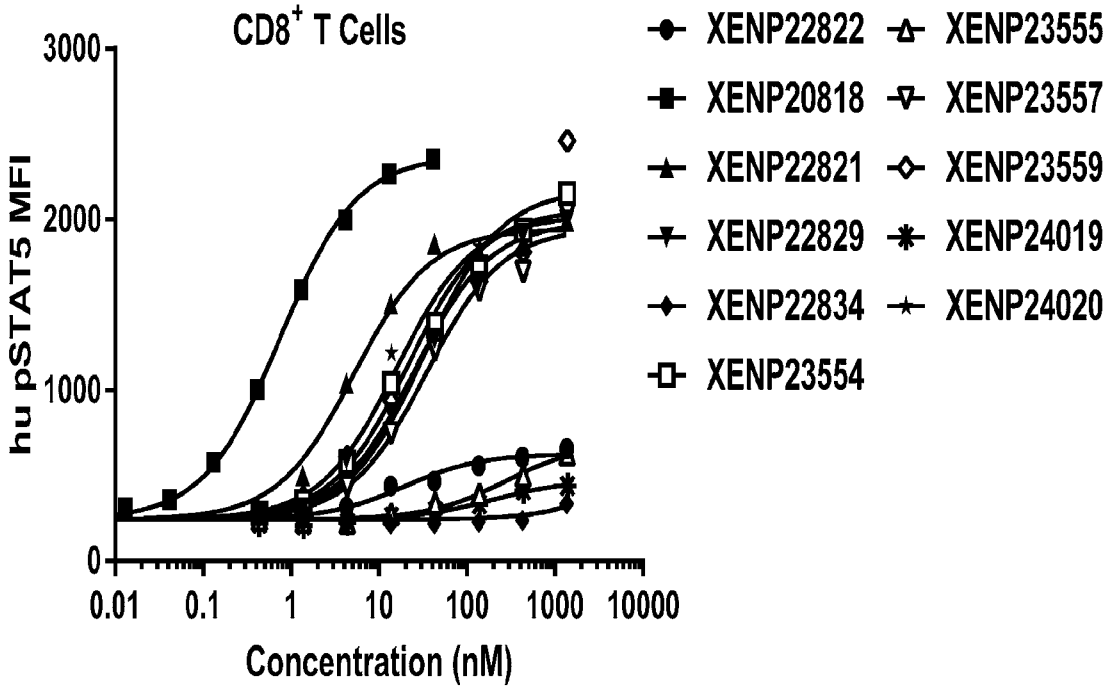


Figure 67B

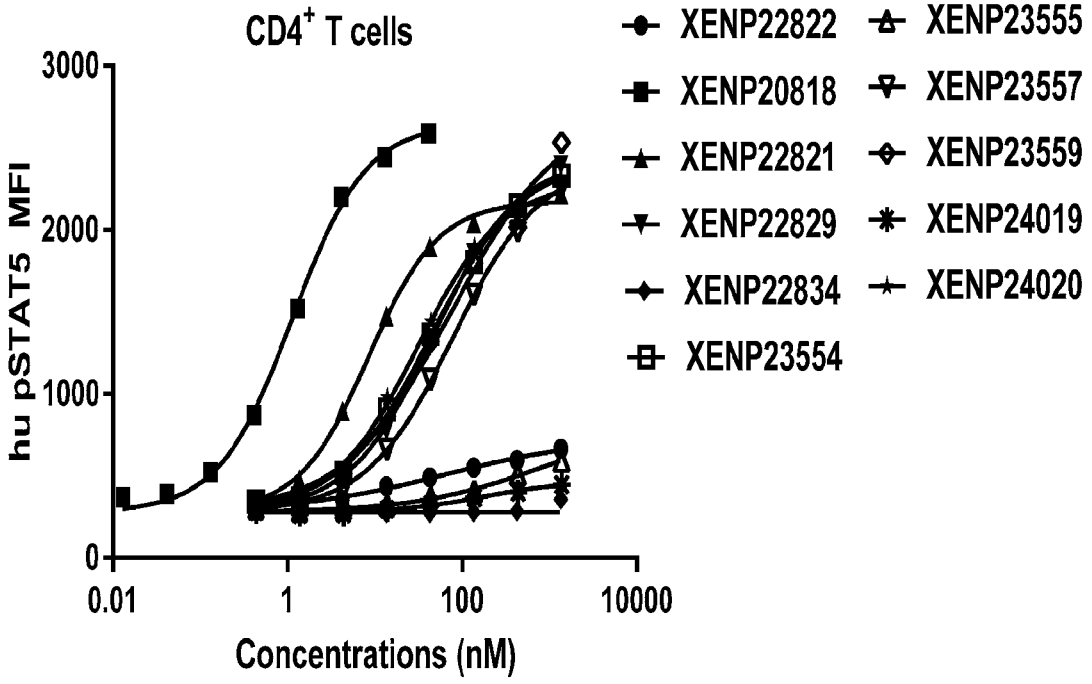
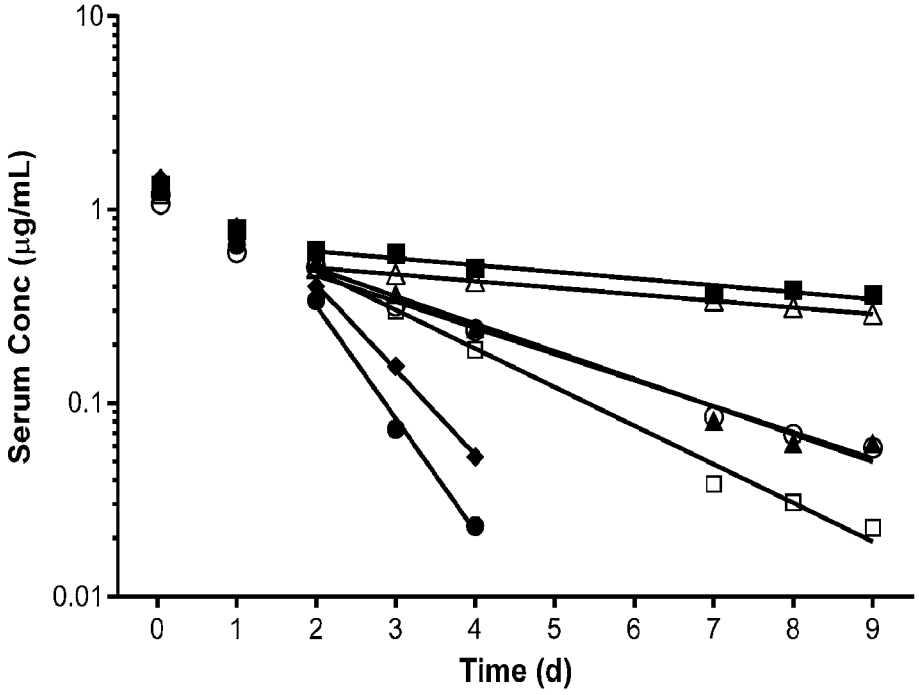


Figure 67C

XENP	EC50 nM (CD8 T cells)	Fold reduced (CD8 T cells)	EC50 nM (CD4 T cells)	Fold reduced (CD4 T cells)
22822	19.34	25.6	61.46	53.8
20818	0.7543	1.0	1.142	1.0
22821	5.196	6.9	8.485	7.4
22829	25.27	33.5	47.11	41.3
22834	ND	ND	ND	ND
23554	21.56	28.6	44.18	38.7
23555	270	357.9	818.2	716.5
23557	34.27	45.4	78.62	68.8
23559	32.91	43.6	76.03	66.6
24019	198.1	262.6	176.7	154.7
24020	15.92	21.1	30.98	27.1

Figure 68



● XENP20818 IL15/IL15Ra-Fc	$t_{1/2}$ ~ 0.5 d
■ XENP22821 IL15/IL15Ra-Fc N65D	$t_{1/2}$ ~ 8.6 d
▲ XENP22818 IL15/IL15Ra-Fc D30N	$t_{1/2}$ ~ 2.1 d
◆ XENP22820 IL15/IL15Ra-Fc E64Q	$t_{1/2}$ ~ 0.7 d
○ XENP21478 IL15/IL15Ra-Fc single-chain	$t_{1/2}$ ~ 2.2 d
□ XENP22819 IL15/IL15Ra-Fc D61N	$t_{1/2}$ ~ 1.5 d
△ XENP22822 IL15/IL15Ra-Fc Q108E	$t_{1/2}$ ~ 8.8 d

Figure 69

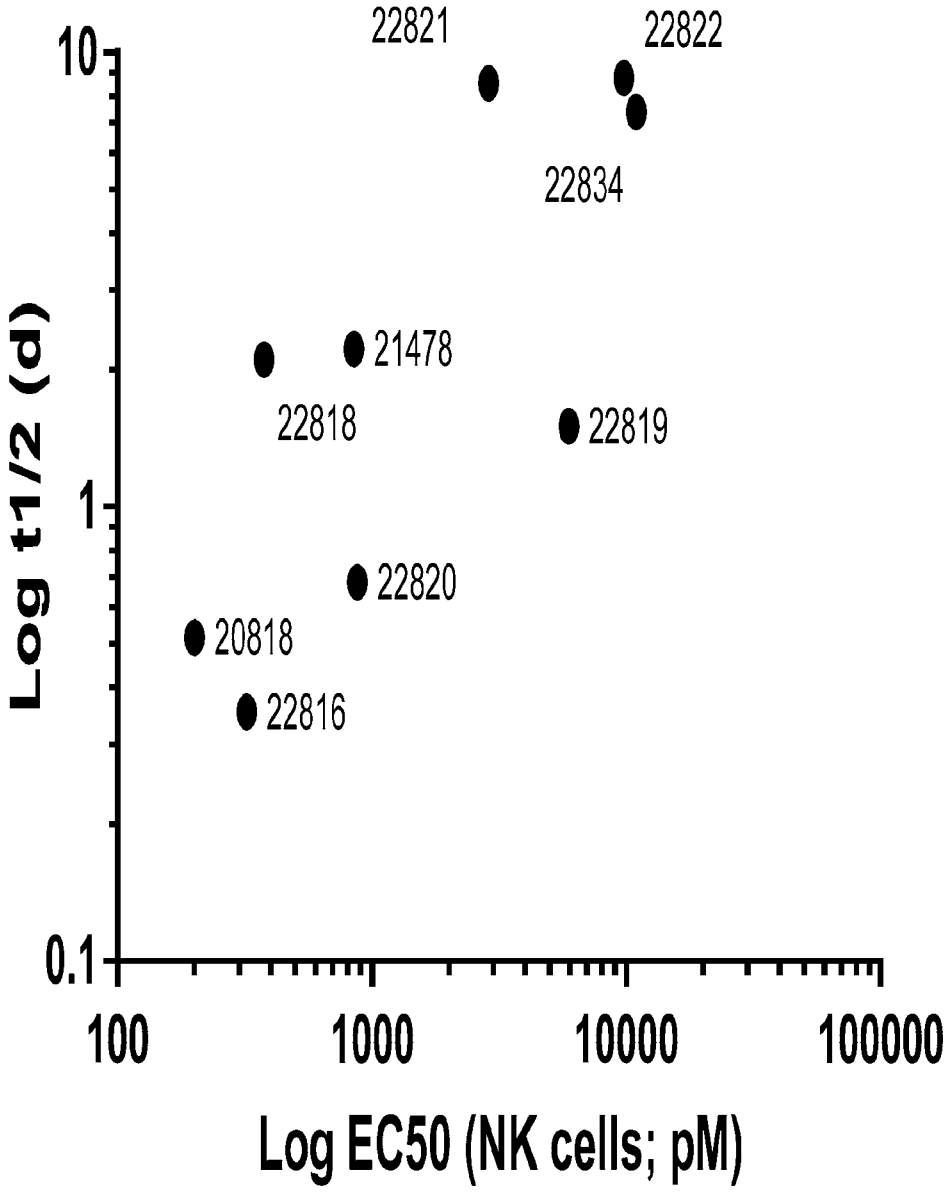

22821
22822
22834
21478
22818
22819
22820
20818
22816
10
1
0.1
Log t1/2 (d)
100
1000
10000
100000
Log EC50 (NK cells; pM)

Figure 70

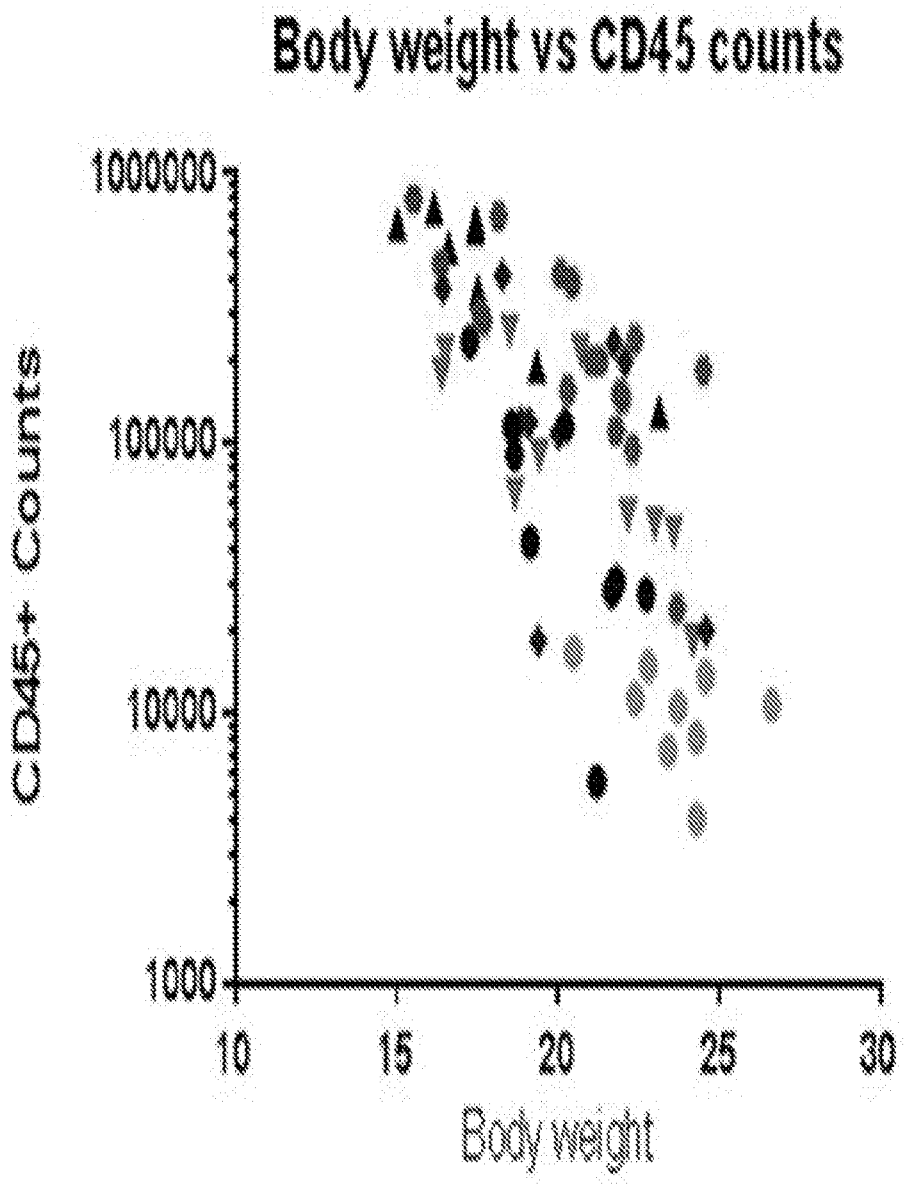

Body weight vs CD45 counts
CD45+ Counts
1000000
100000
10000
1000
10
15
20
25
30
Body weight

Figure 71A

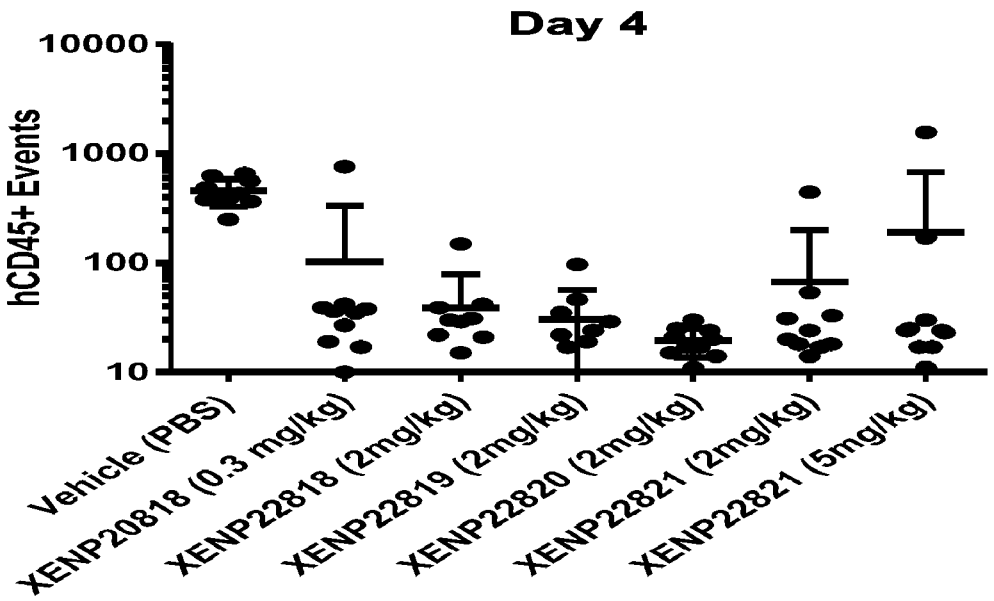


Figure 71B

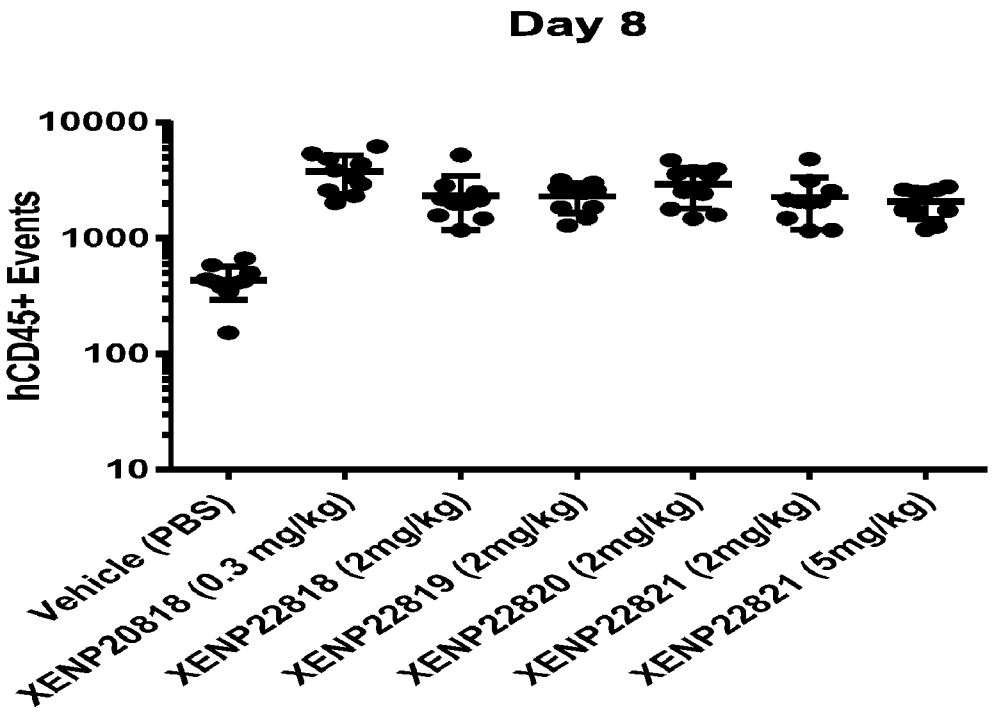


Figure 72A

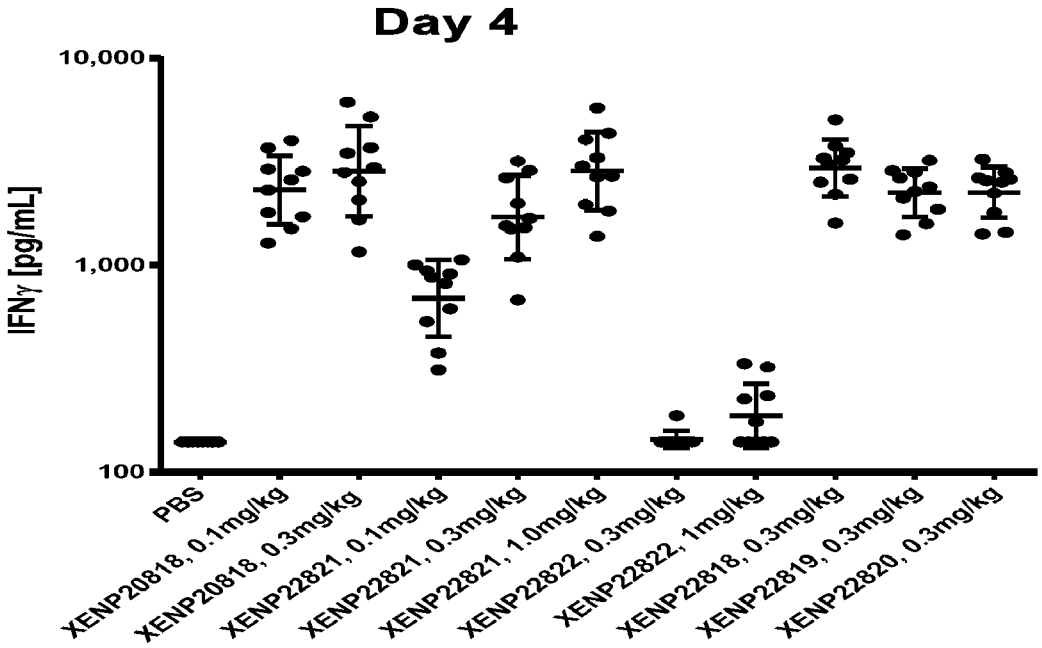


Figure 72B

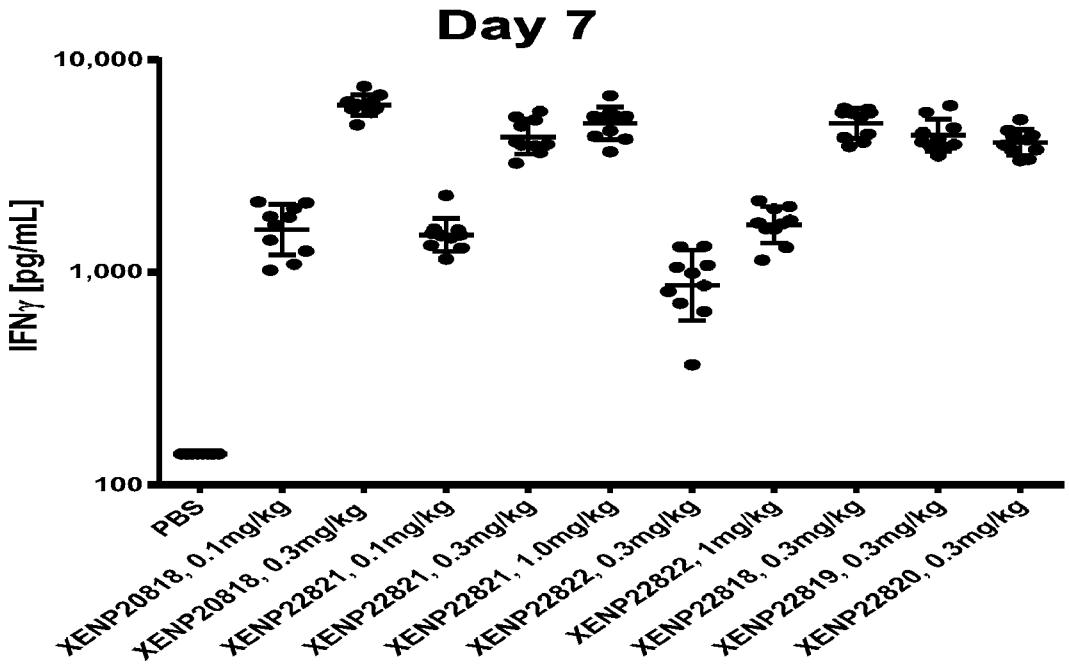


Figure 72C

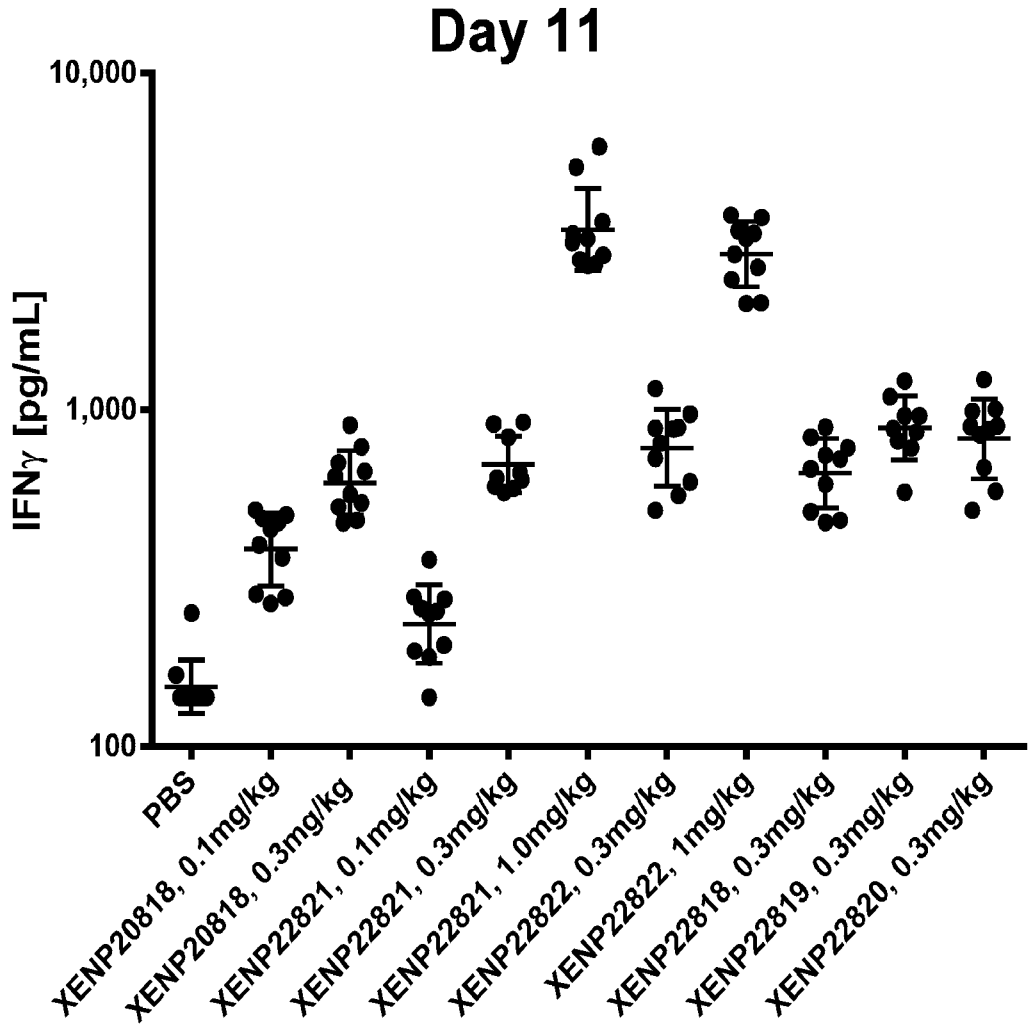

Day 11
10,000
1,000
100
IFNγ [pg/mL]
PBS
XENP20818, 0.1mg/kg
XENP20818, 0.3mg/kg
XENP22821, 0.1mg/kg
XENP22821, 0.3mg/kg
XENP22821, 1.0mg/kg
XENP22822, 0.3mg/kg
XENP22822, 1mg/kg
XENP22818, 0.3mg/kg
XENP22819, 0.3mg/kg
XENP22820, 0.3mg/kg

Figure 73A

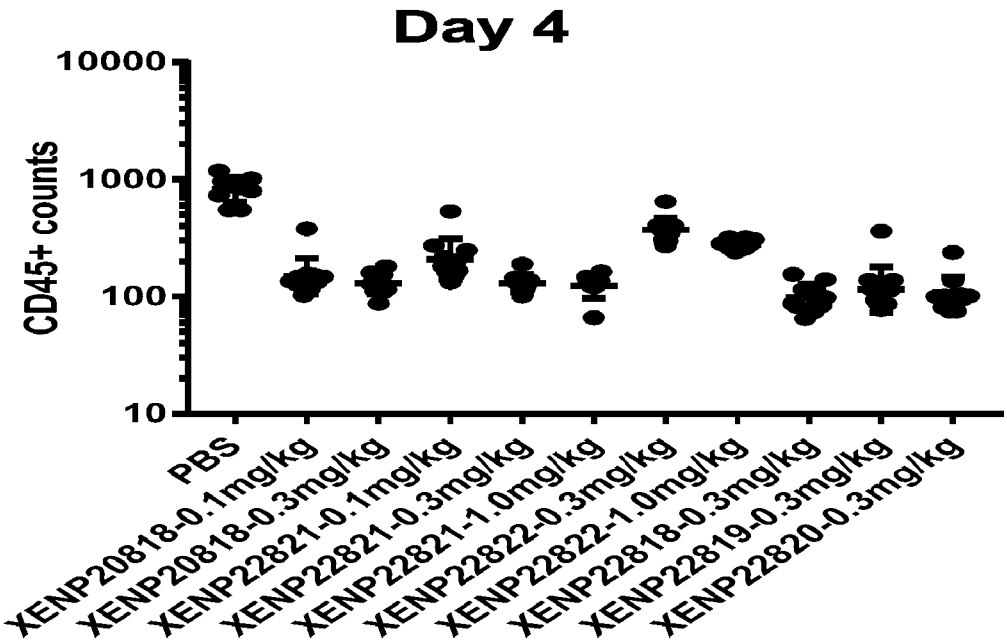


Figure 73B

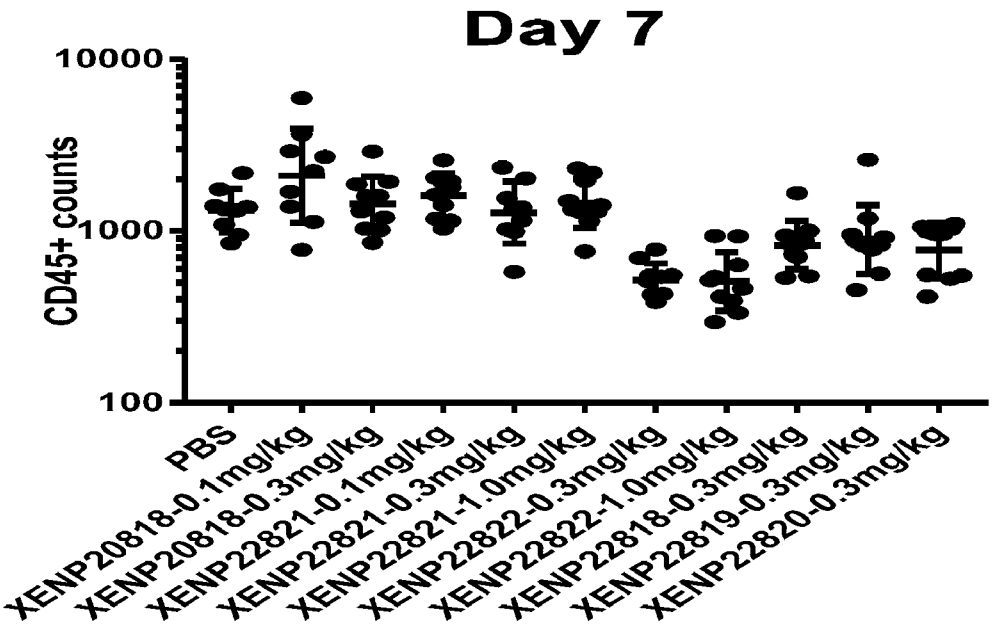


Figure 73C

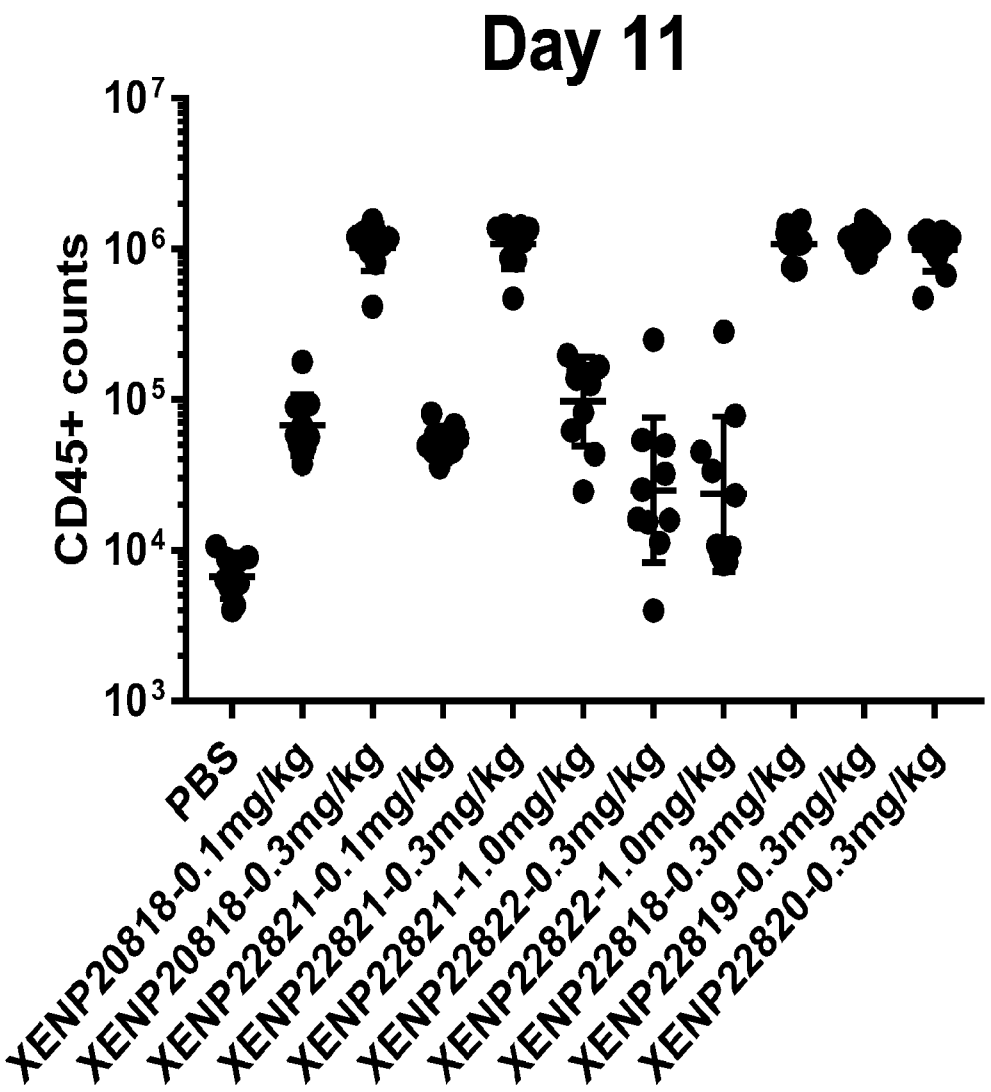

Day 11
CD45+ counts
10^7
10^6
10^5
10^4
10^3
PBS
XENP20818-0.1mg/kg
XENP20818-0.3mg/kg
XENP22821-0.1mg/kg
XENP22821-0.3mg/kg
XENP22821-1.0mg/kg
XENP22822-0.3mg/kg
XENP22822-1.0mg/kg
XENP22818-0.3mg/kg
XENP22819-0.3mg/kg
XENP22820-0.3mg/kg

Figure 74A

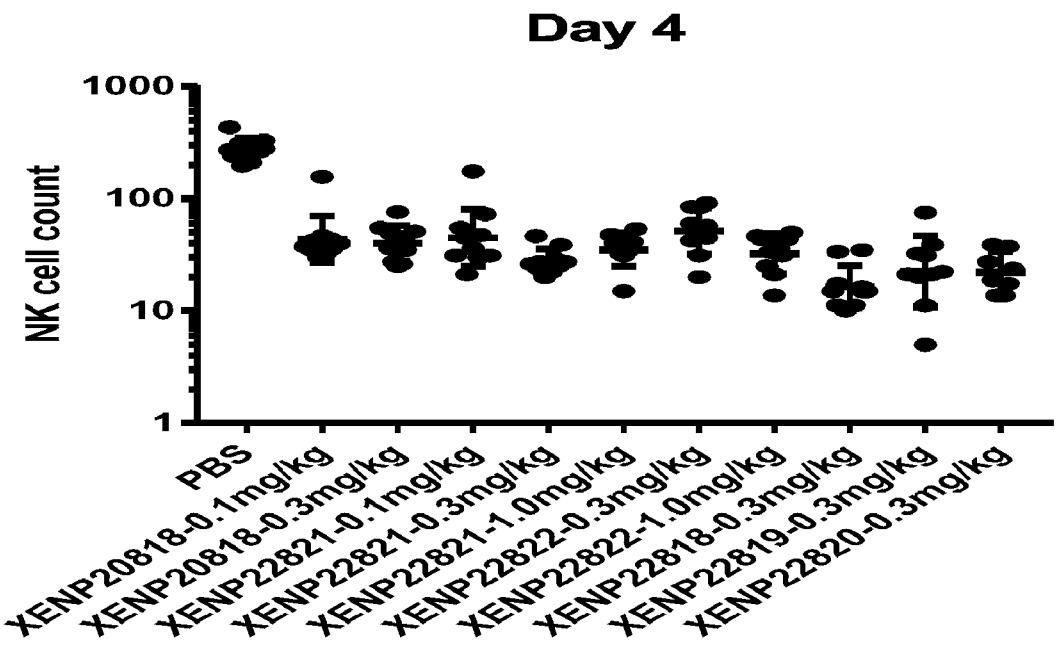


Figure 74B

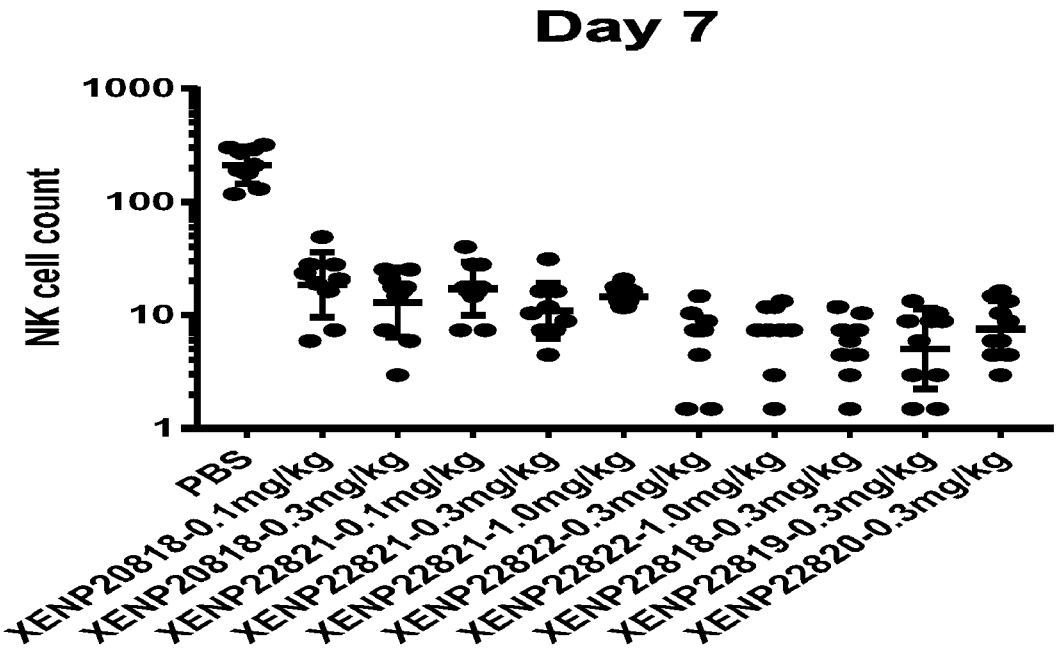


Figure 74C

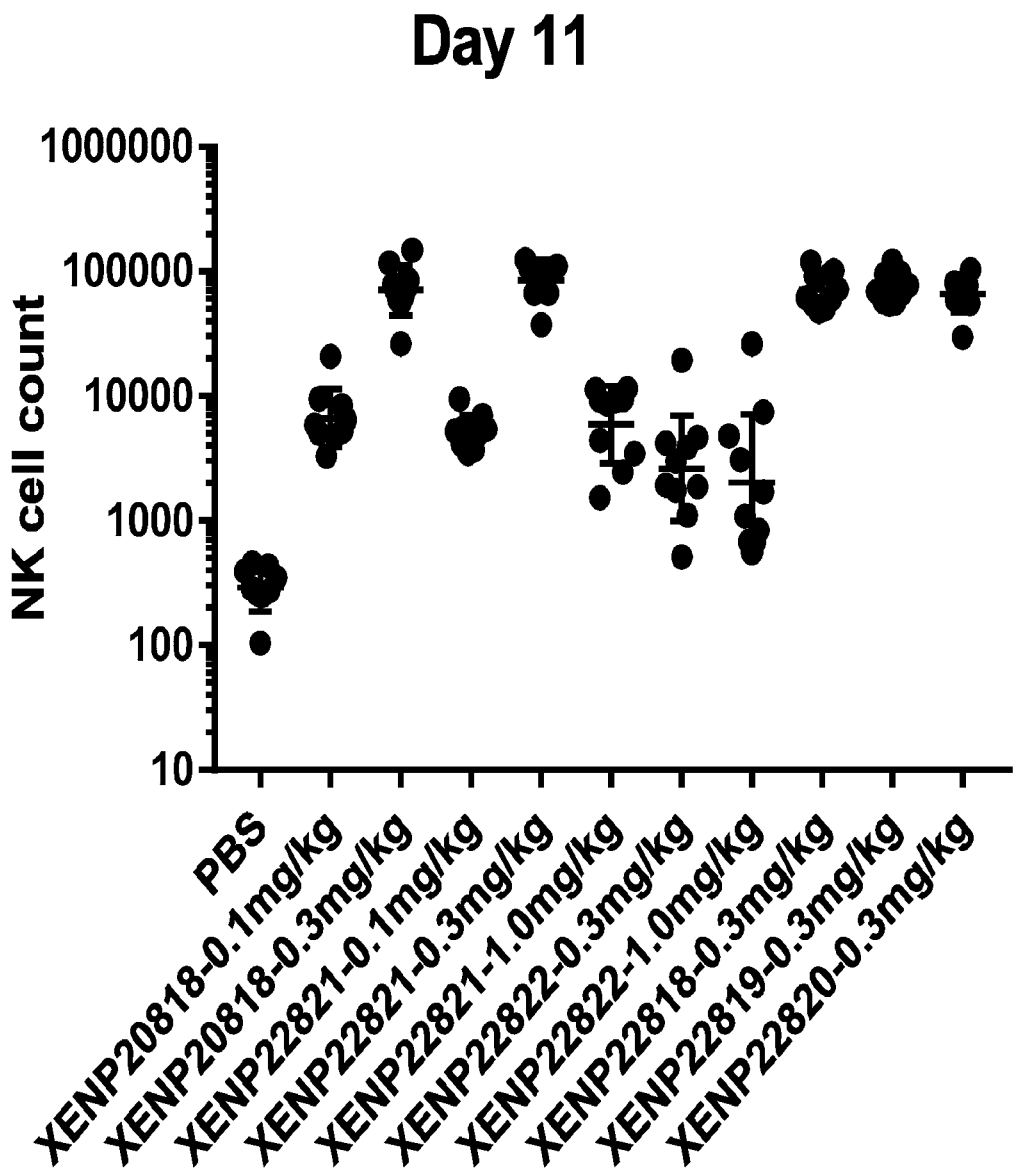

Day 11
NK cell count
1000000
100000
10000
1000
100
10
PBS
XENP20818-0.1mg/kg
XENP20818-0.3mg/kg
XENP22821-0.1mg/kg
XENP22821-0.3mg/kg
XENP22821-1.0mg/kg
XENP22822-0.3mg/kg
XENP22822-1.0mg/kg
XENP22818-0.3mg/kg
XENP22819-0.3mg/kg
XENP22820-0.3mg/kg

Figure 75A

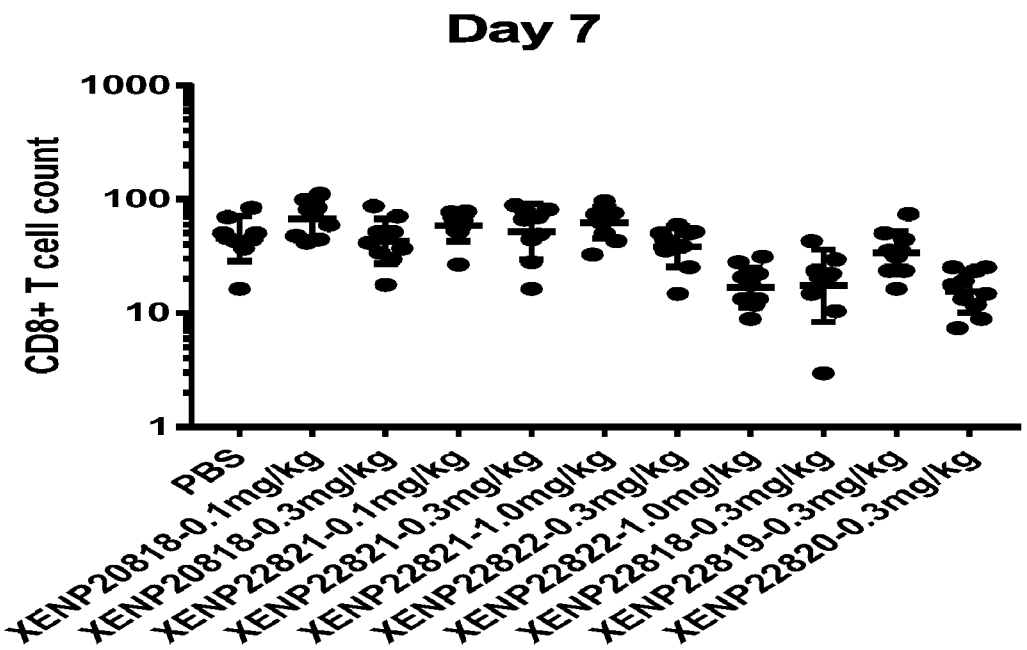


Figure 75B

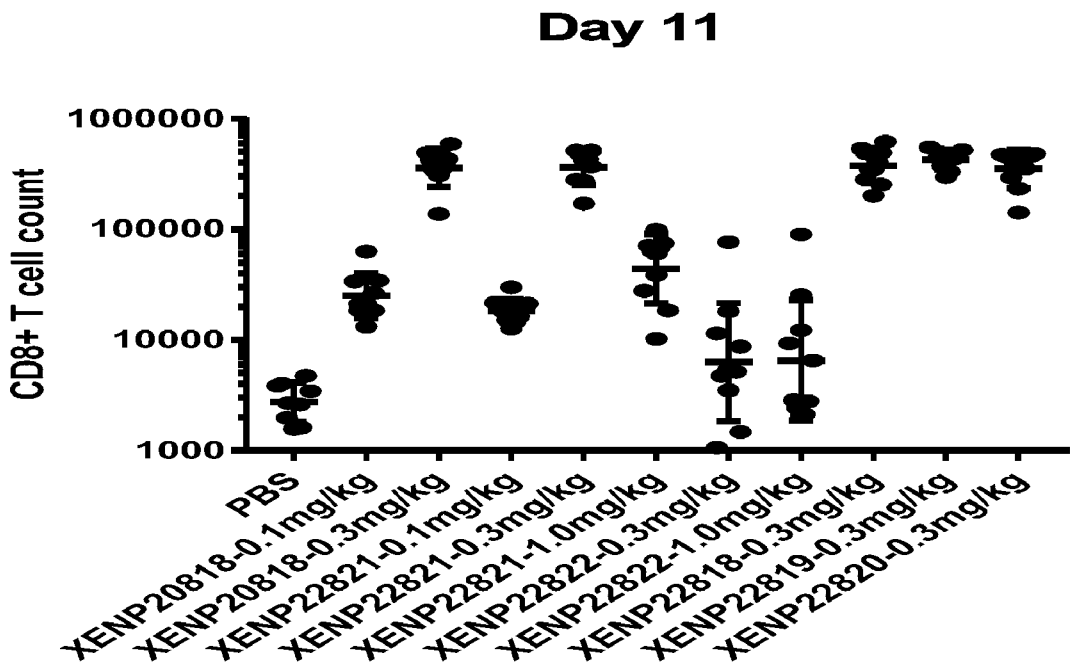


Figure 76A

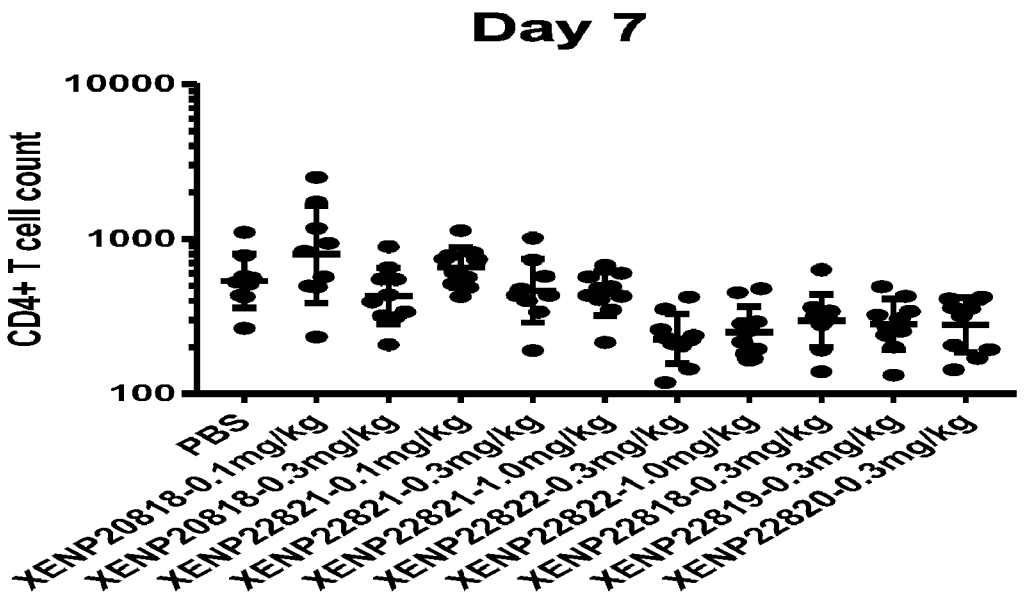


Figure 76B

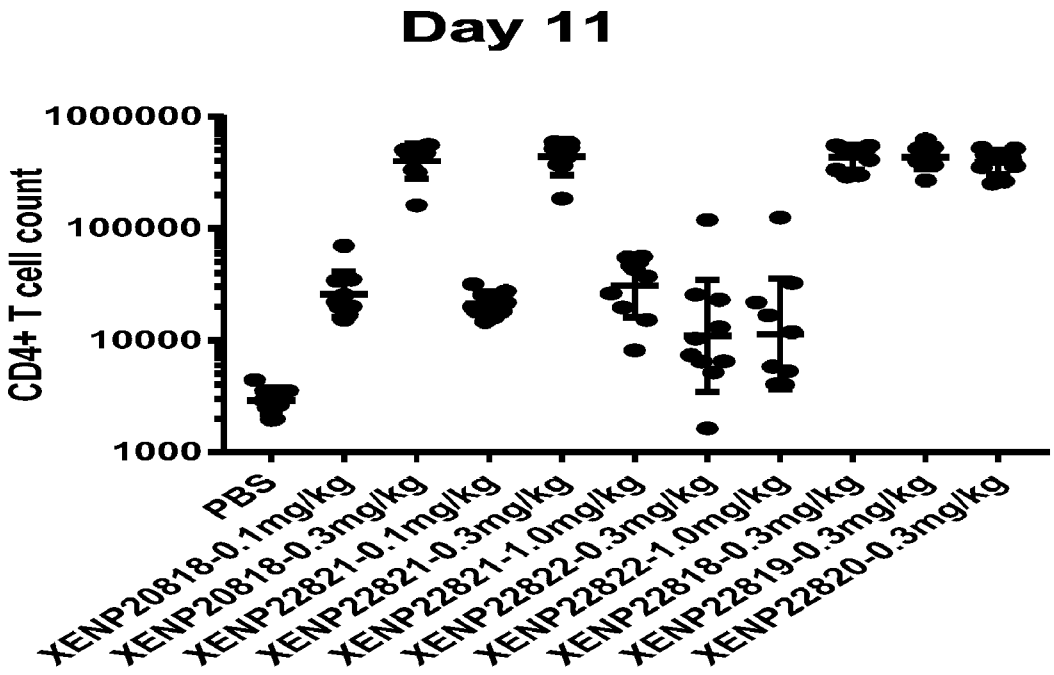


Figure 77

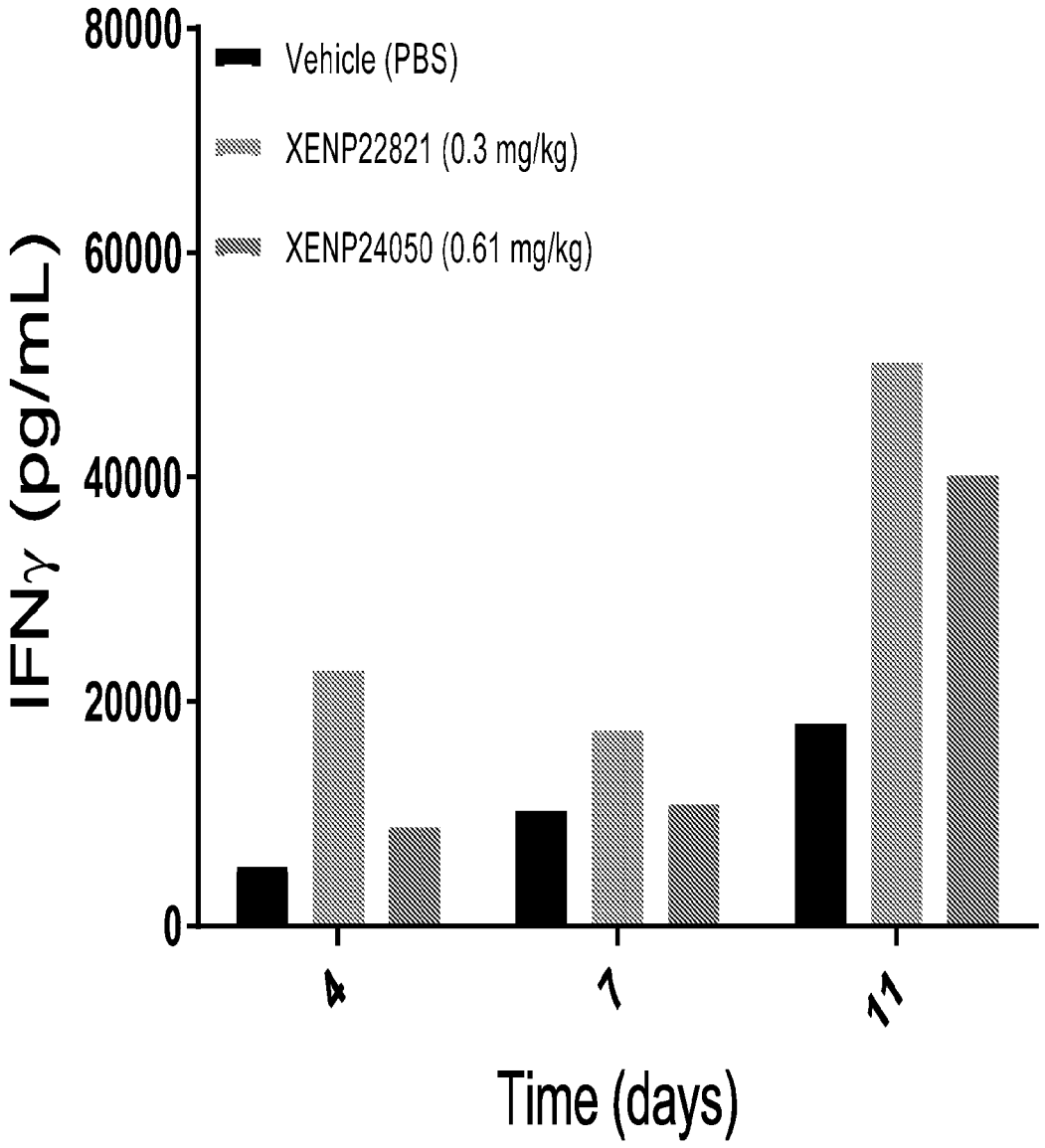

80000
60000
40000
20000
0
IFNγ (pg/mL)
Vehicle (PBS)
XENP22821 (0.3 mg/kg)
XENP24050 (0.61 mg/kg)
4
7
11
Time (days)

Figure 78A

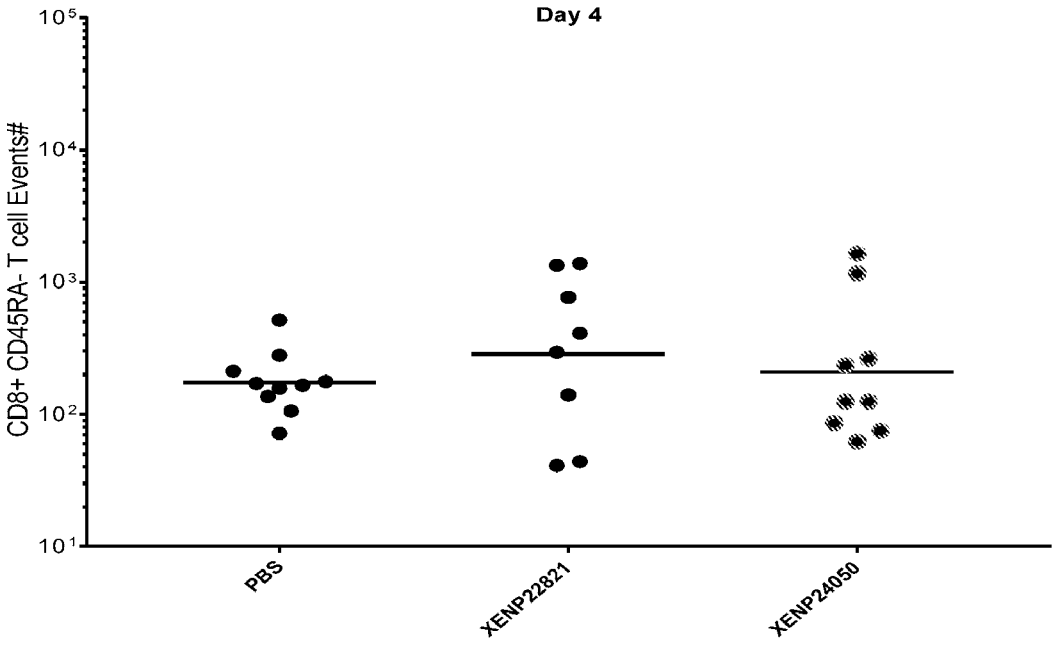


Figure 78B

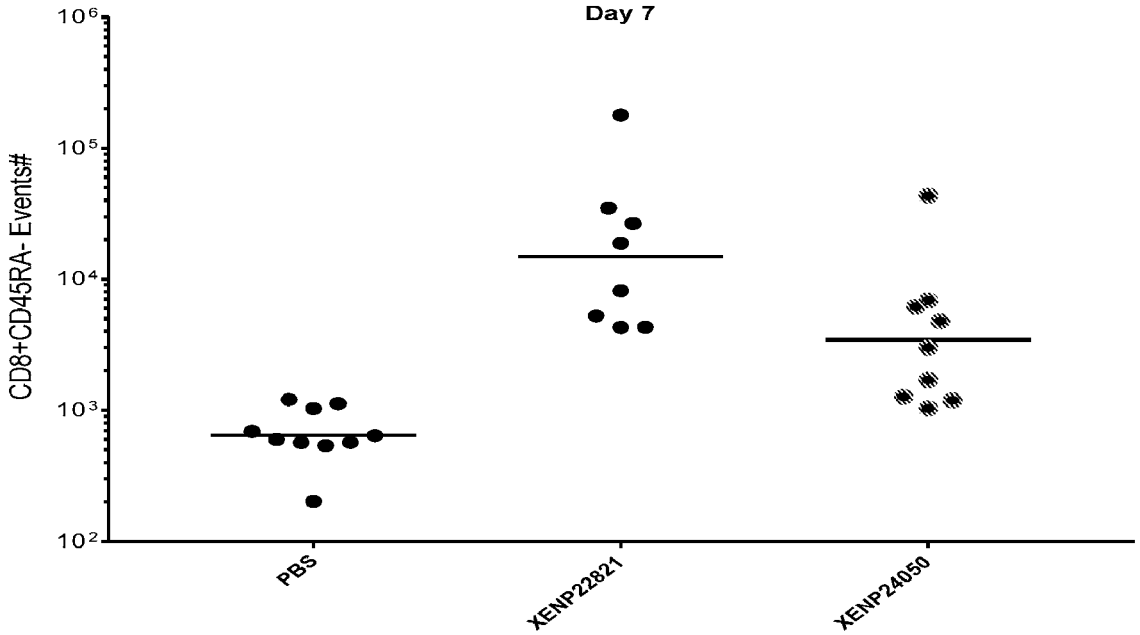


Figure 78C

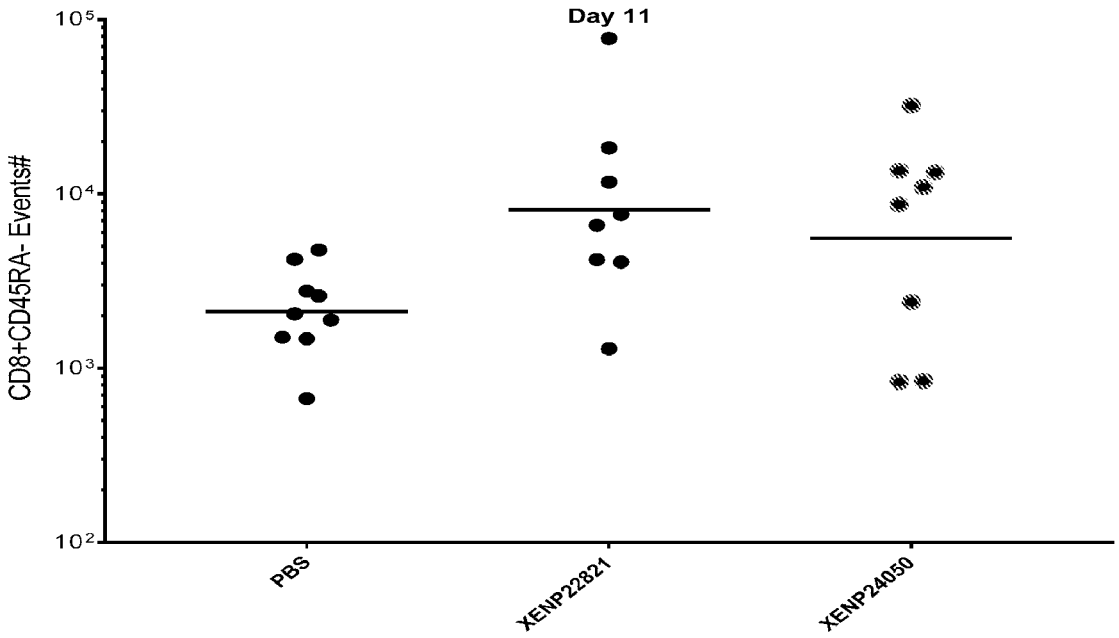

Day 11
CD8+CD45RA- Events#
10⁵
10⁴
10³
10²
PBS
XENP22821
XENP24050

Figure 79A

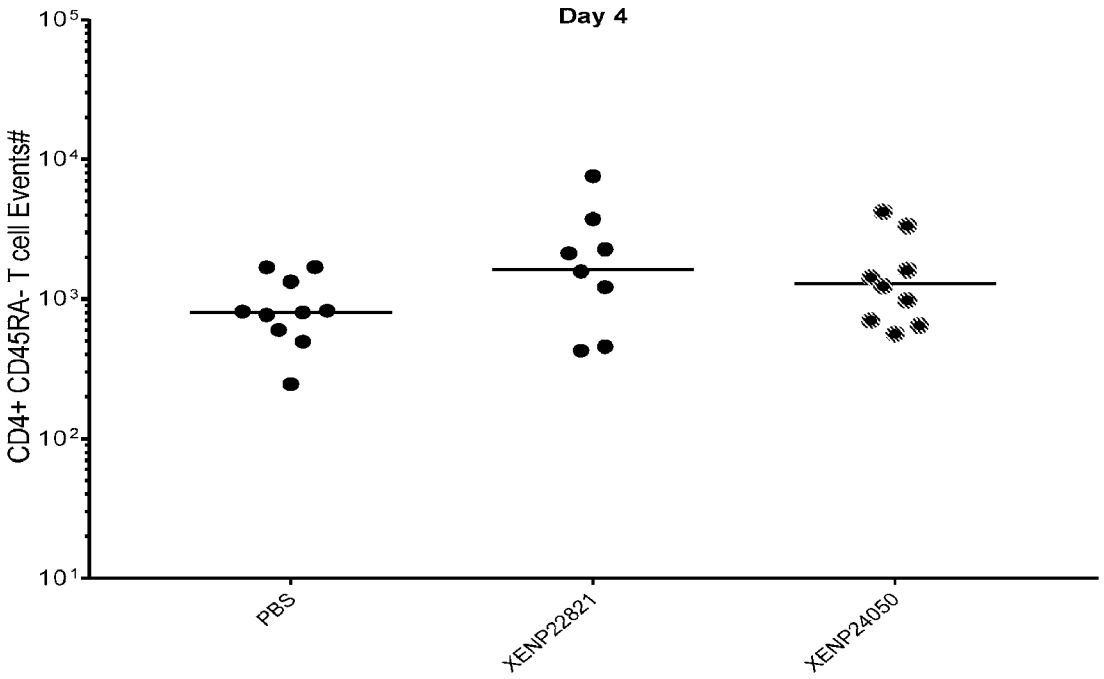


Figure 79B

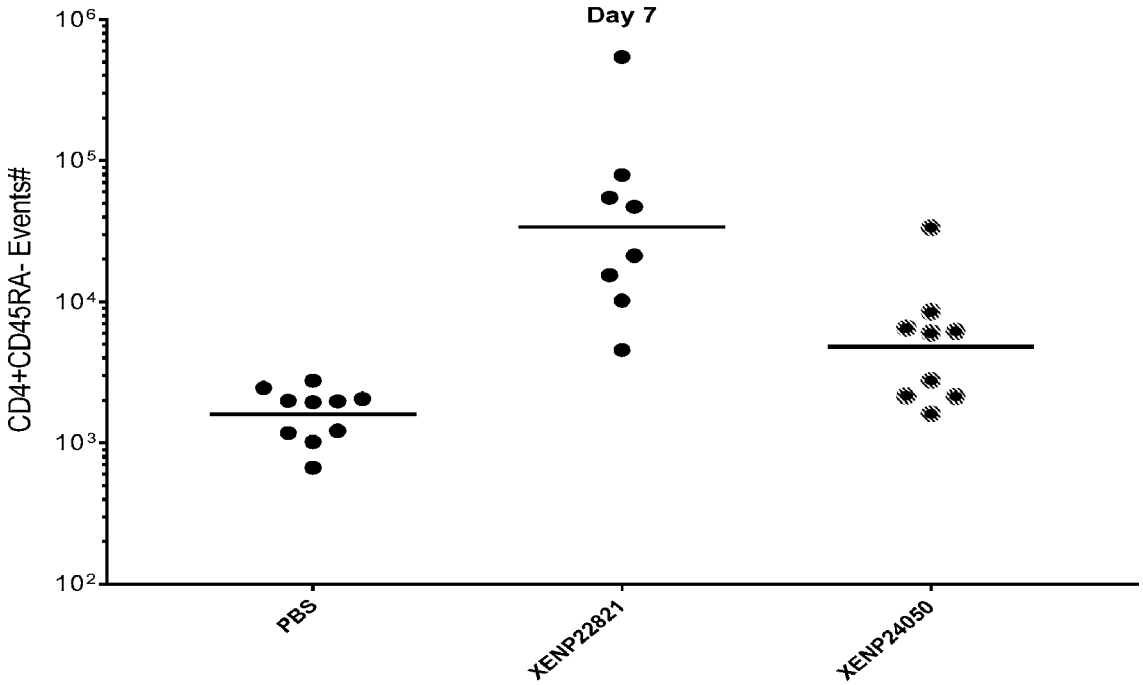


Figure 79C

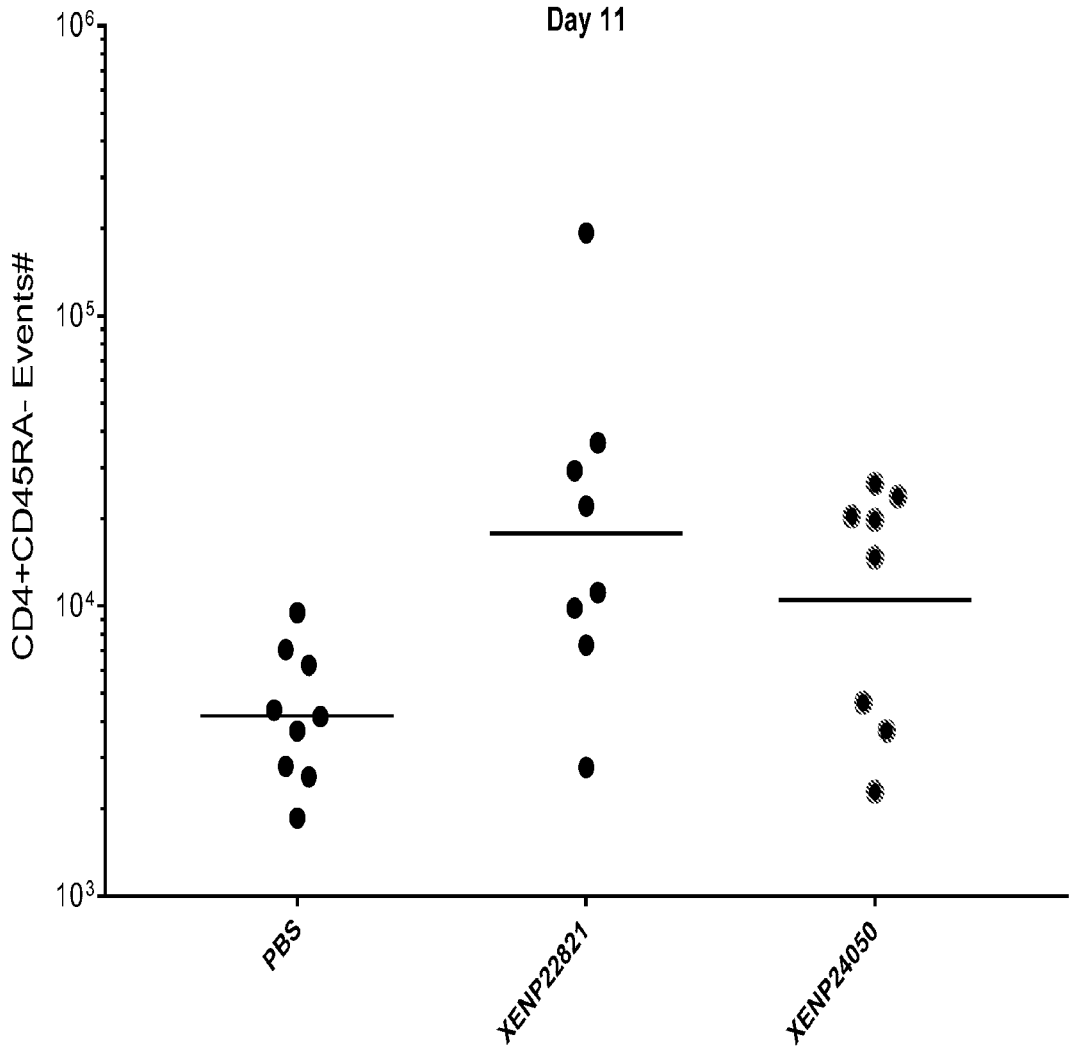

Day 11
CD4+CD45RA- Events#
10^6
10^5
10^4
10^3
PBS
XENP22821
XENP24050

Figure 80A

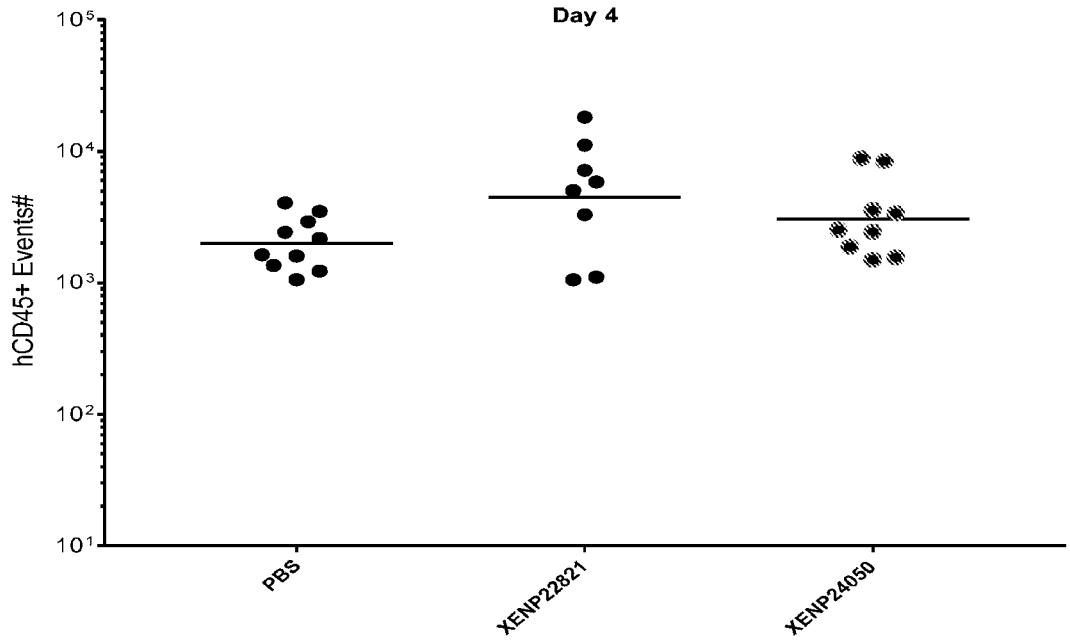


Figure 80B

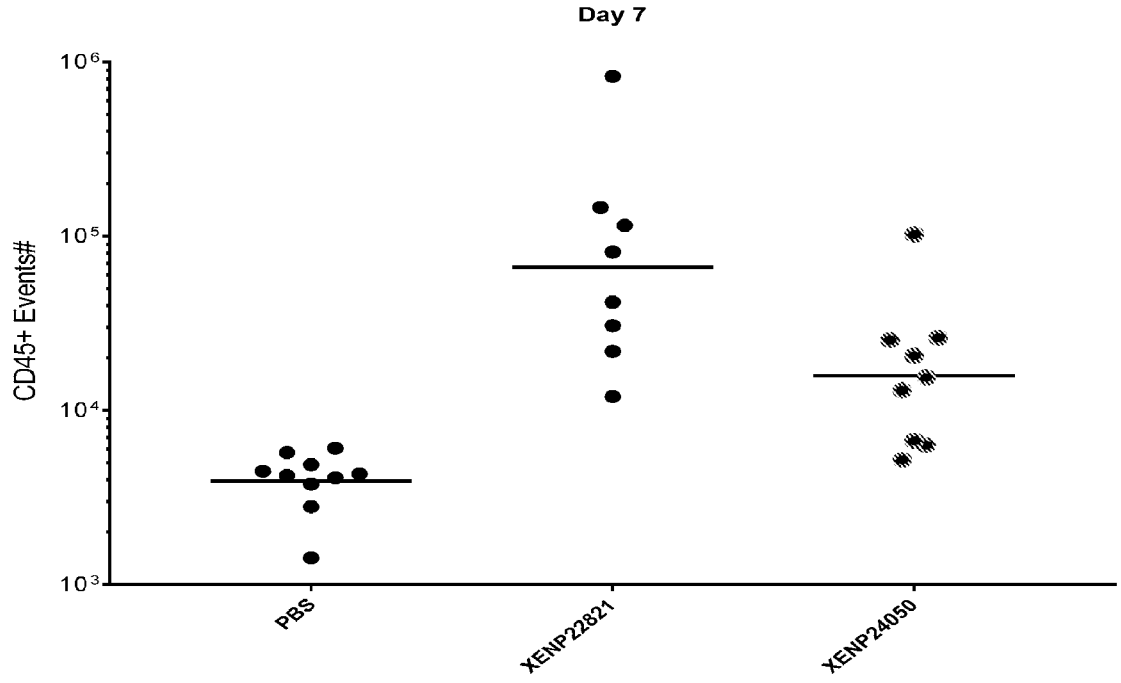


Figure 80C

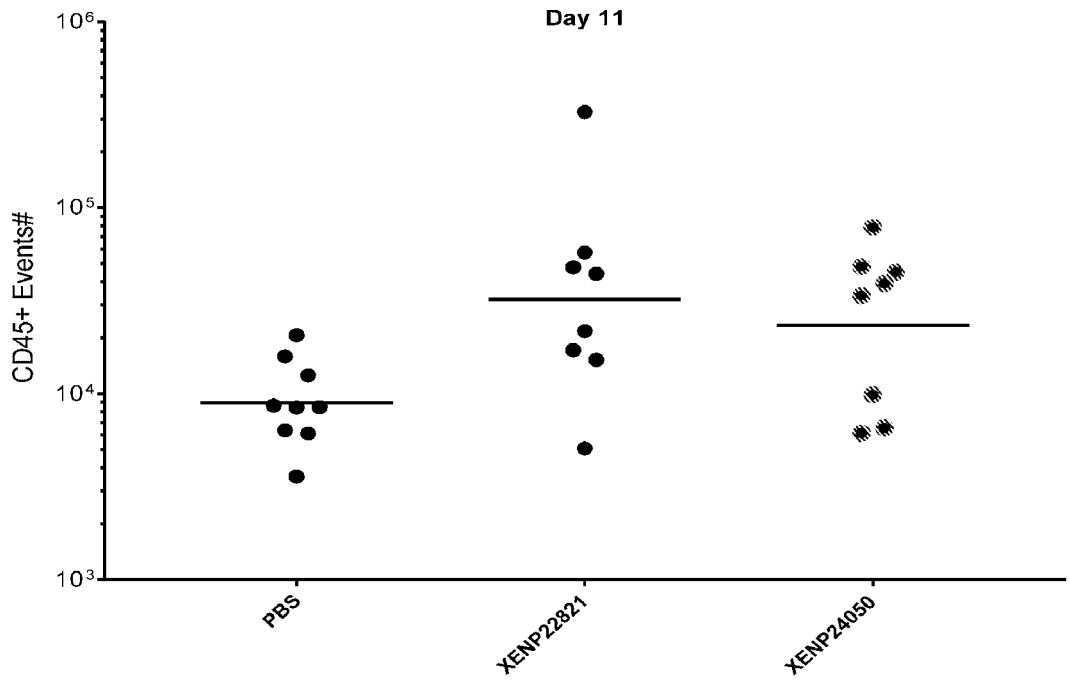


Figure 81A

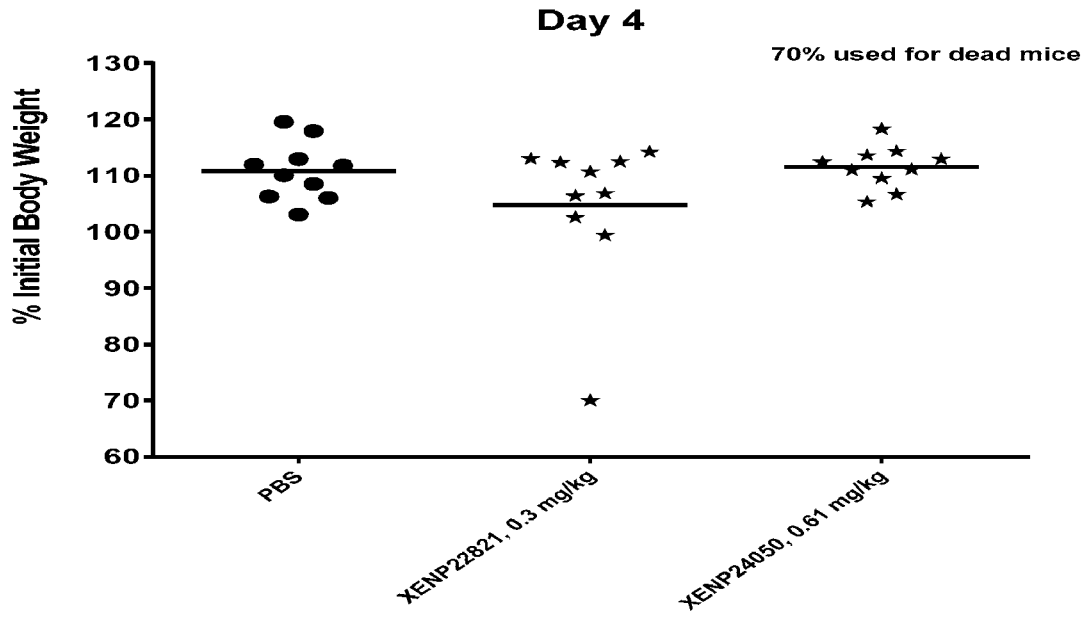


Figure 81B

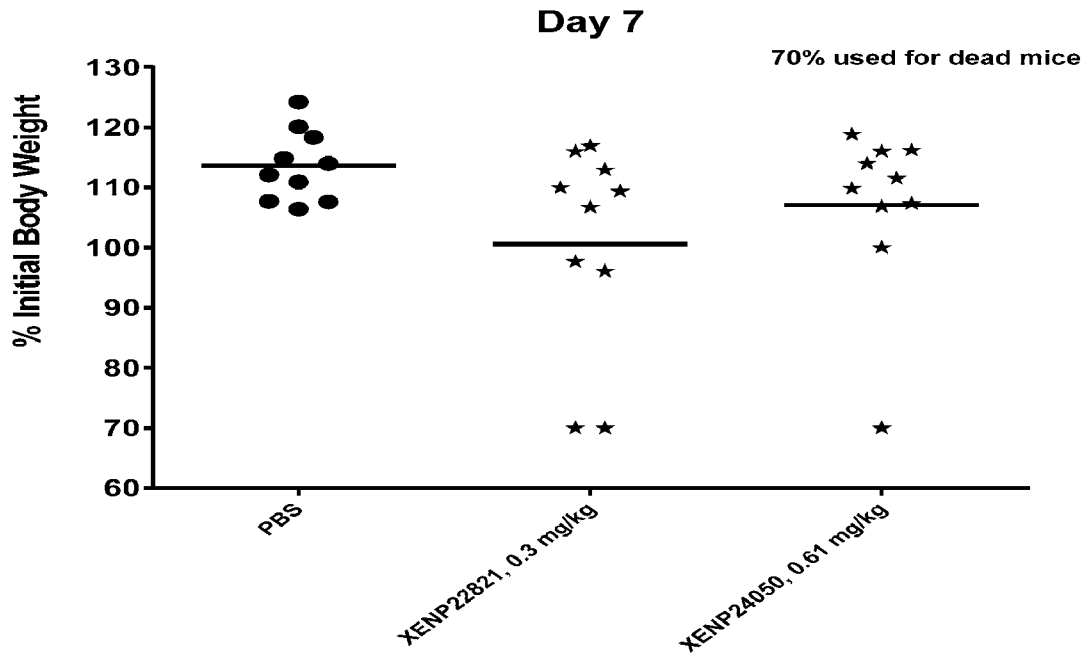


Figure 81C

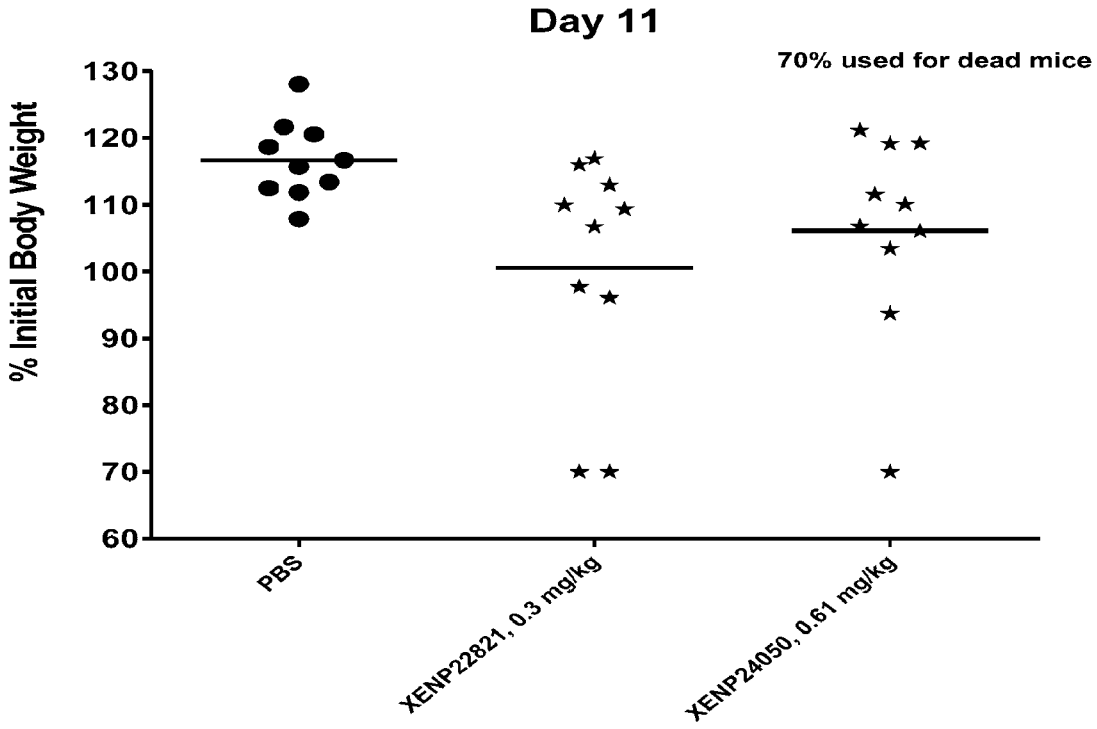

Day 11
70% used for dead mice
% Initial Body Weight
130
120
110
100
90
80
70
60
PBS
XENP22821, 0.3 mg/kg
XENP24050, 0.61 mg/kg

Figure 82A

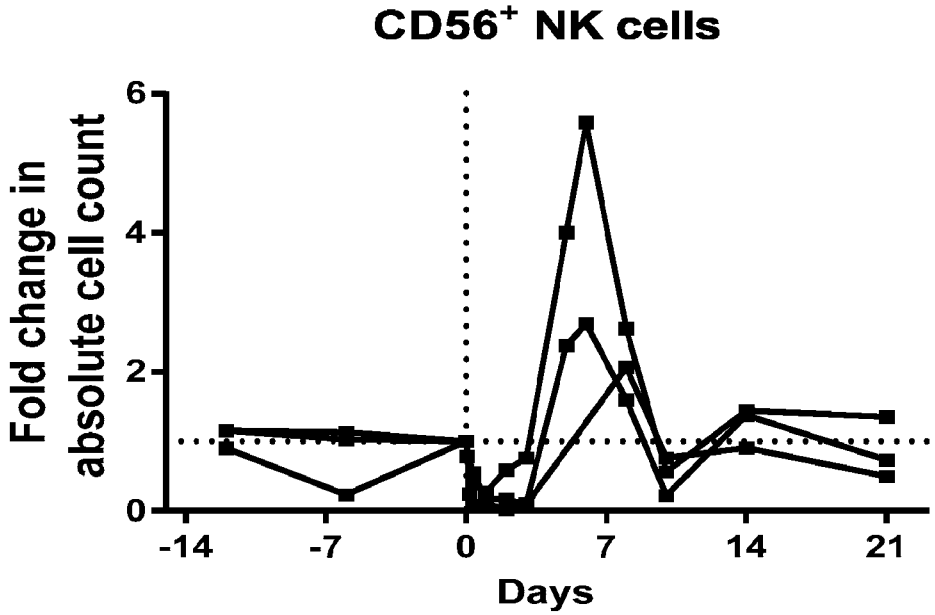


Figure 82B

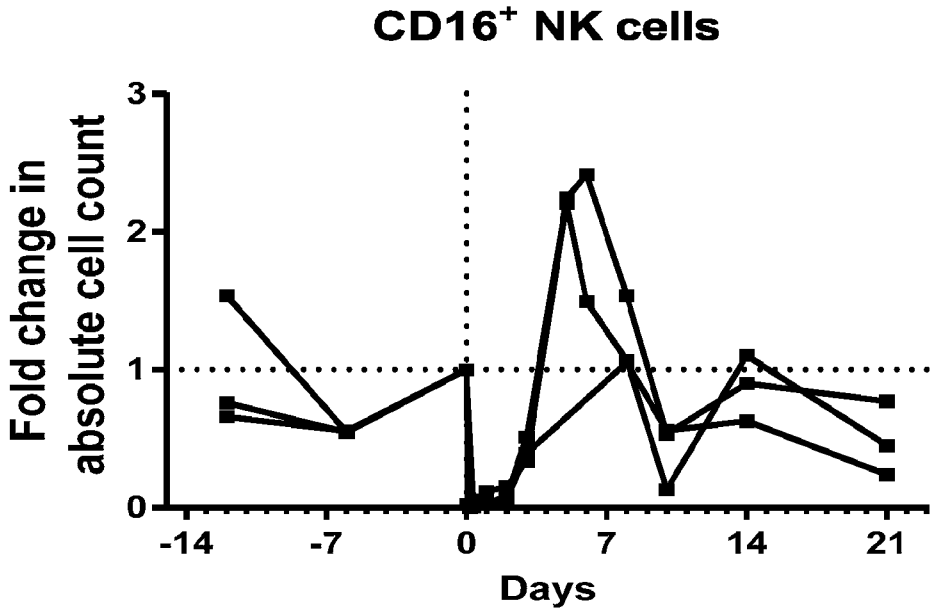


Figure 82C

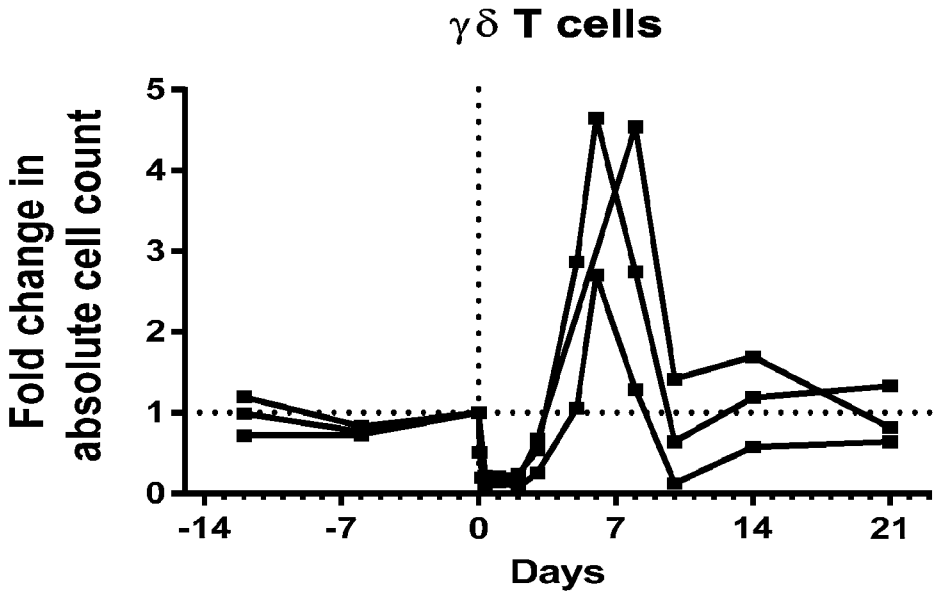


Figure 82D

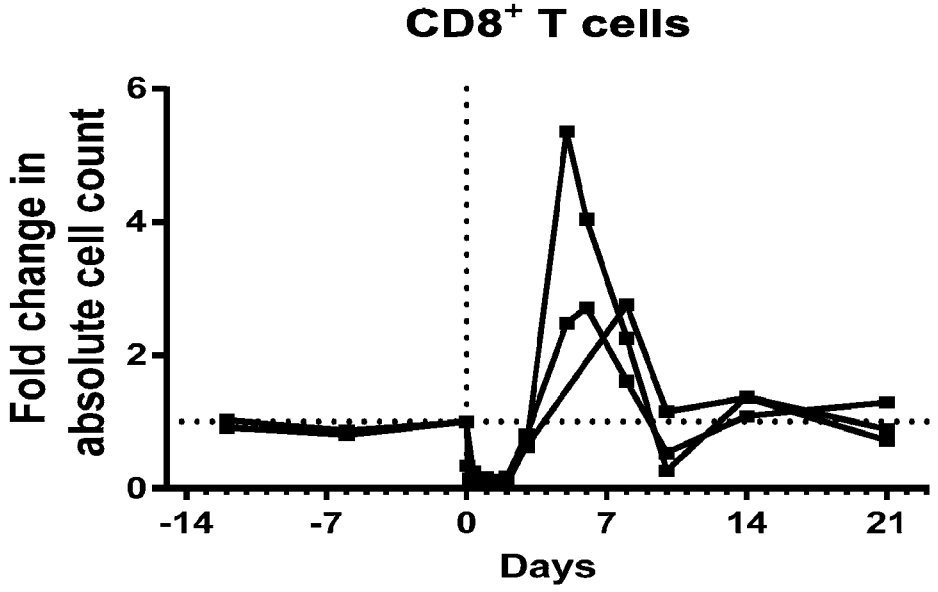


Figure 82E

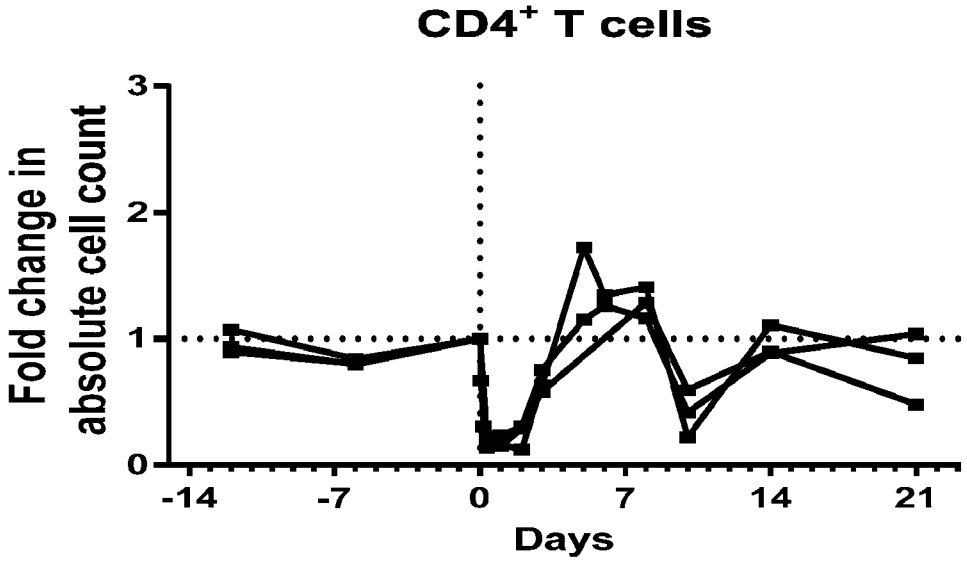

CD4+ T cells
Fold change in absolute cell count
3
2
1
0
-14
-7
0
7
14
21
Days

Figure 83A

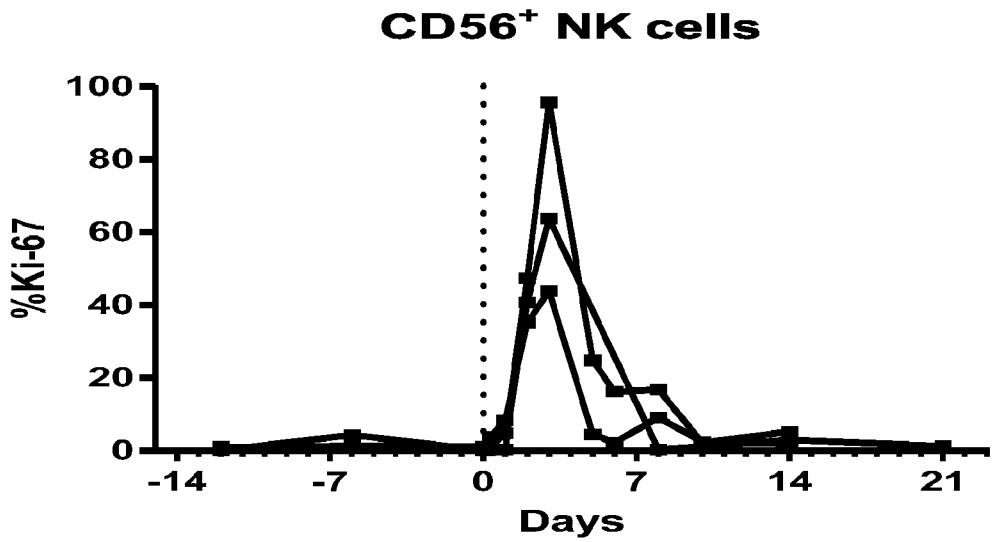


Figure 83B

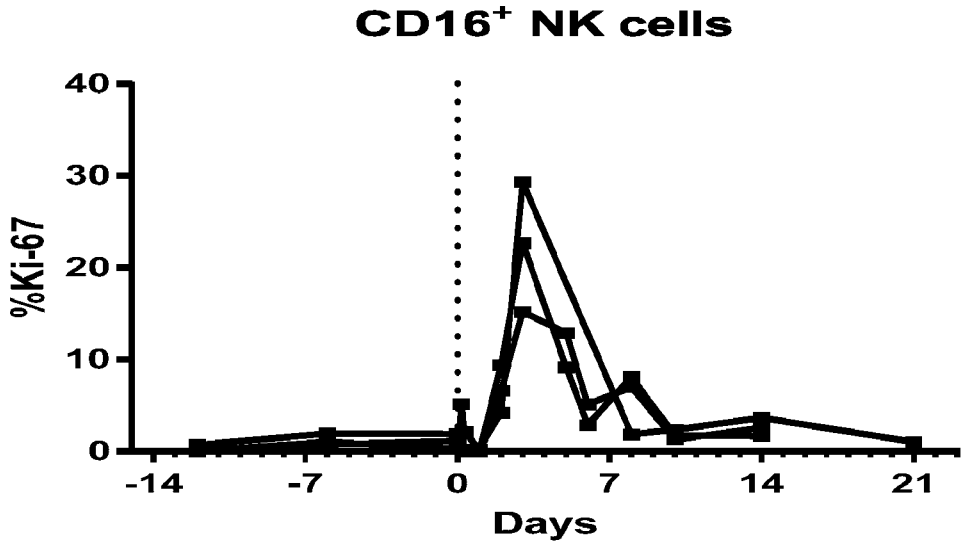


Figure 83C

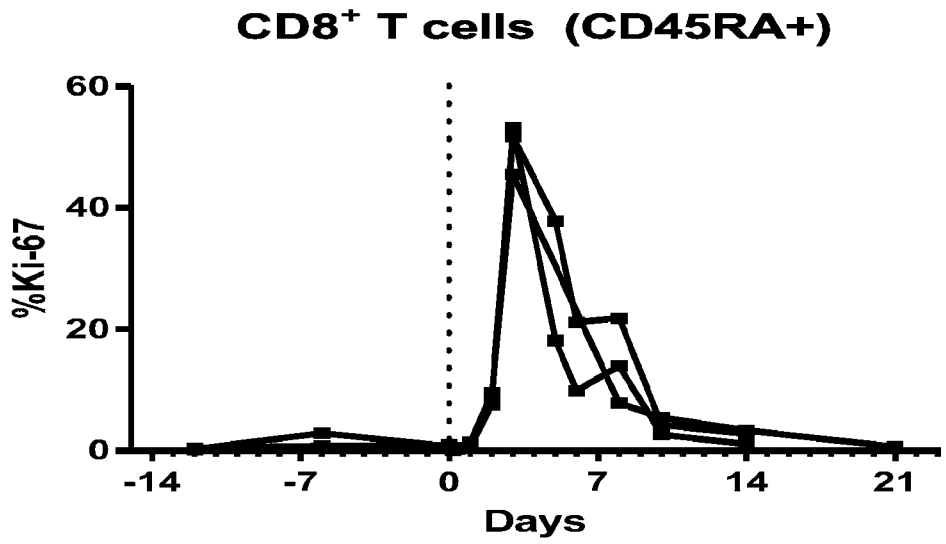


Figure 83D

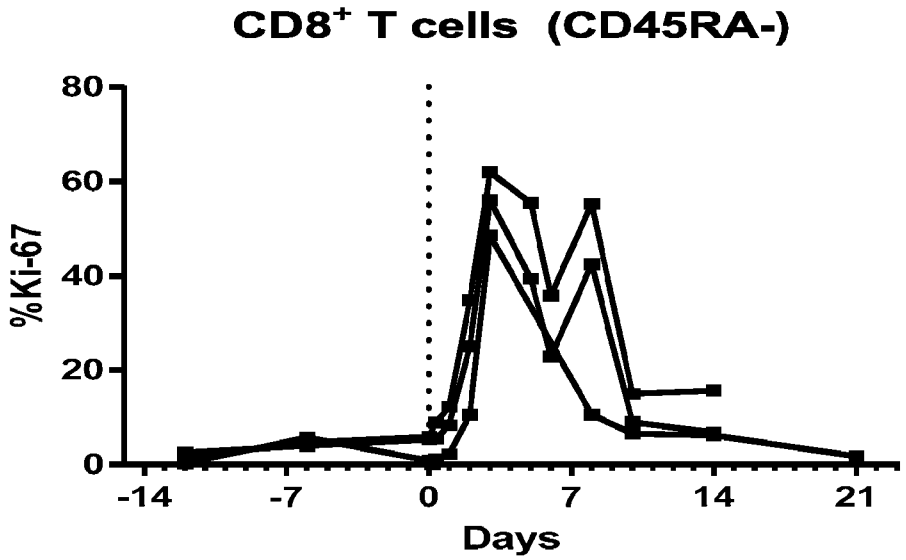


Figure 83E

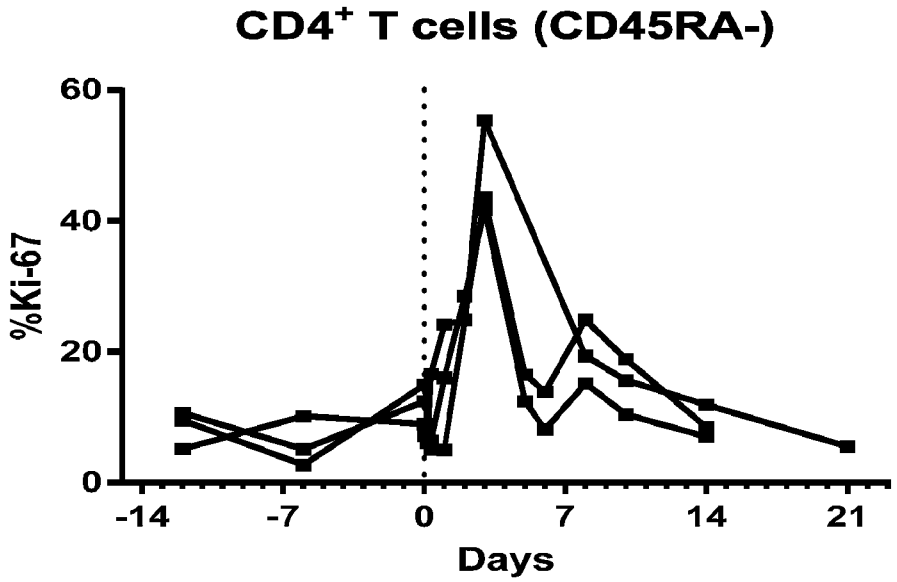


Figure 84A

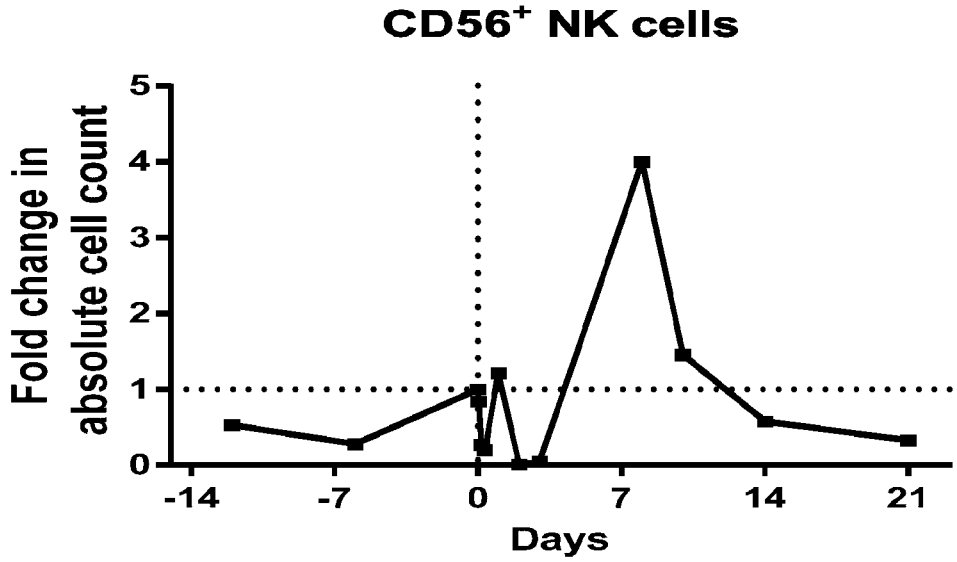


Figure 84B

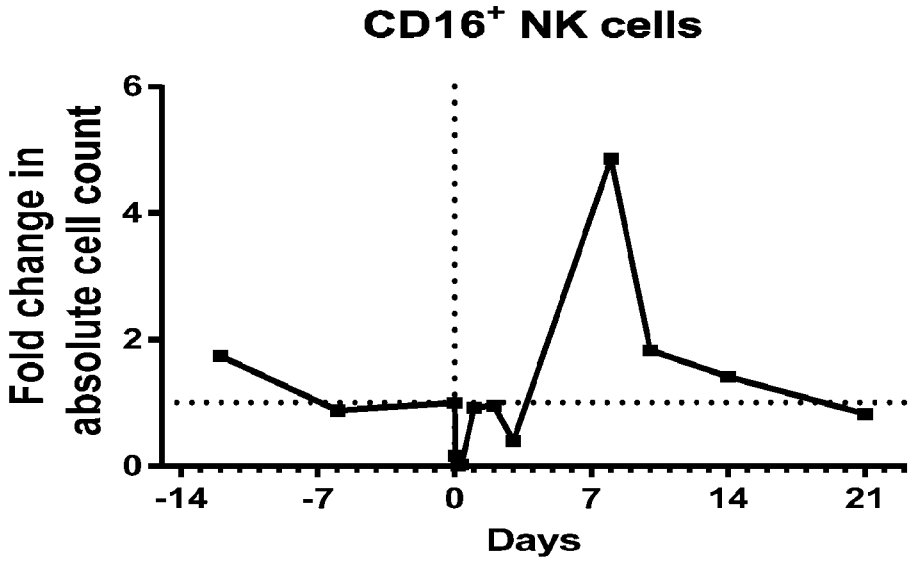


Figure 84C

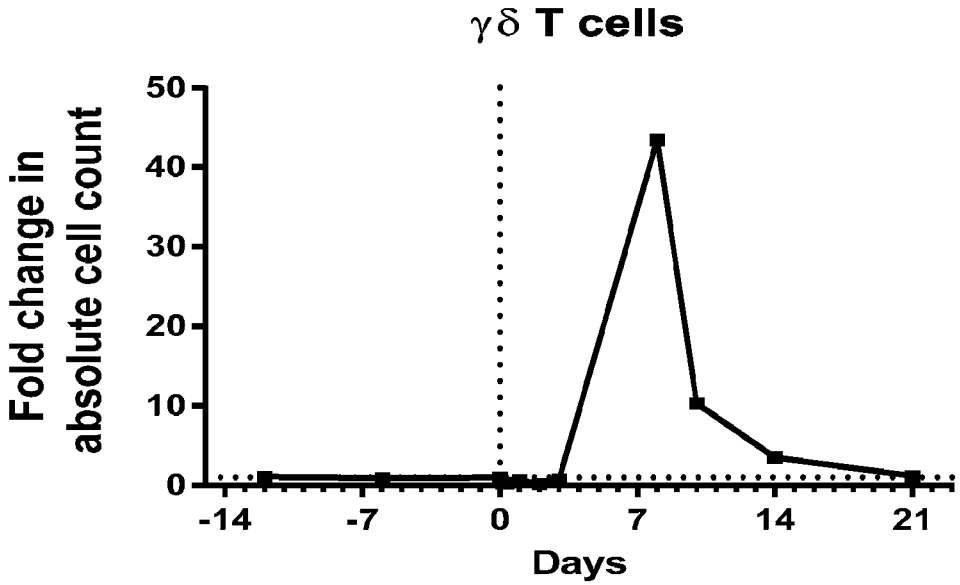


Figure 84D

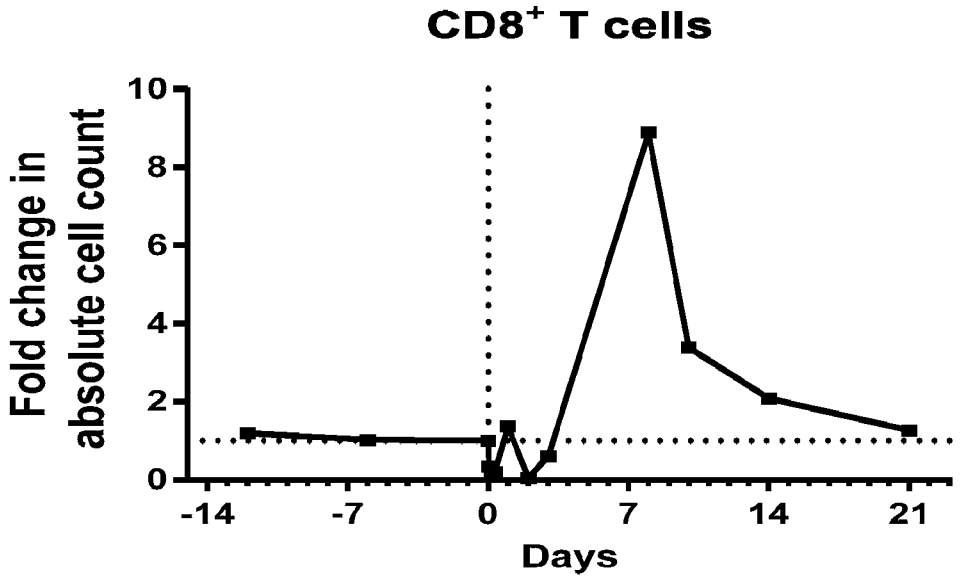


Figure 84E

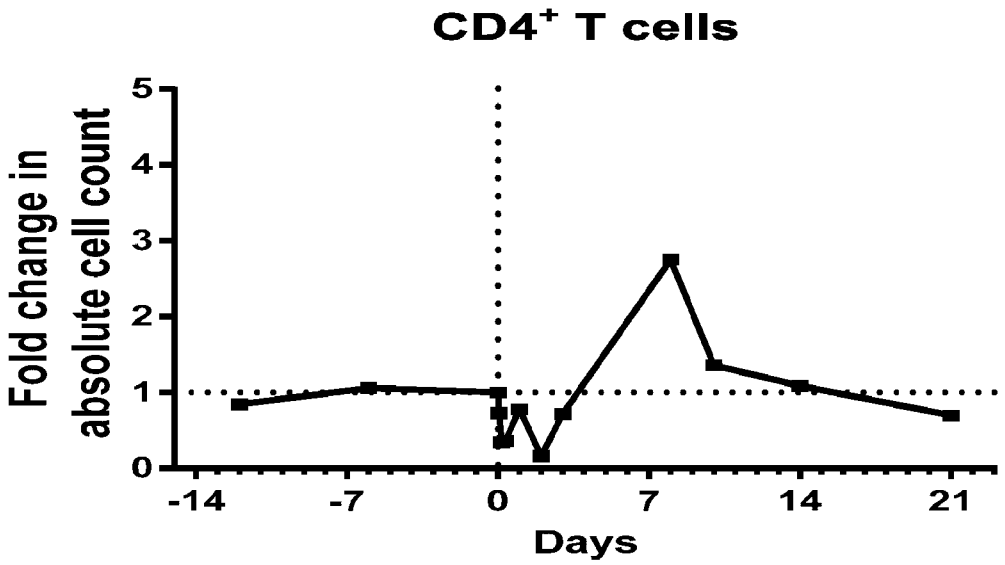

CD4+ T cells
Fold change in absolute cell count
5
4
3
2
1
0
-14
-7
0
7
14
21
Days

Figure 85A

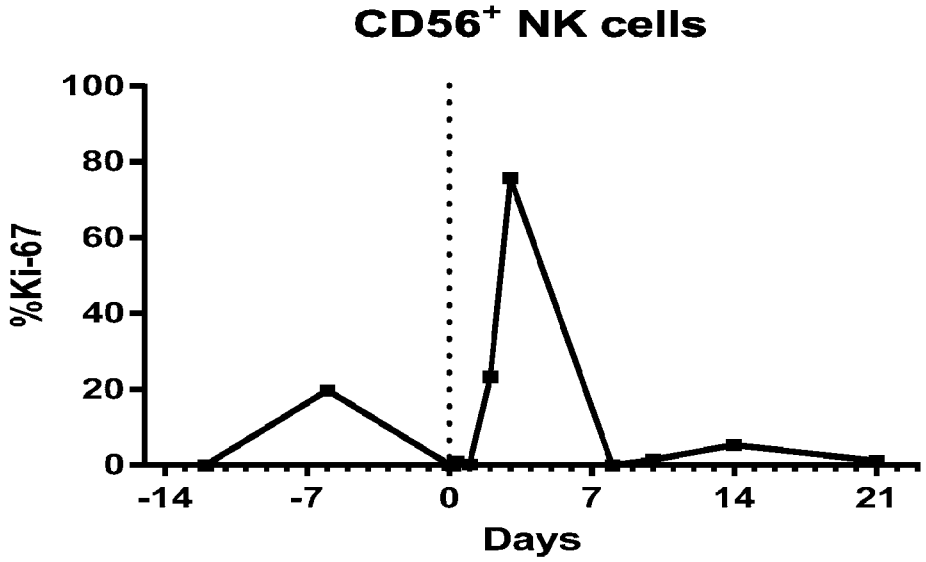


Figure 85B

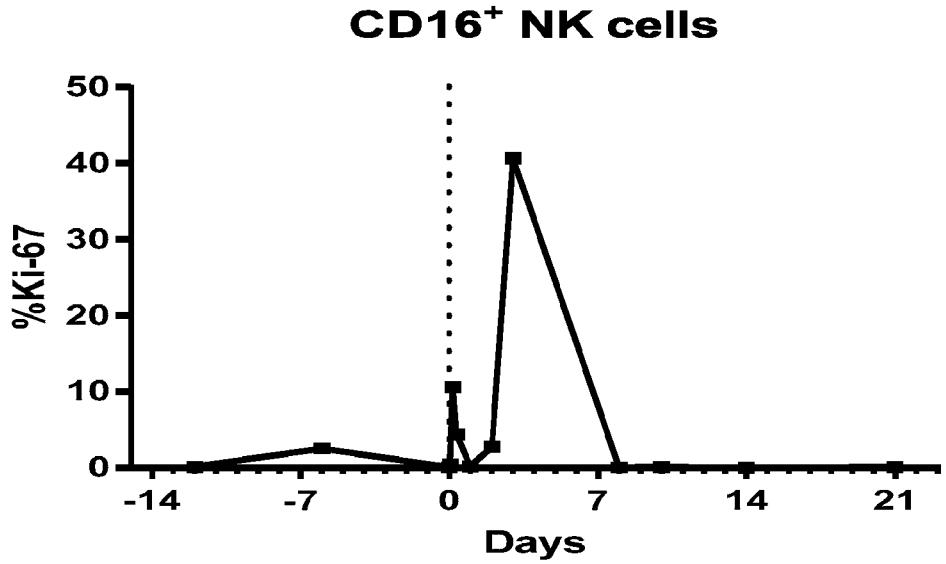


Figure 85C

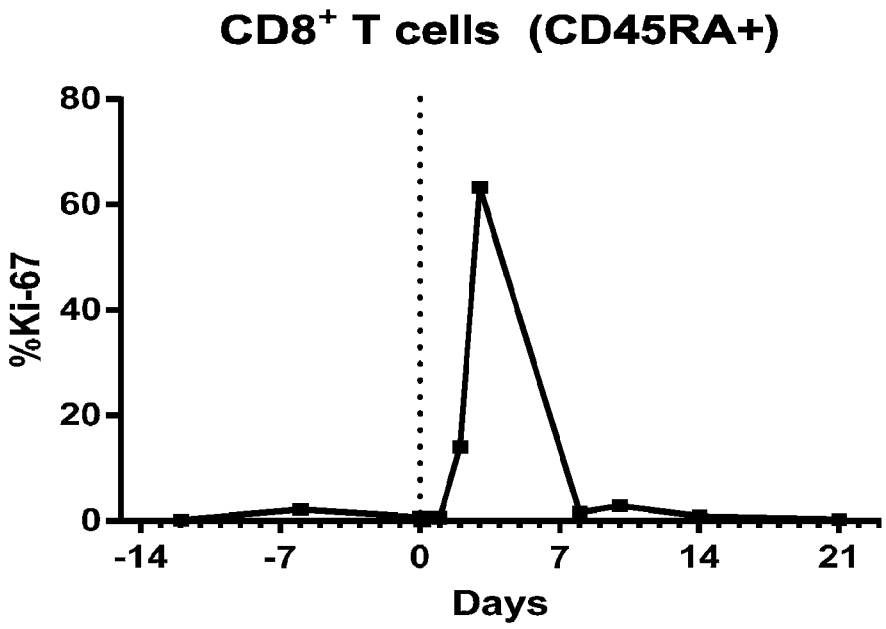


Figure 85D

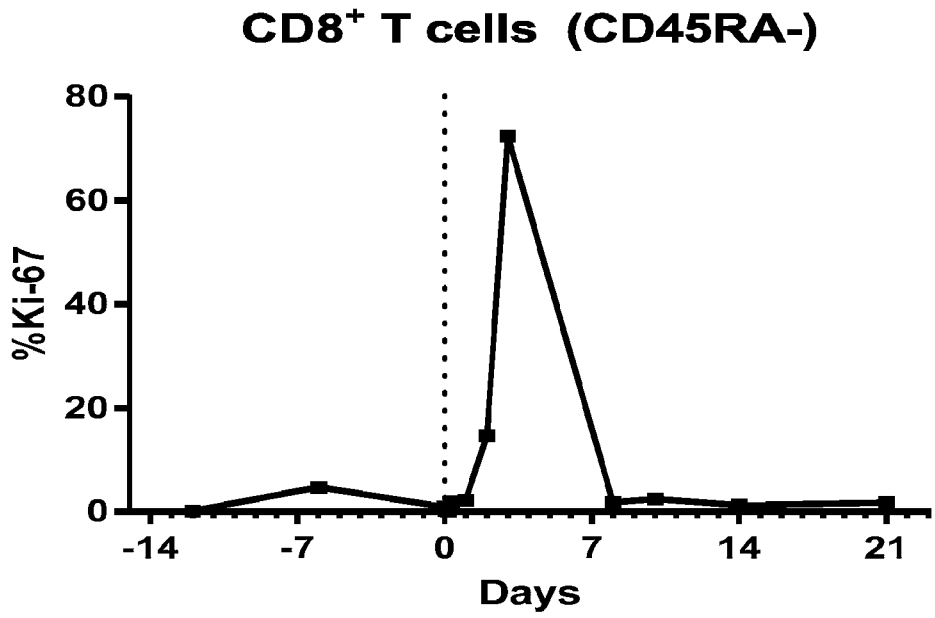


Figure 85E

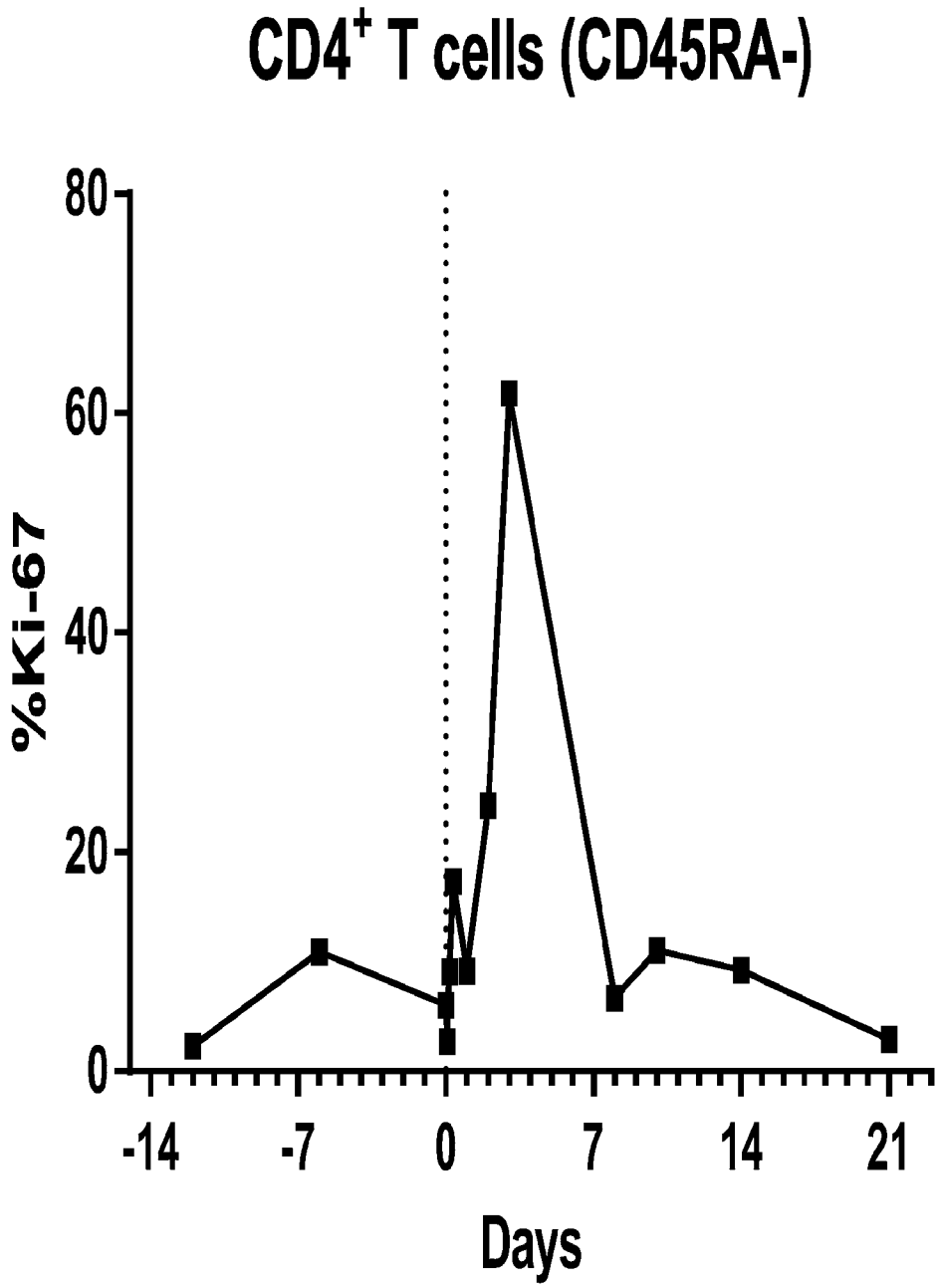


Figure 86A

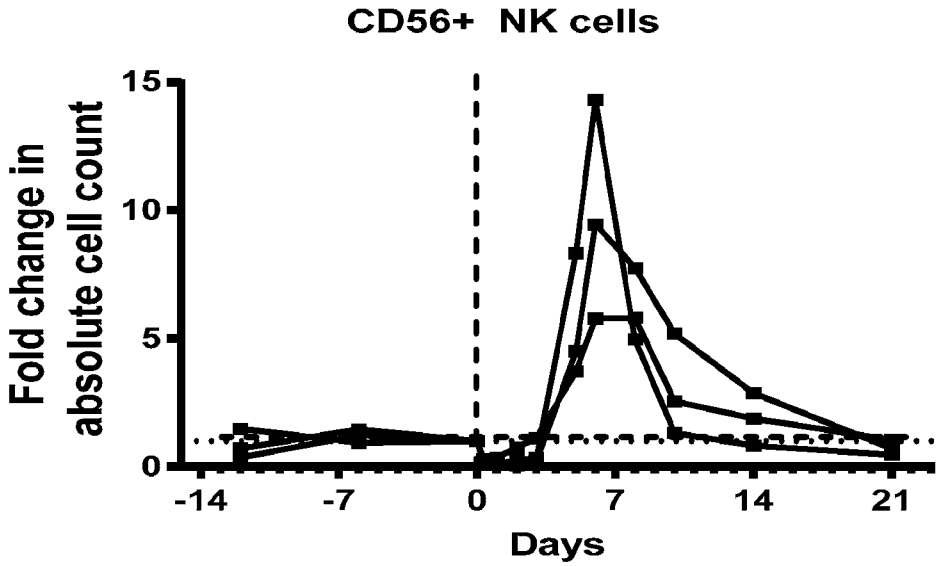


Figure 86B

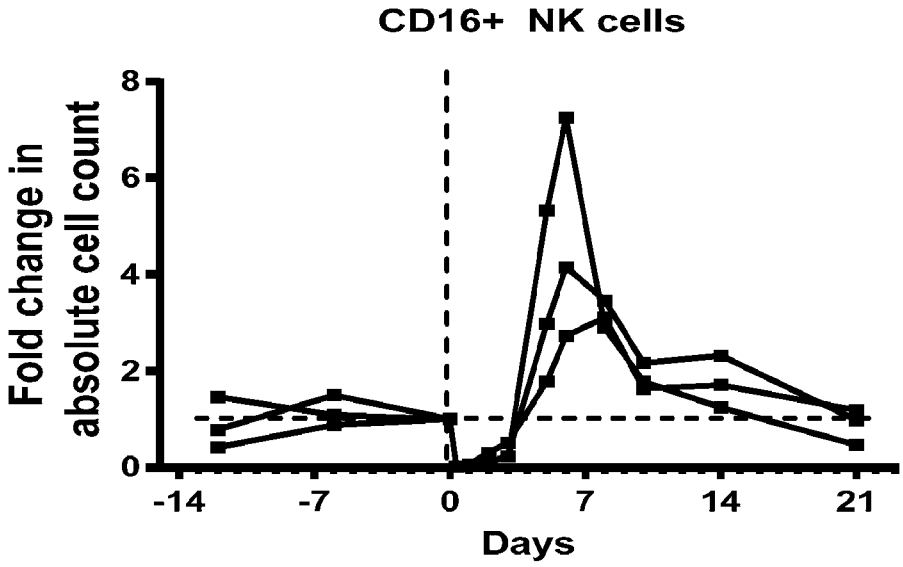


Figure 86C

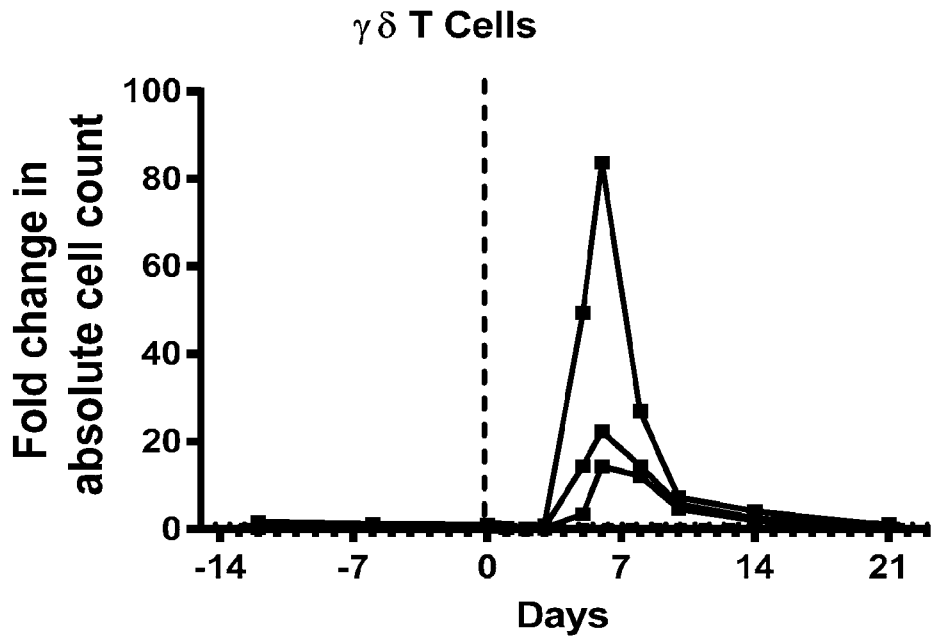


Figure 86D

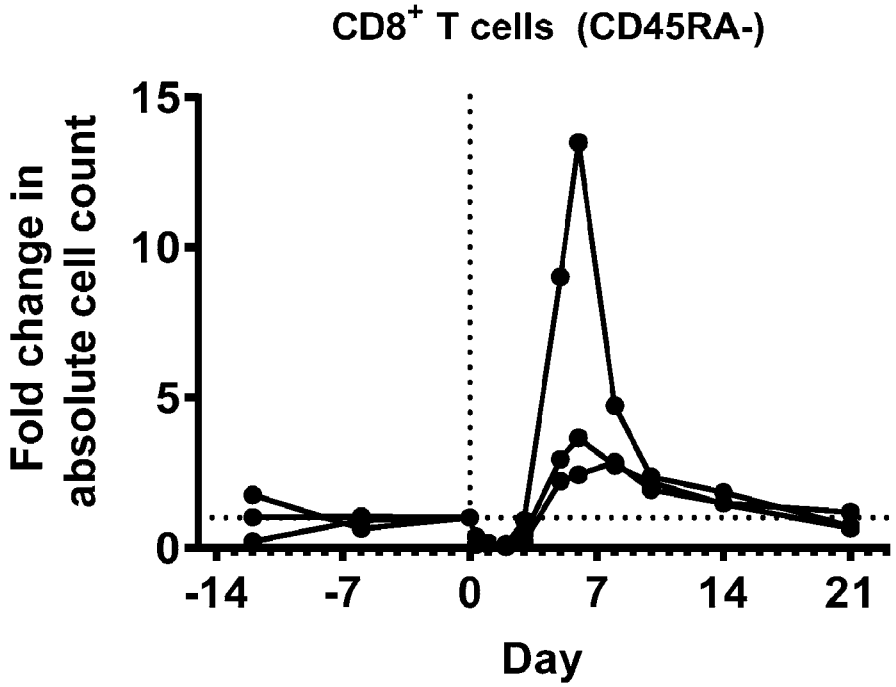


Figure 86E

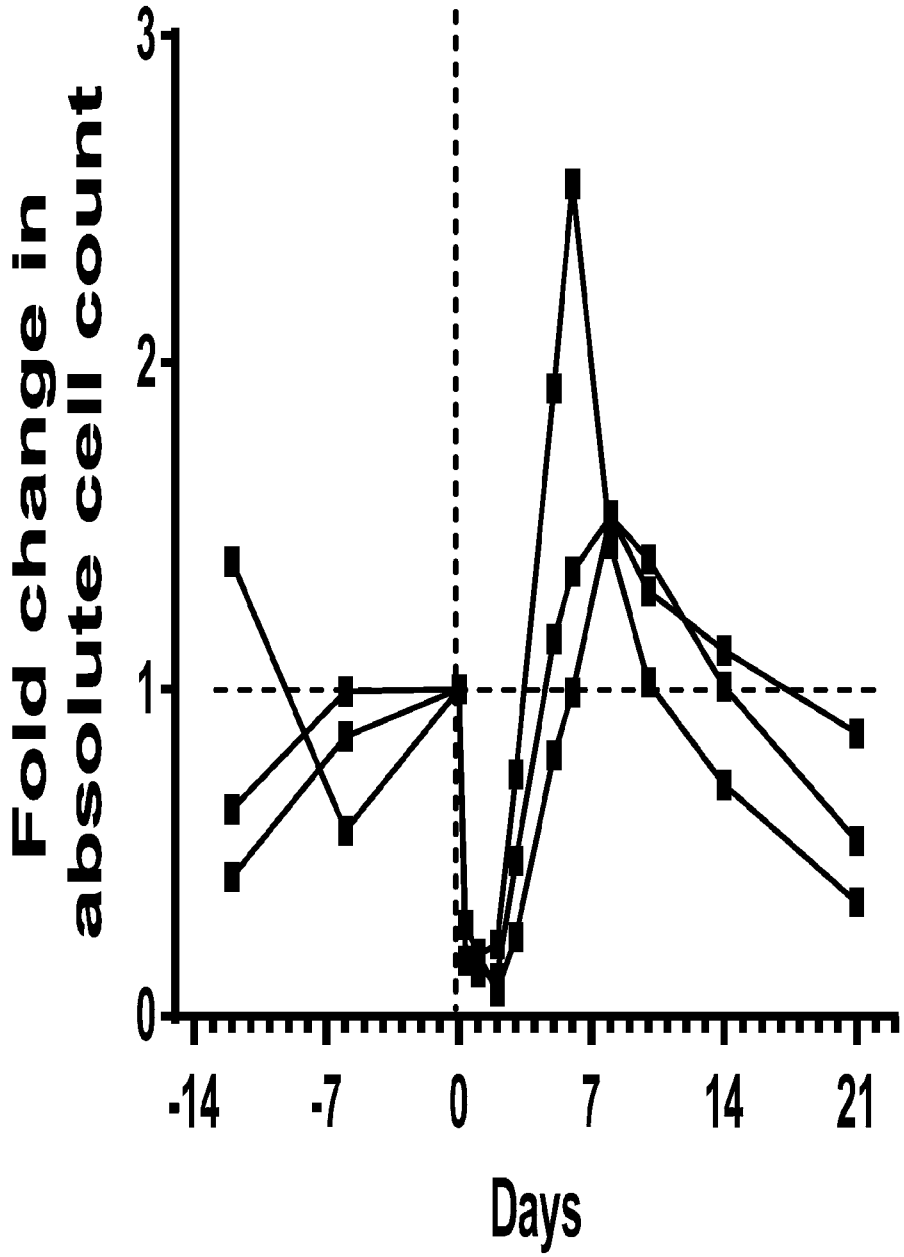


Figure 87A

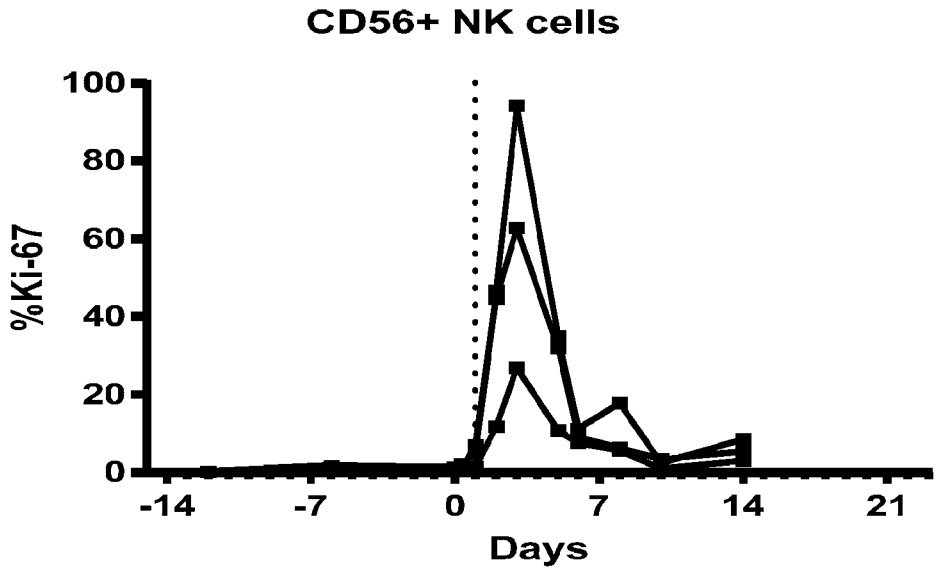


Figure 87B

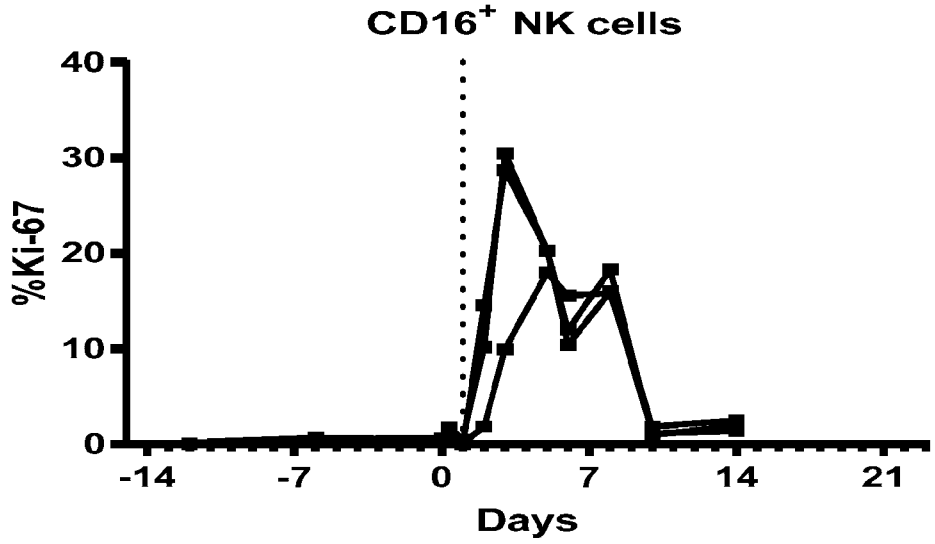


Figure 87C

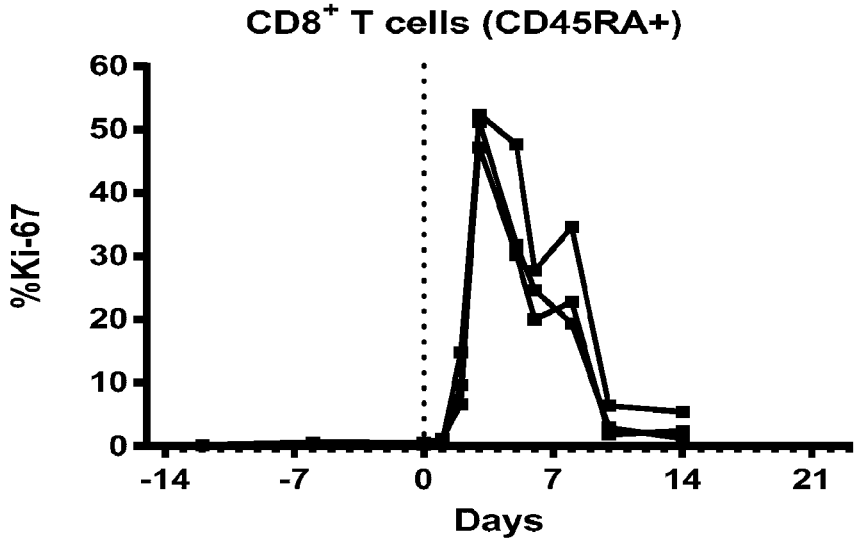


Figure 87D

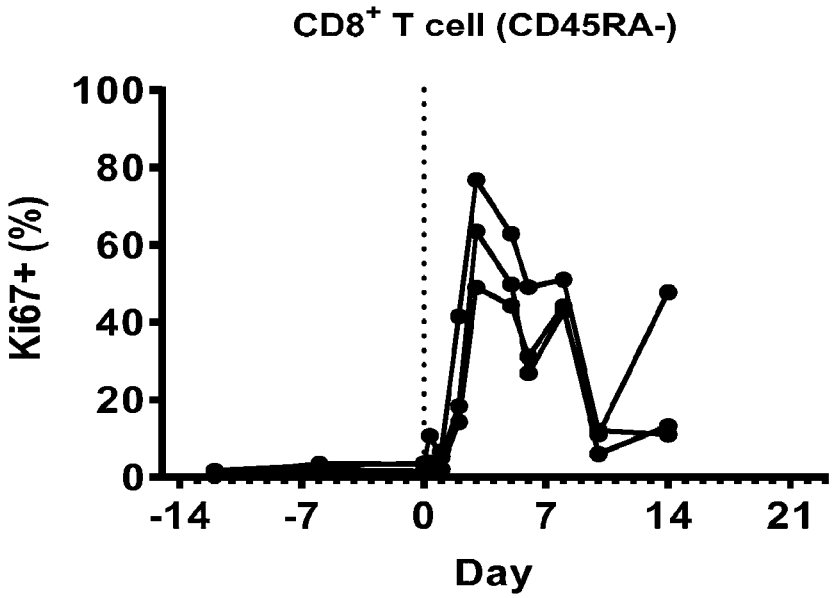


Figure 87E

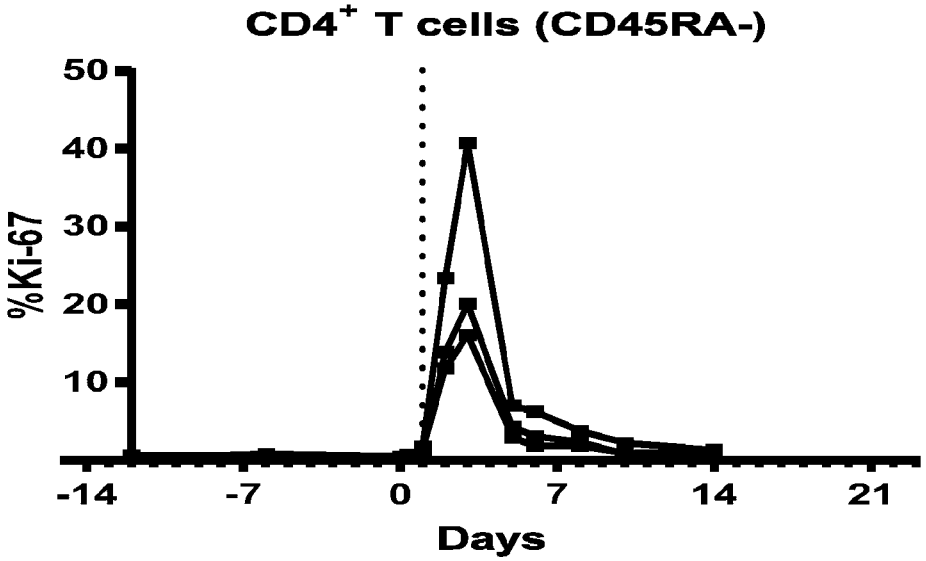


Figure 88A

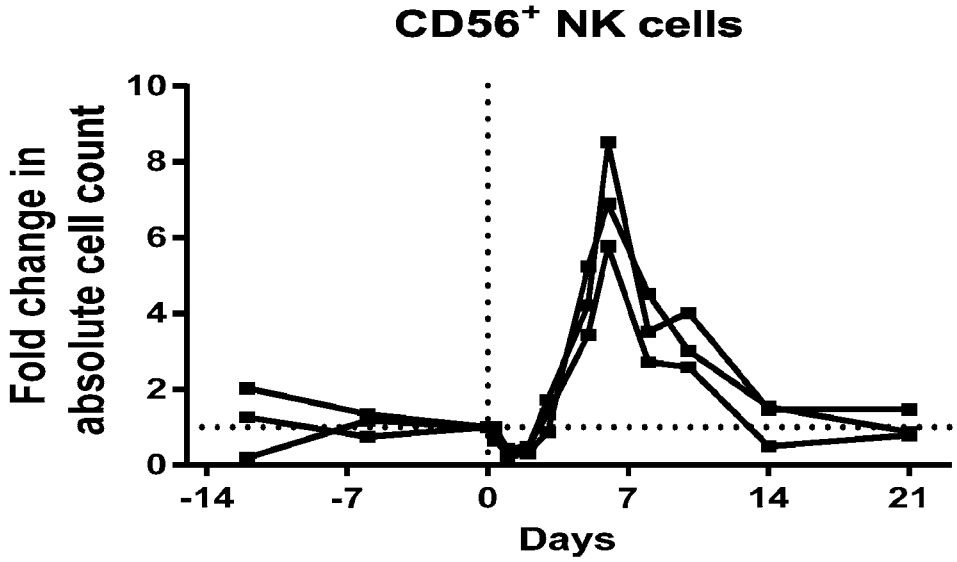


Figure 88B

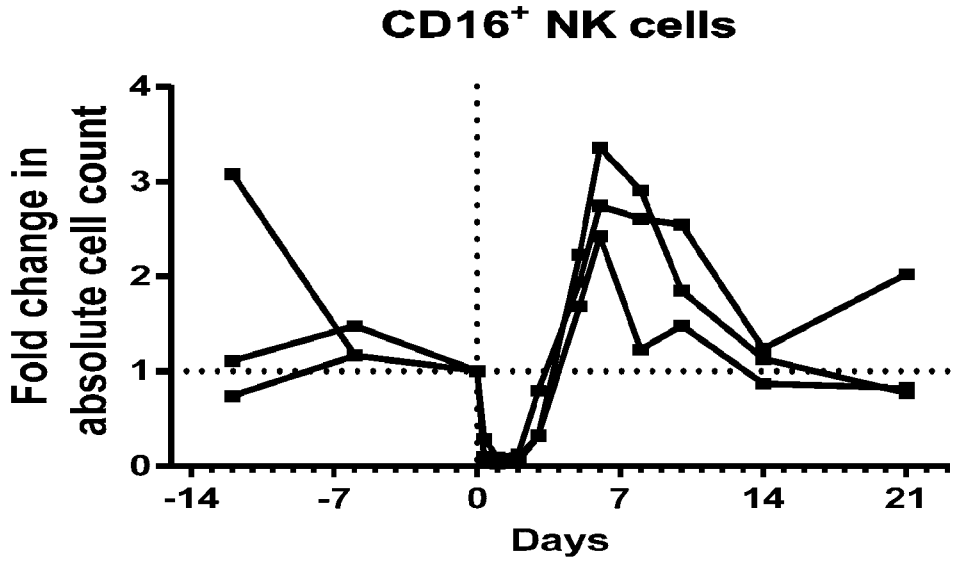


Figure 88C

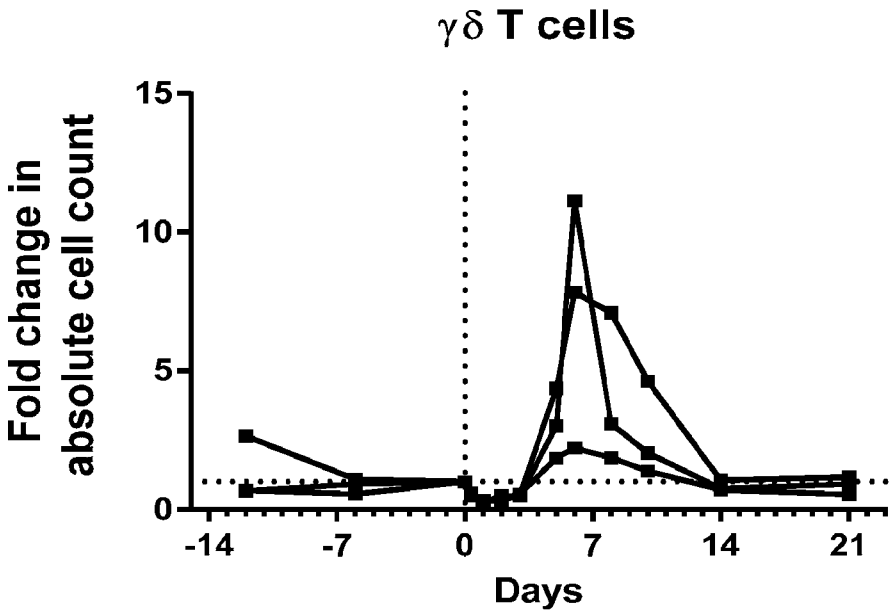


Figure 88D

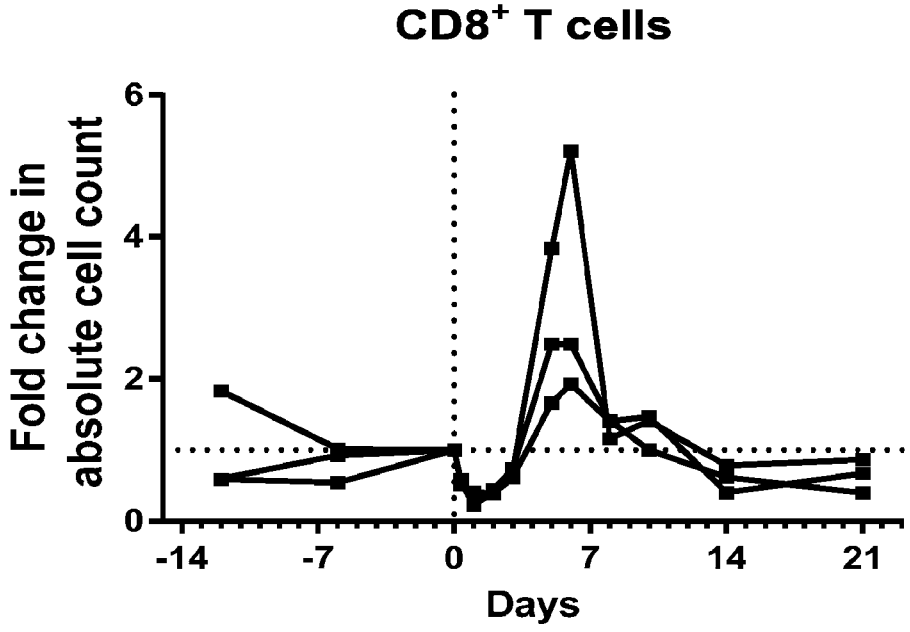


Figure 88E

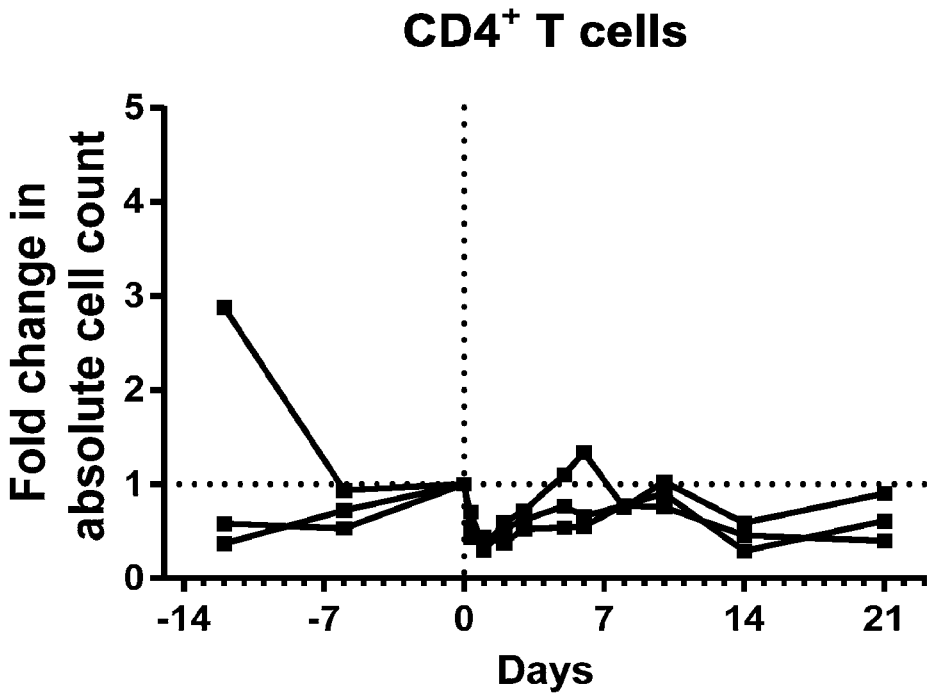

CD4+ T cells
Fold change in absolute cell count
5
4
3
2
1
0
-14
-7
0
7
14
21
Days

Figure 89A

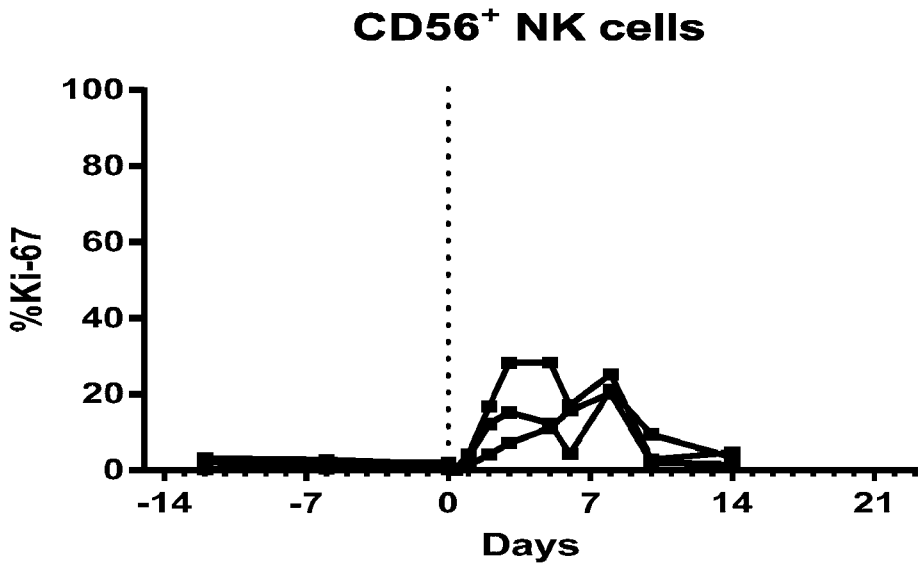


Figure 89B

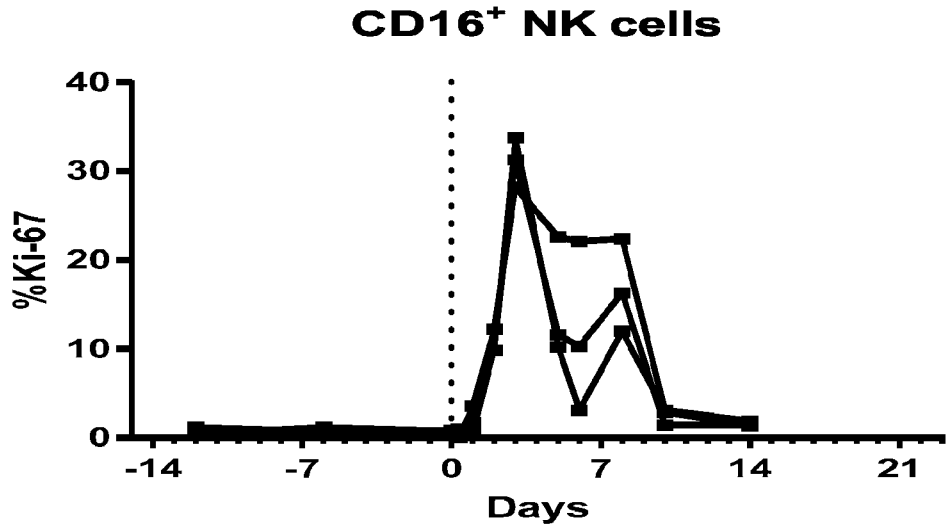


Figure 89C

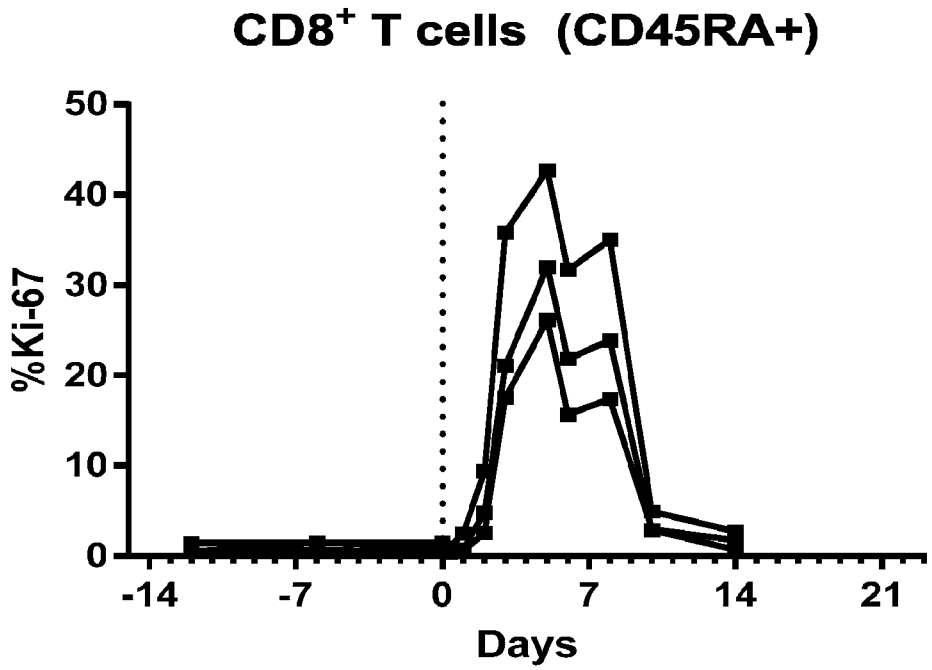


Figure 89D

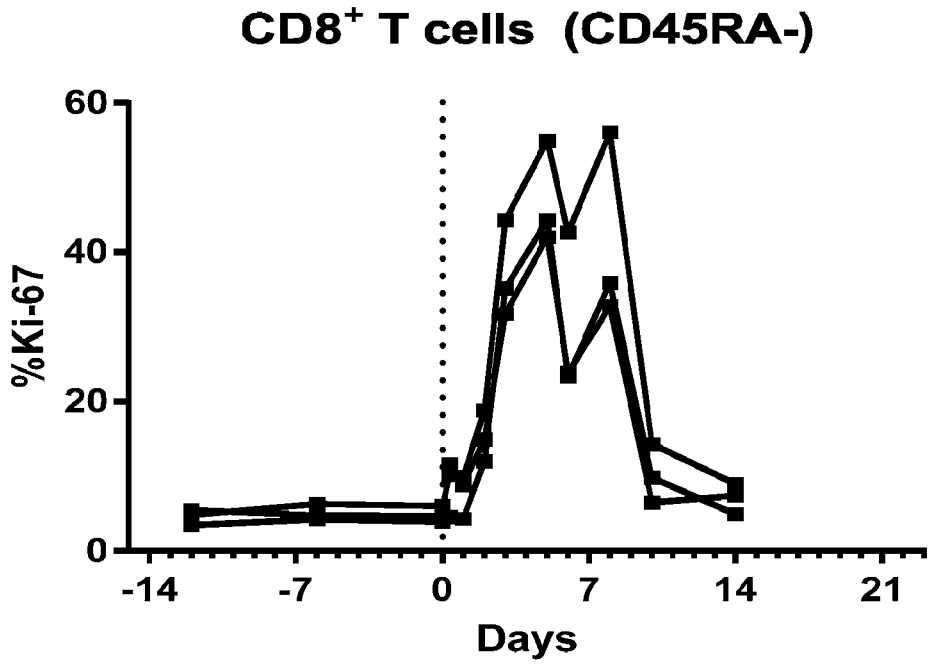


Figure 89E

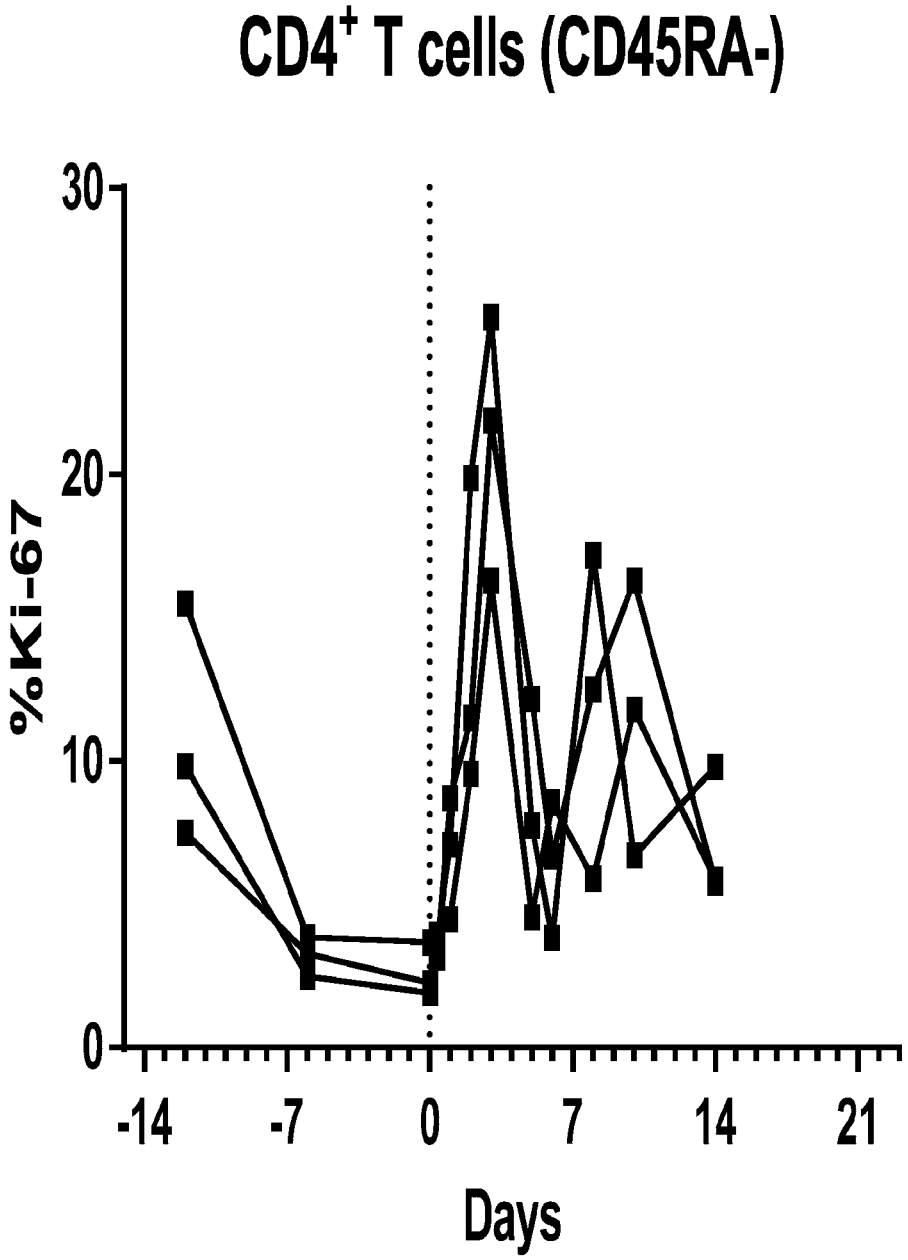


Figure 90A

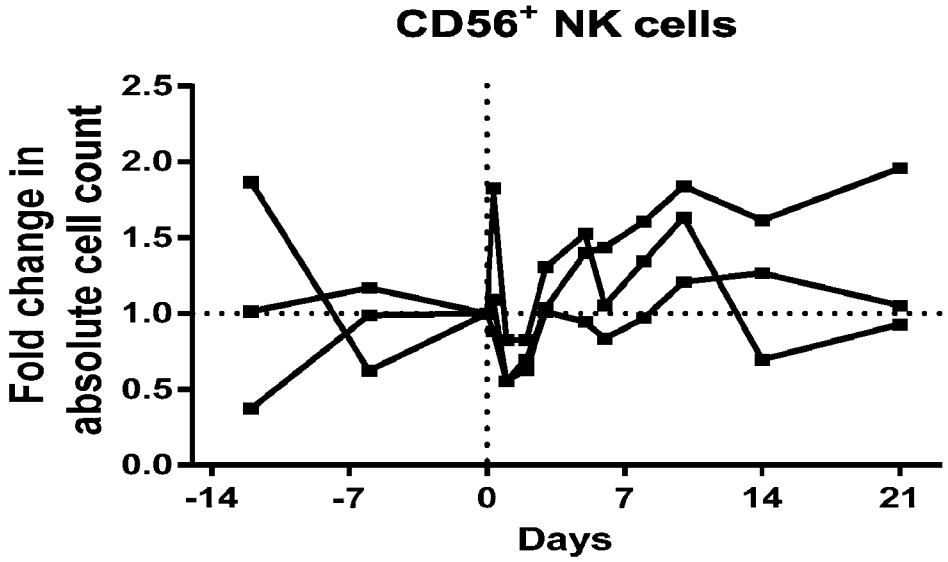


Figure 90B

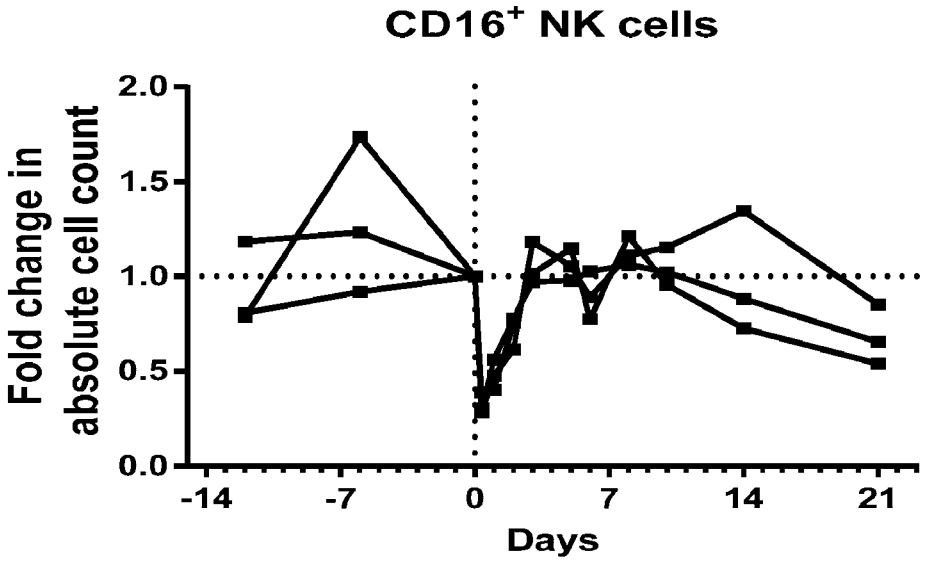


Figure 90C

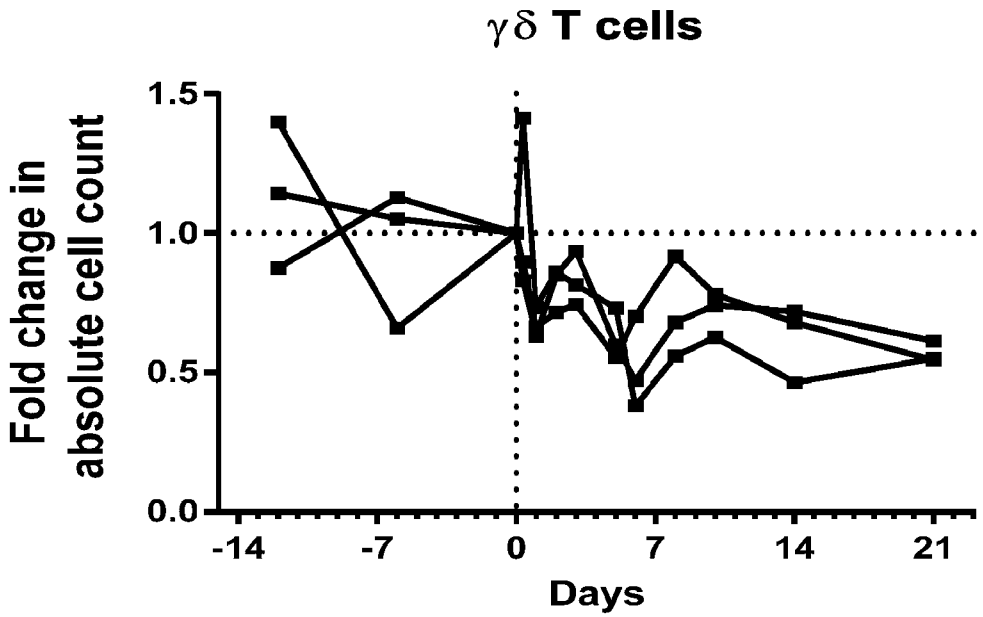


Figure 90D

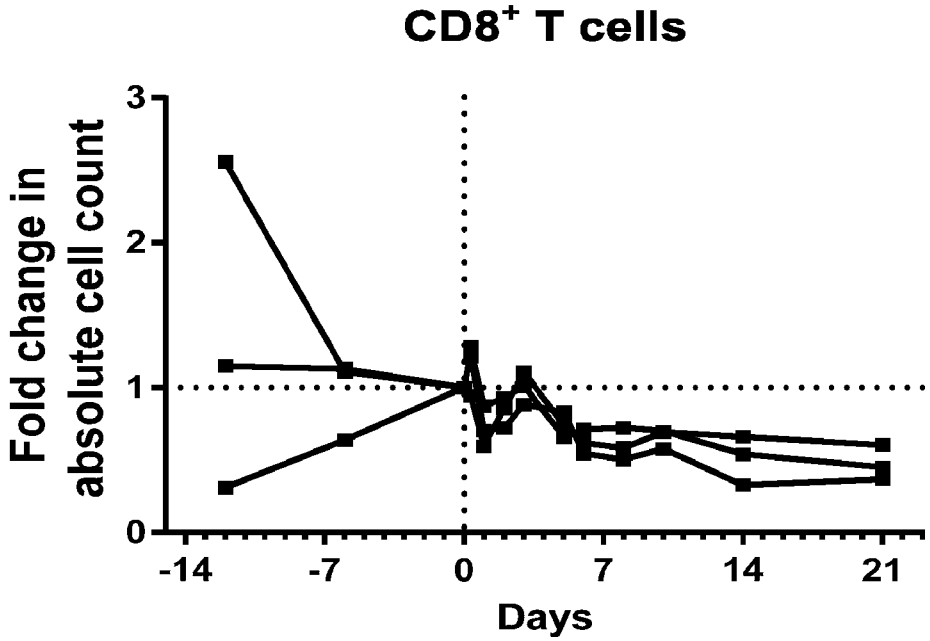
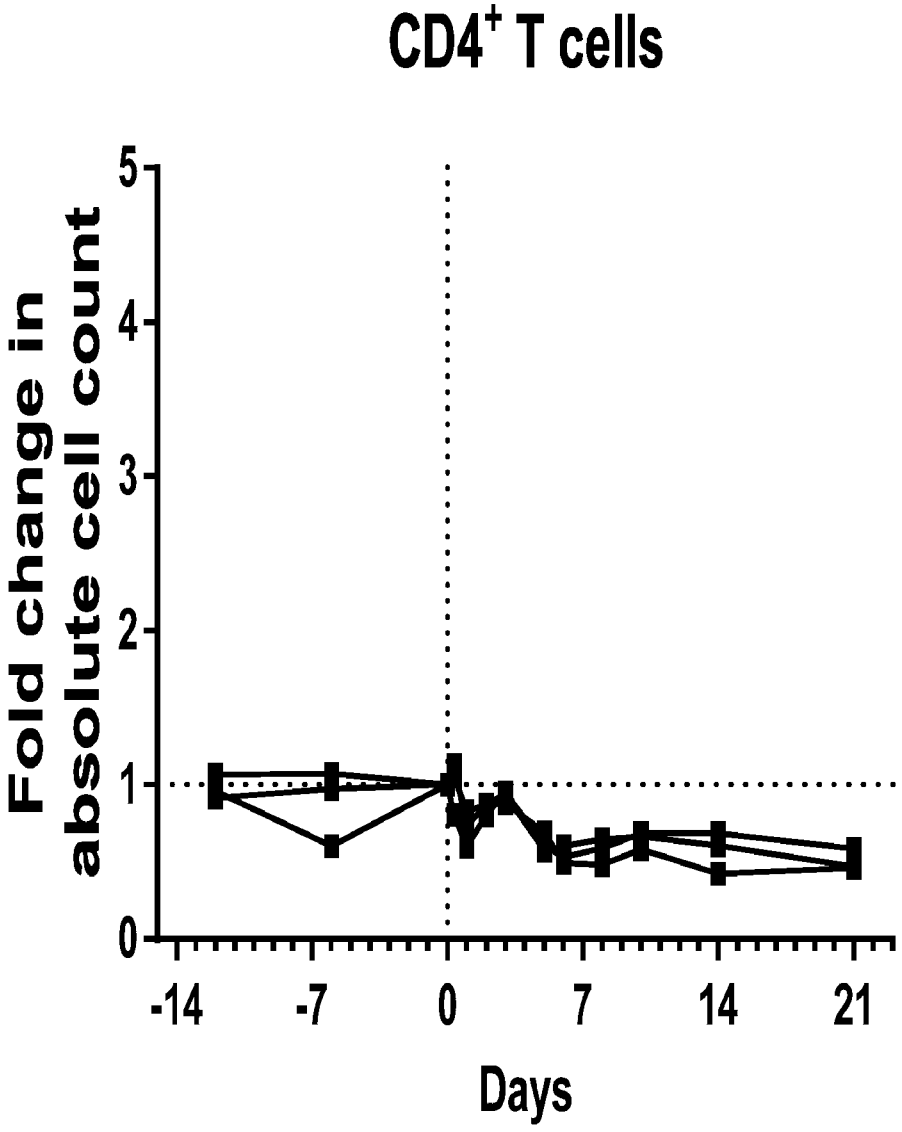


Figure 90E


CD4+ T cells
Fold change in absolute cell count
5
4
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-14
-7
0
7
14
21
Days

Figure 91A

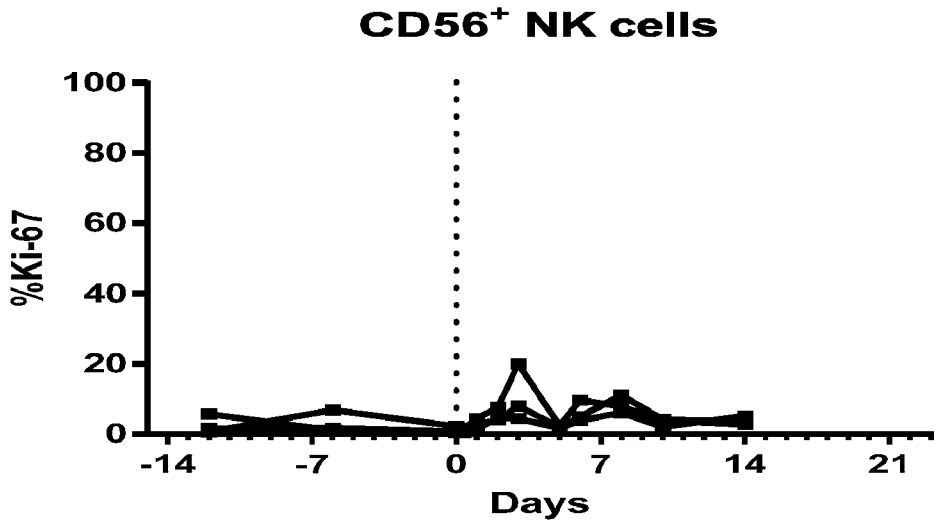

Figure 91B

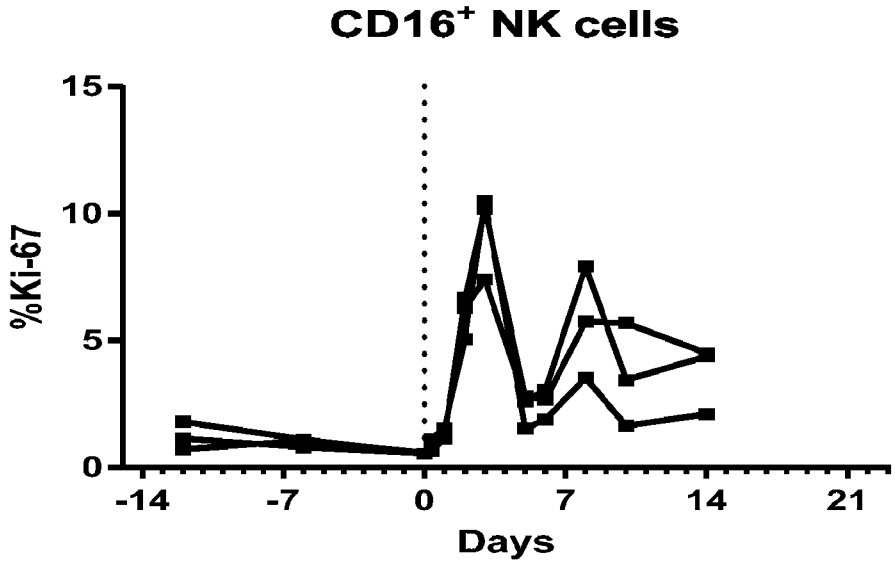

Figure 91C

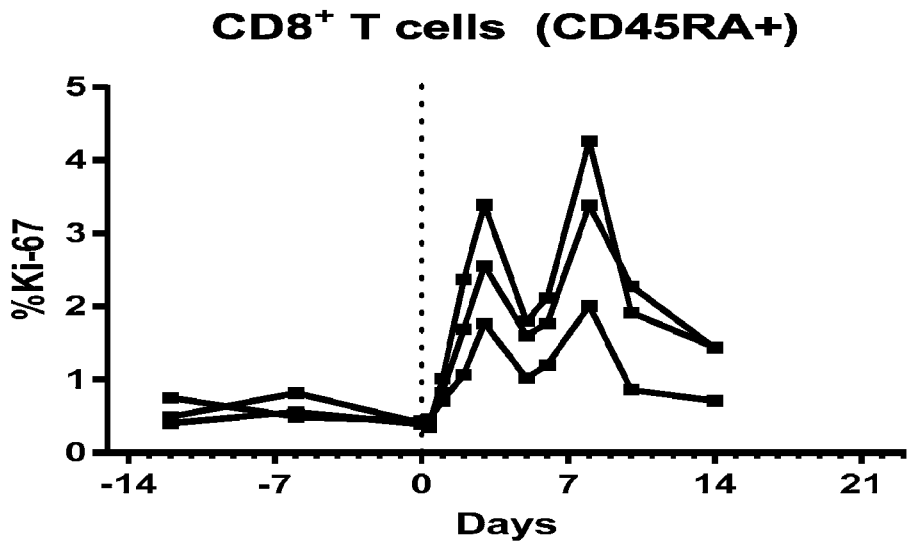

Figure 91D

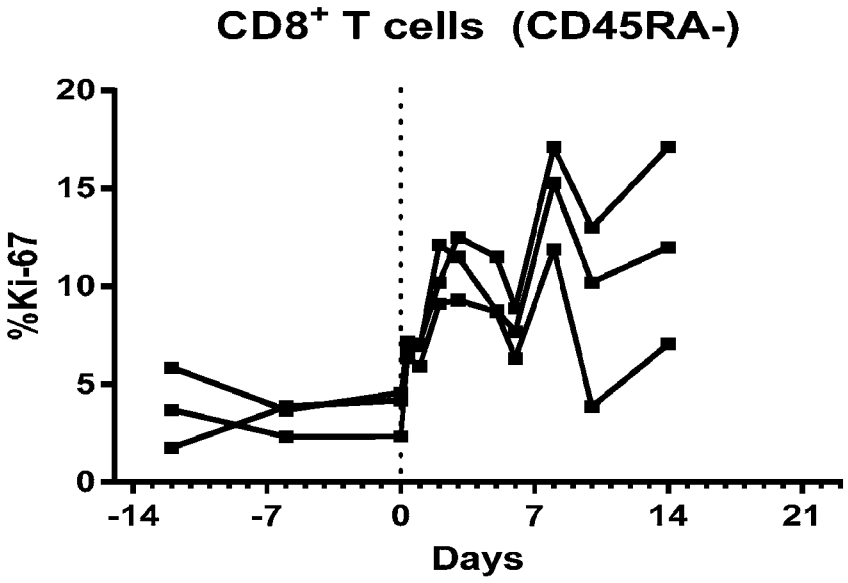

Figure 91E

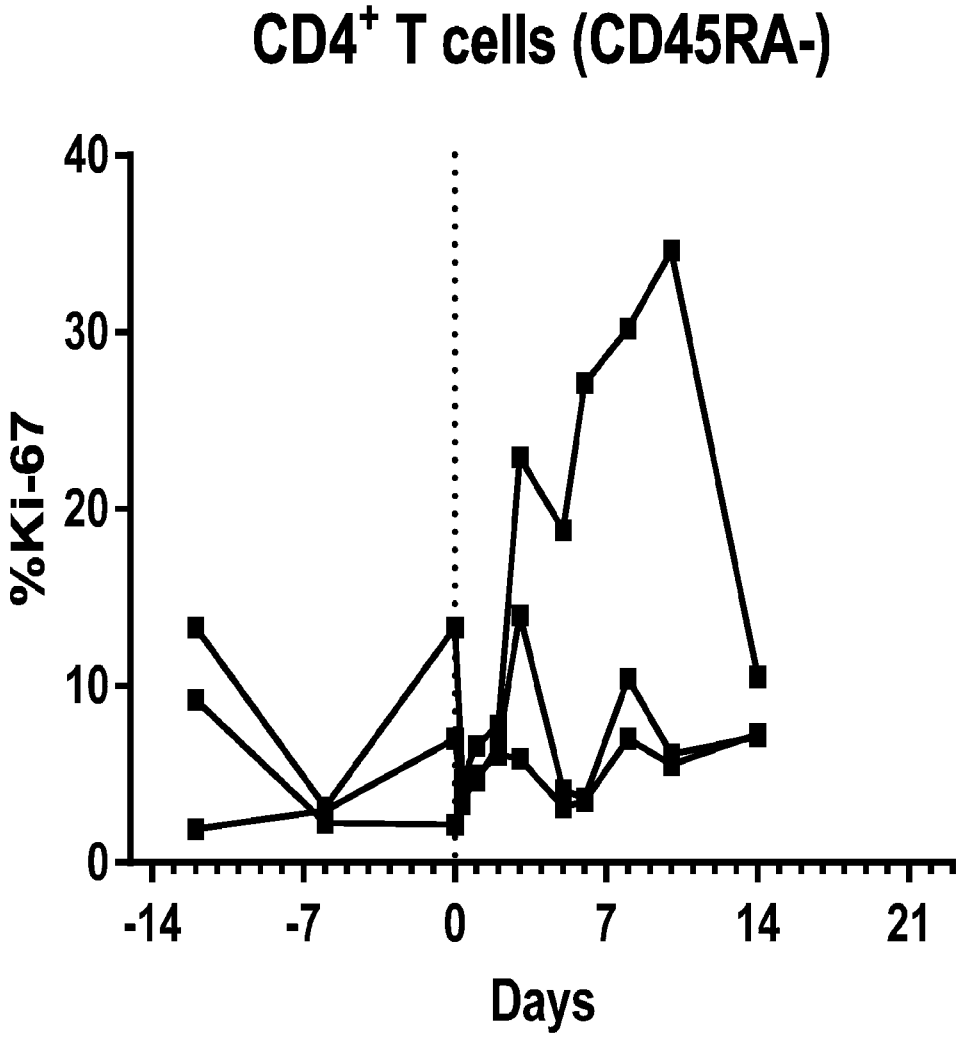

Figure 92A

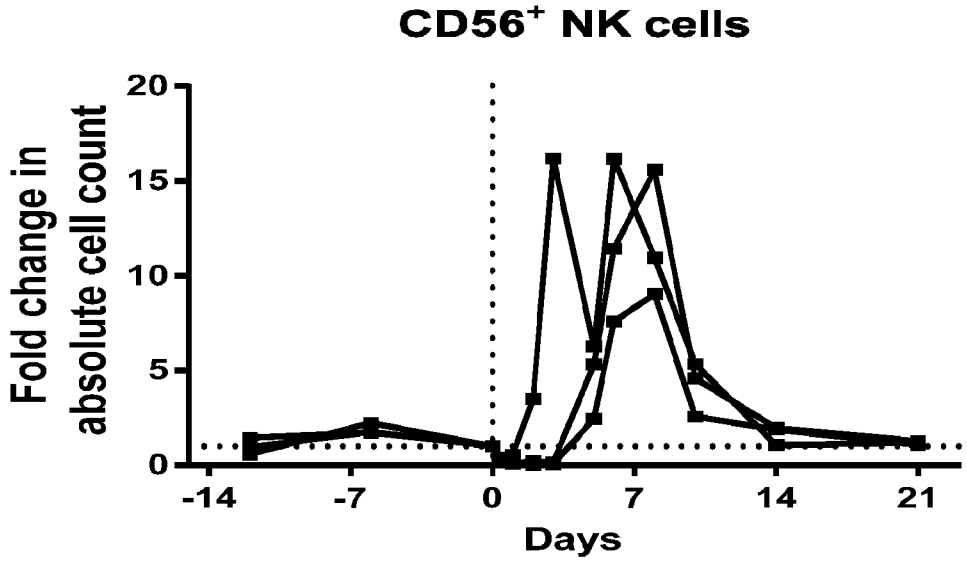

Figure 92B

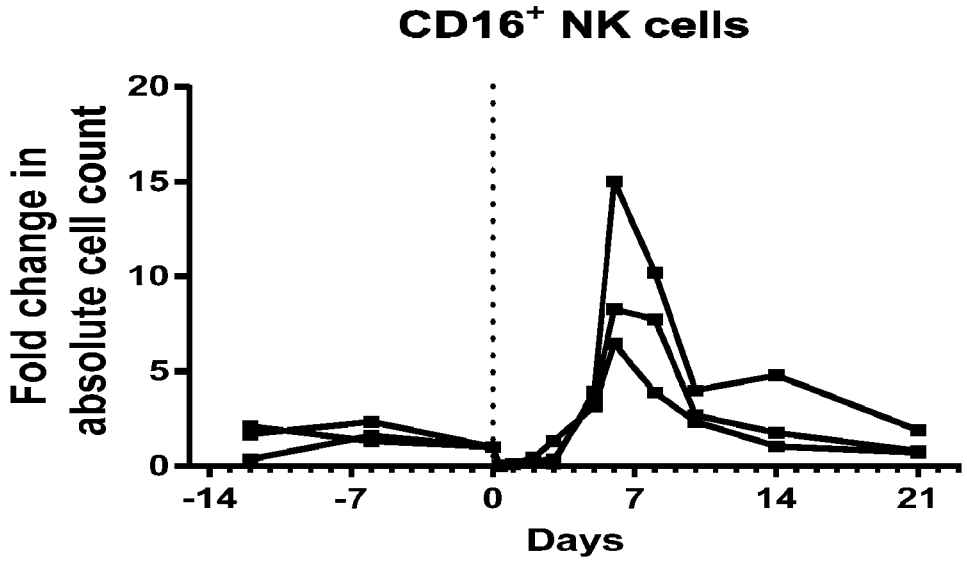

Figure 92C

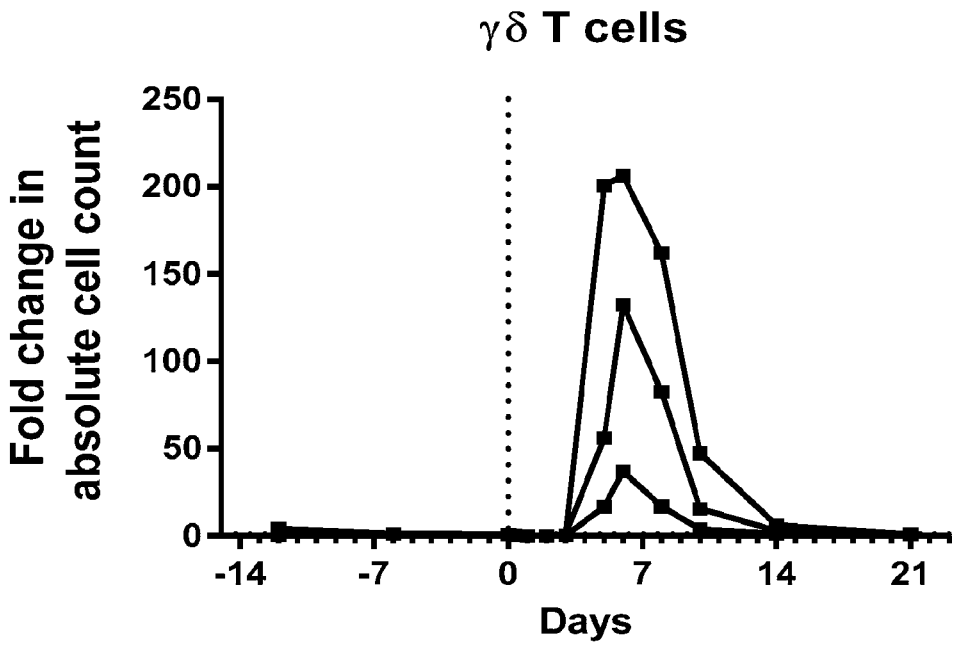

Figure 92D

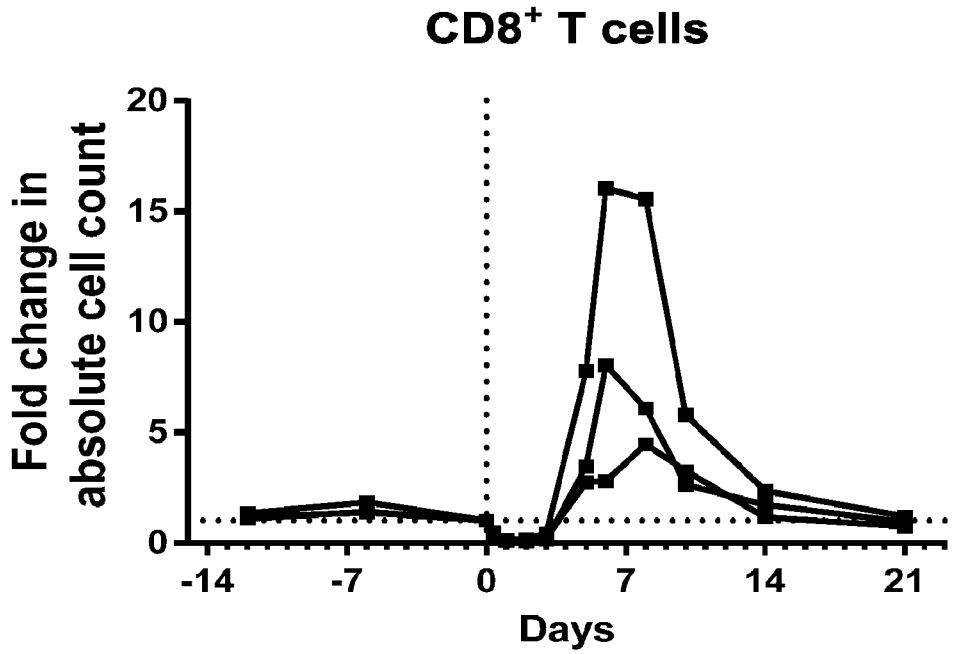

Figure 92E

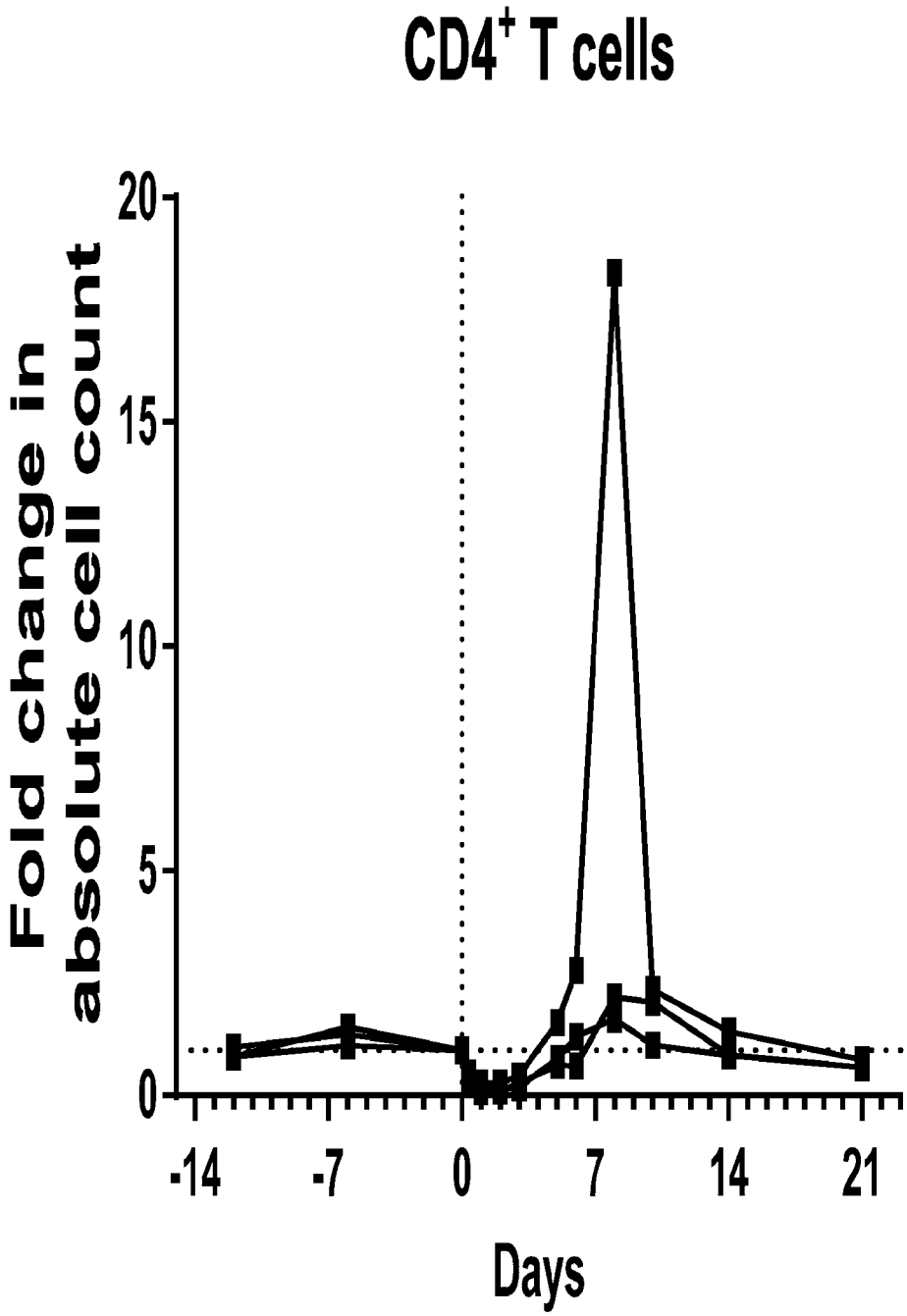
CD4+ T cells
Fold change in absolute cell count
20
15
10
5
0
-14
-7
0
7
14
21
Days

Figure 93A

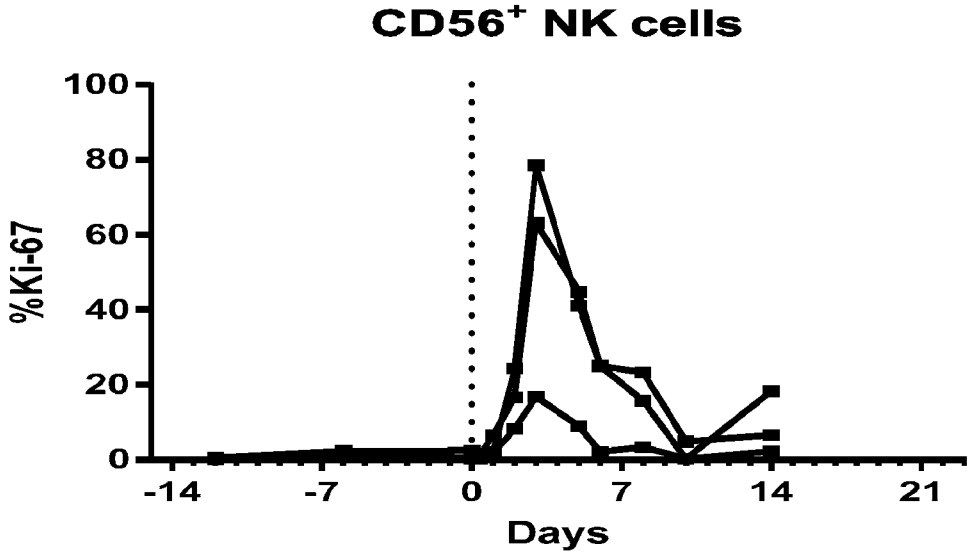

Figure 93B

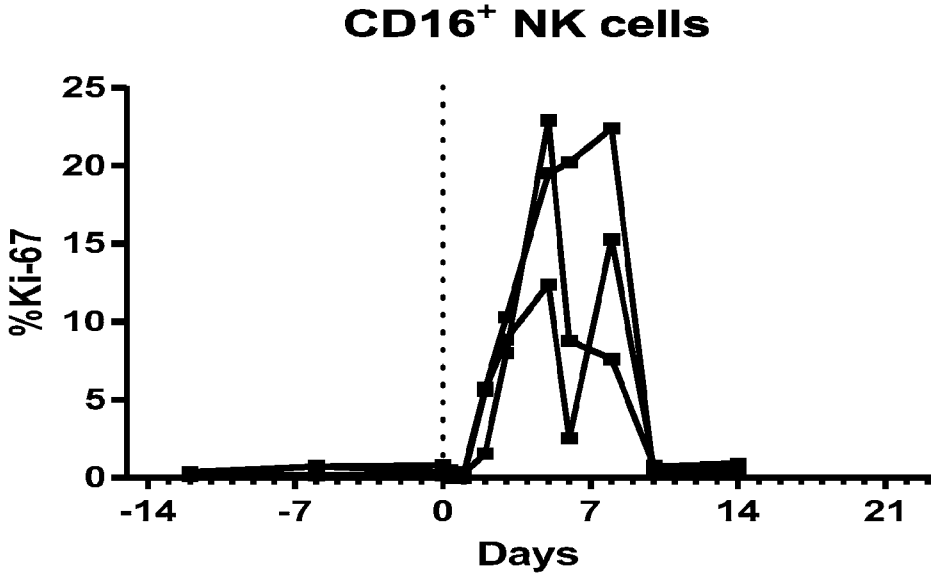

Figure 93C

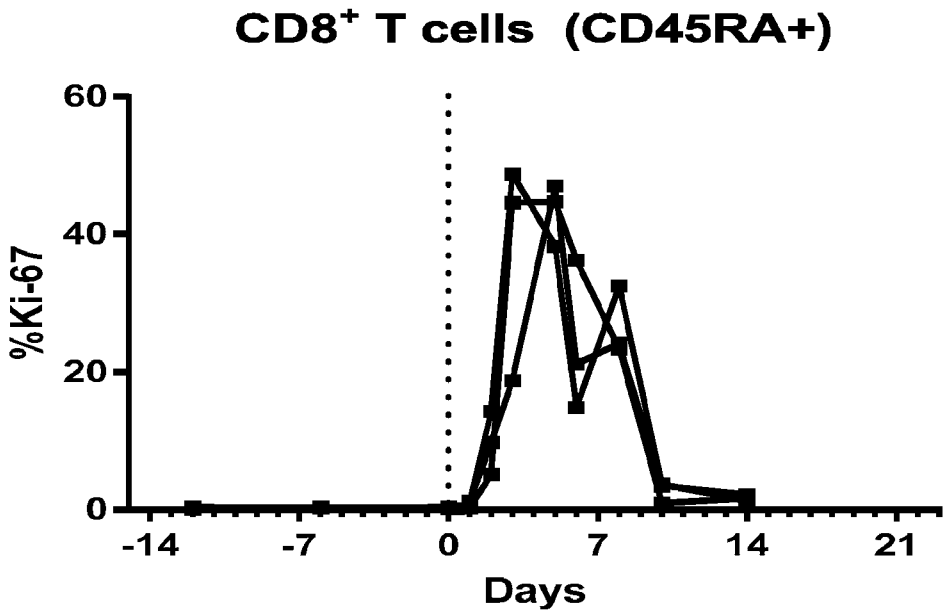

Figure 93D

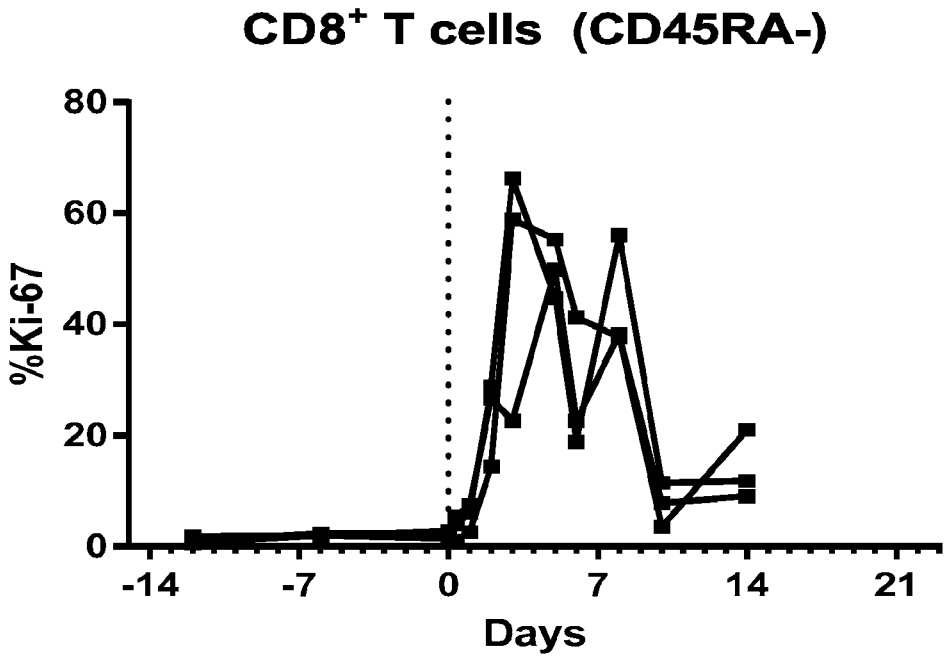

Figure 93E

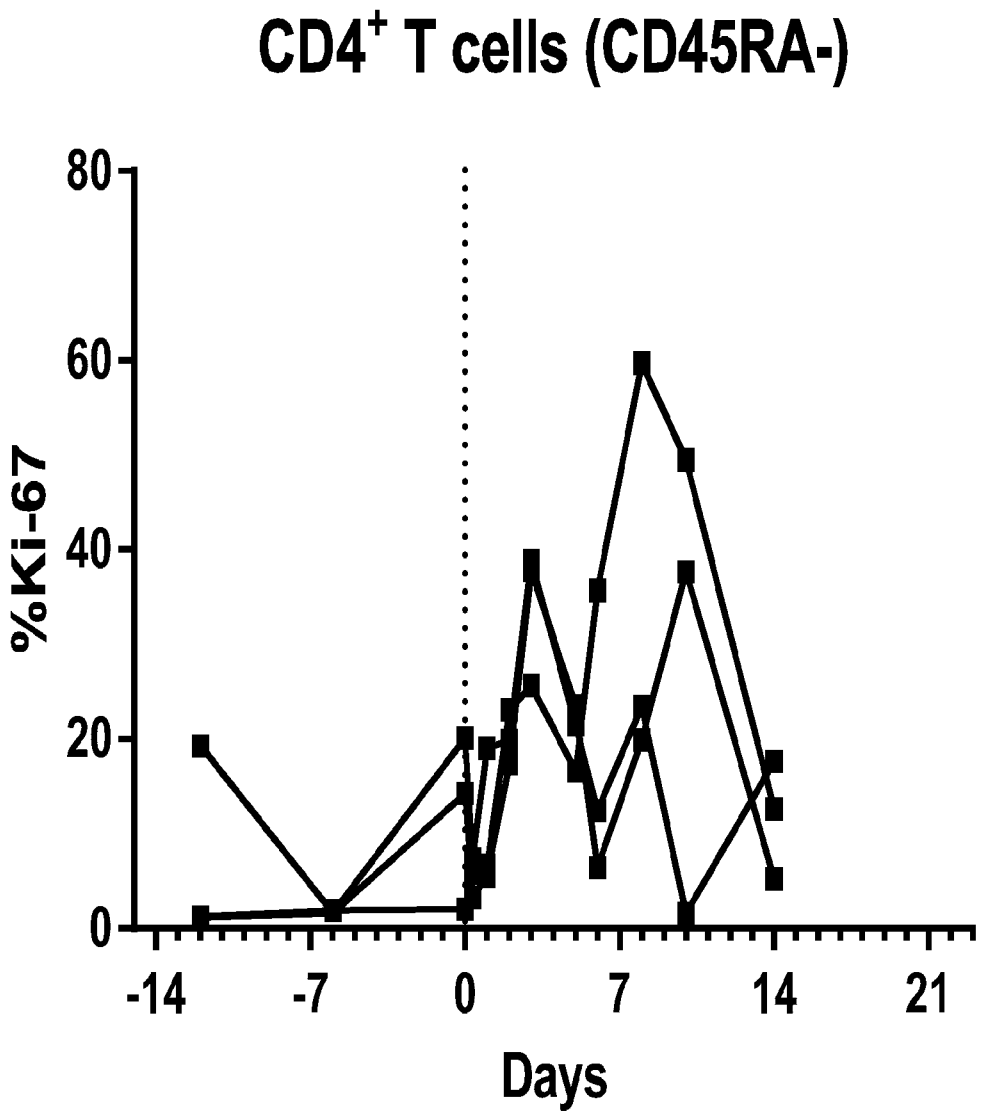

Figure 94A

>XENP023343 - human_IL15_N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - human_IL15_N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (18295) (SEQ ID NOS 358-360)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (17761) (SEQ ID NOS 361-363)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

>XENP023504 human_IL15_Q108E_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 364-366)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 367-369)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

Figure 94B

>XENP024113 human_IL15_N4D/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N4D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 370-372)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 –human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 373-375)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

>XENP024301 human_IL15_N4D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N4D/N65D_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 376-378)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 379-381)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 94C

>XENP024306 human_IL15_D30N/E64Q/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_D30N/E64Q/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 382-384)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 385-387)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

>XENP024341 human_IL15_N1D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N1D/N65D-human_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 388-390)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 391-393)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 94D

>XENP025938 human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 394-397)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 398)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 95

>XENP024383 IL15_Q108E_(non-covalent)-human_IL15Ra(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - IL15_Q108E (SEQ ID NO: 399)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 400-402)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 403)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSL
SLSPGK

Figure 96

>XENP024346 human_IL15(non-covalent; Q108E)-human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S

Chain 1 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S (SEQ ID NOS 404-406)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15(non-covalent; Q108E) (SEQ ID NO: 407)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

>XENP024351 human_IL15(non-covalent; N4D/N65D)-human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S

Chain 1 – IL15(N4D/N65D) (SEQ ID NO: 408)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S (SEQ ID NOS 409-411)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTHTCPPCPAPPVAGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 97A

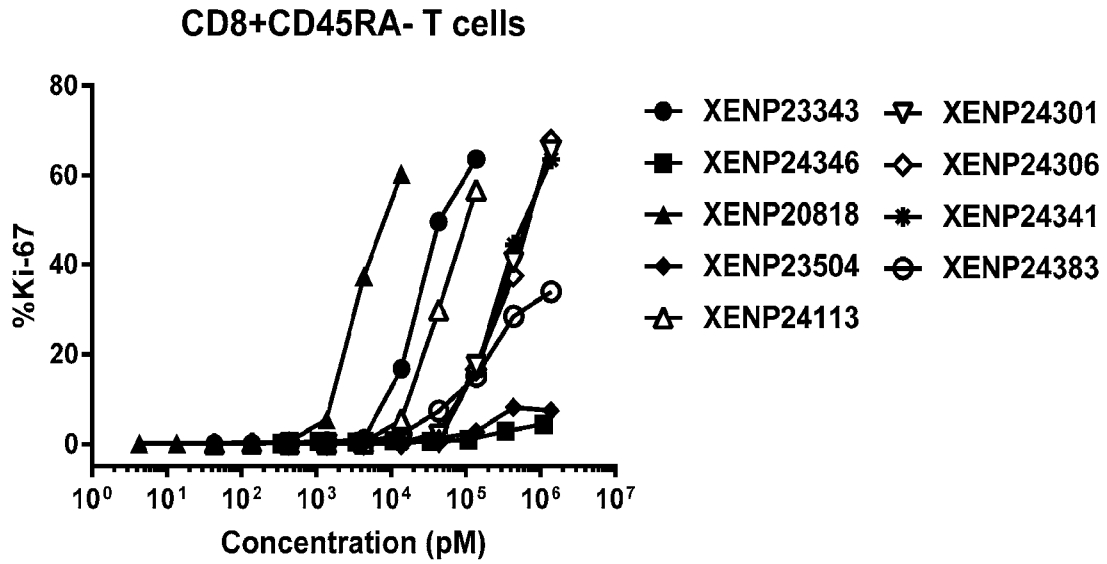

Figure 97B

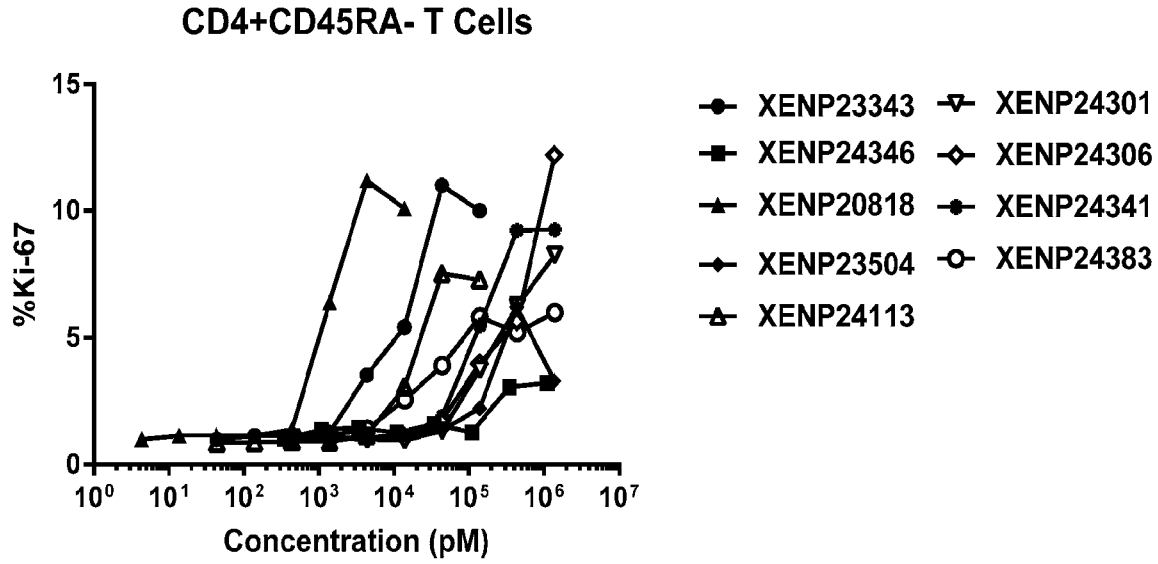

Figure 97C

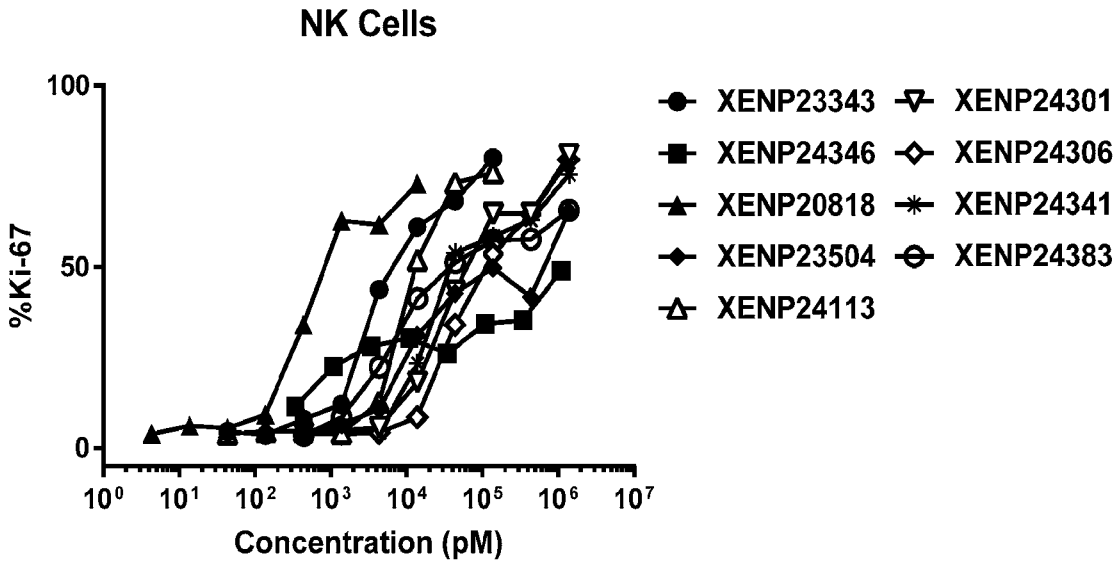
NK Cells
100
50
0
%Ki-67
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP23343
XENP24301
XENP24346
XENP24306
XENP20818
XENP24341
XENP23504
XENP24383
XENP24113

Figure 98A

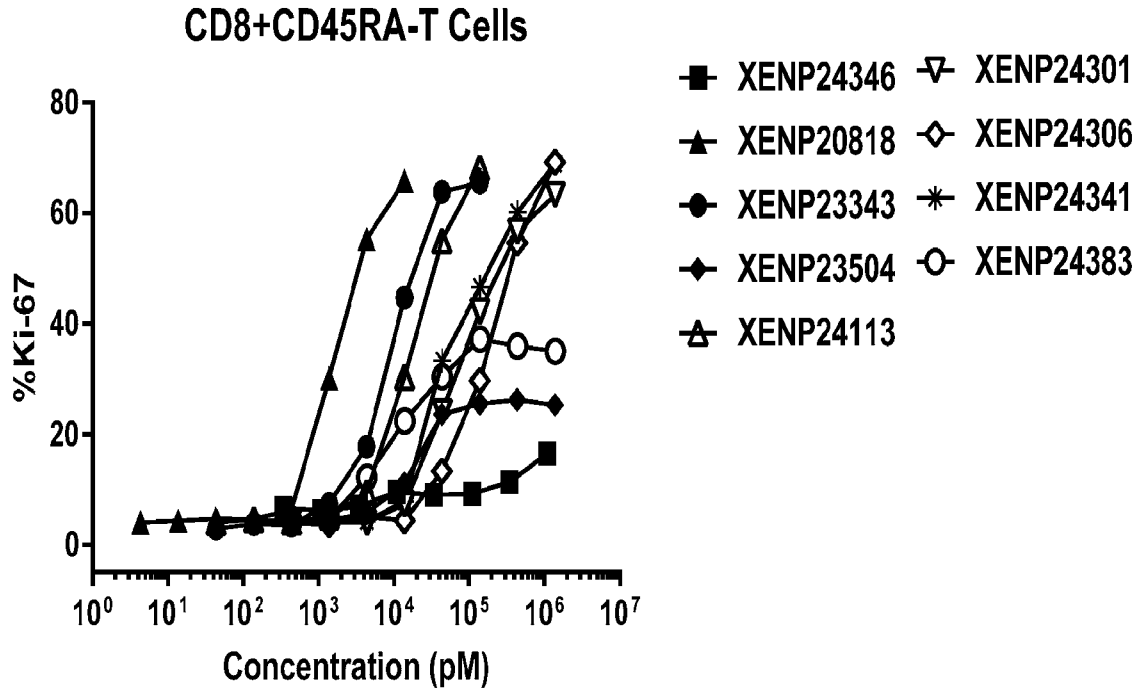

Figure 98B

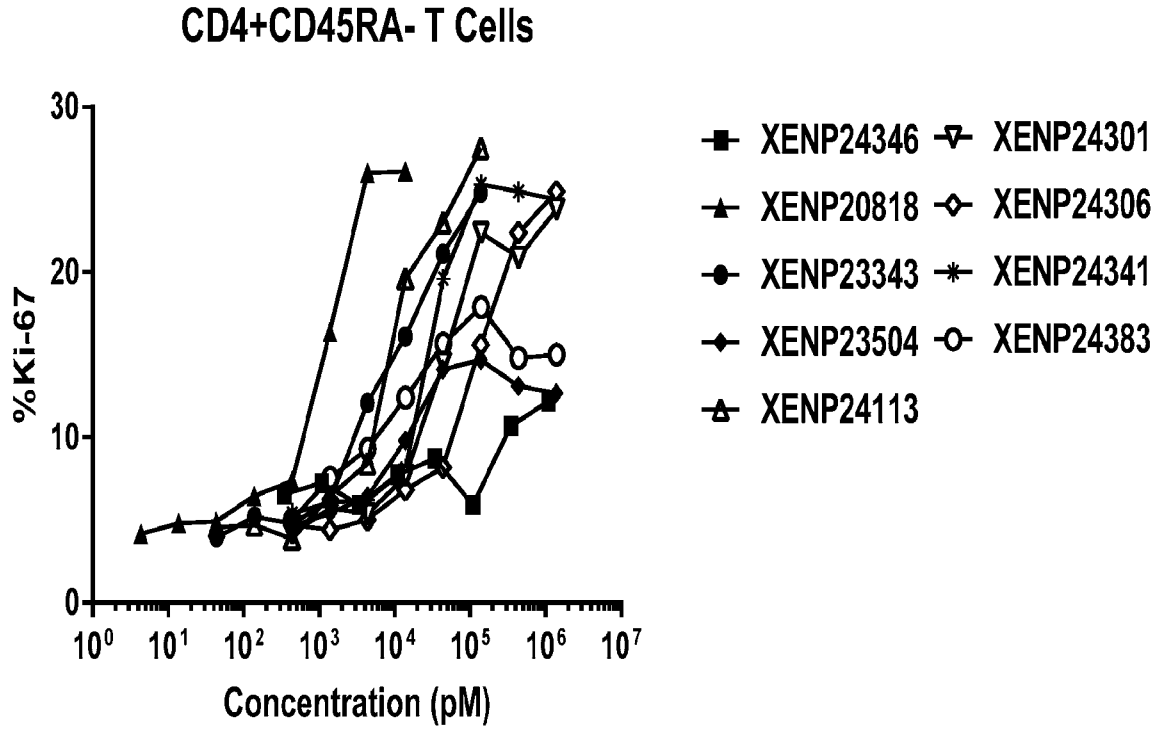

Figure 98C

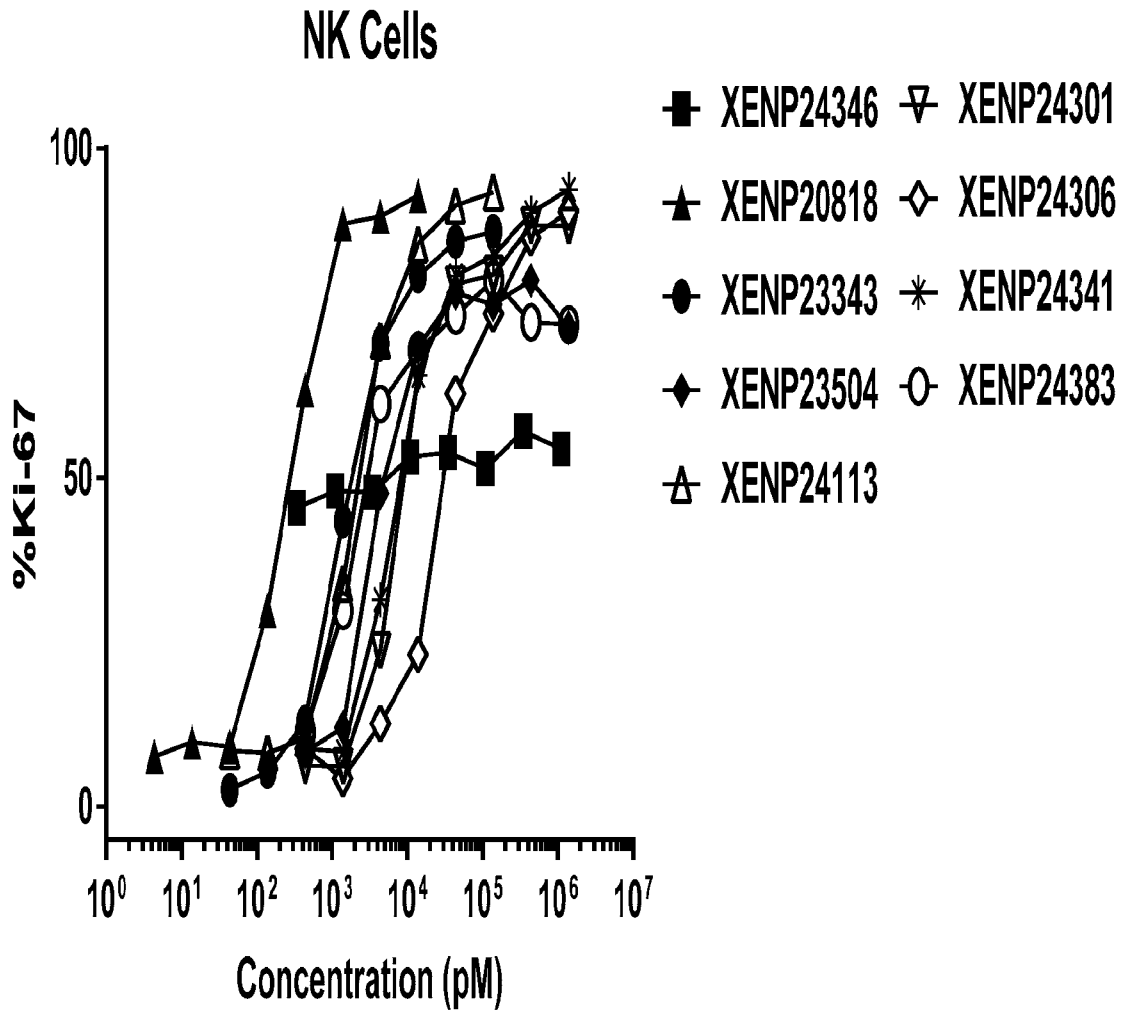
NK Cells
%Ki-67
100
50
0
10^0 10^1 10^2 10^3 10^4 10^5 10^6 10^7
Concentration (pM)
XENP24346
XENP24301
XENP20818
XENP24306
XENP23343
XENP24341
XENP23504
XENP24383
XENP24113

Figure 99A

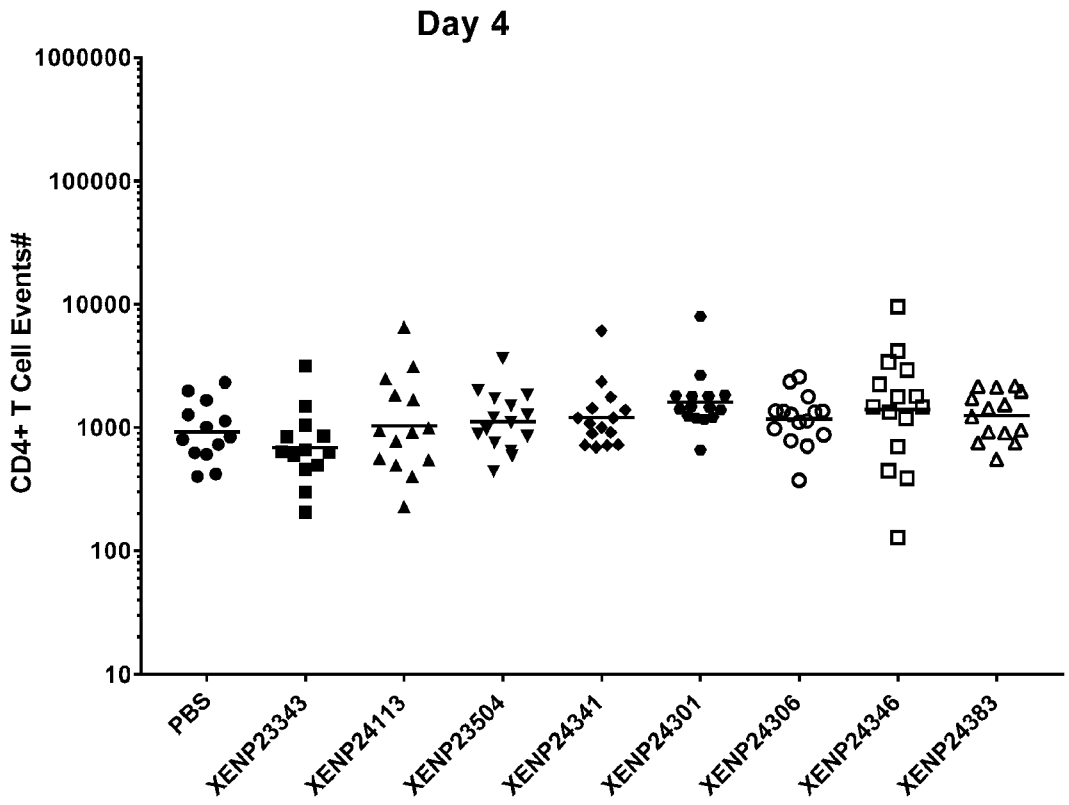

Figure 99B

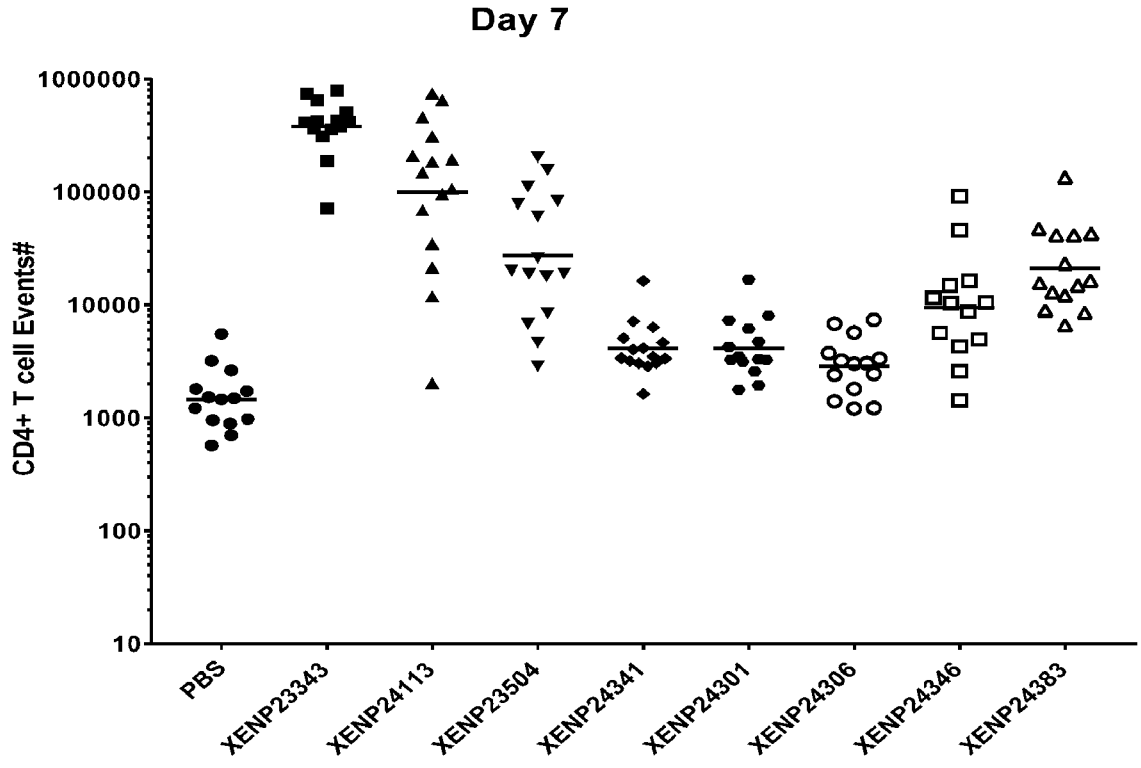

Figure 99C

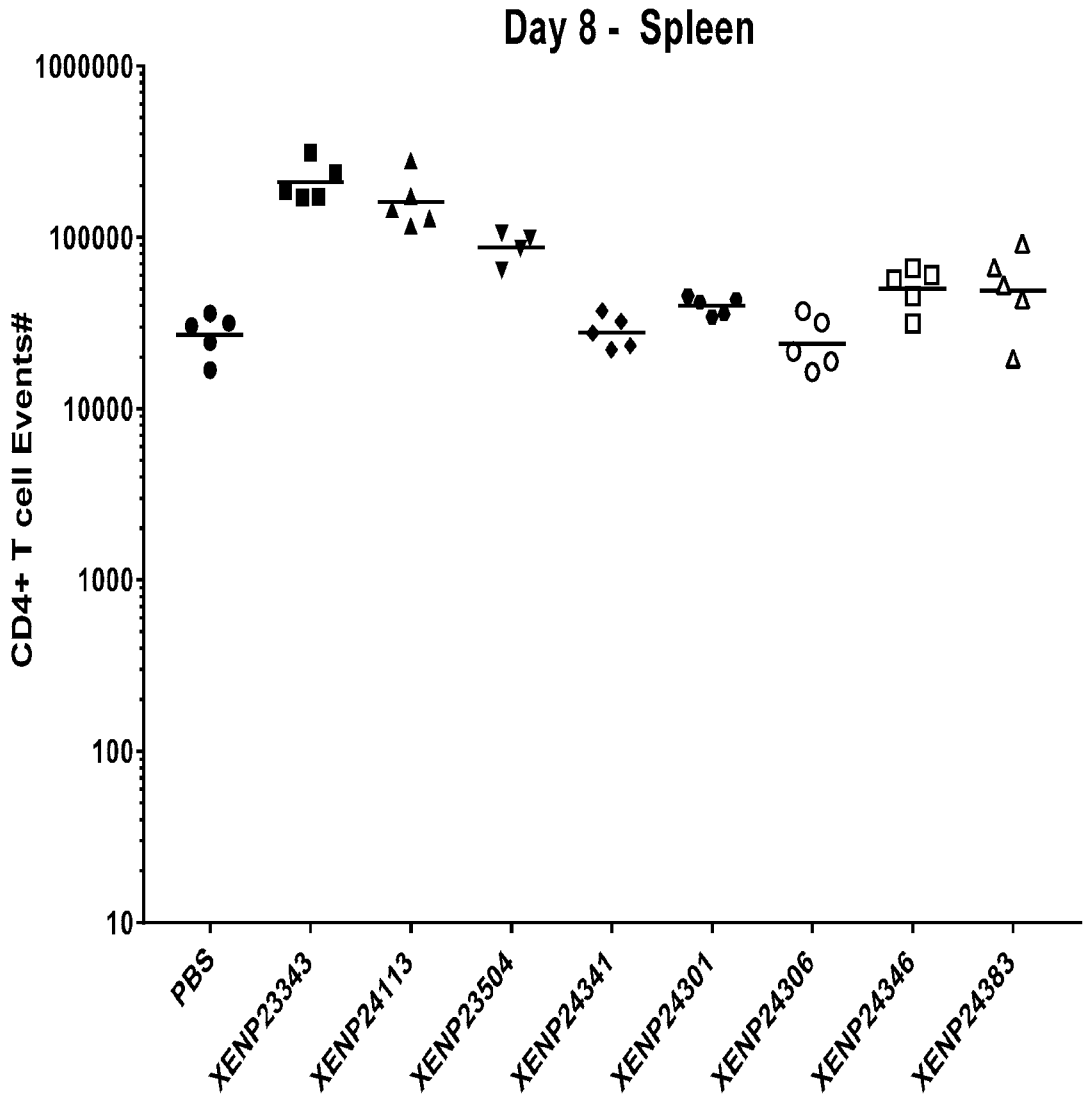
Day 8 - Spleen
CD4+ T cell Events#
1000000
100000
10000
1000
100
10
PBS
XENP23343
XENP24113
XENP23504
XENP24341
XENP24301
XENP24306
XENP24346
XENP24383

Figure 100A

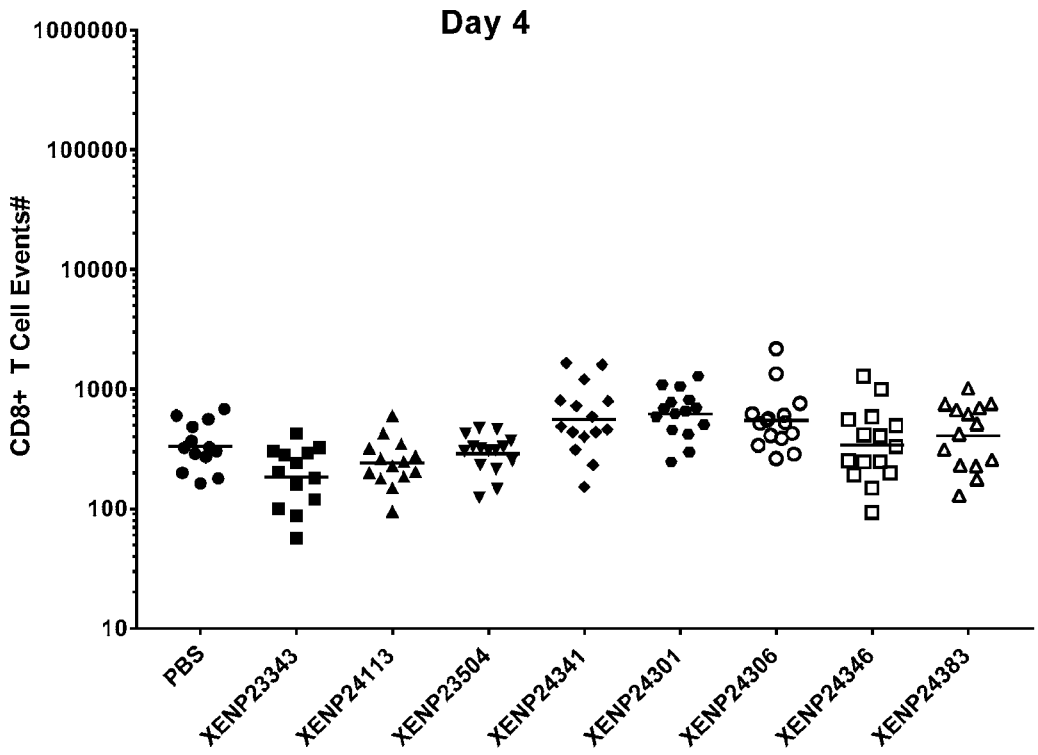

Figure 100B

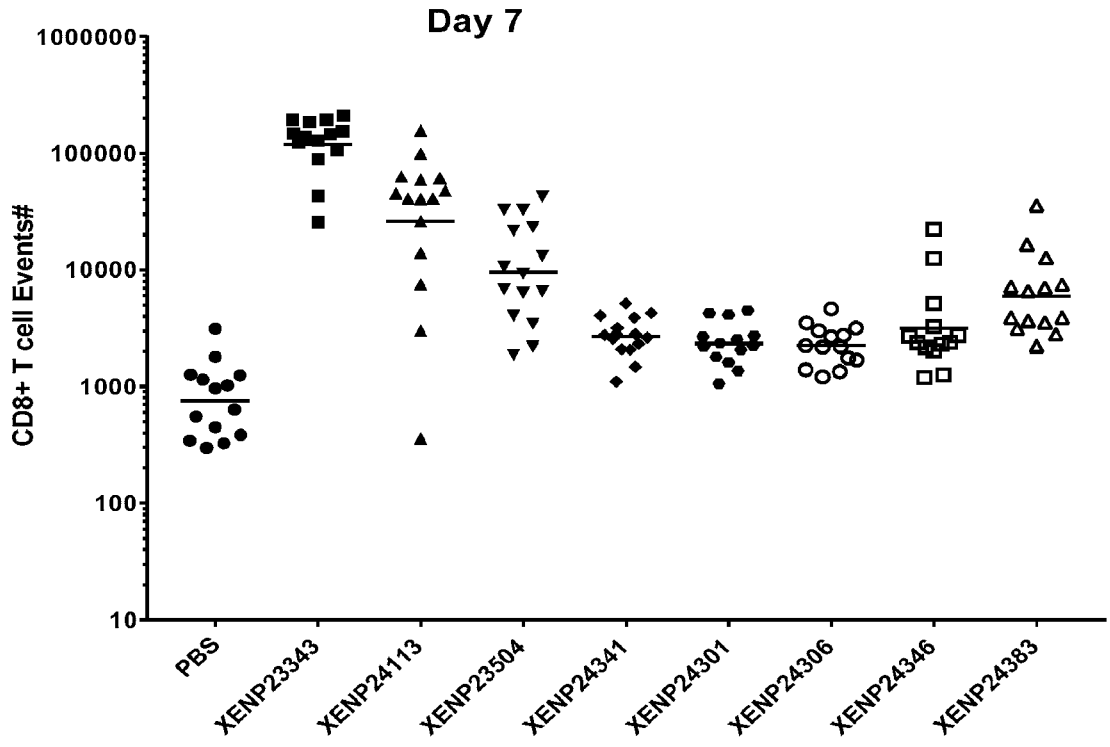

Figure 100C

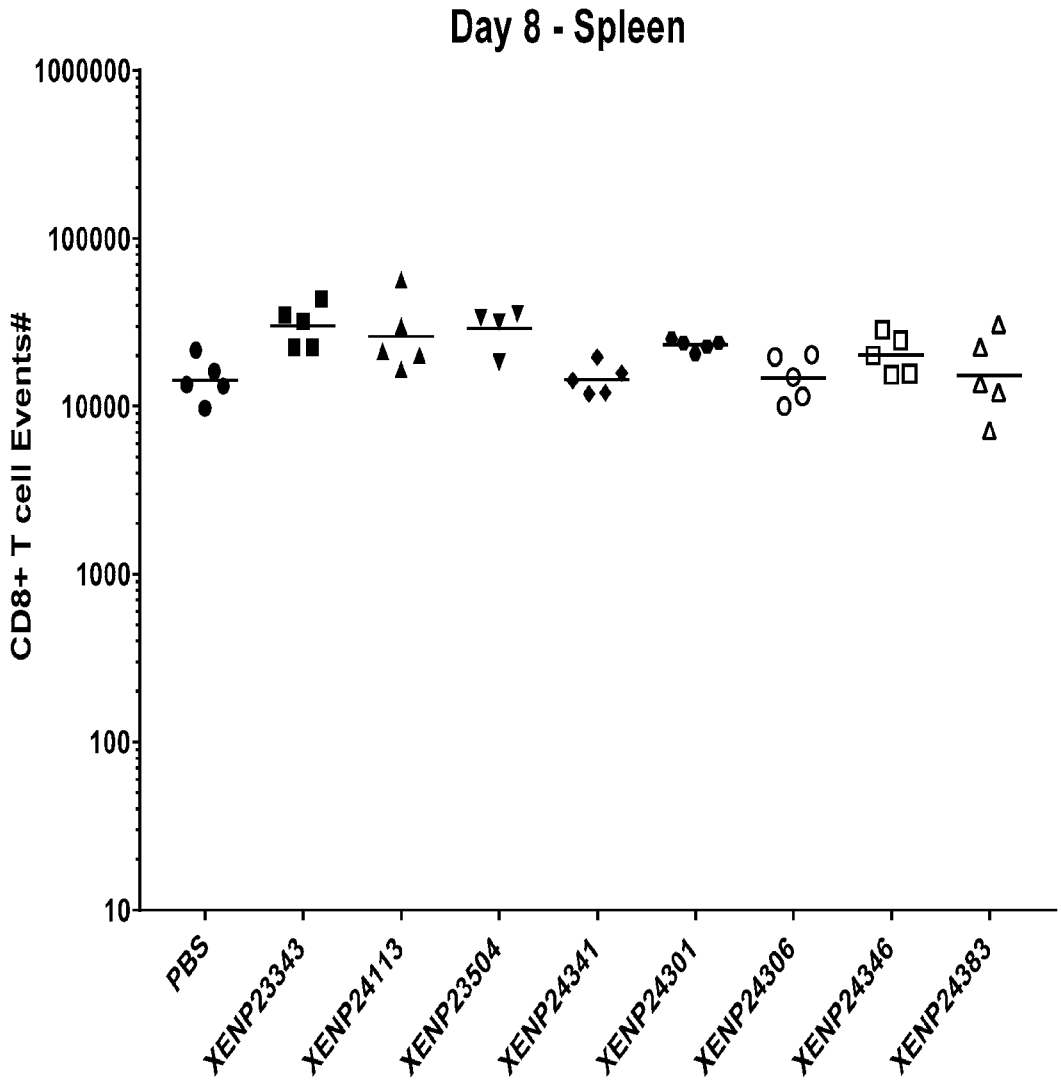
Day 8 - Spleen
CD8+ T cell Events#
1000000
100000
10000
1000
100
10
PBS
XENP23343
XENP24113
XENP23504
XENP24341
XENP24301
XENP24306
XENP24346
XENP24383

Figure 101A

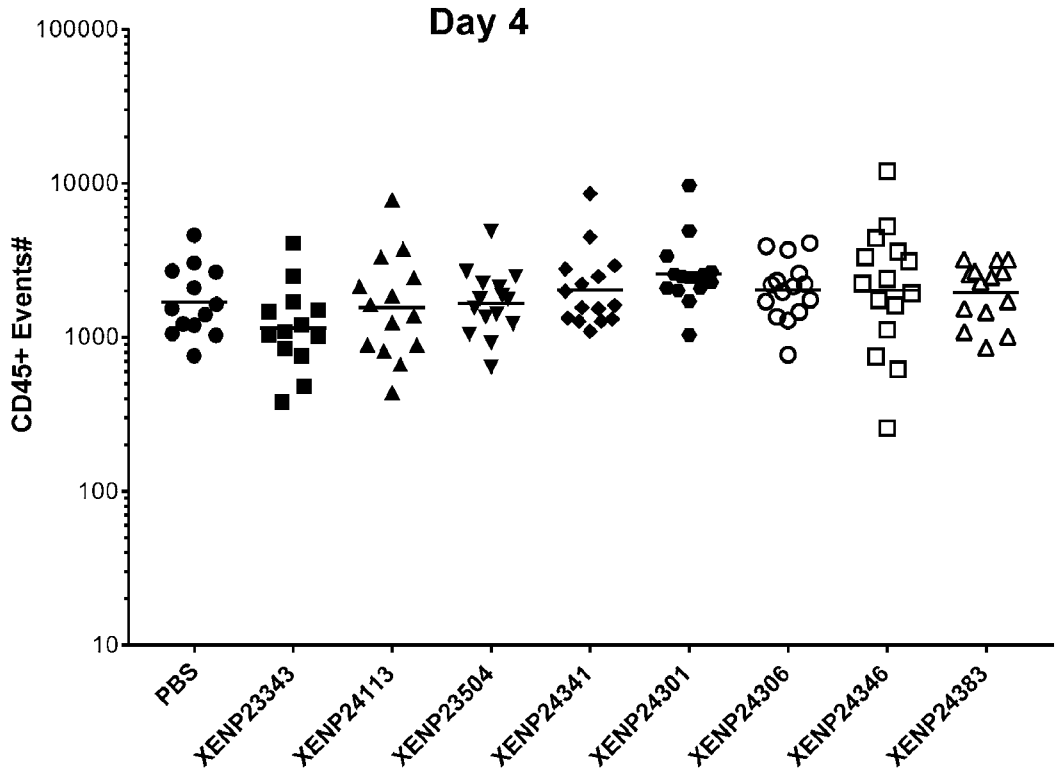

Figure 101B

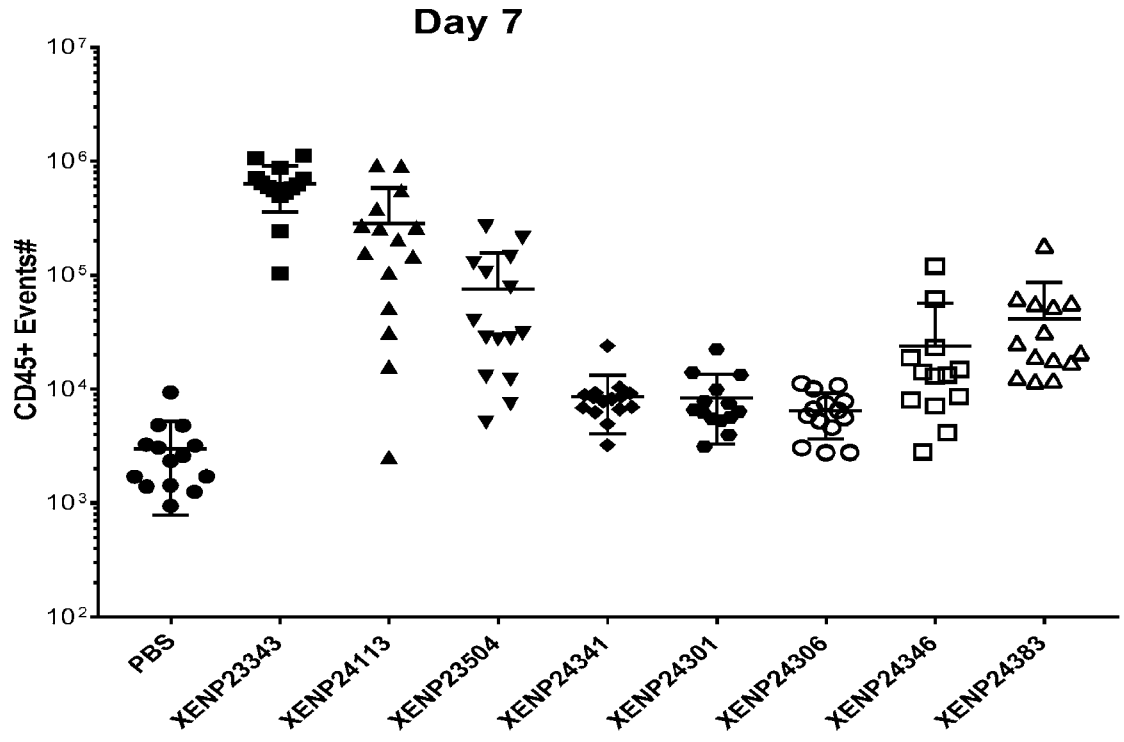

Figure 101C

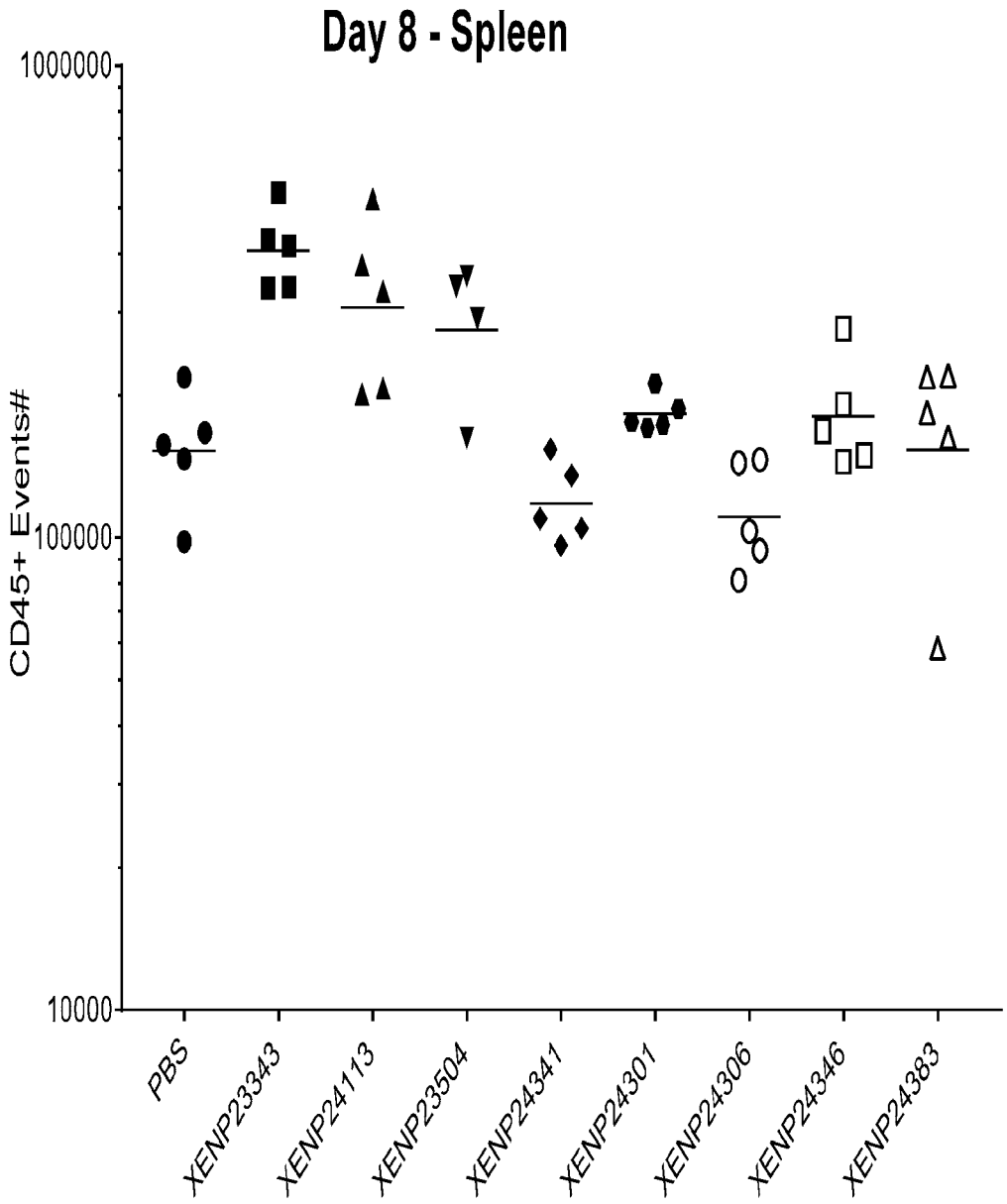
Day 8 - Spleen
CD45+ Events#
1000000
100000
10000
PBS
XENP23343
XENP24113
XENP23504
XENP24341
XENP24301
XENP24306
XENP24346
XENP24383

Figure 102A

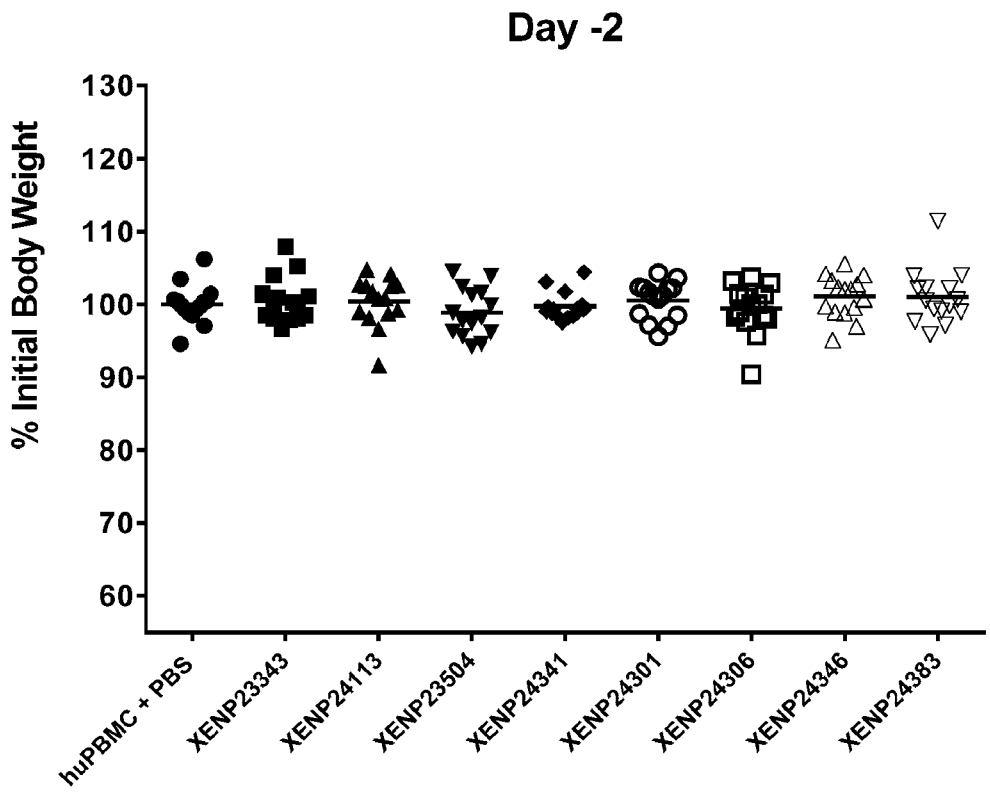

Figure 102B

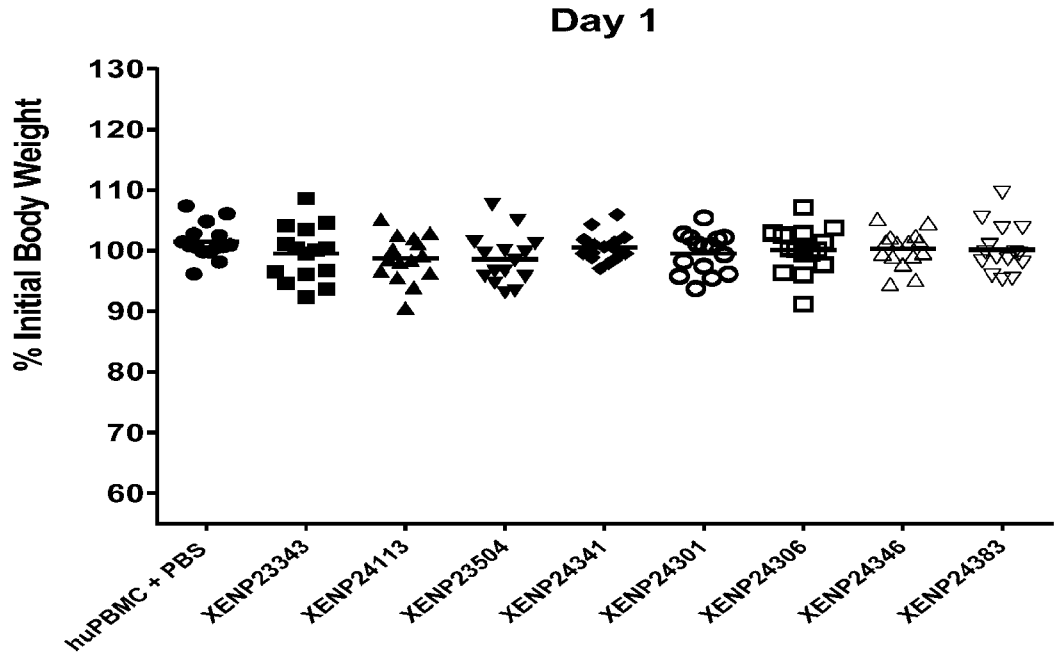

Figure 102C

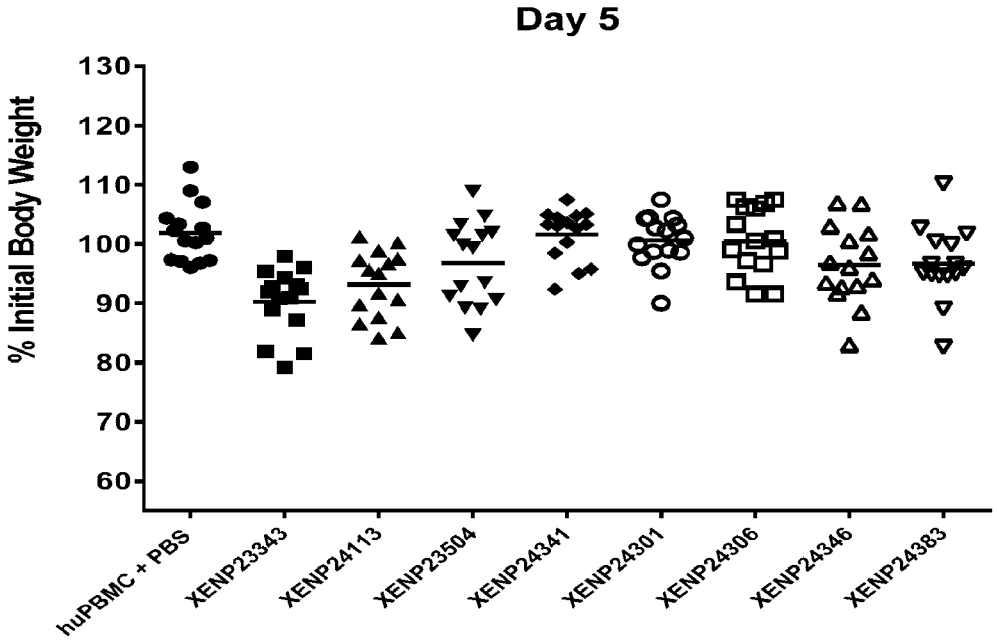

Figure 102D

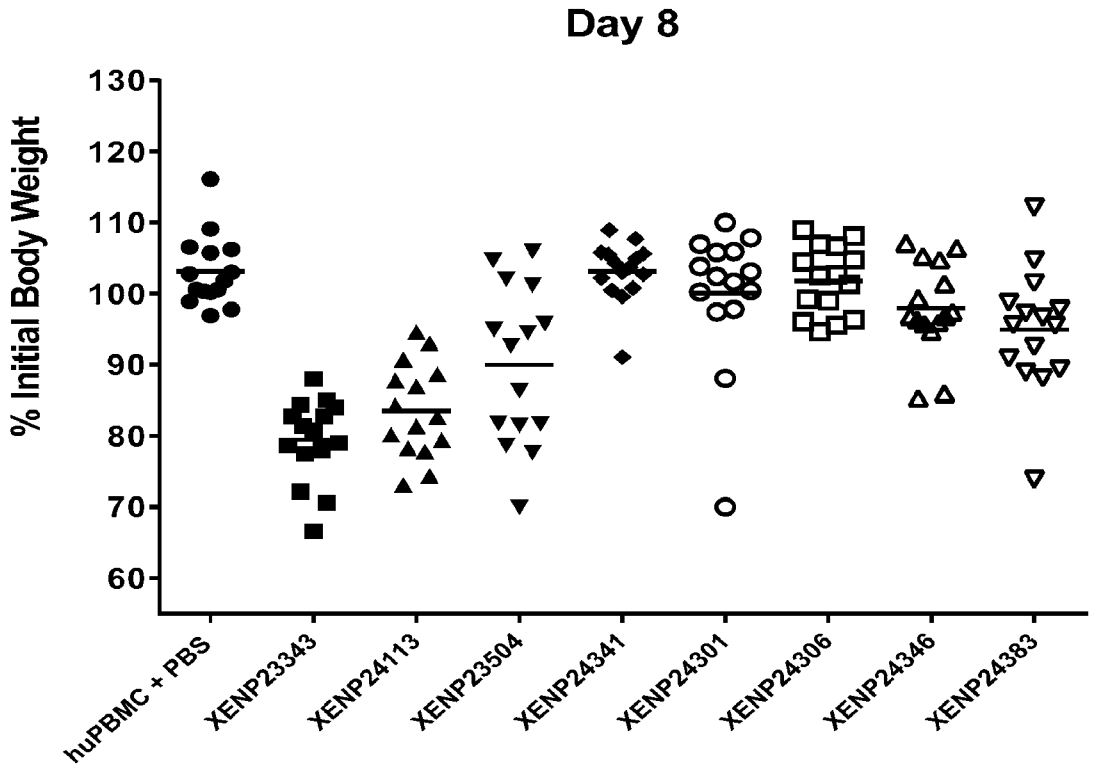

Figure 102E

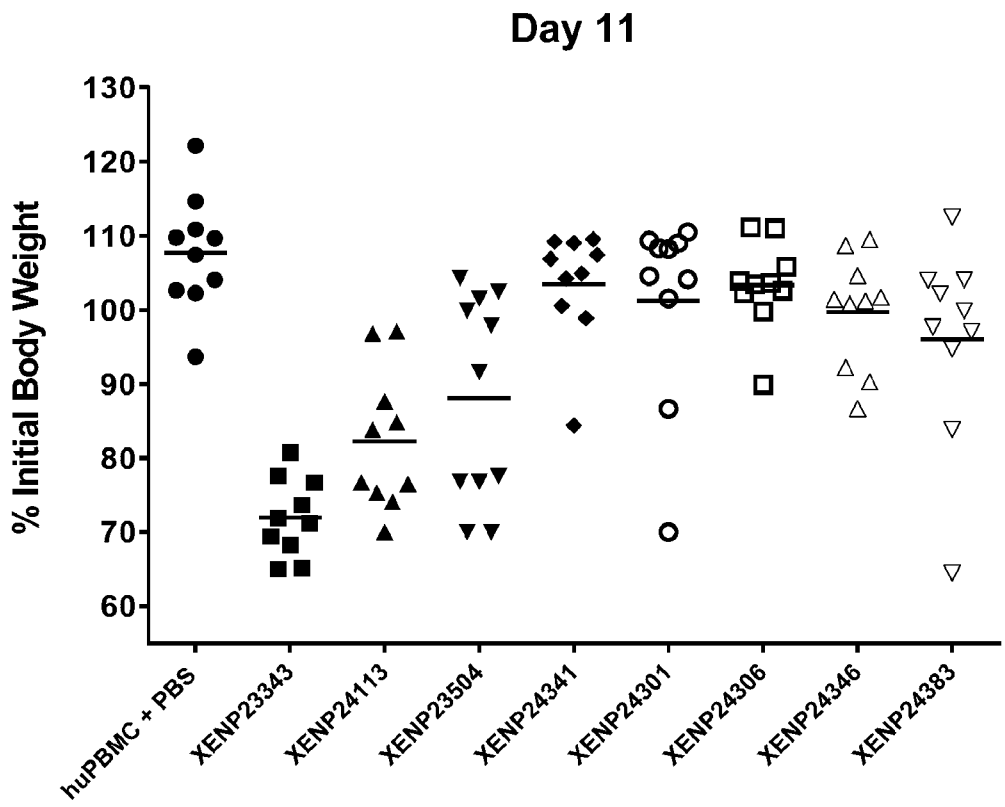

Figure 102F

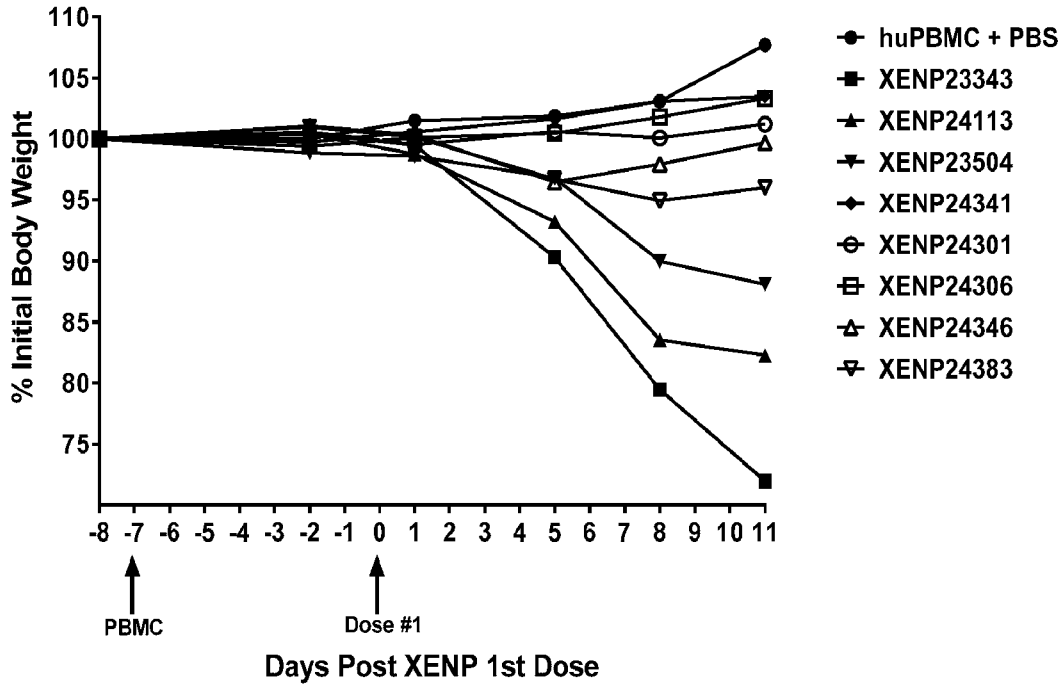

Figure 103A

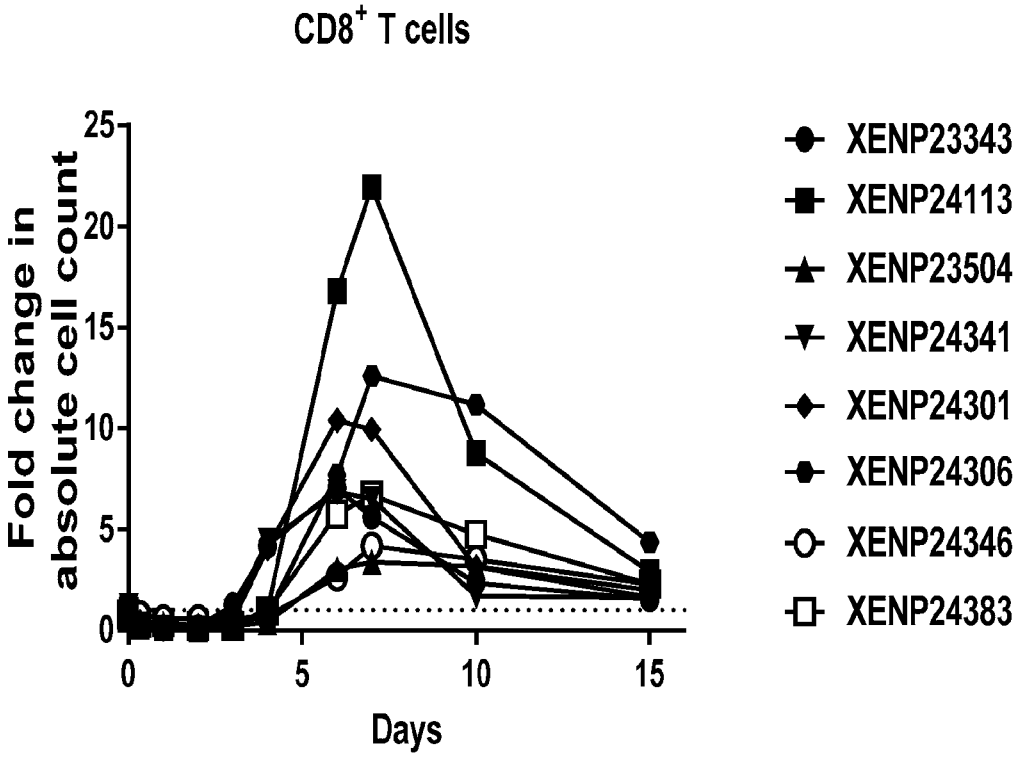

Figure 103B

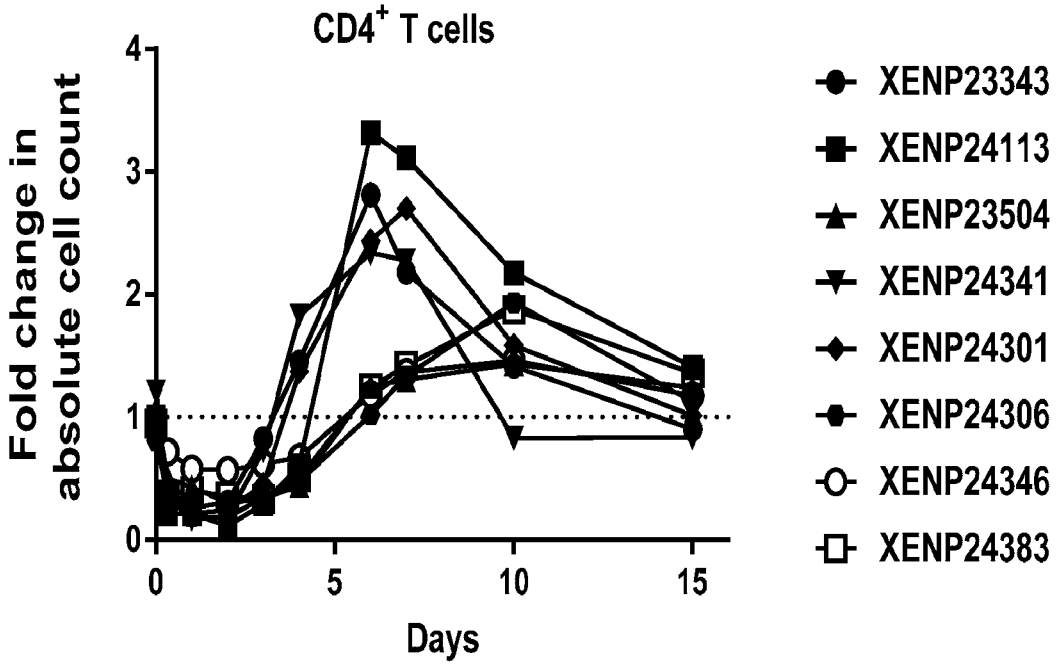

Figure 103C

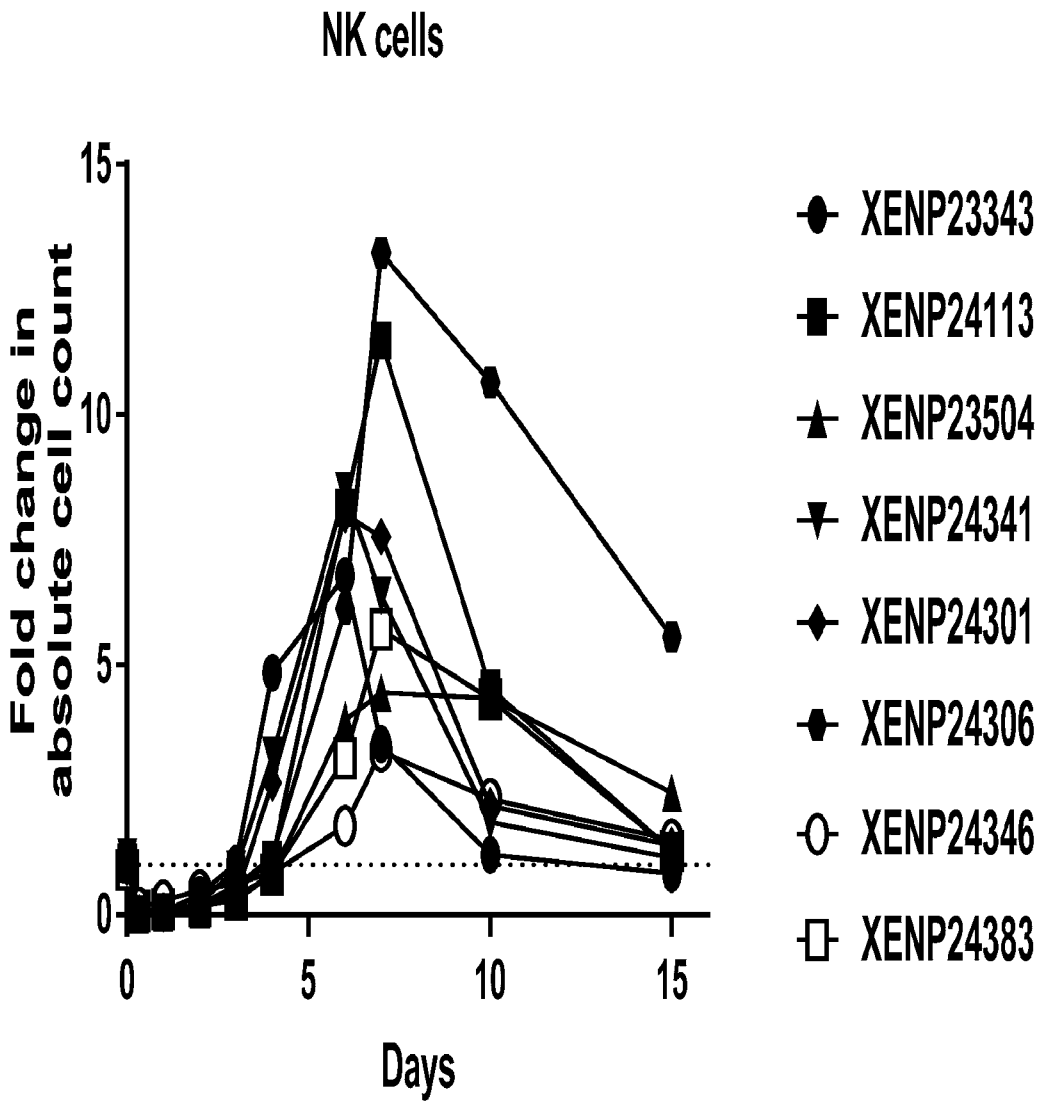
NK cells
Fold change in absolute cell count
15
10
5
0
0
5
10
15
Days
XENP23343
XENP24113
XENP23504
XENP24341
XENP24301
XENP24306
XENP24346
XENP24383

Figure 104A

>XENP20818 – human IL15-(GGGGS)$_1$ x human IL15Rα(Sushi)-(GGGGS)$_1$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (15902) (SEQ ID NOS 412-414)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN
VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSF
FLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 415-417)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP20819 – human IL15-(GGGGS)$_1$ x human IL15Rα(Sushi)-(GGGGS)$_4$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (15902) (SEQ ID NOS 418-420)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN
VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSF
FLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_4$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15909) (SEQ ID NOS 421-423)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSG
GGGSGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
MTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

Figure 104B

>XENP21471 – human IL15 x human IL15Rα(Sushi)-(GGGGS)$_1$ Fc heterodimer

Chain 1 - human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16479) (SEQ ID NOS 424-426)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSC
SVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 427-429)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSDKTHT
CPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP21472 – human IL15-(GGGGS)$_1$ x human IL15Rα(Sushi) Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (15902) (SEQ ID NOS 430-432)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQ
GDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 433-435)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTHTCPPCPA
PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP21473 – human IL15-(GGGGS)$_1$ x human IL15Rα(Sushi)-(GGGGS)$_3$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (15902) (SEQ ID NOS 436-438)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC
VVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQ
GDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_3$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16483) (SEQ ID NOS 439-441)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104C

>XENP21474 – human IL15 x human IL15Rα(Sushi)-(GGGGS)$_4$ Fc heterodimer

Chain 1 - human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16479) (SEQ ID NOS 442-444)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSC
SVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_4$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15909) (SEQ ID NOS 445-447)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGG
SGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP21475 – human IL15 x human IL15Rα(Sushi) Fc heterodimer

Chain 1 - human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16479) (SEQ ID NOS 448-450)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVK
HEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSC
SVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 451-453)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTHTCPPCPA
PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP21476 – human IL15-(GGGGS)$_2$ x human IL15Rα(Sushi)-(GGGGS)$_2$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_2$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16480) (SEQ ID NOS 454-456)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGSGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)$_2$_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16482) (SEQ ID NOS 457-459)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGS/EPKS
SDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104D

>XENP21477 – human IL15-(GGGGS)$_2$ x human IL15Rα(Sushi)-(GGGGS)$_4$ Fc heterodimer

Chain 1 - human_IL15_(GGGGS)$_2$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16480) (SEQ ID NOS 460-462)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN
VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGSGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCK
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15909) (SEQ ID NOS 463-465)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSG
GGGSGGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQ
MTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

>XENP21478 – human IL15Rα(Sushi)-(GGGGS)$_6$-human IL15(single-chain) Fc heterodimer

Chain 1 - human_IL15Rα(sushi)_(GGGGS)$_6$-human_IL15-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (16478) (SEQ ID NOS 466-469)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSG
GGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGD
ASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVA
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQD
WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - empty-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (8924) (SEQ ID NO: 470)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

Figure 104E

>XENP21479 – empty-Fc-IL15(non-covalent)-human_IL15Rα(Sushi) Fc heterodimer

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 471)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGN
VTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 472)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDV
SGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSP
GK

Chain 3 - human_IL15Rα(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 473-475)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021978 – human_IL15(non-covalent)-human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K (17023) (SEQ ID NOS 476-478)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_no_tag (16484) (SEQ ID NO: 479)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

>XENP021979 – human_IL15_N72D_(non-covalent)-human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi)-Fc(216)_IgG1_C220S/PVA_/S267K (17023) (SEQ ID NOS 480-482)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_N72D_no_tag (17076) (SEQ ID NO: 483)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANDSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 104F

>XENP021988 human_IL15_(GGGGS)1-human_IL15Ra(Sushi-D96)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 484-486)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Ra(Sushi-D96)_(GGGGS)1_c(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 487-489)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD/GGGGS/EP
KSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

>XENP021989 human_IL15_(GGGGS)1-human_IL15Ra(Sushi-D96/P97)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_(GGGGS)1_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 490-492)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 493-495)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDP/GGGGS/E
PKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

>XENP021990 human_IL15_(GGGGS)1-human_IL15Ra(Sushi-D96/P97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 496-498)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97/A98)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 499-501)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104G

>XENP021991 human_IL15_(GGGGS)1-human_IL15Ra(Sushi-D96/P97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 502-504)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 505-507)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021992 human_IL15-human_IL15Ra(Sushi-D96/P97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 508-510)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 511-513)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021993 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 514-517)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS
IHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 518)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104H

>XENP021994 human_IL15Ra(sushi)_(GGGGS)4-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)4-human_IL15(single-chain) _Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 519-522)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 523)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021995 human_IL15Ra(sushi)_(GGGGS)3-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)3-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 524-527)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 528)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP021996 - human_IL15(non-covalent)-human_IL15Ra(Sushi)-6x-His

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 529)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi)-6x-His (17033) (SEQ ID NO: 530)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022001 - human_IL15(non-covalent)-human_IL15Ra(Sushi-D96)-6x-His

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 531)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96)-6x-His (17048) (SEQ ID NO: 532)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD

Figure 104I

>XENP022002 - human_IL15(non-covalent)-human_IL15Ra(Sushi-D96/P97)-6x-His

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 533)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/P97)-6x-His (17049) (SEQ ID NO: 534)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDP

>XENP022003 - human_IL15(non-covalent)-human_IL15Ra(Sushi-D96/P97/A98)-6x-His

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 535)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/P97/A98)-6x-His (17050) (SEQ ID NO: 536)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA

>XENP022004 - human_IL15_E87C-human_IL15Ra(Sushi-D96/C97)-6x-His

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 537)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/C97)-6x-His (17051) (SEQ ID NO: 538)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC

>XENP022005 - human_IL15_E87C-human_IL15Ra(Sushi-D96/P97/C98)-6x-His

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 539)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/P97/C98)-6x-His (17052) (SEQ ID NO: 540)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC

>XENP022006 - human_IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)-6x-His

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 541)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-D96/C97/A98)-6x-His (17053) (SEQ ID NO: 542)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA

Figure 104J

>XENP022007 - human_IL15_V49C-human_IL15Ra(Sushi-S40C)-6x-His

Chain 1 - human_IL15_V49C_no_tag (17071) (SEQ ID NO: 543)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQCISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-S40C)-6x-His (17057) (SEQ ID NO: 544)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR

>XENP022008 - human_IL15_L52C-human_IL15Ra(Sushi-S40C)-6x-His

Chain 1 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 545)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-S40C)-6x-His (17057) (SEQ ID NO: 546)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR

>XENP022009 - human_IL15_E89C-human_IL15Ra(Sushi-K34C)-6x-His

Chain 1 - human_IL15_E89C_no_tag (17075) (SEQ ID NO: 547)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECCELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-K34C)-6x-His (17054) (SEQ ID NO: 548)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFCRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022010 - human_IL15_Q48C-human_IL15Ra(Sushi-G38C)-6x-His

Chain 1 - human_IL15_Q48C_no_tag (17070) (SEQ ID NO: 549)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELCVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-G38C)-6x-His (17056) (SEQ ID NO: 550)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKACTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022011 - human_IL15_E53C-human_IL15Ra(Sushi-L42C)-6x-His

Chain 1 - human_IL15_E53C_no_tag (17073) (SEQ ID NO: 551)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLCSGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-L42C)-6x-His (17058) (SEQ ID NO: 552)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSCTECVLNKATNVAHWTTPSLKCIR

Figure 104K

>XENP022012 - human_IL15_C42S-human_IL15Ra(Sushi-A37C)-6x-His

Chain 1 - human_IL15_C42S_no_tag (17083) (SEQ ID NO: 553)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKSFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-L42C)-6x-His (17055) (SEQ ID NO: 554)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022013 human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 555-557)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 558-560)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/GGGGS/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022014 human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 561-563)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 564-566)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC/GGGGS/EPKSS
DKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104K (continued)

>XENP022015human_IL15_E87C_(GGGGS)1-human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 567-569)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 570-572)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/GGGGS/EPKSS
DKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104L

>XENP022017 human_IL15_L52C_(GGGGS)1-human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_L52C_(GGGGS)1-_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 573-575)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF
NWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL
TCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 576-578)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022049 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15-sc-6x-His

Chain 1 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15-sc-6x-His (17032) (SEQ ID NOS 579-581)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE
SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022354 – empty-Fc-IL15(non-covalent)-human_IL15Ra(Sushi-D96)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 582)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 583)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17034) (SEQ ID NOS 584-586)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD/GGGGS/EP
KSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPRE
EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

Figure 104M

>XENP022355 – empty-Fc-IL15(non-covalent)-human_IL15Ra(Sushi-D96/P97)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 587)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 588)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/P97)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 589-591)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDP/GGGGS/E
PKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

>XENP022356 – empty-Fc-IL15(non-covalent)-human_IL15Ra(Sushi-D96/P97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 592)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 593)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/P97/A98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17036) (SEQ ID NOS 594-596)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104N

>XENP022357 – empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 597)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 598)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/C97)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17038) (SEQ ID NOS 599-601)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/GGGGS/E
PKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPR
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTC
LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

>XENP022358 – empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 602)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 603)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/P97/C98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17039) (SEQ ID NOS 604-606)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104O

>XENP022359 – empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 607)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 608)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-D96/C97/A98)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17040) (SEQ ID NOS 609-611)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/GGGGS/
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

>XENP022360 – empty-Fc-IL15_V49C-human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_V49C_no_tag (17071) (SEQ ID NO: 612)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQCISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 613)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17044) (SEQ ID NOS 614-616)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104P

>XENP022361 – empty-Fc-IL15_L52C-human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 617)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 618)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-S40C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17044) (SEQ ID NOS 619-621)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP022362 – empty-Fc-IL15_E89C-human_IL15Ra(Sushi-K34C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E89C_no_tag (17075) (SEQ ID NO: 622)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECCELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 623)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-K34C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17041) (SEQ ID NOS 624-626)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFCRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

Figure 104Q

>XENP022363 – empty-Fc-IL15_Q48C-human_IL15Ra(Sushi-G38C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_Q48C_no_tag (17070) (SEQ ID NO: 627)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELCVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 628)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-G38C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17043) (SEQ ID NOS 629-631)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKACTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP022364 – empty-Fc-IL15_E53C-human_IL15Ra(Sushi-L42C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E53C_no_tag (17073) (SEQ ID NO: 632)
NWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLCSGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 633)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSV_TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPV_DSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-L42C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17045) (SEQ ID NOS 634-636)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSCTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104R

>XENP022365 – empty-Fc-IL15_C42S-human_IL15Ra(Sushi-A37C)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_C42S_no_tag (17083) (SEQ ID NO: 637)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKSFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 638)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi-A37C)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (17042) (SEQ ID NOS 639-641)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022366 – empty-Fc-IL15(non-covalent)-human_IL15Ra(sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_no_tag (16484) (SEQ ID NO: 642)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (8793) (SEQ ID NO: 643)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 644-646)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022493 - human_IL15_L45C-human_IL15Ra(Sushi-G38C)-6x-His

Chain 1 - human_IL15_L45C_no_tag (17069) (SEQ ID NO: 647)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLCELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-G38C)-6x-His (17056) (SEQ ID NO: 648)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKACTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104S

>XENP022494 – human_IL15_L45C-human_IL15Ra(Sushi-A37C)-6x-His

Chain 1 - human_IL15_L45C_no_tag (17069) (SEQ ID NO: 649)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLCELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi-A37C)-6x-His (17055) (SEQ ID NO: 650)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022634 – human_IL15(E87C)-human_IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-D96/C97)-Fc(216)_IgG1_C220S/PVA_/S267K (17581)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/EPKSSDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NOS 651-653)

Chain 2 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 654)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022635 – human_IL15(E87C)-human_IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-D96/C97/A98)-Fc(216)_IgG1_C220S/PVA_/S267K (17582) (SEQ ID NOS 655-657)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/EPKSSD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 658)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022636 – human_IL15(L52C)-human_IL15Ra(Sushi-S40C)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 - human_IL15Ra(Sushi-S40C)-Fc(216)_IgG1_C220S/PVA_/S267K (17583) (SEQ ID NOS 659-661)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHED?EVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE?QVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15_L52C_no_tag (17072) (SEQ ID NO: 662)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 104T

>XENP022637 – empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(non-covalent)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi) (17603) (SEQ ID NOS 663-665)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIR

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 666)
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15_no_tag (16484) (SEQ ID NO: 667)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022638 empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q_(GGGGS)2_IL15Ra(Sushi)_IL15(non-covalent)

Chain 1 – IL15 (SEQ ID NO: 668)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 – empty_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 669)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – Fc(216)_ IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q_(GGGGS)2_IL15Ra(Sushi) (SEQ ID NOS 670-672)
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERY
ICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104U

>XENP022639 – empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi-D96/C97)_IL15(E87C)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi-D96/C97) (17605) (SEQ ID NOS 673-675)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIRDC

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 676)
ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 - human_IL15_E87C_no_tag (17074) (SEQ ID NO: 677)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

>XENP022640 empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q_(GGGGS)2_IL15Ra(Sushi-D96/C97)_IL15(E87C)

Chain 1 – IL15 (SEQ ID NO: 678)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 – empty_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 679)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022684 empty-Fc-IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – IL15_E87C (SEQ ID NO: 680)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 681-683)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/EPKSSDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 684)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104V

>XENP022687 human_IL15_E87C-human_IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 – IL15_E87C (SEQ ID NO: 685)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKCCEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - IL15Ra(Sushi-D96/C97/A98)_Fc(216)_IgG1_C220S/PVA_/S267K (SEQ ID NOS 686-688)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA/EPKSSDKTHTC?PCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQ?REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022791 - human_IL15_N1D(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N1D(non-covalent) (17666) (SEQ ID NO: 689)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 690)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022792 - human_IL15_N4D(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N4D(non-covalent) (17667) (SEQ ID NO: 691)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 692)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022793 - human_IL15_D8N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D8N(non-covalent) (17668) (SEQ ID NO: 693)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 694)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022794 - human_IL15_D30N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D30N(non-covalent) (17669) (SEQ ID NO: 695)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 696)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104W

>XENP022795 - human_IL15_D61N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D61N(non-covalent) (17670) (SEQ ID NO: 697)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 698)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022796 - human_IL15_E64Q(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_E64Q(non-covalent) (17671) (SEQ ID NO: 699)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 700)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022801 - human_IL15_N65D(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N65D(non-covalent) (17672) (SEQ ID NO: 701)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 702)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022802 - human_IL15_Q108E(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_Q108E(non-covalent) (17673) (SEQ ID NO: 703)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 704)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022803 - human_IL15_N1D/D61N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N1D/D61N(non-covalent) (17674) (SEQ ID NO: 705)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 706)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104X

>XENP022804 - human_IL15_N1D/E64Q(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N1D/E64Q(non-covalent) (17675) (SEQ ID NO: 707)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 708)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022805 - human_IL15_N4D/D61N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N4D/D61N(non-covalent) (17676) (SEQ ID NO: 709)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 710)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022806 - human_IL15_N4D/E64Q(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N4D/E64Q(non-covalent) (17677) (SEQ ID NO: 711)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 712)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022807 - human_IL15_D8N/D61N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D8N/D61N(non-covalent) (17678) (SEQ ID NO: 713)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 714)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022808 - human_IL15_D8N/E64Q(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D8N/E64Q(non-covalent) (17679) (SEQ ID NO: 715)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 716)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104Y

>XENP022809 - human_IL15_D61N/E64Q(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D61N/E64Q(non-covalent) (17680) (SEQ ID NO: 717)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 718)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022810 - human_IL15_E64Q/Q108E(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_E64Q/Q108E(non-covalent) (17681) (SEQ ID NO: 719)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 720)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022811 - human_IL15_N1D/N4D/D8N(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N1D/N4D/D8N(non-covalent) (17682) (SEQ ID NO: 721)
DWVDVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 722)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022812 - human_IL15_D61N/E64Q/N65D(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_D61N/E64Q/N65D(non-covalent) (17683) (SEQ ID NO: 723)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 724)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022813 - human_IL15_N1D/D61N/E64Q/Q108E(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N1D/D61N/E64Q/Q108E(non-covalent) (17684) (SEQ ID NO: 725)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 726)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104Z

>XENP022814 - human_IL15_N4D/D61N/E64Q/Q108E(non-covalent)-human_IL15Rα(Sushi)-6x-His

Chain 1 - human_IL15_N4D/D61N/E64Q/Q108E(non-covalent) (17685) (SEQ ID NO: 727)
NWVDVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Rα(Sushi)-6x-His (17033) (SEQ ID NO: 728)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

>XENP022815 - human_IL15_N1D_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D_(GGGGS)$_1$ (17686) (SEQ ID NOS 729-731)
DWVNVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 732-734)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

>XENP022816 - human_IL15_N4D_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D_(GGGGS)$_1$ (17687) (SEQ ID NOS 735-737)
NWVDVISDLKKIED_IQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSK_TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 738-740)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDT_MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTV_HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA_HNHYTQKSLSLS
PGK

Figure 104AA

>XENP022817 - human_IL15_D8N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D8N_(GGGGS)$_1$ (17688) (SEQ ID NOS 741-743)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 744-746)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022818 - human_IL15_D30N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D30N_(GGGGS)$_1$ (17689) (SEQ ID NOS 747-749)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 750-752)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AB

>XENP022819 - human_IL15_D61N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D61N_(GGGGS)$_1$ (17690) (SEQ ID NOS 753-755)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 756-758)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022820 - human_IL15_E64Q_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E64Q_(GGGGS)$_1$ (17691) (SEQ ID NOS 759-761)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 762-764)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022821 - human_IL15_N65D_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N65D_(GGGGS)$_1$ (17692) (SEQ ID NOS 765-767)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 768-770)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AC

>XENP022822 - human_IL15_Q108E_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_Q108E_(GGGGS)$_1$ (17693) (SEQ ID NOS 771-773)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 774-776)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022823 - human_IL15_N1D/D61N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/D61N_(GGGGS)$_1$ (17694) (SEQ ID NOS 777-779)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 780-782)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022824 - human_IL15_N1D/E64Q_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/E64Q_(GGGGS)$_1$ (17695) (SEQ ID NOS 783-785)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 786-788)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AD

>XENP022825 - human_IL15_N4D/D61N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D/D61N_(GGGGS)$_1$ (17696) (SEQ ID NOS 789-791)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 792-794)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022826 - human_IL15_N4D/E64Q_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D/E64Q_(GGGGS)$_1$ (17697) (SEQ ID NOS 795-797)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 798-800)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022827 - human_IL15_D8N/D61N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D8N/D61N_(GGGGS)$_1$ (17698) (SEQ ID NOS 801-803)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 804-806)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AE

>XENP022828 - human_IL15_D8N/E64Q_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D8N/E64Q_(GGGGS)$_1$ (17699) (SEQ ID NOS 807-809)
NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 810-812)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022829 - human_IL15_D61N/E64Q_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D61N/E64Q_(GGGGS)$_1$ (17700) (SEQ ID NOS 813-815)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 816-818)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP022830 - human_IL15_E64Q/Q108E_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E64Q/Q108E_(GGGGS)$_1$ (17701) (SEQ ID NOS 819-821)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 822-824)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AF

>XENP022831 - human_IL15_N1D/N4D/D8N_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/N4D/D8N_(GGGGS)$_1$ (17702) (SEQ ID NOS 825-827)
DWVDVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
DVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNH
YTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 828-830)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GG
GGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP022832 - human_IL15_D61N/E64Q/N65D_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D61N/E64Q/N65D_(GGGGS)$_1$ (17703) (SEQ ID NOS 831-833)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQDLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
DVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNH
YTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 834-836)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GG
GGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVD
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
YTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AF (continued)

>XENP022833 - human_IL15_N1D/D61N/E64Q/Q108E_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/D61N/E64Q/Q108E_(GGGGS)$_1$ (17704) (SEQ ID NOS 837-839)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCP
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC
DVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNH
YTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 840-842)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AG

>XENP022834 - human_IL15_N4D/D61N/E64Q/Q108E_(GGGGS)$_1$-human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D/D61N/E64Q/Q108E_(GGGGS)$_1$ (17705) (SEQ ID NOS 843-845)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Rα(Sushi)_(GGGGS)$_1$_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 846-848)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023174 human_IL15Ra(sushi)_(GKPGS)6-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GKPGS)6-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 849-852)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GKPGSGKPGSGKPGSGKPGSGKPG
SGKPGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTES
GCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS
LTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 853)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP023175 human_IL15Ra(sushi)_(GKPGS)5-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GKPGS)5-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 854-857)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GKPGSGKPGSGKPGSGKPGSGKPG
S/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKEC
EELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYV
DGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDV
SGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 858)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AH

>XENP023343 - human_IL15_N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - human_IL15_N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (18295) (SEQ ID NOS 859-861)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (17761) (SEQ ID NOS 862-864)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

>XENP023472 empty-Fc-IL15_N65D/E87C-human_IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – empty_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 865)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 2 - IL15_N65D/E87C (SEQ ID NO: 866)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

Chain 3 - IL15Ra(Sushi-D96/C97)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 867-869)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC/EPKSSDK
THTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AI

>XENP023473 empty-Fc-IL15_N65D/L52C-human_IL15Ra(Sushi-S40C)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – empty_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NO: 870)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 2 - IL15_N65D/L52C (SEQ ID NO: 871)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 3 - IL15Ra(Sushi-S40C)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 872-874)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHED?EVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE?QVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP023504 human_IL15_Q108E_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 875-877)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 878-880)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

>XENP023554 - human_IL15_N1D/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18783) (SEQ ID NOS 881-883)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 884-886)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AJ

>XENP023555 - human_IL15_N1D/Q108E_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N1D/Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18784) (SEQ ID NOS 887-889)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 890-892)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023557 - human_IL15_N4D/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N4D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18786) (SEQ ID NOS 893-895)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 896-898)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023559 - human_IL15_D30N/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D30N/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (18788) (SEQ ID NOS 899-901)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (15908) (SEQ ID NOS 902-904)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AK

>XENP023560 human_IL15_D30N/Q108E_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_D30N/Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 905-907)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 908-910)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP023561 human_IL15_N65D/Q108E_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_N65D/Q108E_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 911-913)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 914-916)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPKSSDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024013 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(D61N;single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(D61N;single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 917-920)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS
IHNTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 921)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104AL

>XENP024014 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(N65D;single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(N65D;single-chain) _Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 922-925)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 926)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024015 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(Q108E;single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(Q108E;single-chain) _Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 927-930)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 931)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024016 human_IL15Ra(sushi)_(GGGGS)5-human_IL15(N1D/D61N;single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15(N1D/D61N;single-chain) _Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 932-935)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGS/DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 936)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AM

>XENP024017 human_IL15(D61N)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(D61N)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 937-939)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 940-942)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024018 human_IL15(N65D)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 943-945)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 946-948)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024019 - human_IL15(Q108E)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(Q108E)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (19242) (SEQ ID NOS 949-951)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 952-954)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AN

>XENP024020 - human_IL15(N1D/D61N)-human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15(N1D/D61N)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (19243) (SEQ ID NOS 955-957)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (16481) (SEQ ID NOS 958-960)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024043 human_IL15_E64Q/N65D_(GGGGS)1-human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15_E64Q/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 961-963)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 964-966)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP024044 human_IL15_N1D/N4D/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N1D/N4D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 967-969)

DWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTK?REEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 970-972)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

Figure 104AO

>XENP024045 human_IL15_D30N/E64Q/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_D30N/E64Q/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 973-975)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 976-978)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP024048 human_IL15_N4D/D61N/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N4D/D61N/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 979-981)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 982-984)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

>XENP024050 human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 985-988)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDAS
IHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPP
VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AO (continued)

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 989)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104AP

>XENP024051 human_IL15_N1D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N1D/N65D-human_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 990-992)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 993-995)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024052 human_IL15_N4D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15_N4D/N65D-human_ Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 996-998)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NOS 999-1001)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024113 human_IL15_N4D/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N4D/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1002-1004)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 –human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 1005-1007)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

Figure 104AQ

>XENP024301 human_IL15_N4D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N4D/N65D_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1008-1010)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 1011-1013)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

>XENP024306 human_IL15_D30N/E64Q/N65D_(GGGGS)1-human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_D30N/E64Q/N65D_(GGGGS)1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1014-1016)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/GGGGS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_(GGGGS)1_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 1017-1019)

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/EPK
SSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLV
KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLS
PGK

Figure 104AR

>XENP024341 human_IL15_N1D/N65D-human_IL15Rα(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15_N1D/N65D-human_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1020-1022)
DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSD
GSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 1023-1025)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

>XENP024342 human_IL15(non-covalent; Q108E)-human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K

Chain 1 – human_IL15Rα(Sushi) _Fc(216)_IgG1_C220S/PVA_/S267K (SEQ ID NOS 1026-1028)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 –human_IL15(non-covalent; Q108E) (SEQ ID NO: 1029)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

>XENP024346 human_IL15(non-covalent; Q108E)-human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S

Chain 1 – human_IL15Rα(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S (SEQ ID NOS 1030-1032)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – human_IL15(non-covalent; Q108E) (SEQ ID NO: 1033)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Figure 104AS

>XENP024348 IL15(non-covalent)-human_IL15Ra(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – IL15 WT (SEQ ID NO: 1034)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 – human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1035-1037)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1038)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

>XENP024349 IL15_Q108E_(non-covalent)-human_IL15Rα(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 – human_IL15Rα(Sushi)_ Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1039-1041)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty- Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1042)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Chain 3 – IL15_Q108E_(non-covalent) (SEQ ID NO: 1043)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

>XENP024351 human_IL15(non-covalent; N4D/N65D)-human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S

Chain 1 – IL15(N4D/N65D) (SEQ ID NO: 1044)
NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_C220S/PVA_/S267K/M428L/N434S (SEQ ID NOS 1045-1047)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTHTCPPCPAPPVAGPSV
FLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 104AT

>XENP024383 IL15_Q108E_(non-covalent)-human_IL15Ra(Sushi)_empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - IL15_Q108E (SEQ ID NO: 1048)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1049-1051)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1052)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSL
SLSPGK

>XENP024475 human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1053-1056)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGG
SGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE
SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1057)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104AU

>XENP024476 human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;N4D/N65D)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)6-human_IL15(single-chain;N4D/N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1058-1061)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1062)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024477 human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1063-1066)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1067)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024478 human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1068-1071)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1072)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AV

>XENP024479 human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;N4D/N65D)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(GGGGS)7-human_IL15(single-chain;N4D/N65D)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1073-1076)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - empty-Fc_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1077)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>XENP024480 human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1078-1081)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/DPALVHQRPAPPGGGGSGGGGSGGGGSGGG/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1082)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AW

>XENP024481 human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain;Q108E)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - human_IL15Ra(sushi)_(30AA_linker_variant)-human_IL15(single-chain;Q108E)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1083-1086)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/DPALVHQRP
APPGGGGSGGGGSGGGGSGGG/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLE
SGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVEMFINTS/EPKSSDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAV
EWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 – empty_ Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1087)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

>XENP024890 IL15_N4D/N65D_(non-covalent)-human_IL15Ra(Sushi)-empty-Fc_IgG1_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q

Chain 1 – IL-15_N4D/N65D (SEQ ID NOS 1088-1090)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1091-1093)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 – empty_Fc(216)_ IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 1094)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104AX

>XENP25138 IL15_D30N/E64Q/N65D_(non-covalent)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - IL15_D30N/E64Q/N65D (SEQ ID NO: 1095)
NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - human_IL15Ra(Sushi)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S (SEQ ID NOS 1096-1098)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/EPKSSDKTH
TCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPS
DIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - empty_Fc(216)_ IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 1099)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

>XENP025938 human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-empty-Fc_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 – human_IL15Ra(sushi)_(GGGGS)5-human_IL15_N4D/N65D_(single-chain)-_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NOS 1100-1103)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGSGGGGSGGGGSGGGGSGGGG
S/NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKEC
EELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYV
DGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDV
SGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 – empty_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NOS 1104-1108)
EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

human_IL15Ra(sushi)(single-chain)-human_IL15_Fc(216)_IgG1_C220S/PVA_/S267K; corresponding to Figure 14

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR/GGGGS/NWV
NVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNG
NVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104AY

empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(single-chain)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q; corresponding to Figure 16

Chain 1 - empty-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S_(GGGGS)2_IL15Ra(Sushi)_IL15(single-chain) (SEQ ID NOS 1109-1112)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKP
REEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT
CDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSL
SLSPGK/GGGGSGGGGS/ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT
TPSLKCIR/GGGGS/NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIH
DTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Chain 2 - empty-Fc(216)_IgG1_ISO(+RR)_C220S/PVA_/S267K/S364K/E357Q (8927) (SEQ ID NO: 1113)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

Figure 104AZ

IL-15 and IL-15 receptor Sequences – corresponds to Figure 2

Human IL-15 precursor sequence (SEQ ID NO: 1114)

>sp|P40933

MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVFILGCFSAGLPKTEANWVNVISDLKKIEDLIQSMHIDATLYT
ESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQS
FVHIVQMFINTS

Human IL-15 mature form sequence (SEQ ID NO: 1115)

>sp|P40933|49-162

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLS
SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Human IL-15Rα sequence (SEQ ID NO: 1116)

>sp|Q13261

MAPRRARGCRTLGLPALLLLLLLRPPATRGITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTEC
VLNKATNVAHWTTPSLKCIRDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGS
QLMPSKSPSTGTTEISSHESSHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLA
CYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENCSHHL

Human IL-15Rα, extracellular domain (SEQ ID NO: 1117)

>sp|Q13261|31-205

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPALVHQRPA
PPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAAIVPGSQLMPSKSPSTGTTEISSHESSHGTPSQTTA
KNWELTASASHQPPGVYPQGHSDTT

Human IL-15Rα, sushi domain (SEQ ID NO: 1118)

>sp|Q13261|31-95

ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

Human IL-15Rß sequence (SEQ ID NO: 1119)

>sp|P14784

MAAPALSWRLPLLILLLPLATSWASAAVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCE
LLPVSQASWACNLILGAPDSQKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNI
SWEISQASHYFERHLEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQ
PLAFRTKPAALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGPWLKKVLKCNTPDPSKFFSQLSSEHGGDV
QKWLSSPFPSSSFSPGGLAPEISPLEVLERDKVTQLLLQQDKVPEPASLSSNHSLTSCFTNQGYFFFHLPDALEI
EACQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSGEDDAYCTFPSRDDLLLFSPSLLGGPSPPSTAPGGSGA
GEERMPPSLQERVPRDWDPQPLGPPTPGVPDLVDFQPPPELVLREAGEEVPDAGPREGVSFPWSRPPGQGEFRAL
NARLPLNTDAYLSLQELQGQDPTHLV

Human IL-15Rß, extracellular domain (SEQ ID NO: 1120)

>sp|P14784|27-240

AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDSQKLTTV
DIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERHLEFEARTLSPGH
TWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKPAALGKDT

Figure 104BA

Human common gamma chain sequence (SEQ ID NO: 1121)

>sp|P31785

MLKPSLPFTSLLFLQLPLLGVGLNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWN
SSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQN
LVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS
RFNPLCGSAQHWSEWSHPIHWGSNTSKENPFLFALEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLEDLV
TEYHGNFSAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKPET

Human common gamma chain, extracellular domain (SEQ ID NO: 1122)

>sp|P31785|23-262

LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDND
KVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLEL
NWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWG
SNTSKENPFLFALEA

Figure 104BB

Linker Sequences - corresponds to Figure 7

	SEQ ID NO
GGGGS	14
GGGGSGGGGS	15
GGGGSGGGGSGGGGS	16
GGGGSGGGGSGGGGSGGGGS	17
GGGGSGGGGSGGGGSGGGGSGGGGS	18
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	19
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	20
DPALVHQRPAPPGGGGSGGGGSGGGGSGGG	21
GKPGS	22
GKPGSGKPGSGKPGSGKPGSGKPGS	23
GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	24
GGGES	25

Figure 104BC

Backbone Sequences - corresponds to Figure 9

IL-15/Rα-Fc Backbone 1

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1123)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1124)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 2

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1125)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1126)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 3

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1127)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1128)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCEVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104BD

IL-15/Rα-Fc Backbone 4

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1129)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSKGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1130)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTENEVSLTCLVKGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLEVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 5

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1131)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1132)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSRDELTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 6

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1133)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1134)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104BE

IL-15/Rα-Fc Backbone 7

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1135)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1136)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 8

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1137)

ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHN
AKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPS
QEQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNV
FSCSVMHEALHNHYTQKSLSLSLGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1138)

ESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHN
AKTKPREEEFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPS
QEEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWEEGDV
FSCSVMHEALHNHYTQKSLSLSLGK

IL-15/Rα-Fc Backbone 9

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1139)

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA
KTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1140)

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNA
KTKPREEEFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVF
SCSVMHEALHNHYTQKSLSLSPGK

Figure 104BF

IL-15/Rα-Fc Backbone 10

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1141)

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNA
KTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1142)

ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNA
KTKPREEEFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR
EEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVF
SCSVMHEALHNHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 11

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1143)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVLHEALHSHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1144)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVLHEALHSHYTQKSLSLSPGK

IL-15/Rα-Fc Backbone 12

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1145)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1146)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104BG

IL-15/Rα-Fc Backbone 13

>IL-15/Rα-Fc monomer 1 (SEQ ID NO: 1147)

EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEV
HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQG
DVFSCSVMHEALHNHYTQKSLSLSPGK

>IL-15/Rα-Fc monomer 2 (SEQ ID NO: 1148)

ERKSSDKTHTCPRCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
PSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 104BH

Example 2A sequences

IL-15Rα(sushi-D96) of Figure 27 (SEQ ID NO: 1149)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRD

IL-15Rα(sushi-D96/P97) of Figure 27 (SEQ ID NO: 1150)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDP

IL-15Rα(sushi-D96/P97/A98) of Figure 27 (SEQ ID NO: 1151)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA

IL-15(E87C) of Figure 28 (SEQ ID NO: 1152)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKCCEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(V49C) of Figure 28 (SEQ ID NO: 1153)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQCISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(L52C) of Figure 28 (SEQ ID NO: 1154)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISCESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(E89C) of Figure 28 (SEQ ID NO: 1155)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECCELEEKNIKEFLQSFVHIVQMFINTS

IL-15(Q48C) of Figure 28 (SEQ ID NO: 1156)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELCVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(E53C) of Figure 28 (SEQ ID NO: 1157)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLCSGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS
of Figure 28
IL-15(C42S) (SEQ ID NO: 1158)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKSFLLELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

IL-15(L45C) of Figure 28 (SEQ ID NO: 1159)
NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLCELQVISLESGDASIHDTVENLII
LANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 104BI

IL-15Rα(sushi-D96/C97) of Figure 29 (SEQ ID NO: 1160)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDC

IL-15Rα(sushi-D96/P97/C98) of Figure 29 (SEQ ID NO: 1161)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPC

IL-15Rα(sushi-D96/C97/A98) of Figure 29 (SEQ ID NO: 1162)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDCA

IL-15Rα(sushi-S40C) of Figure 29 (SEQ ID NO: 1163)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTCSLTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-K34C) of Figure 29 (SEQ ID NO: 1164)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFCRKAGTSSLTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-G38C) of Figure 29 (SEQ ID NO: 1165)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKACTSSLTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-L42C) of Figure 29 (SEQ ID NO: 1166)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKAGTSSCTECVLNKATNVAHWTTPSLKCIR

IL-15Rα(sushi-A37C) of Figure 29 (SEQ ID NO: 1167)
ITCPPPMSVEHADIWVKSYSLYSRERYICNSGFKRKCGTSSLTECVLNKATNVAHWTTPSLKCIR

Figure 104BJ

IL-15 Variant Sequences – corresponds to Figure 47

N1D (SEQ ID NO: 1168)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

N4D (SEQ ID NO: 1169)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

D8N (SEQ ID NO: 1170)

NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

D30N (SEQ ID NO: 1171)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

D61N (SEQ ID NO: 1172)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

E64Q (SEQ ID NO: 1173)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

N65D (SEQ ID NO: 1174)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Q108E (SEQ ID NO: 1175)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVEMFINTS

N1D/D61N (SEQ ID NO: 1176)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNV
TESGCKECEELEEKNIKEFLQSFVHIVQMFINTS

Figure 104BK

N1D/E64Q (SEQ ID NO: 1177)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/D61N (SEQ ID NO: 1178)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/E64Q (SEQ ID NO: 1179)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D8N/D61N (SEQ ID NO: 1180)

NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D8N/E64Q (SEQ ID NO: 1181)

NWVNVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D61N/E64Q (SEQ ID NO: 1182)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

E64Q/Q108E (SEQ ID NO: 1183)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N1D/N4D/D8N (SEQ ID NO: 1184)

DWVDVISNLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D61N/E64Q/N65D (SEQ ID NO: 1185)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/D61N/E64Q/Q108E (SEQ ID NO: 1186)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N4D/D61N/E64Q/Q108E (SEQ ID NO: 1187)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVQNLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

Figure 104BL

N1D/N65D (SEQ ID NO: 1188)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/Q108E (SEQ ID NO: 1189)

DWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N4D/N65D (SEQ ID NO: 1190)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/N65D (SEQ ID NO: 1191)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/Q108E (SEQ ID NO: 1192)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVENLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

N65D/Q108E (SEQ ID NO: 1193)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVEMFINTS

E64Q/N65D (SEQ ID NO: 1194)

NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N1D/N4D/N65D (SEQ ID NO: 1195)

DWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHDTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

D30N/E64Q/N65D (SEQ ID NO: 1196)

NWVNVISDLKKIEDLIQSMHIDATLYTESNVHPSCKVTAMKCFLLELQVISLESGDASIHDTVQDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

N4D/D61N/N65D (SEQ ID NO: 1197)

NWVDVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHNTVEDLIILANNSLSSNGNVTESGCKECEE
LEEKNIKEFLQSFVHIVQMFINTS

Figure 105

5201

Non-Xtend	Xtend	Format	Substitutions
22822	**23504**	IL-15/Rα-heteroFc	Q108E
24045	**24306**	IL-15/Rα-heteroFc	D30N/E64Q/N65D
22821	23343	IL-15/Rα-heteroFc	N65D
23557	24113	IL-15/Rα-heteroFc	N4D/N65D
24051	24341	IL-15/Rα-heteroFc	N1D/N65D
24052	24301	IL-15/Rα-heteroFc	N1D/N65D
24342	24346	bivalent ncIL-15/Rα-Fc	Q108E
24349	24383	ncIL-15/Rα-Fc	Q108E

Figure 106

XENP	Heterodimer-skewing variant, Chain 1	Heterodimer-skewing variant, Chain 2	Heterodimer Yield (%)	CH3 Tm (°C)
12757	none	none	52.7	83.1
12758	L368D/K370S	S364K	94.4	76.6
12759	L368D/K370S	S364K/E357L	90.2	77.2
12760	L368D/K370S	S364K/E357Q	95.2	77.5
12761	T411E/K360E/Q362E	D401K	85.6	80.6
12496	L368E/K370S	S364K	91.5	n.d.
12511	K370S	S364K	59.9	n.d.
12840	L368E/K370S	S364K/E357Q	59.5	n.d.
12841	K370S	S364K/E357Q	90.4	n.d.
12894	L368E/K370S	S364K	41.0	n.d.
12895	K370S	S364K	49.3	n.d.
12896	L368E/K370S	S364K/E357Q	73.9	n.d.
12901	K370S	S364K/E357Q	87.9	n.d.