Figure 1A

Human CD28 sequence SEQ ID NO: 1

>sp|P10747|CD28_HUMAN T-cell-specific surface glycoprotein CD28 OS=Homo sapiens OX=9606 GN=CD28 PE=1 SV=1

MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQ
VYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFW
VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS

Human CD28, extracellular domain SEQ ID NO: 2

>sp|P10747|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNESV
TFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP

Mouse CD28 sequence SEQ ID NO: 3

>sp|P31041|CD28_MOUSE T-cell-specific surface glycoprotein CD28 OS=Mus musculus OX=10090 GN=Cd28 PE=1 SV=2

MTLRLLFLALNFFSVQVTENKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNGNFTYQP
QFRSNAEFNCDGDFDNETVTFRLWNLHVNHTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHLCHTQSSPKLFWAL
VVVAGVLFCYGLLVTVALCVIWTNSRRNRLLQSDYMNMTPRRPGLTRKPYQPYAPARDFAAYRP

Mouse CD28, extracellular domain SEQ ID NO: 4

>sp|P31041|20-150

NKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNGNFTYQPQFRSNAEFNCDGDFDNETV
TFRLWNLHVNHTDIYFCKIEFMYPPPYLDNERSNGTIIHIKEKHLCHTQSSPKL

Figure 1B

Cynomolgus CD28 sequence SEQ ID NO: 5

>tr|Q0PDN3|Q0PDN3_MACFA CD28 OS=Macaca fascicularis OX=9541 GN=CD28 PE=2 SV=1

MLRLLLALNLLPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQ
VYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFW
ALVVVGGVLACYSLLVTVAFCIFWMRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS

Cynomolgus CD28, extracellular domain SEQ ID NO: 6

>tr|Q0PDN3|19-152

NKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYSKTGFNCDGKLGNESV
TFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKP

Cynomolgus CD28 sequence (predicted) SEQ ID NO: 7

>XP_015308533.1 PREDICTED: CD276 antigen isoform X1 [Macaca fascicularis]

MKLSSDHVFPLFRKLQWLPAAFRIQFTPVSPSAGAAFHHGEPSCQLPHSKMLHRRGSPGMGVHVGAALGALWFCLTG
ALEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGN
ASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDG
QGAPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQVPEDPVVA
LVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASLRLQRVRVADE
GSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGAPLTGNVTTSQ
MANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEALWVTVGLSVCLVALLVALAFVCW
RKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKEDDGQELA

Cynomolgus CD28, extracellular domain SEQ ID NO: 8

>XP_015308533.1|79-516

LEVQVPEDPVVALVGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNA
SLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQ
GAPLTGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSITITPQRSPTGAVEVQVPEDPVVAL
VGTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYANRTALFLDLLAQGNASLRLQRVRVADEG
SFTCFVSIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYRGYPEAEVFWQDGQGAPLTGNVTTSQM
ANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEA

Figure 2A

Human STEAP-1 sequence SEQ ID NO: 9

>sp|Q9UHE8|STEA1_HUMAN Metalloreductase STEAP1 OS=Homo sapiens OX=9606
MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAHADEFDCPSE
LQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPM
VSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSL
SYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPS
VSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIV
VLIFKSILFLPCLRKKILKIRHGWEDVTKINKTEICSQL

Mouse STEAP-1 sequence SEQ ID NO: 10

>sp|Q9CWR7|STEA1_MOUSE Metalloreductase STEAP1 OS=Mus musculus OX=10090
MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLSHLQHAVHVDAFDCPSE
LQHTQEFFPNWRLPVKVAAIISSLTFLYTLLREIIYPLVTSREQYFYKIPILVINKVLPM
VAITLLALVYLPGELAAVVQLRNGTKYKKFPPWLDRWMLARKQFGLLSFFFAVLHAVYSL
SYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRMEIYVSLGIVGLAILALLAVTSIPS
VSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNKWVDVSQFVWYMPPTFMIAVFLPTL
VLICKIALCLPCLRKKILKIRCGWEDVSKINRTEMASRL

Figure 2B

Human CEA sequence SEQ ID NO: 11

>sp|P06731|CEAM5_HUMAN Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens OX=9606 GN=CEACAM5 PE=1 SV=4
MESPSAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEGKEVLLLVHNLPQHLFGYSWYKGERVDGNR
QIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNS
KPVEDKDAVAFTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVIL
NVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAHNSDTGL
NRTTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTR
NDVGPYECGIQNELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGNIQQHTQEL
FISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWWVNGQ
SLPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCH
SASNPSPQYSWRINGIPQQHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSASGTSPGLSAGATVGIMI
GVLVGVALI

Mouse CEA sequence SEQ ID NO: 12

>sp|Q3UKK2|CEAM5_MOUSE Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Mus musculus OX=10090 GN=Ceacam5 PE=2 SV=1
MEASSVLPCKWCTHLQGLLLTASFLTCCHLPTTAQITIELEPPQVIEGENVLIRVNNLTENLITLAWFRGMRIKSPQ
IGQYTPATKVTVLGPGHSGRETLYSNGSLQIYNVTQEDIGFYSLRIINKHAEIVSITSIYLNVYSSLWTCEHPSPHA
KLTIESVPPGISEGGSVLLLVKNLPQNLLSLFWYKGVIAVKKFEIARHIKATNSSVPGPAHTGRETVFSNGSLLLQE
VMQSDTGFYTLRTMSTDLKDEVAHVQLYMDTYLLTCYHPLQVKIESLPQNVAVGKTVLLLVHNLPEDFQAFFWYKSA
YRRDTYKIAEYKRAMDATILGSAYSSREFIYNNGSMLIIDVTEDDAGYFLLEILREDLKIEKAYIQLHVNSFVSNSK
DSASTARLSIESVPPSIVEGGSVLLLVHNLPKNLQSLFWYKGMIAEKKSELIQHIIATSSSLPGPAHSGRETVYNNG
SLLLQRVMQNDTQFYTLQTMDTDLKYEVAHVQLQLDTSLSTWYHPLQVKIESLPRNVAVGKSVLFLVHNFPEVFRAF
SWYKPAYKSHTSKIVEYHRFTDSATVGAAYRGIEVIFTNGSMVMIDVTEDDAGFYMLEILREDFKVEKAYVQLHVNS
FVPNSKVSVSTARLSIESVPPSIVGGESVLLLVHNLPKNLQSLFWYKGVIAEEKSELIQHIIATSSSLPGPAHSGRE
TVYSNGSLLLQRVMQNDTGFYTLLTMSTDLKDEIAHVQLQLDTSTCCSLLTSDQLIIVPVPRNIAVGKSVLLLVCNV
PKDVQTIFWYKSVYRTDIFKIAEYSRSMESTIWGLAHSGKEMVYTNGSLLIQNVTEHDAGLYMLEILHKDYKLERAH
VQVHVNNPVSWPFVRVTDTTVRVQSSVVFTCFSADPGVSIRWLFNKQSLQLTERMTLSPSKCQLSIDPVWREDAGKY
QCEVSNPVSSKSSLPVRLAVIEE

Macaca fascicularis CEA sequence SEQ ID NO: 13

>XP_005589491.2 carcinoembryonic antigen-related cell adhesion molecule 5 isoform X1 [Macaca fascicularis]
MGSPSAPLHRWCIPWQTLLLTASLLTFWNPPTTAQLTIESRPFNVAEGKEVLLLAHNVSQNLFGYIWYKGERVDASR
RIGSCVIRTQQITPGPAHSGRETIDFNASLLIHNVTQSDTGSYTIQVIKEDLVNEEATGQFRVYPELPKPYISSNNS
NPVEDKDAVALTCEPETQDTTYLWWVNNQSLPVSPRLELSSDNRTLTVFNIPRNDTTSYKCETQNPVSVRRSDPVTL
NVLYGPDAPTISPLNTPYRAGENLNLSCHAASNPAAQYSWFVNGTFQQSTQELFIPNITVNNSGSYMCQAHNSATGL
NRTTVTAITVYAELPKPYITSNNSNPIEDKDAVTLTCEPETQDTTYLWWVNNQSLSVSSRLELSNDNRTLTVFNIPR
NDTTFYECETQNPVSVRRSDPVTLNVLYGPDAPTISPLNTPYRAGENLNLSCHAASNPAAQYSWFVNGTFQQSTQEL
FIPNITVNNSGSYMCQAHNSATGLNRTTVTAITVYVELPKPYISSNNSNPIEDKDAVTLTCEPVAENTTYLWWVNNQ
SLSVSPRLQLSNGNRILTLLSVTRNDTGPYECGIQNSESAKRSDPVTLNVTYGPDTPIISPPDLSYRSGANLNLSCH
SDSNPSPQYSWLINGTLRQHTQVLFISKITSNNNGAYACFVSNLATGRNNSIVKNISVSSGDSAPGSSGLSARATVG
IIIGMLVGVALM

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
T366S/L368A/Y407V/S354C	T366W/Y349C
S354C	Y349C
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	P217R/P228R/N276K
K274Q/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
K274Q/R355Q/Q419E/K447_	P217R/P228R/N276K
K274Q/R355Q/Q419E/K447_	N276K
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/N276K
I199T/N203D/K274Q/R355Q/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K274Q/R355Q/Q419E/K447_	Q196K/I199T/N276K

Figure 3F

Monomer 1	Monomer 2
I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447_	
N208D/Q295E/N384D/Q418E/N421D	
N208D/Q295E/Q418E/N421D	
Q196K/I199T/P217R/P228R/N276K	
Q196K/I199T/N276K	
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(-)	I199T/N203D/K274Q/R355Q/N384S/K392N/N397M/Q418E/K447_
pI_ISO(-)-Fc only	K274Q/R355Q/N384S/K392N/V397M/Q418E/K447_
pI_(-)_isosteric_A	N208D/Q295E/N384D/Q418E/N421D
pI_(-)_isosteric A-Fc only	Q295E/N384D/Q418E/N421D
pI_(-)_isosteric_B	N208D/Q295E/Q418E/N421D
pI_(-)_isosteric_B-Fc only	Q295E/Q418E/N421D
pI_ISO(+RR)	Q196K/I199T/P217R/P228R/N276K
pI_ISO(+RR)-Fc only	P217R/P228R/N276K
pI_ISO(+)	Q196K/I199T/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
T299R
T299K
K322A
A327G
A327L
A327N
A327Q
L328E
L328R
P329A
P329H
P329K
A330L
A330S/P331S
I332K
I332R
V266D/A327Q
V266D/P329K
S267R/A327Q
S267R/P329K
G236R/L328R
E233P/L234V/L235A/G236_/S239K
E233P/L234V/L235A/G236_/S267K
E233P/L234V/L235A/G236_/S239K/A327G
E233P/L234V/L235A/G236_/S267K/A327G
E233P/L234V/L235A/G236_
S239K/S267K
S267K/P329K
L234A/L235A/D265S

Figure 6

Positive Charged scFv Linkers

Name	Sequence	Length	Charge	
Gly-Ser 15	GGGGSGGGGSGGGGS	15	0	SEQ ID NO: 14
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	SEQ ID NO: 15
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	SEQ ID NO: 16
+B	GKGGSGKGGSGKGGS	15	+3	SEQ ID NO: 17
+C	GGKGSGGKGSGGKGS	15	+3	SEQ ID NO: 18
+D	GGGKSGGGKSGGGKS	15	+3	SEQ ID NO: 19
+E	GKGKSGKGKSGKGKS	15	+6	SEQ ID NO: 20
+F	GGGKSGGKGSGKGGS	15	+3	SEQ ID NO: 21
+G	GKPGSGKPGSGKPGS	15	+3	SEQ ID NO: 22
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	SEQ ID NO: 24
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	SEQ ID NO: 23

Negative Charged scFv Linkers

Name	Sequence	Length	Charge	
Gly-Ser 20	GGGGSGGGGSGGGGSGGGGS	20	0	SEQ ID NO: 25
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	SEQ ID NO: 26
-B	GEGGSGEGGSGEGGS	15	-3	SEQ ID NO: 27
-C	GGEGSGGEGSGGEGS	15	-3	SEQ ID NO: 28
-D	GGGESGGGESGGGES	15	-3	SEQ ID NO: 29
-E	GEGESGEGESGEGES	15	-6	SEQ ID NO: 30
-F	GGGESGGEGSGEGGS	15	-3	SEQ ID NO: 31
-G	GEGESGEGESGEGESGEGES	20	-8	SEQ ID NO: 32

Additional scFv Linkers

GGGGSGGGGSGGGGS	SEQ ID NO: 14
GGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 25
GSTSGSGKPGSGEGSTKG	SEQ ID NO: 15
PRGASKSGSASQTGSAPGS	SEQ ID NO: 33
GTAAAGAGAAGGAAAGAAG	SEQ ID NO: 34
GTSGSSGSGSGGSGSGGGG	SEQ ID NO: 35
GKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 24

Figure 7

Useful domain linkers

Name	Sequence	SEQ ID NO:
$(GGGGS)_1$ or GGGGS	GGGGS	SEQ ID NO: 36
$(GGGGS)_2$	GGGGSGGGGS	SEQ ID NO: 37
$(GGGGS)_3$	GGGGSGGGGSGGGGS	SEQ ID NO: 14
$(GGGGS)_4$	GGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 25
$(GGGGS)_5$	GGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 38
$(GGGGS)_6$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 39
$(GGGGS)_7$	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	SEQ ID NO: 40
$(GGGGA)_1$ or GGGGA	GGGGA	SEQ ID NO: 41
$(GGGGA)_2$	GGGGAGGGGA	SEQ ID NO: 42
$(GGGGA)_3$	GGGGAGGGGAGGGGA	SEQ ID NO: 43
$(GGGGA)_4$	GGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 44
$(GGGGA)_5$	GGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 45
$(GGGGA)_6$	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 46
$(GGGGA)_7$	GGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGA	SEQ ID NO: 47
30AA-linker	DPALVHQRPAPPGGGGSGGGGSGGGGSGGG	SEQ ID NO: 48
$(GKPGS)_1$ or GKPGS	GKPGS	SEQ ID NO: 49
$(GKPGS)_4$	GKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 24
$(GKPGS)_5$	GKPGSGKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 50
$(GKPGS)_6$	GKPGSGKPGSGKPGSGKPGSGKPGSGKPGS	SEQ ID NO: 51
$(GGGES)_1$ or GGGES	GGGES	SEQ ID NO: 52
"full hinge"	EPKSCDKTHTCPPCP	SEQ ID NO: 53
"lower half hinge"	KTHTCPPCP	SEQ ID NO: 54
"full hinge C220S variant"	EPKSSDKTHTCPPCP	SEQ ID NO: 55
"flex lower half hinge"	GGGGSGGGGSKTHTCPPCP	SEQ ID NO: 56
"charged lower half hinge1"	GKPGSGKPGSKTHTCPPCP	SEQ ID NO: 57
"charged lower half hinge2"	GKPGSKTHTCPPCP	SEQ ID NO: 58
"upper half hinge"	EPKSC	SEQ ID NO: 59
"flex upper half hinge"	EPKSCGGGGSGGGGS	SEQ ID NO: 60
"charged upper half hinge1"	EPKSCGKPGSGKPGS	SEQ ID NO: 61
"charged upper half hinge2"	EPKSCGKPGS	SEQ ID NO: 62

Figure 8

Monomer 1 (scFv-Fc)	**Monomer 2 (HC)**
Heterodimer skew variants S364K/E357Q	Heterodimer skew variants L368D/K370S
	Isosteric pI variant N208D/Q295E/N384D/Q418E/N421D
FcKO E233P/L234V/L235A/G236_/S267K	FcKO E233P/L234V/L235A/G236_/S267K
±M428L/N434S for FcRn	±M428L/N434S for FcRn

Figure 9A

Heterodimeric Fc Backbone 1

>Heterodimeric Fc Backbone 1 monomer 1 (-) (SEQ ID NO: 63)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 1 monomer 2 (+) (SEQ ID NO: 64)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 2

>Heterodimeric Fc Backbone 2 monomer 1 (-) (SEQ ID NO: 65)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone monomer 2 (+) (SEQ ID NO: 66)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 3

>Heterodimeric Fc Backbone 3 monomer 1 (-) (SEQ ID NO: 67)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCEVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 3 monomer 2 (+) (SEQ ID NO: 68)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 4

>Heterodimeric Fc Backbone 4 monomer 1 (-) (SEQ ID NO: 69)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTENEVSLTCLVKGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLEVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 4 monomer 2 (+) (SEQ ID NO: 70)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSKGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9B

Heterodimeric Fc Backbone 5

>Heterodimeric Fc Backbone 5 monomer 1 (-) (SEQ ID NO: 71)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 5 monomer 2 (+) (SEQ ID NO: 72)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 6

>Heterodimeric Fc Backbone 6 monomer 1 (-) (SEQ ID NO: 73)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 6 monomer 2 (+) (SEQ ID NO: 74)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 7

>Heterodimeric Fc Backbone 7 monomer 1 (-) (SEQ ID NO: 75)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 7 monomer 2 (+) (SEQ ID NO: 76)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 8

>Heterodimeric Fc Backbone 8 monomer 1 (-) (SEQ ID NO: 77)
APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCDVSGFYPSDIAVEWESD
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWEEGDVFSCSVMHEALHNHYTQKSLSLSLGK

>Heterodimeric Fc Backbone 8 monomer 2 (+) (SEQ ID NO: 78)
APEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEQMTKNQVKLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

Figure 9C

Heterodimeric Fc Backbone 9

>Heterodimeric Fc Backbone 9 monomer 1 (-) (SEQ ID NO: 79)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 9 monomer 2 (+) (SEQ ID NO: 80)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 10

>Heterodimeric Fc Backbone 10 monomer 1 (-) (SEQ ID NO: 81)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEEFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 10 monomer 2 (+) (SEQ ID NO: 82)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heterodimeric Fc Backbone 11

>Heterodimeric Fc Backbone 11 monomer 1 (-) (SEQ ID NO: 83)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 11 monomer 2 (+) (SEQ ID NO: 84)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Heterodimeric Fc Backbone 12

>Heterodimeric Fc Backbone 12 monomer 1 (-) (SEQ ID NO: 85)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 12 monomer 2 (+) (SEQ ID NO: 86)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 9D

Heterodimeric Fc Backbone 13

>Heterodimeric Fc Backbone 13 monomer 1 (SEQ ID NO: 87)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 13 monomer 2 (SEQ ID NO: 88)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Heterodimeric Fc Backbone 14

>Heterodimeric Fc Backbone 14 monomer 1 (SEQ ID NO: 89)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHAHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 14 monomer 2 (SEQ ID NO: 90)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAHYTQKSLSLSPGK

Heterodimeric Fc Backbone 15

>Heterodimeric Fc Backbone 15 monomer 1 (SEQ ID NO: 91)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHAHYTQKSLSLSPGK

>Heterodimeric Fc Backbone 15 monomer 2 (SEQ ID NO: 92)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDQLTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAHYTQKSLSLSPGK

Figure 10

2 + 1 mAb-scFv Heterodimeric Fc Backbone

>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 1 (SEQ ID NO: 93)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>2 + 1 mAb-scFv Heterodimeric Fc Backbone monomer 2 (SEQ ID NO: 94)
APPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Figure 11

IgG1 CH1(+) (SEQ ID NO: 95)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKV

IgG1 CH1(-) (SEQ ID NO: 96)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSDTKVDKKV

IgG2 CH1(+) (SEQ ID NO: 97)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTV

IgG2 CH1(-) (SEQ ID NO: 98)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSDTKVDKTV

IgG4 CH1(+) (SEQ ID NO: 99)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSNTKVDKRV

IgG4 CH1(-) (SEQ ID NO: 100)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TKTYTCNVDHKPSDTKVDKRV

Figure 12

IgG1 hinge (SEQ ID NO: 101)
EPKSCDKTHTCPPCP

IgG2 hinge (SEQ ID NO: 102)
ERKCCVECPPCP

IgG4 hinge (SEQ ID NO: 103)
ESKYGPPCPSCP

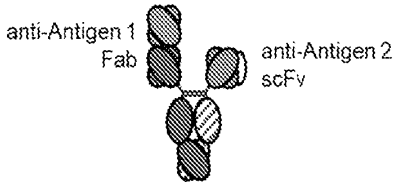
Figure 13

Light Chain Constant Domain – Kappa (SEQ ID NO: 104)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Light Chain Constant Domain – Lambda (SEQ ID NO: 105)
GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPE
QWKSHRSYSCQVTHEGSTVEKTVAPTECS

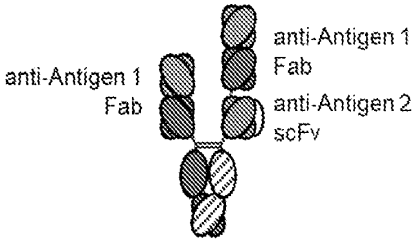
Figures 14A-14F

A)



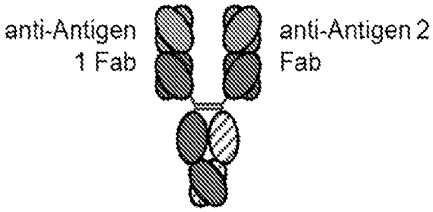
1 + 1 Fab-scFv-Fc

B)



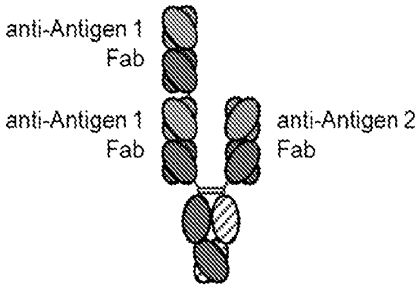
2 + 1 Fab_2-scFv-Fc

C)



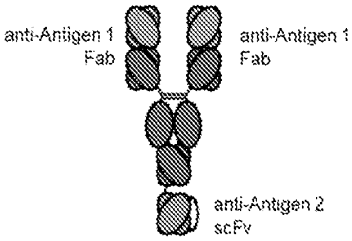
1 + 1 Common Light Chain

D)



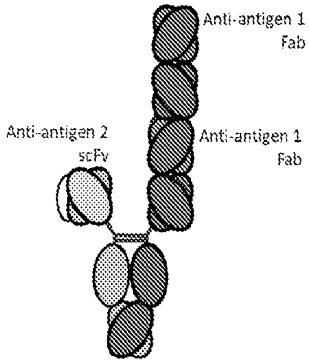
2 + 1 Common Light Chain

E)



2+1 mAb-scFv

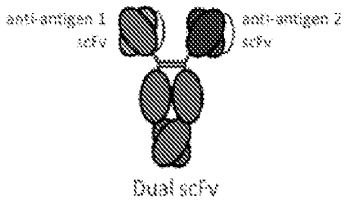
F)



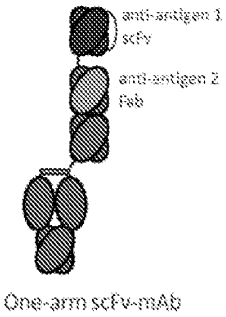
2 + 1 Fab2-Fc x scFv-Fc
or stacked bottle opener

Figures 14G-14J

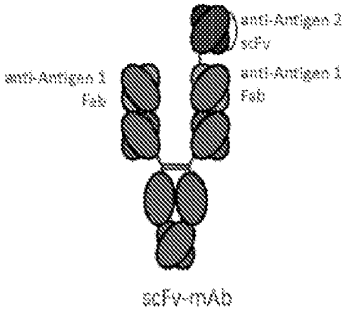
G)



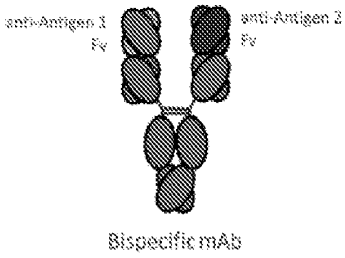
H)



I)

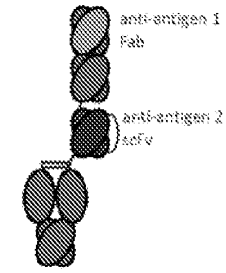


J)



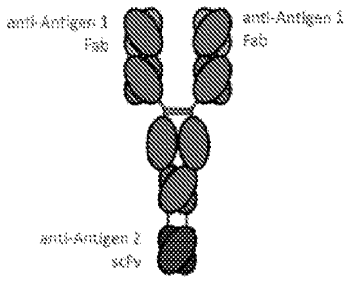
Figures 14K-14N

K)



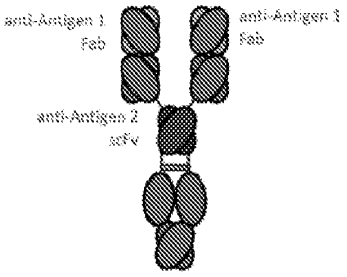
One-arm central-scFv

L)



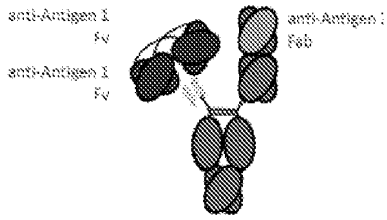
mAb-Fv

M)



central-Fv

N)



Trident

Figure 15

1A7[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLVTVSS	106
vhCDR1	SYAMS	107
vhCDR2	TISGSGDSTYYADSVKG	108
vhCDR3	SGPGLRQVGFDY	109
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PFTFGQGTKLEIK	110
vlCDR1	RASQSISSYLN	111
vlCDR2	AASSLQS	112
vlCDR3	QQSYSTPFT	113

>XENP28428 1A7[CD28]_H1L1_IgG1_PVA_/S267K

Heavy Chain (SEQ ID NO: 114)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Light Chain (SEQ ID NO: 115)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 16A

>**1A7[CD28]_H1.1** SEQ ID NO: 116
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.2** SEQ ID NO: 117
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.3** SEQ ID NO: 118
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.4** SEQ ID NO: 119
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.5** SEQ ID NO: 120
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.6** SEQ ID NO: 121
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.7** SEQ ID NO: 122
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.8** SEQ ID NO: 123
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.9** SEQ ID NO: 124
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.10** SEQ ID NO: 125
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIDGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.11** SEQ ID NO: 126
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIEGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.12** SEQ ID NO: 127
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIYGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.13** SEQ ID NO: 128
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 16B

>**1A7[CD28]_H1.14** SEQ ID NO: 129
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.15** SEQ ID NO: 130
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.16** SEQ ID NO: 131
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.17** SEQ ID NO: 132
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.18** SEQ ID NO: 133
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.19** SEQ ID NO: 134
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.20** SEQ ID NO: 135
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.21** SEQ ID NO: 136
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.22** SEQ ID NO: 137
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIDGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.23** SEQ ID NO: 138
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.24** SEQ ID NO: 139
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.25** SEQ ID NO: 140
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.26** SEQ ID NO: 141
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 16C

>**1A7[CD28]_H1.27** SEQ ID NO: 142
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIEGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.28** SEQ ID NO: 143
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYDSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.29** SEQ ID NO: 144
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.30** SEQ ID NO: 145
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.31** SEQ ID NO: 146
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.32** SEQ ID NO: 147
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIYGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.33** SEQ ID NO: 148
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.34** SEQ ID NO: 149
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.35** SEQ ID NO: 150
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISDSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.36** SEQ ID NO: 151
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGTSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.37** SEQ ID NO: 152
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGYSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.38** SEQ ID NO: 153
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.39** SEQ ID NO: 154
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 16D

>**1A7[CD28]_H1.40** SEQ ID NO: 155
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.41** SEQ ID NO: 156
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIEGSGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.42** SEQ ID NO: 157
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.43** SEQ ID NO: 158
EVQLLESGGGLVQPGGSLRLSCAASGFSFSGNYMTWVRQAPGKGLEWVATITADSDATYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.44** SEQ ID NO: 159
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYSMNWVRQAPGKGLEWVATIYANGSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.45** SEQ ID NO: 160
EVQLLESGGGLVQPGGSLRLSCAASGFNFEEYSMNWVRQAPGKGLEWVATITYNGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.46** SEQ ID NO: 161
EVQLLESGGGLVQPGGSLRLSCAASGFSFRTYYMTWVRQAPGKGLEWVATITSDGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.47** SEQ ID NO: 162
EVQLLESGGGLVQPGGSLRLSCAASGFSFKGYSMNWVRQAPGKGLEWVATIYASSDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.48** SEQ ID NO: 163
EVQLLESGGGLVQPGGSLRLSCAASGFSFGEYSMNWVRQAPGKGLEWVSTIYADGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.49** SEQ ID NO: 164
EVQLLESGGGLVQPGGSLRLSCAASGFTFTDYSMNWVRQAPGKGLEWVATIYADSSSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.50** SEQ ID NO: 165
EVQLLESGGGLVQPGGSLRLSCAASGFTFGGYSMNWVRQAPGKGLEWVATIYYDSTTTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.51** SEQ ID NO: 166
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYSMNWVRQAPGKGLEWVSTIYNDGATTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.52** SEQ ID NO: 167
EVQLLESGGGLVQPGGSLRLSCAASGFSFEAYSMNWVRQAPGKGLEWVATIYYDSSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 16E

>**1A7[CD28]_H1.53** SEQ ID NO: 168
EVQLLESGGGLVQPGGSLRLSCAASGFSFGSYYMSWVRQAPGKGLEWVASIYYGGYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.54** SEQ ID NO: 169
EVQLLESGGGLVQPGGSLRLSCAASGFNFAEYSMSWVRQAPGKGLEWVATIYAGSDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.55** SEQ ID NO: 170
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYSINWVRQAPGKGLEWVATIYYDGSYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.56** SEQ ID NO: 171
EVQLLESGGGLVQPGGSLRLSCAASGFTFSRYYINWVRQAPGKGLEWVASIYDGGADTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.57** SEQ ID NO: 172
EVQLLESGGGLVQPGGSLRLSCAASGFSFGTYSINWVRQAPGKGLEWVSTIYYDGASTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.58** SEQ ID NO: 173
EVQLLESGGGLVQPGGSLRLSCAASGFTFGKYSISWVRQAPGKGLEWVATIYNDGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.59** SEQ ID NO: 174
EVQLLESGGGLVQPGGSLRLSCAASGFSFEKYYISWVRQAPGKGLEWVASIYDGSYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.60** SEQ ID NO: 175
EVQLLESGGGLVQPGGSLRLSCAASGFSFGTYSMNWVRQAPGKGLEWVATIDYDGSNTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.61** SEQ ID NO: 176
EVQLLESGGGLVQPGGSLRLSCAASGFSFAAYSMSWVRQAPGKGLEWVATIYAGSDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.62** SEQ ID NO: 177
EVQLLESGGGLVQPGGSLRLSCAASGFTFTTYSMTWVRQAPGKGLEWVATIYNDGYYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.63** SEQ ID NO: 178
EVQLLESGGGLVQPGGSLRLSCAASGFSFKDYSMNWVRQAPGKGLEWVATIYYDGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.64** SEQ ID NO: 179
EVQLLESGGGLVQPGGSLRLSCAASGFSFAAYSMNWVRQAPGKGLEWVATIYAGGAYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.65** SEQ ID NO: 180
EVQLLESGGGLVQPGGSLRLSCAASGFNFAEYYISWVRQAPGKGLEWVASIYNGGSDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 16F

>**1A7[CD28]_H1.66** SEQ ID NO: 181
EVQLLESGGGLVQPGGSLRLSCAASGFSLGEYYMNWVRQAPGKGLEWVSTIDYDGTYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.67** SEQ ID NO: 182
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYYITWVRQAPGKGLEWVSSIYSSSYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.68** SEQ ID NO: 183
EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYYITWVRQAPGKGLEWVSSIYTSGYDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

>**1A7[CD28]_H1.69** SEQ ID NO: 184
EVQLLESGGGLVQPGGSLRLSCAASGFSFGKYSINWVRQAPGKGLEWVATIYSDGTDTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 17A

>**1A7[CD28]_L1.1** SEQ ID NO: 185
DIQMTQSPSSLSASVGDRVTITCRASQSISAYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.2** SEQ ID NO: 186
DIQMTQSPSSLSASVGDRVTITCRASQSISDYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.3** SEQ ID NO: 187
DIQMTQSPSSLSASVGDRVTITCRASQSISGYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.4** SEQ ID NO: 188
DIQMTQSPSSLSASVGDRVTITCRASQSISHYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.5** SEQ ID NO: 189
DIQMTQSPSSLSASVGDRVTITCRASQSISKYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.6** SEQ ID NO: 190
DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.7** SEQ ID NO: 191
DIQMTQSPSSLSASVGDRVTITCRASQSISQYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.8** SEQ ID NO: 192
DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.9** SEQ ID NO: 193
DIQMTQSPSSLSASVGDRVTITCRASQSISVYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.10** SEQ ID NO: 194
DIQMTQSPSSLSASVGDRVTITCRASQSISYYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.11** SEQ ID NO: 195
DIQMTQSPSSLSASVGDRVTITCRASQSISSALNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.12** SEQ ID NO: 196
DIQMTQSPSSLSASVGDRVTITCRASQSISSDLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.13** SEQ ID NO: 197
DIQMTQSPSSLSASVGDRVTITCRASQSISSFLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 17B

>**1A7[CD28]_L1.14** SEQ ID NO: 198
DIQMTQSPSSLSASVGDRVTITCRASQSISSHLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.15** SEQ ID NO: 199
DIQMTQSPSSLSASVGDRVTITCRASQSISSKLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.16** SEQ ID NO: 200
DIQMTQSPSSLSASVGDRVTITCRASQSISSLLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.17** SEQ ID NO: 201
DIQMTQSPSSLSASVGDRVTITCRASQSISSNLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.18** SEQ ID NO: 202
DIQMTQSPSSLSASVGDRVTITCRASQSISSQLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.19** SEQ ID NO: 203
DIQMTQSPSSLSASVGDRVTITCRASQSISSSLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.20** SEQ ID NO: 204
DIQMTQSPSSLSASVGDRVTITCRASQSISSWLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.21** SEQ ID NO: 205
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.22** SEQ ID NO: 206
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLDWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.23** SEQ ID NO: 207
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLGWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.24** SEQ ID NO: 208
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLHWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.25** SEQ ID NO: 209
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLQWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.26** SEQ ID NO: 210
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 17C

>**1A7[CD28]_L1.27** SEQ ID NO: 211
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.28** SEQ ID NO: 212
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLYWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.29** SEQ ID NO: 213
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.30** SEQ ID NO: 214
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.31** SEQ ID NO: 215
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYKASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.32** SEQ ID NO: 216
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYLASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.33** SEQ ID NO: 217
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYQASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.34** SEQ ID NO: 218
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYSASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.35** SEQ ID NO: 219
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.36** SEQ ID NO: 220
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYWASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.37** SEQ ID NO: 221
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYYASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.38** SEQ ID NO: 222
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASALQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.39** SEQ ID NO: 223
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASDLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 17D

>**1A7[CD28]_L1.40** SEQ ID NO: 224
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASKLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.41** SEQ ID NO: 225
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.42** SEQ ID NO: 226
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASQLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.43** SEQ ID NO: 227
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.44** SEQ ID NO: 228
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASYLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.45** SEQ ID NO: 229
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLASGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.46** SEQ ID NO: 230
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLESGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.47** SEQ ID NO: 231
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLFSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.48** SEQ ID NO: 232
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLHSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.49** SEQ ID NO: 233
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLISGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.50** SEQ ID NO: 234
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLKSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.51** SEQ ID NO: 235
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLNSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.52** SEQ ID NO: 236
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLSSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

Figure 17E

>**1A7[CD28]_L1.53** SEQ ID NO: 237
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLVSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.54** SEQ ID NO: 238
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLYSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.55** SEQ ID NO: 239
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQAGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.56** SEQ ID NO: 240
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQDGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.57** SEQ ID NO: 241
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQGGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.58** SEQ ID NO: 242
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQHGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.59** SEQ ID NO: 243
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQKGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.60** SEQ ID NO: 244
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQQGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.61** SEQ ID NO: 245
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQTGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.62** SEQ ID NO: 246
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQVGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.63** SEQ ID NO: 247
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQYGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.64** SEQ ID NO: 248
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQAYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.65** SEQ ID NO: 249
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQDYSTPFTFGQGTKLEIK

Figure 17F

>**1A7[CD28]_L1.66** SEQ ID NO: 250
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQFYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.67** SEQ ID NO: 251
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQHYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.68** SEQ ID NO: 252
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQKYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.69** SEQ ID NO: 253
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQLYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.70** SEQ ID NO: 254
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQTYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.71** SEQ ID NO: 255
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.72** SEQ ID NO: 256
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQYYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.73** SEQ ID NO: 257
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSASTPFTFGQGTKLEIK

>**1A7[CD28]_L1.74** SEQ ID NO: 258
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSDSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.75** SEQ ID NO: 259
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSFSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.76** SEQ ID NO: 260
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSHSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.77** SEQ ID NO: 261
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSKSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.78** SEQ ID NO: 262
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSLSTPFTFGQGTKLEIK

Figure 17G

>**1A7[CD28]_L1.79** SEQ ID NO: 263
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSQSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.80** SEQ ID NO: 264
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSVSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.81** SEQ ID NO: 265
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSWSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.82** SEQ ID NO: 266
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYATPFTFGQGTKLEIK

>**1A7[CD28]_L1.83** SEQ ID NO: 267
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYDTPFTFGQGTKLEIK

>**1A7[CD28]_L1.84** SEQ ID NO: 268
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYGTPFTFGQGTKLEIK

>**1A7[CD28]_L1.85** SEQ ID NO: 269
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYHTPFTFGQGTKLEIK

>**1A7[CD28]_L1.86** SEQ ID NO: 270
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYKTPFTFGQGTKLEIK

>**1A7[CD28]_L1.87** SEQ ID NO: 271
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYNTPFTFGQGTKLEIK

>**1A7[CD28]_L1.88** SEQ ID NO: 272
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYQTPFTFGQGTKLEIK

>**1A7[CD28]_L1.89** SEQ ID NO: 273
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYTTPFTFGQGTKLEIK

>**1A7[CD28]_L1.90** SEQ ID NO: 274
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYVTPFTFGQGTKLEIK

>**1A7[CD28]_L1.91** SEQ ID NO: 275
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYYTPFTFGQGTKLEIK

Figure 17H

>**1A7[CD28]_L1.92** SEQ ID NO: 276
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSAPFTFGQGTKLEIK

>**1A7[CD28]_L1.93** SEQ ID NO: 277
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSDPFTFGQGTKLEIK

>**1A7[CD28]_L1.94** SEQ ID NO: 278
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSFPFTFGQGTKLEIK

>**1A7[CD28]_L1.95** SEQ ID NO: 279
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSIPFTFGQGTKLEIK

>**1A7[CD28]_L1.96** SEQ ID NO: 280
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSKPFTFGQGTKLEIK

>**1A7[CD28]_L1.97** SEQ ID NO: 281
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSLPFTFGQGTKLEIK

>**1A7[CD28]_L1.98** SEQ ID NO: 282
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSQPFTFGQGTKLEIK

>**1A7[CD28]_L1.99** SEQ ID NO: 283
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSSPFTFGQGTKLEIK

>**1A7[CD28]_L1.100** SEQ ID NO: 284
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSVPFTFGQGTKLEIK

>**1A7[CD28]_L1.101** SEQ ID NO: 285
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSYPFTFGQGTKLEIK

>**1A7[CD28]_L1.102** SEQ ID NO: 286
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPITFGQGTKLEIK

>**1A7[CD28]_L1.103** SEQ ID NO: 287
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPLTFGQGTKLEIK

>**1A7[CD28]_L1.104** SEQ ID NO: 288
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYSTPWTFGQGTKLEIK

Figure 17I

>**1A7[CD28]_L1.105** SEQ ID NO: 289
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGQGTKLEIK

>**1A7[CD28]_L1.106** SEQ ID NO: 290
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLTWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQSYNTPFTFGQGTKLEIK

Figure 18A

1A7[CD28]_H1.1_L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISG SGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQV GFDYWGQGTLVTVSS	291
vhCDR1	SYYMS	292
vhCDR2	TISGSGDSTYYADSVKG	293
vhCDR3	SGPGLRQVGFDY	294
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGQGTKLEI K	295
vlCDR1	RASQSISSYLN	296
vlCDR2	AASSLQS	297
vlCDR3	QQSYSTPFT	298

1A7[CD28]_H1_L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISG SGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQV GFDYWGQGTLVTVSS	299
vhCDR1	SYAMS	300
vhCDR2	TISGSGDSTYYADSVKG	301
vhCDR3	SGPGLRQVGFDY	302
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEI K	303
vlCDR1	RASQSISSYLN	304
vlCDR2	AASSLQS	305
vlCDR3	QQVYSTPFT	306

Figure 18B

1A7[CD28]_H1.1_L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGS GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	307
vhCDR1	SYYMS	308
vhCDR2	TISGSGDSTYYADSVKG	309
vhCDR3	SGPGLRQVGFDY	310
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEIK	311
vlCDR1	RASQSISSYLN	312
vlCDR2	AASSLQS	313
vlCDR3	QQVYSTPFT	314

1A7[CD28]_H1.14_L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISES GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	315
vhCDR1	SYYMS	316
vhCDR2	TISESGDSTYYADSVKG	317
vhCDR3	SGPGLRQVGFDY	318
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGQGTKLEIK	319
vlCDR1	RASQSISSYLN	320
vlCDR2	AASSLQS	321
vlCDR3	QQSYSTPFT	322

Figure 18C

1A7[CD28]_H1.14_L1.71		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIS ESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	323
vhCDR1	SYYMS	324
vhCDR2	TISESGDSTYYADSVKG	325
vhCDR3	SGPGLRQVGFDY	326
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKL EIK	327
vlCDR1	RASQSISSYLN	328
vlCDR2	AASSLQS	329
vlCDR3	QQVYSTPFT	330

Figure 19A

1A7 VH	SEQ	SEQ ID NO:	
HFR1	EVQLLESGGGLVQPGGSLRLSCAASGFX$_1$X$_2$X$_3$	331	X$_1$ is selected from T,S,N; X$_2$ is selected from F, L; and X$_3$ is selected from S, E, R, K, G, T, A, N
HCDR1	X$_1$X$_2$X$_3$X$_4$X$_5$		X$_1$ is selected from S, G, E, T, D, A, R, K; X$_2$ is selected from Y, N; X$_3$ is selected from A, Y, S; X$_4$ is selected from M, I; and X$_5$ is selected from S, T, N
HFR2	WVRQAPGKGLEWVX$_1$	332	X$_1$ is selected from S, A
HCDR2	X$_1$IX$_2$X$_3$X$_4$X$_5$X$_6$X$_7$TYYADSVKG	333	X$_1$ is selected from T, S; X$_2$ is selected from S, D, E, Y, T; X$_3$ is selected from G, D, E, A, Y, S, N, T; X$_4$ is selected from S, D, N, G; X$_5$ is selected from D, T, Y, S, A; X$_6$ is selected from D, T, Y, S, A; and X$_7$ is selected from S, Y, A, T, D, N
HFR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	334	
HCDR3	SGPGLRQVGFDY	335	
HFR4	WGQGTLVTVSS	336	

Figure 19B

1A7 VL			
LFR1	DIQMTQSPSSLSASVGDRVTITC	337	
LCDR1	RASQSISX$_1$X$_2$LX$_3$	338	X$_1$ is selected from S, A, D, G, H, K, N, Q, T, V, Y; X$_2$ is selected from Y, A, D, F, H, K, L, N, Q, S, W; and X$_3$ is selected from N, A, D, G, H, Q, S, T, Y
LFR2	WYQQKPGKAPKLLIY	339	
LCDR2	X$_1$ASX$_2$LX$_3$X$_4$		X$_1$ is selected from A, D, G, K, L, Q, S, T, W, Y; X$_2$ is selected from S, A, D, K, N, Q, T, Y; X$_3$ is selected from Q, A, E, F, H, I, K, N, S, V, Y; and X$_4$ is selected from Q, A, E, F, H, I, K, N, S, V, Y
LFR3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	340	
LCDR3	QQX$_1$X$_2$X$_3$X$_4$PX$_5$T	341	X$_1$ is selected from S, A, D, F, H, K, L, T, V, Y; X$_2$ is selected from Y, A, D, F, H, K, L, Q, V, W; X$_3$ is selected from S, A, D, G, H, K, N, Q, T, V, Y; X$_4$ is selected from T, A, D, F, I, K, L, Q, S, V, Y; and X$_5$ is selected from F, I, L, W
LFR4	FGQGTKLEIK	342	

Figure 20

1A7 VH/VL Pair	VH SEQ ID NO:	VL SQ ID NO:	scFv Orientation	K_D for human CD28 (nM)
H1L1			VHVL	1000
H1.1_L1			VHVL	600
H1.14_L1			VHVL	230
H1_L1.71			VHVL	180
H1.1_L1.71			VHVL	96
H1.14_L1.71			VHVL	37
L1.71_H1.14			VLVH	37
L1_H1.14			VLVH	230

Figure 21A

CD28.3[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLQQSGAELVKPGASVRLSCKASGYTFTEYIIHWIKLRSGQGLEW IGWFYPGSNDIQYNAKFKGKATLTADKSSSTVYMELTGLTSEDSAVY FCARRDDFSGYDALPYWGQGTMVTVSS	343
vhCDR1	EYIIH	344
vhCDR2	WFYPGSNDIQYNAKFKG	345
vhCDR3	RDDFSGYDALPY	346
Variable light (vl) domain	DIQMTQSPASLSVSVGETVTITCRTNENIYSNLAWYQQKQGKSPQLL IYAATHLVEGVPSRFSGSGSGTQYSLKITSLQSEDFGNYYCQHFWGT PCTFGGGTKLEIK	347
vlCDR1	RTNENIYSNLA	348
vlCDR2	AATHLVE	349
vlCDR3	QHFWGTPCT	350

hCD28.3[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGAELKKPGASVKVSCKASGYTFTEYIIHWIKLRSGQGLEW IGWFYPGSNDIQYNAQFKGKATLTADKSSSTVYMELTGLTPEDSAVY FCARRDDFSGYDALPYWGQGTLVTVSA	351
vhCDR1	EYIIH	352
vhCDR2	WFYPGSNDIQYNAQFKG	353
vhCDR3	RDDFSGYDALPY	354
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCKTNENIYSNLAWYQQKDGKSPQLL IYAATHLVEGVPSRFSGSGSGTQYSLTISSLQPEDFGNYYCQHFWGT PCTFGGGTKLEIK	355
vlCDR1	KTNENIYSNLA	356
vlCDR2	AATHLVE	357
vlCDR3	QHFWGTPCT	358

Figure 21B

5.11A1[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQQSGPELVKPGTSVRISCEASGYTFTSYYIHWVKQRPGQGLEW IGCIYPGNVNTNYNEKFKDKATLIVDTSSNTAYMQLSRMTSEDSAVY FCTRSHYGLDWNFDVWGAGTTVTVSS	359
vhCDR1	SYYIH	360
vhCDR2	CIYPGNVNTNYNEKFKD	361
vhCDR3	SHYGLDWNFDV	362
Variable light (vl) domain	DIQMNQSPSSLSASLGDTITITCHASQNIYVWLNWYQQKPGNIPKLL IYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQQGQTY PYTFGGGTKLEIK	363
vlCDR1	HASQNIYVWLN	364
vlCDR2	KASNLHT	365
vlCDR3	QQGQTYPYT	366

TGN1412_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEW IGCIYPGNVNTNYNEKFKDRATLTVDTSISTAYMELSRLRSDDTAVY FCTRSHYGLDWNFDVWGQGTTVTVSS	367
vhCDR1	SYYIH	368
vhCDR2	CIYPGNVNTNYNEKFKD	369
vhCDR3	SHYGLDWNFDV	370
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCHASQNIYVWLNWYQQKPGKAPKLL IYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGQTY PYTFGGGTKVEIK	371
vlCDR1	HASQNIYVWLN	372
vlCDR2	KASNLHT	373
vlCDR3	QQGQTYPYT	374

Figure 21C

341VL34[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCGGSGFTFNNAWMNWVRQAPGKGLEW VGRIKGKTDGGTADYAAPVKGRFTISRDYSKNTLYLQMNSLTTEDTA VYYCNTDLPYYYGSGRYSGMDVWGQGTTVTVSS	375
vhCDR1	NAWMN	376
vhCDR2	RIKGKTDGGTADYAAPVKG	377
vhCDR3	DLPYYYGSGRYSGMDV	378
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNT FGPGTKVDIK	379
vlCDR1	RASQSVSSYLA	380
vlCDR2	DASNRAT	381
vlCDR3	QQRSNT	382

>341VL36[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVKPGGSLRLSCGGSGFTFNNAWMNWVRQAPGKGLEW VGRIKGKTDGGTADYAAPVKGRFTISRDYSKNTLYLQMNSLKTEDTG VYYCTTYLPYYYGSERWSGMDVWGQGTTVTVSS	383
vhCDR1	NAWMN	384
vhCDR2	RIKGKTDGGTADYAAPVKG	385
vhCDR3	YLPYYYGSERWSGMDV	386
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLL IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNT FGPGTKVDIK	387
vlCDR1	RASQSVSSYLA	388
vlCDR2	DASNRAT	389
vlCDR3	QQRSNT	390

Figure 21D

281VL4[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGSELKKPGSSVKVSCKASGGTSRSFAISWVRQAPGQGLEW MGGIIPIFGPANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVY YCARHAIAMGWGVITTNYFDSWGQGTMVTVSS	391
vhCDR1	SFAIS	392
vhCDR2	GIIPIFGPANYAQKFQG	393
vhCDR3	HAIAMGWGVITTNYFDS	394
Variable light (vl) domain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPITFGQGTRLEIK	395
vlCDR1	RASQSVSSSYLA	396
vlCDR2	GASSRAT	397
vlCDR3	QQYGSSPIT	398

HuTN228[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLQESGPGLVKPSETLSLTCAVSGFSLTSYGVHWIRQPPGKGLEW LGVIWPGGGTNFNSALMSRLTISEDTSKNQVSLKLSSVTAADTAVYY CARDRAYGNYLYAMDYWGQGTLVTVSS	399
vhCDR1	SYGVH	400
vhCDR2	VIWPGGGTNFNSALMS	401
vhCDR3	DRAYGNYLYAMDY	402
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASESVEYYVTSLMQWYQQKPGKA PKLLIYAASNVDSGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQ SRKVPFTFGGGTKVEIK	403
vlCDR1	RASESVEYYVTSLMQ	404
vlCDR2	AASNVDS	405
vlCDR3	QQSRKVPFT	406

Figure 21E

PV1[CD28] H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQLKQSGAELVKPGASVKISCKTSGYTFTDGYMNWVEQKPGQGLEW IGRIDPDSGNTRYNQKFQGKATLTRDKSSSTVYMDLRSLTSEDSAVY YCARDGTFYGTYGYWYFDFWGQGTQVTVSS	407
vhCDR1	DGYMN	408
vhCDR2	RIDPDSGNTRYNQKFQG	409
vhCDR3	DGTFYGTYGYWYFDF	410
Variable light (vl) domain	DIVMTQSPYSLAVSAGEKVTMSCRSSQSLYYSGIKKNLLAWYQQKPG QSPKLLIYFTSTRLPGVPDRFTGSGSGTDYTLTITSVQAEDMGHYFC QQGISTPLTFGDGTKLEIR	411
vlCDR1	RSSQSLYYSGIKKNLLA	412
vlCDR2	FTSTRLP	413
vlCDR3	QQGISTPLT	414

m9.3[CD28] H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVKLQQSGPGLVTPSQSLSITCTVSGFSLSDYGVHWVRQSPGQGLEW LGVIWAGGGTNYNSALMSRKSISKDNSKSQVFLKMNSLQADDTAVYY CARDKGYSYYYSMDYWGQGTSVTVSS	415
vhCDR1	DYGVH	416
vhCDR2	VIWAGGGTNYNSALMS	417
vhCDR3	DKGYSYYYSMDY	418
Variable light (vl) domain	DIELTQSPASLAVSLGQRATISCRASESVEYYVTSLMQWYQQKPGQP PKLLIFAASNVESGVPARFSGSGSGTNFSLNIHPVDEDDVAMYFCQQ SRKVPYTFGGGTKLEIK	419
vlCDR1	RASESVEYYVTSLMQ	420
vlCDR2	AASNVES	421
vlCDR3	QQSRKVPYT	422

Figure 21F

hu9.3[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSDYGVHWVRQAPGKGLEW VSAIWAGGGTNYASSVMGRFTISRDNAKNSLYLQMNSLRAEDMAVYY CARDKGYSYYYSMDYWGQGTLVTVSS	423
vhCDR1	DYGVH	424
vhCDR2	AIWAGGGTNYASSVMG	425
vhCDR3	DKGYSYYYSMDY	426
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCRASESVEYYVTSLMAWYQQKPGQP PKLLIYAASNVESGVPDRFSGSGSGTNFSLTISSLQAEDVAVYYCQQ SRKVPYTFGQGTKLEIK	427
vlCDR1	RASESVEYYVTSLMA	428
vlCDR2	AASNVES	429
vlCDR3	QQSRKVPYT	430

9G2[CD28]_H0L0

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGRSLKLSCAASGFTFSNYYMAWVRQAPTKGLEW VASITNTGGSTYYRDSVKGRFTISRDNAKSTLYLQMDSLRSEDTATY YCTRGLIYYYDGRNYYDYVMDAWGQGASVTVSS	431
vhCDR1	NYYMA	432
vhCDR2	SITNTGGSTYYRDSVKG	433
vhCDR3	GLIYYYDGRNYYDYVMDA	434
Variable light (vl) domain	DIQMTQSPASLSASLGETVSIECLASEGISNSLAWYQQKPGKSPQLL IYGASSLQDGVPSRFSGSGSGTQYSLKISGMQPEDEGVYYCQQGYKY PLTFGSGTKLEIK	435
vlCDR1	LASEGISNSLA	436
vlCDR2	GASSLQD	437
vlCDR3	QQGYKYPLT	438

Figure 21G

9G2[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYYMAWVRQAPGKGLEW VSSITNTGGSTYYRDSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVY YCTRGLIYYYDGRNYYDYVMDAWGQGTTVTVSS	439
vhCDR1	NYYMA	440
vhCDR2	SITNTGGSTYYRDSVKG	441
vhCDR3	GLIYYYDGRNYYDYVMDA	442
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASEGISNSLAWYQQKPGKSPKLL IYGASSLQDGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGYKY PLTFGSGTKVEIK	443
vlCDR1	RASEGISNSLA	444
vlCDR2	GASSLQD	445
vlCDR3	QQGYKYPLT	446

2F10A3.140[CD28]_H1L1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLLESGGGLVQPGGSLRLSCAASGFSFGGNSMSWVRQAPGKGLEW VATISDNSYSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCAKSGPGLRQVGFDYWGQGTLVTVSS	447
vhCDR1	GNSMS	448
vhCDR2	TISDNSYSTYYADSVKG	449
vhCDR3	SGPGLRQVGFDY	450
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PFTFGQGTKLEIK	451
vlCDR1	RASQSISSYLN	452
vlCDR2	AASSLQS	453
vlCDR3	QQSYSTPFT	454

Figure 21H

TN228[CD28]_H4L2

	sequence	**SEQ ID NO:**
Variable heavy (vh) domain	QVQLQESGPGLVKPSETLSLTCTVSGFSLTSYGVHWVRQPPGKGLEW IGVIWPGGGTNYNSALKSRVTISEDTSKSQVSLKLSSVTAADTAVYY CARDRAYGNYLYAMDYWGQGTLVTVSS	455
vhCDR1	SYGVH	456
vhCDR2	VIWPGGGTNYNSALKS	457
vhCDR3	DRAYGNYLYAMDY	458
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASESVEYYVTSLMQWYQQKPGQA PRLLIYAASNVDSGVPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQ SRKVPFTFGGGTKVEIK	459
vlCDR1	RASESVEYYVTSLMQ	460
vlCDR2	AASNVDS	461
vlCDR3	QQSRKVPFT	462

Figure 22

STEAP1-A_H0L0		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	DVQVQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYIS NSGSTSYNPSLKSRISITRDTSKNQFFLQLISVTTEDTATYYCARERNYDYDD YYYAMDYWGQGTTLTVSA	463
vhCDR1	SDYAWN	464
vhCDR2	YISNSGSTSYNPSLKS	465
vhCDR3	ERNYDYDDYYYAMDY	466
Variable Light (vl) Domain	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLL IYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYNYPRTFGG GTKVEIK	467
vlCDR1	KSSQSLLYRSNQKNYLA	468
vlCDR2	WASTRES	469
vlCDR3	QQYYNYPRT	470

STEAP1-A_H1L1		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIS NSGSTSYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVYYCARERNYDYDD YYYAMDYWGQGTLVTVSS	471
vhCDR1	SDYAWN	472
vhCDR2	YISNSGSTSYNPSLKS	473
vhCDR3	ERNYDYDDYYYAMDY	474
Variable Light (vl) Domain	DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLL IYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDVAVYYCQQYYNYPRTFGG GTKVEIK	475
vlCDR1	KSSQSLLYRSNQKNYLA	476
vlCDR2	WASTRES	477
vlCDR3	QQYYNYPRT	478

Figure 23A

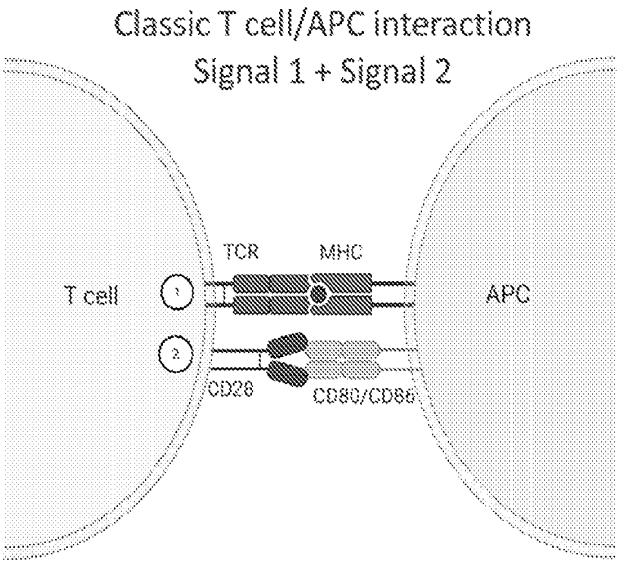


Figure 23B

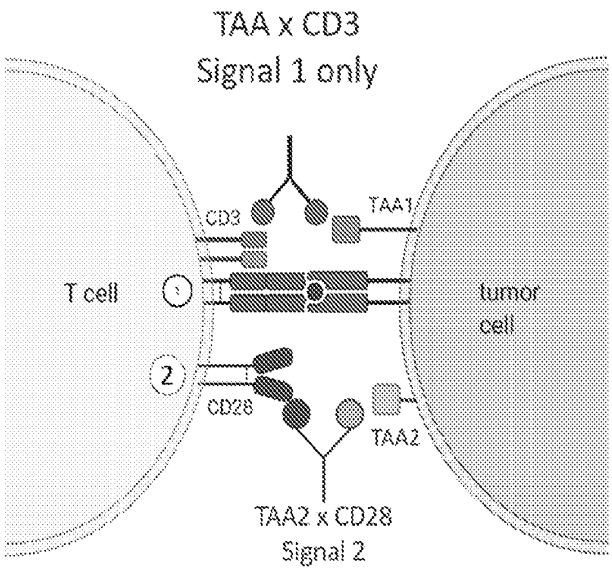


Figure 24A

>XENP45527 STEAP1-A[STEAP1]_H0L0_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q_XENP45527

Chain 1- STEAP1-A[STEAP1]_H0_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 479)

DVQVQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSTSYNPSLKSRISITRDTSKN
QFFLQLISVTTEDTATYYCARERNYDYDDYYYAMDYWGQGTTLTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 480)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3- STEAP1-A[STEAP1]_L0_Light Chain (SEQ ID NO: 481)

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSVKAEDLAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

XENP44652 STEAP1-A[STEAP1]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q_XENP44652

Chain 1- STEAP1-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 482)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 483)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3- STEAP1-A[STEAP1]_L1_Light Chain (SEQ ID NO: 484)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24B

>**XENP46213 STEAP-A[STEAP1]_H1_L1.47_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 485)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4- Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 486)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGQGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
SREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK

Chain 3-STEAP-A[STEAP1]_L1.47_Light Chain (SEQ ID NO: 487)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46214 STEAP-A[STEAP1]_H1_L1.56_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q**

Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 488)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4- Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 489)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGQGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
SREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK

Chain 3-STEAP-A[STEAP1]_L1.56_Light Chain (SEQ ID NO: 490)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAYTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24C

>**XENP46796 STEAP-A[STEAP1] H1 L1.115 Fab-1A7[CD28] H1.129 L1.71 scFv(GKPGS)4-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 491)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- 1A7[CD28]_H1.129_L1.71_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 492)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>**Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 493)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46797 STEAP-A[STEAP1] H1 L1.115 Fab-1A7[CD28] H1.129 L1 scFv(GKPGS)4-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 494)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- 1A7[CD28]_H1.129_L1_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 495)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>**Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 496)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24D

>**XENP46798 STEAP-A[STEAP1] H1 L1.115 Fab-1A7[CD28] H1.14 L1.71 scFv(GKPGS)4-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 497)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 498)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>**Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 499)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46850 STEAP-A[STEAP1] H1.228 L1.115 Fab-1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-Fc(216) IgG1 C220S/PVA /S267K/S364K/E357Q/M428L/N434S**

>**Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 500)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>**Chain 2- 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 501)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVL
HEALHSHYTQKSLSLSPGK

Figure 24E

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 502)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47235 STEAP-A[STEAP1]_H1.230_L1.115_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 503)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 504)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVL
HEALHSHYTQKSLSLSPGK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 505)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP48032 Numax_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- Numax_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 506)

QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYNPSLKDRLTISKDTSK
NQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 24F

>Chain 2- 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 507)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVL
HEALHSHYTQKSLSLSPGK

>Chain 3- Numax_Light Chain (SEQ ID NO: 508)

DIQMTQSPSTLSASVGDRVTITCSASSRVGYMHWYQQKPGKAPKLLIYDTSKLASGVPSRFSGSGSGTEFTLTISSL
QPDDFATYYCFQGSGYPFTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47236_STEAP-A[STEAP1]_H1.230_L1.115_Fab-1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 509)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- 1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 510)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 511)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 24G

>XENP47237_STEAP-A[STEAP1]_H1.230_L1.100_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 512)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 513)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQ
MNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTK
LEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 514)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47238_STEAP-A[STEAP1]_H1.230_L1.100_Fab-1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 515)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- 1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 516)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQ
MNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTK
LEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 24H

>**Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 517)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP47412_STEAP-A[STEAP1]_H1.230_L1.115_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S**

>**Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 518)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>**Chain 2- 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 519)**
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVL
HEALHSHYTQKSLSLSPGK

>**Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 520)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP47413_STEAP-A[STEAP1]_H1.230_L1.100_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S**

>**Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 521)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 24I

>Chain 2- 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 522)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVL
HEALHSHYTQKSLSLSPGK

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 523)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 25A

CD3 High – [anti-CD3]_H1.30_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	524
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	525
vhCDR1	TYAMN	526
vhCDR2	RIRSKYNNYATYYADSVKG	527
vhCDR3	HGNFGDSYVSWFAY	528
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	529
vlCDR1	GSSTGAVTTSNYAN	530
vlCDR2	GTNKRAP	531
vlCDR3	ALWYSNHWV	532
Linker	GKPGSGKPGSGKPGSGKPGS	533

CD3 High-Int #1 – [anti-CD3]_H1.32_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	534
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	535
vhCDR1	TYAMN	536
vhCDR2	RIRSKANNYATYYADSVKG	537
vhCDR3	HGNFGDSYVSWFAY	538
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	539
vlCDR1	GSSTGAVTTSNYAN	540
vlCDR2	GTNKRAP	541
vlCDR3	ALWYSNHWV	542
Linker	GKPGSGKPGSGKPGSGKPGS	543

Figure 25B

CD3 High-Int #2 – [anti-CD3]_H1.89_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	544
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	545
vhCDR1	TYAMN	546
vhCDR2	RIRSKYNNYATYYADSVKG	547
vhCDR3	HGNFGDEYVSWFAY	548
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	549
vlCDR1	GSSTGAVTTSNYAN	550
vlCDR2	GTNKRAP	551
vlCDR3	ALWYSNHWV	552
Linker	GKPGSGKPGSGKPGSGKPGS	553

CD3 High-Int – [anti-CD3]_H1.90_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	554
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	555
vhCDR1	TYAMN	556
vhCDR2	RIRSKYNNYATYYADSVKG	557
vhCDR3	HGNFGDPYVSWFAY	558
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	559
vlCDR1	GSSTGAVTTSNYAN	560
vlCDR2	GTNKRAP	561
vlCDR3	ALWYSNHWV	562
Linker	GKPGSGKPGSGKPGSGKPGS	563

Figure 25C

Anti-CD3-Intermediate – [anti-CD3]_H1.33_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	564
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	565
vhCDR1	TYAMN	566
vhCDR2	RIRSKYNNYATYYADSVKG	567
vhCDR3	HGNFGDSYVSWFDY	568
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	569
vlCDR1	GSSTGAVTTSNYAN	570
vlCDR2	GTNKRAP	571
vlCDR3	ALWYSNHWV	572
Linker	GKPGSGKPGSGKPGSGKPGS	573

CD3 High-Int – [anti-CD3]_H1.31_L1.47_scFv

	Sequence	SEQ ID NO:
scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	574
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	575
vhCDR1	TYAMS	576
vhCDR2	RIRSKYNNYATYYADSVKG	577
vhCDR3	HGNFGDSYVSWFAY	578
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	579
vlCDR1	GSSTGAVTTSNYAN	580
vlCDR2	GTNKRAP	581
vlCDR3	ALWYSNHWV	582
Linker	GKPGSGKPGSGKPGSGKPGS	583

Figure 25D

CD3 High[VL-VH] – [anti-CD3]_L1.47_H1.30_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	584
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	585
vlCDR1	GSSTGAVTTSNYAN	586
vlCDR2	GTNKRAP	587
vlCDR3	ALWYSNHWV	588
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	589
vhCDR1	TYAMN	590
vhCDR2	RIRSKYNNYATYYADSVKG	591
vhCDR3	HGNFGDSYVSWFAY	592
Linker	GKPGSGKPGSGKPGSGKPGS	593

CD3 High-Int #1[VL-VH] – [anti-CD3]_L1.47_H1.32_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	594
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	595
vlCDR1	GSSTGAVTTSNYAN	596
vlCDR2	GTNKRAP	597
vlCDR3	ALWYSNHWV	598
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	599
vhCDR1	TYAMN	600
vhCDR2	RIRSKANNYATYYADSVKG	601
vhCDR3	HGNFGDSYVSWFAY	602
Linker	GKPGSGKPGSGKPGSGKPGS	603

Figure 25E

CD3 High-Int #2[VL-VH] – [anti-CD3]_L1.47_H1.89_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	604
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	605
vlCDR1	GSSTGAVTTSNYAN	606
vlCDR2	GTNKRAP	607
vlCDR3	ALWYSNHWV	608
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS	609
vhCDR1	TYAMN	610
vhCDR2	RIRSKYNNYATYYADSVKG	611
vhCDR3	HGNFGDEYVSWFAY	612
Linker	GKPGSGKPGSGKPGSGKPGS	613

CD3 High-Int[VL-VH] – [anti-CD3]_L1.47_H1.90_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	614
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	615
vlCDR1	GSSTGAVTTSNYAN	616
vlCDR2	GTNKRAP	617
vlCDR3	ALWYSNHWV	618
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS	619
vhCDR1	TYAMN	620
vhCDR2	RIRSKYNNYATYYADSVKG	621
vhCDR3	HGNFGDPYVSWFAY	622
Linker	GKPGSGKPGSGKPGSGKPGS	623

Figure 25F

Anti-CD3-Intermediate[VL-VH] – [anti-CD3]_L1.47_ H1.33_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	624
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	625
vlCDR1	GSSTGAVTTSNYAN	626
vlCDR2	GTNKRAP	627
vlCDR3	ALWYSNHWV	628
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS	629
vhCDR1	TYAMN	630
vhCDR2	RIRSKYNNYATYYADSVKG	631
vhCDR3	HGNFGDSYVSWFDY	632
Linker	GKPGSGKPGSGKPGSGKPGS	633

CD3 High-Int[VL-VH] – [anti-CD3]_L1.47_ H1.31_scFv

	Sequence	SEQ ID NO:
scFv	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL/GKPGSGKPGSGKPGSGKPGS/EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	634
Variable Light (vl) Domain	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL	635
vlCDR1	GSSTGAVTTSNYAN	636
vlCDR2	GTNKRAP	637
vlCDR3	ALWYSNHWV	638
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS	639
vhCDR1	TYAMS	640
vhCDR2	RIRSKYNNYATYYADSVKG	641
vhCDR3	HGNFGDSYVSWFAY	642
Linker	GKPGSGKPGSGKPGSGKPGS	643

Figure 26

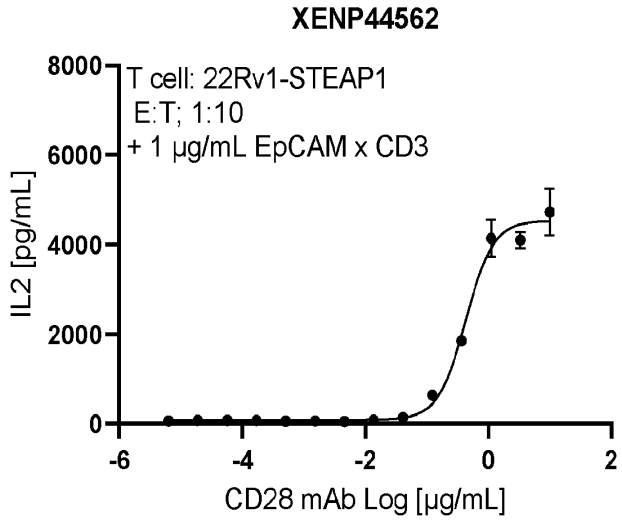

XENP44562
T cell: 22Rv1-STEAP1
E:T; 1:10
+ 1 µg/mL EpCAM x CD3
IL2 [pg/mL]
8000
6000
4000
2000
0
-6
-4
-2
0
2
CD28 mAb Log [µg/mL]

Figure 27A

>XENP44654 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4
Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 644)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSLKLSS
VTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK
Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 645)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSLKLSS
VTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTF
SSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDY
WGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS
SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGTKLEIK
Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 646)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSL
QAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP44802 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4
Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 647)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSLKLSS
VTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 27B

Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 648)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLL
ESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQM
NSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRV
TITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQG
TKLEIK

Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 649)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTL
TISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP45523 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4

Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 650)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27C

Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1_scFv(GKPGS)4 (SEQ ID NO: 651)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLE
SGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMN
SLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGQGT
KLEIK

> Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 652)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTL
TISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP45524 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 653)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27D

Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 654)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLE
SGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMN
SLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGT
KLEIK

> **Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 655)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTL
TISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP45525 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.1_L1.71_scFv(GKPGS)4

Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 656)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27E

Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 657)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLE
SGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMN
SLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGT
KLEIK

Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 658)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTL
TISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP45526 STEAP-A[STEAP1]_H1L1_Fab-STEAP-A[STEAP1]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1- STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 659)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27F

Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 660)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKNQFSL
KLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLE
SGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMN
SLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI
TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGQGT
KLEIK

Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 661)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTL
TISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP45528 STEAP-A[STEAP1]_H0L0_Fab-STEAP-A[STEAP1]_H0L0_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1- STEAP-A[STEAP1]_H0-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 662)

DVQVQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSTSYNPSLKSRISITRDTSKNQFF
LQLISVTTEDTATYYCARERNYDYDDYYYAMDYWGQGTTLTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAP
PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 27G

Chain 2- STEAP-A[STEAP1]_H0_Fab-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 663)

DVQVQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSTSYNPSLKSRISITRDTSKNQFFLQLISVTTE
DTATYYCARERNYDYDDYYYAMDYWGQGTTLTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGGGGGSGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIS
ESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGK
PGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYY
CQQVYSTPFTFGQGTKLEIK

Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 664)

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAE
DLAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP46795_STEAP-A[STEAP1]_H1_L1.115_Fab-STEAP-A[STEAP1]_H1_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 665)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 666)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGG
GSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQVYSTPFTFGQGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 667)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 27H

>XENP46852 STEAP-A[STEAP1] H1.228 L1.115 Fab- STEAP-A[STEAP1] H1.228 L1.115 Fab-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4S)3 1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 668)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 669)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGG
GSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 670)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP46981 STEAP-A[STEAP1] H1.228 L1.115 Fab- STEAP-A[STEAP1] H1.228 L1.115 Fab-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del G4S 1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 671)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27I

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4S_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 672)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY
YMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQG
TLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS
LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 673)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP46982_STEAP-A[STEAP1]_H1.228_L1.115_Fab- STEAP-A[STEAP1]_H1.228_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4A)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 674)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4A)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 675)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGAGGGGAGGGGA/EVQLLESGGGLVQPGGSLRLSC
AASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR
QVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA
PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 676)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 27J

>XENP46983 STEAP-A[STEAP1] H1.228 L1.115 Fab- STEAP-A[STEAP1] H1.228 L1.115 Fab-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del (G4A)2 1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 677)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4A)2_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 678)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGAGGG
GA/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQSYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 679)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP46984 STEAP-A[STEAP1] H1.228 L1.115 Fab- STEAP-A[STEAP1] H1.228 L1.115 Fab-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del G4A 1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 680)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27K

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 681)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EV
QLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
SYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 682)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47242_STEAP-A[STEAP1]_H1.230_L1.100_Fab-STEAP-A[STEAP1]_H1.230_L1.100_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 683)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 684)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGG
GSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQVYSTPFTFGCGTKLEIK

Figure 27L

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 685)
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47239_STEAP-A[STEAP1]_H1.230_L1.115_Fab- STEAP-A[STEAP1]_H1.230_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 686)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 687)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGGGSGGGGS/EVQLLESGGGLVQPGGSLRLSC
AASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR
QVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKA
PKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 688)
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47240_STEAP-A[STEAP1]_H1.230_L1.115_Fab- STEAP-A[STEAP1]_H1.230_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 689)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27M

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 690)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGG
GSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQVYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 691)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47241_STEAP-A[STEAP1]_H1.230_L1.100_Fab-STEAP-A[STEAP1]_H1.230_L1.100_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 692)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_(G4S)3_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 693)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGSGGG
GSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQ
MTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSTPFTFGCGTKLEIK

Figure 27N

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 694)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47414 STEAP-A[STEAP1]_H1.230_L1.115_Fab- STEAP-A[STEAP1]_H1.230_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 695)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 696)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EV
QLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 697)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47415 STEAP-A[STEAP1]_H1.230_L1.115_Fab- STEAP-A[STEAP1]_H1.230_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 698)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Figure 27O

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 699)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGGGGGAEVQL
LESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASV
GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSY
STPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 700)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47416 STEAP-A[STEAP1]_H1.230_L1.115_Fab- STEAP-A[STEAP1]_H1.230_L1.115_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 701)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 702)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EV
QLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 703)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 27P

>XENP47417_STEAP-A[STEAP1]_H1.230_L1.100_Fab- STEAP-A[STEAP1]_H1.230_L1.100_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 704)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 705)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY
YMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQG
TLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS
LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 706)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTIS
SLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47418_STEAP-A[STEAP1]_H1.230_L1.100_Fab- STEAP-A[STEAP1]_H1.230_L1.100_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4

>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 707)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 708)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLK
LSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPVAGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSY
YMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQG
TLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASS
LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK

Figure 27Q

>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 709)
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>XENP47419 STEAP-A[STEAP1] H1.230 L1.100 Fab- STEAP-A[STEAP1] H1.230 L1.100 Fab-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-IgG1 PVA /S267K/S364K/E357Q/M428L/N434S/K447del G4A 1A7[CD28] H1.129 L1.71 VH G46C VL Q108C scFv(GKPGS)4
>Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 710)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK
>Chain 2- STEAP-A[STEAP1]_H1.230_Fab-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S/K447del_G4A_1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4 (SEQ ID NO: 711)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSP/GGGGGA/EV
QLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGCGTKLEIK
>Chain 3- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 712)
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 28

>XENP44658 STEAP-A[STEAP1]_H1L1_Fab_(G4A)2_STEAP-A[STEAP1]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1_Fab_(G4A)2_STEAP-A[STEAP1]_H1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 713)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGG
GAGGGGAQVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTI
SRDTSKNQFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVE
PKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREE
EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSG
FYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 714)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSA
SVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQ
VYSTPFTFGQGTKLEIKEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
SREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHE
ALHSHYTQKSLSLSPGK

> Chain 3-STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 715)

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 29

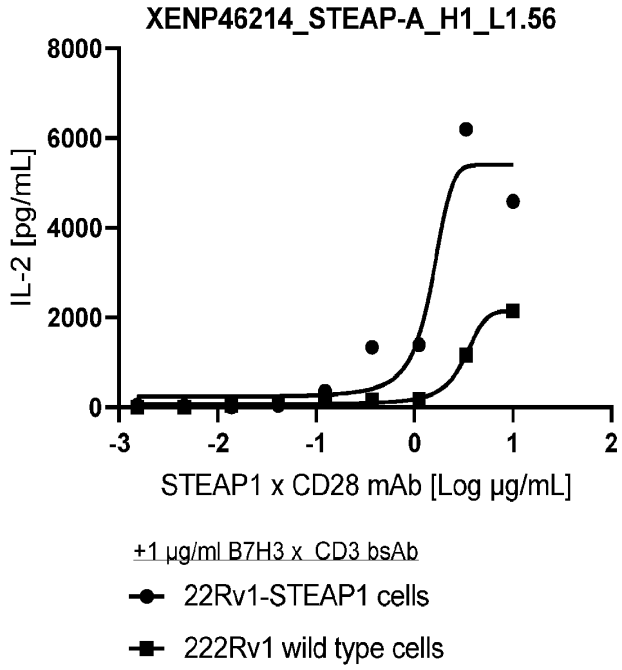

XENP46214_STEAP-A_H1_L1.56
8000
6000
4000
2000
0
IL-2 [pg/mL]
-3
-2
-1
0
1
2
STEAP1 x CD28 mAb [Log µg/mL]
+1 µg/ml B7H3 x CD3 bsAb
22Rv1-STEAP1 cells
222Rv1 wild type cells

Figure 30A

>**XENP44680 STEAP-A[STEAP1]_H1L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 716)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 717)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44804 STEAP-A[STEAP1]_H1.1_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.1_IgG1_PVA_/S267K (SEQ ID NO: 718)**
QVQLQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 719)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44805 STEAP-A[STEAP1]_H1.2_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.2_IgG1_PVA_/S267K (SEQ ID NO: 720)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKGLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 721)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44806 STEAP-A[STEAP1]_H1.3_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.3_IgG1_PVA_/S267K (SEQ ID NO: 722)**
QVQLQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKGLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30B

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 723)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44807 STEAP-A[STEAP1]_H1.4_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.4_IgG1_PVA_/S267K (SEQ ID NO: 724)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYADYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 725)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44808 STEAP-A[STEAP1]_H1.5_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.5_IgG1_PVA_/S267K (SEQ ID NO: 726)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 727)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44809 STEAP-A[STEAP1]_H1.6_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.6_IgG1_PVA_/S267K (SEQ ID NO: 728)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 729)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30C

>**XENP44810 STEAP-A[STEAP1]_H1.7_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.7_IgG1_PVA_/S267K (SEQ ID NO: 730)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 731)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44811 STEAP-A[STEAP1]_H1.8_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.8_IgG1_PVA_/S267K (SEQ ID NO: 732)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 733)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44812 STEAP-A[STEAP1]_H1.9_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.9_IgG1_PVA_/S267K (SEQ ID NO: 734)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 735)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44813 STEAP-A[STEAP1]_H1.10_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.10_IgG1_PVA_/S267K (SEQ ID NO: 736)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30D

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 737)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44814 STEAP-A[STEAP1]_H1.11_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.11_IgG1_PVA_/S267K (SEQ ID NO: 738)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDLYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 739)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44815 STEAP-A[STEAP1]_H1.12_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.12_IgG1_PVA_/S267K (SEQ ID NO: 740)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 741)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44816 STEAP-A[STEAP1]_H1.13_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.13_IgG1_PVA_/S267K (SEQ ID NO: 742)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDTYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 743)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30E

>**XENP44817 STEAP-A[STEAP1]_H1.14_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.14_IgG1_PVA_/S267K (SEQ ID NO: 744)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 745)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44818 STEAP-A[STEAP1]_H1.15_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.15_IgG1_PVA_/S267K (SEQ ID NO: 746)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 747)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44819 STEAP-A[STEAP1]_H1.16_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.16_IgG1_PVA_/S267K (SEQ ID NO: 748)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYALYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 749)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44820 STEAP-A[STEAP1]_H1.17_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.17_IgG1_PVA_/S267K (SEQ ID NO: 750)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30F

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 751)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44821 STEAP-A[STEAP1]_H1.18_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.18_IgG1_PVA_/S267K (SEQ ID NO: 752)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYATYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 753)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44822 STEAP-A[STEAP1]_H1.19_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.19_IgG1_PVA_/S267K (SEQ ID NO: 754)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 755)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44823 STEAP-A[STEAP1]_H1.20_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.20_IgG1_PVA_/S267K (SEQ ID NO: 756)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 757)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30G

>**XENP44824 STEAP-A[STEAP1]_H1.21_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 758)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 759)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44825 STEAP-A[STEAP1]_H1.22_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.22_IgG1_PVA_/S267K (SEQ ID NO: 760)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 761)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44826 STEAP-A[STEAP1]_H1.23_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.23_IgG1_PVA_/S267K (SEQ ID NO: 762)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYETYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 763)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44827 STEAP-A[STEAP1]_H1.24_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.24_IgG1_PVA_/S267K (SEQ ID NO: 764)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30H

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 765)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44828 STEAP-A[STEAP1]_H1.25_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.25_IgG1_PVA_/S267K (SEQ ID NO: 766)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 767)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44829 STEAP-A[STEAP1]_H1.26_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.26_IgG1_PVA_/S267K (SEQ ID NO: 768)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLLYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 769)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44830 STEAP-A[STEAP1]_H1.27_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.27_IgG1_PVA_/S267K (SEQ ID NO: 770)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 771)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30I

>**XENP44831 STEAP-A[STEAP1]_H1.28_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.28_IgG1_PVA_/S267K (SEQ ID NO: 772)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLTYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 773)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44832 STEAP-A[STEAP1]_H1.29_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.29_IgG1_PVA_/S267K (SEQ ID NO: 774)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 775)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44833 STEAP-A[STEAP1]_H1.30_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.30_IgG1_PVA_/S267K (SEQ ID NO: 776)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 777)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44834 STEAP-A[STEAP1]_H1.31_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.31_IgG1_PVA_/S267K (SEQ ID NO: 778)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQLYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30J

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 779)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44835 STEAP-A[STEAP1]_H1.32_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.32_IgG1_PVA_/S267K (SEQ ID NO: 780)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 781)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44836 STEAP-A[STEAP1]_H1.33_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.33_IgG1_PVA_/S267K (SEQ ID NO: 782)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQTYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 783)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44837 STEAP-A[STEAP1]_H1.34_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.34_IgG1_PVA_/S267K (SEQ ID NO: 784)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 785)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30K

>**XENP44838 STEAP-A[STEAP1]_H1.35_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.35_IgG1_PVA_/S267K (SEQ ID NO: 786)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTEYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 787)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44839 STEAP-A[STEAP1]_H1.36_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.36_IgG1_PVA_/S267K (SEQ ID NO: 788)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTLYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 789)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44840 STEAP-A[STEAP1]_H1.37_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.37_IgG1_PVA_/S267K (SEQ ID NO: 790)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTQYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 791)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44841 STEAP-A[STEAP1]_H1.38_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.38_IgG1_PVA_/S267K (SEQ ID NO: 792)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTTYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30L

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 793)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44842 STEAP-A[STEAP1]_H1_L1.1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1__IgG1_PVA_/S267K (SEQ ID NO: 794)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.1_Light Chain (SEQ ID NO: 795)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44843 STEAP-A[STEAP1]_H1_L1.2_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 796)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.2_Light Chain (SEQ ID NO: 797)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP44844 STEAP-A[STEAP1]_H1_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 798)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 799)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30M

>**XENP45529 STEAP-A[STEAP1]_H0L0_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H0_IgG1_PVA_/S267K (SEQ ID NO: 800)**
DVQVQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISNSGSTSYNPSLKSRISITRDTSKN
QFFLQLISVTTEDTATYYCARERNYDYDDYYYAMDYWGQGTTLTVSA/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L0_Light Chain (SEQ ID NO: 801)**
DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSVKAEDLAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45530 STEAP-A[STEAP1]_H1.21_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 802)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 803)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45531 STEAP-A[STEAP1]_H1.34_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.34_IgG1_PVA_/S267K (SEQ ID NO: 804)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 805)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45632 STEAP-A[STEAP1]_H1.39_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.39_IgG1_PVA_/S267K (SEQ ID NO: 806)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSEYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30N

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 807)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45633 STEAP-A[STEAP1]_H1.40_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.40_IgG1_PVA_/S267K (SEQ ID NO: 808)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSNYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 809)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45634 STEAP-A[STEAP1]_H1.41_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.41_IgG1_PVA_/S267K (SEQ ID NO: 810)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSRYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 811)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45635 STEAP-A[STEAP1]_H1.42_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.42_IgG1_PVA_/S267K (SEQ ID NO: 812)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 813)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30O

>**XENP45636 STEAP-A[STEAP1]_H1.43_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.43_IgG1_PVA_/S267K (SEQ ID NO: 814)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSYYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 815)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45637 STEAP-A[STEAP1]_H1.44_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.44_IgG1_PVA_/S267K (SEQ ID NO: 816)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDAAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 817)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45638 STEAP-A[STEAP1]_H1.45_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.45_IgG1_PVA_/S267K (SEQ ID NO: 818)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDDAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 819)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45639 STEAP-A[STEAP1]_H1.46_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.46_IgG1_PVA_/S267K (SEQ ID NO: 820)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDKAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30P

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 821)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45640 STEAP-A[STEAP1]_H1.47_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.47_IgG1_PVA_/S267K (SEQ ID NO: 822)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDLAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 823)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45641 STEAP-A[STEAP1]_H1.48_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.48_IgG1_PVA_/S267K (SEQ ID NO: 824)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDQAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 825)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45642 STEAP-A[STEAP1]_H1.49_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.49_IgG1_PVA_/S267K (SEQ ID NO: 826)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYDWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 827)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30Q

>**XENP45643 STEAP-A[STEAP1]_H1.50_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.50_IgG1_PVA_/S267K (SEQ ID NO: 828)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYFWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 829)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45644 STEAP-A[STEAP1]_H1.51_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.51_IgG1_PVA_/S267K (SEQ ID NO: 830)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYGWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 831)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45645 STEAP-A[STEAP1]_H1.52_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.52_IgG1_PVA_/S267K (SEQ ID NO: 832)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYHWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 833)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45646 STEAP-A[STEAP1]_H1.53_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.53_IgG1_PVA_/S267K (SEQ ID NO: 834)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYKWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30R

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 835)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45647 STEAP-A[STEAP1]_H1.54_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.54_IgG1_PVA_/S267K (SEQ ID NO: 836)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYLWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 837)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45648 STEAP-A[STEAP1]_H1.55_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.55_IgG1_PVA_/S267K (SEQ ID NO: 838)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYQWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 839)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45649 STEAP-A[STEAP1]_H1.56_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.56_IgG1_PVA_/S267K (SEQ ID NO: 840)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 841)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30S

>**XENP45650 STEAP-A[STEAP1]_H1.57_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.57_IgG1_PVA_/S267K (SEQ ID NO: 842)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYTWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 843)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45651 STEAP-A[STEAP1]_H1.58_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.58_IgG1_PVA_/S267K (SEQ ID NO: 844)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWGWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 845)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45652 STEAP-A[STEAP1]_H1.59_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.59_IgG1_PVA_/S267K (SEQ ID NO: 846)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWHWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 847)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45653 STEAP-A[STEAP1]_H1.60_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.60_IgG1_PVA_/S267K (SEQ ID NO: 848)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWSWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30T

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 849)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45654 STEAP-A[STEAP1]_H1.61_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.61_IgG1_PVA_/S267K (SEQ ID NO: 850)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWTWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 851)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45655 STEAP-A[STEAP1]_H1.62_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.62_IgG1_PVA_/S267K (SEQ ID NO: 852)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGAISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 853)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45656 STEAP-A[STEAP1]_H1.63_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.63_IgG1_PVA_/S267K (SEQ ID NO: 854)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGDISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 855)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30U

>**XENP45657 STEAP-A[STEAP1]_H1.64_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.64_IgG1_PVA_/S267K (SEQ ID NO: 856)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGFISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 857)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45658 STEAP-A[STEAP1]_H1.65_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.65_IgG1_PVA_/S267K (SEQ ID NO: 858)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGHISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 859)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45659 STEAP-A[STEAP1]_H1.66_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.66_IgG1_PVA_/S267K (SEQ ID NO: 860)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGKISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 861)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45660 STEAP-A[STEAP1]_H1.67_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.67_IgG1_PVA_/S267K (SEQ ID NO: 862)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGLISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30V

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 863)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45661 STEAP-A[STEAP1]_H1.68_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.68_IgG1_PVA_/S267K (SEQ ID NO: 864)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGQISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 865)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45662 STEAP-A[STEAP1]_H1.69_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.69_IgG1_PVA_/S267K (SEQ ID NO: 866)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGVISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 867)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45663 STEAP-A[STEAP1]_H1.70_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.70_IgG1_PVA_/S267K (SEQ ID NO: 868)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGWISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 869)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30W

>**XENP45664 STEAP-A[STEAP1]_H1.71_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.71_IgG1_PVA_/S267K (SEQ ID NO: 870)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIANSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 871)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45665 STEAP-A[STEAP1]_H1.72_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.72_IgG1_PVA_/S267K (SEQ ID NO: 872)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIDNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 873)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45666 STEAP-A[STEAP1]_H1.73_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.73_IgG1_PVA_/S267K (SEQ ID NO: 874)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 875)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45667 STEAP-A[STEAP1]_H1.74_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.74_IgG1_PVA_/S267K (SEQ ID NO: 876)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIHNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30X

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 877)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45668 STEAP-A[STEAP1]_H1.75_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.75_IgG1_PVA_/S267K (SEQ ID NO: 878)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIKNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 879)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45669 STEAP-A[STEAP1]_H1.76_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.76_IgG1_PVA_/S267K (SEQ ID NO: 880)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIQNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 881)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45670 STEAP-A[STEAP1]_H1.77_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.77_IgG1_PVA_/S267K (SEQ ID NO: 882)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYITNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 883)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30Y

>**XENP45671 STEAP-A[STEAP1]_H1.78_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.78_IgG1_PVA_/S267K (SEQ ID NO: 884)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIVNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 885)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45672 STEAP-A[STEAP1]_H1.79_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.79_IgG1_PVA_/S267K (SEQ ID NO: 886)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIYNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 887)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45673 STEAP-A[STEAP1]_H1.80_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.80_IgG1_PVA_/S267K (SEQ ID NO: 888)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISESGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 889)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45674 STEAP-A[STEAP1]_H1.81_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.81_IgG1_PVA_/S267K (SEQ ID NO: 890)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30Z

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 891)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45675 STEAP-A[STEAP1]_H1.82_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.82_IgG1_PVA_/S267K (SEQ ID NO: 892)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISLSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 893)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45676 STEAP-A[STEAP1]_H1.83_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.83_IgG1_PVA_/S267K (SEQ ID NO: 894)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISQSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 895)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45677 STEAP-A[STEAP1]_H1.84_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.84_IgG1_PVA_/S267K (SEQ ID NO: 896)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISRSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 897)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AA

>**XENP45678 STEAP-A[STEAP1]_H1.85_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.85_IgG1_PVA_/S267K (SEQ ID NO: 898)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNAGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 899)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45679 STEAP-A[STEAP1]_H1.86_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.86_IgG1_PVA_/S267K (SEQ ID NO: 900)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNEGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 901)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45680 STEAP-A[STEAP1]_H1.87_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.87_gG1_PVA_/S267K (SEQ ID NO: 902)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 903)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45681 STEAP-A[STEAP1]_H1.88_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.88_IgG1_PVA_/S267K (SEQ ID NO: 904)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AB

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 905)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45682 STEAP-A[STEAP1]_H1.89_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.89_IgG1_PVA_/S267K (SEQ ID NO: 906)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNIGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 907)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45683 STEAP-A[STEAP1]_H1.90_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.90_IgG1_PVA_/S267K (SEQ ID NO: 908)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNKGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 909)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45684 STEAP-A[STEAP1]_H1.91_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.91_IgG1_PVA_/S267K (SEQ ID NO: 910)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNQGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 911)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AC

>**XENP45685 STEAP-A[STEAP1]_H1.92_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.92_IgG1_PVA_/S267K (SEQ ID NO: 912)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNTGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 913)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45686 STEAP-A[STEAP1]_H1.93_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.93_IgG1_PVA_/S267K (SEQ ID NO: 914)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNYGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 915)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45687 STEAP-A[STEAP1]_H1.94_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.94_IgG1_PVA_/S267K (SEQ ID NO: 916)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSASTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 917)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45688 STEAP-A[STEAP1]_H1.95_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.95_IgG1_PVA_/S267K (SEQ ID NO: 918)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSESTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AD

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 919)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45689 STEAP-A[STEAP1]_H1.96_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.96_IgG1_PVA_/S267K (SEQ ID NO: 920)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSHSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 921)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45690 STEAP-A[STEAP1]_H1.97_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.97_IgG1_PVA_/S267K (SEQ ID NO: 922)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSQSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 923)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45691 STEAP-A[STEAP1]_H1.98_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.98_IgG1_PVA_/S267K (SEQ ID NO: 924)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSRSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 925)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AE

>**XENP45692 STEAP-A[STEAP1]_H1.99_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.99_IgG1_PVA_/S267K (SEQ ID NO: 926)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGATSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 927)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45693 STEAP-A[STEAP1]_H1.100_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.100_IgG1_PVA_/S267K (SEQ ID NO: 928)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGDTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 929)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45694 STEAP-A[STEAP1]_H1.101_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.101_IgG1_PVA_/S267K (SEQ ID NO: 930)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGGTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 931)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45695 STEAP-A[STEAP1]_H1.102_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.102_IgG1_PVA_/S267K (SEQ ID NO: 932)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGHTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AF

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 933)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45696 STEAP-A[STEAP1]_H1.103_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.102_IgG1_PVA_/S267K (SEQ ID NO: 934)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGKTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 935)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45697 STEAP-A[STEAP1]_H1.104_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.104_IgG1_PVA_/S267K (SEQ ID NO: 936)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGQTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 937)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45698 STEAP-A[STEAP1]_H1.105_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.105_IgG1_PVA_/S267K (SEQ ID NO: 938)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGTTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 939)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AG

>**XENP45699 STEAP-A[STEAP1]_H1.106_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.106_IgG1_PVA_/S267K (SEQ ID NO: 940)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGVTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 941)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45700 STEAP-A[STEAP1]_H1.107_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.107_IgG1_PVA_/S267K (SEQ ID NO: 942)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 943)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45701 STEAP-A[STEAP1]_H1.108_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.108_IgG1_PVA_/S267K (SEQ ID NO: 944)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 945)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45702 STEAP-A[STEAP1]_H1.109_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.109_IgG1_PVA_/S267K (SEQ ID NO: 946)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AH

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 947)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45703 STEAP-A[STEAP1]_H1.110_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.110_IgG1_PVA_/S267K (SEQ ID NO: 948)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTDYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 949)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45704 STEAP-A[STEAP1]_H1.111_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.111_IgG1_PVA_/S267K (SEQ ID NO: 950)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTGYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 951)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45705 STEAP-A[STEAP1]_H1.112_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.112_IgG1_PVA_/S267K (SEQ ID NO: 952)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTHYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 953)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AI

>**XENP45706 STEAP-A[STEAP1]_H1.113_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.113_IgG1_PVA_/S267K (SEQ ID NO: 954)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTQYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 955)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45707 STEAP-A[STEAP1]_H1.114_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.114_IgG1_PVA_/S267K (SEQ ID NO: 956)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTTYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 957)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45708 STEAP-A[STEAP1]_H1.115_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.115_IgG1_PVA_/S267K (SEQ ID NO: 958)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 959)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45709 STEAP-A[STEAP1]_H1.116_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.116_IgG1_PVA_/S267K (SEQ ID NO: 960)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTYYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AJ

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 961)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45710 STEAP-A[STEAP1]_H1.117_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.117_IgG1_PVA_/S267K (SEQ ID NO: 962)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARHRNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 963)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45711 STEAP-A[STEAP1]_H1.118_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.118_IgG1_PVA_/S267K (SEQ ID NO: 964)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARIRNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 965)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45712 STEAP-A[STEAP1]_H1.119_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.119_IgG1_PVA_/S267K (SEQ ID NO: 966)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARKRNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 967)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AK

>**XENP45713 STEAP-A[STEAP1]_H1.120_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.120_IgG1_PVA_/S267K (SEQ ID NO: 968)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARQRNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 969)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45714 STEAP-A[STEAP1]_H1.121_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.121_IgG1_PVA_/S267K (SEQ ID NO: 970)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARSRNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 971)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45715 STEAP-A[STEAP1]_H1.122_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.122_IgG1_PVA_/S267K (SEQ ID NO: 972)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREENYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 973)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45716 STEAP-A[STEAP1]_H1.123_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.123_IgG1_PVA_/S267K (SEQ ID NO: 974)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREHNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AL

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 975)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45717 STEAP-A[STEAP1]_H1.124_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.124_IgG1_PVA_/S267K (SEQ ID NO: 976)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREINYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 977)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45718 STEAP-A[STEAP1]_H1.125_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.125_IgG1_PVA_/S267K (SEQ ID NO: 978)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREKNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 979)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45719 STEAP-A[STEAP1]_H1.126_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.126_IgG1_PVA_/S267K (SEQ ID NO: 980)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREQNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 981)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AM

>**XENP45720 STEAP-A[STEAP1]_H1.127_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.127_IgG1_PVA_/S267K (SEQ ID NO: 982)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERDYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 983)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45721 STEAP-A[STEAP1]_H1.128_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.128_IgG1_PVA_/S267K (SEQ ID NO: 984)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERGYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 985)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45722 STEAP-A[STEAP1]_H1.129_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.129_IgG1_PVA_/S267K (SEQ ID NO: 986)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERHYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 987)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45723 STEAP-A[STEAP1]_H1.130_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.130_IgG1_PVA_/S267K (SEQ ID NO: 988)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERLYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AN

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 989)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45724 STEAP-A[STEAP1]_H1.131_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.131_IgG1_PVA_/S267K (SEQ ID NO: 990)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERQYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 991)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45725 STEAP-A[STEAP1]_H1.132_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.132_IgG1_PVA_/S267K (SEQ ID NO: 992)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERRYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 993)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45726 STEAP-A[STEAP1]_H1.133_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.133_IgG1_PVA_/S267K (SEQ ID NO: 994)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERSYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 995)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AO

>**XENP45727 STEAP-A[STEAP1]_H1.134_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.134_IgG1_PVA_/S267K (SEQ ID NO: 996)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERTYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 997)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45728 STEAP-A[STEAP1]_H1.135_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.135_IgG1_PVA_/S267K (SEQ ID NO: 998)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNADYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 999)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45729 STEAP-A[STEAP1]_H1.136_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.136_IgG1_PVA_/S267K (SEQ ID NO: 1000)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNFDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1001)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45730 STEAP-A[STEAP1]_H1.137_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.137_IgG1_PVA_/S267K (SEQ ID NO: 1002)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNHDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AP

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1003)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45731 STEAP-A[STEAP1]_H1.138_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.138_IgG1_PVA_/S267K (SEQ ID NO: 1004)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNKDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1005)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45732 STEAP-A[STEAP1]_H1.139_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.139_IgG1_PVA_/S267K (SEQ ID NO: 1006)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNLDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1007)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45733 STEAP-A[STEAP1]_H1.140_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.140_IgG1_PVA_/S267K (SEQ ID NO: 1008)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNQDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1009)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AQ

>**XENP45734 STEAP-A[STEAP1]_H1.141_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.141_IgG1_PVA_/S267K (SEQ ID NO: 1010)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNVDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1011)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45735 STEAP-A[STEAP1]_H1.142_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.142_IgG1_PVA_/S267K (SEQ ID NO: 1012)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYEYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1013)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45736 STEAP-A[STEAP1]_H1.143_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.143_IgG1_PVA_/S267K (SEQ ID NO: 1014)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYGYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1015)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45737 STEAP-A[STEAP1]_H1.144_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.144_IgG1_PVA_/S267K (SEQ ID NO: 1016)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYHYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AR

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1017)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45738 STEAP-A[STEAP1]_H1.145_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.145_IgG1_PVA_/S267K (SEQ ID NO: 1018)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYLYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1019)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45739 STEAP-A[STEAP1]_H1.146_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.146_IgG1_PVA_/S267K (SEQ ID NO: 1020)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYNYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1021)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45740 STEAP-A[STEAP1]_H1.147_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.147_IgG1_PVA_/S267K (SEQ ID NO: 1022)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYRYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1023)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AS

>**XENP45741 STEAP-A[STEAP1]_H1.148_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.148_IgG1_PVA_/S267K (SEQ ID NO: 1024)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYSYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1025)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45742 STEAP-A[STEAP1]_H1.149_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.149_IgG1_PVA_/S267K (SEQ ID NO: 1026)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYTYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1027)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45743 STEAP-A[STEAP1]_H1.150_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.150_IgG1_PVA_/S267K (SEQ ID NO: 1028)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDADDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1029)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45744 STEAP-A[STEAP1]_H1.151_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.151_IgG1_PVA_/S267K (SEQ ID NO: 1030)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDFDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AT

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1031)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45745 STEAP-A[STEAP1]_H1.152_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.152_IgG1_PVA_/S267K (SEQ ID NO: 1032)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDHDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1033)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45746 STEAP-A[STEAP1]_H1.153_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.153_IgG1_PVA_/S267K (SEQ ID NO: 1034)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDKDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1035)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45747 STEAP-A[STEAP1]_H1.154_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.154_IgG1_PVA_/S267K (SEQ ID NO: 1036)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDLDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1037)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AU

>**XENP45748 STEAP-A[STEAP1]_H1.155_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.155_IgG1_PVA_/S267K (SEQ ID NO: 1038)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDQDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1039)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45749 STEAP-A[STEAP1]_H1.156_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.156_IgG1_PVA_/S267K (SEQ ID NO: 1040)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDVDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1041)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45750 STEAP-A[STEAP1]_H1.157_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.157_IgG1_PVA_/S267K (SEQ ID NO: 1042)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYGDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1043)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45751 STEAP-A[STEAP1]_H1.158_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.158_IgG1_PVA_/S267K (SEQ ID NO: 1044)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYHDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AV

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1045)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45752 STEAP-A[STEAP1]_H1.159_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.159_IgG1_PVA_/S267K (SEQ ID NO: 1046)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYNDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1047)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45753 STEAP-A[STEAP1]_H1.160_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.160_IgG1_PVA_/S267K (SEQ ID NO: 1048)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYRDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1049)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45754 STEAP-A[STEAP1]_H1.161_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.161_IgG1_PVA_/S267K (SEQ ID NO: 1050)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1051)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AW

>**XENP45755 STEAP-A[STEAP1]_H1.162_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.162_IgG1_PVA_/S267K (SEQ ID NO: 1052)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDGYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1053)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45756 STEAP-A[STEAP1]_H1.163_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.163_IgG1_PVA_/S267K (SEQ ID NO: 1054)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDHYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1055)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45757 STEAP-A[STEAP1]_H1.164_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.164_IgG1_PVA_/S267K (SEQ ID NO: 1056)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDIYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1057)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45758 STEAP-A[STEAP1]_H1.165_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.165_IgG1_PVA_/S267K (SEQ ID NO: 1058)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDNYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AX

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1059)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45759 STEAP-A[STEAP1]_H1.166_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.166_IgG1_PVA_/S267K (SEQ ID NO: 1060)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDRYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1061)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45760 STEAP-A[STEAP1]_H1.167_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.167_IgG1_PVA_/S267K (SEQ ID NO: 1062)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDSYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1063)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45761 STEAP-A[STEAP1]_H1.168_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.168_IgG1_PVA_/S267K (SEQ ID NO: 1064)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDVYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1065)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30AY

>**XENP45762 STEAP-A[STEAP1]_H1.169_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.169_IgG1_PVA_/S267K (SEQ ID NO: 1066)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEGYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1067)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45763 STEAP-A[STEAP1]_H1.170_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.170_IgG1_PVA_/S267K (SEQ ID NO: 1068)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEHYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1069)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45764 STEAP-A[STEAP1]_H1.171_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.171_IgG1_PVA_/S267K (SEQ ID NO: 1070)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEIYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1071)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45765 STEAP-A[STEAP1]_H1.172_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.172_IgG1_PVA_/S267K (SEQ ID NO: 1072)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYENYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30AZ

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1073)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45766 STEAP-A[STEAP1]_H1.173_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.173_IgG1_PVA_/S267K (SEQ ID NO: 1074)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYERYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1075)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45767 STEAP-A[STEAP1]_H1.174_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.174_IgG1_PVA_/S267K (SEQ ID NO: 1076)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYESYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1077)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45768 STEAP-A[STEAP1]_H1.175_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.175_IgG1_PVA_/S267K (SEQ ID NO: 1078)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEVYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1079)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BA

>**XENP45769 STEAP-A[STEAP1]_H1.176_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.176_IgG1_PVA_/S267K (SEQ ID NO: 1080)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDAYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1081)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45770 STEAP-A[STEAP1]_H1.177_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.177_IgG1_PVA_/S267K (SEQ ID NO: 1082)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDFYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1083)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45771 STEAP-A[STEAP1]_H1.178_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.178_IgG1_PVA_/S267K (SEQ ID NO: 1084)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDHYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1085)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45772 STEAP-A[STEAP1]_H1.179_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.179_IgG1_PVA_/S267K (SEQ ID NO: 1086)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDKYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BB

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1087)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45773 STEAP-A[STEAP1]_H1.180_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.180_IgG1_PVA_/S267K (SEQ ID NO: 1088)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDLYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1089)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45774 STEAP-A[STEAP1]_H1.181_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.181_IgG1_PVA_/S267K (SEQ ID NO: 1090)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDQYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1091)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45775 STEAP-A[STEAP1]_H1.182_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.182_IgG1_PVA_/S267K (SEQ ID NO: 1092)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDVYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1093)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BC

>**XENP45776 STEAP-A[STEAP1]_H1.183_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.183_IgG1_PVA_/S267K (SEQ ID NO: 1094)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYAYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1095)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45777 STEAP-A[STEAP1]_H1.184_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.184_IgG1_PVA_/S267K (SEQ ID NO: 1096)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYFYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1097)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45778 STEAP-A[STEAP1]_H1.185_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.185_IgG1_PVA_/S267K (SEQ ID NO: 1098)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYHYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1099)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45779 STEAP-A[STEAP1]_H1.186_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.186_IgG1_PVA_/S267K (SEQ ID NO: 1100)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYKYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BD

>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1101)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45780 STEAP-A[STEAP1]_H1.187_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.187_IgG1_PVA_/S267K (SEQ ID NO: 1102)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYLYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1103)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45781 STEAP-A[STEAP1]_H1.188_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.188_IgG1_PVA_/S267K (SEQ ID NO: 1104)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYQYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1105)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45782 STEAP-A[STEAP1]_H1.189_L1_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.189_IgG1_PVA_/S267K (SEQ ID NO: 1106)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYVYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1_Light Chain (SEQ ID NO: 1107)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BE

>**XENP45783 STEAP-A[STEAP1]_H1_L1.4_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1108)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.4_Light Chain (SEQ ID NO: 1109)**
DIVMTQSPDSLAVSLGERATINCKSSQALLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45784 STEAP-A[STEAP1]_H1_L1.5_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1110)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.5_Light Chain (SEQ ID NO: 1111)**
DIVMTQSPDSLAVSLGERATINCKSSQDLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45785 STEAP-A[STEAP1]_H1_L1.6_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1112)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.6_Light Chain (SEQ ID NO: 1113)**
DIVMTQSPDSLAVSLGERATINCKSSQGLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45786 STEAP-A[STEAP1]_H1_L1.7_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1114)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BF

>**Chain 2- STEAP-A[STEAP1]_L1.7_Light Chain (SEQ ID NO: 1115)**
DIVMTQSPDSLAVSLGERATINCKSSQHLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45787 STEAP-A[STEAP1]_H1_L1.8_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1116)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.8_Light Chain (SEQ ID NO: 1117)**
DIVMTQSPDSLAVSLGERATINCKSSQKLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45788 STEAP-A[STEAP1]_H1_L1.9_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1118)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.9_Light Chain (SEQ ID NO: 1119)**
DIVMTQSPDSLAVSLGERATINCKSSQQLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45789 STEAP-A[STEAP1]_H1_L1.10_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1120)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.10_Light Chain (SEQ ID NO: 1121)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BG

>**XENP45790 STEAP-A[STEAP1]_H1_L1.11_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1122)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.11_Light Chain (SEQ ID NO: 1123)**
DIVMTQSPDSLAVSLGERATINCKSSQVLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45791 STEAP-A[STEAP1]_H1_L1.12_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1124)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.12_Light Chain (SEQ ID NO: 1125)**
DIVMTQSPDSLAVSLGERATINCKSSQYLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45792 STEAP-A[STEAP1]_H1_L1.13_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1126)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.13_Light Chain (SEQ ID NO: 1127)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLERSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45793 STEAP-A[STEAP1]_H1_L1.14_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1128)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BH

>**Chain 2- STEAP-A[STEAP1]_L1.14_Light Chain (SEQ ID NO: 1129)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLFRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45794 STEAP-A[STEAP1]_H1_L1.15_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1130)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.15_Light Chain (SEQ ID NO: 1131)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLHRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45795 STEAP-A[STEAP1]_H1_L1.16_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1132)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.16_Light Chain (SEQ ID NO: 1133)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLQRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45796 STEAP-A[STEAP1]_H1_L1.17_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1134)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.17_Light Chain (SEQ ID NO: 1135)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLRRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BI

>**XENP45797 STEAP-A[STEAP1]_H1_L1.18_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1136)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.18_Light Chain (SEQ ID NO: 1137)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYESNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45798 STEAP-A[STEAP1]_H1_L1.19_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1138)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.19_Light Chain (SEQ ID NO: 1139)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYKSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45799 STEAP-A[STEAP1]_H1_L1.20_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1140)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.20_Light Chain (SEQ ID NO: 1141)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYLSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45800 STEAP-A[STEAP1]_H1_L1.21_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1142)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BJ

>**Chain 2- STEAP-A[STEAP1]_L1.21_Light Chain (SEQ ID NO: 1143)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYQSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45801 STEAP-A[STEAP1]_H1_L1.22_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1144)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.22_Light Chain (SEQ ID NO: 1145)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45802 STEAP-A[STEAP1]_H1_L1.23_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1146)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.23_Light Chain (SEQ ID NO: 1147)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRDNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45803 STEAP-A[STEAP1]_H1_L1.24_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1148)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.24_Light Chain (SEQ ID NO: 1149)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRENQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BK

>**XENP45804 STEAP-A[STEAP1]_H1_L1.25_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1150)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.25_Light Chain (SEQ ID NO: 1151)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRHNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45805 STEAP-A[STEAP1]_H1_L1.26_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1152)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.26_Light Chain (SEQ ID NO: 1153)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRINQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45806 STEAP-A[STEAP1]_H1_L1.27_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1154)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.27_Light Chain (SEQ ID NO: 1155)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRKNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45807 STEAP-A[STEAP1]_H1_L1.28_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1156)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BL

>**Chain 2- STEAP-A[STEAP1]_L1.28_Light Chain (SEQ ID NO: 1157)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRLNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45808 STEAP-A[STEAP1]_H1_L1.29_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1158)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.29_Light Chain (SEQ ID NO: 1159)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRQNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45809 STEAP-A[STEAP1]_H1_L1.30_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1160)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.30_Light Chain (SEQ ID NO: 1161)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRTNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45810 STEAP-A[STEAP1]_H1_L1.31_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1162)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.31_Light Chain (SEQ ID NO: 1163)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRYNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BM

>**XENP45811 STEAP-A[STEAP1]_H1_L1.32_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1164)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.32_Light Chain (SEQ ID NO: 1165)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSDQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45812 STEAP-A[STEAP1]_H1_L1.33_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1166)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.33_Light Chain (SEQ ID NO: 1167)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSIQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45813 STEAP-A[STEAP1]_H1_L1.34_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1168)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.34_Light Chain (SEQ ID NO: 1169)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSKQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45814 STEAP-A[STEAP1]_H1_L1.35_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1170)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BN

>**Chain 2- STEAP-A[STEAP1]_L1.35_Light Chain (SEQ ID NO: 1171)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSLQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45815 STEAP-A[STEAP1]_H1_L1.36_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1172)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.36_Light Chain (SEQ ID NO: 1173)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSQQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45816 STEAP-A[STEAP1]_H1_L1.37_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1174)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.37_Light Chain (SEQ ID NO: 1175)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSRQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45817 STEAP-A[STEAP1]_H1_L1.38_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1176)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.38_Light Chain (SEQ ID NO: 1177)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BO

>**XENP45818 STEAP-A[STEAP1]_H1_L1.39_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1178)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.39_Light Chain (SEQ ID NO: 1179)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSTQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45819 STEAP-A[STEAP1]_H1_L1.40_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1180)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.40_Light Chain (SEQ ID NO: 1181)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSYQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45820 STEAP-A[STEAP1]_H1_L1.41_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1182)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.41_Light Chain (SEQ ID NO: 1183)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNEKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45821 STEAP-A[STEAP1]_H1_L1.42_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1184)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BP

>**Chain 2- STEAP-A[STEAP1]_L1.42_Light Chain (SEQ ID NO: 1185)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNHKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45822 STEAP-A[STEAP1]_H1_L1.43_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1186)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.43_Light Chain (SEQ ID NO: 1187)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNKKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45823 STEAP-A[STEAP1]_H1_L1.44_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1188)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.44_Light Chain (SEQ ID NO: 1189)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNNKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45824 STEAP-A[STEAP1]_H1_L1.45_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1190)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.45_Light Chain (SEQ ID NO: 1191)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNYKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BQ

>**XENP45825 STEAP-A[STEAP1]_H1_L1.46_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1192)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.46_Light Chain (SEQ ID NO: 1193)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQQNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45826 STEAP-A[STEAP1]_H1_L1.47_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1194)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.47_Light Chain (SEQ ID NO: 1195)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45827 STEAP-A[STEAP1]_H1_L1.48_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1196)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.48_Light Chain (SEQ ID NO: 1197)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQSNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45828 STEAP-A[STEAP1]_H1_L1.49_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1198)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BR

>**Chain 2- STEAP-A[STEAP1]_L1.49_Light Chain (SEQ ID NO: 1199)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKKYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45829 STEAP-A[STEAP1]_H1_L1.50_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1200)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.50_Light Chain (SEQ ID NO: 1201)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKRYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45830 STEAP-A[STEAP1]_H1_L1.51_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1202)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.51_Light Chain (SEQ ID NO: 1203)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKYYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45831 STEAP-A[STEAP1]_H1_L1.52_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1204)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.52_Light Chain (SEQ ID NO: 1205)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAETRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BS

>**XENP45832 STEAP-A[STEAP1]_H1_L1.53_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1206)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.53_Light Chain (SEQ ID NO: 1207)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAKTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45833 STEAP-A[STEAP1]_H1_L1.54_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1208)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.54_Light Chain (SEQ ID NO: 1209)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWALTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45834 STEAP-A[STEAP1]_H1_L1.55_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1210)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.55_Light Chain (SEQ ID NO: 1211)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAQTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45835 STEAP-A[STEAP1]_H1_L1.56_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1212)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BT

>**Chain 2- STEAP-A[STEAP1]_L1.56_Light Chain (SEQ ID NO: 1213)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAYTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45836 STEAP-A[STEAP1]_H1_L1.57_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1214)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.57_Light Chain (SEQ ID NO: 1215)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASERESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45837 STEAP-A[STEAP1]_H1_L1.58_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1216)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.58_Light Chain (SEQ ID NO: 1217)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASKRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45838 STEAP-A[STEAP1]_H1_L1.59_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1218)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.59_Light Chain (SEQ ID NO: 1219)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASLRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BU

>**XENP45839 STEAP-A[STEAP1]_H1_L1.60_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1220)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.60_Light Chain (SEQ ID NO: 1221)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASQRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45840 STEAP-A[STEAP1]_H1_L1.61_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1222)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.61_Light Chain (SEQ ID NO: 1223)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASYRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45841 STEAP-A[STEAP1]_H1_L1.62_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1224)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.62_Light Chain (SEQ ID NO: 1225)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYANYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45842 STEAP-A[STEAP1]_H1_L1.63_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1226)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BV

>**Chain 2- STEAP-A[STEAP1]_L1.63_Light Chain (SEQ ID NO: 1227)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYDNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45843 STEAP-A[STEAP1]_H1_L1.64_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1228)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.64_Light Chain (SEQ ID NO: 1229)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYHNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45844 STEAP-A[STEAP1]_H1_L1.65_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1230)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.65_Light Chain (SEQ ID NO: 1231)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYKNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45845 STEAP-A[STEAP1]_H1_L1.66_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1232)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.66_Light Chain (SEQ ID NO: 1233)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYLNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BW

>**XENP45846 STEAP-A[STEAP1]_H1_L1.67_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1234)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.67_Light Chain (SEQ ID NO: 1235)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYQNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45847 STEAP-A[STEAP1]_H1_L1.68_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1236)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.68_Light Chain (SEQ ID NO: 1237)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYRNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45848 STEAP-A[STEAP1]_H1_L1.69_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1238)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.69_Light Chain (SEQ ID NO: 1239)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYVNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45849 STEAP-A[STEAP1]_H1_L1.70_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1240)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 30BX

>**Chain 2- STEAP-A[STEAP1]_L1.70_Light Chain (SEQ ID NO: 1241)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYDYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45850 STEAP-A[STEAP1]_H1_L1.71_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1242)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.71_Light Chain (SEQ ID NO: 1243)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYHYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45851 STEAP-A[STEAP1]_H1_L1.72_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1244)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.72_Light Chain (SEQ ID NO: 1245)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45852 STEAP-A[STEAP1]_H1_L1.73_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1246)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.73_Light Chain (SEQ ID NO: 1247)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYLYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BY

>**XENP45853 STEAP-A[STEAP1]_H1_L1.74_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1248)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.74_Light Chain (SEQ ID NO: 1249)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYQYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45854 STEAP-A[STEAP1]_H1_L1.75_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1250)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.75_Light Chain (SEQ ID NO: 1251)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYRYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45855 STEAP-A[STEAP1]_H1_L1.76_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1252)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.76_Light Chain (SEQ ID NO: 1253)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYSYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45856 STEAP-A[STEAP1]_H1_L1.77_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1254)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.77_Light Chain (SEQ ID NO: 1255)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYTYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30BZ

>**XENP45857 STEAP-A[STEAP1]_H1_L1.78_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1256)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.78_Light Chain (SEQ ID NO: 1257)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNAPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45858 STEAP-A[STEAP1]_H1_L1.79_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1258)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.79_Light Chain (SEQ ID NO: 1259)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNDPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45859 STEAP-A[STEAP1]_H1_L1.80_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1260)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.80_Light Chain (SEQ ID NO: 1261)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNHPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45860 STEAP-A[STEAP1]_H1_L1.81_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1262)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.81_Light Chain (SEQ ID NO: 1263)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNKPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CA

>**XENP45861 STEAP-A[STEAP1]_H1_L1.82_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1264)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.82_Light Chain (SEQ ID NO: 1265)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNLPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45862 STEAP-A[STEAP1]_H1_L1.83_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1266)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.83_Light Chain (SEQ ID NO: 1267)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNQPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45863 STEAP-A[STEAP1]_H1_L1.84_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1268)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.84_Light Chain (SEQ ID NO: 1269)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNRPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP45864 STEAP-A[STEAP1]_H1_L1.85_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1_IgG1_PVA_/S267K (SEQ ID NO: 1270)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.85_Light Chain (SEQ ID NO: 1271)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNVPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CB

>**XENP46211 STEAP-A[STEAP1]_H1.42_L1.47_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.42_IgG1_PVA_/S267K (SEQ ID NO: 1272)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.47_Light Chain (SEQ ID NO: 1273)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46212 STEAP-A[STEAP1]_H1.42_L1.56_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.42_IgG1_PVA_/S267K (SEQ ID NO: 1274)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.56_Light Chain (SEQ ID NO: 1275)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAYTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46440 STEAP-A[STEAP1]_H1.190_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.190_IgG1_PVA_/S267K (SEQ ID NO: 1276)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSAYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1277)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46441 STEAP-A[STEAP1]_H1.191_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.191_IgG1_PVA_/S267K (SEQ ID NO: 1278)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSLYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1279)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CC

>**XENP46442 STEAP-A[STEAP1]_H1.192_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.192_IgG1_PVA_/S267K (SEQ ID NO: 1280)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSVYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1281)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46443 STEAP-A[STEAP1]_H1.195_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1282)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1283)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46444 STEAP-A[STEAP1]_H1.196_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1284)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1285)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46445 STEAP-A[STEAP1]_H1.197_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.197_IgG1_PVA_/S267K (SEQ ID NO: 1286)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1287)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CD

>**XENP46446 STEAP-A[STEAP1]_H1.198_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.198_IgG1_PVA_/S267K (SEQ ID NO: 1288)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1289)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46447 STEAP-A[STEAP1]_H1.199_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.199_IgG1_PVA_/S267K (SEQ ID NO: 1290)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1291)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46448 STEAP-A[STEAP1]_H1.200_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.200_IgG1_PVA_/S267K (SEQ ID NO: 1292)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1293)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46449 STEAP-A[STEAP1]_H1.201_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.201_IgG1_PVA_/S267K (SEQ ID NO: 1294)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1295)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CE

>**XENP46450 STEAP-A[STEAP1]_H1.202_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.202_IgG1_PVA_/S267K (SEQ ID NO: 1296)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1297)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46451 STEAP-A[STEAP1]_H1.203_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.203_IgG1_PVA_/S267K (SEQ ID NO: 1298)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1299)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46452 STEAP-A[STEAP1]_H1.204_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.204_IgG1_PVA_/S267K (SEQ ID NO: 1300)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1301)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46453 STEAP-A[STEAP1]_H1.205_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1302)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1303)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CF

>**XENP46454 STEAP-A[STEAP1]_H1.206_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.206_IgG1_PVA_/S267K (SEQ ID NO: 1304)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1305)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46455 STEAP-A[STEAP1]_H1.207_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.207_IgG1_PVA_/S267K (SEQ ID NO: 1306)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1307)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46456 STEAP-A[STEAP1]_H1.208_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.208_IgG1_PVA_/S267K (SEQ ID NO: 1308)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1309)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46457 STEAP-A[STEAP1]_H1.209_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.209_IgG1_PVA_/S267K (SEQ ID NO: 1310)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1311)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CG

>**XENP46458 STEAP-A[STEAP1]_H1.210_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.210_IgG1_PVA_/S267K (SEQ ID NO: 1312)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1313)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46459 STEAP-A[STEAP1]_H1.211_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.211_IgG1_PVA_/S267K (SEQ ID NO: 1314)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1315)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46460 STEAP-A[STEAP1]_H1.212_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.212_IgG1_PVA_/S267K (SEQ ID NO: 1316)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1317)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46461 STEAP-A[STEAP1]_H1.213_L1.3_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.213_IgG1_PVA_/S267K (SEQ ID NO: 1318)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1319)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CH

>**XENP46462 STEAP-A[STEAP1]_H1.214_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.214_IgG1_PVA_/S267K (SEQ ID NO: 1320)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1321)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46463 STEAP-A[STEAP1]_H1.215_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.215_IgG1_PVA_/S267K (SEQ ID NO: 1322)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1323)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46464 STEAP-A[STEAP1]_H1.216_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.216_IgG1_PVA_/S267K (SEQ ID NO: 1324)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1325)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46465 STEAP-A[STEAP1]_H1.217_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.217_IgG1_PVA_/S267K (SEQ ID NO: 1326)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1327)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CI

>**XENP46466 STEAP-A[STEAP1]_H1.218_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.218_IgG1_PVA_/S267K (SEQ ID NO: 1328)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1329)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46467 STEAP-A[STEAP1]_H1.219_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.219_IgG1_PVA_/S267K (SEQ ID NO: 1330)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1331)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46468 STEAP-A[STEAP1]_H1.220_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.220_IgG1_PVA_/S267K (SEQ ID NO: 1332)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1333)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46469 STEAP-A[STEAP1]_H1.221_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.221_IgG1_PVA_/S267K (SEQ ID NO: 1334)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1335)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CJ

>**XENP46470 STEAP-A[STEAP1]_H1.222_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.222_IgG1_PVA_/S267K (SEQ ID NO: 1336)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1337)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46471 STEAP-A[STEAP1]_H1.223_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.223_IgG1_PVA_/S267K (SEQ ID NO: 1338)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1339)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46472 STEAP-A[STEAP1]_H1.224_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.224_IgG1_PVA_/S267K (SEQ ID NO: 1340)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1341)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46473 STEAP-A[STEAP1]_H1.225_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.225_IgG1_PVA_/S267K (SEQ ID NO: 1342)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1343)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CK

>**XENP46474 STEAP-A[STEAP1]_H1.226_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.226_IgG1_PVA_/S267K (SEQ ID NO: 1344)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1345)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46475 STEAP-A[STEAP1]_H1.227_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.227_IgG1_PVA_/S267K (SEQ ID NO: 1346)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1347)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46476 STEAP-A[STEAP1]_H1.228_L1.3_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_PVA_/S267K (SEQ ID NO: 1348)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.3_Light Chain (SEQ ID NO: 1349)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46477 STEAP-A[STEAP1]_H1.21_L1.92_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1350)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.92_Light Chain (SEQ ID NO: 1351)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CL

>**XENP46478 STEAP-A[STEAP1]_H1.21_L1.93_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1352)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.93_Light Chain (SEQ ID NO: 1353)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46479 STEAP-A[STEAP1]_H1.21_L1.94_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1354)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.94_Light Chain (SEQ ID NO: 1355)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46480 STEAP-A[STEAP1]_H1.21_L1.95_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1356)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.95_Light Chain (SEQ ID NO: 1357)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46481 STEAP-A[STEAP1]_H1.21_L1.96_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1358)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.96_Light Chain (SEQ ID NO: 1359)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CM

>**XENP46482 STEAP-A[STEAP1]_H1.21_L1.97_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1360)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.97_Light Chain (SEQ ID NO: 1361)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46483 STEAP-A[STEAP1]_H1.21_L1.98_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1362)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.98_Light Chain (SEQ ID NO: 1363)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46484 STEAP-A[STEAP1]_H1.21_L1.99_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1364)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.99_Light Chain (SEQ ID NO: 1365)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46485 STEAP-A[STEAP1]_H1.21_L1.100_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1366)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 1367)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CN

>**XENP46486 STEAP-A[STEAP1]_H1.21_L1.101_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1368)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.101_Light Chain (SEQ ID NO: 1369)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46487 STEAP-A[STEAP1]_H1.21_L1.102_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1370)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.102_Light Chain (SEQ ID NO: 1371)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46488 STEAP-A[STEAP1]_H1.21_L1.103_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1372)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.103_Light Chain (SEQ ID NO: 1373)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46489 STEAP-A[STEAP1]_H1.21_L1.104_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1374)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.104_Light Chain (SEQ ID NO: 1375)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CO

>**XENP46490 STEAP-A[STEAP1]_H1.21_L1.105_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1376)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.105_Light Chain (SEQ ID NO: 1377)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46491 STEAP-A[STEAP1]_H1.21_L1.106_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1378)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.106_Light Chain (SEQ ID NO: 1379)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46492 STEAP-A[STEAP1]_H1.21_L1.107_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1380)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.107_Light Chain (SEQ ID NO: 1381)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46493 STEAP-A[STEAP1]_H1.21_L1.108_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1382)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.108_Light Chain (SEQ ID NO: 1383)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CP

>**XENP46494 STEAP-A[STEAP1]_H1.21_L1.109_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1384)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.109_Light Chain (SEQ ID NO: 1385)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46495 STEAP-A[STEAP1]_H1.21_L1.110_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1386)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.110_Light Chain (SEQ ID NO: 1387)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46496 STEAP-A[STEAP1]_H1.21_L1.111_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1388)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.111_Light Chain (SEQ ID NO: 1389)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46497 STEAP-A[STEAP1]_H1.21_L1.112_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1390)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.112_Light Chain (SEQ ID NO: 1391)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CQ

>**XENP46498 STEAP-A[STEAP1]_H1.21_L1.113_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1392)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.113_Light Chain (SEQ ID NO: 1393)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46499 STEAP-A[STEAP1]_H1.21_L1.114_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1394)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.114_Light Chain (SEQ ID NO: 1395)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46500 STEAP-A[STEAP1]_H1.21_L1.115_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1396)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1397)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46501 STEAP-A[STEAP1]_H1.21_L1.116_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1398)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.116_Light Chain (SEQ ID NO: 1399)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CR

>**XENP46502 STEAP-A[STEAP1]_H1.21_L1.117_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1400)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.117_Light Chain (SEQ ID NO: 1401)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46503 STEAP-A[STEAP1]_H1.21_L1.118_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1402)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.118_Light Chain (SEQ ID NO: 1403)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46504 STEAP-A[STEAP1]_H1.21_L1.119_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.21_IgG1_PVA_/S267K (SEQ ID NO: 1404)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.119_Light Chain (SEQ ID NO: 1405)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46505 STEAP-A[STEAP1]_H1.195_L1.92_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1406)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.92_Light Chain (SEQ ID NO: 1407)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CS

>**XENP46506 STEAP-A[STEAP1]_H1.195_L1.94_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1408)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.94_Light Chain (SEQ ID NO: 1409)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46507 STEAP-A[STEAP1]_H1.195_L1.95_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1410)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.95_Light Chain (SEQ ID NO: 1411)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46508 STEAP-A[STEAP1]_H1.195_L1.104_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1412)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.104_Light Chain (SEQ ID NO: 1413)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46509 STEAP-A[STEAP1]_H1.195_L1.105_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1414)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.105_Light Chain (SEQ ID NO: 1415)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CT

>**XENP46510 STEAP-A[STEAP1]_H1.195_L1.109_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.195_IgG1_PVA_/S267K (SEQ ID NO: 1416)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.109_Light Chain (SEQ ID NO: 1417)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46511 STEAP-A[STEAP1]_H1.196_L1.92_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1418)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.92_Light Chain (SEQ ID NO: 1419)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46512 STEAP-A[STEAP1]_H1.196_L1.94_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1420)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.94_Light Chain (SEQ ID NO: 1421)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46513 STEAP-A[STEAP1]_H1.196_L1.95_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1422)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.95_Light Chain (SEQ ID NO: 1423)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CU

>**XENP46514 STEAP-A[STEAP1]_H1.196_L1.104_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1424)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.104_Light Chain (SEQ ID NO: 1425)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46515 STEAP-A[STEAP1]_H1.196_L1.105_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1426)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.105_Light Chain (SEQ ID NO: 1427)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46516 STEAP-A[STEAP1]_H1.196_L1.109_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.196_IgG1_PVA_/S267K (SEQ ID NO: 1428)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.109_Light Chain (SEQ ID NO: 1429)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46517 STEAP-A[STEAP1]_H1.205_L1.92_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1430)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.92_Light Chain (SEQ ID NO: 1431)**

DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CV

>**XENP46518 STEAP-A[STEAP1]_H1.205_L1.94_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1432)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.94_Light Chain (SEQ ID NO: 1433)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46519 STEAP-A[STEAP1]_H1.205_L1.95_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1434)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.95_Light Chain (SEQ ID NO: 1435)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46520 STEAP-A[STEAP1]_H1.205_L1.104_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1436)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.104_Light Chain (SEQ ID NO: 1437)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46521 STEAP-A[STEAP1]_H1.205_L1.105_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1438)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.105_Light Chain (SEQ ID NO: 1439)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CW

>**XENP46522 STEAP-A[STEAP1]_H1.205_L1.109_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.205_IgG1_PVA_/S267K (SEQ ID NO: 1440)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.109_Light Chain (SEQ ID NO: 1441)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46523 STEAP-A[STEAP1]_H1.193_L1.91_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.193_IgG1_PVA_/S267K (SEQ ID NO: 1442)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGETSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.91_Light Chain (SEQ ID NO: 1443)**
DIVMTQSPDSLAVSLGERATINCKSSKSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46524 STEAP-A[STEAP1]_H1.194_L1.86_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.194_IgG1_PVA_/S267K (SEQ ID NO: 1444)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTIRRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.86_Light Chain (SEQ ID NO: 1445)**
DIDMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46525 STEAP-A[STEAP1]_H1.194_L1.87_IgG1_PVA_/S267K**
>**Chain 1- STEAP-A[STEAP1]_H1.194_IgG1_PVA_/S267K (SEQ ID NO: 1446)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTIRRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
>**Chain 2- STEAP-A[STEAP1]_L1.87_Light Chain (SEQ ID NO: 1447)**
DIVMTQSPDSLAVSLGERATINCKSDQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CX

>**XENP46526 STEAP-A[STEAP1]_H1.194_L1.88_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.194_IgG1_PVA_/S267K (SEQ ID NO: 1448)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTIRRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.88_Light Chain (SEQ ID NO: 1449)**

DIVMTQSPDSLAVSLGERATINCKSEQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46527 STEAP-A[STEAP1]_H1.194_L1.89_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.194_IgG1_PVA_/S267K (SEQ ID NO: 1450)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTIRRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.89_Light Chain (SEQ ID NO: 1451)**

DIVMTQSPDSLAVSLGERATINCKSSDSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46528 STEAP-A[STEAP1]_H1.194_L1.90_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.194_IgG1_PVA_/S267K (SEQ ID NO: 1452)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTIRRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.90_Light Chain (SEQ ID NO: 1453)**

DIVMTQSPDSLAVSLGERATINCKSSESLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CY

>**XENP46889 STEAP-A[STEAP1]_H1.228_L1.115_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_PVA_/S267K (SEQ ID NO: 1454)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1455)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46890 STEAP-A[STEAP1]_H1.229_L1.115_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.229_IgG1_PVA_/S267K (SEQ ID NO: 1456)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGESGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1457)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46891 STEAP-A[STEAP1]_H1.230_L1.115_IgG1_PVA_/S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_PVA_/S267K (SEQ ID NO: 1458)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1459)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 30CZ

>**XENP46892 STEAP-A[STEAP1] H1.231 L1.115 IgG1 PVA /S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.231_IgG1_PVA_/S267K (SEQ ID NO: 1460)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNQGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1461)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP46893 STEAP-A[STEAP1] H1.232 L1.115 IgG1 PVA /S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.232_IgG1_PVA_/S267K (SEQ ID NO: 1462)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNTGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1463)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>**XENP47373 STEAP-A[STEAP1] H1.230 L1.100 IgG1 PVA /S267K**

>**Chain 1- STEAP-A[STEAP1]_H1.230_IgG1_PVA_/S267K (SEQ ID NO: 1464)**

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

>**Chain 2- STEAP-A[STEAP1]_L1.100_Light Chain (SEQ ID NO: 1465)**

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 31A

>**STEAP-A [STEAP1] _H1 (SEQ ID NO: 1466)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.1 (SEQ ID NO: 1467)**
QVQLQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.2 (SEQ ID NO: 1468)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKGLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.3 (SEQ ID NO: 1469)**
QVQLQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKGLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.4 (SEQ ID NO: 1470)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYADYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.5 (SEQ ID NO: 1471)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.6 (SEQ ID NO: 1472)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.7 (SEQ ID NO: 1473)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.8 (SEQ ID NO: 1474)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.9 (SEQ ID NO: 1475)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.10 (SEQ ID NO: 1476)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDEYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.11 (SEQ ID NO: 1477)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDLYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.12 (SEQ ID NO: 1478)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDQYYYAMDYWGQGTLVTVSS

Figure 31B

>**STEAP-A [STEAP1] _H1.13 (SEQ ID NO: 1479)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDTYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.14 (SEQ ID NO: 1480)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.15 (SEQ ID NO: 1481)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAEYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.16 (SEQ ID NO: 1482)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYALYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.17 (SEQ ID NO: 1483)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYAQYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.18 (SEQ ID NO: 1484)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYATYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.19 (SEQ ID NO: 1485)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.20 (SEQ ID NO: 1486)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEEYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.21 (SEQ ID NO: 1487)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.22 (SEQ ID NO: 1488)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEQYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.23 (SEQ ID NO: 1489)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYETYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.24 (SEQ ID NO: 1490)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.25 (SEQ ID NO: 1491)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLEYYYAMDYWGQGTLVTVSS

Figure 31C

>**STEAP-A [STEAP1] _H1.26 (SEQ ID NO: 1492)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLLYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.27 (SEQ ID NO: 1493)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLQYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.28 (SEQ ID NO: 1494)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYLTYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.29 (SEQ ID NO: 1495)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.30 (SEQ ID NO: 1496)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQEYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.31 (SEQ ID NO: 1497)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQLYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.32 (SEQ ID NO: 1498)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQQYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.33 (SEQ ID NO: 1499)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYQTYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.34 (SEQ ID NO: 1500)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTAYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.35 (SEQ ID NO: 1501)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTEYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.36 (SEQ ID NO: 1502)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTLYYYAMDYWGQGTLVTVSS

Figure 31D

>**STEAP-A [STEAP1] _H1.37 (SEQ ID NO: 1503)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTQYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.38 (SEQ ID NO: 1504)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYTTYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.39 (SEQ ID NO: 1505)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.40 (SEQ ID NO: 1506)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSYYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.41 (SEQ ID NO: 1507)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDAAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.42 (SEQ ID NO: 1508)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDDAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.43 (SEQ ID NO: 1509)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDKAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.44 (SEQ ID NO: 1510)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDLAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.45 (SEQ ID NO: 1511)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDQAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.46 (SEQ ID NO: 1512)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYDWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.47 (SEQ ID NO: 1513)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYFWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31E

>**STEAP-A [STEAP1] _H1.48 (SEQ ID NO: 1514)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYGWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.49 (SEQ ID NO: 1515)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYHWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.50 (SEQ ID NO: 1516)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYKWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.51 (SEQ ID NO: 1517)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYLWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.52 (SEQ ID NO: 1518)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYQWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.53 (SEQ ID NO: 1519)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.54 (SEQ ID NO: 1520)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYTWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.55 (SEQ ID NO: 1521)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWGWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.56 (SEQ ID NO: 1522)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWHWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.57 (SEQ ID NO: 1523)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWSWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.58 (SEQ ID NO: 1524)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWTWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31F

>**STEAP-A [STEAP1] _H1.59 (SEQ ID NO: 1525)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGAISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.60 (SEQ ID NO: 1526)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGDISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.61 (SEQ ID NO: 1527)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGFISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.62 (SEQ ID NO: 1528)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGHISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.63 (SEQ ID NO: 1529)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGKISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.64 (SEQ ID NO: 1530)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGLISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.65 (SEQ ID NO: 1531)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGQISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.66 (SEQ ID NO: 1532)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGVISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.67 (SEQ ID NO: 1533)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGWISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.68 (SEQ ID NO: 1534)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIANSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.69 (SEQ ID NO: 1535)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIDNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31G

>**STEAP-A [STEAP1] _H1.70 (SEQ ID NO: 1536)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.71 (SEQ ID NO: 1537)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIHNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.72 (SEQ ID NO: 1538)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIKNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.73 (SEQ ID NO: 1539)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIQNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.74 (SEQ ID NO: 1540)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYITNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.75 (SEQ ID NO: 1541)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIVNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.76 (SEQ ID NO: 1542)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIYNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.77 (SEQ ID NO: 1543)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISESGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.78 (SEQ ID NO: 1544)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.79 (SEQ ID NO: 1545)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISLSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.80 (SEQ ID NO: 1546)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISQSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31H

>**STEAP-A [STEAP1] _H1.81 (SEQ ID NO: 1547)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISRSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.82 (SEQ ID NO: 1548)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNAGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.83 (SEQ ID NO: 1549)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNEGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.84 (SEQ ID NO: 1550)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.85 (SEQ ID NO: 1551)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.86 (SEQ ID NO: 1552)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNIGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.87 (SEQ ID NO: 1553)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNKGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.88 (SEQ ID NO: 1554)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNQGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.89 (SEQ ID NO: 1555)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNTGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.90 (SEQ ID NO: 1556)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNYGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.91 (SEQ ID NO: 1557)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSASTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31I

>**STEAP-A [STEAP1] _H1.92 (SEQ ID NO: 1558)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSESTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.93 (SEQ ID NO: 1559)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSHSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.94 (SEQ ID NO: 1560)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSQSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.95 (SEQ ID NO: 1561)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSRSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.96 (SEQ ID NO: 1562)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGATSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.97 (SEQ ID NO: 1563)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGDTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.98 (SEQ ID NO: 1564)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGGTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.99 (SEQ ID NO: 1565)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGHTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.100 (SEQ ID NO: 1566)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGKTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.101 (SEQ ID NO: 1567)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGQTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.102 (SEQ ID NO: 1568)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGTTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31J

>**STEAP-A [STEAP1] _H1.103 (SEQ ID NO: 1569)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGVTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.104 (SEQ ID NO: 1570)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.105 (SEQ ID NO: 1571)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.106 (SEQ ID NO: 1572)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.107 (SEQ ID NO: 1573)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTDYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.108 (SEQ ID NO: 1574)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTGYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.109 (SEQ ID NO: 1575)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTHYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.110 (SEQ ID NO: 1576)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTQYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.111 (SEQ ID NO: 1577)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTTYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.112 (SEQ ID NO: 1578)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.113 (SEQ ID NO: 1579)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTYYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

Figure 31K

>**STEAP-A [STEAP1] _H1.114 (SEQ ID NO: 1580)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARHRNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.115 (SEQ ID NO: 1581)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARIRNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.116 (SEQ ID NO: 1582)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARKRNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.117 (SEQ ID NO: 1583)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARQRNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.118 (SEQ ID NO: 1584)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARSRNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.119 (SEQ ID NO: 1585)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREENYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.120 (SEQ ID NO: 1586)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREHNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.121 (SEQ ID NO: 1587)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREINYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.122 (SEQ ID NO: 1588)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREKNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.123 (SEQ ID NO: 1589)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCAREQNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.124 (SEQ ID NO: 1590)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERDYDYDDYYYAMDYWGQGTLVTVSS

Figure 31L

>**STEAP-A [STEAP1] _H1.125 (SEQ ID NO: 1591)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERGYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.126 (SEQ ID NO: 1592)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERHYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.127 (SEQ ID NO: 1593)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERLYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.128 (SEQ ID NO: 1594)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERQYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.129 (SEQ ID NO: 1595)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERRYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.130 (SEQ ID NO: 1596)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERSYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.131 (SEQ ID NO: 1597)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERTYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.132 (SEQ ID NO: 1598)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNADYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.133 (SEQ ID NO: 1599)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNFDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.134 (SEQ ID NO: 1600)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNHDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.135 (SEQ ID NO: 1601)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNKDYDDYYYAMDYWGQGTLVTVSS

Figure 31M

>**STEAP-A [STEAP1] _H1.136 (SEQ ID NO: 1602)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNLDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.137 (SEQ ID NO: 1603)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNQDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.138 (SEQ ID NO: 1604)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNVDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.139 (SEQ ID NO: 1605)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYEYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.140 (SEQ ID NO: 1606)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYGYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.141 (SEQ ID NO: 1607)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYHYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.142 (SEQ ID NO: 1608)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYLYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.143 (SEQ ID NO: 1609)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYNYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.144 (SEQ ID NO: 1610)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYRYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.145 (SEQ ID NO: 1611)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYSYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.146 (SEQ ID NO: 1612)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYTYDDYYYAMDYWGQGTLVTVSS

Figure 31N

>**STEAP-A [STEAP1] _H1.147 (SEQ ID NO: 1613)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDADDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.148 (SEQ ID NO: 1614)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDFDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.149 (SEQ ID NO: 1615)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDHDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.150 (SEQ ID NO: 1616)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDKDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.151 (SEQ ID NO: 1617)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDLDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.152 (SEQ ID NO: 1618)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDQDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.153 (SEQ ID NO: 1619)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDVDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.154 (SEQ ID NO: 1620)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYGDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.155 (SEQ ID NO: 1621)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYHDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.156 (SEQ ID NO: 1622)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYNDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.157 (SEQ ID NO: 1623)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYRDYYYAMDYWGQGTLVTVSS

Figure 31O

>**STEAP-A [STEAP1] _H1.158 (SEQ ID NO: 1624)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.159 (SEQ ID NO: 1625)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDGYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.160 (SEQ ID NO: 1626)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDHYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.161 (SEQ ID NO: 1627)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDIYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.162 (SEQ ID NO: 1628)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDNYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.163 (SEQ ID NO: 1629)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDRYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.164 (SEQ ID NO: 1630)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDSYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.165 (SEQ ID NO: 1631)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDVYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.166 (SEQ ID NO: 1632)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEGYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.167 (SEQ ID NO: 1633)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEHYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.168 (SEQ ID NO: 1634)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEIYYYAMDYWGQGTLVTVSS

Figure 31P

>**STEAP-A [STEAP1] _H1.169 (SEQ ID NO: 1635)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYENYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.170 (SEQ ID NO: 1636)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYERYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.171 (SEQ ID NO: 1637)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYESYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.172 (SEQ ID NO: 1638)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYEVYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.173 (SEQ ID NO: 1639)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDAYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.174 (SEQ ID NO: 1640)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDFYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.175 (SEQ ID NO: 1641)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDHYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.176 (SEQ ID NO: 1642)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDKYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.177 (SEQ ID NO: 1643)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDLYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.178 (SEQ ID NO: 1644)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDQYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.179 (SEQ ID NO: 1645)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDVYYAMDYWGQGTLVTVSS

Figure 31Q

>**STEAP-A [STEAP1] _H1.180 (SEQ ID NO: 1646)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYAYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.181 (SEQ ID NO: 1647)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYFYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.182 (SEQ ID NO: 1648)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYHYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.183 (SEQ ID NO: 1649)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYKYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.184 (SEQ ID NO: 1650)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYLYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.185 (SEQ ID NO: 1651)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYQYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.186 (SEQ ID NO: 1652)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYVYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.187 (SEQ ID NO: 1653)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.188 (SEQ ID NO: 1654)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.189 (SEQ ID NO: 1655)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNIGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYDDYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.190 (SEQ ID NO: 1656)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSAYYYAMDYWGQGTLVTVSS

Figure 31R

>**STEAP-A [STEAP1] _H1.191 (SEQ ID NO: 1657)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSLYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.192 (SEQ ID NO: 1658)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYSVYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.195 (SEQ ID NO: 1659)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.196 (SEQ ID NO: 1660)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.197 (SEQ ID NO: 1661)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.198 (SEQ ID NO: 1662)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.199 (SEQ ID NO: 1663)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.200 (SEQ ID NO: 1664)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.201 (SEQ ID NO: 1665)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.202 (SEQ ID NO: 1666)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.203 (SEQ ID NO: 1667)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

Figure 31S

>**STEAP-A [STEAP1] _H1.204 (SEQ ID NO: 1668)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.205 (SEQ ID NO: 1669)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.206 (SEQ ID NO: 1670)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.207 (SEQ ID NO: 1671)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.208 (SEQ ID NO: 1672)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGHSGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.209 (SEQ ID NO: 1673)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNGGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.210 (SEQ ID NO: 1674)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNHGSTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.211 (SEQ ID NO: 1675)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.212 (SEQ ID NO: 1676)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.213 (SEQ ID NO: 1677)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYIGNSGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.214 (SEQ ID NO: 1678)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

Figure 31T

>**STEAP-A [STEAP1] _H1.215 (SEQ ID NO: 1679)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYISNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.216 (SEQ ID NO: 1680)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISHSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.217 (SEQ ID NO: 1681)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNGGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.218 (SEQ ID NO: 1682)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.219 (SEQ ID NO: 1683)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.220 (SEQ ID NO: 1684)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.221 (SEQ ID NO: 1685)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGYTSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.222 (SEQ ID NO: 1686)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.223 (SEQ ID NO: 1687)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNHGSTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.224 (SEQ ID NO: 1688)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYKSYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A [STEAP1] _H1.225 (SEQ ID NO: 1689)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGYTAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

Figure 31U

>**STEAP-A** [**STEAP1**] **_H1.226 (SEQ ID NO: 1690)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYAWNWIRQPPGKKLEWIGYISNSGSKAYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A** [**STEAP1**] **_H1.227 (SEQ ID NO: 1691)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSTYAWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>**STEAP-A** [**STEAP1**] **_H1.228 (SEQ ID NO: 1692)**
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>STEAP-A[STEAP1]_H1.229 (SEQ ID NO: 1693)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGESGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>STEAP-A[STEAP1]_H1.230 (SEQ ID NO: 1694)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGTSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>STEAP-A[STEAP1]_H1.231 (SEQ ID NO: 1695)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNQGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

>STEAP-A[STEAP1]_H1.232 (SEQ ID NO: 1696)
QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNTGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS

Figure 32A

>**STEAP-A [STEAP1] _L1 . 1 (SEQ ID NO: 1697)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 2 (SEQ ID NO: 1698)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 3 (SEQ ID NO: 1699)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 4 (SEQ ID NO: 1700)**
DIVMTQSPDSLAVSLGERATINCKSSQALLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 5 (SEQ ID NO: 1701)**
DIVMTQSPDSLAVSLGERATINCKSSQDLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 6 (SEQ ID NO: 1702)**
DIVMTQSPDSLAVSLGERATINCKSSQGLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 7 (SEQ ID NO: 1703)**
DIVMTQSPDSLAVSLGERATINCKSSQHLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 8 (SEQ ID NO: 1704)**
DIVMTQSPDSLAVSLGERATINCKSSQKLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 9 (SEQ ID NO: 1705)**
DIVMTQSPDSLAVSLGERATINCKSSQQLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 10 (SEQ ID NO: 1706)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 11 (SEQ ID NO: 1707)**
DIVMTQSPDSLAVSLGERATINCKSSQVLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 12 (SEQ ID NO: 1708)**
DIVMTQSPDSLAVSLGERATINCKSSQYLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 13 (SEQ ID NO: 1709)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLERSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32B

>**STEAP-A [STEAP1] _L1 . 14 (SEQ ID NO: 1710)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLFRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 15 (SEQ ID NO: 1711)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLHRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 16 (SEQ ID NO: 1712)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLQRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 17 (SEQ ID NO: 1713)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLRRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 18 (SEQ ID NO: 1714)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYESNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 19 (SEQ ID NO: 1715)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYKSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 20 (SEQ ID NO: 1716)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYLSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 21 (SEQ ID NO: 1717)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYQSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 22 (SEQ ID NO: 1718)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 23 (SEQ ID NO: 1719)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRDNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 24 (SEQ ID NO: 1720)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRENQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 25 (SEQ ID NO: 1721)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRHNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 26 (SEQ ID NO: 1722)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRINQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32C

>**STEAP-A [STEAP1] _L1 . 27 (SEQ ID NO: 1723)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRKNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 28 (SEQ ID NO: 1724)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRLNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 29 (SEQ ID NO: 1725)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRQNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 30 (SEQ ID NO: 1726)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRTNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 31 (SEQ ID NO: 1727)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRYNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 32 (SEQ ID NO: 1728)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSDQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 33 (SEQ ID NO: 1729)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSIQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 34 (SEQ ID NO: 1730)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSKQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 35 (SEQ ID NO: 1731)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSLQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 36 (SEQ ID NO: 1732)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSQQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 37 (SEQ ID NO: 1733)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSRQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 38 (SEQ ID NO: 1734)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 39 (SEQ ID NO: 1735)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSTQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32D

>**STEAP-A [STEAP1] _L1 . 40 (SEQ ID NO: 1736)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSYQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 41 (SEQ ID NO: 1737)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNEKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 42 (SEQ ID NO: 1738)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNHKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 43 (SEQ ID NO: 1739)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNKKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 44 (SEQ ID NO: 1740)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNNKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 45 (SEQ ID NO: 1741)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNYKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 46 (SEQ ID NO: 1742)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQQNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 47 (SEQ ID NO: 1743)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 48 (SEQ ID NO: 1744)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQSNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 49 (SEQ ID NO: 1745)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKKYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 50 (SEQ ID NO: 1746)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKRYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 51 (SEQ ID NO: 1747)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKYYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 52 (SEQ ID NO: 1748)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAETRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32E

>**STEAP-A [STEAP1]_L1.53 (SEQ ID NO: 1749)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAKTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.54 (SEQ ID NO: 1750)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWALTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.55 (SEQ ID NO: 1751)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAQTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.56 (SEQ ID NO: 1752)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWAYTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.57 (SEQ ID NO: 1753)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASERESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.58 (SEQ ID NO: 1754)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASKRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.59 (SEQ ID NO: 1755)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASLRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.60 (SEQ ID NO: 1756)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASQRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.61 (SEQ ID NO: 1757)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASYRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.62 (SEQ ID NO: 1758)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYANYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.63 (SEQ ID NO: 1759)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYDNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.64 (SEQ ID NO: 1760)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYHNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.65 (SEQ ID NO: 1761)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYKNYPRTFGGGTKVEIK

Figure 32F

>**STEAP-A [STEAP1]_L1.66 (SEQ ID NO: 1762)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYLNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.67 (SEQ ID NO: 1763)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYQNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.68 (SEQ ID NO: 1764)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYRNYPRTFGGGTKVEIK
>**STEAP-A [STEAP1]_L1.69 (SEQ ID NO: 1765)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYVNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.70 (SEQ ID NO: 1766)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYDYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.71 (SEQ ID NO: 1767)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYHYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.72 (SEQ ID NO: 1768)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.73 (SEQ ID NO: 1769)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYLYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.74 (SEQ ID NO: 1770)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYQYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.75 (SEQ ID NO: 1771)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYRYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.76 (SEQ ID NO: 1772)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYSYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.77 (SEQ ID NO: 1773)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYTYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.78 (SEQ ID NO: 1774)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNAPRTFGGGTKVEIK

Figure 32G

>**STEAP-A [STEAP1]_L1.79 (SEQ ID NO: 1775)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNDPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.80 (SEQ ID NO: 1776)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNHPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.81 (SEQ ID NO: 1777)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNKPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.82 (SEQ ID NO: 1778)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNLPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.83 (SEQ ID NO: 1779)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNQPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.84 (SEQ ID NO: 1780)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNRPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.85 (SEQ ID NO: 1781)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNVPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.86 (SEQ ID NO: 1782)**
DIDMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.87 (SEQ ID NO: 1783)**
DIVMTQSPDSLAVSLGERATINCKSDQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.88 (SEQ ID NO: 1784)**
DIVMTQSPDSLAVSLGERATINCKSEQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.89 (SEQ ID NO: 1785)**
DIVMTQSPDSLAVSLGERATINCKSSDSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.90 (SEQ ID NO: 1786)**
DIVMTQSPDSLAVSLGERATINCKSSESLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.91 (SEQ ID NO: 1787)**
DIVMTQSPDSLAVSLGERATINCKSSKSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32H

>**STEAP-A [STEAP1]_L1.92 (SEQ ID NO: 1788)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.93 (SEQ ID NO: 1789)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.94 (SEQ ID NO: 1790)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.95 (SEQ ID NO: 1791)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.96 (SEQ ID NO: 1792)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.97 (SEQ ID NO: 1793)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.98 (SEQ ID NO: 1794)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.99 (SEQ ID NO: 1795)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.100 (SEQ ID NO: 1796)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.101 (SEQ ID NO: 1797)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.102 (SEQ ID NO: 1798)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.103 (SEQ ID NO: 1799)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1]_L1.104 (SEQ ID NO: 1800)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

Figure 32I

>**STEAP-A [STEAP1] _L1 . 105 (SEQ ID NO: 1801)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 106 (SEQ ID NO: 1802)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 107 (SEQ ID NO: 1803)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 108 (SEQ ID NO: 1804)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 109 (SEQ ID NO: 1805)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 110 (SEQ ID NO: 1806)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 111 (SEQ ID NO: 1807)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 112 (SEQ ID NO: 1808)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 113 (SEQ ID NO: 1809)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYNYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 114 (SEQ ID NO: 1810)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 115 (SEQ ID NO: 1811)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 116 (SEQ ID NO: 1812)**
DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 117 (SEQ ID NO: 1813)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWALTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

Figure 32J

>**STEAP-A [STEAP1] _L1 . 118 (SEQ ID NO: 1814)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

>**STEAP-A [STEAP1] _L1 . 119 (SEQ ID NO: 1815)**
DIVMTQSPDSLAVSLGERATINCKSSQSLLYRSNQRNYLAWYQQKPGQPPKLLIYWASKRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK

Figure 33

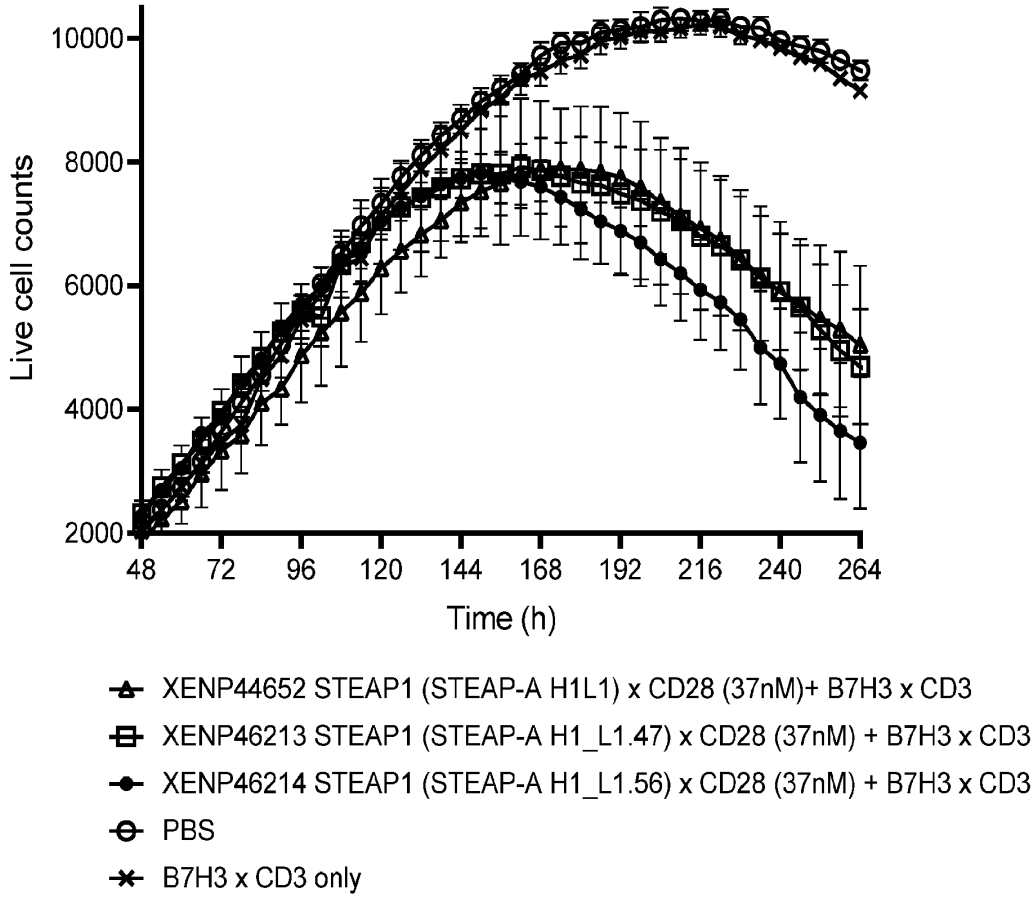

Live cell counts
10000
8000
6000
4000
2000
48
72
96
120
144
168
192
216
240
264
Time (h)
XENP44652 STEAP1 (STEAP-A H1L1) x CD28 (37nM)+ B7H3 x CD3
XENP46213 STEAP1 (STEAP-A H1_L1.47) x CD28 (37nM) + B7H3 x CD3
XENP46214 STEAP1 (STEAP-A H1_L1.56) x CD28 (37nM) + B7H3 x CD3
PBS
B7H3 x CD3 only

Figure 34A

XENP	Substitutions (VH | VL)	Max MFI	AUC	EC50 (nM)
XENP46500	mu120 H1.21_L1.115, D109E/D110L | S28T/S49P/S58Y/T69S/N99K	25967	732955091	246.6
XENP46514	mu120 H1.196_L1.104, S63V/D109E/D110L | K36R/S49P/S58Y/T69S	25227	712740077	254
XENP46512	mu120 H1.196_L1.94, S63V/D109E/D110L | S49P/S58Y/T69S	24404	706297688	198.1
XENP46503	mu120 H1.21_L1.118, D109E/D110L | K36R/S49P/S58Y/T69S/N99K	24404	686711134	261.9
XENP46495	mu120 H1.21_L1.110, D109E/D110L | S49P/S58Y/T69S/N99K	23873	681426236	201.7
XENP46506	mu120 H1.195_L1.94, S54G/D109E/D110L | S49P/S58Y/T69S	23406	665625836	221.5
XENP46499	mu120 H1.21_L1.114, D109E/D110L | S28T/S49P/S58L/T69S/N99K	23304	676339129	184.4
XENP46485	mu120 H1.21_L1.100, D109E/D110L | S28T/S49P/S58Y/T69S	22851	604571533	442.7
XENP46502	mu120 H1.21_L1.117, D109E/D110L | K36R/S49P/S58L/T69S/N99K	21975	621725256	238.9
XENP46489	mu120 H1.21_L1.104, D109E/D110L | K36R/S49P/S58Y/T69S	21692	606092329	304.3
XENP46516	mu120 H1.196_L1.109, S63V/D109E/D110L | S49P/S58Y/T59K/T69S	21552	616335122	215.6
XENP46493	mu120 H1.21_L1.108, D109E/D110L | S49P/S58L/T69S/N99K	21460	591634742	342.9
XENP46501	mu120 H1.21_L1.116, D109E/D110L | S28T/S49P/T59K/T69S/N99K	21414	587870533	320.4
XENP46515	mu120 H1.196_L1.105, S63V/D109E/D110L | K36R/S49P/T59K/T69S	21368	600616481	266
XENP46479	mu120 H1.21_L1.94, D109E/D110L | S49P/S58Y/T69S	20428	549451607	392.5
XENP46497	mu120 H1.21_L1.112, D109E/D110L | K36R/S49P/S58L/T59K/T69S	20384	571984811	239.8
XENP46504	mu120 H1.21_L1.119, D109E/D110L | K36R/S49P/T59K/T69S/N99K	20126	554545519	315.1
XENP46484	mu120 H1.21_L1.99, D109E/D110L | S28T/S49P/S58L/T69S	20126	535329180	418.8
XENP46487	mu120 H1.21_L1.102, D109E/D110L | S28T/S49P/T69S/N99K	19829	511106033	544.4
XENP46461	mu120 H1.213_L1.3, S54G/S63A/D109E/D110L | S49P/T69S	19745	538253957	387.8
XENP46488	mu120 H1.21_L1.103, D109E/D110L | K36R/S49P/S58L/T69S	19496	521670662	416.5

Figure 34B

XENP	Substitutions (VH | VL)	Max MFI	AUC	EC50 (nM)
XENP46498	mu120 H1.21_L1.113, D109E/D110L | K36R/S49P/S58Y/T59K/T69S	19373	535596403	276.3
XENP46476	mu120 H1.228_L1.3, A35S/S54G/S63V/D109E/D110L | S49P/T69S	19129	501631778	433.1
XENP46505	mu120 H1.195_L1.92, S54G/D109E/D110L | K36R/S49P/T69S	18929	514517340	335.3
XENP46473	mu120 H1.225_L1.3, S61Y/S63A/D109E/D110L | S49P/T69S	18771	483185901	541.1
XENP46460	mu120 H1.212_L1.3, S54G/T62K/D109E/D110L | S49P/T69S	18268	495439476	374.8
XENP46507	mu120 H1.195_L1.95, S54G/D109E/D110L | S49P/T59K/T69S	18192	503784881	305.4
XENP46454	mu120 H1.206_L1.3, D32T/S54G/D109E/D110L | S49P/T69S	18078	482268735	405.6
XENP46490	mu120 H1.21_L1.105, D109E/D110L | K36R/S49P/T59K/T69S	18003	477904993	438.1
XENP46475	mu120 H1.227_L1.3, D32T/S54G/S63V/D109E/D110L | S49P/T69S	17891	485833907	333.6
XENP46472	mu120 H1.224_L1.3, S61Y/T62K/D109E/D110L | S49P/T69S	17561	450847485	541.4
XENP46483	mu120 H1.21_L1.98, D109E/D110L | S28T/K36R/S49P/T69S	17488	444667866	593.8
XENP46478	mu120 H1.21_L1.93, D109E/D110L | S49P/S58L/T69S	17131	434181398	579.1
XENP45835	**mu120 H1_L1.56, S58Y**	**17096**	**447009069**	**434.2**
XENP46443	mu120 H1.195_L1.3, S54G/D109E/D110L | S49P/T69S	16956	439989591	489.7
XENP46496	mu120 H1.21_L1.111, D109E/D110L | S49P/T59K/T69S/N99K	16921	441734503	439.2
XENP46491	mu120 H1.21_L1.106, D109E/D110L | K36R/S49P/T69S/N99K	16851	432167196	565.1
XENP46492	mu120 H1.21_L1.107, D109E/D110L | S49P/S58L/T59K/T69S	16680	429837677	531.1
XENP46513	mu120 H1.196_L1.95, S63V/D109E/D110L | S49P/T59K/T69S	16646	449163064	343.4
XENP46455	mu120 H1.207_L1.3, A35S/S54G/D109E/D110L | S49P/T69S	16376	427521126	467.2
XENP46486	mu120 H1.21_L1.101, D109E/D110L | S28T/S49P/T59K/T69S	16243	408242443	-
XENP46474	mu120 H1.226_L1.3, T62K/S63A/D109E/D110L | S49P/T69S	15851	406004588	531.3
XENP46459	mu120 H1.211_L1.3, S54G/S61Y/D109E/D110L | S49P/T69S	15628	395323785	629

Figure 34C

XENP	Substitutions (VH | VL)	Max MFI	AUC	EC50 (nM)
XENP46469	mu120 H1.221_L1.3, S56H/S61Y/D109E/D110L | S49P/T69S	15102	415318922	338.6
XENP46468	mu120 H1.220_L1.3, T62K/S63V/D109E/D110L | S49P/T69S	15072	405844097	384.9
XENP46456	mu120 H1.208_L1.3, S54G/N55H/D109E/D110L | S49P/T69S	14891	378846581	588
XENP46463	mu120 H1.215_L1.3, A35S/S63V/D109E/D110L | S49P/T69S	14862	398226724	384.6
XENP46494	mu120 H1.21_L1.109, D109E/D110L | S49P/S58Y/T59K/T69S	14802	380783762	542
XENP46462	mu120 H1.214_L1.3, D32T/S63V/D109E/D110L | S49P/T69S	14743	394639179	399.4
XENP46467	mu120 H1.219_L1.3, S61Y/S63V/D109E/D110L | S49P/T69S	14655	398823300	353
XENP46444	mu120 H1.196_L1.3, S63V/D109E/D110L | S49P/T69S	14338	374101474	460
XENP46457	mu120 H1.209_L1.3, S54G/S56G/D109E/D110L | S49P/T69S	14196	362359296	586.5
XENP46465	mu120 H1.217_L1.3, S56G/S63V/D109E/D110L | S49P/T69S	13890	376940822	353.8
XENP46458	mu120 H1.210_L1.3, S54G/S56H/D109E/D110L | S49P/T69S	13700	357872078	482.5
XENP46464	mu120 H1.216_L1.3, N55H/S63V/D109E/D110L | S49P/T69S	13380	347632562	447.8
XENP46448	mu120 H1.200_L1.3, S63A/D109E/D110L | S49P/T69S	13302	340177496	555.5
XENP46471	mu120 H1.223_L1.3, S56H/S63A/D109E/D110L | S49P/T69S	13198	317357190	870.1
XENP46482	mu120 H1.21_L1.97, D109E/D110L | S49P/T69S/N99K	12693	314888591	714.2
XENP46481	mu120 H1.21_L1.96, D109E/D110L | S28T/S49P/T69S	12546	299214624	931.4
XENP46466	mu120 H1.218_L1.3, S56H/S63V/D109E/D110L | S49P/T69S	12377	321149828	500.3
XENP46477	mu120 H1.21_L1.92, D109E/D110L | K36R/S49P/T69S	12047	283504641	1027
XENP46446	mu120 H1.198_L1.3, S61Y/D109E/D110L | S49P/T69S	11594	276573583	933
XENP46480	mu120 H1.21_L1.95, D109E/D110L | S49P/T59K/T69S	11288	257519409	1295
XENP46447	mu120 H1.199_L1.3, T62K/D109E/D110L | S49P/T69S	11096	269287808	800.7
XENP46452	mu120 H1.204_L1.3, S56G/D109E/D110L | S49P/T69S	10346	239645064	1156
XENP46451	mu120 H1.203_L1.3, N55H/D109E/D110L | S49P/T69S	9946	212614988	2065
XENP46470	mu120 H1.222_L1.3, S56H/T62K/D109E/D110L | S49P/T69S	9581	225157766	1038
XENP46450	mu120 H1.202_L1.3, A35S/D109E/D110L | S49P/T69S	7828	171184431	1716
XENP46449	mu120 H1.201_L1.3, D32T/D109E/D110L | S49P/T69S	7309	154673526	2243
XENP45530	mu120 H1.21_L1.3, D109E/D110L | S49P/T69S	7016	150503014	2047

Figure 34D

XENP	Substitutions (VH | VL)	Max MFI	AUC	EC50 (nM)
XENP46524	mu120 H1.194_L1.86, S75R/D109E/D110L | V3D/S49P/T69S	6913	151547218	1659
XENP45531	mu120 H1.34_L1.3, D109T/D110A | S49P/T69S	6861	149665826	2051
XENP44824	mu120 H1.21_L1, D109E/D110L	6609	140246184	2420
XENP46445	mu120 H1.197_L1.3, S56H/D109E/D110L | S49P/T69S	6450	133784201	2588
XENP44844	mu120 H1_L1.3, S49P/T69S	5135	102876949	3868
XENP46526	mu120 H1.194_L1.88, S75R/D109E/D110L | S26E/S49P/T69S	4893	103145134	2025
XENP44680	**mu120 H1L1**	**4676**	**91807050**	**5529**
XENP46442	mu120 H1.192_L1.3, D109S/D110V | S49P/T69S	4288	81403268	4110
XENP46525	mu120 H1.194_L1.87, S75R/D109E/D110L | S26D/S49P/T69S	4014	79937655	2799
XENP46441	mu120 H1.191_L1.3, D109S/D110L | S49P/T69S	2462	43209741	12173
XENP46440	mu120 H1.190_L1.3, D109S/D110A | S49P/T69S	1533	26819177	8153
XENP46523	mu120 H1.193_L1.91, S61E/D109E/D110L | Q27K/S49P/T69S	1200	20772439	2593
XENP46528	mu120 H1.194_L1.90, S75R/D109E/D110L | Q27E/S49P/T69S	478	8852777	-
XENP46527	mu120 H1.194_L1.89, S75R/D109E/D110L | Q27D/S49P/T69S	260	6075167	-

Figure 35A

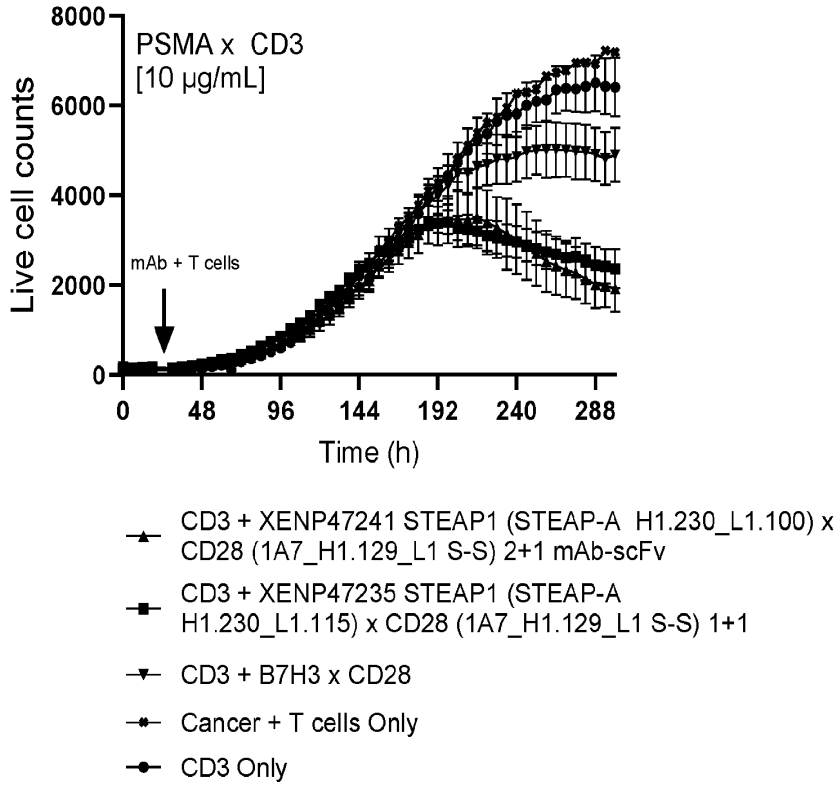

PSMA x CD3
[10 µg/mL]
Live cell counts
8000
6000
4000
2000
0
mAb + T cells
0
48
96
144
192
240
288
Time (h)
CD3 + XENP47241 STEAP1 (STEAP-A H1.230_L1.100) x CD28 (1A7_H1.129_L1 S-S) 2+1 mAb-scFv
CD3 + XENP47235 STEAP1 (STEAP-A H1.230_L1.115) x CD28 (1A7_H1.129_L1 S-S) 1+1
CD3 + B7H3 x CD28
Cancer + T cells Only
CD3 Only

Figure 35B

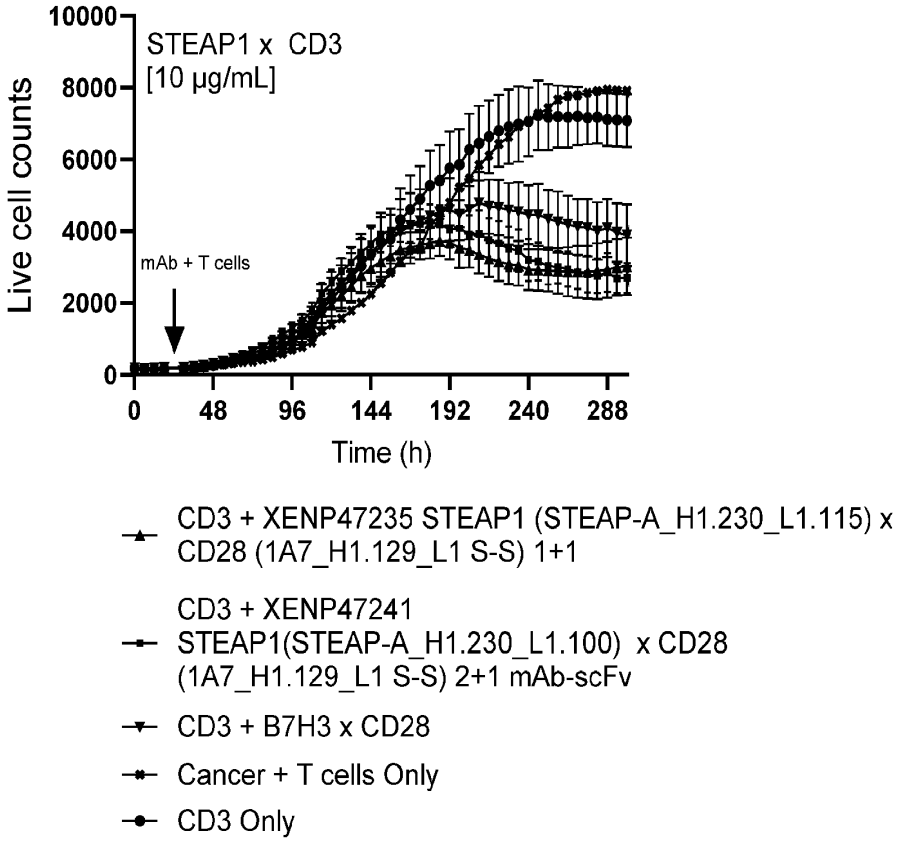
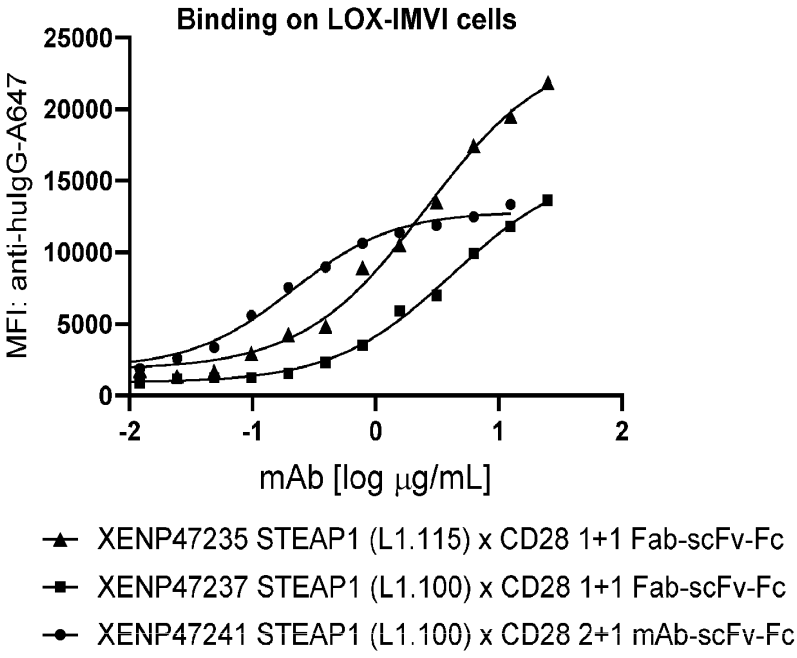

STEAP1 x CD3
[10 µg/mL]
Live cell counts
10000
8000
6000
4000
2000
0
mAb + T cells
0
48
96
144
192
240
288
Time (h)
CD3 + XENP47235 STEAP1 (STEAP-A_H1.230_L1.115) x CD28 (1A7_H1.129_L1 S-S) 1+1
CD3 + XENP47241 STEAP1(STEAP-A_H1.230_L1.100) x CD28 (1A7_H1.129_L1 S-S) 2+1 mAb-scFv
CD3 + B7H3 x CD28
Cancer + T cells Only
CD3 Only

Figure 36


Binding on LOX-IMVI cells
MFI: anti-huIgG-A647
25000
20000
15000
10000
5000
0
-2
-1
0
1
2
mAb [log μg/mL]
XENP47235 STEAP1 (L1.115) x CD28 1+1 Fab-scFv-Fc
XENP47237 STEAP1 (L1.100) x CD28 1+1 Fab-scFv-Fc
XENP47241 STEAP1 (L1.100) x CD28 2+1 mAb-scFv-Fc

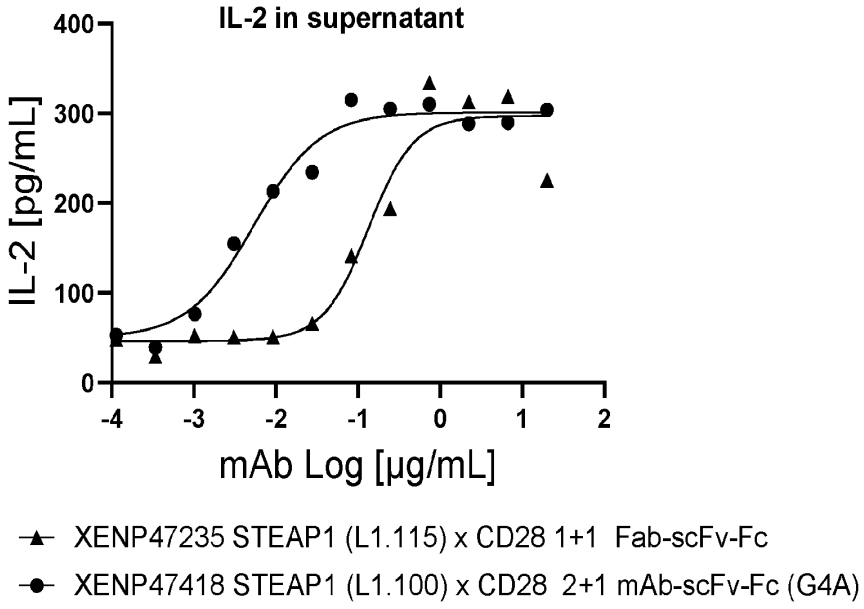

IL-2 in supernatant
IL-2 [pg/mL]
400
300
200
100
0
-4
-3
-2
-1
0
1
2
mAb Log [μg/mL]
XENP47235 STEAP1 (L1.115) x CD28 1+1 Fab-scFv-Fc
XENP47418 STEAP1 (L1.100) x CD28 2+1 mAb-scFv-Fc (G4A)

Figure 37

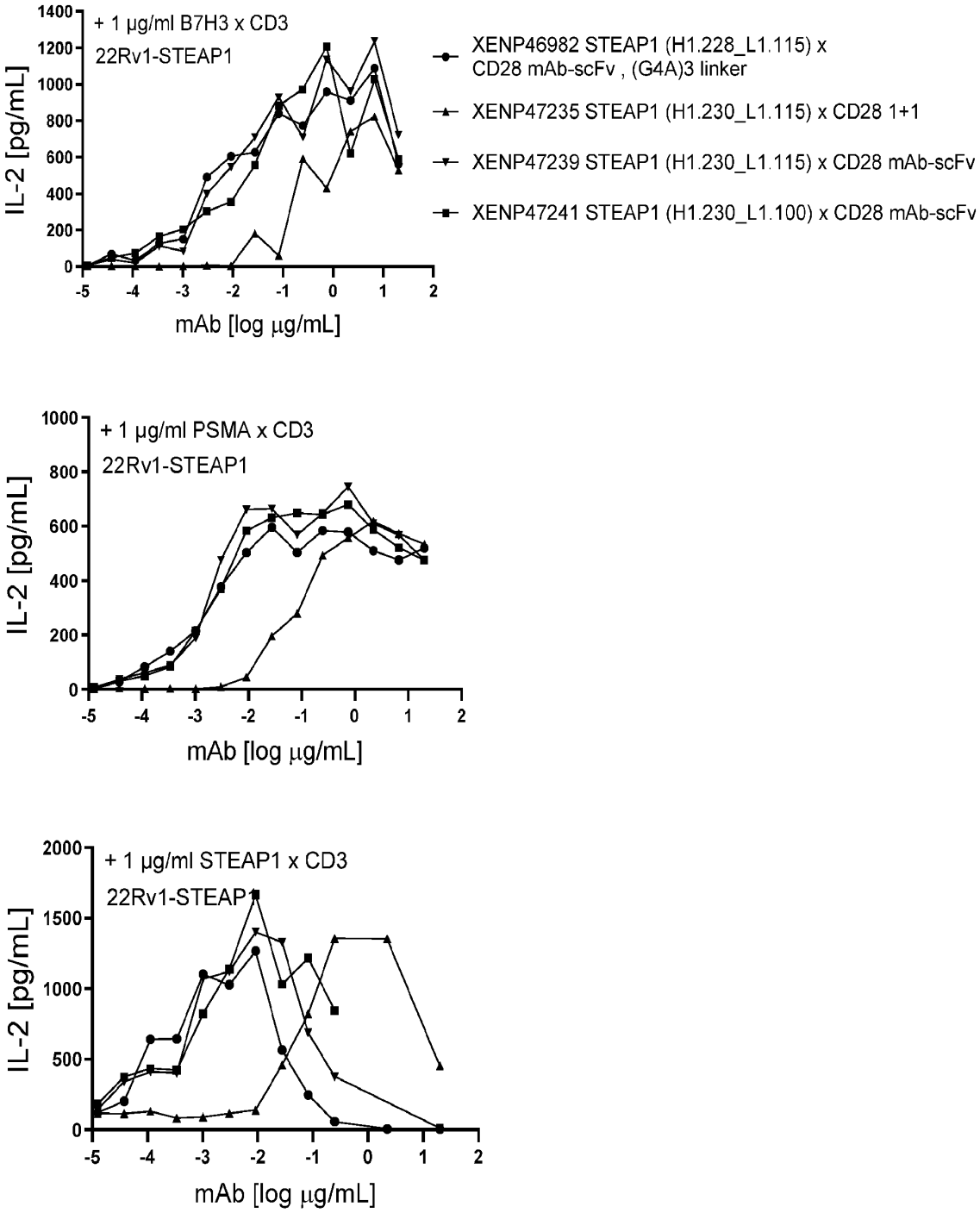
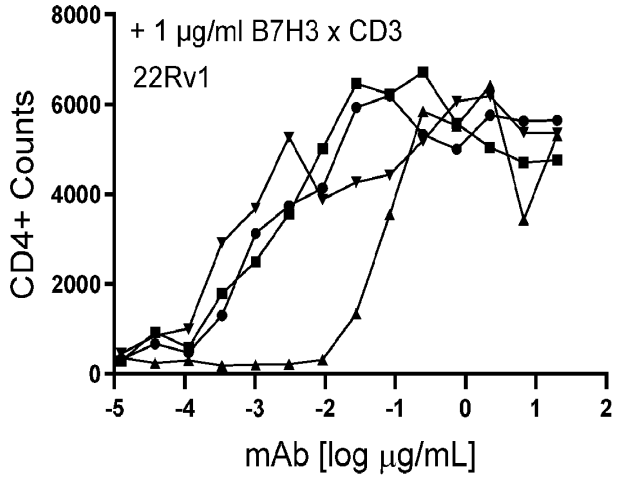
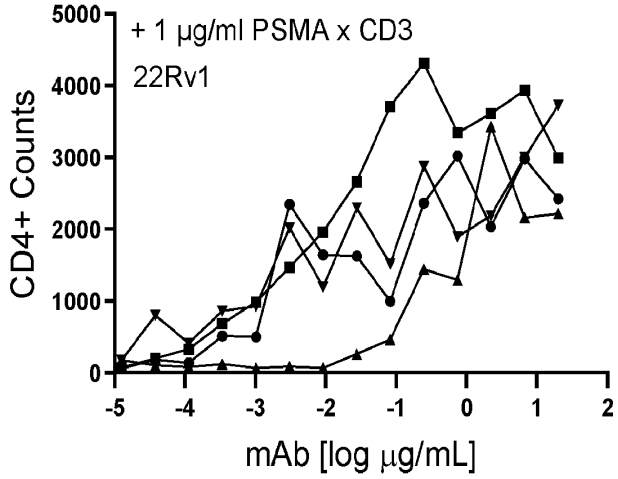

+ 1 µg/ml B7H3 x CD3
22Rv1-STEAP1
IL-2 [pg/mL]
mAb [log µg/mL]
XENP46982 STEAP1 (H1.228_L1.115) x CD28 mAb-scFv , (G4A)3 linker
XENP47235 STEAP1 (H1.230_L1.115) x CD28 1+1
XENP47239 STEAP1 (H1.230_L1.115) x CD28 mAb-scFv
XENP47241 STEAP1 (H1.230_L1.100) x CD28 mAb-scFv
+ 1 µg/ml PSMA x CD3
22Rv1-STEAP1
IL-2 [pg/mL]
mAb [log µg/mL]
+ 1 µg/ml STEAP1 x CD3
22Rv1-STEAP1
IL-2 [pg/mL]
mAb [log µg/mL]

Figure 38





XENP46982 STEAP1 (H1.228_L1.115) x CD28 mAb-scFv, (G4A)3 linker
XENP47235 STEAP1 (H1.230_L1.115) x CD28 1+1
XENP47239 STEAP1 (H1.230_L1.115) x CD28 mAb-scFv
XENP47241 STEAP1 (H1.230_L1.100) x CD28 mAb-scFv

Figure 39

[STEAP-A] H1.230 L1.100

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLE WIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVY YCARERNYDYELYYYAMDYWGQGTLVTVSS	1816
vhCDR1	SDYSWN	1817
vhCDR2	YIGTSGSTVYNPSLKS	1818
vhCDR3	ERNYDYELYYYAMDY	1819
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPG QPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QQYYNYPRTFGGGTKVEIK	1820
vlCDR1	KSSQTLLYRSNQKNYLA	1821
vlCDR2	WAYTRES	1822
vlCDR3	QQYYNYPRT	1823

[STEAP-A] H1.230 L1.115

	sequence	SEQ ID NO:
Variable heavy (vh) domain	QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLE WIGYIGTSGSTVYNPSLKSRVTISRDTSKNQFSLKLSSVTAADTAVY YCARERNYDYELYYYAMDYWGQGTLVTVSS	1824
vhCDR1	SDYSWN	1825
vhCDR2	YIGTSGSTVYNPSLKS	1826
vhCDR3	ERNYDYELYYYAMDY	1827
Variable light (vl) domain	DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPG QPPKLLIYWAYTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QQYYKYPRTFGGGTKVEIK	1828
vlCDR1	KSSQTLLYRSNQKNYLA	1829
vlCDR2	WAYTRES	1830
vlCDR3	QQYYKYPRT	1831

Figure 40

>XENP46851 STEAP-A[STEAP1] H1.228 L1.115 Fab- STEAP-A[STEAP1] H1.228 L1.115 Fab (G4S)2 1A7[CD28] H1.129 L1 VH G46C VL Q108C scFv(GKPGS)4 (G4S)2-IgG1 pI(-) Isosteric A PVA /S267K/L368D/K370S/M428L/N434S-Fc(222) IgG1 PVA /S267K/S364K/E357Q/M428L/N434S

>Chain 1- STEAP-A[STEAP1]_H1.228_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1832)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 2- STEAP-A[STEAP1]_H1.228_Fab_(G4S)2_1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_(G4S)2-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1833)

QVQVQESGPGLVKPSQTLSLTCTVSGYSITSDYSWNWIRQPPGKKLEWIGYIGNSGSTVYNPSLKSRVTISRDTSKN
QFSLKLSSVTAADTAVYYCARERNYDYELYYYAMDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC/GG
GGSGGGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DI
QMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCQQSYSTPFTFGCGTKLEIK/GGGGSGGGGSKTHTCPPCP/APPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

>Chain 3- STEAP-A[STEAP1]_L1.115_Light Chain (SEQ ID NO: 1834)

DIVMTQSPDSLAVSLGERATINCKSSQTLLYRSNQKNYLAWYQQKPGQPPKLLIYWAYTRESGVPDRFSGSGSGTDF
TLTISSLQAEDVAVYYCQQYYKYPRTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ
WKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 41A

CEA-A		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGN KANGYTTEYSASVKGRFTISRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRF YFDYWGQGTTLTVSS	1835
vhCDR1	GFTFTDYYMN	1836
vhCDR2	FIGNKANGYTTEYSASVKG	1837
vhCDR3	DRGLRFYFDY	1838
Variable Light (vl) Domain	QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNL ASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK	1839
vlCDR1	RASSSVTYIH	1840
vlCDR2	ATSNLAS	1841
vlCDR3	QHWSSKPPT	1842

CEA-B		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDP ANGNSKYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAPFGYYVSDY AMAYWGQGTLVTVSS	1843
vhCDR1	GFNIKDTYMH	1844
vhCDR2	RIDPANGNSKYADSVKG	1845
vhCDR3	FGYYVSDYAMAY	1846
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIY RASNLESGVPSRFSGSGSRTDFTLTISSLQPEDFATYYCQQTNEDPYTFGQGT KVEIK	1847
vlCDR1	RAGESVDIFGVGFLH	1848
vlCDR2	RASNLES	1849
vlCDR3	QQTNEDPYT	1850

Figure 41B

CEA-C		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDP ENGDTEYAPKFQGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPTGPYY FDYWGQGTTVTVSS	1851
vhCDR1	GFNIKDSYMH	1852
vhCDR2	WIDPENGDTEYAPKFQG	1853
vhCDR3	GTPTGPYYFDY	1854
Variable Light (vl) Domain	ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNL ASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK	1855
vlCDR1	SASSSVSYMH	1856
vlCDR2	STSNLAS	1857
vlCDR3	QQRSSYPLT	1858

CEA-D		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHP DSSTINYAPSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWF AYWGQGTPVTVSS	1859
vhCDR1	GFDFTTYWMS	1860
vhCDR2	EIHPDSSTINYAPSLKD	1861
vhCDR3	LYFGFPWFAY	1862
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTST RHTGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYSLYRSFGQGTKVEIK	1863
vlCDR1	KASQDVGTSVA	1864
vlCDR2	WTSTRHT	1865
vlCDR3	QQYSLYRS	1866

Figure 41C

CEA-E		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKNTLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS	1867
vhCDR1	GFVFSSYDMS	1868
vhCDR2	YISSGGGITYAPSTVKG	1869
vhCDR3	HYFGSSGPFAY	1870
Variable Light (vl) Domain	DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISSLQPEDFATYYCQHHYGTPFTFGSGTKLEIK	1871
vlCDR1	RASENIFSYLA	1872
vlCDR2	NTRTLAE	1873
vlCDR3	QHHYGTPFT	1874

CEA-F		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTSTAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS	1875
vhCDR1	GYTFTEFGMN	1876
vhCDR2	WINTKTGEATYVEEFKG	1877
vhCDR3	WDFAYYVEAMDY	1878
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQYYTYPLFTFGQGTKLEIK	1879
vlCDR1	KASAAVGTYVA	1880
vlCDR2	SASYRKR	1881
vlCDR3	HQYYTYPLFT	1882

Figure 41D

B9		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGRSLRLSCAASGFTVSSYWMHWVRQAPGKGLEWVGFIRN KANGGTTEYAASVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDRGLRF YFDYWGQGTTVTVSS	1883
vhCDR1	GFTVSSYWMH	1884
vhCDR2	FIRNKANGGTTEYAASVKG	1885
vhCDR3	DRGLRFYFDY	1886
Variable Light (vl) Domain	QAVLTQPASLSASPGASASLTCTLRRGINVGAYSIYWYQQKPGSPPQYLLRYK SDSDKQQGSGVSSRFSASKDASANAGILLISGLQSEDEADYYCMIWHSGASAV FGGGTKLTVL	1887
vlCDR1	TLRRGINVGAYSIY	1888
vlCDR2	SDKQQGS	1889
vlCDR3	MIWHSGASAV	1890

E12		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGRSLRLSCAASGFTVSSYWMHWVRQAPGKGLEWVGFILN KANGGTTEYAASVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDRGLRF YFDYWGQGTTVTVSS	1891
vhCDR1	GFTVSSYWMH	1892
vhCDR2	FILNKANGGTTEYAASVKG	1893
vhCDR3	DRGLRFYFDY	1894
Variable Light (vl) Domain	QAVLTQPASLSASPGASASLTCTLRRGINVGAYSIYWYQQKPGSPPQYLLRYK SDSDKQQGSGVSSRFSASKDASANAGILLISGLQSEDEADYYCMIWHSGASAV FGGGTKLTVL	1895
vlCDR1	TLRRGINVGAYSIY	1896
vlCDR2	SDKQQGS	1897
vlCDR3	MIWHSGASAV	1898

Figure 41E

A5		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGVVQPGRSLRLSCAASGFTLSTYAMHWVRQAPGKGLEWVALISN DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGLRFYF DYWGQGTTVTVSS	1899
vhCDR1	GFTLSTYAMH	1900
vhCDR2	LISNDGSNKYYADSVKG	1901
vhCDR3	DRGLRFYFDY	1902
Variable Light (vl) Domain	QAVLTQPASLSASPGASASLTCTLRRGINVGAYSIYWYQQKPGSPPQYLLRYK SDSDKQQGSGVSSRFSASKDASANAGILLISGLQSEDEADYYCMIWHSGASAV FGGGTKLTVL	1903
vlCDR1	TLRRGINVGAYSIY	1904
vlCDR2	SDKQQGS	1905
vlCDR3	MIWHSGASAV	1906

D8		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGVVQPGRSLRLSCAASGFTLSTYAMHWVRQAPGKGLEWVALISN DGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRDRGLRFYF DYWGQGTTVTVSS	1907
vhCDR1	GFTLSTYAMH	1908
vhCDR2	LISNDGSNKYYADSVKG	1909
vhCDR3	DRGLRFYFDY	1910
Variable Light (vl) Domain	QAVLTQPASLSASPGASASLTCTLRRGINVGAYSIYWYQQKPGSPPQYLLRYK SDSDKQQGSGVSSRFSASKDASANAGILLISGLQSEDEADYYCMIWHSGASAV FGGGTKLTVL	1911
vlCDR1	TLRRGINVGAYSIY	1912
vlCDR2	SDKQQGS	1913
vlCDR3	MIWHSGASAV	1914

Figure 41F

T84.66		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLQQSGAELVEPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDP ANGNSKYVPKFQGKATITADTSSNTAYLQLTSLTSEDTAVYYCAPFGYYVSDY AMAYWGQGTSVTVSS	1915
vhCDR1	GFNIKDTYMH	1916
vhCDR2	RIDPANGNSKYVPKFQG	1917
vhCDR3	FGYYVSDYAMAY	1918
Variable Light (vl) Domain	DIVLTQSPASLAVSLGQRATMSCRAGESVDIFGVGFLHWYQQKPGQPPKLLIY RASNLESGIPVRFSGTGSRTDFTLIIDPVEADDVATYYCQQTNEDPYTFGGGT KLEIK	1919
vlCDR1	RAGESVDIFGVGFLH	1920
vlCDR2	RASNLES	1921
vlCDR3	QQTNEDPYT	1922

M5B		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDP ANGNSKYVPKFQGRATISADTSKNTAYLQMNSLRAEDTAVYYCAPFGYYVSDY AMAYWGQGTLVTVSS	1923
vhCDR1	GFNIKDTYMH	1924
vhCDR2	RIDPANGNSKYVPKFQG	1925
vhCDR3	FGYYVSDYAMAY	1926
Variable Light (vl) Domain	DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIY RASNLESGVPSRFSGSGSRTDFTLTISSLQPEDFATYYCQQTNEDPYTFGQGT KVEIK	1927
vlCDR1	RAGESVDIFGVGFLH	1928
vlCDR2	RASNLES	1929
vlCDR3	QQTNEDPYT	1930

Figure 41G

Shanghai Haikang		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	QVQLQQSGAELVRSGASIKLSCTASGFNIKHYYMHWVKQRPEQGLEWIGWINP ENVDTEYAPKFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYCNHYRYAGGGA LDYWGQGTTVTVSS	1931
vhCDR1	GFNIKHYYMH	1932
vhCDR2	WINPENVDTEYAPKFQG	1933
vhCDR3	YRYAGGGALDY	1934
Variable Light (vl) Domain	DIQLTQSPAIMSASPGEKVTMTCSASSSVSYIHWYQQKSGTSPKRWVYDTSKL ASGVPARFSGSGSGTSYSLTISTMEAEDAATYYCQQWNNNPYSFGGGTKVVI	1935
vlCDR1	SASSSVSYIH	1936
vlCDR2	DTSKLAS	1937
vlCDR3	QQWNNNPYS	1938

Figure 42A

>XENP44329 CEA-D[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1939)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1940)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-D[CEACAM5]_L1 (SEQ ID NO: 1941)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42B

>XENP44330 CEA-E[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1942)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1943)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-E[CEACAM5]_L1 (SEQ ID NO: 1944)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42C

>XENP44331 CEA-F[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1945)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1946)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-F[CEACAM5]_L1 (SEQ ID NO: 1947)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42D

>XENP44332 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1948)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1949)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1950)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42E

>XENP44333 CEA-B[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1951)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1952)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_L1 (SEQ ID NO: 1953)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42F

>XENP44335 CEA-D[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1954)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1955)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-D[CEACAM5]_L1 (SEQ ID NO: 1956)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42G

>XENP44336 CEA-E[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1957)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1958)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-E[CEACAM5]_L1 (SEQ ID NO: 1959)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42H

>XENP44337 CEA-F[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1960)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1961)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-F[CEACAM5]_L1 (SEQ ID NO: 1962)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42I

>XENP44338 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1963)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1964)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1965)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42J

>XENP44339 CEA-B[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1966)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1967)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_L1 (SEQ ID NO: 1968)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42K

>XENP44560 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1969)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1970)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1971)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42L

>XENP44561 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.14_L1_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1972)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1973)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1974)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42M

>XENP44562 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1975)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1976)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1977)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42N

>XENP44563 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1978)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1979)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GKPGSGKPGSGKPGSGKPGS/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 1980)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42O

>XENP44666 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1981)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1982)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 1983)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42P

>XENP44667 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1984)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1985)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 1986)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42Q

>XENP44669 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1987)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1988)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 1989)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42R

>XENP44670 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_VH_K43C_VL_Q103C_scFv(staple)-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1990)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_K43C_VL_Q103C_scFv(staple)_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 1991)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGCGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGGGSGGSGGCPPCGGSGGDIQMTQSPSSLSASV
GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVY
STPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
REQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEA
LHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 1992)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42S

>XENP44671 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_VH_K43C_VL_Q103C_scFv(staple)-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1993)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_K43C_VL_Q103C_scFv(staple)_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 1994)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGCGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGGGSGGSGGCPPCGGSGGDIQMTQSPSSLSASV
GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVY
STPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNW
YVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
REEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEA
LHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 1995)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42T

>XENP44732 CEA-C[CEACAM5]_H0L0_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1996)

QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSN
TAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 1997)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L0 (SEQ ID NO: 1998)

ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAE
DAATYYCQQRSSYPLTFGAGTKLELK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42U

>XENP44734 CEA-C[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 1999)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWLRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTTDTSIN
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2000)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L1 (SEQ ID NO: 2001)

ENVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQKPGQSPRLLIYSTSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQQRSSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42V

>XENP44755 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2002)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2003)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2004)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42W

>XENP44756 CEA-A[CEACAM5]_H1L2_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2005)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2006)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2 (SEQ ID NO: 2007)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42X

>XENP44849 CEA-A[CEACAM5]_H1L2_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2008)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2009)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2 (SEQ ID NO: 2010)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42Y

>XENP44889 CEA-A[CEACAM5]_H1_L1.2_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2011)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2012)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1.2 (SEQ ID NO: 2013)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPKSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42Z

>XENP44890 CEA-A[CEACAM5]_H1_L1.3_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2014)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2015)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1.3 (SEQ ID NO: 2016)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSWIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42AA

>XENP44891 CEA-A[CEACAM5]_H1_L2.5_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2017)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2018)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.5 (SEQ ID NO: 2019)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42BB

>XENP44892 CEA-A[CEACAM5]_H1_L2.8_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2020)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2021)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.8 (SEQ ID NO: 2022)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42CC

>XENP44893 CEA-A[CEACAM5]_H1_L2.9_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2023)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2024)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.9 (SEQ ID NO: 2025)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42DD

>XENP44894 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2026)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2027)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2028)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42EE

>XENP44895 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2029)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2030)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2031)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42FF

>XENP44896 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2032)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2033)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GGGGAGGGGAGGGGAGGGGA/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2034)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42GG

>XENP44897 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2035)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2036)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2037)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42HH

>XENP44898 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2038)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2039)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GGGGAGGGGAGGGGAGGGGA/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2040)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42II

>XENP44911 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2041)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2042)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2043)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42JJ

>XENP44912 CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2044)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2045)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GKPGSGKPGSGKPGSGKPGS/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2046)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42KK

>XENP44913 CEA-A[CEACAM5]_H1_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2047)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2048)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2049)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42LL

>XENP44914 CEA-A[CEACAM5]_H1.7_L1_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2050)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2051)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2052)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42MM

>XENP44915 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2053)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2054)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2055)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42NN

>XENP45226 CEA-C[CEACAM5]_H1.1_L1.1_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-C[CEACAM5]_H1.1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2056)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWVRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTRDTSIS
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2057)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L1.1 (SEQ ID NO: 2058)

EIVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQKPGQSPRLLIYSTSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQQRSSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42OO

>XENP45227 CEA-C[CEACAM5]_H1.2_L1.1_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-C[CEACAM5]_H1.2_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2059)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWVRQAPGQGLEWMGWIDPEQGDTEYAPKFQGRVTMTRDTSIS
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2060)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L1.1 (SEQ ID NO: 2061)

EIVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQKPGQSPRLLIYSTSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQQRSSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42PP

>XENP45229 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1_L1.71_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2062)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2063)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2064)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42QQ

>XENP45230 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2065)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2066)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2067)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42RR

>XENP45231 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2068)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.14_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2069)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GGGGAGGGGAGGGGAGGGGA/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2070)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42SS

>XENP45232 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2071)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.1_L1.71_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2072)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GGGGAGGGGAGGGGAGGGGA/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2073)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42TT

>XENP45233 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(G4A)4-IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S-Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2074)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_L1.71_H1.1_VH_G46C_VL_Q108C_scFv(G4A)4_Fc(216)_IgG1_pI(-)_Isosteric_A_C220S/PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2075)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCQQVYSTPFTFGCGTKLEIK/GGGGAGGGGAGGGGAGGGGA/EVQLLESGGGLVQPGGSLRLSCAAS
GFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPG
LRQVGFDYWGQGTLVTVSS/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2076)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42UU

>XENP45558 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2077)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2078)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2079)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42VV

>XENP45559 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.129_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2080)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.129_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2081)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2082)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42WW

>XENP45560 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2083)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.129_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2084)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2085)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42XX

>XENP45561 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.106_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2086)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.106_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2087)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2088)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42YY

>XENP45904 CEA-A[CEACAM5]_H1.10_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.10_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2089)

EVQLVESGGGLVQPGGSLRLSCAASGFTFIDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2090)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2091)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42ZZ

>XENP45905 CEA-A[CEACAM5]_H1.12_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.12_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2092)

EVQLVESGGGLVQPGGSLRLSCAASGFTFQDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2093)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2094)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42AAA

>XENP45906 CEA-A[CEACAM5]_H1.13_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.13_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2095)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2096)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2097)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42BBB

>XENP45907 CEA-A[CEACAM5]_H1.17_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.17_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2098)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTHYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2099)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2100)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42CCC

>XENP45908 CEA-A[CEACAM5]_H1.49_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.49_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2101)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFISNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2102)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2103)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42DDD

>XENP45909 CEA-A[CEACAM5]_H1.79_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.79_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2104)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANQYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2105)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2106)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42EEE

>XENP45910 CEA-A[CEACAM5]_H1.150_L2.15_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.150_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2107)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFVFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2108)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2109)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42FFF

>XENP45911 CEA-A[CEACAM5]_H1.7_L2.20_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2110)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2111)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.20 (SEQ ID NO: 2112)

EIVLTQSPATLSLSPGERATLSCRASQSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42GGG

>XENP45912 CEA-A[CEACAM5]_H1.7_L2.67_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2113)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2114)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.67 (SEQ ID NO: 2115)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSRLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42HHH

>XENP45913 CEA-A[CEACAM5]_H1.7_L2.81_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2116)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2117)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.81 (SEQ ID NO: 2118)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAQGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42III

>XENP45914 CEA-A[CEACAM5]_H1.7_L2.102_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2119)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2120)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.102 (SEQ ID NO: 2121)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSQPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42JJJ

>XENP45915 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2122)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2123)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2124)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42KKK

>XENP45916 CEA-A[CEACAM5]_H1.7_L2.15_Fab-1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1.7_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2125)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2126)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2127)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42LLL

>XENP45930 CEA-A[CEACAM5]_H1.17_L2.20_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.17_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2128)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTHYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2129)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.20 (SEQ ID NO: 2130)

EIVLTQSPATLSLSPGERATLSCRASQSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42MMM

>XENP45931 CEA-A[CEACAM5]_H1.17_L2.67_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.17_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2131)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTHYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2132)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.67 (SEQ ID NO: 2133)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSRLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42NNN

>XENP45932 CEA-A[CEACAM5]_H1.49_L2.20_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.49_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2134)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFISNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2135)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.20 (SEQ ID NO: 2136)

EIVLTQSPATLSLSPGERATLSCRASQSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42OOO

>XENP45933 CEA-A[CEACAM5]_H1.49_L2.67_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.49_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2137)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFISNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2138)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.67 (SEQ ID NO: 2139)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSRLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42PPP

>XENP46035 CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2140)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2141)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2142)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42QQQ

>XENP46036 CEA-A[CEACAM5]_H0.1_L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2143)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKVNGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2144)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2145)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42RRR

>XENP46037 CEA-A[CEACAM5]_H0.2_L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.2_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2146)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGIRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2147)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2148)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42SSS

>XENP46038 CEA-A[CEACAM5]_H0.3_L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.3_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2149)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGVRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2150)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2151)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42TTT

>XENP46039 CEA-A[CEACAM5]_H0.4_L0_Fab-1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.4_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2152)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFAFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2153)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2154)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42UUU

>XENP46238 CEA-A[CEACAM5]_H1.49_L2.67_Fab-1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.49_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2155)

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFISNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2156)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.67 (SEQ ID NO: 2157)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSRLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42VVV

>XENP46322 CEA-A[CEACAM5]_H1.13_L2.15_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.13_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2158)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2159)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2160)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42WWW

>XENP46323 CEA-A[CEACAM5]_H0.1_L0_Fab-1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2161)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKVNGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.129_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2162)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2163)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42XXX

>XENP46327 CEA-A[CEACAM5]_H1.13_L2.15_Fab-1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1.13_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2164)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2165)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2166)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 42YYY

>XENP46328 CEA-A[CEACAM5]_H0.1_L0_Fab-1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H0.1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2167)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKVNGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.106_L1_VH_G46C_VL_Q108C_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2168)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQSYSTPFTFGCGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
LHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2169)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 43A-43F

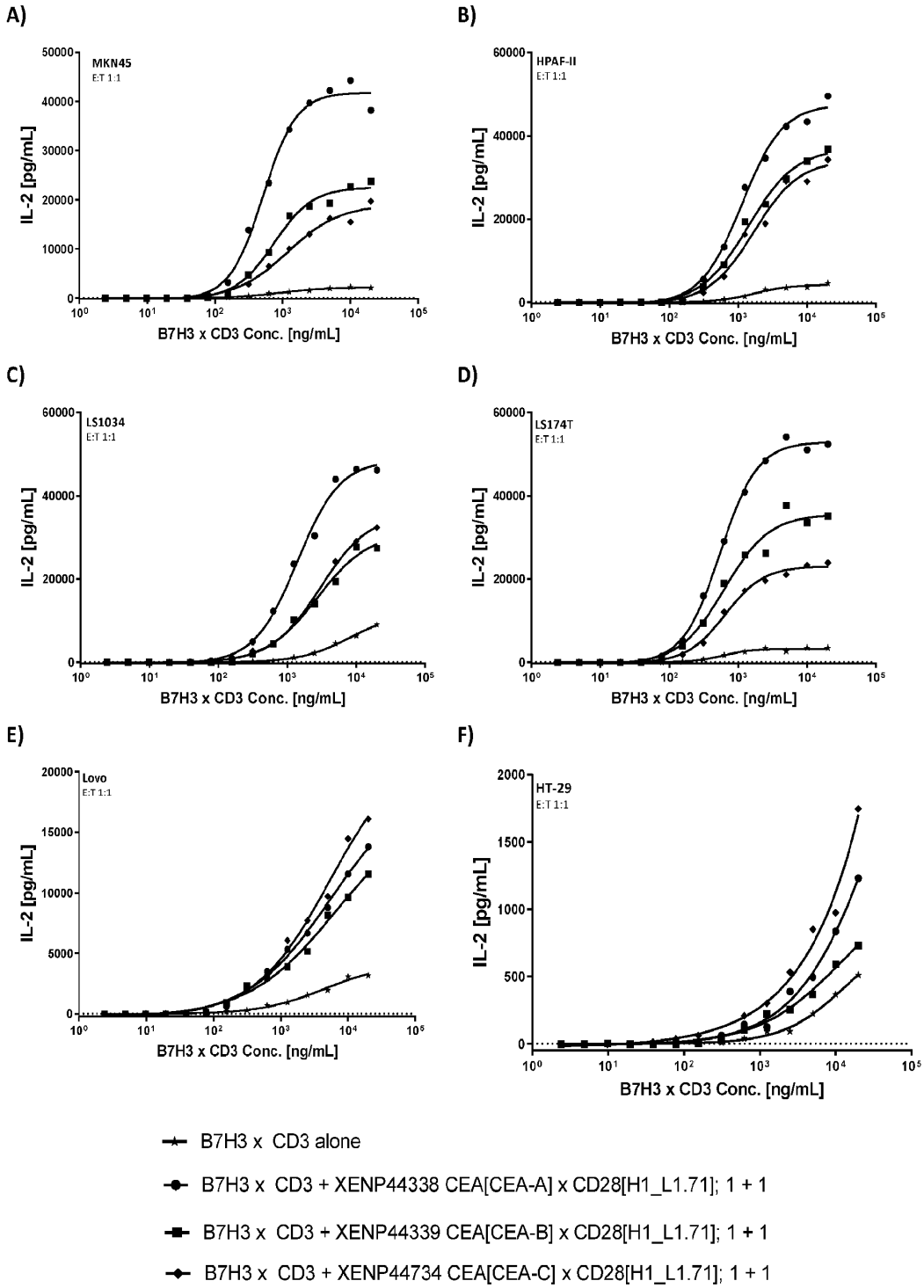


Figure 44A-44F

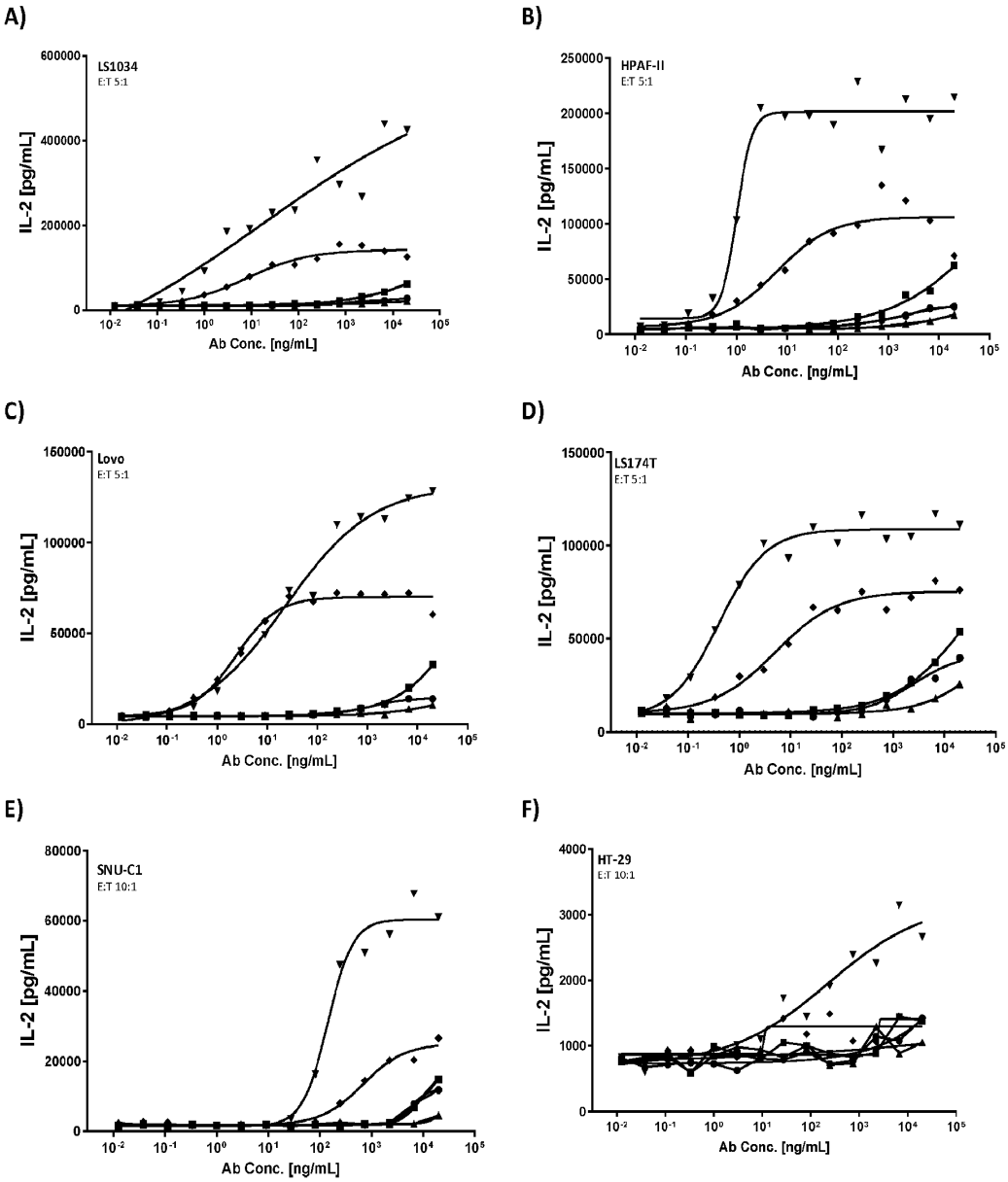


Figure 45A

CEA-A H1

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEW VGFIGNKANGYTTEYSASVKGRFTISRDKSKSSLYLQMNSLKTEDTA VYYCTRDRGLRFYFDYWGQGTLVTVSS	2170
vhCDR1	GFTFTDYYMN	2171
vhCDR2	FIGNKANGYTTEYSASVKG	2172
vhCDR3	DRGLRFYFDY	2173

CEA-A L1

	sequence	SEQ ID NO:
Variable light (vl) domain	QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLI YATSNLASGVPARFSGSGSGTDYTLTISSLEPEDFAVYYCQHWSSKP PTFGGGTKVEIK	2174
vlCDR1	RASSSVTYIH	2175
vlCDR2	ATSNLAS	2176
vlCDR3	QHWSSKPPT	2177

CEA-A L2

	sequence	SEQ ID NO:
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLI YATSNLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHWSSKP PTFGGGTKVEIK	2178
vlCDR1	RASSSVTYIH	2179
vlCDR2	ATSNLAS	2180
vlCDR3	QHWSSKPPT	2181

CEA-A H1.13 L2.15

	sequence	SEQ ID NO:
Variable heavy (vh) domain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMNWVRQAPGKGLEW VGFIGNKANAYTTEYSASVKGRFTISRDKSKSSLYLQMNSLKTEDTA VYYCTRDRGLRFYFDYWGQGTLVTVSS	2182
vhCDR1	GFTFSDYYMN	2183
vhCDR2	FIGNKANAYTTEYSASVKG	2184
vhCDR3	DRGLRFYFDY	2185
Variable light (vl) domain	EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLI YATSNLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHWSSKP PTFGGGTKVEIK	2186
vlCDR1	RASSSVTYIH	2187
vlCDR2	ATSNLAS	2188
vlCDR3	QHWSSKPPT	2189

Figure 45B

>CEA-A[CEACAM5]_H1.1(SEQ ID NO: 2190)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.2(SEQ ID NO: 2191)
EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.3(SEQ ID NO: 2192)
EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.4(SEQ ID NO: 2193)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.5(SEQ ID NO: 2194)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKALEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.6(SEQ ID NO: 2195)
EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.7(SEQ ID NO: 2196)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.8(SEQ ID NO: 2197)
EVQLVESGGGLVQPGGSLRLSCAASGFTFADYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.9(SEQ ID NO: 2198)
EVQLVESGGGLVQPGGSLRLSCAASGFTFEDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.10(SEQ ID NO: 2199)
EVQLVESGGGLVQPGGSLRLSCAASGFTFIDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.11(SEQ ID NO: 2200)
EVQLVESGGGLVQPGGSLRLSCAASGFTFKDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.12(SEQ ID NO: 2201)
EVQLVESGGGLVQPGGSLRLSCAASGFTFQDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.13(SEQ ID NO: 2202)
EVQLVESGGGLVQPGGSLRLSCAASGFTFSDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.14(SEQ ID NO: 2203)
EVQLVESGGGLVQPGGSLRLSCAASGFTFVDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.15(SEQ ID NO: 2204)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTAYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.16(SEQ ID NO: 2205)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTEYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.17(SEQ ID NO: 2206)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTHYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS

Figure 45C

>CEA-A[CEACAM5]_H1.18(SEQ ID NO: 2207)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTKYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.19(SEQ ID NO: 2208)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTNYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.20(SEQ ID NO: 2209)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.21(SEQ ID NO: 2210)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTTYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.22(SEQ ID NO: 2211)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDAYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.23(SEQ ID NO: 2212)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDEYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.24(SEQ ID NO: 2213)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDFYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.25(SEQ ID NO: 2214)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDHYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.26(SEQ ID NO: 2215)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDKYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.27(SEQ ID NO: 2216)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDLYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.28(SEQ ID NO: 2217)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDVYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.29(SEQ ID NO: 2218)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYAMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.30(SEQ ID NO: 2219)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYDMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.31(SEQ ID NO: 2220)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYFMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.32(SEQ ID NO: 2221)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYHMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.33(SEQ ID NO: 2222)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYKMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.34(SEQ ID NO: 2223)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYLMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS

Figure 45D

>CEA-A[CEACAM5]_H1.35(SEQ ID NO: 2224)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYVMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.36(SEQ ID NO: 2225)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYINWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.37(SEQ ID NO: 2226)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYLNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.38(SEQ ID NO: 2227)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYVNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.39(SEQ ID NO: 2228)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMDWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.40(SEQ ID NO: 2229)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMGWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.41(SEQ ID NO: 2230)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMHWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.42(SEQ ID NO: 2231)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMSWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.43(SEQ ID NO: 2232)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMTWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.44(SEQ ID NO: 2233)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIANKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.45(SEQ ID NO: 2234)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIDNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.46(SEQ ID NO: 2235)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIHNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.47(SEQ ID NO: 2236)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIKNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.48(SEQ ID NO: 2237)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIQNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.49(SEQ ID NO: 2238)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFISNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.50(SEQ ID NO: 2239)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFITNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.51(SEQ ID NO: 2240)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGEKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS

Figure 45E

>CEA-A[CEACAM5]_H1.52(SEQ ID NO: 2241)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGHKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.53(SEQ ID NO: 2242)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGQKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.54(SEQ ID NO: 2243)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGRKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.55(SEQ ID NO: 2244)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGSKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.56(SEQ ID NO: 2245)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGTKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.57(SEQ ID NO: 2246)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGYKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.58(SEQ ID NO: 2247)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKENAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.59(SEQ ID NO: 2248)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKGNAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.60(SEQ ID NO: 2249)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKKNAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.61(SEQ ID NO: 2250)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKLNAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.62(SEQ ID NO: 2251)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKQNAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.63(SEQ ID NO: 2252)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKVNAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.64(SEQ ID NO: 2253)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAEAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.65(SEQ ID NO: 2254)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAHAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.66(SEQ ID NO: 2255)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAQAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.67(SEQ ID NO: 2256)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKARAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.68(SEQ ID NO: 2257)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKASAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS

Figure 45F

>CEA-A[CEACAM5]_H1.69(SEQ ID NO: 2258)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKATAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.70(SEQ ID NO: 2259)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAYAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.71(SEQ ID NO: 2260)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAAGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.72(SEQ ID NO: 2261)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAEGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.73(SEQ ID NO: 2262)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKAQGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.74(SEQ ID NO: 2263)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKASGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.75(SEQ ID NO: 2264)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANEYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.76(SEQ ID NO: 2265)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANHYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.77(SEQ ID NO: 2266)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANKYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.78(SEQ ID NO: 2267)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANLYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.79(SEQ ID NO: 2268)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANQYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.80(SEQ ID NO: 2269)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANTYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.81(SEQ ID NO: 2270)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAATTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.82(SEQ ID NO: 2271)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAFTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.83(SEQ ID NO: 2272)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAGTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.84(SEQ ID NO: 2273)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAHTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.85(SEQ ID NO: 2274)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANALTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS

Figure 45G

>CEA-A[CEACAM5]_H1.86(SEQ ID NO: 2275)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANASTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.87(SEQ ID NO: 2276)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAVTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.88(SEQ ID NO: 2277)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYATEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.89(SEQ ID NO: 2278)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYETEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.90(SEQ ID NO: 2279)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYITEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.91(SEQ ID NO: 2280)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYKTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.92(SEQ ID NO: 2281)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYQTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.93(SEQ ID NO: 2282)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYSTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.94(SEQ ID NO: 2283)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYVTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.95(SEQ ID NO: 2284)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTAYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.96(SEQ ID NO: 2285)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTDYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.97(SEQ ID NO: 2286)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTGYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.98(SEQ ID NO: 2287)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTHYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.99(SEQ ID NO: 2288)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTKYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.100(SEQ ID NO: 2289)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTQYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.101(SEQ ID NO: 2290)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTSYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.102(SEQ ID NO: 2291)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRERGLRFYFDYWGQGTLVTVSS

Figure 45H

>CEA-A[CEACAM5]_H1.103(SEQ ID NO: 2292)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRGRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.104(SEQ ID NO: 2293)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRHRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.105(SEQ ID NO: 2294)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRNRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.106(SEQ ID NO: 2295)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRRRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.107(SEQ ID NO: 2296)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRSRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.108(SEQ ID NO: 2297)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRTRGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.109(SEQ ID NO: 2298)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDDGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.110(SEQ ID NO: 2299)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDGGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.111(SEQ ID NO: 2300)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDHGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.112(SEQ ID NO: 2301)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDKGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.113(SEQ ID NO: 2302)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDQGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.114(SEQ ID NO: 2303)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDSGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.115(SEQ ID NO: 2304)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDYGLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.116(SEQ ID NO: 2305)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRALRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.117(SEQ ID NO: 2306)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRDLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.118(SEQ ID NO: 2307)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRHLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.119(SEQ ID NO: 2308)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRKLRFYFDYWGQGTLVTVSS

Figure 45I

>CEA-A[CEACAM5]_H1.120(SEQ ID NO: 2309)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRQLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.121(SEQ ID NO: 2310)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRSLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.122(SEQ ID NO: 2311)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRTLRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.123(SEQ ID NO: 2312)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGARFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.124(SEQ ID NO: 2313)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGERFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.125(SEQ ID NO: 2314)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGFRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.126(SEQ ID NO: 2315)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGIRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.127(SEQ ID NO: 2316)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGKRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.128(SEQ ID NO: 2317)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGVRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.129(SEQ ID NO: 2318)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGYRFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.130(SEQ ID NO: 2319)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLDFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.131(SEQ ID NO: 2320)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLGFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.132(SEQ ID NO: 2321)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLHFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.133(SEQ ID NO: 2322)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLKFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.134(SEQ ID NO: 2323)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLQFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.135(SEQ ID NO: 2324)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLSFYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.136(SEQ ID NO: 2325)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLYFYFDYWGQGTLVTVSS

Figure 45J

>CEA-A[CEACAM5]_H1.137(SEQ ID NO: 2326)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRDYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.138(SEQ ID NO: 2327)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRHYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.139(SEQ ID NO: 2328)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRIYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.140(SEQ ID NO: 2329)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRKYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.141(SEQ ID NO: 2330)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRLYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.142(SEQ ID NO: 2331)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRSYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.143(SEQ ID NO: 2332)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRYYFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.144(SEQ ID NO: 2333)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFAFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.145(SEQ ID NO: 2334)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFDFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.146(SEQ ID NO: 2335)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFFFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.147(SEQ ID NO: 2336)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFHFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.148(SEQ ID NO: 2337)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFKFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.149(SEQ ID NO: 2338)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFLFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_H1.150(SEQ ID NO: 2339)
EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYYMNWVRQAPGKGLEWVGFIGNKANAYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFVFDYWGQGTLVTVSS
>CEA-A[CEACAM5]_L1.1 (SEQ ID NO: 2340)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGSSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.2 (SEQ ID NO: 2341)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPKSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.3 (SEQ ID NO: 2342)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSWIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45K

>CEA-A[CEACAM5]_L1.4 (SEQ ID NO: 2343)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGSSPKSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.5 (SEQ ID NO: 2344)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPKSWIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.6 (SEQ ID NO: 2345)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.7 (SEQ ID NO: 2346)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTSYSLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.8 (SEQ ID NO: 2347)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHFSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L1.9 (SEQ ID NO: 2348)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHYSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.1 (SEQ ID NO: 2349)
QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.2 (SEQ ID NO: 2350)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGVPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.3 (SEQ ID NO: 2351)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGIPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.4 (SEQ ID NO: 2352)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRLLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.5 (SEQ ID NO: 2353)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.6 (SEQ ID NO: 2354)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.7 (SEQ ID NO: 2355)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.8 (SEQ ID NO: 2356)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.9 (SEQ ID NO: 2357)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.10 (SEQ ID NO: 2358)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.11 (SEQ ID NO: 2359)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPKSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45L

>CEA-A[CEACAM5]_L2.12 (SEQ ID NO: 2360)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.13 (SEQ ID NO: 2361)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHFSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.14 (SEQ ID NO: 2362)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRSWIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHYSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.15 (SEQ ID NO: 2363)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.16 (SEQ ID NO: 2364)
EIVLTQSPATLSLSPGERATLSCRASASVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.17 (SEQ ID NO: 2365)
EIVLTQSPATLSLSPGERATLSCRASESVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.18 (SEQ ID NO: 2366)
EIVLTQSPATLSLSPGERATLSCRASGSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.19 (SEQ ID NO: 2367)
EIVLTQSPATLSLSPGERATLSCRASKSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.20 (SEQ ID NO: 2368)
EIVLTQSPATLSLSPGERATLSCRASQSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.21 (SEQ ID NO: 2369)
EIVLTQSPATLSLSPGERATLSCRASTSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.22 (SEQ ID NO: 2370)
EIVLTQSPATLSLSPGERATLSCRASVSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.23 (SEQ ID NO: 2371)
EIVLTQSPATLSLSPGERATLSCRASSAVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.24 (SEQ ID NO: 2372)
EIVLTQSPATLSLSPGERATLSCRASSDVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.25 (SEQ ID NO: 2373)
EIVLTQSPATLSLSPGERATLSCRASSGVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.26 (SEQ ID NO: 2374)
EIVLTQSPATLSLSPGERATLSCRASSKVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.27 (SEQ ID NO: 2375)
EIVLTQSPATLSLSPGERATLSCRASSQVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.28 (SEQ ID NO: 2376)
EIVLTQSPATLSLSPGERATLSCRASSTVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45M

>CEA-A[CEACAM5]_L2.29 (SEQ ID NO: 2377)
EIVLTQSPATLSLSPGERATLSCRASSVVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.30 (SEQ ID NO: 2378)
EIVLTQSPATLSLSPGERATLSCRASSSATYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.31 (SEQ ID NO: 2379)
EIVLTQSPATLSLSPGERATLSCRASSSETYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.32 (SEQ ID NO: 2380)
EIVLTQSPATLSLSPGERATLSCRASSSITYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.33 (SEQ ID NO: 2381)
EIVLTQSPATLSLSPGERATLSCRASSSKTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.34 (SEQ ID NO: 2382)
EIVLTQSPATLSLSPGERATLSCRASSSLTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.35 (SEQ ID NO: 2383)
EIVLTQSPATLSLSPGERATLSCRASSSTTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.36 (SEQ ID NO: 2384)
EIVLTQSPATLSLSPGERATLSCRASSSYTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.37 (SEQ ID NO: 2385)
EIVLTQSPATLSLSPGERATLSCRASSSVAYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.38 (SEQ ID NO: 2386)
EIVLTQSPATLSLSPGERATLSCRASSSVDYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.39 (SEQ ID NO: 2387)
EIVLTQSPATLSLSPGERATLSCRASSSVIYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.40 (SEQ ID NO: 2388)
EIVLTQSPATLSLSPGERATLSCRASSSVKYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.41 (SEQ ID NO: 2389)
EIVLTQSPATLSLSPGERATLSCRASSSVQYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.42 (SEQ ID NO: 2390)
EIVLTQSPATLSLSPGERATLSCRASSSVSYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.43 (SEQ ID NO: 2391)
EIVLTQSPATLSLSPGERATLSCRASSSVVYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.44 (SEQ ID NO: 2392)
EIVLTQSPATLSLSPGERATLSCRASSSVTAIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.45 (SEQ ID NO: 2393)
EIVLTQSPATLSLSPGERATLSCRASSSVTDIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45N

>CEA-A[CEACAM5]_L2.46 (SEQ ID NO: 2394)
EIVLTQSPATLSLSPGERATLSCRASSSVTFIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.47 (SEQ ID NO: 2395)
EIVLTQSPATLSLSPGERATLSCRASSSVTHIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.48 (SEQ ID NO: 2396)
EIVLTQSPATLSLSPGERATLSCRASSSVTKIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.49 (SEQ ID NO: 2397)
EIVLTQSPATLSLSPGERATLSCRASSSVTLIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.50 (SEQ ID NO: 2398)
EIVLTQSPATLSLSPGERATLSCRASSSVTVIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.51 (SEQ ID NO: 2399)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIAWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.52 (SEQ ID NO: 2400)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIDWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.53 (SEQ ID NO: 2401)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIGWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.54 (SEQ ID NO: 2402)
EIVLTQSPATLSLSPGERATLSCRASSSVTYINWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.55 (SEQ ID NO: 2403)
EIVLTQSPATLSLSPGERATLSCRASSSVTYISWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.56 (SEQ ID NO: 2404)
EIVLTQSPATLSLSPGERATLSCRASSSVTYITWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.57 (SEQ ID NO: 2405)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYDTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.58 (SEQ ID NO: 2406)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYGTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.59 (SEQ ID NO: 2407)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYKTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.60 (SEQ ID NO: 2408)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYLTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.61 (SEQ ID NO: 2409)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYSTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.62 (SEQ ID NO: 2410)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYTTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45O

>CEA-A[CEACAM5]_L2.63 (SEQ ID NO: 2411)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYVTSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.64 (SEQ ID NO: 2412)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSDLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.65 (SEQ ID NO: 2413)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSHLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.66 (SEQ ID NO: 2414)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSQLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.67 (SEQ ID NO: 2415)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSRLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.68 (SEQ ID NO: 2416)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSSLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.69 (SEQ ID NO: 2417)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSTLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.70 (SEQ ID NO: 2418)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSYLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.71 (SEQ ID NO: 2419)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLESGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.72 (SEQ ID NO: 2420)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLGSGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.73 (SEQ ID NO: 2421)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLKSGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.74 (SEQ ID NO: 2422)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLLSGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.75 (SEQ ID NO: 2423)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLQSGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.76 (SEQ ID NO: 2424)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLVSGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.77 (SEQ ID NO: 2425)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAAGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.78 (SEQ ID NO: 2426)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAEGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.79 (SEQ ID NO: 2427)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAGGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK

Figure 45P

>CEA-A[CEACAM5]_L2.80 (SEQ ID NO: 2428)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAKGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.81 (SEQ ID NO: 2429)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAQGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.82 (SEQ ID NO: 2430)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLATGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.83 (SEQ ID NO: 2431)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLAVGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.84 (SEQ ID NO: 2432)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWASKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.85 (SEQ ID NO: 2433)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWESKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.86 (SEQ ID NO: 2434)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWGSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.87 (SEQ ID NO: 2435)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWKSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.88 (SEQ ID NO: 2436)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWQSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.89 (SEQ ID NO: 2437)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWTSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.90 (SEQ ID NO: 2438)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWVSKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.91 (SEQ ID NO: 2439)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSAKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.92 (SEQ ID NO: 2440)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSDKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.93 (SEQ ID NO: 2441)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSGKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.94 (SEQ ID NO: 2442)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSKKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.95 (SEQ ID NO: 2443)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSQKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.96 (SEQ ID NO: 2444)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSTKPPTFGGGTKVEIK

Figure 45Q

>CEA-A[CEACAM5]_L2.97 (SEQ ID NO: 2445)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSVKPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.98 (SEQ ID NO: 2446)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSAPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.99 (SEQ ID NO: 2447)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSEPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.100 (SEQ ID NO: 2448)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSGPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.101 (SEQ ID NO: 2449)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSHPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.102 (SEQ ID NO: 2450)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSQPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.103 (SEQ ID NO: 2451)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSRPPTFGGGTKVEIK
>CEA-A[CEACAM5]_L2.104 (SEQ ID NO: 2452)
EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPKSLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSSPPTFGGGTKVEIK

Figure 45R

CEA-A VH	SEQ	SEQ ID NO:	
HFR1	EVQLVESGGGLVQPGGSLRLSCAXS	2453	X is selected from A, T
HCDR1	GFTFX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$	2454	X$_1$ is selected from T, A, E, I, K, Q, S, V; X$_2$ is selected from D, A, E, H, K, N, S, T; X$_3$ is selected from Y, A, E, F, H, K, L, V; X$_4$ is selected from Y, A, D, F, H, K, L, V; X$_5$ is selected from M, I, L, V; X$_6$ is selected from N, D, G, H, S, T
HFR2	WVRQAPGKXLEWVG	2455	X is selected from A, G
HCDR2	FIX$_1$X$_2$KX$_3$X$_4$X$_5$X$_6$X$_7$TX$_8$YSASVKG	2456	X$_1$ is selected from G, A, D, H, K, Q, S, T; X$_2$ is selected from N, E, H, Q, R, S, T, Y; X$_3$ is selected from A, E, G, K, L, Q, V; X$_4$ is selected from N, E, H, Q, R, S, T, Y, A; X$_5$ is selected from G, A, E, H, K, L, Q, T; X$_6$ is selected from Y, A, F, G, H, L, S, V; X$_7$ is selected from T, A, E, I, K, Q, S, V; X$_8$ is selected from E, A, D, G, H, K, Q, S
HFR3	RFTISRDKSKSSLYLQMNSLKTEDTAVYYCTR	2457	
HCDR3	X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$FDY		X$_1$ is selected from D, E, G, H, N, R, S, T; X$_2$ is selected from R, D, G, H, K, Q, S, Y; X$_3$ is selected from G, A, D, H, K, Q, S, T; X$_4$ is selected from L, A, E, F, I, K, V, Y; X$_5$ is selected from R, D, G, H, K, Q, S, Y; X$_6$ is selected from F, D, H, I, K, L, S, Y; X$_7$ is selected from Y, A, D, F, H, K, L, V
HFR4	WGQGTLVTVSS	2458	

Figure 45S

CEA-A VL			
LFR1	X_1X_2VLTQSPATLSLSPGERATLSC	2459	X_1 is selected from Q, E; X_2 is selected from T, I
LCDR1	RAS$X_1X_2X_3X_4X_5$IX_6	2460	X_1 is selected from S, A, E, G, K, Q, T, V; X_2 is selected from S, A, D, G, K, Q, T, V; X_3 is selected from V, A, E, I, K, L, T, Y; X_4 is selected from T, A, D, I, K, Q, S, V; X_5 is selected from Y, A, D, F, H, K, L, V; X_6 is selected from H, A, D, G, N, S, T
LFR2	WYQQKPGX_1X_2P$X_3X_4X_5$IY	2461	X_1 is selected from S, Q; X_2 is selected from S, A; X_3 is selected from R, K; X_4 is selected from S, L; X_5 is selected from L, W
LCDR2	X_1TSX_2LX_3X_4		X_1 is selected from A, D, G, K, L, S, T, V; X_2 is selected from N, D, H, Q, R, S, T, Y; X_3 is selected from A, E, G, K, L, Q, V; X_4 is selected from S, A, E, G, K, Q, T
LFR3	GX_1PARFSGSGSGT$X_2X_3X_4$LTISSLEPEDFAVYYC	2462	X_1 is selected from V, I; X_2 is selected from D, S; X_3 is selected from Y, F; X_4 is selected from T, S
LCDR3	QH$X_1X_2X_3X_4$PPT	2463	X_1 is selected from W, F, Y; X_2 is selected from S, A, E, G, K, Q, T, V; X_3 is selected from S, A, D, G, K, Q, T, V; X_4 is selected from K, A, E, G, H, Q, R, S
LFR4	FGGGTKVEIK	2464	

Figure 46A

>1A7[CD28]_H1.103 (SEQ ID NO: 2465)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERMDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.104 (SEQ ID NO: 2466)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.105 (SEQ ID NO: 2467)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERLDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.106 (SEQ ID NO: 2468)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.107 (SEQ ID NO: 2469)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESSDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.108 (SEQ ID NO: 2470)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERNDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.109 (SEQ ID NO: 2471)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERRDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.110 (SEQ ID NO: 2472)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVWTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.111 (SEQ ID NO: 2473)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERSDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.112 (SEQ ID NO: 2474)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERQDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.113 (SEQ ID NO: 2475)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERTDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.114 (SEQ ID NO: 2476)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.115 (SEQ ID NO: 2477)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVMTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.116 (SEQ ID NO: 2478)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERKDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.117 (SEQ ID NO: 2479)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERHDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 46B

>1A7[CD28]_H1.118 (SEQ ID NO: 2480)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIAESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.119 (SEQ ID NO: 2481)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTIVERGDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.120 (SEQ ID NO: 2482)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERYDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.121 (SEQ ID NO: 2483)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDYTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.122 (SEQ ID NO: 2484)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVTTISESGDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.123 (SEQ ID NO: 2485)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISENLDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.124 (SEQ ID NO: 2486)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESADVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.125 (SEQ ID NO: 2487)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISEHGLSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.126 (SEQ ID NO: 2488)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERDDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.127 (SEQ ID NO: 2489)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISENRDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.128 (SEQ ID NO: 2490)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERFDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.129 (SEQ ID NO: 2491)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERADSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.130 (SEQ ID NO: 2492)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERGDVTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.131 (SEQ ID NO: 2493)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISEREDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.132 (SEQ ID NO: 2494)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESSMSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 46C

>1A7[CD28]_H1.133 (SEQ ID NO: 2495)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESVDPTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.134 (SEQ ID NO: 2496)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVMTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.135 (SEQ ID NO: 2497)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESWDHTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.136 (SEQ ID NO: 2498)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISERIDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.137 (SEQ ID NO: 2499)
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVVTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS
>1A7[CD28]_H1.138 (SEQ ID NO: 2500
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVTTISERGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS

Figure 46D

1A7 VH	SEQ	SEQ ID NO:	
HFR1	EVQLLESGGGLVQPGGSLRLSCAASGFTFS	2501	
HCDR1	SYYMS	2502	
HFR2	WVRQAPGKGLEWVX	2503	X is selected from S, W, M, T, V
HCDR2	TIX$_1$EX$_2$X$_3$X$_4$X$_5$TYYADSVKG	2504	X$_1$ is selected from A, V, S; X$_2$ is selected from S, N, H, R; X$_3$ is selected from G, L, S, N, R, Q, T, K, H, Y, A, D, F, E, V, W, I, M; X$_4$ is selected from L, M, D; and X$_5$ is selected from S, P, V, Y, H
HFR3	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	334	
HCDR3	SGPGLRQVGFDY	335	
HFR4	WGQGTLVTVSS	336	

Figure 47

huCD28 KD (nM)	CD28 Mutations
20	1A7_H1.111_IGKV1-39_L1
21	1A7_H1.129_IGKV1-39_L1
28	1A7_H1.125_IGKV1-39_L1
29	1A7_H1.113_IGKV1-39_L1
38	1A7_H1.14_L1.71, 37 nM
43	1A7_H1.106_IGKV1-39_L1
44	1A7_H1.114_IGKV1-39_L1
46	1A7_H1.130_IGKV1-39_L1
57	1A7_H1.107_IGKV1-39_L1
63	1A7_H1.118_IGKV1-39_L1

Figure 48A

>XENP44341 CEA-D[CEACAM5]_H1L1_Fab-CEA-D[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2505)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-D[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2506)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGG
S/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPS
SLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY
YCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-D[CEACAM5]_H1 (SEQ ID NO: 2507)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48B

>XENP44342 CEA-E[CEACAM5]_H1L1_Fab-CEA-E[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2508)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-E[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2509)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGG
GS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-E[CEACAM5]_H1 (SEQ ID NO: 2510)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48C

>XENP44343 CEA-F[CEACAM5]_H1L1_Fab-CEA-F[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2511)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-F[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2512)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-F[CEACAM5]_H1 (SEQ ID NO: 2513)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48D

>XENP44344 CEA-A[CEACAM5]_H0L0_Fab-CEA-A[CEACAM5]_H0L0_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2514)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-A[CEACAM5]_H0_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2515)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-A[CEACAM5]_H0 (SEQ ID NO: 2516)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48E

>XENP44345 CEA-B[CEACAM5]_H1L1_Fab-CEA-B[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2517)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-B[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2518)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-B[CEACAM5]_H1 (SEQ ID NO: 2519)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48F

>XENP44347 CEA-D[CEACAM5]_H1L1_Fab-CEA-D[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2520)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-D[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2521)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGGG
S/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNS
KNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPS
SLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY
YCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-D[CEACAM5]_H1 (SEQ ID NO: 2522)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48G

>XENP44348 CEA-E[CEACAM5]_H1L1_Fab-CEA-E[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2523)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-E[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2524)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGGG
GS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-E[CEACAM5]_H1 (SEQ ID NO: 2525)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48H

>XENP44349 CEA-F[CEACAM5]_H1L1_Fab-CEA-F[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2526)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-F[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2527)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-F[CEACAM5]_H1 (SEQ ID NO: 2528)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48I

>XENP44350 CEA-A[CEACAM5]_H0L0_Fab-CEA-A[CEACAM5]_H0L0_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2529)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-A[CEACAM5]_H0_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2530)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-A[CEACAM5]_H0 (SEQ ID NO: 2531)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 48J

>XENP44351 CEA-B[CEACAM5]_H1L1_Fab-CEA-B[CEACAM5]_H1L1_Fab-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2532)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-B[CEACAM5]_H1_IgG1_PVA_/S267K/S364K/E357Q/K447del_(G4S)3_1A7[CD28]_H1_L1.71_scFv(GKPGS)4 (SEQ ID NO: 2533)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK

Chain 3 - CEA-B[CEACAM5]_H1 (SEQ ID NO: 2534)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49A

>XENP44353 CEA-D[CEACAM5]_H1L1_Fab-CEA-D[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2535)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-D[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2536)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGG
GS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-D[CEACAM5]_H1 (SEQ ID NO: 2537)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49B

>XENP44354 CEA-E[CEACAM5]_H1L1_Fab-CEA-E[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2538)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-E[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2539)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-E[CEACAM5]_H1 (SEQ ID NO: 2540)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49C

>XENP44355 CEA-F[CEACAM5]_H1L1_Fab-CEA-F[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2541)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-F[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2542)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-F[CEACAM5]_H1 (SEQ ID NO: 2543)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49D

>XENP44356 CEA-A[CEACAM5]_H0L0_Fab-CEA-A[CEACAM5]_H0L0_Fab_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2544)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-A[CEACAM5]_H0_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2545)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_H0 (SEQ ID NO: 2546)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49E

>XENP44357 CEA-B[CEACAM5]_H1L1_Fab-CEA-B[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2547)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-B[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2548)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_H1 (SEQ ID NO: 2549)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49F

>XENP44359 CEA-D[CEACAM5]_H1L1_Fab-CEA-D[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-D[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2550)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVL
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWES
DGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-D[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2551)

EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSLKDRFTISRDNAKN
TLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGGG
GS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSP
SSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
KHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
NVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-D[CEACAM5]_H1 (SEQ ID NO: 2552)

DIQLTQSPSSLSASVGDRVTITCKASQDVGTSVAWYQQKPGKAPKLLIYWTSTRHTGVPSRFSGSGSGTDFTFTISS
LQPEDIATYYCQQYSLYRSFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49G

>XENP44360 CEA-E[CEACAM5]_H1L1_Fab-CEA-E[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-E[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2553)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-E[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2554)

EVQLQESGPGLVKPGGSLSLSCAASGFVFSSYDMSWVRQTPERGLEWVAYISSGGGITYAPSTVKGRFTVSRDNAKN
TLYLQMNSLTSEDTAVYYCAAHYFGSSGPFAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-E[CEACAM5]_H1 (SEQ ID NO: 2555)

DIQMTQSPASLSASVGDRVTITCRASENIFSYLAWYQQKPGKSPKLLVYNTRTLAEGVPSRFSGSGSGTDFSLTISS
LQPEDFATYYCQHHYGTPFTFGSGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49H

>XENP44361 CEA-F[CEACAM5]_H1L1_Fab-CEA-F[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-F[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2556)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-F[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2557)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTEFGMNWVRQAPGQGLEWMGWINTKTGEATYVEEFKGRVTFTTDTSTS
TAYMELRSLRSDDTAVYYCARWDFAYYVEAMDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-F[CEACAM5]_H1 (SEQ ID NO: 2558)

DIQMTQSPSSLSASVGDRVTITCKASAAVGTYVAWYQQKPGKAPKLLIYSASYRKRGVPSRFSGSGSGTDFTLTISS
LQPEDFATYYCHQYYTYPLFTFGQGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49I

>XENP44362 CEA-A[CEACAM5]_H0L0_Fab-CEA-A[CEACAM5]_H0L0_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2559)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-A[CEACAM5]_H0_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2560)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_H0 (SEQ ID NO: 2561)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49J

>XENP44363 CEA-B[CEACAM5]_H1L1_Fab-CEA-B[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2562)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-B[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2563)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_H1 (SEQ ID NO: 2564)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49K

>XENP44668 CEA-A[CEACAM5]_H1L1_Fab-CEA-A[CEACAM5]_H1L1_Fab_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S

Chain 1 - CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S/M428L/N434S (SEQ ID NO: 2565)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC
PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW
ESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - CEA-A[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q/M428L/N434S (SEQ ID NO: 2566)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSG
GGGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISR
DNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQ
SPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF
ATYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_H1 (SEQ ID NO: 2567)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49L

>XENP44735 CEA-C[CEACAM5]_H0L0_Fab-CEA-C[CEACAM5]_H0L0_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2568)

QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSN
TAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-C[CEACAM5]_H0L0_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2569)

QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSN
TAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_H0 (SEQ ID NO: 2570)

ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRM
EAEDAATYYCQQRSSYPLTFGAGTKLELK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 49M

>XENP44737 CEA-C[CEACAM5]_H1L1_Fab-CEA-C[CEACAM5]_H1L1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(222)_IgG1_PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2571)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWLRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTTDTSIN
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCP
PCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWE
SDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 2 - CEA-C[CEACAM5]_H1_(G4S)2_1A7[CD28]_H1_L1.71_scFv(GKPGS)4_(G4S)2_Fc(222)_IgG1_PVA_/S267K/S364K/E357Q (SEQ ID NO: 2572)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWLRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTTDTSIN
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGGGSGG
GGS/EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQS
PSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
TYYCQQVYSTPFTFGQGTKLEIK/GGGGSGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_H1 (SEQ ID NO: 2573)

ENVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQKPGQSPRLLIYSTSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQQRSSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50A

>XENP44565 CEA-A[CEACAM5]_H0L0_Fab_(G4A)2_CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_(G4A)2_CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2574)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTI
SRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2575)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2576)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50B

>XENP44566 CEA-B[CEACAM5]_H1L1_Fab_(G4A)2_CEA-B[CEACAM5]_H1L1_Fab-1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_(G4A)2_CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2577)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISA
DTSKNTAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2578)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKGLEWVSTISESGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_L1 (SEQ ID NO: 2579)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50C

>XENP44567 CEA-A[CEACAM5]_H0L0_Fab_(G4A)2_CEA-A[CEACAM5]_H0L0_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H0_(G4A)2_CEA-A[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2580)

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKS
QSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTI
SRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2581)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L0 (SEQ ID NO: 2582)

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRV
EAEDAATYYCQHWSSKPPTFGGGTKLEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50D

>XENP44568 CEA-B[CEACAM5]_H1L1_Fab_(G4A)2_CEA-B[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-B[CEACAM5]_H1_(G4A)2_CEA-B[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2583)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISADTSKN
TAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYMHWVRQAPGKGLEWVARIDPANGNSKYADSVKGRFTISA
DTSKNTAYLQMNSLRAEDTAVYYCAPFGYYVSDYAMAYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2584)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-B[CEACAM5]_L1 (SEQ ID NO: 2585)

DIQLTQSPSSLSASVGDRVTITCRAGESVDIFGVGFLHWYQQKPGKAPKLLIYRASNLESGVPSRFSGSGSRTDFTL
TISSLQPEDFATYYCQQTNEDPYTFGQGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK
VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50E

>XENP44738 CEA-C[CEACAM5]_H0L0_Fab_(G4A)2_CEA-C[CEACAM5]_H0L0_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H0_(G4A)2_CEA-C[CEACAM5]_H0_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2586)

QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSN
TAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAGG
GGA/QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTD
TSSNTAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2587)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L0 (SEQ ID NO: 2588)

ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRM
EAEDAATYYCQQRSSYPLTFGAGTKLELK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50F

>XENP44740 CEA-C[CEACAM5]_H1L1_Fab_(G4A)2_CEA-C[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-C[CEACAM5]_H1_(G4A)2_CEA-C[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2589)

QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWLRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTTDTSIN
TAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAGG
GGA/QVQLVQSGAEVKKPGASVKVSCKASGFNIKDSYMHWLRQAPGQGLEWMGWIDPENGDTEYAPKFQGRVTMTTD
TSINTAYMELSRLRSDDTAVYYCNEGTPTGPYYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLV
KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKT
HTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIA
VEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2590)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-C[CEACAM5]_L1 (SEQ ID NO: 2591)

ENVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQKPGQSPRLLIYSTSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQQRSSYPLTFGAGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50G

>XENP44757 CEA-A[CEACAM5]_H1L1_Fab_(G4A)2_CEA-A[CEACAM5]_H1L1_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1_(G4A)2_CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2592)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTI
SRDKSKSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2593)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L1 (SEQ ID NO: 2594)

QTVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQSPRSLIYATSNLASGVPARFSGSGSGTDYTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 50H

>XENP44758 CEA-A[CEACAM5]_H1L2_Fab_(G4A)2_CEA-A[CEACAM5]_H1L2_Fab-1A7[CD28]_H1_L1.71_scFv(GKPGS)4-IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S-Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q

Chain 1 - CEA-A[CEACAM5]_H1_(G4A)2_CEA-A[CEACAM5]_H1_IgG1_pI(-)_Isosteric_A_PVA_/S267K/L368D/K370S (SEQ ID NO: 2595)

EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTISRDKS
KSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCGGGGAG
GGGA/EVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKALEWVGFIGNKANGYTTEYSASVKGRFTI
SRDKSKSSLYLQMNSLKTEDTAVYYCTRDRGLRFYFDYWGQGTLVTVSS/ASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCD
KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNST
YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSD
IAVEWESDGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVLHEALHSHYTQKSLSLSPGK

Chain 2 - 1A7[CD28]_H1_L1.71_scFv(GKPGS)4_Fc(216)_IgG1_C220S/PVA_/S267K/S364K/E357Q (SEQ ID NO: 2596)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS/GKPGSGKPGSGKPGSGKPGS/DIQMTQSPSSL
SASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC
QQVYSTPFTFGQGTKLEIK/EPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK

Chain 3 - CEA-A[CEACAM5]_L2 (SEQ ID NO: 2597)

EIVLTQSPATLSLSPGERATLSCRASSSVTYIHWYQQKPGQAPRLLIYATSNLASGIPARFSGSGSGTDFTLTISSL
EPEDFAVYYCQHWSSKPPTFGGGTKVEIK/RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 51A-51D

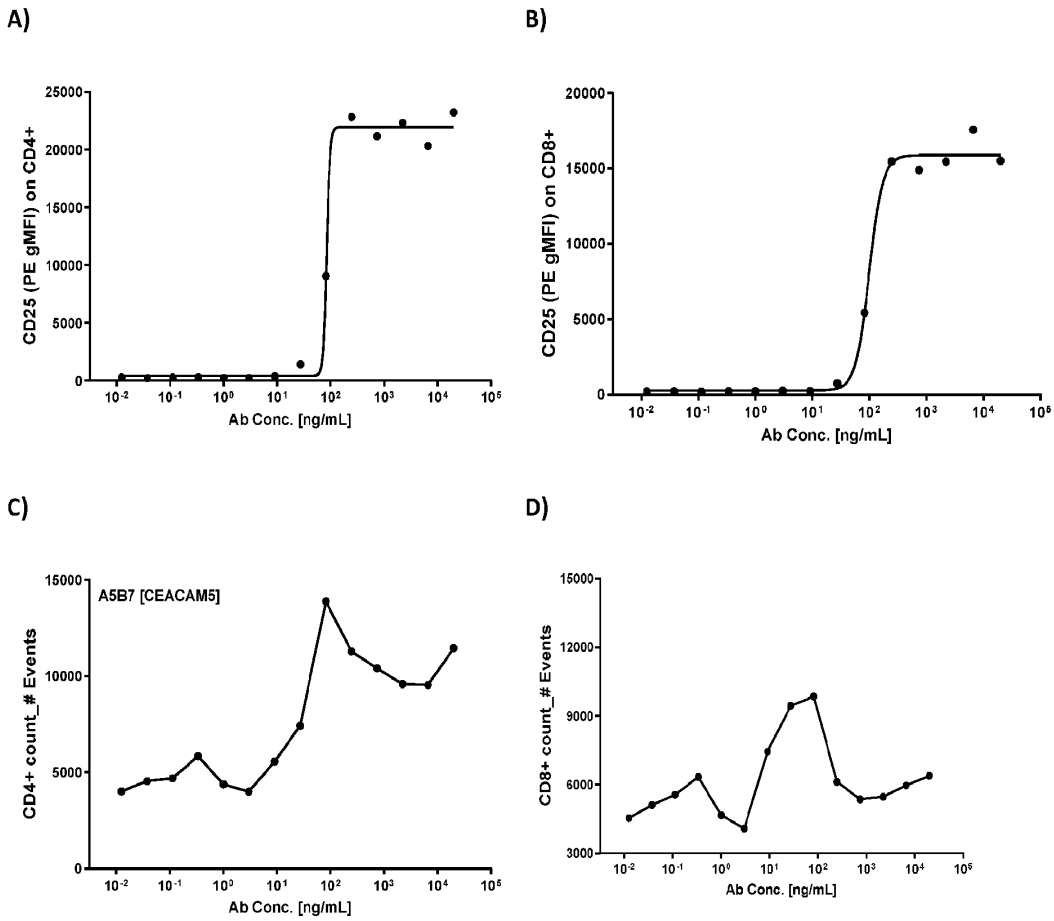


Figure 52A-52E

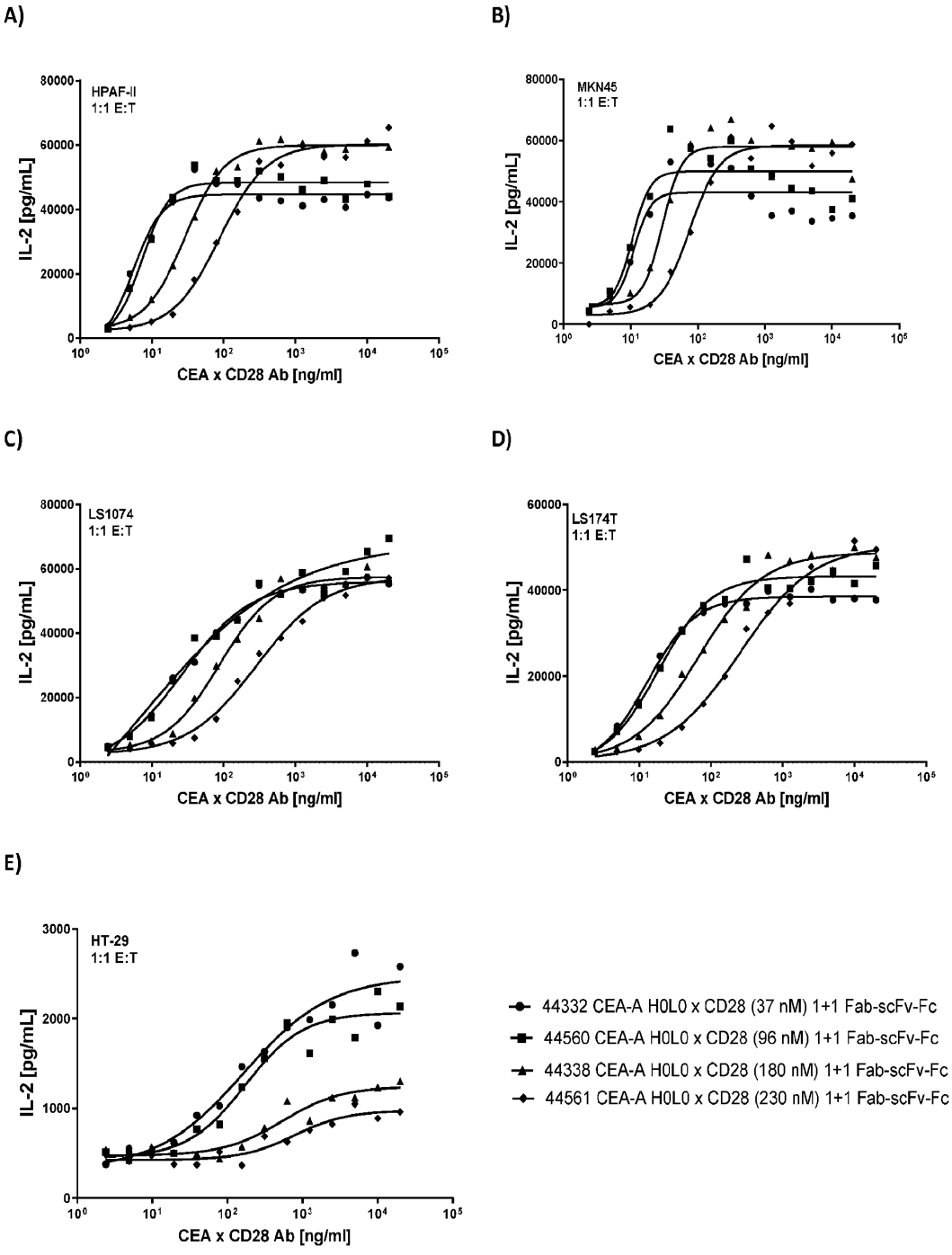


Figure 53A-53E

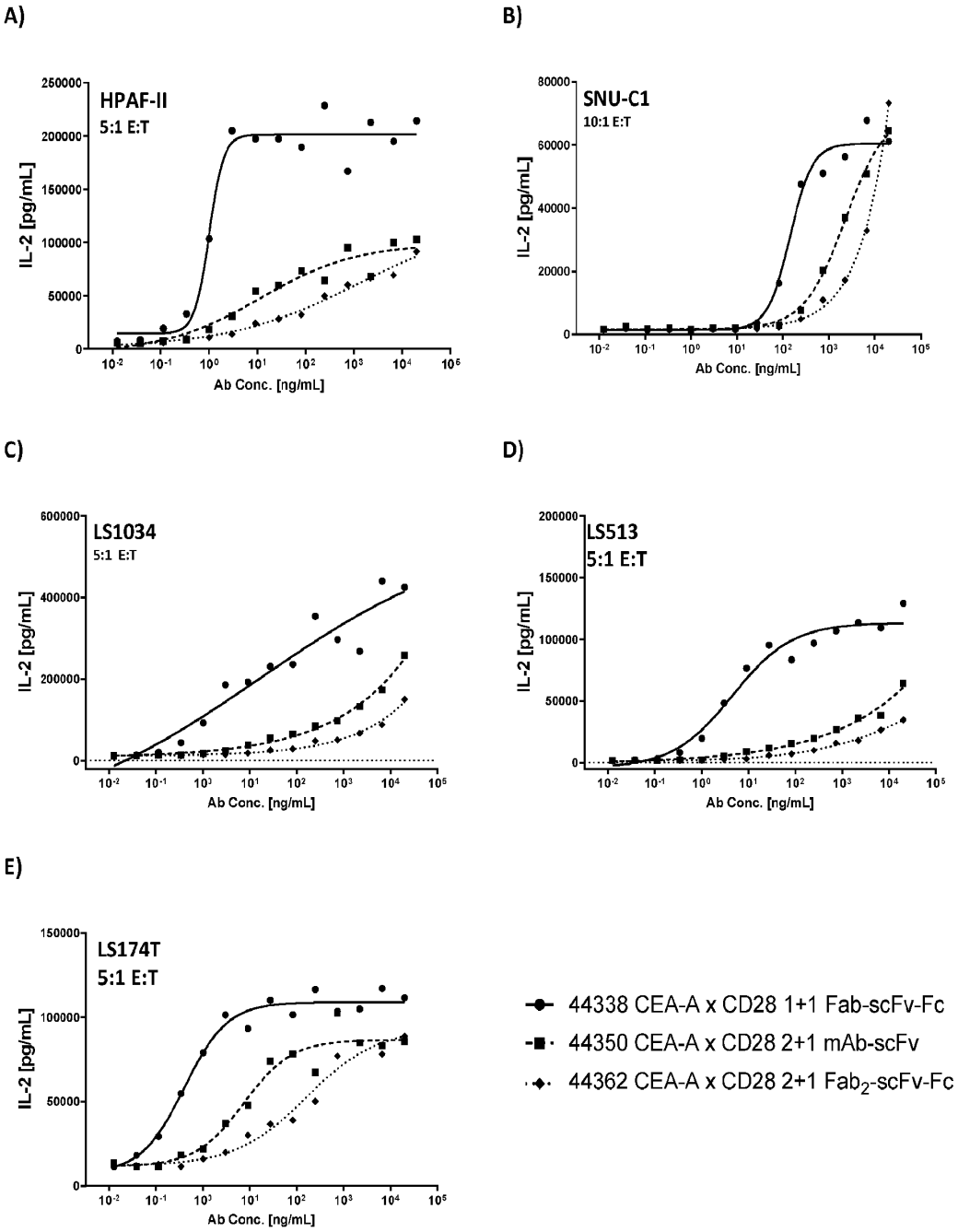
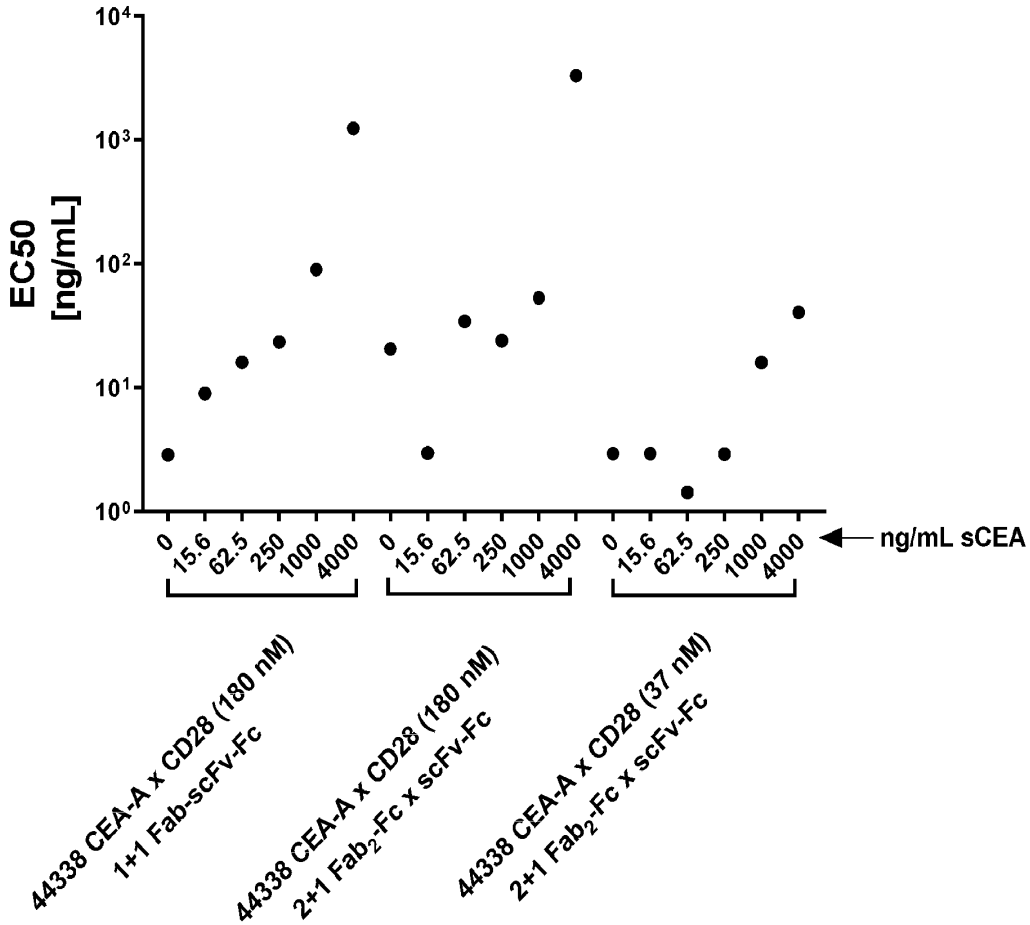


Figure 54


EC50 [ng/mL]
10⁴
10³
10²
10¹
10⁰
0 15.6 62.5 250 1000 4000
0 15.6 62.5 250 1000 4000
0 15.6 62.5 250 1000 4000
ng/mL sCEA
44338 CEA-A x CD28 (180 nM) 1+1 Fab-scFv-Fc
44338 CEA-A x CD28 (180 nM) 2+1 Fab2-Fc x scFv-Fc
44338 CEA-A x CD28 (37 nM) 2+1 Fab2-Fc x scFv-Fc

Figures 55A-55C

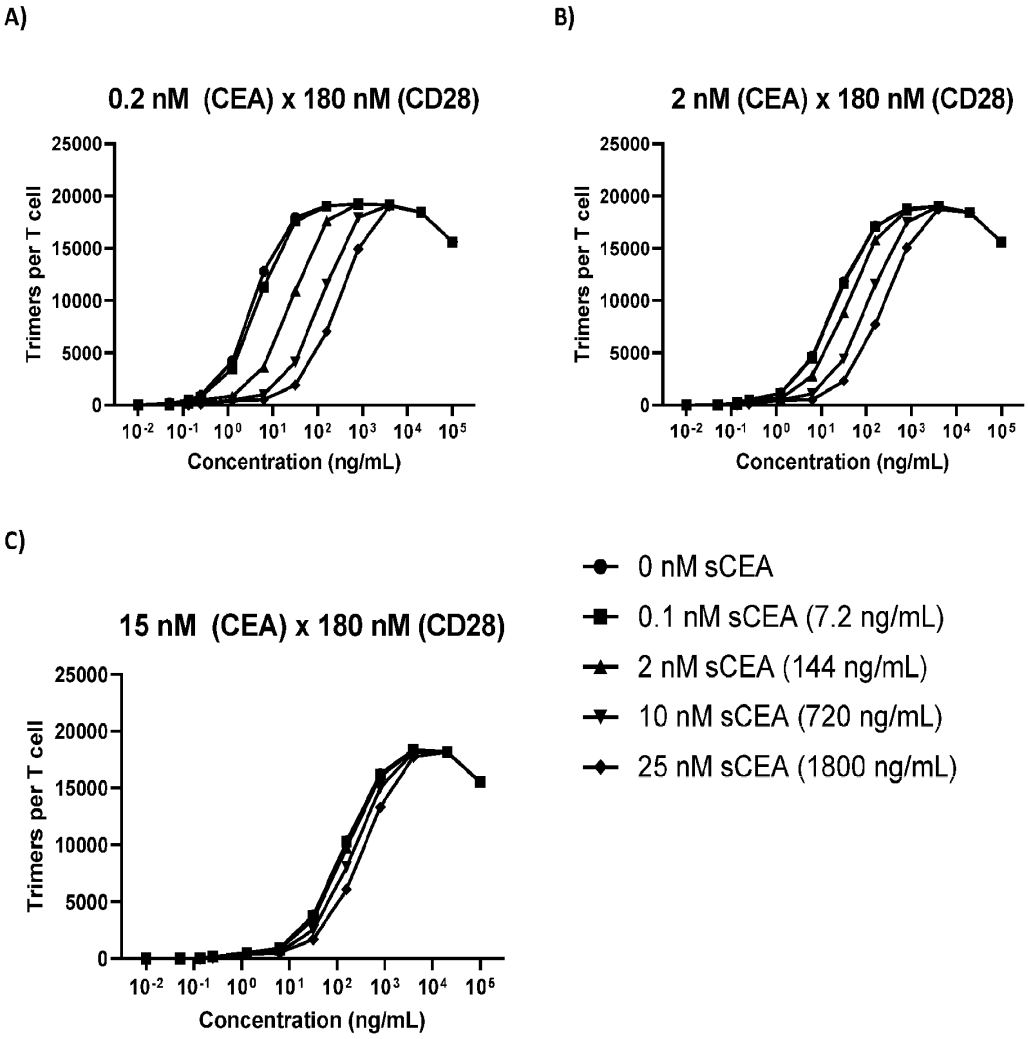


Figure 56

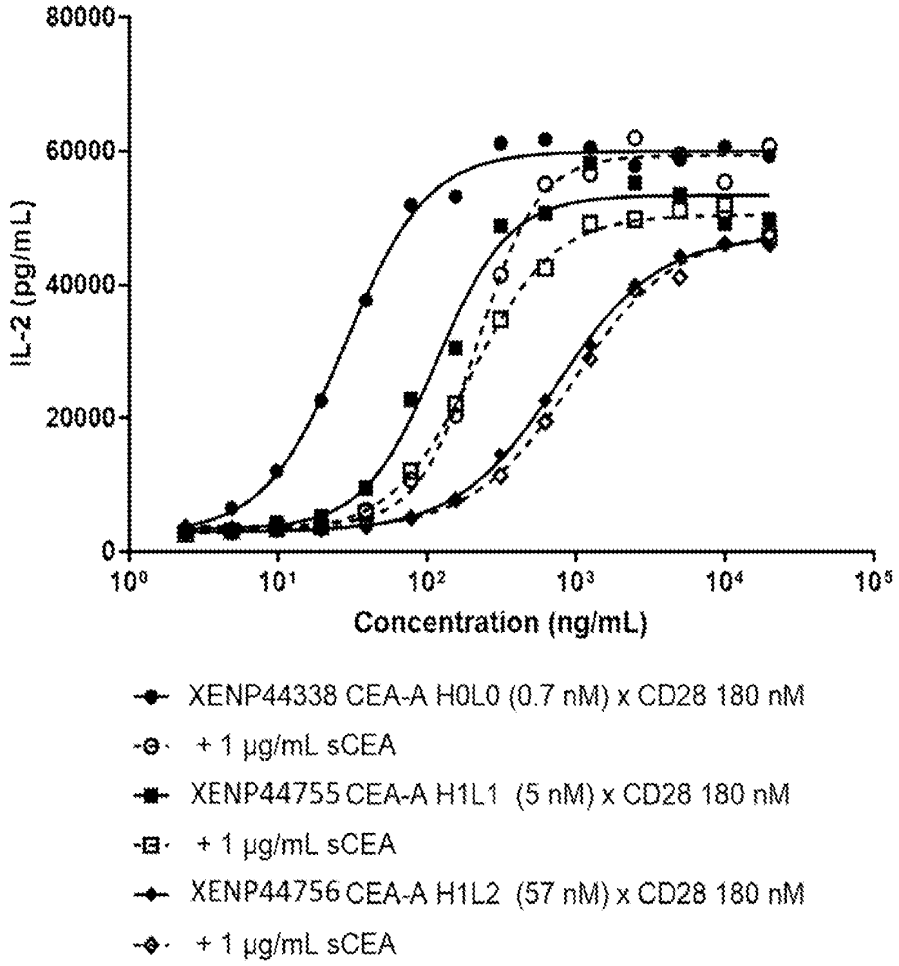

80000
60000
40000
20000
0
IL-2 (pg/mL)
10⁰
10¹
10²
10³
10⁴
10⁵
Concentration (ng/mL)
XENP44338 CEA-A H0L0 (0.7 nM) x CD28 180 nM
+ 1 µg/mL sCEA
XENP44755 CEA-A H1L1 (5 nM) x CD28 180 nM
+ 1 µg/mL sCEA
XENP44756 CEA-A H1L2 (57 nM) x CD28 180 nM
+ 1 µg/mL sCEA

Figure 57

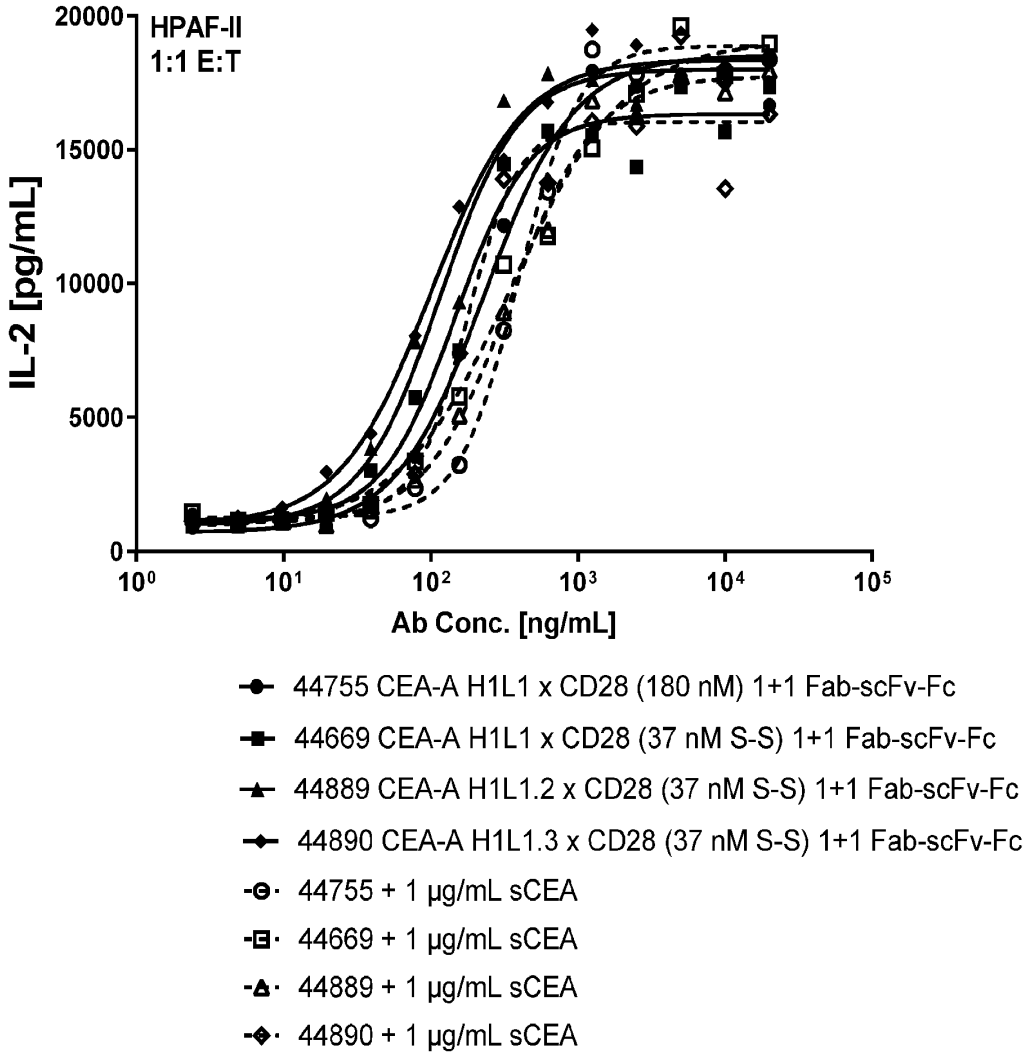

HPAF-II
1:1 E:T
IL-2 [pg/mL]
20000
15000
10000
5000
0
10^0
10^1
10^2
10^3
10^4
10^5
Ab Conc. [ng/mL]
44755 CEA-A H1L1 x CD28 (180 nM) 1+1 Fab-scFv-Fc
44669 CEA-A H1L1 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44889 CEA-A H1L1.2 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44890 CEA-A H1L1.3 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44755 + 1 µg/mL sCEA
44669 + 1 µg/mL sCEA
44889 + 1 µg/mL sCEA
44890 + 1 µg/mL sCEA

Figure 58

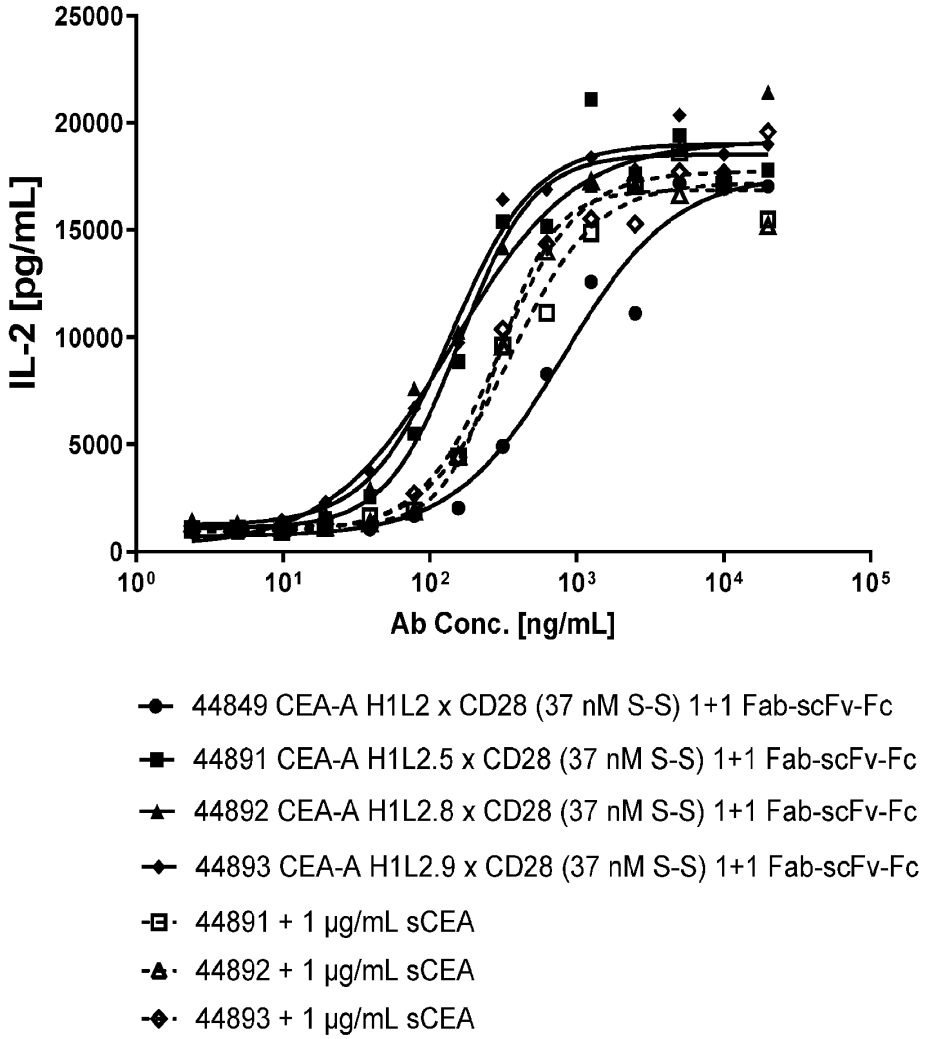
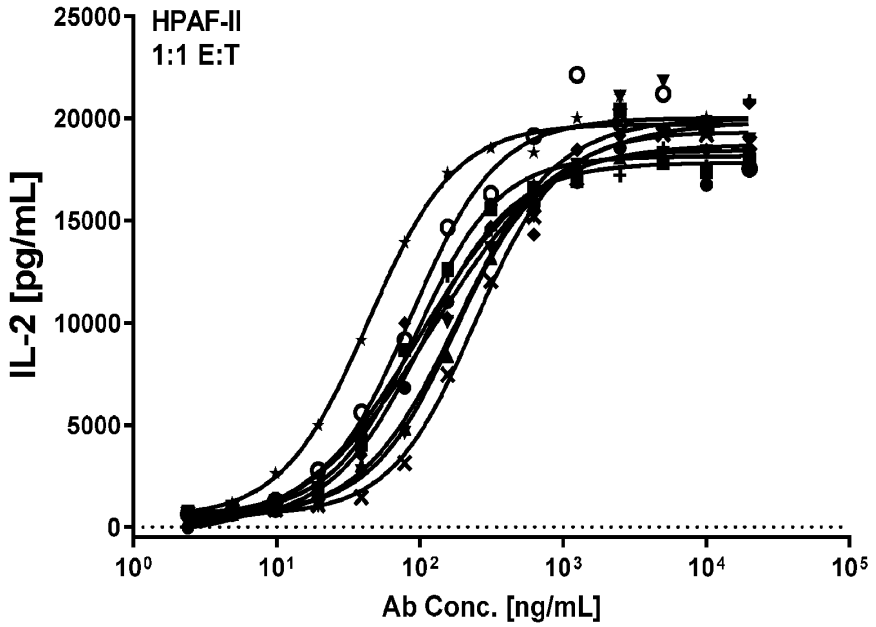

25000
20000
15000
10000
5000
0
IL-2 [pg/mL]
10⁰
10¹
10²
10³
10⁴
10⁵
Ab Conc. [ng/mL]
44849 CEA-A H1L2 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44891 CEA-A H1L2.5 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44892 CEA-A H1L2.8 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44893 CEA-A H1L2.9 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
44891 + 1 µg/mL sCEA
44892 + 1 µg/mL sCEA
44893 + 1 µg/mL sCEA

Figure 59



44338 CEA-A H0L0 x CD28 (180 nM) 1+1 Fab-scFv-Fc

44755 CEA-A H1L1 x CD28 (180 nM) 1+1 Fab-scFv-Fc

44669 CEA-A H1L1 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44889 CEA-A H1_L1.2 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44890 CEA-A H1_L1.3 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44893 CEA-A H1_L2.9 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44913 CEA-A H1_L2.15 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44914 CEA-A H1.7_L1 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 Fab-scFv-Fc

44915 CEA-A H1.7_L2.15 x CD28 (1A7_H1.14_L1.71, 37 nM S-S) 1+1 BO

Figure 60

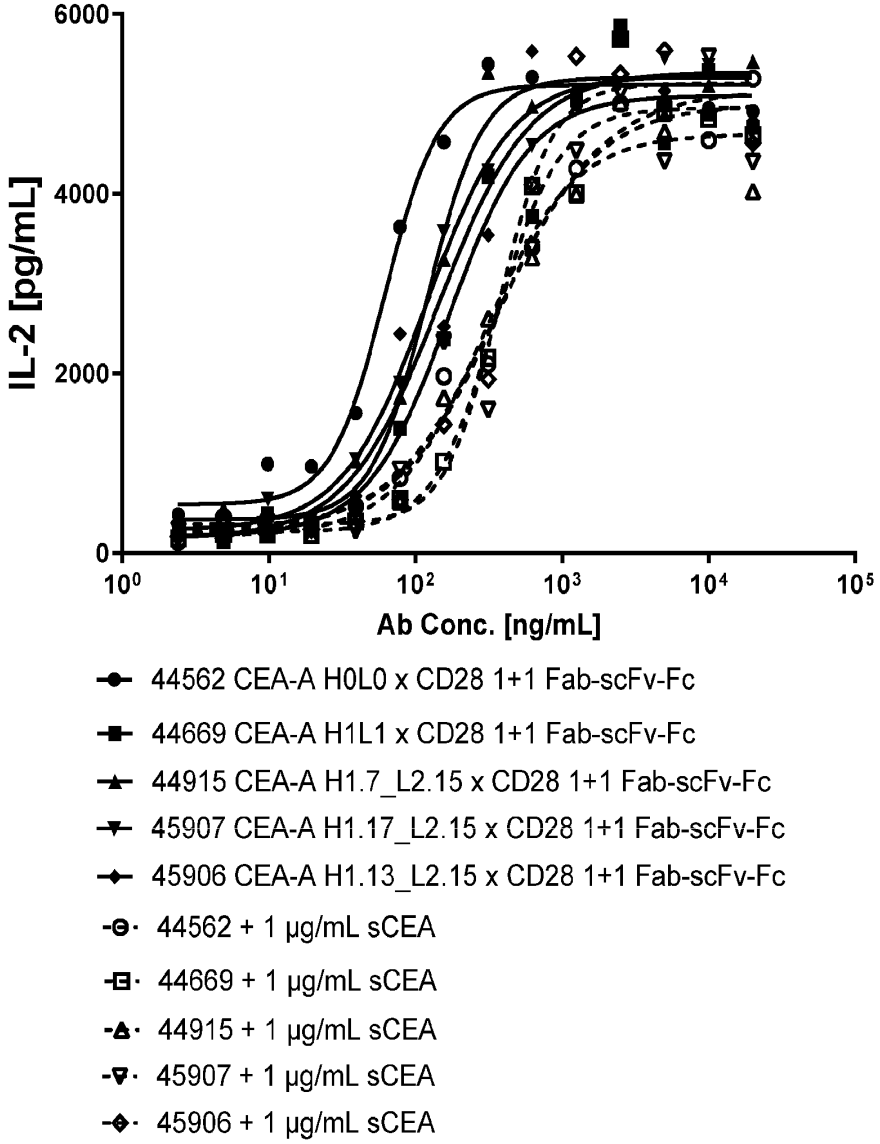
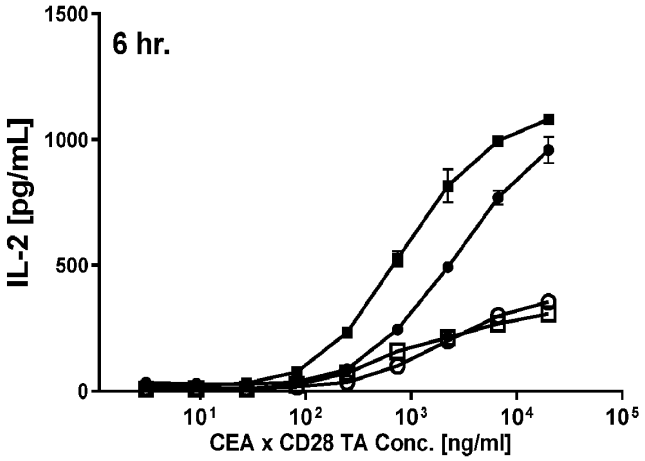
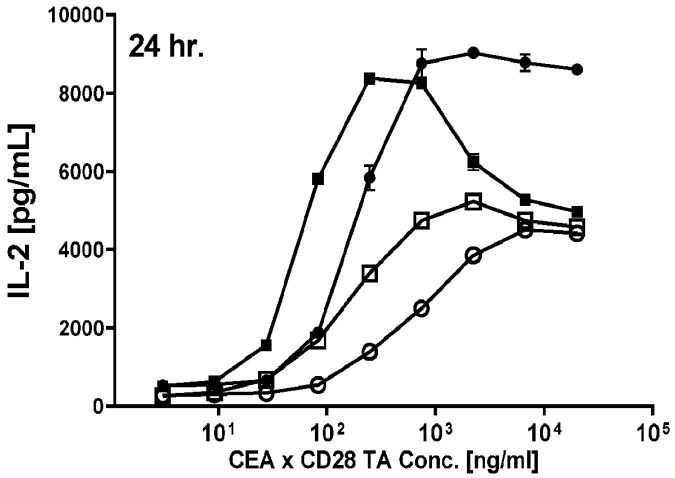

6000
4000
2000
0
IL-2 [pg/mL]
10^0
10^1
10^2
10^3
10^4
10^5
Ab Conc. [ng/mL]
44562 CEA-A H0L0 x CD28 1+1 Fab-scFv-Fc
44669 CEA-A H1L1 x CD28 1+1 Fab-scFv-Fc
44915 CEA-A H1.7_L2.15 x CD28 1+1 Fab-scFv-Fc
45907 CEA-A H1.17_L2.15 x CD28 1+1 Fab-scFv-Fc
45906 CEA-A H1.13_L2.15 x CD28 1+1 Fab-scFv-Fc
44562 + 1 µg/mL sCEA
44669 + 1 µg/mL sCEA
44915 + 1 µg/mL sCEA
45907 + 1 µg/mL sCEA
45906 + 1 µg/mL sCEA

Figure 61A-61B

A)



B)



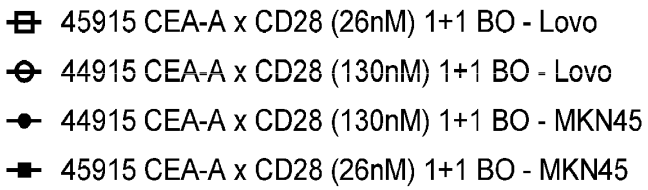


Figure 62

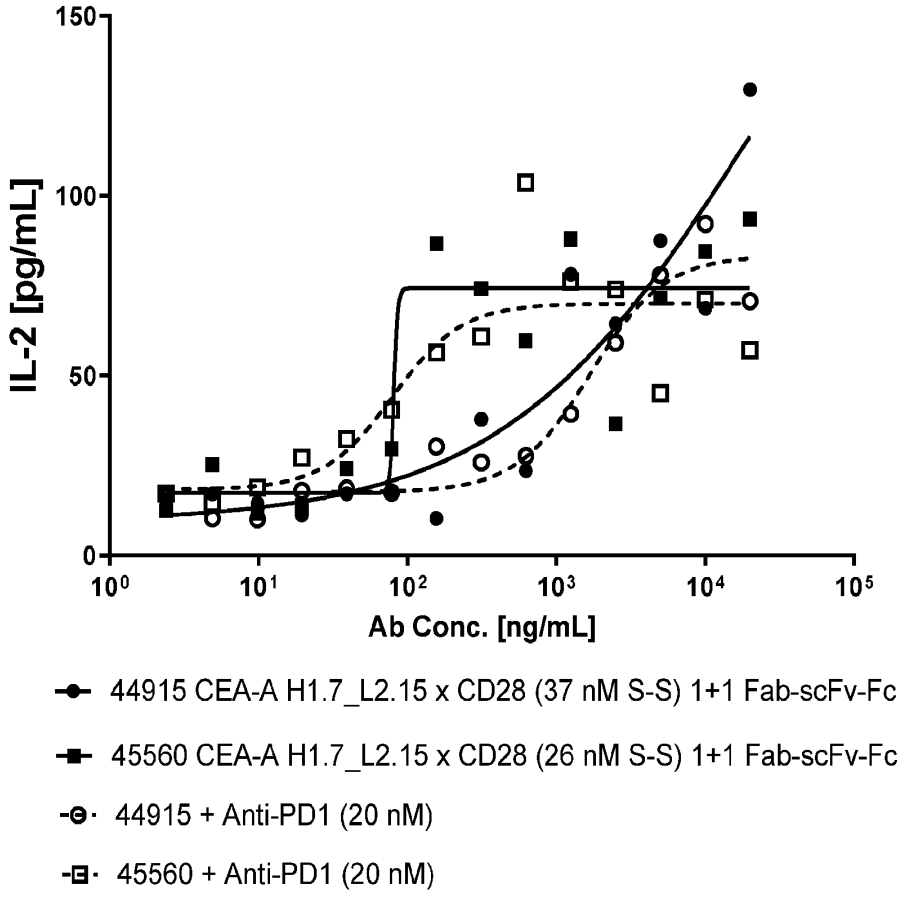

150
100
50
0
IL-2 [pg/mL]
10^0
10^1
10^2
10^3
10^4
10^5
Ab Conc. [ng/mL]
44915 CEA-A H1.7_L2.15 x CD28 (37 nM S-S) 1+1 Fab-scFv-Fc
45560 CEA-A H1.7_L2.15 x CD28 (26 nM S-S) 1+1 Fab-scFv-Fc
44915 + Anti-PD1 (20 nM)
45560 + Anti-PD1 (20 nM)

Figure 63

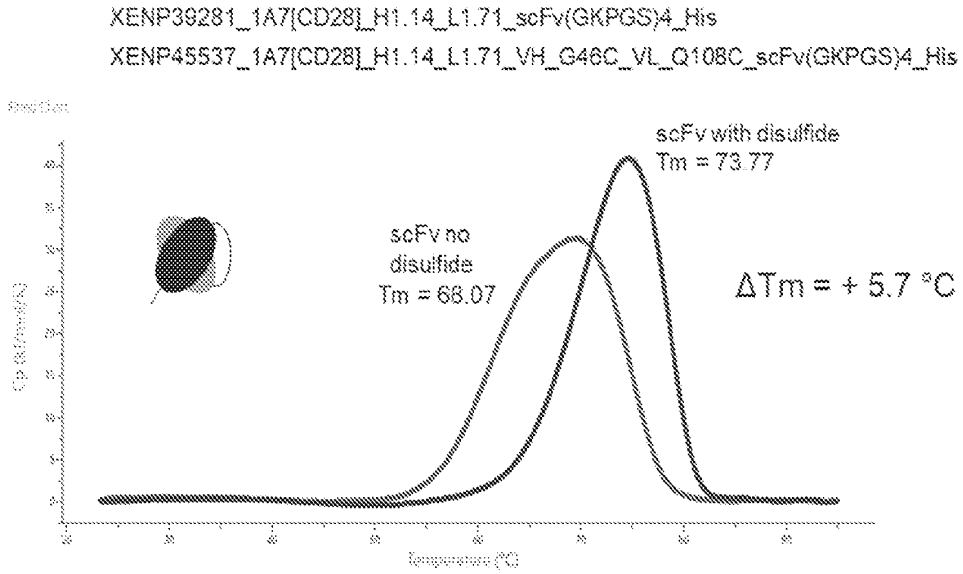

XENP39281_1A7[CD28]_H1.14_L1.71_scFv(GKPGS)4_His
XENP45537_1A7[CD28]_H1.14_L1.71_VH_G46C_VL_Q108C_scFv(GKPGS)4_His
scFv with disulfide
Tm = 73.77
scFv no
disulfide
Tm = 68.07
ΔTm = + 5.7 °C

Figure 64

	KD (M)	kon(1/Ms)	kdis(1/s)	KD (nM)
1A7_L1.71_H1.129	1.67E-09	2.33E+05	3.90E-04	1.67
1A7_H1.129_L1.71	1.73E-09	2.22E+05	3.85E-04	1.73
1A7_L1.71_H1.129 [S-S]	4.22E-09	1.82E+05	7.66E-04	4.22
1A7_H1.129_L1.71 [S-S]	5.32E-09	1.56E+05	8.31E-04	5.32
1A7_L1.71_H1.106	4.56E-09	2.53E+05	1.16E-03	4.56
1A7_H1.106_L1.71	5.59E-09	2.10E+05	1.18E-03	5.59
1A7_L1_H1.129	1.11E-08	3.41E+05	3.79E-03	11.1
1A7_H1.129_L1	1.17E-08	3.11E+05	3.63E-03	11.7
1A7_L1.71_H1.106 [S-S]	1.16E-08	1.97E+05	2.28E-03	11.6
1A7_H1.106_L1.71 [S-S]	1.48E-08	1.62E+05	2.38E-03	14.8
1A7_L1_H1.106	2.61E-08	3.73E+05	9.71E-03	26.1
1A7_H1.106_L1	3.15E-08	3.23E+05	1.02E-02	31.5
1A7_H1.14_L1.71 [S-S]	7.40E-08	1.61E+05	1.19E-02	74
1A7_H1.14_L1.71 [S-S]	7.60E-08	1.55E+05	1.18E-02	76
1A7_H1.14_L1.71 [S-S]	8.24E-08	1.43E+05	1.18E-02	82.4
1A7_H1.1_L1.71 [S-S]	1.61E-07	1.59E+05	2.56E-02	161
1A7_H1_L1.71	1.23E-07	2.74E+05	3.36E-02	123
1A7_H1.14_L1	1.67E-07	4.26E+05	7.10E-02	167
1A7_H1.14_L1.71	2.31E-08	2.26E+05	5.22E-03	23.1
1A7_H1.14_L1.71 [S-S]	1.3E-07			130
1A7_H1.106_L1 [S-S]	8.9E-08	2.39E+05	2.12E-02	89
1A7_H1.129_L1 [S-S]	2.6E-08	3.36E+05	9.41E-03	28

Figure 65A

1A7[CD28]_H1.1_L1 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS	2598
vhCDR1	SYYMS	2599
vhCDR2	TISGSGDSTYYADSVKG	2600
vhCDR3	SGPGLRQVGFDY	2601
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2602
vlCDR1	RASQSISSYLN	2603
vlCDR2	AASSLQS	2604
vlCDR3	QQSYSTPFT	2605
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2606

1A7[CD28]_H1_L1.71 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSS	2607
vhCDR1	SYAMS	2608
vhCDR2	TISGSGDSTYYADSVKG	2609
vhCDR3	SGPGLRQVGFDY	2610
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2611
vlCDR1	RASQSISSYLN	2612
vlCDR2	AASSLQS	2613
vlCDR3	QQVYSTPFT	2614
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSTISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2615

Figure 65B

1A7[CD28]_H1.1_L1.71 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGS GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	2616
vhCDR1	SYYMS	2617
vhCDR2	TISGSGDSTYYADSVKG	2618
vhCDR3	SGPGLRQVGFDY	2619
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2620
vlCDR1	RASQSISSYLN	2621
vlCDR2	AASSLQS	2622
vlCDR3	QQVYSTPFT	2623
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISGS GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTI SSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2624

1A7[CD28]_H1.14_L1 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISES GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSS	2625
vhCDR1	SYYMS	2626
vhCDR2	TISESGDSTYYADSVKG	2627
vhCDR3	SGPGLRQVGFDY	2628
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2629
vlCDR1	RASQSISSYLN	2630
vlCDR2	AASSLQS	2631
vlCDR3	QQSYSTPFT	2632
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTISES GDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLRQVGF DYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTI SSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2633

Figure 65C

1A7[CD28]_H1.14_L1.71 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	2634
vhCDR1	SYYMS	2635
vhCDR2	TISESGDSTYYADSVKG	2636
vhCDR3	SGPGLRQVGFDY	2637
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKL EIK	2638
vlCDR1	RASQSISSYLN	2639
vlCDR2	AASSLQS	2640
vlCDR3	QQVYSTPFT	2641
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ESGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASV GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2642

1A7[CD28]_H1.129_L1.71 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	2643
vhCDR1	SYYMS	2644
vhCDR2	TISERADSTYYADSVKG	2645
vhCDR3	SGPGLRQVGFDY	2646
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKL EIK	2647
vlCDR1	RASQSISSYLN	2648
vlCDR2	AASSLQS	2649
vlCDR3	QQVYSTPFT	2650
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASV GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2651

Figure 65D

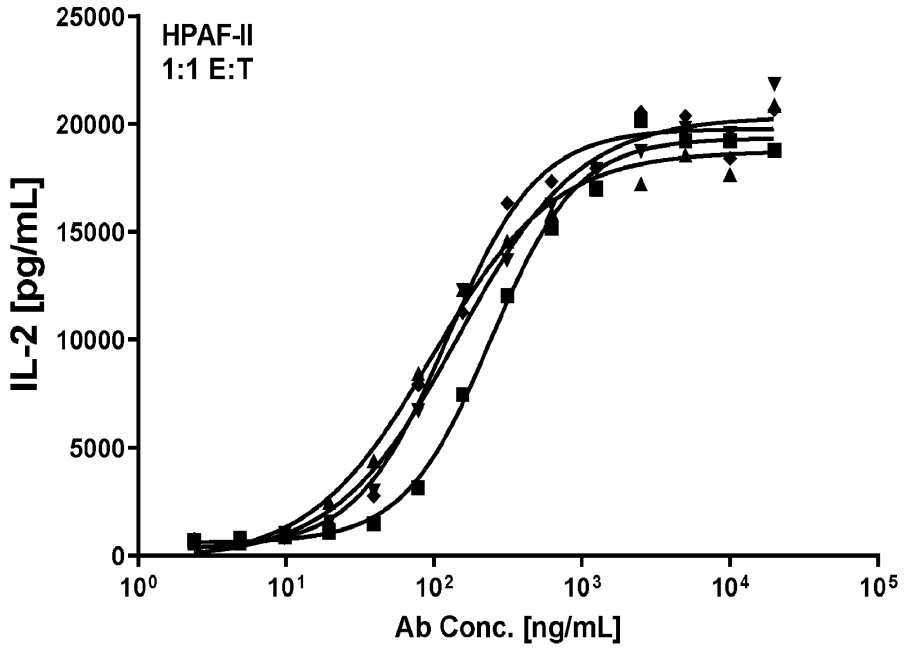
1A7[CD28]_H1.106_L1.71 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	2652
vhCDR1	SYYMS	2653
vhCDR2	TISERGDSTYYADSVKG	2654
vhCDR3	SGPGLRQVGFDY	2655
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKL EIK	2656
vlCDR1	RASQSISSYLN	2657
vlCDR2	AASSLQS	2658
vlCDR3	QQVYSTPFT	2659
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASV GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQVYSTPFTFGCGTKLEIK	2660

1A7[CD28]_H1.129_L1 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	2661
vhCDR1	SYYMS	2662
vhCDR2	TISERADSTYYADSVKG	2663
vhCDR3	SGPGLRQVGFDY	2664
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKL EIK	2665
vlCDR1	RASQSISSYLN	2666
vlCDR2	AASSLQS	2667
vlCDR3	QQSYSTPFT	2668
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERADSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASV GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2669

Figure 65E

1A7[CD28]_H1.106_L1 [S-S]		
	Sequence	SEQ ID NO:
Variable Heavy (vh) Domain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSS	2670
vhCDR1	SYYMS	2671
vhCDR2	TISERGDSTYYADSVKG	2672
vhCDR3	SGPGLRQVGFDY	2673
Variable Light (vl) Domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAS SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKL EIK	2674
vlCDR1	RASQSISSYLN	2675
vlCDR2	AASSLQS	2676
vlCDR3	QQSYSTPFT	2677
scFv	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYYMSWVRQAPGKCLEWVSTIS ERGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSGPGLR QVGFDYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSDIQMTQSPSSLSASV GDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQSYSTPFTFGCGTKLEIK	2678

Figure 66



- 44755 CEA-A H1L1 x CD28 (1A7_H1_L1.71, 180 nM) 1+1 Fab-scFv-Fc
- 44911 CEA-A H1L1 x CD28 (1A7_H1.1_L1.71, 96 nM [S-S]) 1+1 Fab-scFv-Fc
- 44912 CEA-A H1L1 x CD28 (1A7_L1.71_H1.1, 96 nM [S-S]) 1+1 Fab-scFv-Fc
- 44669 CEA-A H1L1 x CD28 (1A7_H1.14_L1.71, 37 nM [S-S]) 1+1 Fab-scFv-Fc

Figure 67

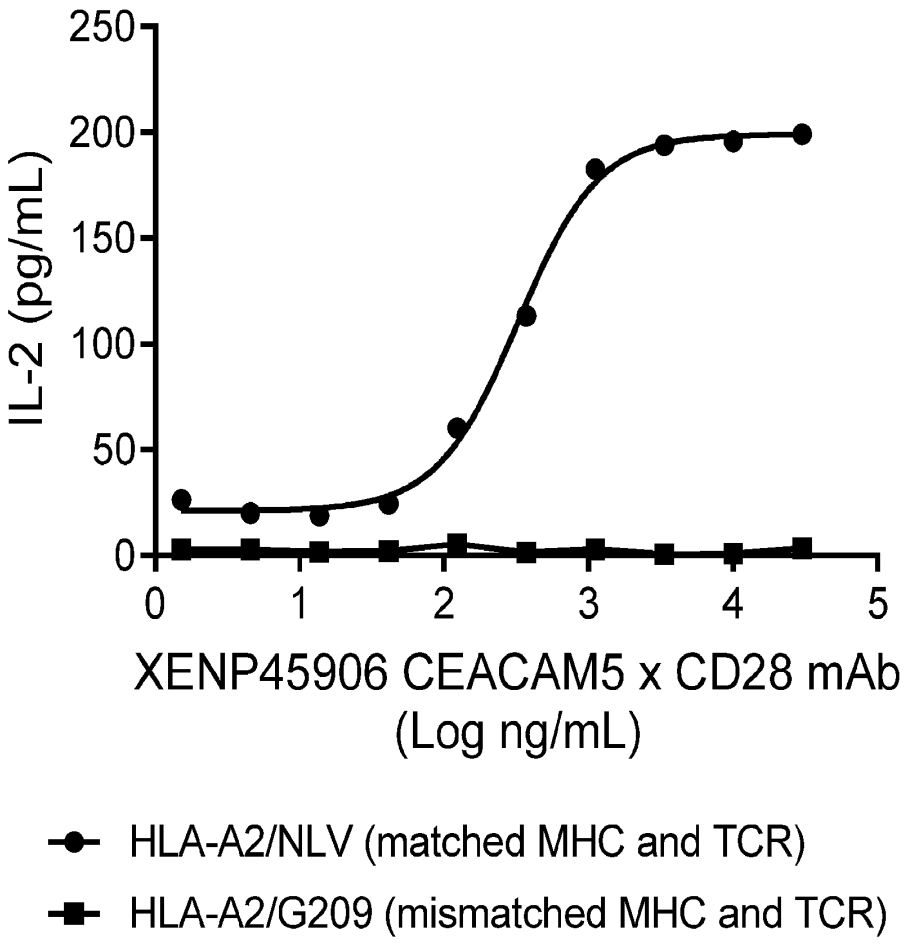

250
200
150
100
50
0
IL-2 (pg/mL)
0
1
2
3
4
5
XENP45906 CEACAM5 x CD28 mAb
(Log ng/mL)
HLA-A2/NLV (matched MHC and TCR)
HLA-A2/G209 (mismatched MHC and TCR)

Figure 68

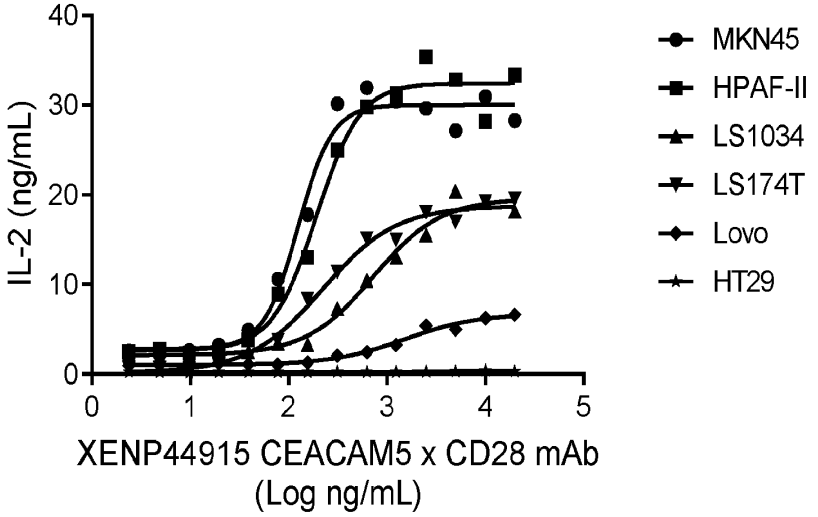
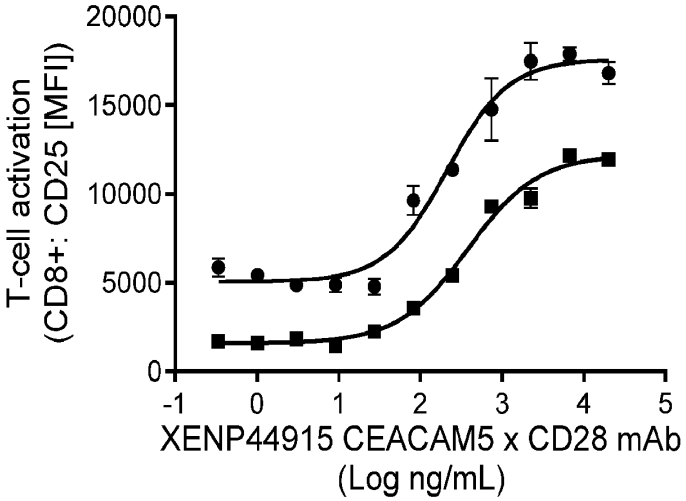

40
30
20
10
0
IL-2 (ng/mL)
0
1
2
3
4
5
XENP44915 CEACAM5 x CD28 mAb
(Log ng/mL)
MKN45
HPAF-II
LS1034
LS174T
Lovo
HT29

Figure 69A-69B

A)



B)

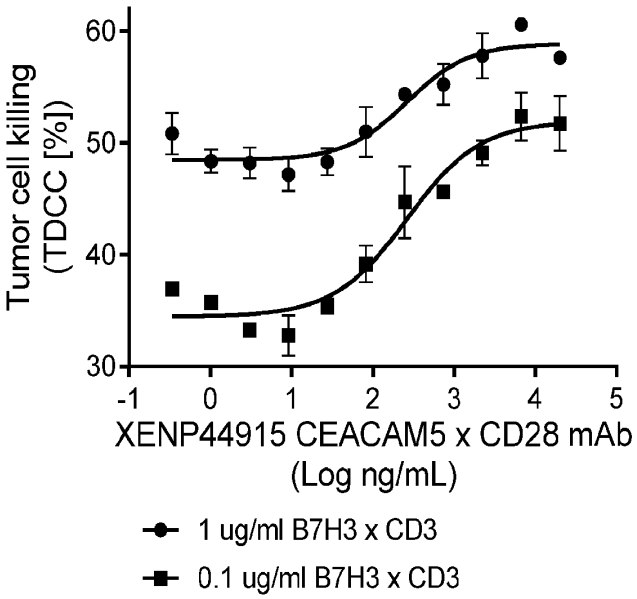
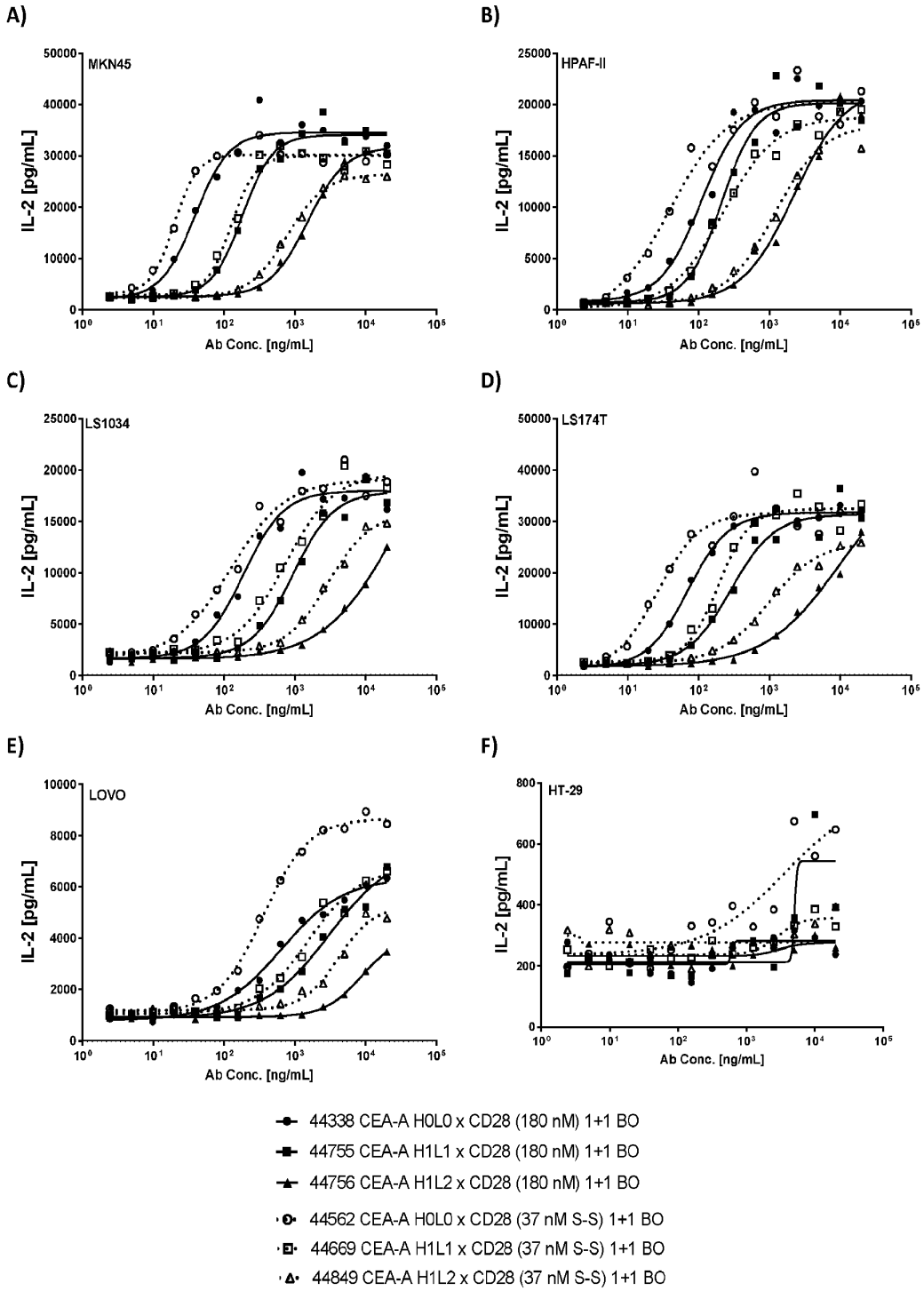


Figure 70A-70F



Figures 71A-71D

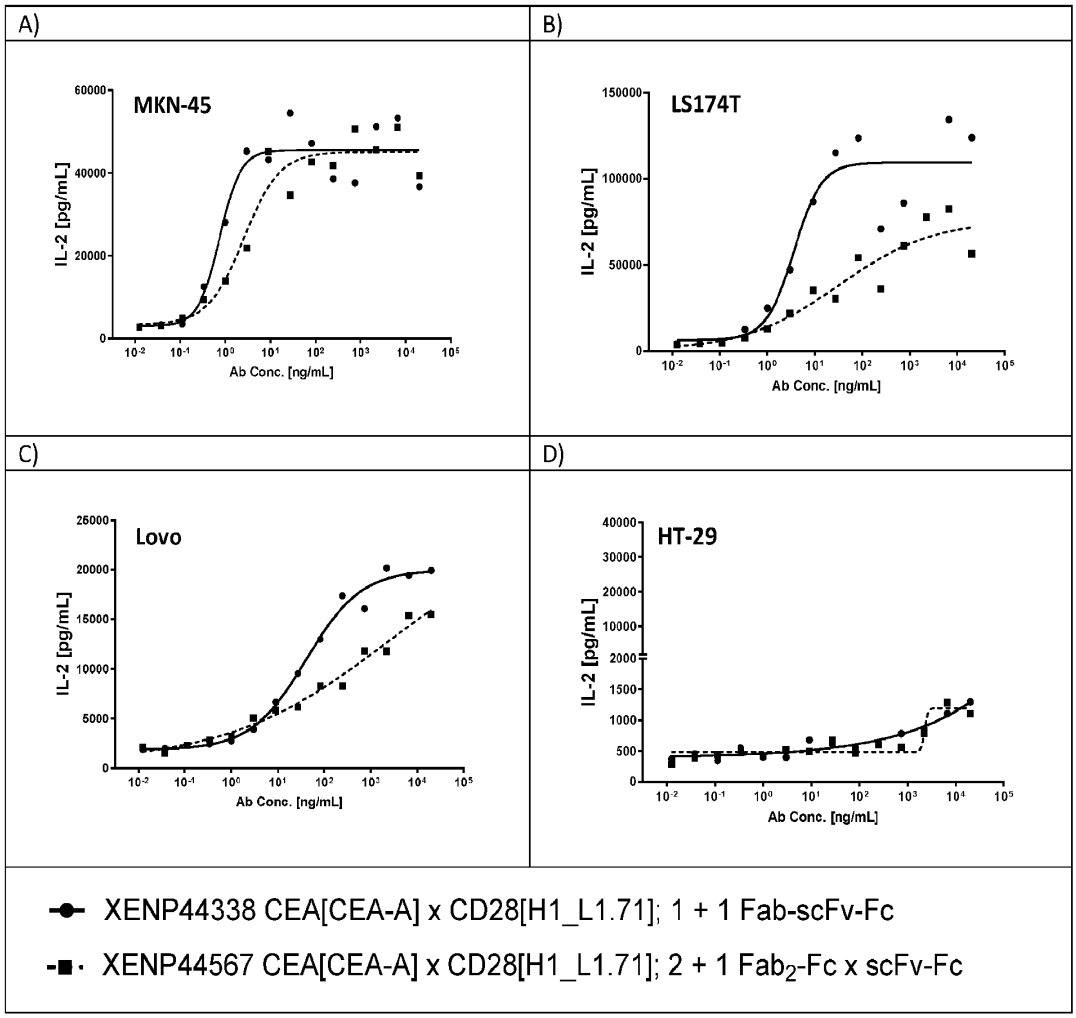
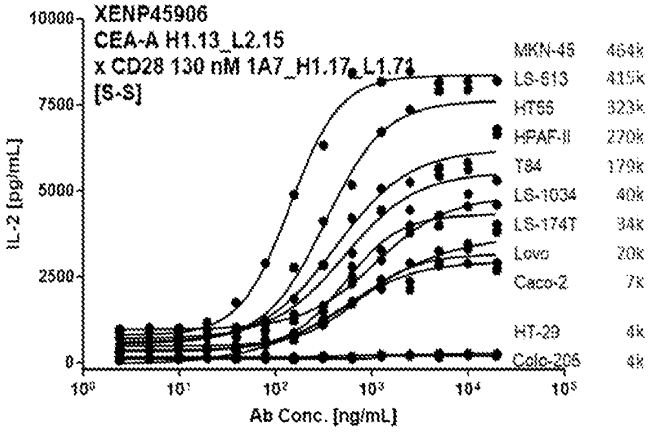


Figure 72A-72B

A)



B)

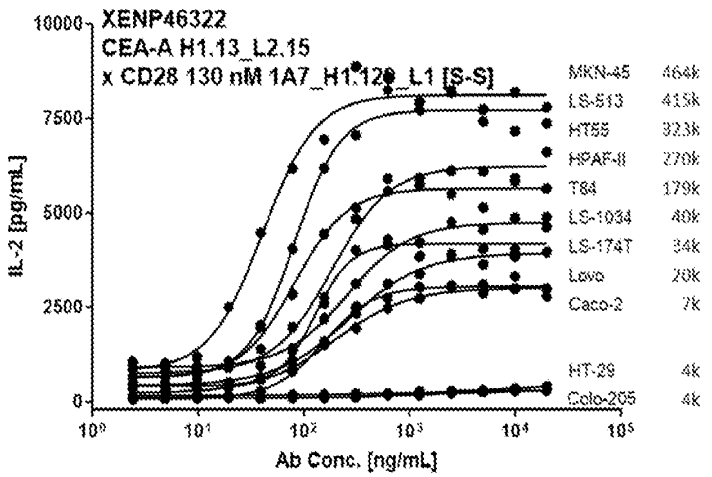


Figure 73

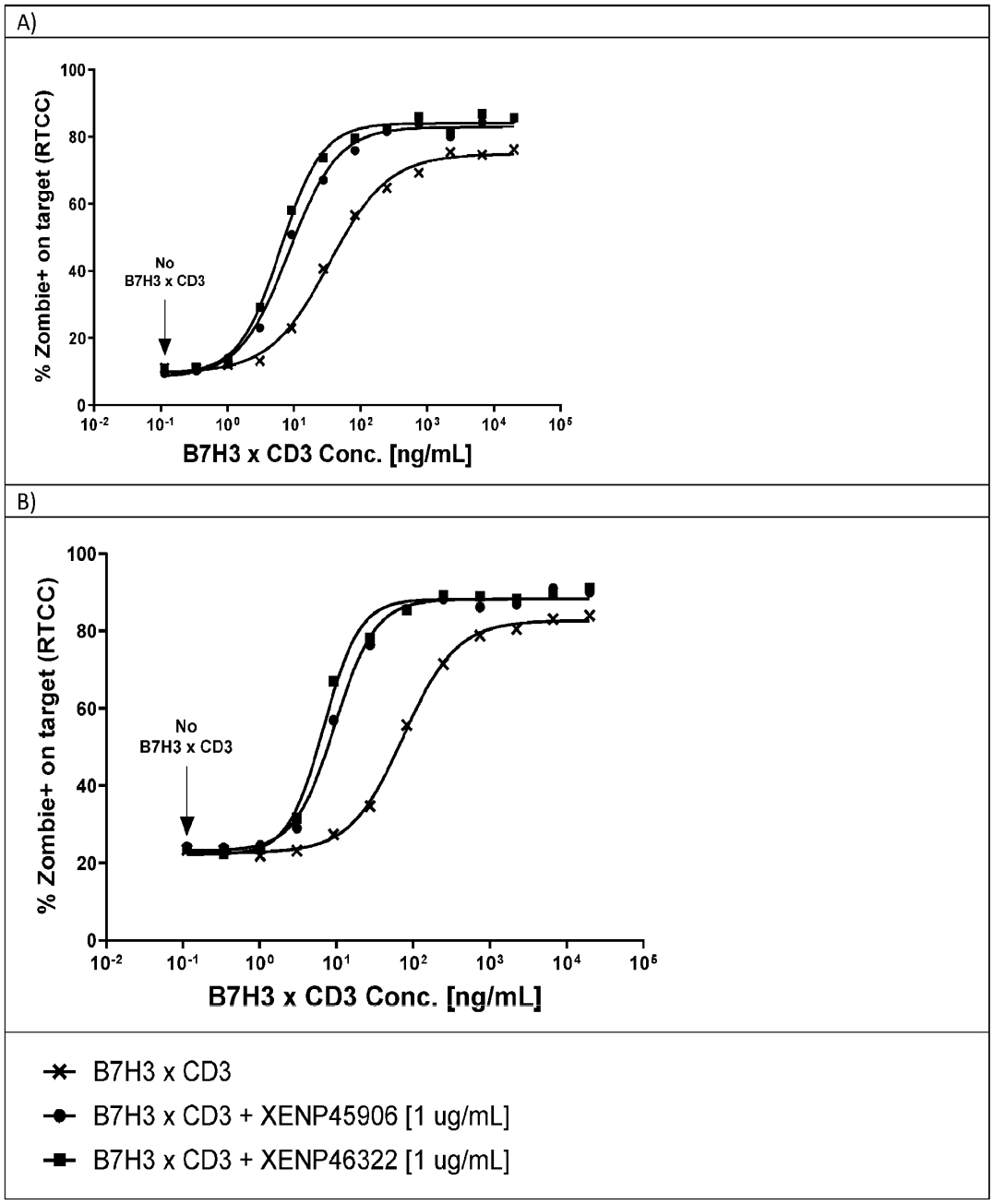

A)
% Zombie+ on target (RTCC)
100
80
60
40
20
0
No
B7H3 x CD3
10-2
10-1
100
101
102
103
104
105
B7H3 x CD3 Conc. [ng/mL]
B)
% Zombie+ on target (RTCC)
100
80
60
40
20
0
No
B7H3 x CD3
10-2
10-1
100
101
102
103
104
105
B7H3 x CD3 Conc. [ng/mL]
B7H3 x CD3
B7H3 x CD3 + XENP45906 [1 ug/mL]
B7H3 x CD3 + XENP46322 [1 ug/mL]

Figure 74

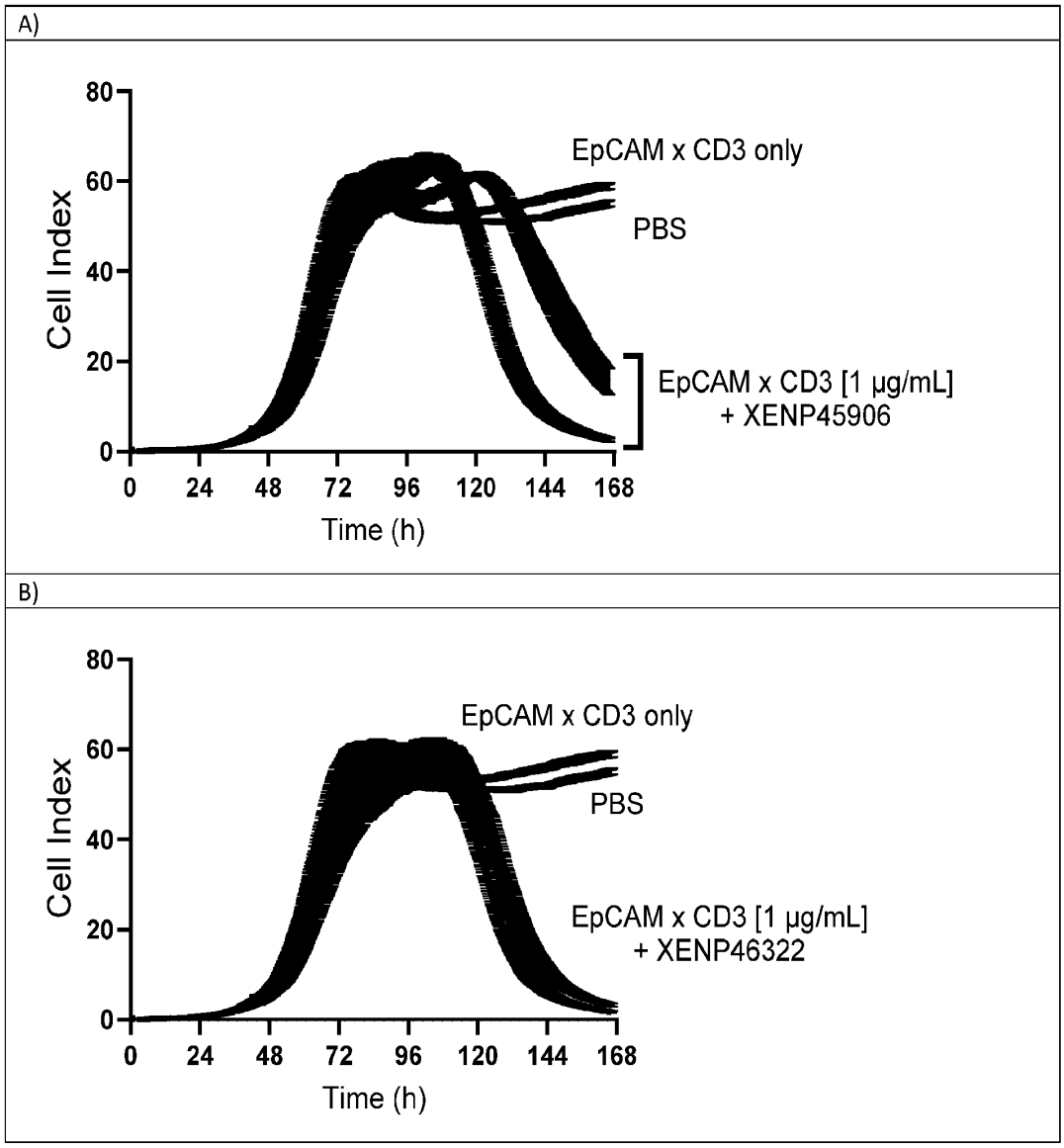

A)
Cell Index
80
60
40
20
0
0 24 48 72 96 120 144 168
Time (h)
EpCAM x CD3 only
PBS
EpCAM x CD3 [1 µg/mL]
+ XENP45906
B)
Cell Index
80
60
40
20
0
0 24 48 72 96 120 144 168
Time (h)
EpCAM x CD3 only
PBS
EpCAM x CD3 [1 µg/mL]
+ XENP46322

Figure 75

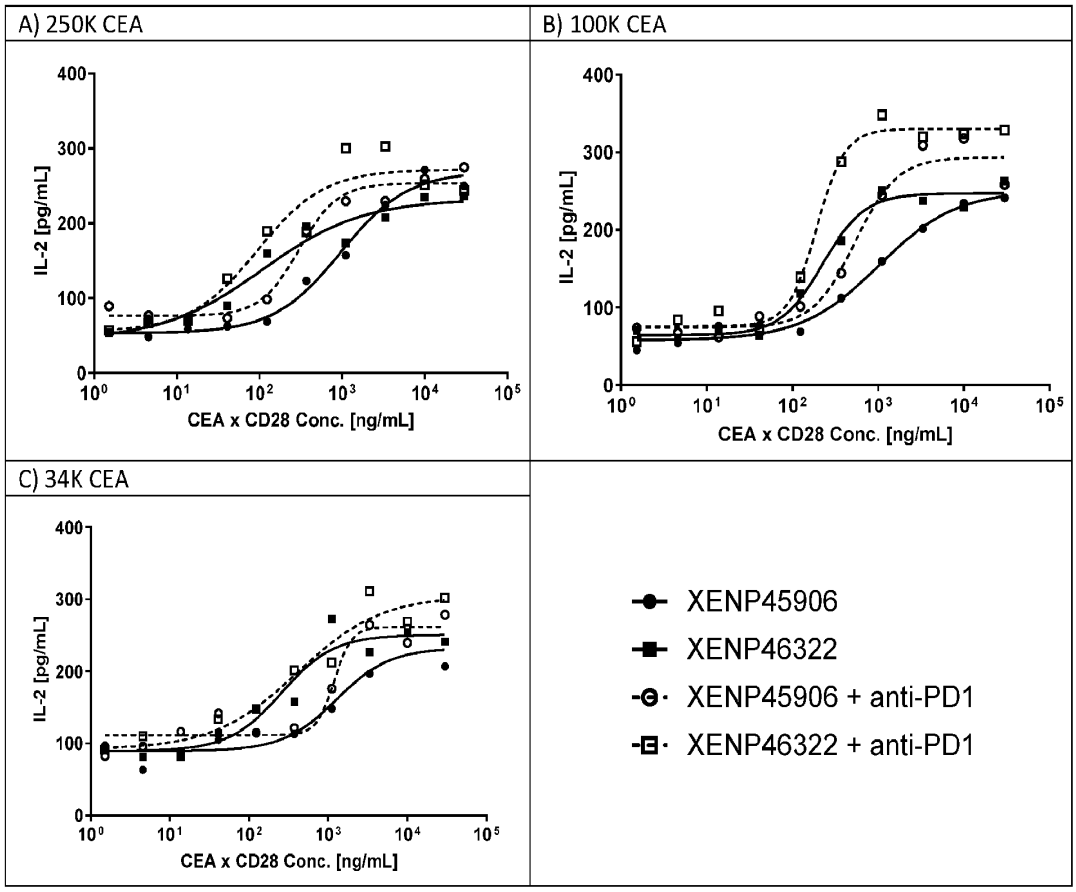
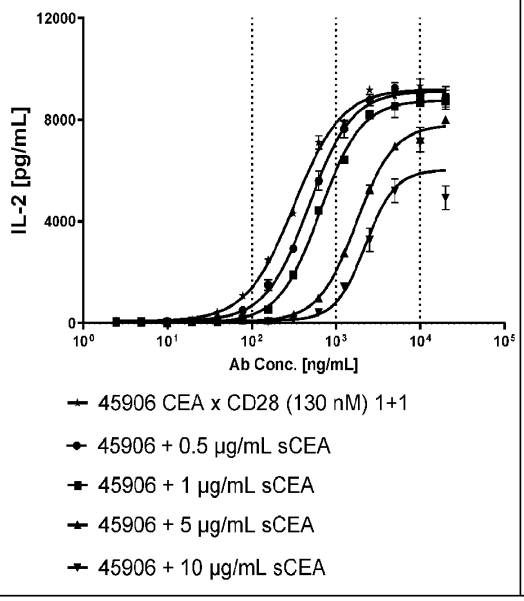
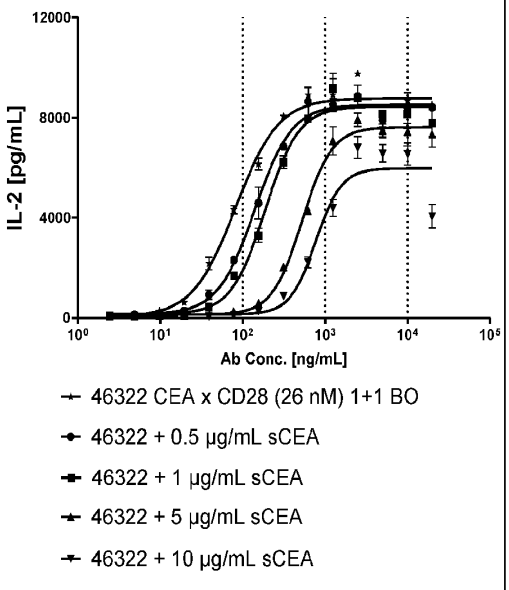

A) 250K CEA
B) 100K CEA
C) 34K CEA
IL-2 [pg/mL]
CEA x CD28 Conc. [ng/mL]
XENP45906
XENP46322
XENP45906 + anti-PD1
XENP46322 + anti-PD1

Figure 76

A)



B)

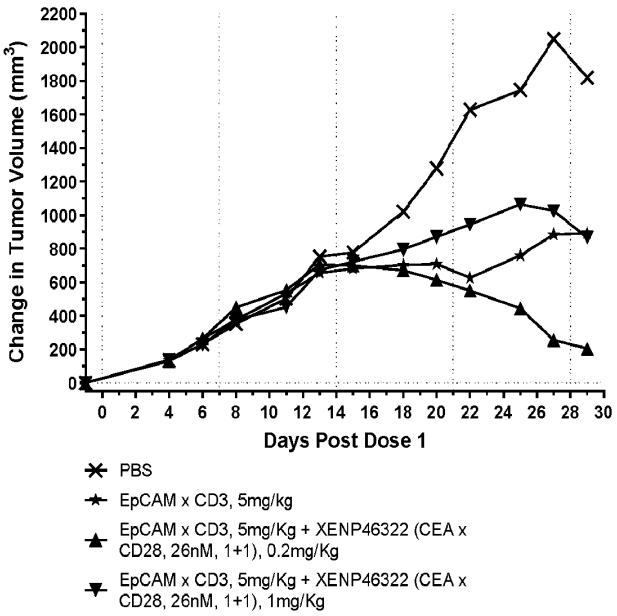


C)

	46322 CEA x CD28 (26 nM)		45906 CEA x CD28 (130 nM)	
	EC50 [ng/mL]	**Fold Change**	**EC50 [ng/mL]**	**Fold Change**
No sCEA	82.22	1.00	318.4	1.00
0.5 µg/mL sCEA	140.9	1.71	476	1.49
1 µg/mL sCEA	187.2	2.28	647.6	2.03
5 µg/mL sCEA	527.5	6.42	1741	5.47
10 µg/mL sCEA	772.3	9.39	2239	7.03

Figure 77

A)


Change in Tumor Volume (mm3)
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
Days Post Dose 1
PBS
EpCAM x CD3, 5mg/kg
EpCAM x CD3, 5mg/Kg + XENP46322 (CEA x CD28, 26nM, 1+1), 0.2mg/Kg
EpCAM x CD3, 5mg/Kg + XENP46322 (CEA x CD28, 26nM, 1+1), 1mg/Kg

B)

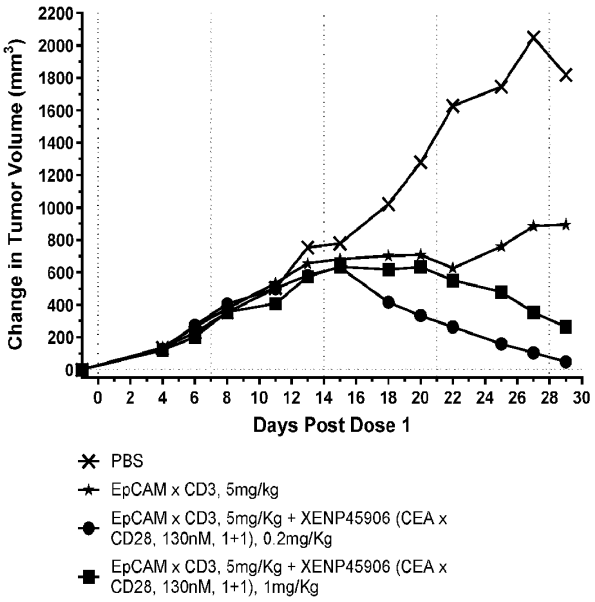

Change in Tumor Volume (mm3)
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
Days Post Dose 1
PBS
EpCAM x CD3, 5mg/kg
EpCAM x CD3, 5mg/Kg + XENP45906 (CEA x CD28, 130nM, 1+1), 0.2mg/Kg
EpCAM x CD3, 5mg/Kg + XENP45906 (CEA x CD28, 130nM, 1+1), 1mg/Kg

Figure 78

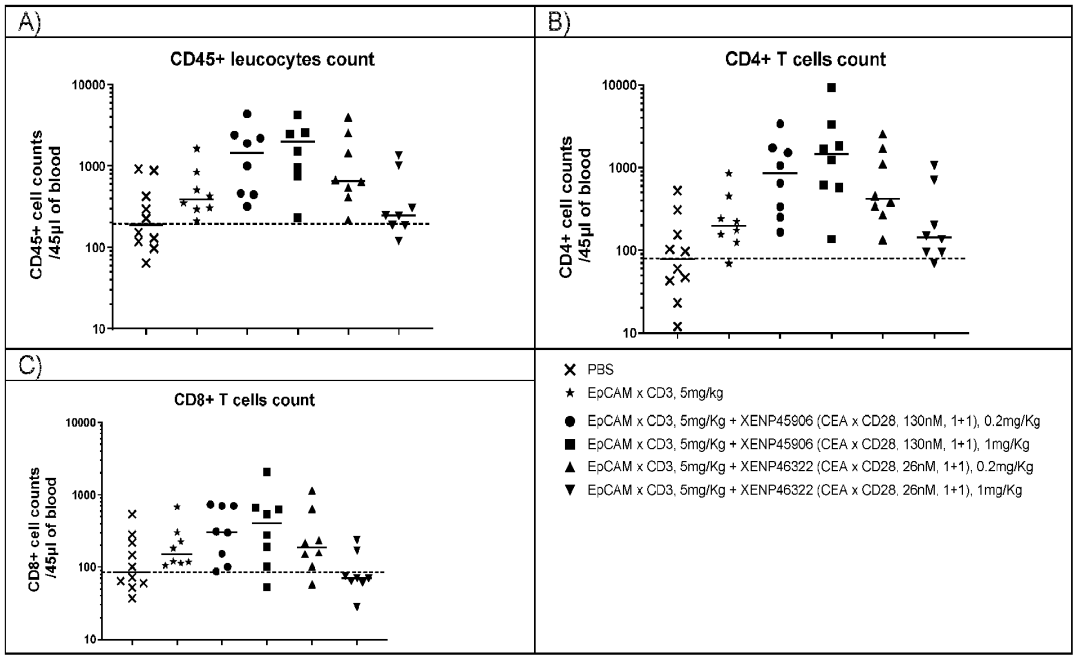

A)
CD45+ leucocytes count
CD45+ cell counts /45µl of blood
10000
1000
100
10
B)
CD4+ T cells count
CD4+ cell counts /45µl of blood
10000
1000
100
10
C)
CD8+ T cells count
CD8+ cell counts /45µl of blood
10000
1000
100
10
PBS
EpCAM x CD3, 5mg/kg
EpCAM x CD3, 5mg/Kg + XENP45906 (CEA x CD28, 130nM, 1+1), 0.2mg/Kg
EpCAM x CD3, 5mg/Kg + XENP45906 (CEA x CD28, 130nM, 1+1), 1mg/Kg
EpCAM x CD3, 5mg/Kg + XENP46322 (CEA x CD28, 26nM, 1+1), 0.2mg/Kg
EpCAM x CD3, 5mg/Kg + XENP46322 (CEA x CD28, 26nM, 1+1), 1mg/Kg

Figure 79

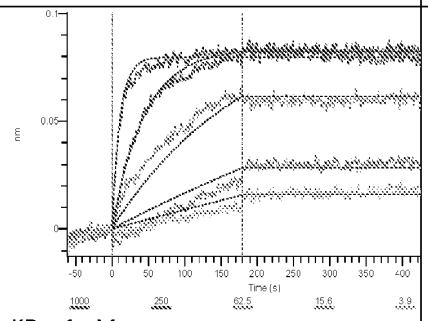
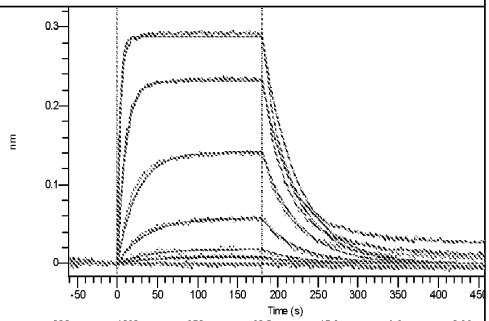
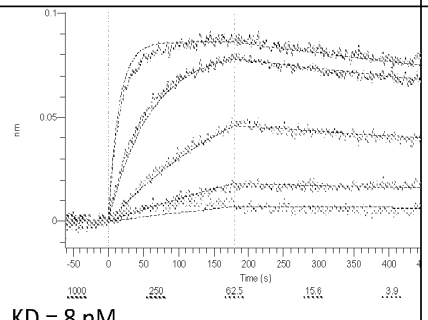
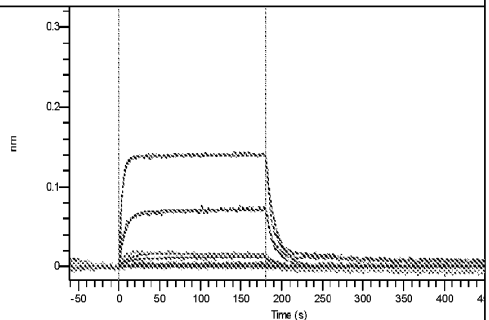
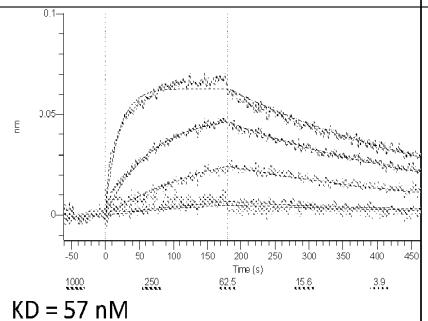
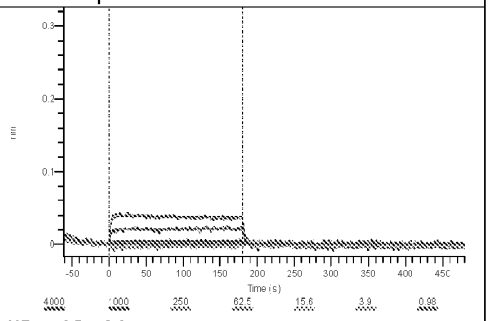
	CEACAM5	CEACAM8
XENP44560 CEA-A H0L0	 KD < 1 nM	 KD = 310 nM
XENP44755 CEA-A H1L1	 KD = 8 nM	 KD = 1.8 µM
XENP44756 CEA-A H1L2	 KD = 57 nM	 KD ~ 10 µM

Figure 80

XENP	CEA-A Variant	CEACAM5 KD (nM)	CEACAM8 KD (nM)
44915	H1.7_L2.15	15	3330
45905	H1.12_L2.15	17	6336
45906	H1.13_L2.15	18	10890
45907	H1.17_L2.15	16	7646
45908	H1.49_L2.15	15	2957
45912	H1.17_L2.67	9	2966
45933	H1.49_L2.67	12	4090

Figure 81

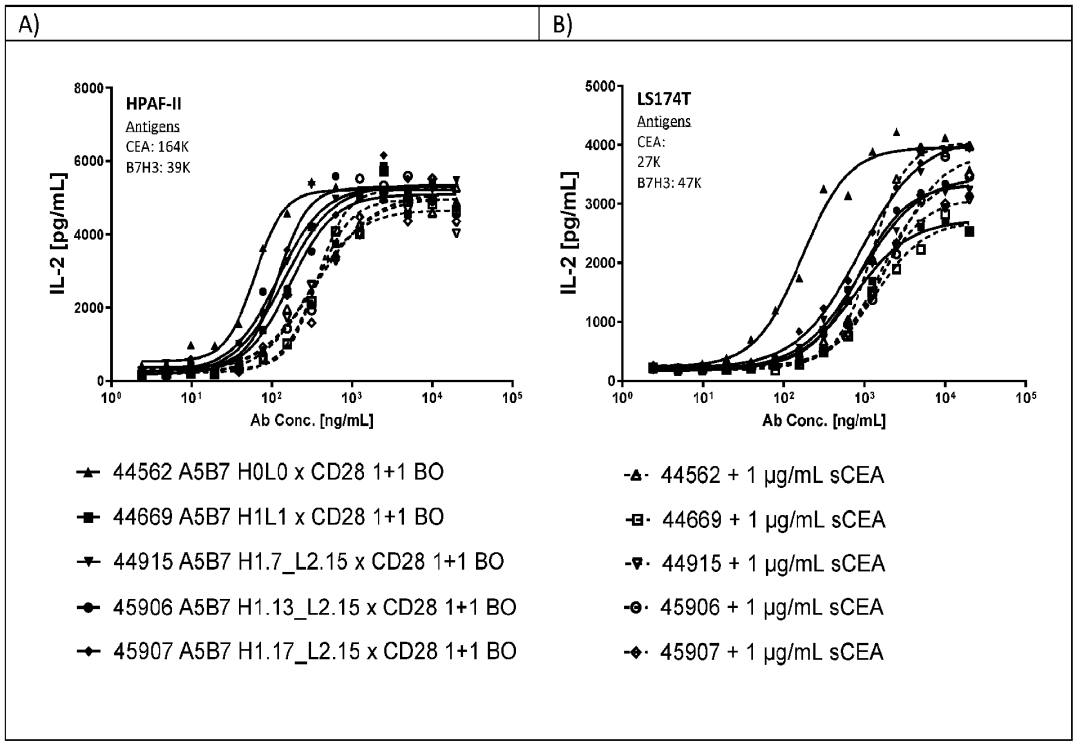

A)
B)
HPAF-II
Antigens
CEA: 164K
B7H3: 39K
IL-2 [pg/mL]
Ab Conc. [ng/mL]
LS174T
Antigens
CEA:
27K
B7H3: 47K
44562 A5B7 H0L0 x CD28 1+1 BO
44669 A5B7 H1L1 x CD28 1+1 BO
44915 A5B7 H1.7_L2.15 x CD28 1+1 BO
45906 A5B7 H1.13_L2.15 x CD28 1+1 BO
45907 A5B7 H1.17_L2.15 x CD28 1+1 BO
44562 + 1 µg/mL sCEA
44669 + 1 µg/mL sCEA
44915 + 1 µg/mL sCEA
45906 + 1 µg/mL sCEA
45907 + 1 µg/mL sCEA

Figure 82

IGKV1-39 Germline VL

	sequence	**SEQ ID NO:**
Variable light (vl) domain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST PYTFGQGTKLEIK	2679
vlCDR1	RASQSISSYLN	2680
vlCDR2	AASSLQS	2681
vlCDR3	QQSYSTPYT	2682