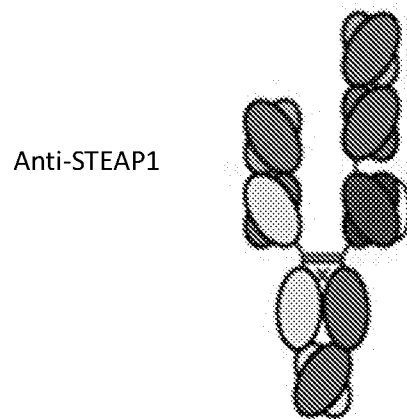


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FIGURE 1**FIGURE 2**

MQSGTHWRVLGLCLLSVGWVGQDGNEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDE
DDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDVMSVATIVIVDICITGG
LLLLVYYWSKNRKAKAKPVTRGAGAGGRQRGQNKERPPPVPNPDYEPKRGQRDLYSGLNQRRRI (**SEQ ID
NO: 1**)

FIGURE 3

MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAAHADEFDCPSE
LQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPM
VSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSL
SYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPS
VSDSLTWREFHYIQSKLGIVSLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIV
VLIFKSILFLPCLRKKILKIRHGWEDVTKINKTEICSQL (**SEQ ID NO: 2**)

FIGURE 4A

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

FIGURE 4B

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

FIGURE 4C

Monomer 1	Monomer 2
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 4D

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 4E

Monomer 1	Monomer 2
K392D/K409D	E356K/D399K
K370D/K392D/K409D	E356K/E357K/D399K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/N384S/K392N/V397M/Q419E/K447_	Q196K/I199T/N276K
N384S/K392N/V397M/Q419E	N276K
D221E/P228E/L368E	D221R/P228R/K409R
C220E/P228E/L368E	C220R/E224R/P228R/K409R
F405L	K409R
T366I/K392M/T394W	F405A/Y407V
T366V/K409F	L351Y/Y407A
T366A/K392E/K409F/T411E	D399R/S400R/Y407A
L351K	L351E
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/P217R/P228R/N276K
I199T/N203D/K247Q/R355Q/Q419E/K447_	Q196K/I199T/N276K
I199T N203D K274Q R355Q N384S K392N V397M Q419E DEL447	
N208D Q295E N384D Q418E N421D	
N208D Q295E Q418E N421D	
Q196K I199T P217R P228R N276K	
Q196K I199T N276K	
E269Q E272Q E283Q E357Q	
E269Q E272Q E283Q	
E269Q E272Q	
E269Q E283Q	
E272Q E283Q	
E269Q	

FIGURE 5

pI variants

<u>Variant constant region</u>	<u>Substitutions</u>
pI_ISO(-)	I199T N203D K274Q R355Q N384S K392N V397M Q419E DEL447
pI_(-)_isosteric_A	N208D Q295E N384D Q418E N421D
pI_(-)_isosteric_B	N208D Q295E Q418E N421D
pI_ISO(+RR)	Q196K I199T P217R P228R N276K
pI_ISO(+)	Q196K I199T 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 6

Ablation variants

Variant	Variant(s), cont.
G236R	P329K
S239G	A330L
S239K	A330S/P331S
S239Q	I332K
S239R	I332R
V266D	V266D/A327Q
S267K	V266D/P329K
S267R	S267R/A327Q
H268K	S267R/P329K
E269R	G236R/L328R
299R	E233P/L234V/L235A/G236del/S239K
299K	E233P/L234V/L235A/G236del/S267K
K322A	E233P/L234V/L235A/G236del/S239K/A327G
A327G	E233P/L234V/L235A/G236del/S267K/A327G
A327L	E233P/L234V/L235A/G236del
A327N	S239K/S267K
A327Q	267K/P329K
L328E	
L328R	
P329A	
P329H	

FIGURE 7**scFv monomer (+)****Heterodimerization skew variants
S364K/E357Q****Optional scFv charged linker including
but not limited to (GKPGS)₄****FcKO
E233P/L234V/L235A/G236del/S267K****± 428L/434S for FcRn****scFv of anti-CD3****Fab monomer (-)****Heterodimerization skew variants L368D/K370S****Isosteric pl substitutions
N208D/Q295E/N384D/Q418E/N421D****FcKO E233P/L234V/L235A/G236del/S267K****± 428L/434S for FcRn****Fv sequences for anti-STEAP1****scFv monomer****Heterodimerization skew variants
S364K/E357Q****Optional scFv charged linker including,
but not limited to (GKPGS)₄****FcKO
E233P/L234V/L235A/G236del/S267K****± 428L/434S for FcRn (optional)****scFv of anti-CD3****Fab monomer****Heterodimerization skew variants L368D/K370S****pl substitutions I199T N203D K274Q R355Q Q419E K447del****FcKO E233P/L234V/L235A/G236del/S267K****± 428L/434S for FcRn (optional)****scFv of anti-STEAP1**

FIGURE 8A**Positive charged scFv linkers**

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGS GGGGS GGGGS	15	0	143
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	144
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	145
+B	GKGGSGKGGSGKGGG	15	+3	146
+C	GGKGS GGKGS GGKGS	15	+3	147
+D	GGGKS GGGKS GGGKS	15	+3	148
+E	GKGKSGKGKSGKGKS	15	+6	149
+F	GGGKS GGKGS GKGGG	15	+3	150
+G	GKPGSGKPGSGKPGS	15	+3	151
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	152
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	153

Negative charged scFv linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGS GGGGS GGGGS GGGGS	20	0	154
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	155
-B	GEGGS GEGGS GEGGS	15	-3	156
-C	GGEGS GEGS GGEGS	15	-3	157
-D	GGGES GGGES GGGES	15	-3	158
-E	GEGES GEGES GEGES	15	-6	159
-F	GGGES GGGES GEGGS	15	-3	160
-G	GEGES GEGES GEGES GEGES	20	-8	161

FIGURE 8B**scFv Linkers**

GGGGSGGGSGGGGS	(SEQ ID NO: 162)
GGGGSGGGSGGGSGGGGS	(SEQ ID NO: 163)
GSTSGSGKPGSGEGSTKG	(SEQ ID NO: 164)
PRGASKSGSASQTGSAPGS	(SEQ ID NO: 165)
GTAAAGAGAAGGAAAGAAG	(SEQ ID NO: 166)
GTSGSSGSGSGSGSGGGG	(SEQ ID NO: 167)
GKPGSGKPGSGKPGSGKPGS	(SEQ IS NO: 168)

Useful domain linkers

KTHTCPPCP ("half hinge")	SEQ ID NO:210
EPKSSDKTHTCPPCP ("full hinge C220S variant")	SEQ ID NO:211
GGGGSGGGSGKTHTCPPCP ("flex half hinge")	SEQ ID NO:212
GKPGSGKPGSKTHTCPPCP ("charged half hinge1")	SEQ ID NO:213
GKPGSKTHTCPPCP ("charged half hinge2")	SEQ ID NO:214

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FIGURE 9

XENP	Heterodimer-skewing variant, Chain 1	Heterodimer-skewing variant, Chain 2	Heterodimer Yield (%)	CH3 Tm (°C)
12757	none	none	52.7	83.1
12758	L368D/K370S	S364K	94.4	76.6
12759	L368D/K370S	S364K/E357L	90.2	77.2
12760	L368D/K370S	S364K/E357Q	95.2	77.5
12761	T411E/K360E/Q362E	D401K	85.6	80.6
12496	L368E/K370S	S364K	91.5	n.d.
12511	K370S	S364K	59.9	n.d.
12840	L368E/K370S	S364K/E357Q	59.5	n.d.
12841	K370S	S364K/E357Q	90.4	n.d.
12894	L368E/K370S	S364K	41.0	n.d.
12895	K370S	S364K	49.3	n.d.
12896	L368E/K370S	S364K/E357Q	73.9	n.d.
12901	K370S	S364K/E357Q	87.9	n.d.

FIGURE 10A

VH ID	VL ID	VH Substitutions	VL Substitutions
H1	L1.4		
H1.30	L1.47	N30S/N100D	Q42K/A43S/L75I/E85D/L95H
H1.33	L1.47	N30S/N100D/A101D	Q42K/A43S/L75I/E85D/L95H
H1.31	L1.47	N30S/N35S/N100D	Q42K/A43S/L75I/E85D/L95H
H1.32	L1.47	N30S/Y52CA/N100D	Q42K/A43S/L75I/E85D/L95H
H1.88	L1.47	N30S/N100P	Q42K/A43S/L75I/E85D/L95H
H1.89	L1.47	N30S/N100D/S100AE	Q42K/A43S/L75I/E85D/L95H
H1.90	L1.47	N30S/N100D/S100AP	Q42K/A43S/L75I/E85D/L95H
H1.91	L1.47	N30S/Y52CA/N100D	Q42K/A43S/L75I/E85D/L95H
H1.92	L1.47	N30S/Y58A/N100D	Q42K/A43S/L75I/E85D/L95H
H1.93	L1.47	N30S/N100E	Q42K/A43S/L75I/E85D/L95H
H1.94	L1.47	N30S/N100Q	Q42K/A43S/L75I/E85D/L95H
H1.96	L1.47	N30S/N100D/S100AN	Q42K/A43S/L75I/E85D/L95H
H1.97	L1.47	N30S/N100D/S100AQ	Q42K/A43S/L75I/E85D/L95H
H1.98	L1.47	N30S/Y52CA/N100D/A101D	Q42K/A43S/L75I/E85D/L95H
H1.99	L1.47	N30S/Y58A/N100D/A101D	Q42K/A43S/L75I/E85D/L95H
H1.100	L1.47	N30S/N100A/A101D	Q42K/A43S/L75I/E85D/L95H
H1.101	L1.47	N30S/N100Q/A101D	Q42K/A43S/L75I/E85D/L95H
H1.102	L1.47	N30S/N100D/S100AE/A101D	Q42K/A43S/L75I/E85D/L95H
H1.103	L1.47	N30S/N100D/S100AN/A101D	Q42K/A43S/L75I/E85D/L95H
H1.104	L1.47	N30S/N100D/S100AP/A101D	Q42K/A43S/L75I/E85D/L95H
H1.105	L1.47	N30S/N100D/S100AQ/A101D	Q42K/A43S/L75I/E85D/L95H

FIGURE 10B

VH ID	VL ID	VH Substitutions	VL Substitutions
H1.106	L1.47	N30S/Y52CA/Y58A/N100D	Q42K/A43S/L75I/E85D/L95H
H1.107	L1.47	N30S/Y52CA/Y58A/N100A	Q42K/A43S/L75I/E85D/L95H
H1.108	L1.47	N30S/Y52CA/Y58A/N100Q	Q42K/A43S/L75I/E85D/L95H
H1.109	L1.47	N30S/Y52CA/Y58A/N100D/A101D	Q42K/A43S/L75I/E85D/L95H

FIGURE 11

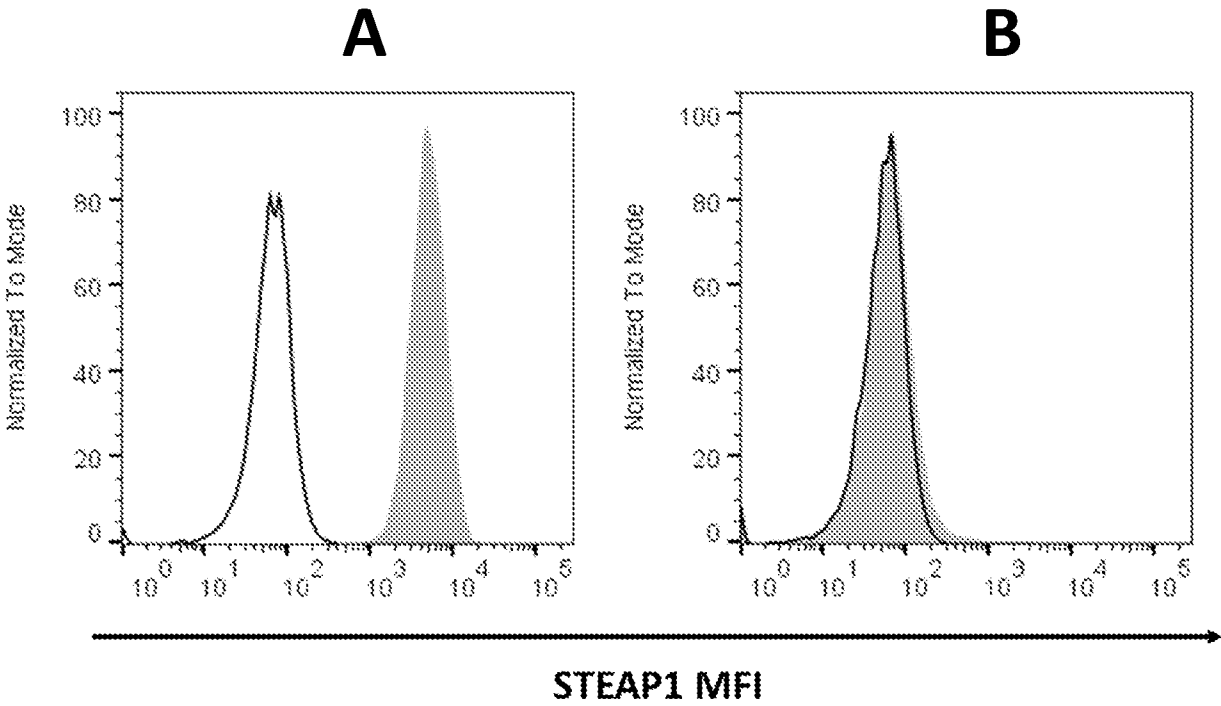


FIGURE 12A

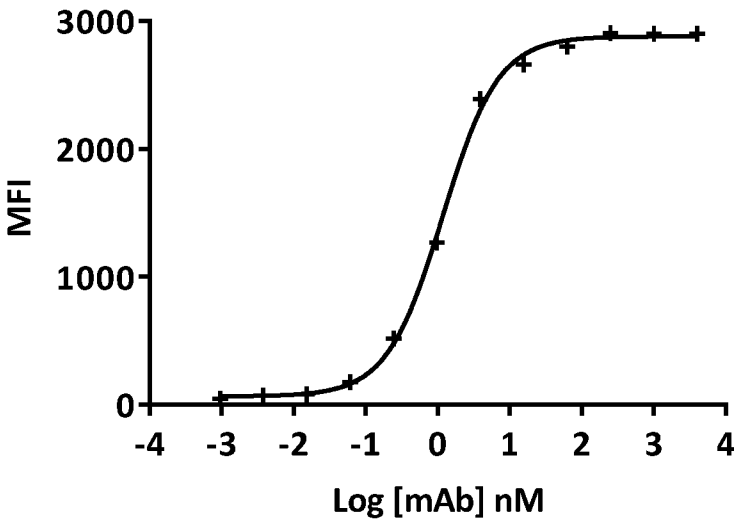


FIGURE 12B

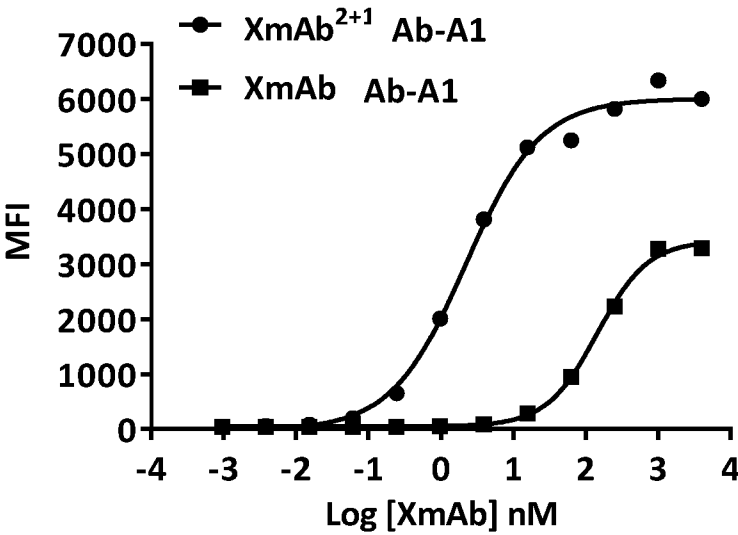


FIGURE 12C

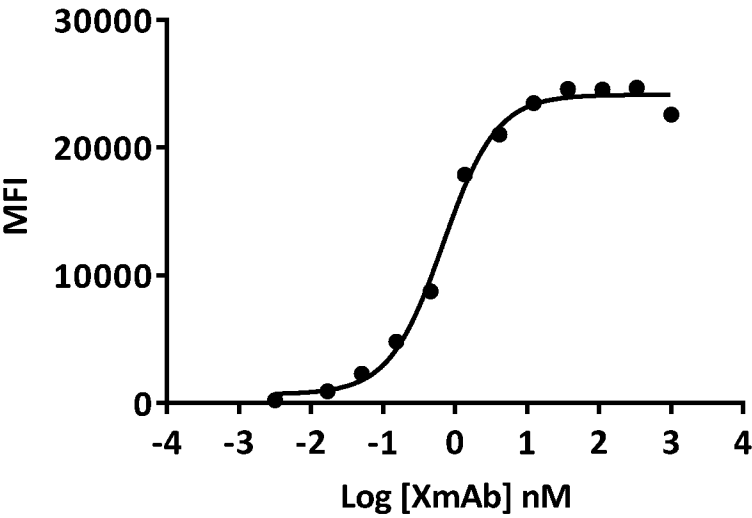


FIGURE 13

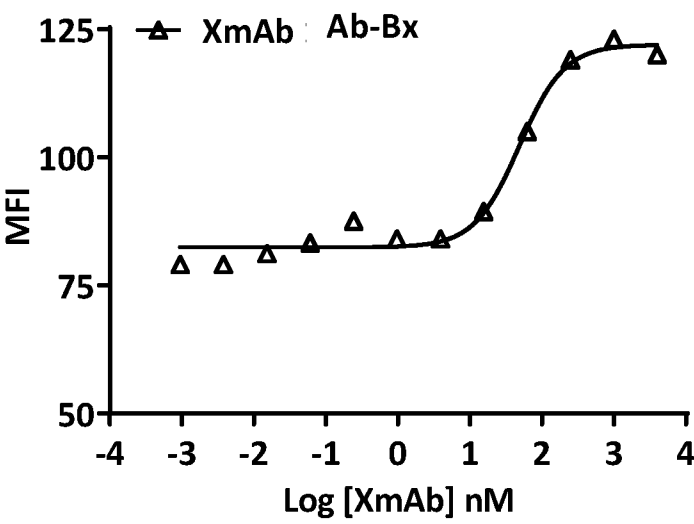


FIGURE 14

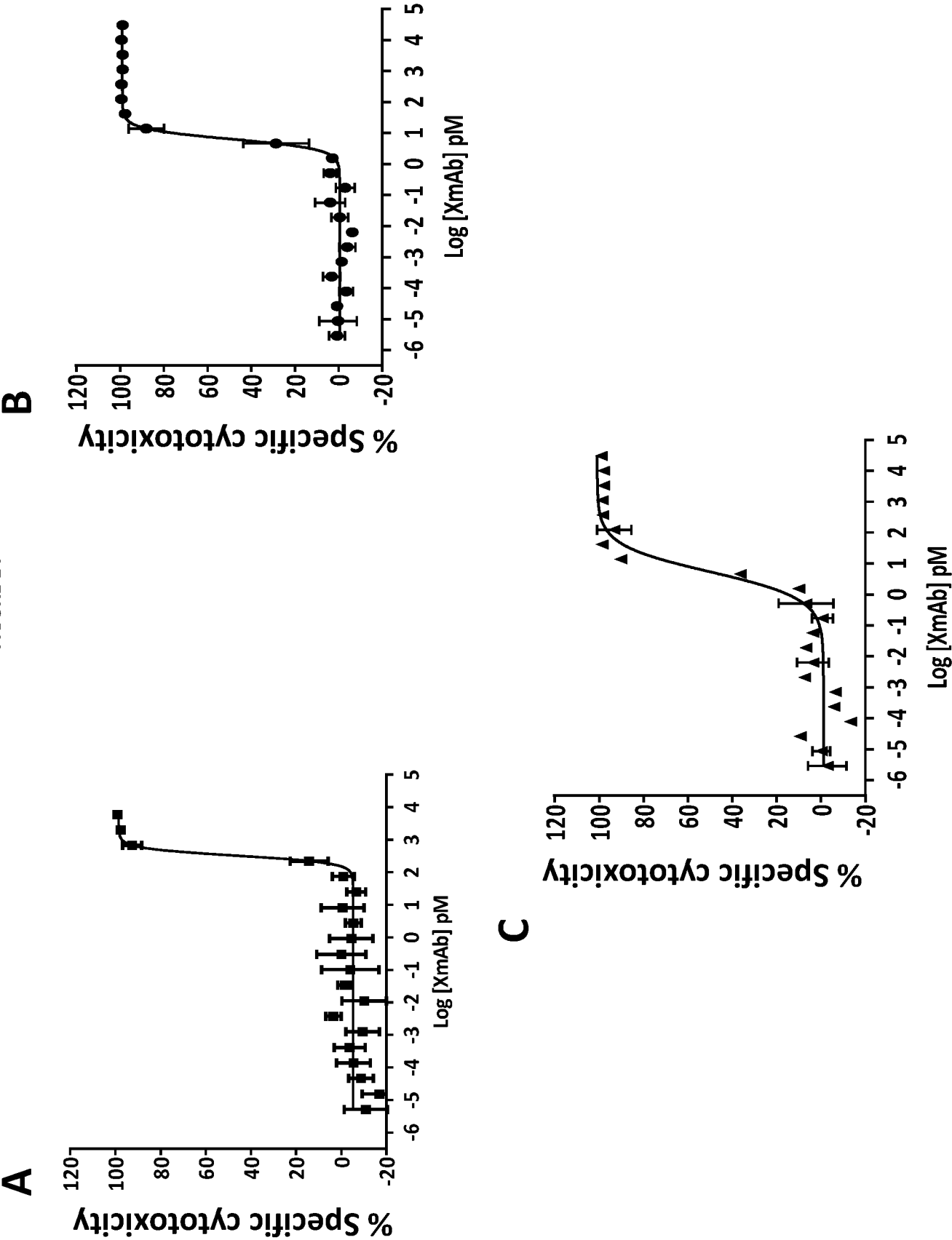


FIGURE 15

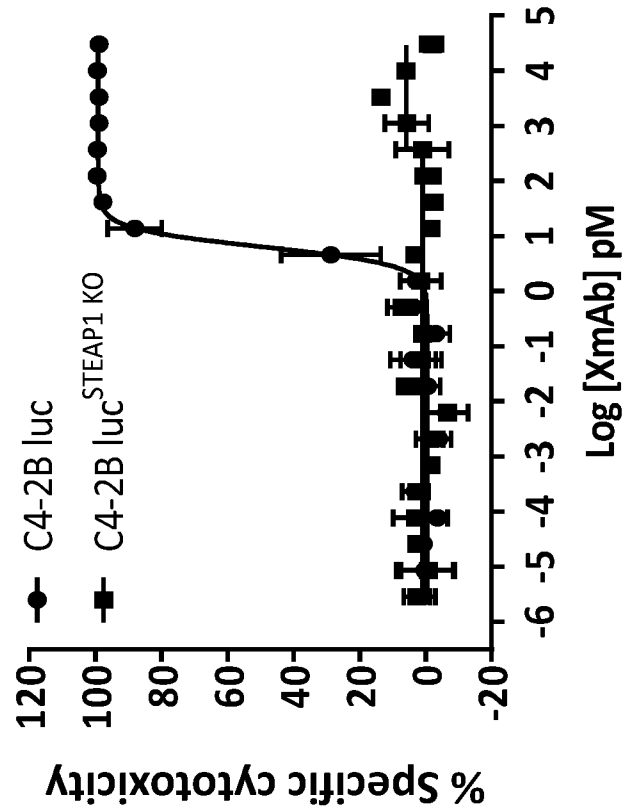


FIGURE 16

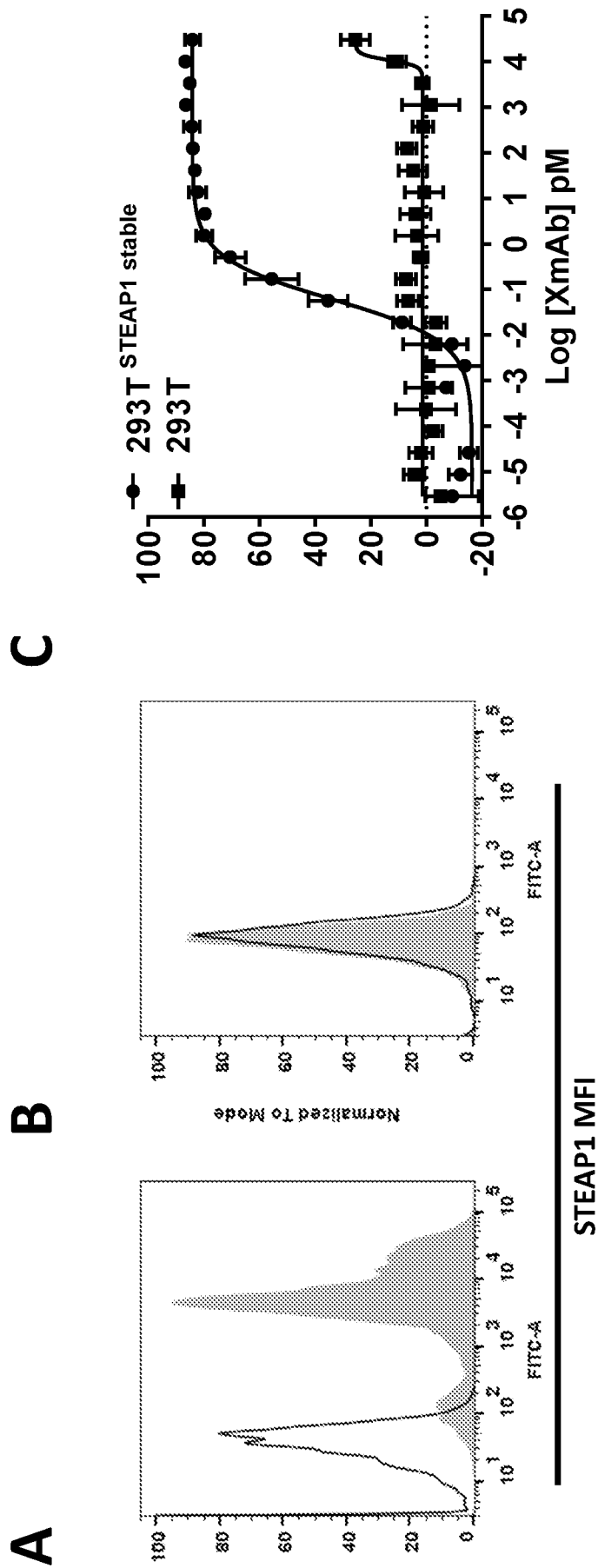


FIGURE 17

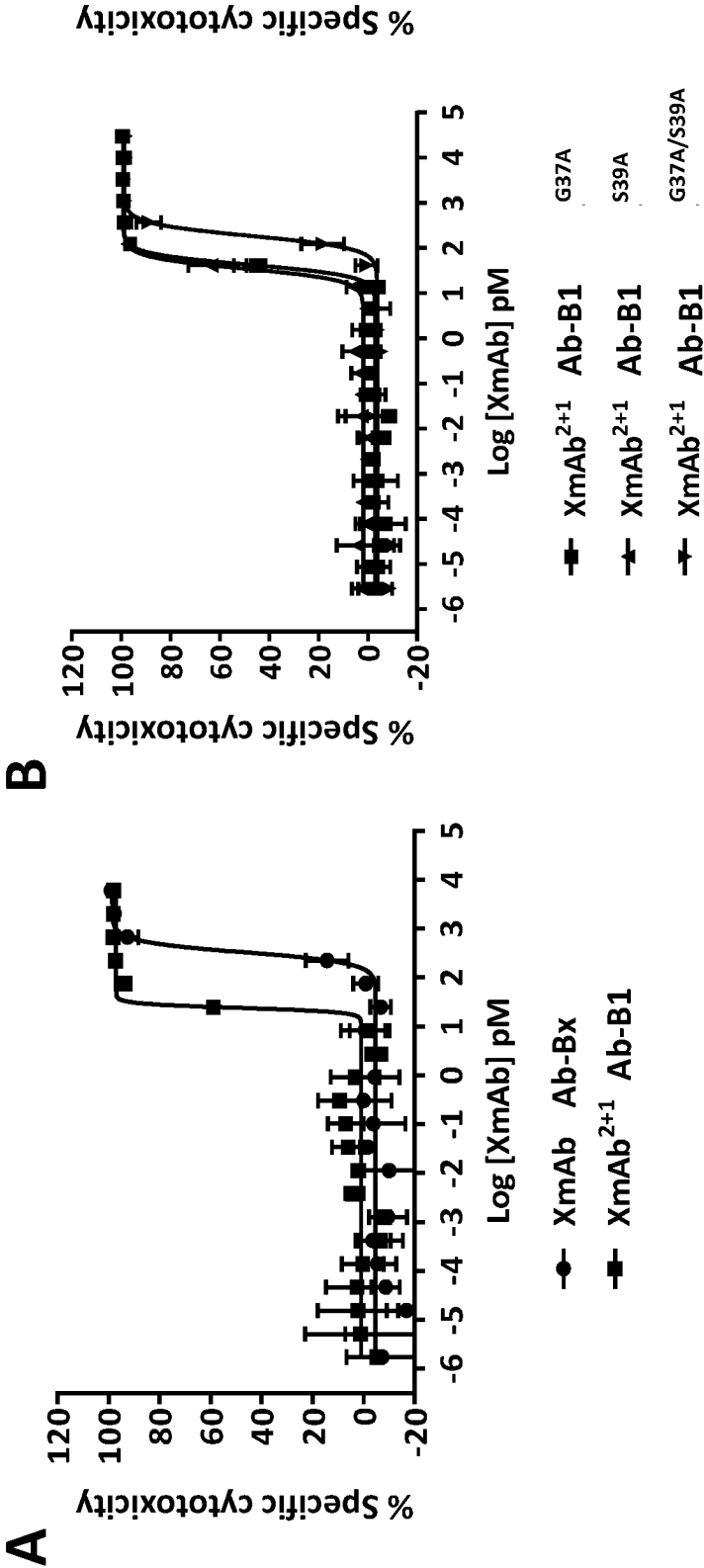


FIGURE 17C

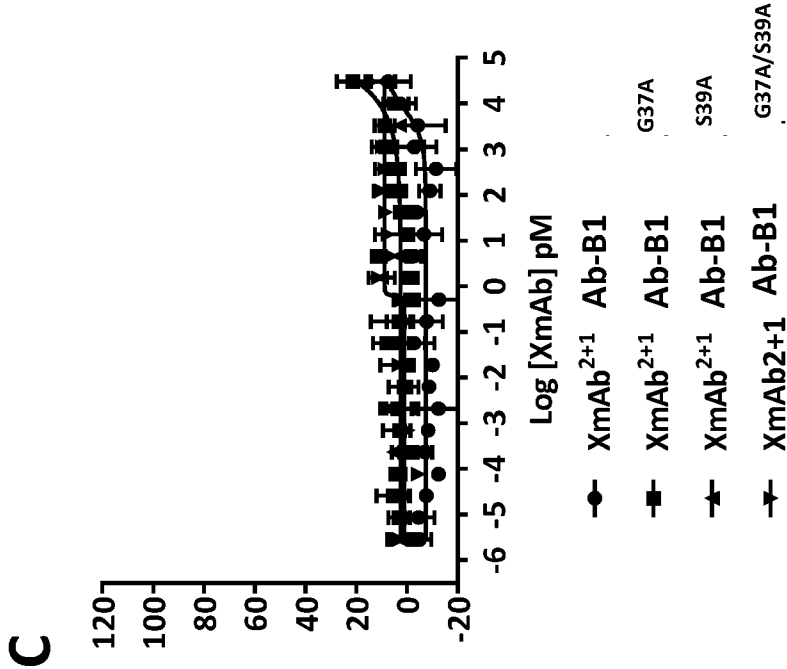


FIGURE 18A-E

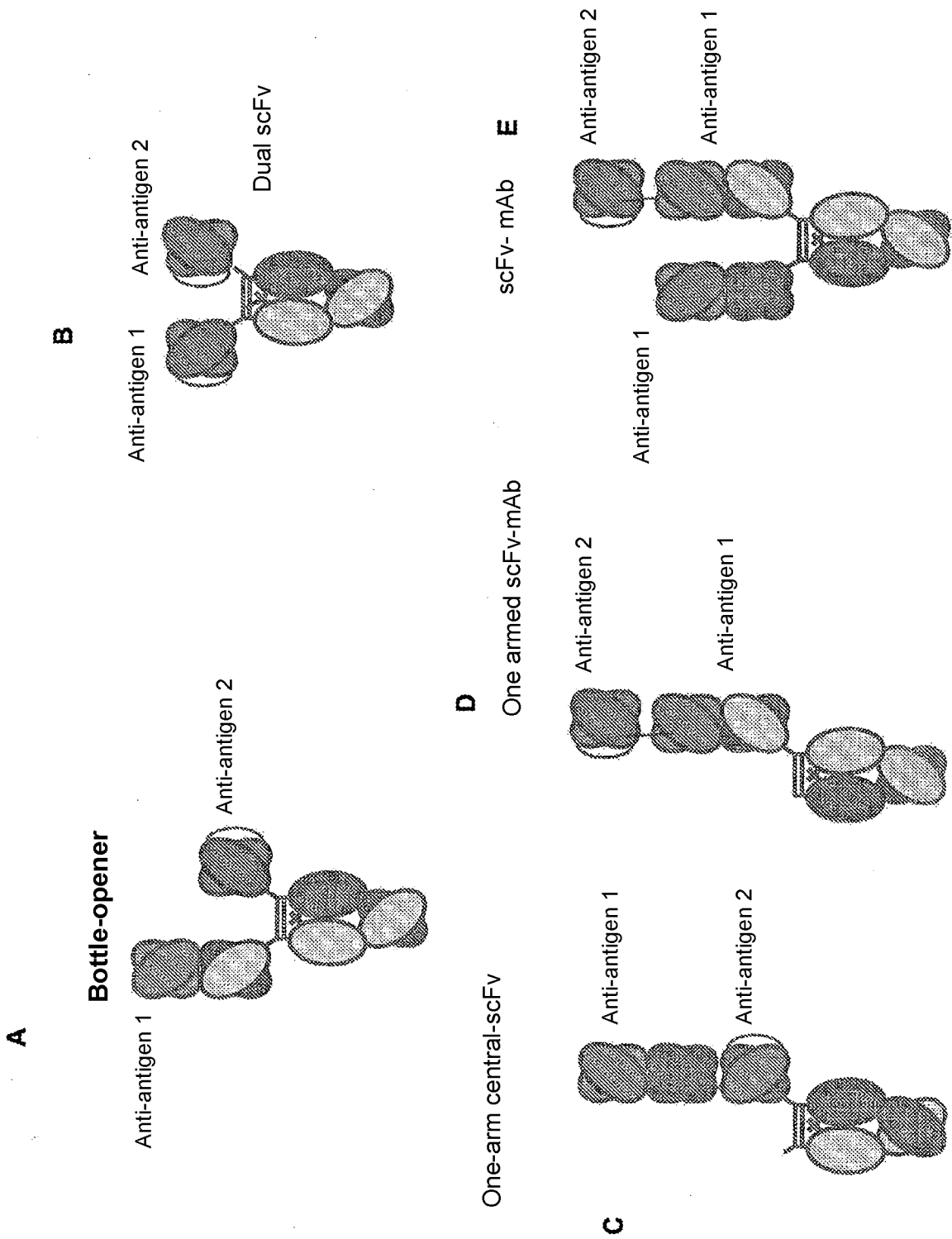


FIGURE 18F-I

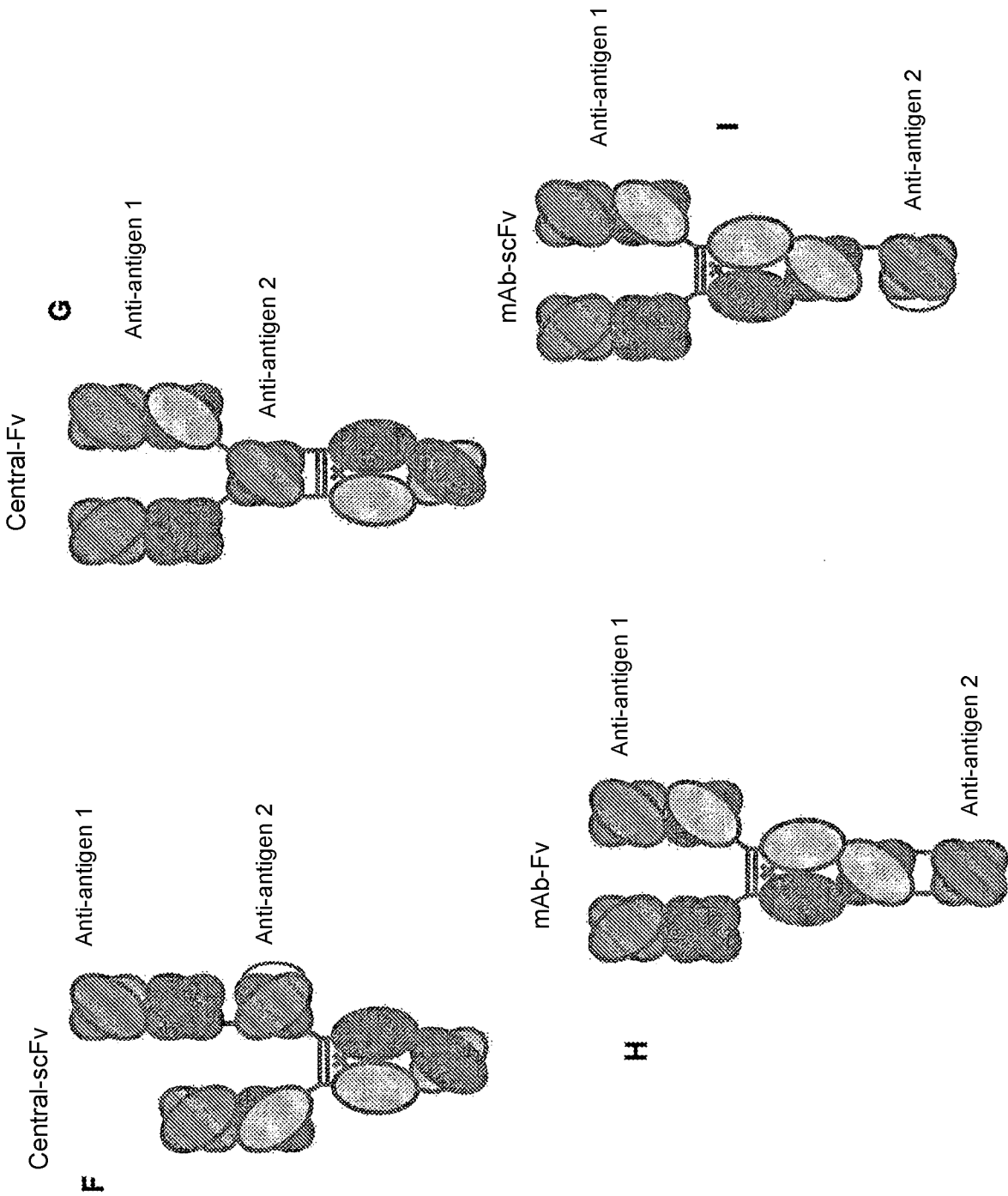


FIGURE 19

SEQ ID NO:	Description	Sequence
1.	CD3 epsilon chain - human	MQSGTHWRVILGLCLLSVGWVGQDNGNEEMGGITQTPYKVISGTTVILTCQYPGSEILWQHNDKNIGGDEDDKNI GSEDEHLSLKEFSELEQSGYVVCYPRGSKPEDANFYLYLRARVCENCMEMDVMMSVATIVIDICITGGLLLVVYWSK NRKAKAPVTRGAGAGGRQGRQNKERPPVPNPDPYPIRKQQRDLYSGLNQRRRI
2.	STEAP-1 – human	MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAAHAEFDCPSE LQHTQELFPQWHLPIKIAAIIASLTFLYTLREVIHPLATSHQQYFYKIPILVINKVLPM VSITLLALVLPGVIAAIVQLHNGTKYKKFPHWLDKWWMLTRKQFGLSFFFAVLHAIYSL SYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPS VSDSLTWREFHYIQSKLGVSLLLGTIHALIFAWNKWIDIKQFVWVYTPPTFMIAVFLPIV VLIFKSILFLPCLRKKILKIRHGWEDVTKINKTEICSQL
3.	Ab-A HC variable	QVQLQQSGAEMMKPGASVKISCKATGYTFSTYWIEWVKQRPQGHGLEWIGELPGSGNTDFNEKFKGKATFTADTS SDTAYMHLSSLTSEDSAVVYCTRW/GYYGTRGYFNWVGAGSTVTVSS
4.	Ab-A HCDR1	TYWIE
5.	Ab-A HCDR2	EILPGSGNTDFNEKFKG
6.	Ab-A HCDR3	WGYYGTRGYFNV
7.	Ab-A LC variable	QIVLTQSPAIMSASPGEKVTTITCSASSSVSYMHWVFQQKPGTSPKLIWYSTSNLASGVPARFSGSGSGTSYSLTISRME AEDAATYYCQQRSPFYTFGGGKLEIK
8.	Ab-A LCDR1	SASSSVSYM
9.	Ab-A LCDR2	STSNLAS
10.	Ab-A LCDR3	QQRSPFYT
11.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ LCDR1	RASSSVSYM

FIGURE 19 Cont.

12.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ LCDR2	STSNLAS
13.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ LCDR3	QQRRSFPYT
14.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ HCDR1	TYWIE
15.	Ab-A1 Xmab ²⁺¹ HCDR2	EILPGSGNTDFNEKFQG
16.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ HCDR3	WGYGTRGYFNV
17.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ light chain	MGWSCILFLVATATGVHSEIVLTQSPATLSLSPGERATLSCRASSVSYMHWFQKPGQAPRLIYSTSNLASGIPAR FSGSGSDTYLTISILEPEDFAVYCCQRRSPFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
18.	Ab-A1 Xmab ²⁺¹ heavy chain	MGWSCILFLVATATGVHSEIVLTQSPATLSLSPGERATLSCRASSVSYMHWFQKPGQAPRLIYSTSNLASGIPAR NTDFNEKFQGRVFTADTSSDTAYMELSSLRSEDTAVYCTRWGYGTRGYFNVWVGQGLTVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPS DTKVDKVEPKSCDKTHTCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEV HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKN QVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYT QKSLSLSPGK
19.	Ab-A1 Xmab ²⁺¹ XVHMx	MGWSCILFLVATATGVHSEIVLTQSPATLSLSPGERATLSCRASSVSYMHWFQKPGQAPRLIYSTSNLASGIPAR NTDFNEKFQGRVFTADTSSDTAYMELSSLRSEDTAVYCTRWGYGTRGYFNVWVGQGLTVTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPS NTKVDKVEPKSCDKTHTCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEV RSKYNNTATYADSVKGRFTISRDDSKNTLYLQMNSLRSEDTAVYCTRWGYGTRGYFNVWVGQGLTVTVSSG KPGSGKPGSGKPGSGKPGSQAVVTQEPSTVSPGGTTLTCSGSTGAVTTSNANWVQKPGKSPRGLIGGTNKR APGVPARFSGSLGGKAAALTSGAQPEDEADYICWYNSHWVFGGGLTTLVGGGGGGGSKTHTCPPCAPP VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREQMTKNQVLTCLVKGFYPSDIAVEWESNGQ PENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNGVFCSVMHEALHNHYTQKSLSLSPGK

FIGURE 19 Cont.

20.	Ab-A2 (N67Q) Xmab ²⁺¹ XVHMx	MDMRVPAQLLGLLLWLRGARQCQLVQSGAEVKPGASVKVCKASGYTFSTYWIEWVRQAPGQRLEWMGEIL PGSGQTDNFNEKFGQRTFTADTSSDTAYMELSLRSEDATVYCTRWGYGTRGFNVWGGGTLTVSSASTKGPS VFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWNVRQAPGKGLEW VGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNGFGDSVYVFWFAYWGQGLTVTV SSGKPGSGKPGSGKPGSGQAVTQEPSTVSPGGTVTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGGGGSGGGGSKTHTCPPCPA PPVAGPSVFLFPKPKDITLMISRTPEVTCVVDVKHEDPEVKFNWVYDGVGVHNAKTKPCEEQYGSTYRCVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSGFLYSLKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK EILPGSGQTDNFNEKFGQ
21.	Ab-A2 (N67Q) Xmab ²⁺¹ HCDR2 (all other CDRs the same as Ab-A1 Xmab ²⁺¹)	
22.	Ab-B1 heavy variable	QIQLVQSGPELKKPGETVKISKASGYTFNTYGMNWWKQAPGKGLQWGMWNTYTGEPTYADDFKGRFAFSLET SARTVSLDINDLKNETATYFCTRAGGQLRPGAMIDYWGGGTSVTSS
23.	Ab-B1 HCDR1	NYGMN
24.	Ab-B1 HCDR2	WMNTYTGEPTYADDFKG
25.	Ab-B1 HCDR3	AGGQLRPGAMIDY
26.	Ab-B1 light variable	DIVLTQSPASLAVSLGQRATISCKASQSDYDGDGDFMNVWYQKPGQPPKLLIYVASNLESVIPDRFSGSGSGTDFTLN IHPVEEEDAATYYCQQSNEEPTFGGGTKLEIK KASQSDYDGDGDFMN
27.	Ab-B1 LCDR1	
28.	Ab-B1 LCDR2	VASNLES
29.	Ab-B1 LCDR3	QQSNEEPT
30.	Ab-B1 Xmab ²⁺¹	KASQSDYDGDGDFMN

FIGURE 19 Cont.

	LCDR1	
31.	Ab-B1 Xmab ²⁺¹ LCDR2	VASNLES
32.	Ab-B1 Xmab ²⁺¹ LCDR3	QQSNEEPPT
33.	Ab-B1 Xmab ²⁺¹ HCDR1	NYGMN
34.	Ab-B1 Xmab ²⁺¹ HCDR2	WMNTYTGEPTYADKFQG
35.	Ab-B1 Xmab ²⁺¹ HCDR3	AGGQLRPGAMIDY
36.	Ab-B1 Xmab ²⁺¹ Light chain	MGWSCILFLVATATGVHSDIVLTQTPLSLSVTPGQPASISCKASQSVDDYDGSFMNWWYQKPGQPQLLIYVASNL ESGVDPDRFSGSGGTDFTLKISRVEAEDVGWYQCQSQNEEPPTFGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKVKVACEVTHQGLSSPVTKSFN RGE
37.	Ab-B1 Xmab ²⁺¹ Heavy chain	MGWSCILFLVATATGVHSEIQLVQSGAEVKKPGATVKISCKASGYTFTNYGMNWWVQQAPGQGLEWMGMWNTY TGEPTYADKFQGRVFTFLDTSARTVYMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSS ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ TYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKF NWWVDGVEVHNAKTPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGGQPENNYKTPPVLDSDGSEFFLYSKLTVDKSRWEQDGVFSCSVMI HEALHNHYTQKSLSLSPGK
38.	Ab-B1 Xmab ²⁺¹ XMHx	MGWSCILFLVATATGVHSEIQLVQSGAEVKKPGATVKISCKASGYTFTNYGMNWWVQQAPGQGLEWMGMWNTY TGEPTYADKFQGRVFTFLDTSARTVYMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCGGGGGGSEVQLVESGGGLVQPGGSLRSCAASGFTFTYAMNWWVRAQPGKGLEWV GRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNGFSDSVSWFAYWGQGLTVTS SGKPGSGKPGSGKPGSGKPGSQAVWTQEPSTLSPGGLTTCGSSGTAVTTSYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYNSHWVFGGGLTKLTVLGGGSGGGGSKTHTCPPCPA PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTPREEEYNSTYRVVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTPPSREQMTKNQVTKLCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
39.	Anti-CD3 H1_L1.4	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWWVRAQPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNGFSDSVSWFAYWGQGLTVTSVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

		TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
40.	Anti-CD3 H1_L1.4	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
41.	Anti-CD3 H1_L1.4	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSS
42.	Anti-CD3 H1_L1.4	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
43.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
44.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
45.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSS
46.	Anti-CD3 H1.30_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
47.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
48.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
49.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFSDSYVSFWAYWGQGLTVTVSS
50.	Anti-CD3 H1.33_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

51.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD SKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV QEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQP EDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
52.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD SKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV QEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQP EDEADYYCALWYSNHWVFGGGTKLTVL
53.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD SKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSS
54.	Anti-CD3 H1.31_L147	QAVVTQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
55.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
56.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
57.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVWFAYWGQGTLLTVSS
58.	Anti-CD3 H1.32_L147	QAVVTQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
59.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGPSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
60.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGPSYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPLSTVSPGGTTLTSGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
61.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMSVVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISRDD DSKNTLYQMNSLRAEDTAVYCVRHGNFGPSYVWFAYWGQGTLLTVSS

FIGURE 19 Cont.

62.	Anti-CD3 H1.88_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
63.	Anti-CD3 H1.89_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDEYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
64.	Anti-CD3 H1.89_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDEYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
65.	Anti-CD3 H1.89_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDEYVSWFAYWGQGLTVTVSS
66.	Anti-CD3 H1.89_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
67.	Anti-CD3 H1.90_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDPYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
68.	Anti-CD3 H1.90_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDPYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
69.	Anti-CD3 H1.90_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDPYVSWFAYWGQGLTVTVSS
70.	Anti-CD3 H1.90_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
71.	Anti-CD3 H1.91_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
72.	Anti-CD3 H1.91_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

73.	Anti-CD3 H1.91_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSS
74.	Anti-CD3 H1.91_L1.47	QAVVTQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
75.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
76.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
77.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSS
78.	Anti-CD3 H1.92_L1.47	QAVVTQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
79.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGESYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
80.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGESYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
81.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGESYVSFWAYWGQGLTVTVSS
82.	Anti-CD3 H1.93_L1.47	QAVVTQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
83.	Anti-CD3 H1.94_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTVTLTSGSSTGAVTTSNYANWVQQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
84.	Anti-CD3 H1.94_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSFWAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

		TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVL
85.	Anti-CD3 H1.94_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGQSVSWFAYWGQGLTVTVSS
86.	Anti-CD3 H1.94_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYVCALWYSNHWVFGGGTKLTVL
87.	Anti-CD3 H1.96_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVW TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVLGSHHHHHH
88.	Anti-CD3 H1.96_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVW TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVL
89.	Anti-CD3 H1.96_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSS
90.	Anti-CD3 H1.96_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYVCALWYSNHWVFGGGTKLTVL
91.	Anti-CD3 H1.97_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVW TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVLGSHHHHHH
92.	Anti-CD3 H1.97_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVW TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVL
93.	Anti-CD3 H1.97_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSS
94.	Anti-CD3 H1.97_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYVCALWYSNHWVFGGGTKLTVL
95.	Anti-CD3 H1.98_L1.47	EVQLVSGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFGDYSWVFWYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVW TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEEADYVCALWYSNHWVFGGGTKLTVLGSHHHHHH

FIGURE 19 Cont.

96.	Anti-CD3 H1.98_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYNSHNWVFGGGTKLTVL
97.	Anti-CD3 H1.98_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSS
98.	Anti-CD3 H1.98_L1.47	QAVVTQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYNSHNWVFGGGTKLTVL
99.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYNSHNWVFGGGTKLTVLGSHHHHH
100.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYNSHNWVFGGGTKLTVL
101.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSS
102.	Anti-CD3 H1.99_L1.47	QAVVTQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYNSHNWVFGGGTKLTVL
103.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYNSHNWVFGGGTKLTVLGSHHHHH
104.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYNSHNWVFGGGTKLTVL
105.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSS
106.	Anti-CD3 H1.100_L1.47	QAVVTQPSLTSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGINKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYNSHNWVFGGGTKLTVL
107.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGDSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

		TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
108.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
109.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSS
110.	Anti-CD3 H1.101_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
111.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
112.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
113.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSS
114.	Anti-CD3 H1.102_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
115.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
116.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
117.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNNWVRQAPGKLEWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFQSYVSWFDYWGQGLTVTVSS
118.	Anti-CD3 H1.103_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

119.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
120.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
121.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSS
122.	Anti-CD3 H1.104_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
123.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGA QPEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
124.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGA QPEDEADYCALWYSNHWVFGGGTKLTVL
125.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSS
126.	Anti-CD3 H1.105_L1.47	QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYCALWYSNHWVFGGGTKLTVL
127.	Anti-CD3 H1.106_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVLGSHHHHH
128.	Anti-CD3 H1.106_L1.47 (ScFv)	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPGKSPRGLIGGTTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYCALWYSNHWVFGGGTKLTVL
129.	Anti-CD3 H1.106_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNGFDYVSWFQGTTLTVSS

FIGURE 19 Cont.

130.	Anti-CD3 H1.106_L1.47	QAVVTQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADY ~~CALWYSNHWVFGGGTKLTVL~~
131.	Anti-CD3 H1.107_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGASYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~ SGSHHHHH
132.	Anti-CD3 H1.107_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGASYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~
133.	Anti-CD3 H1.107_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGASYVSWFAYWGQGT ~~LVTVSS~~
134.	Anti-CD3 H1.107_L1.47	QAVVTQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADY ~~CALWYSNHWVFGGGTKLTVL~~
135.	Anti-CD3 H1.108_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGQSYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~ SGSHHHHH
136.	Anti-CD3 H1.108_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGQSYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~
137.	Anti-CD3 H1.108_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGQSYVSWFAYWGQGT ~~LVTVSS~~
138.	Anti-CD3 H1.108_L1.47	QAVVTQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADY ~~CALWYSNHWVFGGGTKLTVL~~
139.	Anti-CD3 H1.109_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~ SGSHHHHH
140.	Anti-CD3 H1.109_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNFGDSYVSWFAYWGQGT ~~LVTVSSGKPGSGKPGSGKPGSQAVV~~ TQEPSLTVSPGGT ~~TVLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGG~~ TNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADY ~~CALWYSNHWVFGGGTKLTVL~~

FIGURE 19 Cont.

141.	Anti-CD3 H1.109_L1.47	EVQLVESGGGLVQP ^{GG} SLRLSCAASGFTFTSTYAMN ^{WVR} QAPGKGL ^{EWVGR} IRSKANNYATAYADSVKGRFTISRD DSKNTLYLQMNSLRAEDTAVYVCVRHGNFGDSYVS ^{WFDYW} GQGT ^{LVTVSS}
142.	Anti-CD3 H1.109_L1.47	QAVVTQPSLTVSPGGT ^{VTLT} CGSSTGAVTTSN ^{YANWV} QKPGKSPRGLIGG ^{TNKR} APGV ^{PAR} FSGSLGGKAALTI SQAQPEDEADYYCALWY ^{SNHWV} FGGGTK ^{LTVL}
143.	Linker	GGGGGGGGGGGG
144.	Whitlow linker	GSTSGGKPGSGEGSTKG
145.	Linker	IRPRAIGGSKPRVA
146.	Linker	GKGGSGKGGSGGKGS
147.	Linker	GGKSGGKGGSGGKGS
148.	Linker	GGGKSGGKGGGGKS
149.	Linker	GKGS ^{GKGS} GKGS
150.	Linker	GGKSGGKGGSGGKGS
151.	Linker	GKPGSGKPGSGKPGS
152.	Linker	GKPGSGKPGSGKPGSGKPGS
153.	Linker	GKGS ^{GKGS} GKGS ^{GKGS}
154.	Linker	GGGGGGGGGGGGGGGGGS
155.	Linker	STAGDTHLGEDFD
156.	Linker	GEGSGEGSGEGGS
157.	Linker	GGEGSGEGSGEGGS
158.	Linker	GGEGSGEGSGEGGS
159.	Linker	GEGSGEGSGEGGS
160.	Linker	GGEGSGEGSGEGGS
161.	Linker	GEGSGEGSGEGSGEGGS
162.	Linker	GGGGGGGGGGGG
163.	Linker	GGGGGGGGGGGGGGGGGS
164.	Linker	GSTSGGKPGSGEGSTKG
165.	Linker	PRGASKSGSASQTGSAPGS
166.	Linker	GTAAAGAGAGGAAAGAAAG
167.	Linker	GTSGSGSGSGSGSGGGG
168.	Linker	GKPGSGKPGSGKPGSGKPGS
169.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹	EVQLVESGGGLVQP ^{GG} SLRLSCAASGFTFTSTYAMN ^{WVR} QAPGKGL ^{EWVGR} IRSKYNNYATYADSVKGRFTISRD DSKNTLYLQMNSLRAEDTAVYVCVRHGNFGDSYVS ^{WFAW} GQGT ^{LVTVSS}

FIGURE 19 Cont.

	Anti-CD3, heavy variable	
170.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, HCDR1	TYAMN
171.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, HCDR2	RIRSKYNNYATYYADSVKG
172.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, HCDR3	HGNFGDSYVSWFAY
173.	Ab-A1 XmAb ²⁺ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, light variable	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQPKGSPRGLGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
174.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, LCDR1	GSSTGAVTTSNYAN
175.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, LCDR2	GTNKRAP
176.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹ Anti-CD3, LCDR3	ALWYSNHWV
177.	STEAP2 - human	MESISMIMGSPKSLSETFLPNGINGIKDARKVTGVIGSGDFAKSLTIRLCGYHVVIGS RNPKFASEFFPHVVDVTHEDALTKNIIFVAIHREHYTSLWDLRLHLLVGKILIDVSNM RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE

FIGURE 19 Cont.

		LARQLNFIPIDLGSLSSAREIENLPRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA RNQQSDFYKIPIEIVNKTLPVAVITLLSLVLAGLAAAYQLYGYTKYRRFPFWLETWLQ CRKQLGLSFFAMVHVAYSCLPMRRSERYFLN MAYQQVHANIENSWNEEEVWRIEMY ISFGIMSLGLLSLAVTSIPSVSNALNWREFSFIQSTGLGYVALLISTFHVLIYGWKRAFE EEYRYFTPPNFVLA LVPISVILGKIILFLPCISRKLKRIKKGWKSEKQFLEEGMGGTIP HVSPERVTVM
178.	Linker	GSGGS
179.	Linker	GSGGS
180.	Linker	GSGGS
181.	Linker	GFLG
182.	Ab-A1 Xmab ²⁺¹ heavy variable	QVQLVQSGAEVKKPGASVKVCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGNTDFNEKFQGRVTFADTS SDTAYMELSSLRSEDTAVYCTRWGYGTRGYFNVWVGQGLTVTVSS
183.	Ab-A1/A2(N67Q) Xmab ²⁺¹ light variable	EIVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQKPKGQAPRLLIYSTSNLASGIPARFSGSGGTDYTLTISSLEPE DFAVYYCQQRRSFPTFGQGTKLEIK
184.	Ab-A2 (N67Q) Xmab ²⁺¹ heavy variable	QVQLVQSGAEVKKPGASVKVCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGQTDNEKFQGRVTFADTS SDTAYMELSSLRSEDTAVYCTRWGYGTRGYFNVWVGQGLTVTVSS
185.	Ab-B1 Xmab ²⁺¹ heavy variable	EIQLVQSGAEVKKPGATVKISKASGYTFSTYGMNWWVQQAPGQGLEWMGMWNTYTGEPTYADKFQGRVTFILD TSARTVMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGMVTVSS
186.	Ab-B1 Xmab ²⁺¹ light variable	DIVLTQTPLSLVTPGQPASISCKASQSDYDGDGDFMNNWYLQKPGQPPQLLIYVSNLESVGPDRFSGSGGTDFTLK ISRVEAEDVGVYCCQQNEEPPTFGQGTKLEIK
187.	human PD-1	PGWFLDSPDRPWNPPTFSPALLVVTEDGNATFTCSFNTSEFVLNWMSPSNQTDKLAAPFEDRSQPGQDCRF RVTQLPNGRDFHMSVVRARRNDSTYLCGALSAPKAQIKESLRAELRVTERRAEVPTAHPSPPRAGQFQTLVVG VVGGLLSLVLLVWVLAIVCSRAARGTIGARRTGQPLKEDPSAVPVFSDYDGLDFQWREKTPPPVPCVPEQTEYA TIVFSGMGTSPPARRGSADGPRSAQPLRPEDGHCSWPL
188.	cynomologous PD-1	MIQIPQAPWPVWAVLQLGWRPGWFLESPDRPWNAPTFSPALLVTEGDNATFTCSFNASEFVLNWMSPS NQTDKLAAPFEDRSQPGQDCRFVTRLPNGRDFHMSVVRARRNDSTYLCGALSAPKAQIKESLRAELRVTERRAE VPTAHPSPPRAGQFQALVGVWGGLLGSLVLLVWVLAIVCSRAAQGTIEARRTGQPLKEDPSAVPVFSDYDGLD FQWREKTPPPVPCVPEQTEYATIVFPSGLTSSPARRGSADGPRSPRPLRPEDGHCSWPL
189.	Anti-PD-1 antibody HC	SYDMS

FIGURE 19 Cont.

	CDR1	
190.	Anti-PD-1 antibody HC CDR2	LISGGGQTYVAESVK
191.	Anti-PD-1 antibody HC CDR3	PSGHYFYAMDV
192.	Anti-PD-1 antibody LC CDR1	RASQGISNWLA
193.	Anti-PD-1 antibody LC CDR2	AASSLQS
194.	Anti-PD-1 antibody LC CDR3	QQAESFPH
195.	Anti-PD-1 antibody HC VARIABLE	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYDMSWVRQAPGKGLWVSLISGGGQTYVAESVKGRFTISRDNK NTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITVTVSS
196.	Anti-PD-1 antibody LC VARIABLE	DIQMTQSPSSVSASVGDRTITCRASQGISNWLAWYQQKPKAPKLLIFAASSLQSGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQAESFPHFTGGGKVEIK
197.	Anti-PD-1 antibody HC FULL LENGTH	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASGFTSSYDMSWVRQAPGKGLWVSLISG GGSTQTYVAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITVTVSSASTKGPSVF PLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWVVDGV EVHNAKTKPCEEQYGSTYRCVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQWYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN HYTQKSLISLSPGK
198.	Anti-PD-1 antibody LC	MDMRVPAQLLGLLLWLRGARCDIQMTQSPSSVSASVGDRTITCRASQGISNWLAWYQQKPKAPKLLIFAASSL QSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQAESFPHFTGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVW

FIGURE 19 Cont.

	FULL LENGTH	CLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTKSFN RGE
199.	Ab-A2 (N67Q) X _{mab} 2+1 heavy chain	MDMRVPAQLLLWLRGARCQQLVQSGAEVKKPGASVKVSKASGYTFSTYIEWVRQAPGQRLEWMGEIL PGSGQTDNEKFQGRVTFADTSSDTAYMELSSRSEDYAVYYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVN HKPSDTKVDKKVEPKSCDKTHCTCPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDG VEVHNAKTKPCEEEYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMT KNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNH YTQKSLSLSPGK
200.	Ab-A1/A2 (N67Q) X _{mab} ²⁺¹ light chain minus signal sequence	EIVLTQSPATLSLSPGERATLSCRASSVSYMHWFQKPGQAPRLLIYSTSNLASGIPARFSGSGSDYTLTISSLEPE DFAVYCCQRRSFYTFGQGTLEIKRTVAAPSFIFFPSDEQLKSGTASVCLLNINFPYFREAKVQWKVDNALQSGN SQESVTEQDSKDYSLSTLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC
201.	Ab-A1 X _{mab} ²⁺¹ heavy chain minus the signal sequence	QVQLVQSGAEVKKPGASVKVSKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGNTDFNEKFQGRVTFADTTS SDTAYMELSSRSEDYAVYYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPSFPLAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHNKPSDTKVDKKVEPKSCDKTHCT PPCPAPPVAGPSVFLPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNHYTQKSLSLSPGK
202.	Ab-A1 X _{mab} ²⁺¹ XVHMx minus the signal sequence	QVQLVQSGAEVKKPGASVKVSKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGNTDFNEKFQGRVTFADTTS SDTAYMELSSRSEDYAVYYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPSFPLAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCGGGS GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKLEWVGRIRSKYNNYATYYADSVKGR FTISRDTSKNTLYLQMNSLRAEDTAVYCVRHNGFSDYSVWFAYWGQGLTVTVSSGKPGSGKPGSGKPG SQAVVTQEPSTLVSPGGTVTLTSGSSTGAVTTSNYANWVQKPGKSPRLIGGTNKRAPGVPARFSGSLGGKAAL TISGAQPEDEADYYCALWYSNHWVFGGGLTKLTVLGGGGGGGSKTHCTCPAPPVAGPSVFLPPKPKDTLMIS

FIGURE 19 Cont.

		RTPEVTCVVVDVKHEDPEVKFNWVVDGVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREQMTKNQKLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
203.	Ab-A2 (N67Q) Xmab 2+1 heavy chain minus signal sequence	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGQTDFNEKFQGRVTFITADTS SDTAYMELSSLRSEDTAVYYCTRWGYGTRGYFNVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTC PPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVVDGVEVHNAKTPKEEYGGSTYRCVS VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW ESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK
204.	Ab-B1 Xmab ²⁺¹ light chain minus signal sequence	DIVLTQTPLSLVTPGPASISCKASQSDYDGDGDFMNMWYLQKPGQPQLLIYVASNLESGVPDRFSGSGSGTDFTLK ISRVEAEDGVVYCCQQNEEPPTFGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN ALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
205.	Ab-B1 Xmab ²⁺¹ heavy chain minus signal sequence	QLVQSGAEVKKPGATVKISCKASGYFTFTNYGMNWWVQQAPGQGLEWMGMWMNTYTGEPTYADKFQGRVTFITLDT SARTVMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTH TCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVVDGVEVHNAKTPREEYNSTYRV VSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE WESDGGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK
206.	Ab-B1 Xmab ²⁺¹ XMVHx minus signal sequence	QLVQSGAEVKKPGATVKISCKASGYFTFTNYGMNWWVQQAPGQGLEWMGMWMNTYTGEPTYADKFQGRVTFITLDT SARTVMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCGGG GSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVK GRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNGDSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSGK PGSAVVTQEPSTLVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKA ALTISGAQPEDEADYYCALWYSNHWVFGGGLTLVLGGGSGGGGSKTHTCPAPPVAGPSVFLFPPKPKDTL MISRTPEVTCVVVDVKHEDPEVKFNWVVDGVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
207.	Ab-A2 (N67Q) Xmab ²⁺¹ XVHMx	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSGQTDFNEKFQGRVTFITADTS SDTAYMELSSLRSEDTAVYYCTRWGYGTRGYFNVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD

FIGURE 19 Cont.

	minus signal sequence	YFEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVWTVPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCGGGGS GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTSTYAMNWWRQAPGKGLEWVGRIRSKYNNYATYYADSVKGR FTISRDTSKNTLYLQMNSLRAEDTAVYCVRHGNGFSDSYVWFAYWGQGLTVTVSSGKPGSGKPGSGKPG SQAVVTQEPSTLVSPGGTTLTSGSSTGAVTTSNYANVWQKPKGSPRGLIGGTNKRAPGVPAFSGSLGGKAAL TISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGGGGSGGGGSKTHTCPPCAPPVAGPSVFLFPKPKDMLIS RTPEVTCVWVDVKHEDPEVKFNWVVDGVEVHNATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
208.	Anti-PD-1 antibody HC FULL LENGTH minus signal sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSVDMSWVWRQAPGKGLEWVSLISGGGQTYVAESVKGRFTISRDNK NTLYLQMNSLRAEDTAVYFCASPSSGHYFAMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSVWTVPSSSLGTQTYICNVNHHKPSNTKVDKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWVVDGVEVHNATKPCEEQYGSTYRCVS VLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
209.	Anti-PD-1 antibody LC FULL LENGTH minus signal sequence	DIQMTQSPSSVSASVGDRVTITCRASQGISNWLAWYQQKPGKAPKLLIFAAASSLQSGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQAESEFPHTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

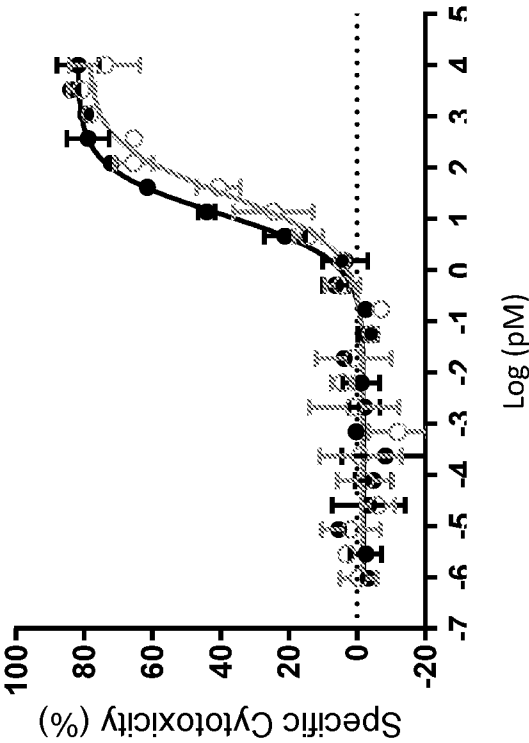


FIGURE 20A

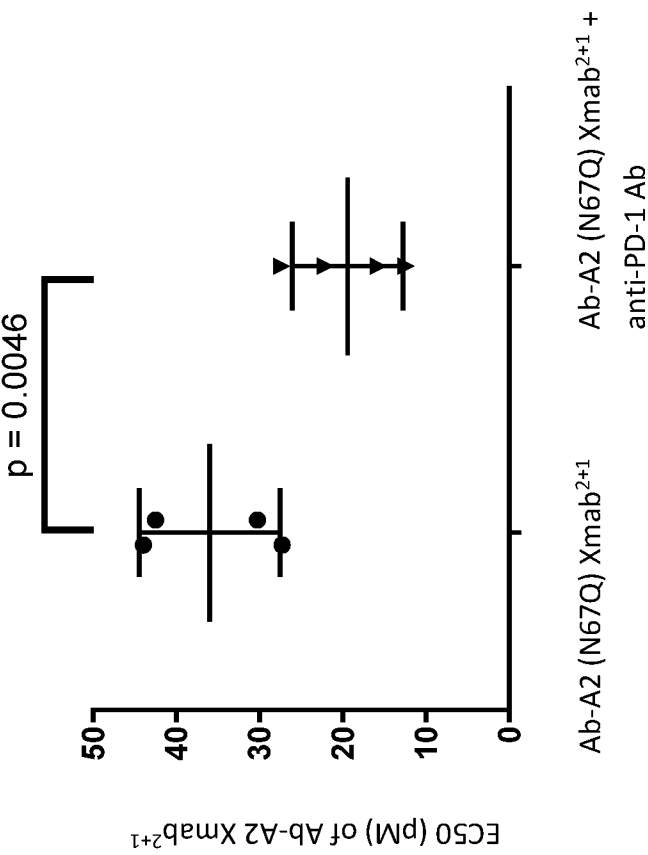


FIGURE 20B

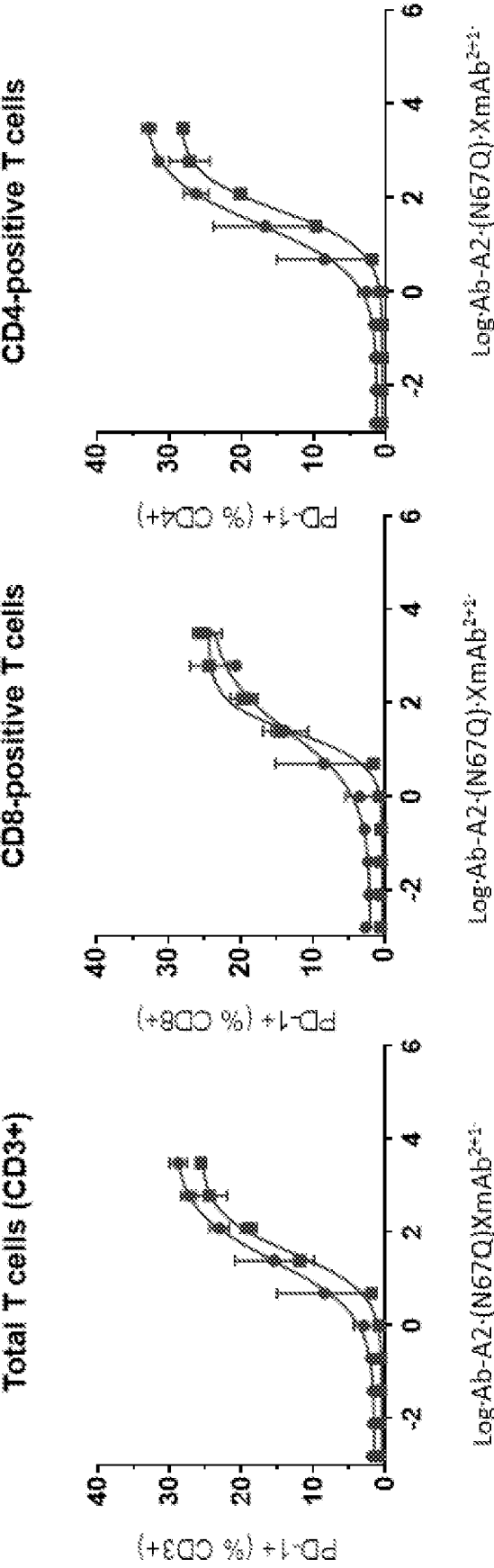


FIGURE 21A

FIGURE 21B

FIGURE 21C

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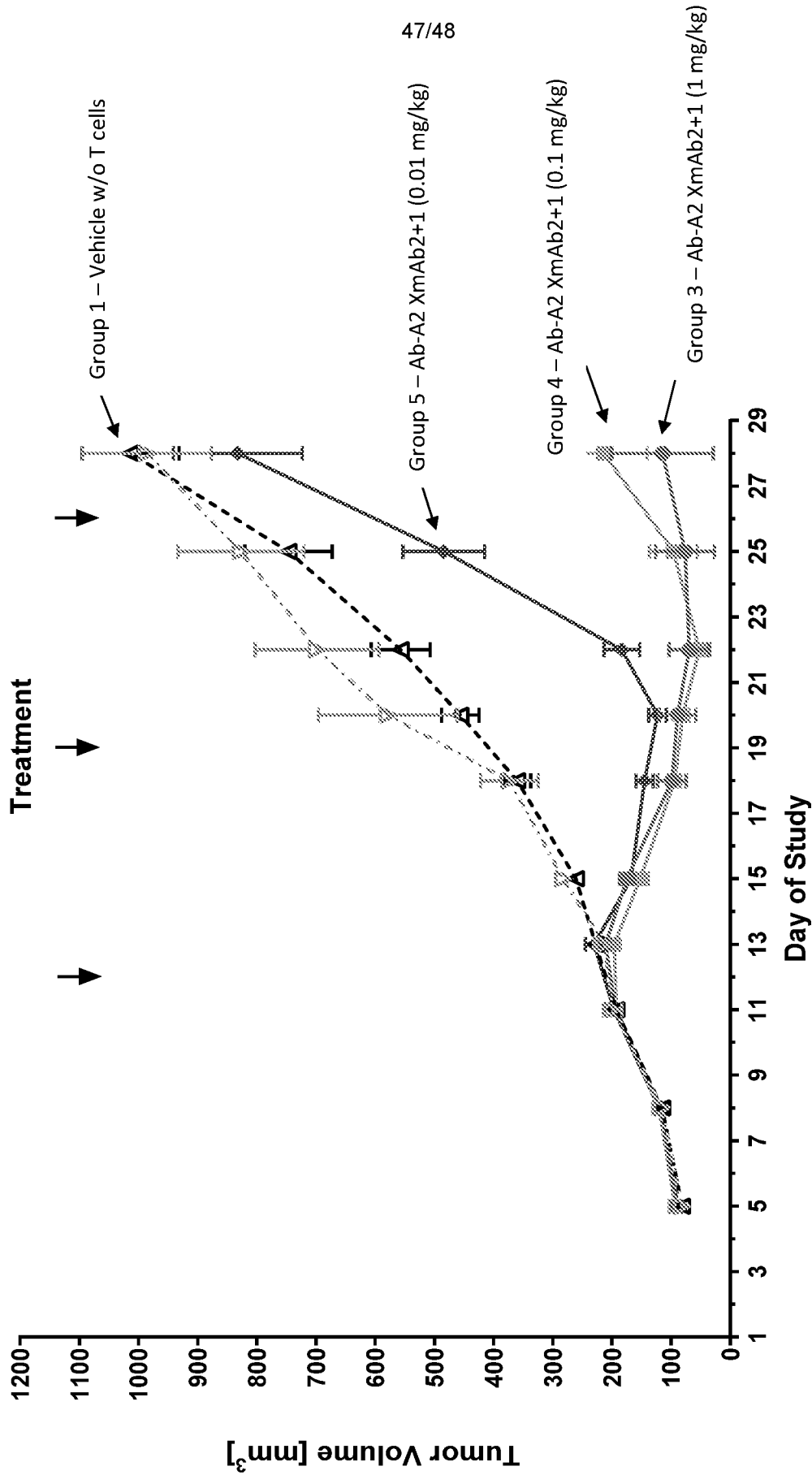


FIGURE 22

FIGURE 23. Mean and Median SK-N-MC Human Neuroblastoma Tumor Volumes in Female NOD/SCID Mice

Dose Group	Parameter	Tumor Volume [mm ³]									
		Day 5	Day 8	Day 11	Day 13	Day 15	Day 18	Day 20	Day 22	Day 25	Day 28
1 Vehicle w/o T cells	Mean	81.42	115.24	198.79	212.62	282.70	373.05	578.73	698.38	827.31	985.94
	Median	90.28	122.85	203.63	229.86	286.81	323.09	563.09	598.48	673.42	885.10
	SEM	9.84	10.43	15.69	18.48	12.75	48.70	117.46	104.52	106.45	108.87
	Animals [N]	5	5	5	5	5	5	5	5	5	5
	Significance	n.p.	n.p.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
2 Vehicle	Mean	81.70	115.59	192.91	227.63	260.98	360.22	456.04	557.15	746.68	1013.67
	Median	80.44	118.24	196.61	225.01	253.27	348.93	468.93	590.08	837.07	955.14
	SEM	3.26	5.84	5.65	8.43	8.27	22.88	31.99	49.93	73.79	82.53
	Animals [N]	10	10	10	10	10	10	10	10	10	10
	Significance	n.p.	n.p.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
3 Ab-A2 XmAb2+1 (1.0 mg/kg)	Mean	90.20	116.48	194.16	210.85	174.59	98.67	89.06	69.26	76.53	114.65
	Median	87.90	115.14	197.87	206.94	166.09	78.41	59.90	33.53	27.07	29.77
	SEM	6.06	6.83	5.86	10.05	12.61	24.54	30.99	34.20	49.48	85.58
	Animals [N]	10	10	10	10	10	10	10	10	10	10
	Significance	n.p.	n.p.	n.s.	n.s.	***	***	***	***	***	***
4 Ab-A2 XmAb2+1 (0.1 mg/kg)	Mean	92.85	120.80	192.45	196.10	152.32	94.10	80.21	52.33	96.21	214.04
	Median	92.42	117.60	197.59	198.67	144.59	88.07	76.73	41.56	55.86	106.87
	SEM	4.26	7.36	5.14	12.56	14.21	9.02	10.31	12.89	40.62	73.43
	Animals [N]	10	10	10	10	10	10	10	10	10	10
	Significance	n.p.	n.p.	n.s.	n.s.	***	***	***	***	***	***
5 Ab-A2 XmAb2+1 (0.01 mg/kg)	Mean	88.12	120.82	196.68	230.31	168.00	145.00	122.92	183.51	484.07	832.45
	Median	90.29	119.04	200.97	217.31	150.74	121.75	115.60	202.07	431.89	867.08
	SEM	5.07	7.38	5.23	15.01	13.55	14.25	14.81	29.98	69.24	109.11
	Animals [N]	10	10	10	10	10	10	10	10	10	10
	Significance	n.p.	n.p.	n.s.	n.s.	***	***	***	***	*	n.s.

One-way ANOVA and assessment of experimental results for tumor growth by Dunnett's post-test in comparison to group 2; significant: * = p < 0.05; ** = p < 0.01; *** = p < 0.001. Statistical analysis from day 11 (one day before treatment start) until day 28.

N = number of animals; n.p. = not performed; n.s. = not significant; SEM = standard error of the mean; w/o = without.