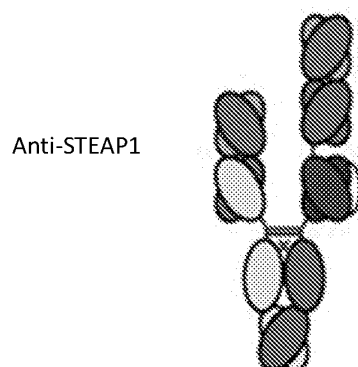


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FIGURE 1**FIGURE 2**

MQSGTHWRVLGLCLLSVGWVGQDGN EEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDE
DDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSKPEDANFYLYLRARVCENCMEMDVMSVATIVIVDITGG
LLLLVYYWSKNRKAKAKPVTRGAGAGGRQRGQNKERPPVPNPDYEPKRGQRDLYSGLNQRRI (SEQ ID
NO: 1)

FIGURE 3

MESRKDITNQEELWKMKPRRNLEEDDY LHKDTGETSMLKRPVLLHLHQT AHAEFDCPSE
LQHTQELFPQWHLPIKIAAIIASLTFLY TLLREVIHPLATSHQQYFYKIPILVINKVLPM
VSITLLALVYLPGVIAAIVQLHNGTKYKK FPHWLDKWMLTRKQFGLLSFFF AVLHAIYSL
SYPMRRSYRYKLLNWAYQQVQQNKEDAW IEHDVWRMEIYVSLGIVGLAILALLAVTSIPS
VSDSLTWREFHYIQSKLGIVSLLGTIHAL IFAWNKWIDIKQFVWYTPPTFMIAVFLPIV
VLIFKSILFLPCLRKKILKIRHGWEDVT KINKTEICSQL (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	GGGGSGGGGSGGGGS	15	0	143
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	144
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	145
+B	GKGGSGKGGSGKGGGS	15	+3	146
+C	GGKGS GGKGS GGKGS	15	+3	147
+D	GGGKSGGGKSGGGKS	15	+3	148
+E	GKGKSGKGKSGKGKS	15	+6	149
+F	GGGKSGGKSGKGGGS	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	GGGGSGGGGSGGGGSGGGGS	20	0	154
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	155
-B	GEGSGEGGSGEGGS	15	-3	156
-C	GGEGSGEGSGEGGS	15	-3	157
-D	GGGESGGGESGGGES	15	-3	158
-E	GEGESGEGESGEGES	15	-6	159
-F	GGGESGGEGSGEGGS	15	-3	160
-G	GEGESGEGESGEGESGEGES	20	-8	161

FIGURE 8B**scFv Linkers**

GGGGS GGGGS GGGGS	(SEQ ID NO: 162)
GGGGS GGGGS GGGGS GGGGS	(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
GGGGS GGGGS KTHTCPPCP ("flex half hinge")	SEQ ID NO:212
GKPGSGKPGSKTHTCPPCP ("charged half hinge1")	SEQ ID NO:213
GKPGSKTHTCPPCP ("charged half hinge2")	SEQ ID NO:214

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

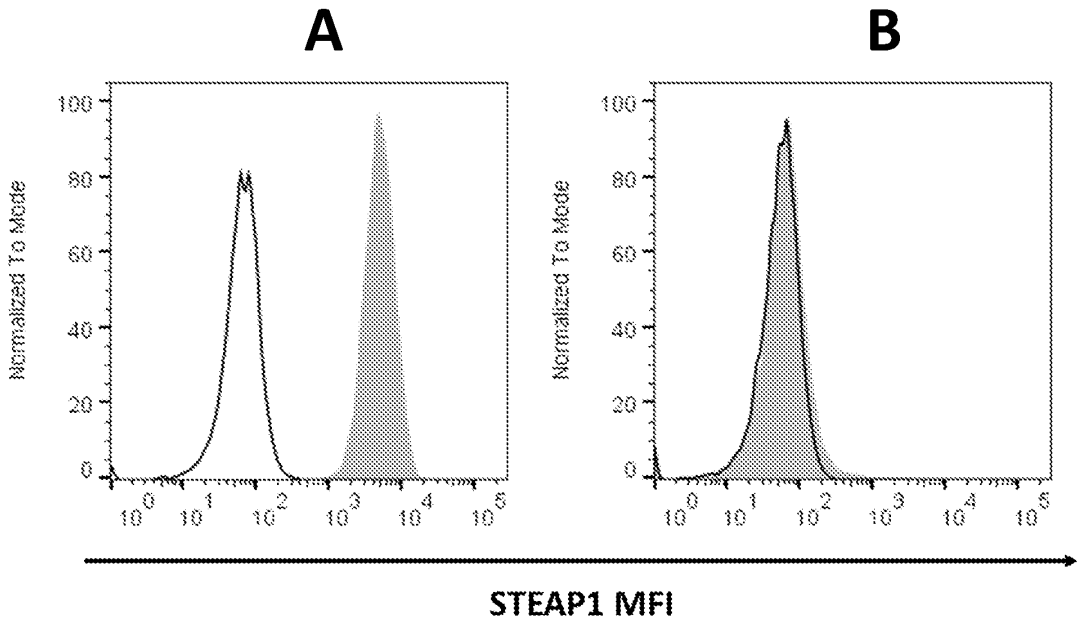


FIGURE 12A

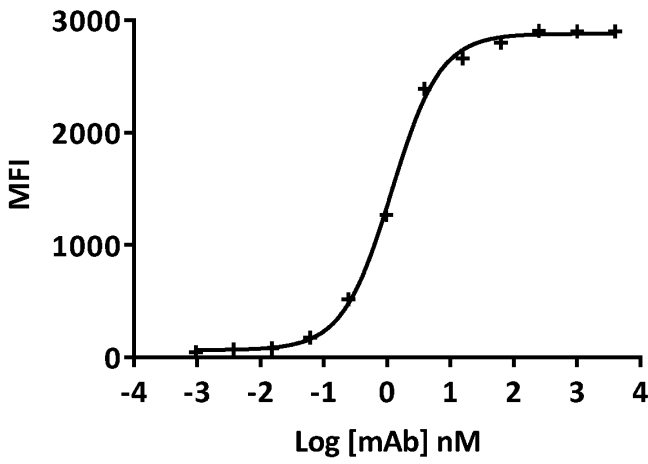


FIGURE 12B

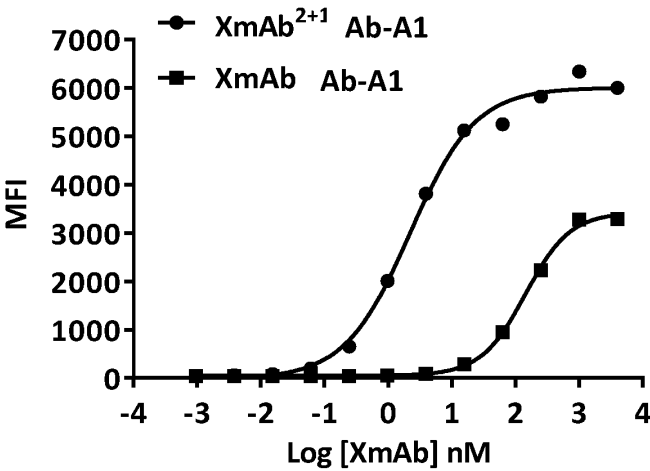


FIGURE 12C

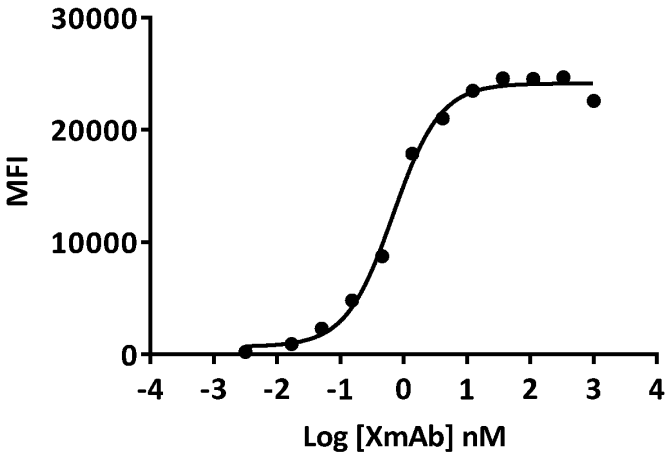


FIGURE 13

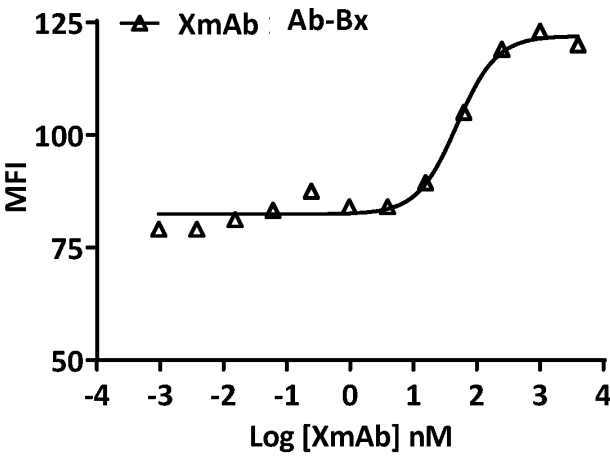


FIGURE 14

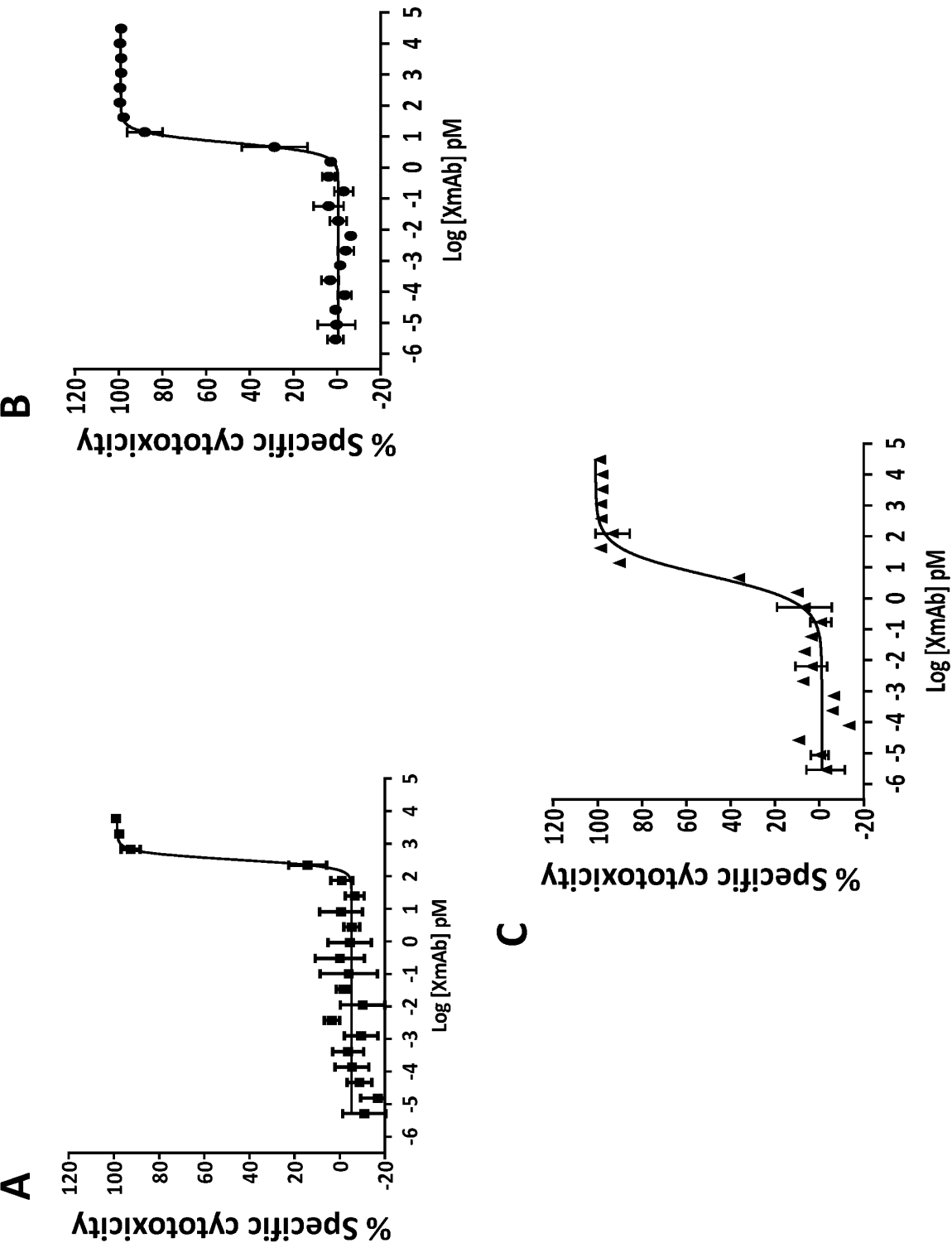


FIGURE 15

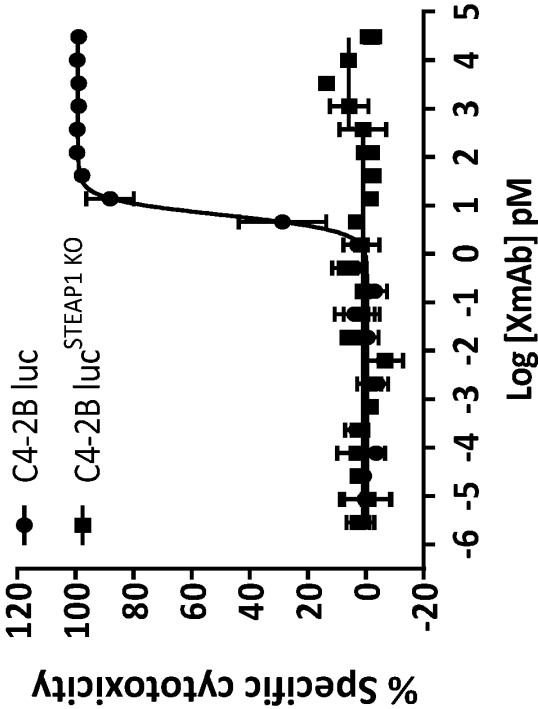


FIGURE 16

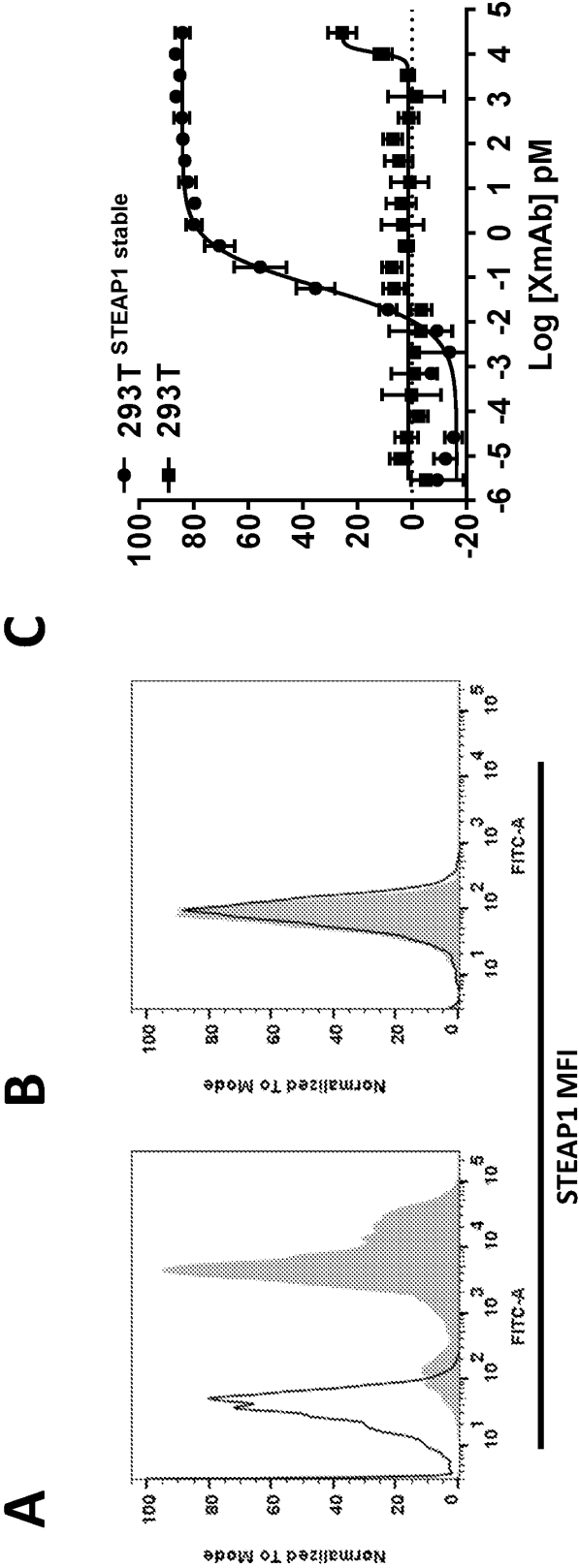


FIGURE 17

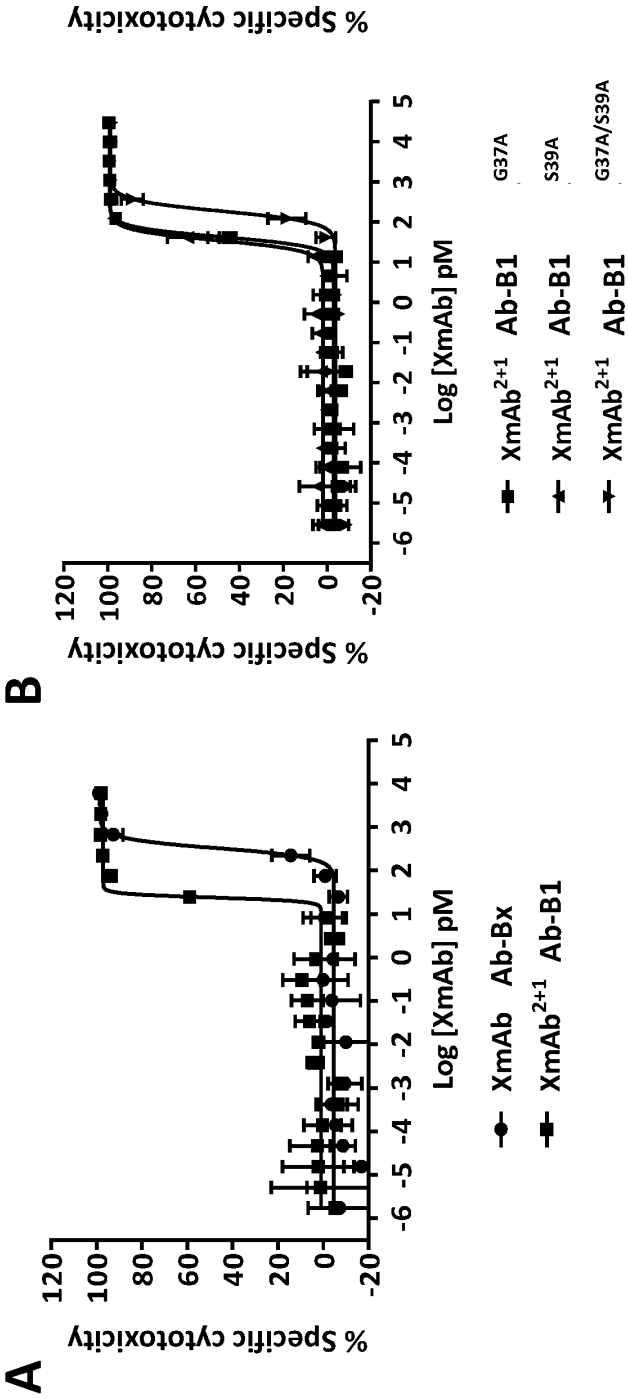


FIGURE 17C

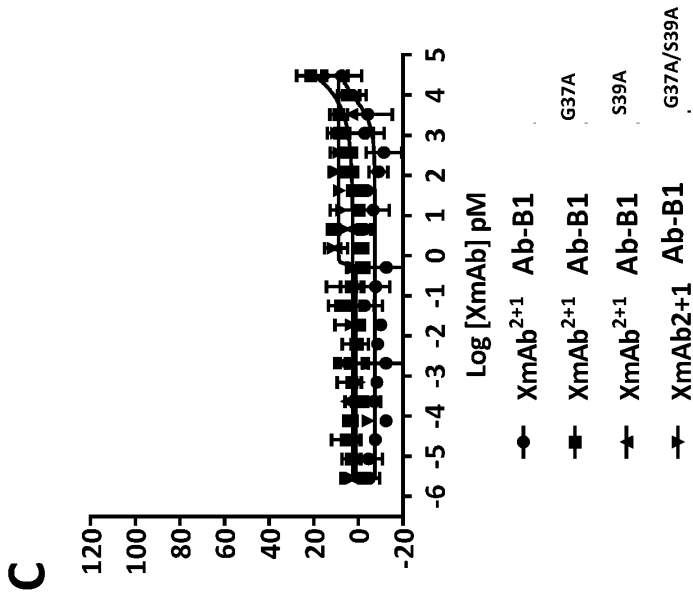


FIGURE 18A-E

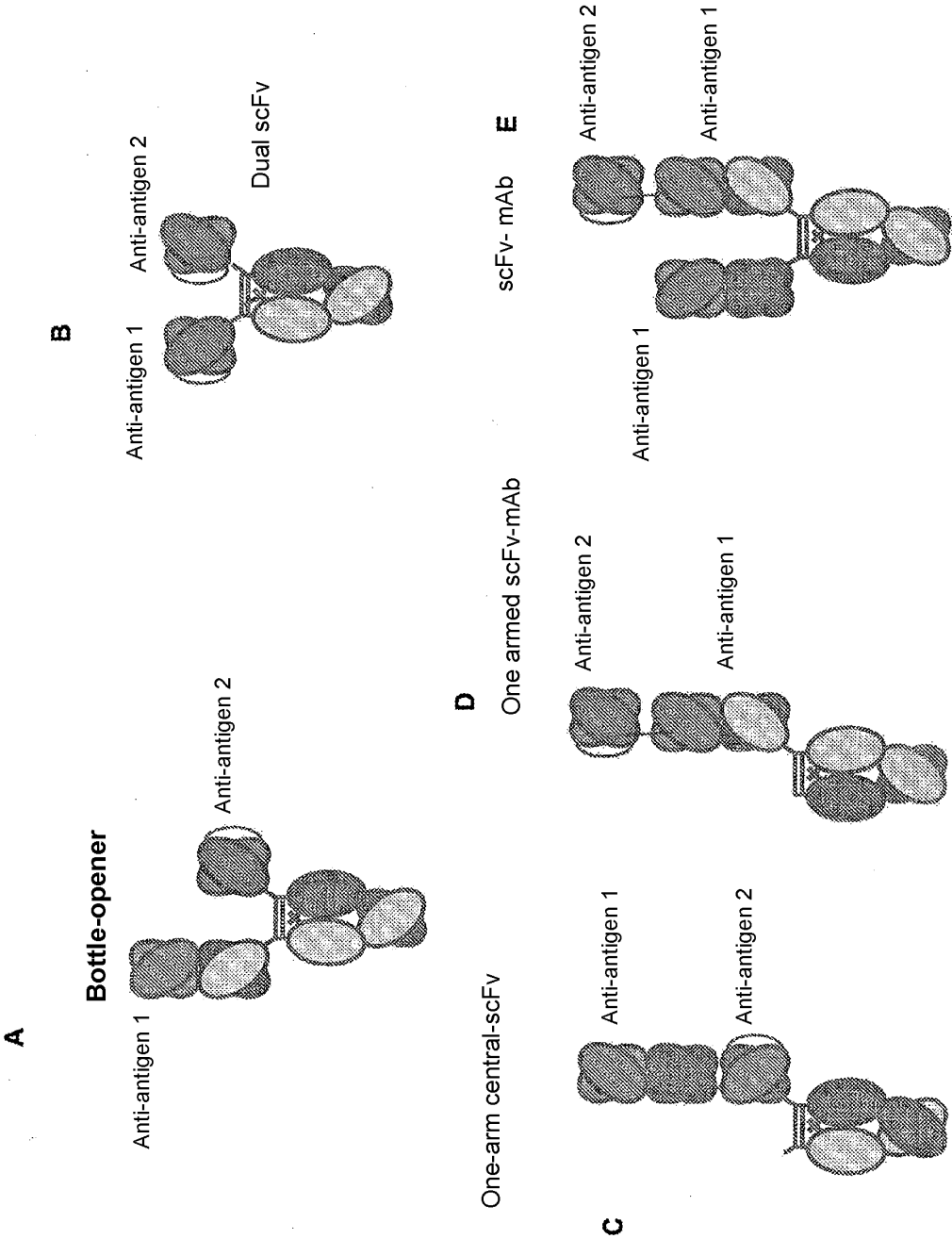


FIGURE 18F-I

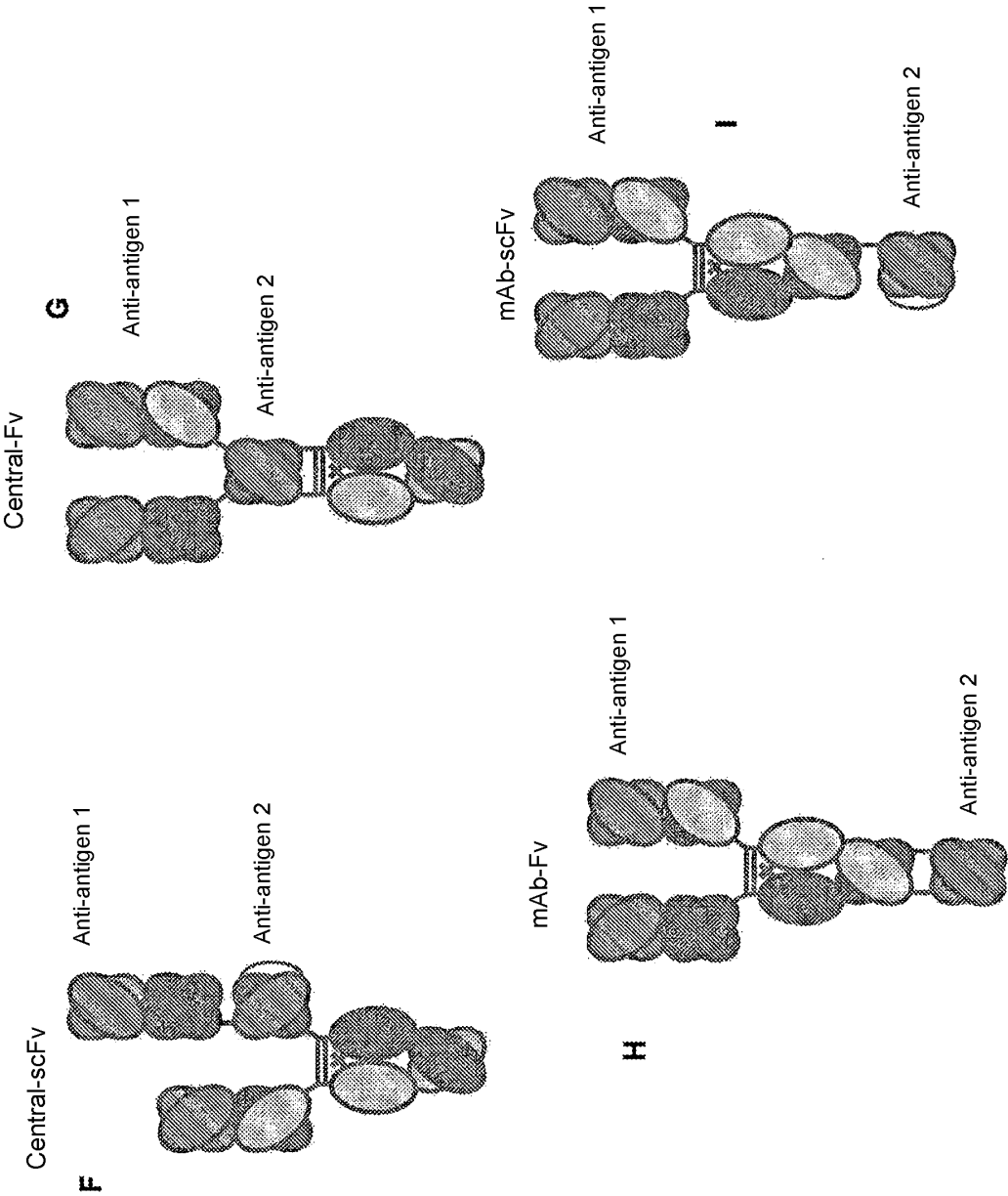


FIGURE 19

SEQ ID NO:	Description	Sequence
1.	CD3 epsilon chain - human	MQSGTHWRVLGLCLLVGVWGQDNGNEEMGGITQTTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNI GSEDEDHLSLKEFSELEQSGYVVCYPRGSKPEDANFYLYLRARVCENCMEMDMVMSVATIVDICTGGILLLVVYWSK NRKAKAPVTRGAGAGGRQRGQNKERPPVNPDPYPIRKGQRDLVSLNQRRRI
2.	STEAP-1 – human	MESRKDITNQEELWKMFKPRNLEDDYLLHKDGTGETSMILKRPVLLHLHQTAAHAEFDCPSE LQHTQELFPQWHLPIKAAIIASLTFLYLLREVHPLATSHQQYFYKIPILVINKVLPM VSITLLALVLPGVAAINQLHNGTKYKKFPHWLDKWMMLTRKQFGLLSFFFAVLHAIYSL SYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPS VSDSLTWREFHYIQSLGIVSLLGTIHALIFAWNKNWIDIKQFVWVYPTPTFMIAVFLPIV VLIFKSILFPLCKRKKILIRHGWEDVTKINKTEICSQL
3.	Ab-A HC variable	QVQLQQSGAEMMKPGASVKISCKATGYTFTSYWIEWVKQRPGHGLEWIGEILPGSGNTDFNEKFKGKATFTADTS SDTAYMHLSSLTSEDSAVVYCTRWGYGTRGVFNWVGAGSTVTYVS
4.	Ab-A HCDR1	TYWIE
5.	Ab-A HCDR2	EILPGSGNTDFNEKFKG
6.	Ab-A HCDR3	WGYYGTRGVFN
7.	Ab-A LC variable	QIVLTQSPAIMASAPGKVTITCSASSSVSYMHWFQQKPGTSPKLIWYSTNLSAGVPARFSGSGTSYSLTISRME AEDAATYCCQRRSFPTYFGGGTKLEIK
8.	Ab-A LCDR1	SASSSVSYMH
9.	Ab-A LCDR2	STSNLAS
10.	Ab-A LCDR3	QQRSSFPT
11.	Ab-A1/A2 (N67Q) Xmab ³⁺¹ LCDR1	RASSSVSYMH

FIGURE 19 Cont.

12.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ LCDR2	STSNLAS	
13.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ LCDR3	QQRSPVPT	
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	WGYGTRGFENV	
17.	Ab-A1/A2 (N67Q) Xmab ²⁺¹ light chain	MGWSCILFLVATATGVHSEIVLTQSPATLSLSPGERATLSCRASSSVSYMHWFQQPGQAPRLLIYSTNLSASGIPAR FSGSGSDTYLTLSISLEPEDEFAVYCCQRRSPFTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASWVCLLNNFYP REAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	
18.	Ab-A1 Xmab ²⁺¹ heavy chain	MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSG NTDFNEKFQGRVTFADTSSDTAYMELSLRSEDATVYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPSVFPL APSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHKPS DTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVYVDGVEV HNAKTKPREEEYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQGVFSCSVMHEALHNHYT QKSLSLSPGK	
19.	Ab-A1 Xmab ²⁺¹ XVHMx	MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFSTYIEWVRQAPGQRLEWMGEILPGSG NTDFNEKFQGRVTFADTSSDTAYMELSLRSEDATVYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPSVFPL APSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCGGGGGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKGLEWVGRI RSKYNRYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNFGDSVSWFAYWVGQGLTVTVSSG KPGSGKPGSGKPGSQAVVTQEPSLTVSPGGTTLTCSGSTGAVTTSYANWVWQKPGKSPRGLIGGTNKR APGVPARFSGSLGGKAALTISGAQPEDEADYCALWVSNHWVFGGGLTVLGGGGGGGGSKTHTCPPCAPP VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVYVDGVEVHNKAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVCLTCLVKGFYPSDIAVEWESNGQ PENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK	

FIGURE 19 Cont.

20.	Ab-A2 (N67Q) X _{mab} ²⁺¹ XVHMx	MDMRVPAQLGLLLWLRGARQVQLVQSGAEVKKPGASVKVCKASGYFTSTYIEWVRQAPGQRLEWMIGEIL PGSGQTDENEKFGQRTVFTADTSSDTAYMELSSLRSEDTAVYYCTRWGYGTRGFNVWVGQGTLLTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVWTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCGGGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKGLEW VGRIRSKYNNYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNGDSVSWFAYWGQGTLLTV SSGKPGSGKPGSGKPGSQAVVTQEPSTLVSPGGTVTLTCSGSTGAVTTSNVANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGGGGGGGGSKTHTCPPCPA PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWVVDGVEVHNAKTKPCEEQYGGSTYRCVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK EILPGSGQTDENEKFGQ
21.	Ab-A2 (N67Q) X _{mab} ²⁺¹ HCDR2 (all other CDRs the same as Ab-A1 X _{mab} ²⁺¹)	
22.	Ab-B1 heavy variable	QIQLVQSGPELKKPGETVKISCKASGYFTFTNYGMNWKQAPGKGLQWGMWMMINTYTGPTYADDFKGRFASLET SARTVSLDINDLNKEDTATYFCTRAGGQLRPGAMIDYWGGQTSVTVSS
23.	Ab-B1 HCDR1	NYGMN
24.	Ab-B1 HCDR2	WMINTYTGPTYADDFKG
25.	Ab-B1 HCDR3	AGGQLRPGAMDY
26.	Ab-B1 light variable	DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSFMNWWYQQKPGQPKLLIYVASNLESIPDRFSGSGSGTDFTLN IHPVEEEDAATYCCQSNEEPPTFGGGTKLEIK
27.	Ab-B1 LCDR1	KASQSDVDGDSFMN
28.	Ab-B1 LCDR2	VASNLES
29.	Ab-B1 LCDR3	QQSNEEPT
30.	Ab-B1 X _{mab} ²⁺¹	KASQSDVDGDSFMN

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	WMINTYTGEPTYADKFKQ
35.	Ab-B1 Xmab ²⁺¹ HCDR3	AGGQLRPGAMDY
36.	Ab-B1 Xmab ²⁺¹ light chain	MGWSCILFLVATATGVHSDIVLTQTPLSLVTPGQPASISCKASQSDYDGDGDFMNMWYLQKPGQPPQLLIYVASNL ESGVPDRFSGSGGTDFTLKISRVEADVGVYCCQSNEEPTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPRKAVQWVKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGECL
37.	Ab-B1 Xmab ²⁺¹ Heavy chain	MGWSCILFLVATATGVHSEIQLVQSGAEVKKPGATVKISCKASGYTFITNYGMNWWQQAPGQGLEWMGMWNTY TGEPTYADKFKQGRVTFITLDTARTVMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSS ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVWTPVSSSLGTQ TYICNVNHKPSDTKVDKKVEPKSCDKHTCCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKF NWYVDGVEVHNATKPREEEYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLTP PSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEEQDGFVSCVM HEALHNHYTQKSLSLSPGK
38.	Ab-B1 Xmab ²⁺¹ XMHx	MGWSCILFLVATATGVHSEIQLVQSGAEVKKPGATVKISCKASGYTFITNYGMNWWQQAPGQGLEWMGMWNTY TGEPTYADKFKQGRVTFITLDTARTVMELSSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSVWTPVSSSLGTQTYICNVNH KPSNTKVDKKVEPKSCGGGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKGLEWV GRIRSKYNNVATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYCVRHGNGFDSYVSWFAYWGQGTITVTVS SGKPGSGKPGSGKPGSQAVVTQEPSTVSPGGTTLTCGSTGAVTTSNYANWVQQKPGKSPRGLIGGTN KRAPGVPARFSGSLGGKAAALTSGAQPEDEADYYCALWYNHWFVGGGTLTVLGGGGGGGSKTHTCPCPA PPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVL HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKTCLVKGFPYPSDIAVEWESNG QPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNGVFSCSMHEALHNHYTQKSLSLSPGK
39.	Anti-CD3 H1_L1.4	EVQLVDSGGGLVQPGGSLRLSCAASGFTSTYAMNWRQAPGKGLEWVGRIRSKYNNVATYYADSVKGRFTISRDR DSKNTLYLQMNSLRAEDTAVYCVRHGNGFDSYVSWFAYWGQGTITVTVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

		TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
40.	Anti-CD3 H1_L1.4	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
41.	Anti-CD3 H1_L1.4	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSS
42.	Anti-CD3 H1_L1.4	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
43.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
44.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
45.	Anti-CD3 H1.30_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSS
46.	Anti-CD3 H1.30_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
47.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
48.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
49.	Anti-CD3 H1.33_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFAYWGQGTLLTVSS
50.	Anti-CD3 H1.33_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

51.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV QEPLSLTSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQP EDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
52.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV QEPLSLTSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQP EDEADYYCALWYSNHWVFGGGTKLTVL
53.	Anti-CD3 H1.31_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMSWVRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSS
54.	Anti-CD3 H1.31_L147	QAVVTQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
55.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKANNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
56.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKANNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
57.	Anti-CD3 H1.32_L147	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKANNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGDSYVSWFAYWGQGTLLTVSS
58.	Anti-CD3 H1.32_L147	QAVVTQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
59.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGPSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
60.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGPSYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSTVSPGGTVTLTCSGSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
61.	Anti-CD3 H1.88_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWRQAPGKGLWVGRIIRSKYNNYATYYADSVKGRFTISR DSKNTLYLQMNSLRAEDTAVYCVRHGNEFGPSYVSWFAYWGQGTLLTVSS

FIGURE 19 Cont.

62.	Anti-CD3 H1.88_L1.47	QAVVTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
63.	Anti-CD3 H1.89_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
64.	Anti-CD3 H1.89_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVL
65.	Anti-CD3 H1.89_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSS
66.	Anti-CD3 H1.89_L1.47	QAVVTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
67.	Anti-CD3 H1.90_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
68.	Anti-CD3 H1.90_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVL
69.	Anti-CD3 H1.90_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSS
70.	Anti-CD3 H1.90_L1.47	QAVVTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
71.	Anti-CD3 H1.91_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
72.	Anti-CD3 H1.91_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAAALISGAQ PEADYYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

73.	Anti-CD3 H1.91_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSS
74.	Anti-CD3 H1.91_L1.47	QAVWTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
75.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTSGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
76.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTSGAQ PEADYYCALWYSNHWVFGGGTKLTVL
77.	Anti-CD3 H1.92_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSS
78.	Anti-CD3 H1.92_L1.47	QAVWTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
79.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTSGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
80.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTSGAQ PEADYYCALWYSNHWVFGGGTKLTVL
81.	Anti-CD3 H1.93_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSS
82.	Anti-CD3 H1.93_L1.47	QAVWTQPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
83.	Anti-CD3 H1.94_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTSGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
84.	Anti-CD3 H1.94_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDGSYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

		TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
85.	Anti-CD3 H1.94_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSS
86.	Anti-CD3 H1.94_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
87.	Anti-CD3 H1.96_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
88.	Anti-CD3 H1.96_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
89.	Anti-CD3 H1.96_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSS
90.	Anti-CD3 H1.96_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
91.	Anti-CD3 H1.97_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
92.	Anti-CD3 H1.97_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
93.	Anti-CD3 H1.97_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSS
94.	Anti-CD3 H1.97_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
95.	Anti-CD3 H1.98_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDQYVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH

FIGURE 19 Cont.

96.	Anti-CD3 H1.98_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYNSHNHWVFGGGTKLTVL
97.	Anti-CD3 H1.98_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSS
98.	Anti-CD3 H1.98_L1.47	QAVVTQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEDEADYYCALWYNSHNHWVFGGGTKLTVL
99.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYNSHNHWVFGGGTKLTVLGSHHHHH
100.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYNSHNHWVFGGGTKLTVL
101.	Anti-CD3 H1.99_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSS
102.	Anti-CD3 H1.99_L1.47	QAVVTQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEDEADYYCALWYNSHNHWVFGGGTKLTVL
103.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGASYSVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYNSHNHWVFGGGTKLTVLGSHHHHH
104.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGASYSVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQ PEDEADYYCALWYNSHNHWVFGGGTKLTVL
105.	Anti-CD3 H1.100_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGASYSVSWFEDYWGQGTLLTVSS
106.	Anti-CD3 H1.100_L1.47	QAVVTQEPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTI SGAQPEDEADYYCALWYNSHNHWVFGGGTKLTVL
107.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEGDSYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV

FIGURE 19 Cont.

108.	Anti-CD3 H1.101_L1.47	TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
109.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSS QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
110.	Anti-CD3 H1.101_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
111.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
112.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
113.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSS QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
114.	Anti-CD3 H1.102_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH
115.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
116.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYSNHWVFGGGTKLTVL
117.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSS QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL
118.	Anti-CD3 H1.103_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKYNNYATYYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGQSYVSFEDYWGQGTLLTVSS QAVVTQEPSLTVSPGGTTLTCSSTGAVTTSNYANWVQKPKGSPRGLIGGTNKRAPGVPARFSGSLGGKAALT SGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

119.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYNSHNWVFEGGDKLTVLGSHHHHH
120.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYNSHNWVFEGGDKLTVL
121.	Anti-CD3 H1.104_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSS
122.	Anti-CD3 H1.104_L1.47	QAVVTQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYNSHNWVFEGGDKLTVL
123.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGA QPDEADYYCALWYNSHNWVFEGGDKLTVLGSHHHHH
124.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV VTQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGA QPDEADYYCALWYNSHNWVFEGGDKLTVL
125.	Anti-CD3 H1.105_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKYNNYATYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFEDYWGQGTLLTVSS
126.	Anti-CD3 H1.105_L1.47	QAVVTQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SGAQPEDEADYYCALWYNSHNWVFEGGDKLTVL
127.	Anti-CD3 H1.106_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYNSHNWVFEGGDKLTVLGSHHHHH
128.	Anti-CD3 H1.106_L1.47 (ScFv)	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAV TQEPSLTVSPGGTVTLTCSGSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTISGAQ PEDEADYYCALWYNSHNWVFEGGDKLTVL
129.	Anti-CD3 H1.106_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTSTYAMNWVRQAPGKGLIEWVGRIRSKANNYATAYADSVKGRFTISRD DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYVSWFAYWGQGTLLTVSS

FIGURE 19 Cont.

130.	Anti-CD3 H1.106_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
131.	Anti-CD3 H1.107_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
132.	Anti-CD3 H1.107_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVL
133.	Anti-CD3 H1.107_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSS
134.	Anti-CD3 H1.107_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
135.	Anti-CD3 H1.108_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
136.	Anti-CD3 H1.108_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVL
137.	Anti-CD3 H1.108_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGASYVWFAYWGQGTLLTVSS
138.	Anti-CD3 H1.108_L1.47	QAVVTQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTI SGAQPEADYYCALWYSNHWVFGGGTKLTVL
139.	Anti-CD3 H1.109_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDSYVWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVLGSHHHHH
140.	Anti-CD3 H1.109_L1.47	EVQLVSGGGLVQPGSLRLSCAASGFTSTYAMNWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFGDSYVWFEDYWGQGTLLTVSSGKPGSGKPGSGKPGSQAVV TQEPSLTVSPGGTTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGTNKRAPGVPARFSGSLGGKAALTISGAQ PEADYYCALWYSNHWVFGGGTKLTVL

FIGURE 19 Cont.

141.	Anti-CD3 H1.109_L1.47	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWWVRQAPGKGLWVGRIRSKANNYATAYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYSYVWFYWGQGTLLTVSS
142.	Anti-CD3 H1.109_L1.47	QAVTQPSLTVSPGGTTLTCSGSTGAVTTSNYANWVQKPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI SQAQPEADYYCALWYSNHWVFGGGTKLTVL
143.	Linker	GGGGGGGGGGGG
144.	Whitlow linker	GSTSGKPGSGEGSTKG
145.	Linker	IRPRAIGGSKPRVA
146.	Linker	GKGGSGKGGSGKGG
147.	Linker	GGKGGSGKGGSGKGG
148.	Linker	GGKGGSGKGGSGKGG
149.	Linker	GKGGSGKGGSGKGG
150.	Linker	GGKGGSGKGGSGKGG
151.	Linker	GKGGSGKGGSGKGG
152.	Linker	GKGGSGKGGSGKGGSGKGG
153.	Linker	GKGGSGKGGSGKGGSGKGG
154.	Linker	GGGGGGGGGGGGGGGGGG
155.	Linker	STAGDTHLGGEDFD
156.	Linker	GEGSGEGSGEGSG
157.	Linker	GGEGSGEGSGEGSG
158.	Linker	GGEGSGEGSGEGSG
159.	Linker	GEGSGEGSGEGSG
160.	Linker	GGEGSGEGSGEGSG
161.	Linker	GEGSGEGSGEGSGEGSG
162.	Linker	GGGGGGGGGGGGGGGGGG
163.	Linker	GGGGGGGGGGGGGGGGGG
164.	Linker	GSTSGKPGSGEGSTKG
165.	Linker	PRGASKGSASQTGSAPGS
166.	Linker	GTAAGAGAGAGAGAGAG
167.	Linker	GTSGGSGSGSGSGGGGG
168.	Linker	GKPGSGKPGSGKPGSGKPGS
169.	Ab-A1 XmAb ²⁺¹ , Ab-A2 (N67Q) XmAb ²⁺¹ , Ab-B1 XmAb ²⁺¹	EVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWWVRQAPGKGLWVGRIRSKYNNYATYADSVKGRFTISR DSKNTLYQMNSLRAEDTAVYCVRHGNEFDYSYVWFYWGQGTLLTVSS

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	RIRSKYNINATYYADSVKG
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	QAVTQEPSLTVSPGGTTLTGSSTGAVTTSNYANWVQQPKGKSPRGLIGGTNKRAPGVPARFSGSLGGKAALTI 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	MESISMMGSPKSLSETFLPNGLNGIKDARKVTGVIGSGDFAKSLTIRLCGYHVVIGS RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGGKILIDVSNM RINQYPESNAEVLASLFPDSLIVKGFNVVSAWALQLGPKDASRVYICSNNIQARQQVIE

FIGURE 19 Cont.

		LARQLNFIPIDLGSLSSAREIENLPRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPVA RNQSDFYKPIEIVNKTLPVIAITLLSLVLAGLAAAYQLYGTKYRRFPFWLEWLQ CRKQLGLSFFAMVHVAYSLCLPMRRSERYFLNNMAYQQVQHANIENSWNEEEVWRIEMV ISFGIMSLGLLSLAVTSPSVSNALNWREFSQSTLGYVALLISTFHVLIYGWKRAFE EYYRYFTPPNFVLALVLPISVILGKIILPCISRKLIKRIKKGWKSQFLEEGMGGTIP HVSPEVTVVM
178.	Linker	GSGGS
179.	Linker	GGGS
180.	Linker	GGGS
181.	Linker	GFLG
182.	Ab-A1 Xmap ²⁺¹ heavy variable	QVQLVQSGAEVKKPGASVKVCKASGYTFSTWIEWVRQAPGQRLLEWMGEILPGSGNTDFNEKFQGRVFTTADTS SDTAYMELSSLRSEDTAVYYCTRWGYGTRGVFNWVGQGLTVTVSS
183.	Ab-A1/A2 (N67Q) Xmap ²⁺¹ light variable	EIVLTQSPATLSLSPGERATLSCRASSSVSMHWFAQKPGQAPRLLIYSTNLSASGIPARFSGSGSGTDYTLTISSLEPE DFAVYYCQRRSFPTFGQGTKLEIK
184.	Ab-A2 (N67Q) Xmap ²⁺¹ heavy variable	QVQLVQSGAEVKKPGASVKVCKASGYTFSTWIEWVRQAPGQRLLEWMGEILPGSGQTDNEKFQGRVFTTADTS SDTAYMELSSLRSEDTAVYYCTRWGYGTRGVFNWVGQGLTVTVSS
185.	Ab-B1 Xmap ²⁺¹ heavy variable	EIQLVQSGAEVKKPGATVKISCKASGYTFSTWYGMNWWQQAPGQGLEWMGMWMTNTYGEPTYADKFGQGRVFTLD TSARTVYMELSLRSEDTAVYFCARAGGQLRPGAMDYWGQGTMTVTVSS
186.	Ab-B1 Xmap ²⁺¹ light variable	DIVLTQTLPLSLVTPGQPASISCKASQSDYDGDGSMNWYLQKPGQPPQLLIYVASNLESQVPDFSGSGSGTDFTLK ISRVEAEDGVVYCYCQSNPEPTFGQGTKLEIK
187.	human PD-1	PGWFLDSPDRPWNPPTFSPALLVVTGEDNATFTCSFNTSESFVFNWYRMSPSNQTKLAAFPEDRSQPGQDCRF RVTQLPNGRDFHMSVVRARRNDSTYLCGAILAPKAKIKESLRAELRVTERRAEVPTAHPSPSRPAGQFQTLVWG VVGGLLSLVLLVWLVAVICRAARGTIGARTGQPLKEDPSAVPVFSDYDGLDFQWREKTPPEPPVPCVPEQTEYA TIVFSGMGTSSPARRGSADGPRSAQPLRPEDGHCSWPL
188.	cynomologous PD-1	MQIPQAPWPVWVAVLQLGWRPWFLESFDRPWNPAPTSPALLVTEGDNATFTCSFNSASEFVFNWYRMSPS NQTDKLAAPFEDRSQPGQDCRFVTRIPNGRDFHMSVVRARRNDSTYLCGAILAPKAKIKESLRAELRVTERRAE VPTAHPSPSRPAGQFQALVWGWGGLLSLVLLVWLVAVICRAAQGTIEARRTGQPLKEDPSAVPVFSDYDGLD FQWREKTPPEPPVPCVPEQTEYATIVFSGIGTSSPARRGSADGPRSPRLRPEDGHCSWPL
189.	Anti-PD-1 antibody HC	SYDMS

FIGURE 19 Cont.

	CDR1	
190.	Anti-PD-1 antibody HC CDR2	LISGGGSQTYAESVK
191.	Anti-PD-1 antibody HC CDR3	PSGHYFYAMDV
192.	Anti-PD-1 antibody LC CDR1	RASQGISNWL
193.	Anti-PD-1 antibody LC CDR2	AASSLQS
194.	Anti-PD-1 antibody LC CDR3	QQAESFPHT
195.	Anti-PD-1 antibody HC VARIABLE	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYDMSWVRQAPGKGLWVSLISGGGSQTYAESVKGRFTISRDNK NTLYQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITVTVSS
196.	Anti-PD-1 antibody LC VARIABLE	DIQMTQSPSSVSASVGDRTTITCRASQGISNWLAWYQQKPGKAPKLLIFAAASSLQSGVPSRFSGGSGGTDFTLTISL QPEDFATYCCQAESFPHTFGGGTKVEIK
197.	Anti-PD-1 antibody HC FULL LENGTH	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASGFTSSYDMSWVRQAPGKGLWVSLISG GGSQTYAESVKGRFTISRDNKNTLYQMNSLRAEDTAVYFCASPSGHYFYAMDVWGQGTITVTVSSASTKGPSVF PLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHHK PSNTKYVDKKVEPKSCDKTHCTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV EVHNAKTKPCEEQYGSTYRCVSLTLVHLDSDGSFFLYSKLTVDKSRWQQQGNVFSCSVMHEALHN KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQQGNVFSCSVMHEALHN HYTQKSLISLSPGK
198.	Anti-PD-1 antibody LC	MDMRVPAQLLGLLLWLRGARCDIQMTQSPSSVSASVGDRTTITCRASQGISNWLAWYQQKPGKAPKLLIFAASSL QSGVPSRFSGGSGGTDFTLTISLQPEDFATYCCQAESFPHTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVV

FIGURE 19 Cont.

	FULL LENGTH	
199.	Ab-A2 (N67Q) X _{mab} 2+1 heavy chain	CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFN RGEK MDMRVPAQLLGLLLWLIRGARCQQLVQSGAEVKKPGASVKVCKASGYFTFTYWIEWVRQAPGQRLEWMIGEIL PGSGQTDENEKFGQGRVFTADTSSDTAYMELSLRSEDATVYCTRWGYGTRGFNVWVGQGLTVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTICNVN HKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAGPSVFLFPPKPKDRLMISRTPEVTCVVVDVKHEDPEVKFNWYVDG VEVHNAKTKPCEEYGGSTYRCVSLTVLHQQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMT KNQVSLTCDVSGFYPSDIAVEWESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNNH YTQKSLSLSPGK
200.	Ab-A1/A2 (N67Q) X _{mab} ²⁺¹ light chain minus signal sequence	EIVLTQSPATLSLSPGERATLSCRASSSVYMHWFQQKPGQAPRLLVYSTNLSASIPARFSGSGGTVDYTLTISSLEPE DFAVYCCQRRSFYTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC
201.	Ab-A1 X _{mab} ²⁺¹ heavy chain minus the signal sequence	QVQLVQSGAEVKKPGASVKVCKASGYFTFTYWIEWVRQAPGQRLEWMGEILPGSGNTDFNEKFQGRVFTADTS SDTAYMELSLRSEDATVYCTRWGYGTRGFNVWVGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTICNVNHNKPSDTKVDKKVEPKSCDKTHTC PPCPAPPVAGPSVFLFPPKPKDRLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVS VLTVLHQQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW ESDGPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCFSVMHEALHNNHYTQKSLSLSPGK
202.	Ab-A1 X _{mab} ²⁺¹ X _{VHMx} minus the signal sequence	QVQLVQSGAEVKKPGASVKVCKASGYFTFTYWIEWVRQAPGQRLEWMGEILPGSGNTDFNEKFQGRVFTADTS SDTAYMELSLRSEDATVYCTRWGYGTRGFNVWVGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTICNVNHNKPSNTKVDKKVEPKSCGGGS GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWNVRQAPGKLEWVGRIRSKYNVATYVADSVKGR FTISRDTSKNTLYLQMNSLRAEDTAVYCVRHGNGFDVSVWFAYWGQGLTVTVSSGKPGSGKPGSGKPG SQAVTQEPSTLSPGGTVTLTCSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAAL TISGAQPEDEADYICALWYSNHNWVFGGGLTTLVGGGGGGGGGSKTHTCPPCPAPPVAGPSVFLFPPKPKDRLMIS

FIGURE 19 Cont.

203.	Ab-A2 (N67Q) Xmab ²⁺¹ heavy chain minus signal sequence	RTPEVTVVDVKHEDPEVKFNWVYDGVGVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSFFLY SKLTVDKSRWQQGKVFSCVMHEALHNHYTQKSLSLSPGK
204.	Ab-B1 Xmab ²⁺¹ light chain minus signal sequence	QVQLVQSGAEVKKPGASVKVSCKASGYTFSTYVIEWVRQAPGQRLIEWMGEILPGSGGQTDNFNEKFQGRVFTTADTS SDTAYMELSSLRSEDTAVYYCTRWGYGTRGVFNWVGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTHTC PPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPCEEEYGSYRCSV VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEW ESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK
205.	Ab-B1 Xmab ²⁺¹ heavy chain minus signal sequence	DIVLTQTPLSLSVTPGQPAISCKASQSDVDYDGSFMNWWYLQKPGQPPQLLIYVASNLESGVPDRFSGSGSDTFLTK ISRVEAEDVGYYCQSQSNEEPPTFGQGTGLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWVKVDN ALQSGNSQESVTEQDSKDSYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
206.	Ab-B1 Xmab ²⁺¹ XMHx minus signal sequence	QLVQSGAEVKKPGATVKISKASGYTFITNYGMNWWVQAPGQGLEWMGMWMTYTGPTYADKFQGRVFTFLDT SARTVYMELSSLRSEDTAVYFCARAGGQLRPAMDYWGQGMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSDTKVDKKEPKSCDKTH TCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVE WESDGGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWEQGDVFCSCVMHEALHNHYTQKSLSLSPGK
207.	Ab-A2 (N67Q) Xmab ²⁺¹ XVHMx	QLVQSGAEVKKPGATVKISKASGYTFITNYGMNWWVQAPGQGLEWMGMWMTYTGPTYADKFQGRVFTFLDT SARTVYMELSSLRSEDTAVYFCARAGGQLRPAMDYWGQGMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCGGG GSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTYAMNWWVRQAPGKLEWVRGRISKYNNYATYYADSVK GRFTISRDSDSKNTLYLQMNSLRAEDTAVYCVRHGNGFSDYVSWFAVWGQGLTVTVSSGKPGSGKPGSGKPGSGK PGSAVVTQEPSTLSPGGTVTLTCSSTGAVTTSNVANWVQKPGKSPRLIGGTNKRAPGVPARFSGSLGGA ALTISGAQPEDEADYYCALWYSNHWVFGGGLTVLGGGGSGGGGSKTHTCPCPAPPVAGPSVFLFPPKPKDTL MISRTPEVTCVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREQMTKNQVKLTCLVKGYFSPDIAVEWESNGQPENNYKTPPVLDSDGSF FLYSKLTVDKSRWQQGKVFSCVMHEALHNHYTQKSLSLSPGK

FIGURE 19 Cont.

	minus signal sequence	YFPEPVTWNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCGGGGS GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTSYAMNWWRQAPGKGLWVGRIRSKYNNVATYYADSVKGR FTISRDTSKNTLYLQMNSLRAEDTAVYCVRHGNFGDSVSWFAYWGQGLTVTVSSGKPGSGKPGSGKPGKPG SQAVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQKPGKSPRGLIGGTNKRAPGVPARFSGSLGGKAAL TISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGGGGGGGGSKTHTCPPAPPVAGPSVFLPPKPKDTLMIS RTPEVTCVVDVKHEDPEVKFNWVDGVEVHNAKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNAKLP APIEKTISKAKGQPREPQVYTLPPSREQMTKNQVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
208.	Anti-PD-1 antibody HC FULL LENGTH minus signal sequence	EVQLLEGGGLVQPGGSLRLSCAASGFTFSYDMMSWVRQAPGKGLWVSLISGGGSQTYVAESVKGRFTISRDNK NTLYLQMNSLRAEDTAVYFCASPSPGHYFYAMDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTWNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEVHNAKTPCEEQYGSTYRCVS VLTVLHQDWLNGKEYCKKVSNAKLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
209.	Anti-PD-1 antibody LC FULL LENGTH minus signal sequence	DIQMTQSPSSVSASVGDRTVITTCRASQGISNWLAWYQQKPGKAPKLLIFAAASSLSQSGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQAESEFPHTFGGGTKVEIKRTVAAPSVFIFPPSDEQLIKSGTASVVCCLINNFYPREAKVQWKVDNALQ SGNSQESVTEQDSKDSSTYSLSSTLTLSKADVEKHKVYACEVTHQGLSSPVTKSFRGEC

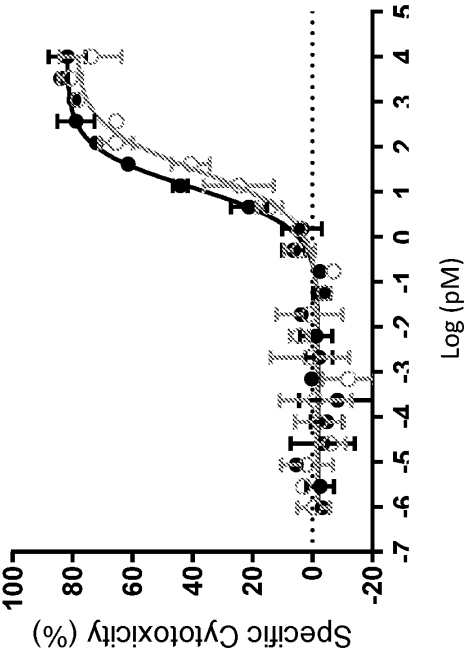


FIGURE 20A

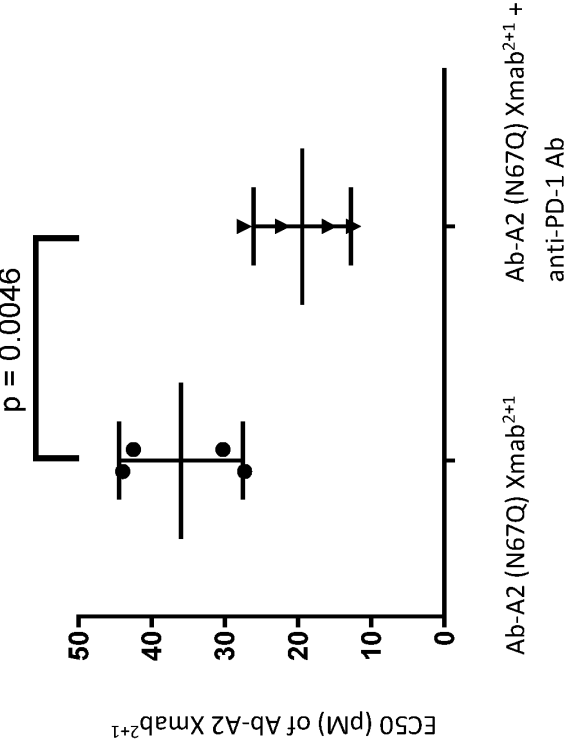


FIGURE 20B

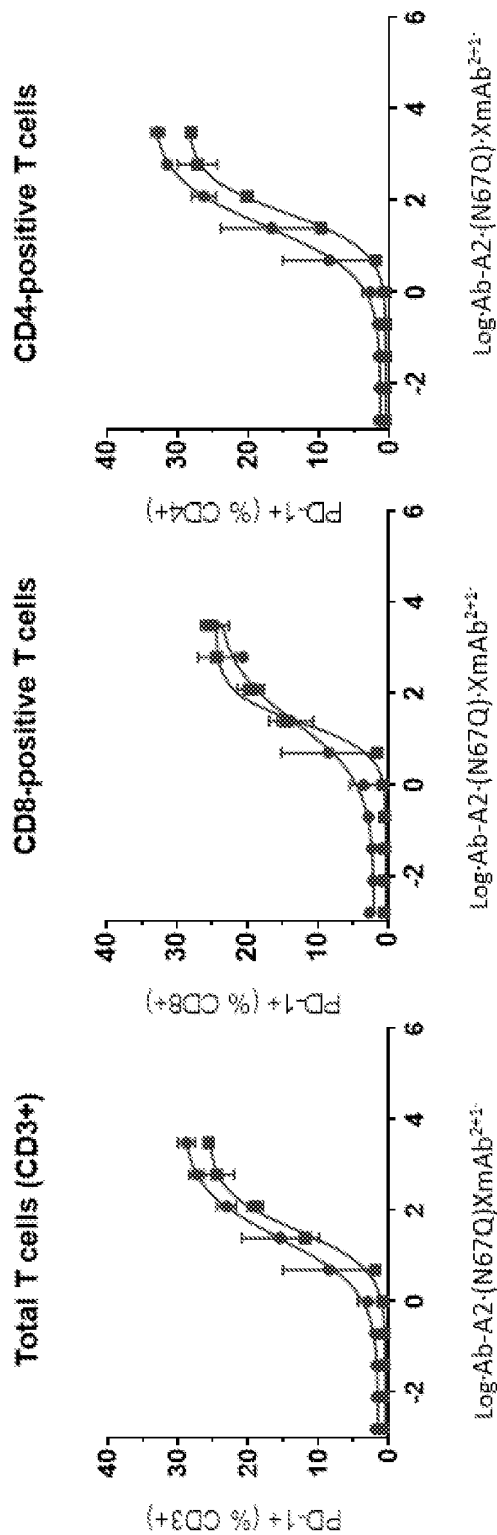


FIGURE 21A

FIGURE 21B

FIGURE 21C

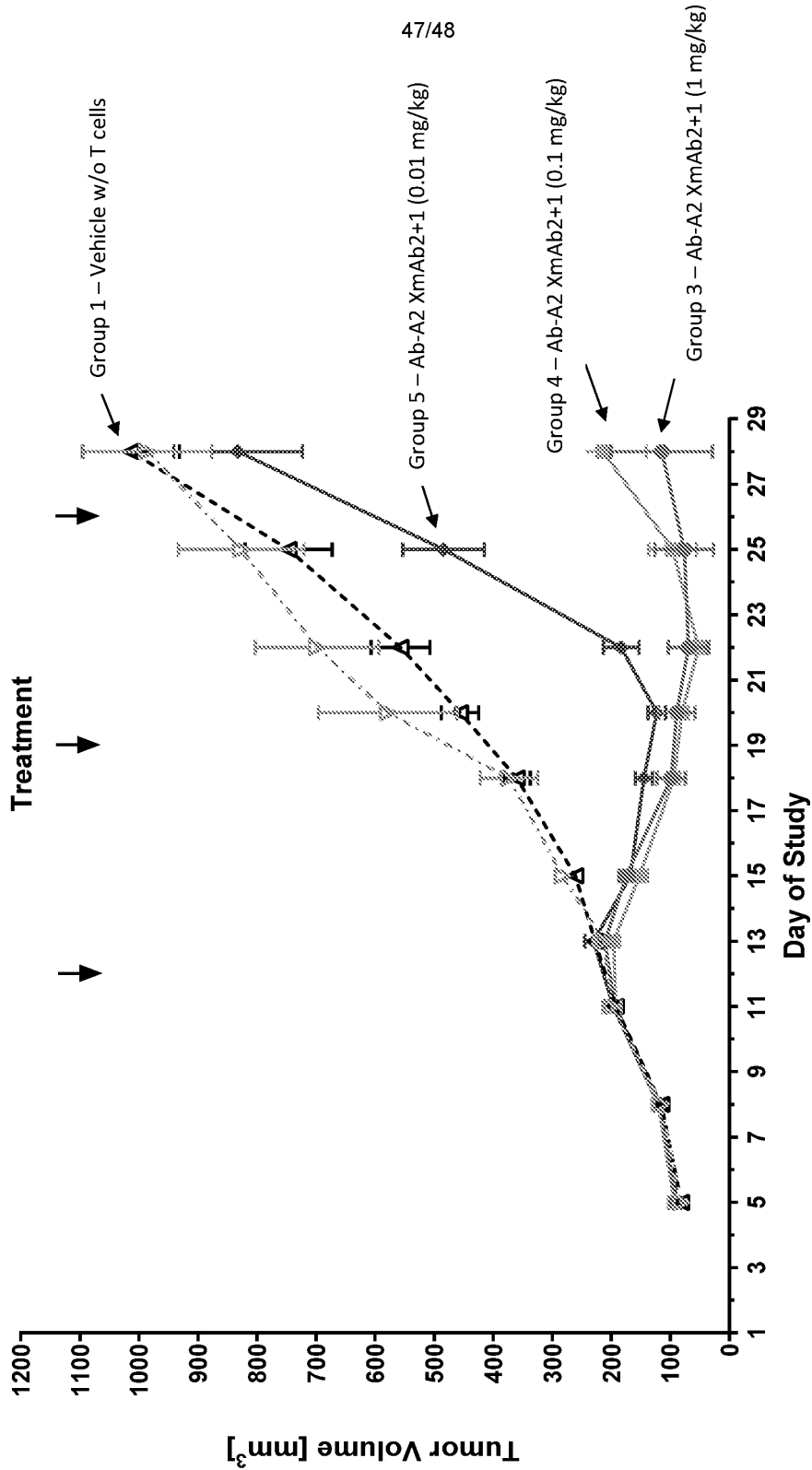


FIGURE 22

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.	n.s.	n.s.	n.s.	n.s.	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.	n.s.	n.s.	n.s.	n.s.	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.	n.s.	n.s.	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.