

A3 clone

DIQMTQSPSFMSASVGDRVITTCRASQDIGSYLAWYQQKPGKAPKLLIYAASTL
QSGVPSRFSSGSGSGTDFTLTINSLQPEDFATYYCQQSYSSPPTFGPGTTLEIK
 (SEQ ID NO:1)

LC-CDR1: RASQDIGSYLA (SEQ ID NO:6)

LC-CDR2: AASTLQS (SEQ ID NO:7)

LC-CDR3: QQSYSSPPT (SEQ ID NO:8)

B10 clone

EIVLTQSPATLSFSPGERATLSCRASQSVGSYLAWYQQRPGQAPRPLIYDATN
RATGIPTRFSGSGSGTDFTLTISSELEPEDFATYYCQHRRTFGRGTKLEIK
 (SEQ ID NO:2)

LC-CDR1: RASQSVGSYLA (SEQ ID NO:9)

LC-CDR2: DATNRAT (SEQ ID NO:10)

LC-CDR3: QHRRT (SEQ ID NO:11)

G6 clone

DVVMTQSPLSLPVTGPGEPAISCRRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI
YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPTFGQ
 GTKVELK (SEQ ID NO:3)

LC-CDR1: RSSQSLLHSNGYNYLD (SEQ ID NO:12)

LC-CDR2: LGSNRAS (SEQ ID NO:13)

LC-CDR3: MQGTHWPPT (SEQ ID NO:14)

Figure 1

G7 clone

ETTLTQSPGTL~~SLSPGERATL~~SCRASQSVSSSYLAWYQQTPGQAPRLLIYGAS
SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRLEIK
 (SEQ ID NO:4)

LC-CDR1: RASQSVSSSYLA (SEQ ID NO:15)

LC-CDR2: GASSRAT (SEQ ID NO:16)

LC-CDR3: QQYGSSPIT (SEQ ID NO:17)

G9 clone

ETTLTQSPGTL~~SLSPGERATL~~SCRASQSVSSSYLAWYQQKIGQAPRLLIYGASS
RATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRLEIK
 (SEQ ID NO:5)

LC-CDR1: RASQSVSSSYLA (SEQ ID NO:15)

LC-CDR2: GASSRAT (SEQ ID NO:16)

LC-CDR3: QQYGSSPIT (SEQ ID NO:17)

A11 clone

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNNYVSWYQQLPGTAPKLLIYGNN
WRPSGIPDRFSGSKSGTSATLAISGLQTGDEADYYCETWDSSLSAGVFGGGT
 KLTVL (SEQ ID NO:45)

LC-CDR1: SGSSSNIGNNNYVS (SEQ ID NO:47)

LC-CDR2: GNNWRPS (SEQ ID NO:48)

LC-CDR3: ETWDSSLSAGV (SEQ ID NO:49)

Figure 1 (Cont.)

A11_q1 clone

QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGNN
WRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCETWDSSLSAGVFGGGT
KLTVL (SEQ ID NO:46)

LC-CDR1: SGSSSNIGNNYVS (SEQ ID NO:47)

LC-CDR2: GNNWRPS (SEQ ID NO:48)

LC-CDR3: ETWDSSLSAGV (SEQ ID NO:49)

Figure 1 (Cont.)

A3 clone

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSY¹YMH²WVRQAPGQGLEWMGII³
NPSGGSTSYAQKFQG⁴RV⁵TM⁶TR⁷DT⁸ST⁹SV¹⁰YME¹¹LS¹²SL¹³RS¹⁴ED¹⁵TAV¹⁶YY¹⁷CAR¹⁸SPGVV¹⁹
TALFDYWGQGTLVTVSS (SEQ ID NO:19)

HC-CDR1:	GYTFTSYMH	(SEQ ID NO:24), or
	SYMH	(SEQ ID NO:58)
HC-CDR2:	IINPSGGSTSYAQKFQG	(SEQ ID NO:25)
HC-CDR3:	SPGVVTALFDY	(SEQ ID NO:26)

B10 clone

QVQLQESGPGLVKASETSLTCTVSGGSIGSSDYYWGWIRQPPGKGLEWIGSI³
YYSGSTYYNPSLKS⁴RV⁵TMS⁶VD⁷TP⁸NN⁹QF¹⁰SL¹¹KL¹²SS¹³VT¹⁴AAD¹⁵TAV¹⁶YY¹⁷CAR¹⁸GEHRGEF¹⁹
DYWGQGTLVTVSS (SEQ ID NO:20)

HC-CDR1:	GGSIGSSDYYWG	(SEQ ID NO:27), or
	SSDYYWG	(SEQ ID NO:59)
HC-CDR2:	SIYYSGSTYYNPSLKS	(SEQ ID NO:28)
HC-CDR3:	GEHRGEFDY	(SEQ ID NO:29)

G6 clone

QVQLQESGPGLVKPSGTLSTCAVSGGSISSN¹WWS²WVRQPPGKGLEWIGE³I⁴
YHSGSTNYNPSLKS⁵RV⁶TIS⁷VD⁸KSK⁹NQ¹⁰FSL¹¹KL¹²SS¹³VT¹⁴AAD¹⁵TAV¹⁶YY¹⁷CAR¹⁸VAVAGTV¹⁹
DYWGQGTLVTVSS (SEQ ID NO:21)

HC-CDR1:	GGSISSN ¹ WWS	(SEQ ID NO:30), or
	SSN ¹ WWS	(SEQ ID NO:60)
HC-CDR2:	EIYHSGSTNYNPSLKS	(SEQ ID NO:31)
HC-CDR3:	VVAVAGTVDY	(SEQ ID NO:32)

Figure 2

G7 clone

EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWRQAPGQGLEWMGIIN
PSGGSTSYAQKFQGGRVTMTRDTSTSTVYMELSSLRSED~~TAVYYCARD~~DQYSSG
WYYYGMDVWGQGTTVTVSS (SEQ ID NO:22)

HC-CDR1:	GYTFTSYMH	(SEQ ID NO:24), or
	SYMH	(SEQ ID NO:58)
HC-CDR2:	IINPSGGSTSYAQKFQG	(SEQ ID NO:25)
HC-CDR3:	DQYSSGWYYYGMDV	(SEQ ID NO:33)

G9 clone

QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYMHWRQAPGQGLEWMGIIN
NPSGGSTSYAQKFQGGRVTMTRDTSTSTVYMELSSLRSED~~TAVYYCARD~~DLYSY
GFYYYGMDVWGQGTTVTVSS (SEQ ID NO:23)

HC-CDR1:	GYTFTSYMH	(SEQ ID NO:24), or
	SYMH	(SEQ ID NO:58)
HC-CDR2:	IINPSGGSTSYAQKFQG	(SEQ ID NO:25)
HC-CDR3:	DLYSYGFYYYGMDV	(SEQ ID NO:34)

A11 clone

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIN
HSGSTNYNPSLKSRVTVISVDTSKNQFSLKLSSVTAAD~~TAVYYCARG~~GYVAGFDY
WGQGTLVTVSS (SEQ ID NO:50)

HC-CDR1:	GGSFSGYYWS	(SEQ ID NO:52), or
	GYWS	(SEQ ID NO: 61)
HC-CDR2:	EINHSGSTNYNPSLKS	(SEQ ID NO:53)
HC-CDR3:	GYVAGFDY	(SEQ ID NO:54)

Figure 2 (Cont.)

A11 gl clone

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEIN
HSGSTNYNPSLKSSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGYVAGFDY
WGQGTLVTVSS (SEQ ID NO:51)

HC-CDR1:	GGSFSGYYWS	(SEQ ID NO:52), or
	GYYS	(SEQ ID NO: 61)
HC-CDR2:	EINHSGSTNYNPSLKS	(SEQ ID NO:53)
HC-CDR3:	GYVAGFDY	(SEQ ID NO:54)

Figure 2 (Cont.)

Clone	CDR L1	CDR L2	CDR L3
Light Chain			
A3	RASQDIGSYLA (SEQ ID NO:6)	AASTLQS (SEQ ID NO:7)	QQSYSSPPT (SEQ ID NO:8)
B10	RASQSVGSYLA (SEQ ID NO:9)	DATNRAT (SEQ ID NO:10)	QHRRT (SEQ ID NO:11)
G6	RSSQSLHSHNGYNYLD (SEQ ID NO:12)	LGSNRAS (SEQ ID NO:13)	MQGTHWPPT (SEQ ID NO:14)
G7	RASQSVSSSYLA (SEQ ID NO:15)	GASSRAT (SEQ ID NO:16)	QQYGSSPIT (SEQ ID NO:17)
G9	RASQSVSSSYLA (SEQ ID NO:15)	GASSRAT (SEQ ID NO:16)	QQYGSSPIT (SEQ ID NO:17)
A11	SGSSSNIGNNYVS (SEQ ID NO:47)	GNNWRPS (SEQ ID NO:48)	ETWDSSLSAGV (SEQ ID NO:49)
A11_gI	SGSSSNIGNNYVS (SEQ ID NO:47)	GNNWRPS (SEQ ID NO:48)	ETWDSSLSAGV (SEQ ID NO:49)

Figure 3

Clone	CDR L1	CDR L2	CDR L3
Heavy Chain			
A3	GYTFTSYMH (SEQ ID NO:24), or SYMH (SEQ ID NO:58)	IINPSGGSTSYAQKFQG (SEQ ID NO:25)	SPGVVTALFDY (SEQ ID NO:26)
B10	GGSIGSSDYYWG (SEQ ID NO:27), or SSDYYWG (SEQ ID NO: 59)	SIYSGSTYYNPSLKS (SEQ ID NO:28)	GEHRGEFDY (SEQ ID NO:29)
G6	GGSISSSNWWS (SEQ ID NO:30), or SSNWWS (SEQ ID NO:60)	EIYHSGSTNYNPSLKS (SEQ ID NO:31)	VVAVAGTVDY (SEQ ID NO:32)
G7	GYTFTSYMH (SEQ ID NO:24), or SYMH (SEQ ID NO:58)	IINPSGGSTSYAQKFQG (SEQ ID NO:25)	DQYSSGWYYYGMDV (SEQ ID NO:33)
G9	GYTFTSYMH (SEQ ID NO:24), or SYMH (SEQ ID NO:58)	IINPSGGSTSYAQKFQG (SEQ ID NO:25)	DLYSYGFYYYGMDV (SEQ ID NO:34)
A11	GGSFSGYYWS (SEQ ID NO:52), or SGYYWS (SEQ ID NO:61)	EINHSGSTNYNPSLKS (SEQ ID NO:53)	GYVAGFDY (SEQ ID NO:54)
A11_gI	GGSFSGYYWS (SEQ ID NO:52), or SGYYWS (SEQ ID NO:61)	EINHSGSTNYNPSLKS (SEQ ID NO:53)	GYVAGFDY (SEQ ID NO:54)

Figure 3 (Cont.)

Light chain variable domains**A3 clone**

>A3_aa_L

DIQMTQSPSFMSASVGDRTITCRASQDIGSYLAWYQQKPGKAPKLLIYAASTLQSGVP
 SRFSGSGSGTDFTLTINSLQPEDFATYYCQQSYSSPPTFGPGTTLEIK [SEQ ID
 NO. 1]

>A3_ntd_L

GACATCCAGATGACCCAGTCTCCCTCCTTCATGTCTGCATCTGTAGGAGACAGAGTCAC
 CATCACTTGCCGGGCCAGTCAGGACATTGGCAGTTATTTAGCCTGGTATCAGCAAAAAC
 CAGGGAAAGCCCCTAAACTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCA
 TCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCA
 ACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTCCCCCTCCGACTTTCG
 GCCCTGGGACCACATTGGAGATCAAA [SEQ ID NO. 35]

B10 clone

>B10_aa_L

EIVLTQSPATLSFSPGERATLSCRASQSVGSYLAWEYQQKPGQAPRPLIYDATNRATGIP
 TRFSGSGSGTDFTLTISLSEPEDFATYYCQHRRTFGRGTKLEIK [SEQ ID NO. 2]

>B10_ntd_L

GAAATTGTGCTGACTCAGTCTCCAGCCACCCTGTCTTTTTCTCCGGGTGAAAGAGCCAC
 CCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCTACTTAGCCTGGTACCAGCAGAGAC
 CTGGCCAGGCTCCCAGGCCCTCATCTATGATGCAACCAACAGGGCCACTGGCATCCCA
 ACCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGA
 GCCTGAAGATTTTGCAACTTATTACTGTCAACACCGAAGGACTTTTGGCCGGGGGACCA
 AGTTGGAGATCAAA [SEQ ID NO. 36]

Figure 4

G6 clone

>G6_aa_L

DVVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNR
 ASGVDPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPTFGQGTKVELK [SEQ
 ID NO. 3]

>G6_ntd_L

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTC
 CATCTCCTGCAGGTCTAGTCAGAGCCTCCTACATAGTAATGGATACAACCTATTTGGATT
 GGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTCTAATCGG
 GCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAA
 AATCAGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTACACACT
 GGCCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAACCTCAA [SEQ ID NO. 37]

G7 clone

>G7_aa_L

ETTLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQTPGQAPRLLIYGASSRATGI
 PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGRLEIK [SEQ ID
 NO. 4]

>G7_ntd_L

GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
 CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGA
 CACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATC
 CCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACT
 GGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCCATCACCT
 TCGGCCAAGGGACACGACTGGAGATTAAA [SEQ ID NO. 38]

Figure 4 (Cont.)

G9 clone

>G9_aa_L

ETTLTQSPGTLSSLSPGERATLSCRASQSVSSSYLAWYQQKIGQAPRLLIYGASSRATGI
PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPITFGQGTRLEIK [SEQ ID
NO. 5]

>G9_ntd_L

GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCAC
CCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAAA
AAATTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATC
CCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACT
GGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCAATCACCT
TCGGCCAAGGGACACGACTGGAGATTAAA [SEQ ID NO. 39]

A11 clone

>A11_aa_L

QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGNNWRPSGI
PDRFSGSKSGTSATLAISGLQTGDEADYYCETWDSSLSAGVFGGGTKLTVL [SEQ ID
NO. 45]

>A11_ntd_L

CAGTCTGTCTGTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAAGTCACCAT
CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGC
TCCAGGAACAGCCCCCAAACCTCCTCATTTATGGCAATAATTGGCGACCCTCAGGGATT
CCTGACCGCTTCTCTGGCTCCAAGTCTGGCACCTCAGCCACCCTGGCCATCAGCGGACT
TCAGACTGGGGACGAGGCCGATTATTACTGCGAAACATGGGATAGCAGCCTGAGTGCTG
GGGTATTTCGGCGGAGGGACCAAGCTGACCGTCCTA [SEQ ID NO. 55]

Figure 4 (Cont.)

A11_gl clone

>A11_gl_aa_L

QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGNNWRPSGI
PDRFSGSKSGTSATLGITGLQTGDEADYYCETWDSSLSAGVFGGGTKLTVL [SEQ ID
NO. 46]

>A11_gl_ntd_L

CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGCGGCCCCAGGACAGAAAGTCACCAT
CTCCTGCTCTGGAAGCAGCTCCAACATTGGGAATAATTATGTATCCTGGTACCAGCAGC
TCCCAGGAACAGCCCCCAAACCTCCTCATTTATGGCAATAATTGGCGACCCTCAGGGATT
CCTGACCGCTTCTCTGGCTCCAAGTCTGGCACCTCAGCCACCCTGGGCATCACCGGACT
TCAGACTGGGGACGAGGCCGATTATTACTGCGAAACATGGGATAGCAGCCTGAGTGCTG
GGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA [SEQ ID NO. 56]

Figure 4 (Cont.)

Heavy chain variable domains**A3 clone**

>A3_aa_H

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHWVRQAPGQGLEWMGIINPSGGSTS
 YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDVAVYYCARSPGVVTALFDYWQGTLVTV
 SS [SEQ ID NO. 19]

>A3_ntd_H

CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
 TTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGG
 CCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAGC
 TACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGT
 CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAA
 GCCCTGGGGTGGTGA CTGCCCTCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC
 TCAAGC [SEQ ID NO. 40]

B10 clone

>B10_aa_H

QVQLQESGPGLVKASETSLTCTVSGGSIGSSDYWGWRQPPGKGLEWIGSIYYSGST
 YYNPSLKSRTMSVDTPNNQFSLKLSSVTAADTAVYYCARGEHRGEFDYWQGTLTVS
 S [SEQ ID NO. 20]

>B10_ntd_H

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGGCTTCGGAGACCCTGTCCCT
 CACCTGCACTGTCTCTGGTGGCTCCATCGGCAGTAGTGATTACTACTGGGGCTGGATCC
 GCCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGAGTATCTATTATAGTGGGAGCACC
 TACTACAACCCCTCCCTCAAGAGTCGAGTCACCATGTCAGTAGACACGCCCAACAATCA
 GTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGA
 GAGGAGAACATAGAGGGGAATTTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCA
 AGC [SEQ ID NO. 41]

Figure 4 (Cont.)

G6 clone

>G6_aa_H

QVQLQESGPGGLVKPSGTLSTLCAVSGGSISSSNWWSWVRQPPGKGLEWIGEIIYHSGSTN
 YNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARVVAVAGTVDYWGQGTLLVTVS
 S [SEQ ID NO. 21]

>G6_ntd_H

CAGGTGCAGCTGCAGGAGTCCGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCT
 CACCTGCGCTGTCTCTGGTGGCTCCATTAGCAGTAGTAAGTGGTGGAGTTGGGTCCGCC
 AGCCCCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCTATCATAGTGGGAGCACCAAC
 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTT
 CTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAG
 TAGTAGCAGTGGCTGGTACGGTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCA
 AGC [SEQ ID NO. 42]

G7 clone

>G7_aa_H

EVQLVQSGAEVKKPGASVKVSKASGYTFTSYMHWVRQAPGQGLEWMGIINPSGGSTS
 YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDVAVYYCARDQYSSGWYYYGMDVWGQGT
 VTVSS [SEQ ID NO. 22]

>G7_ntd_H

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
 TTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGG
 CCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAAGC
 TACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGT
 CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG
 ATCAGTATAGCAGTGGCTGGTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
 GTCACCGTCTCAAGC [SEQ ID NO. 43]

Figure 4 (Cont.)

G9 clone

>G9_aa_H

QVQLQQSGAEVKKPGASVKVSCKASGYTFTSYIMHWVRQAPGQGLEWMGIINPSGGSTS
 YAQKFQGRVTMTRDTSTSTVYMELSSLRSEDVAVYYCARDLYSYGFYYYGMDVWGQGTT
 VTVSS [SEQ ID NO. 23]

>G9_ntd_H

CAGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGT
 TTCTTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATGCACTGGGTGCGACAGG
 CCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTAGCACAAAGC
 TACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGT
 CTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG
 ATTTATACAGCTATGGTTTTTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACG
 GTCACCGTCTCAAGC [SEQ ID NO. 44]

A11 clone

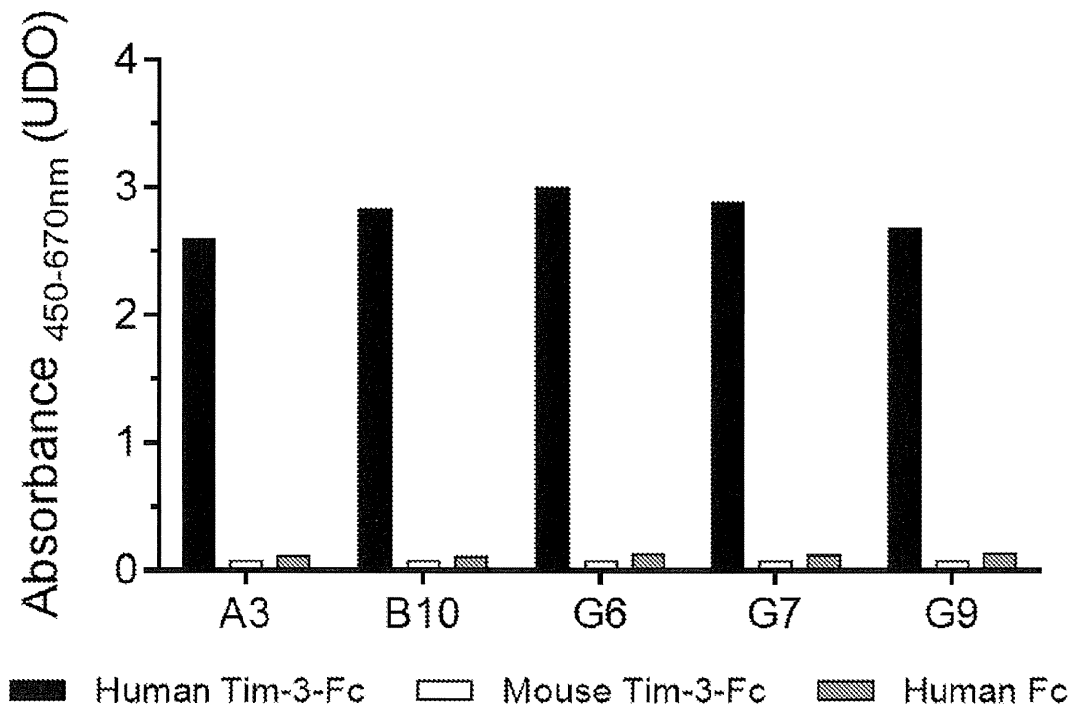
>A11_aa_H

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNY
 NPSTLSRVTTISVDTSKNQFSLKLSVTAADTAVYYCARGYVAGFDYWGQGTTLVTSS
 [SEQ ID NO. 50]

>A11_ntd_H

CAGGTGCAGCTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCT
 CACCTGCGCTGTCTATGGTGGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGC
 CCCCAGGGAAGGGGCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTAC
 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTC
 CTTGAAACTGAGCTCTGTGACCGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGGCT
 ACGTGGCTGGCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCAAGC [SEQ
 ID NO. 57]

A11 gl clone heavy chain is identical to A11**Figure 4 (Cont.)**

**Figure 5**

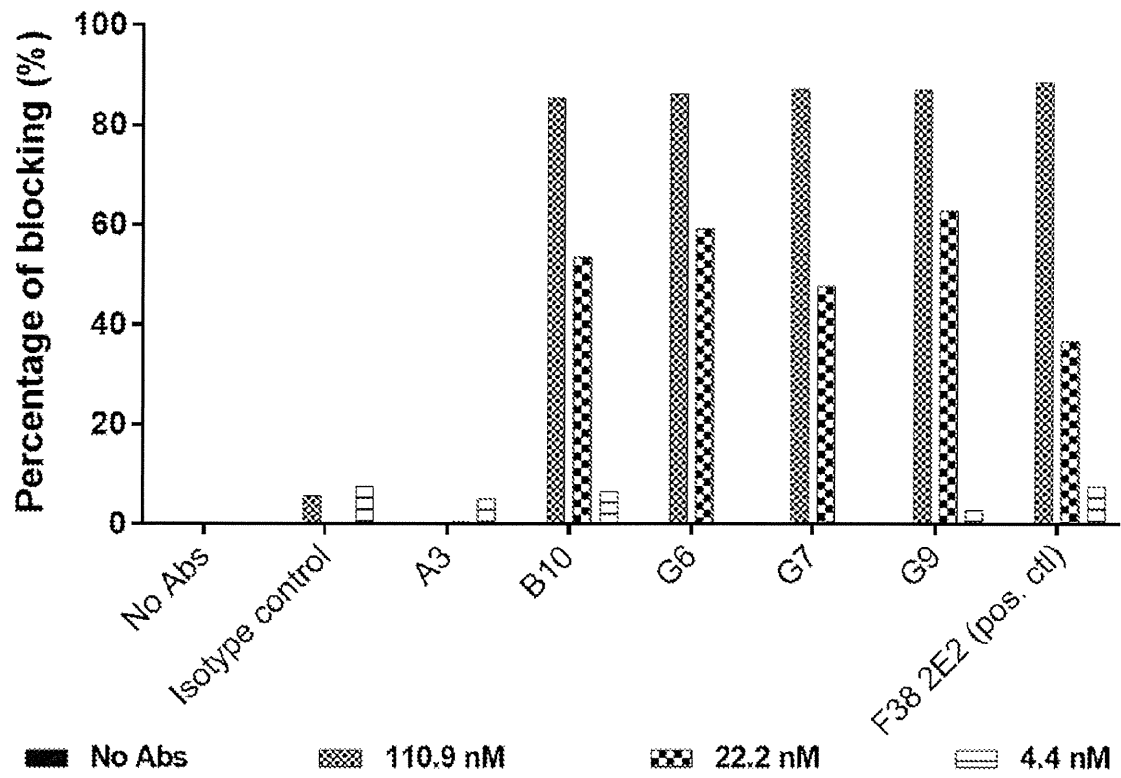


Figure 6

	Affinity (K_D in nM)
A3	0.44
B10	0.26
G6	2.52
G7	0.62
G9	0.63

Figure 7

OCI-AML3 (M4)

THP-1 (M5)

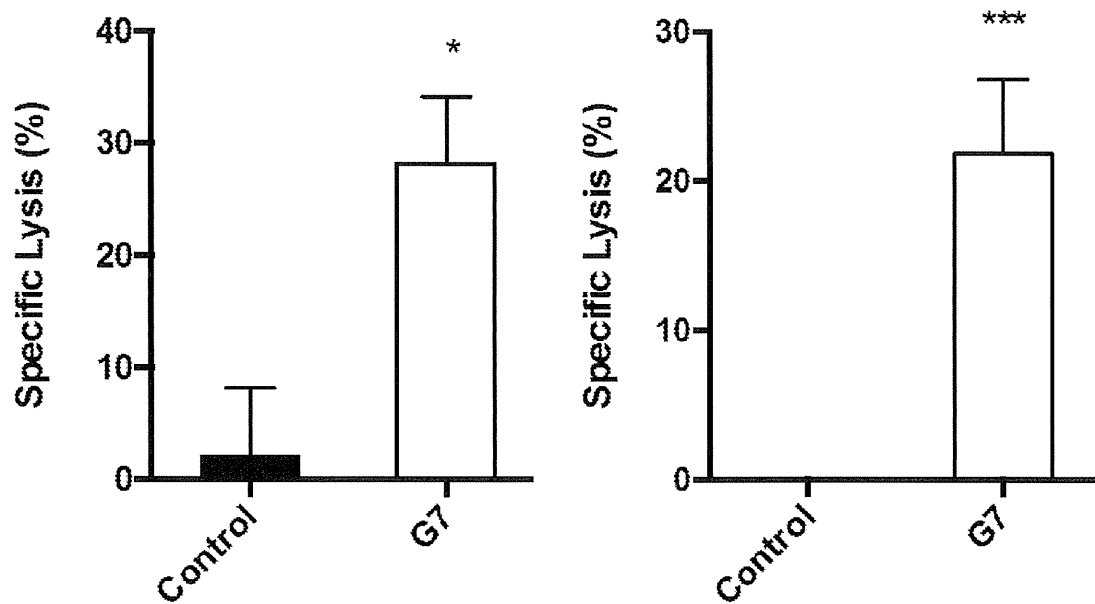


Figure 8

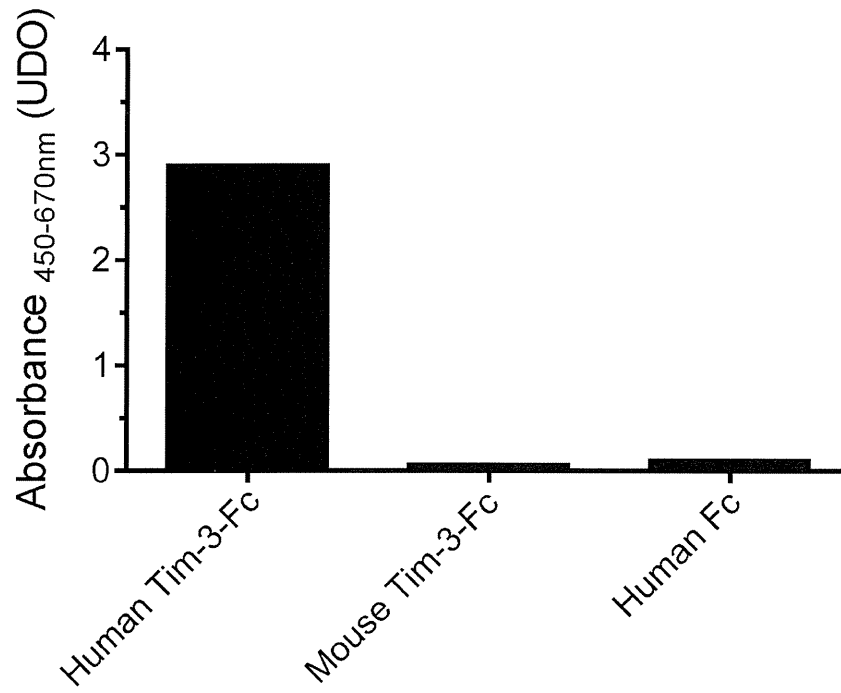


Figure 9

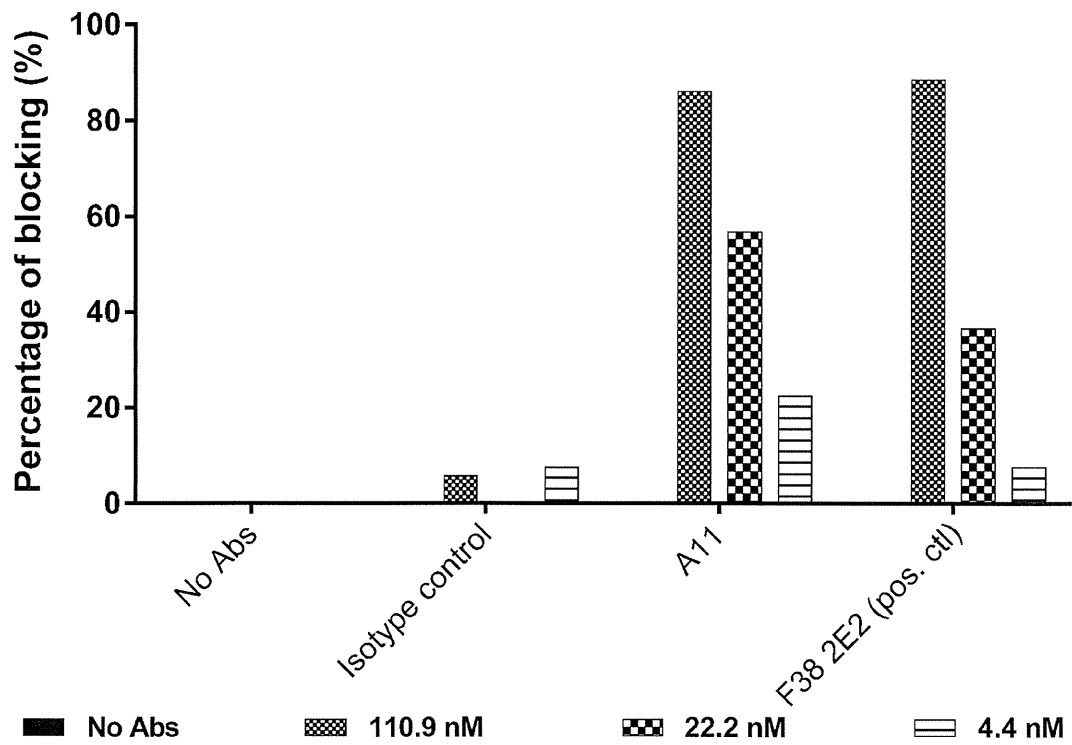


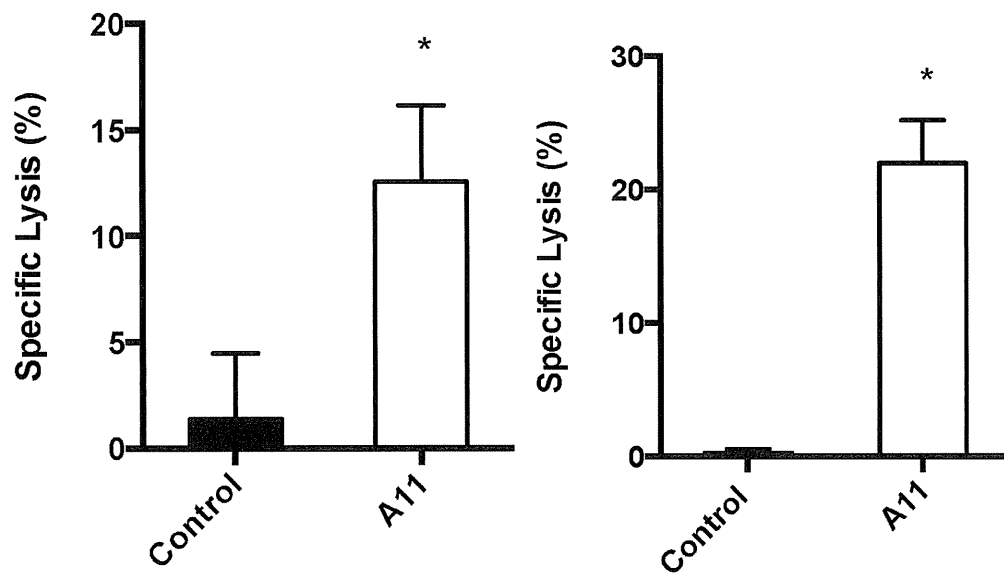
Figure 10

	Affinity (K_D in nM)
A11	1.26

Figure 11

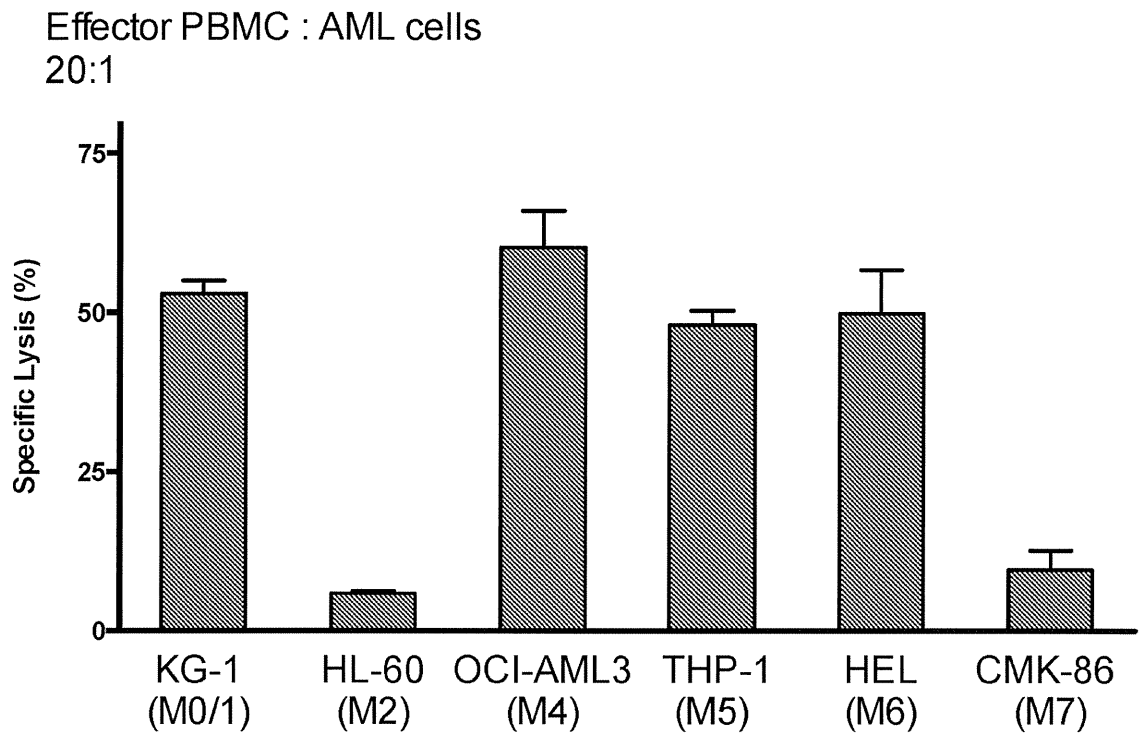
HEL (M6)

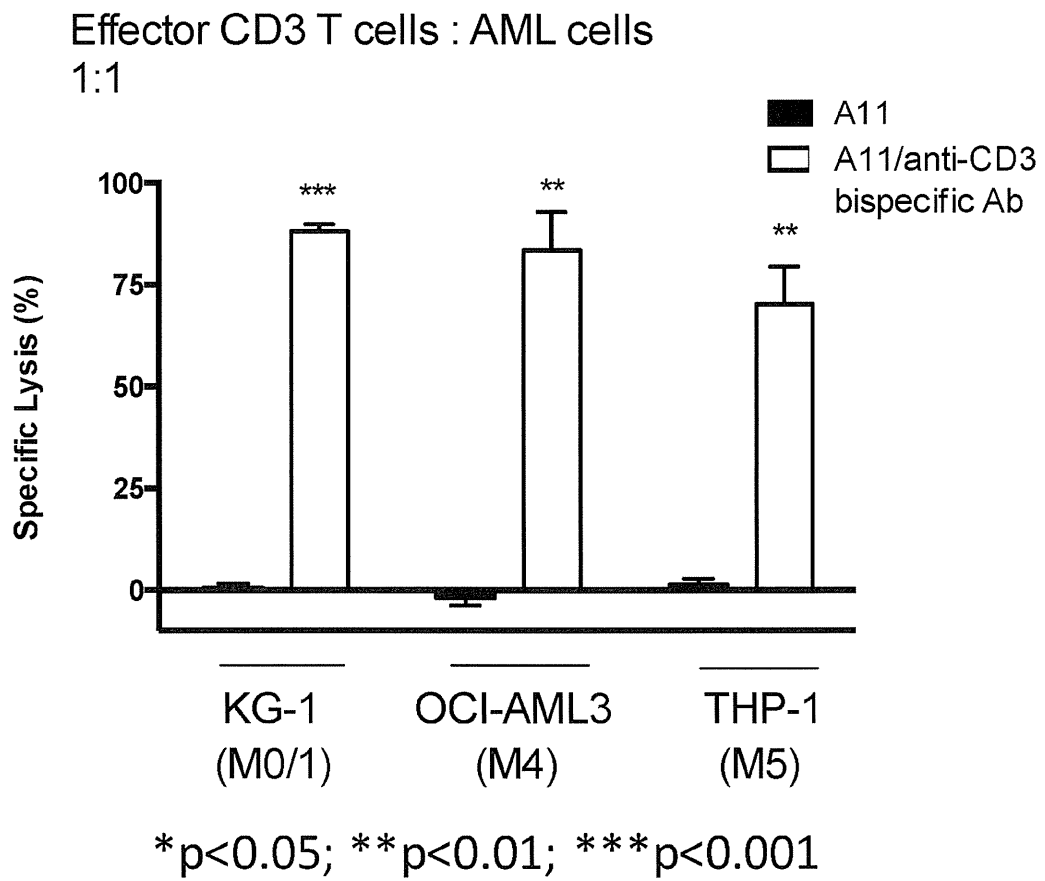
CMK-86 (M7)



*p<0.05; ***p<0.001

Figure 12

**Figure 13**

**Figure 14**

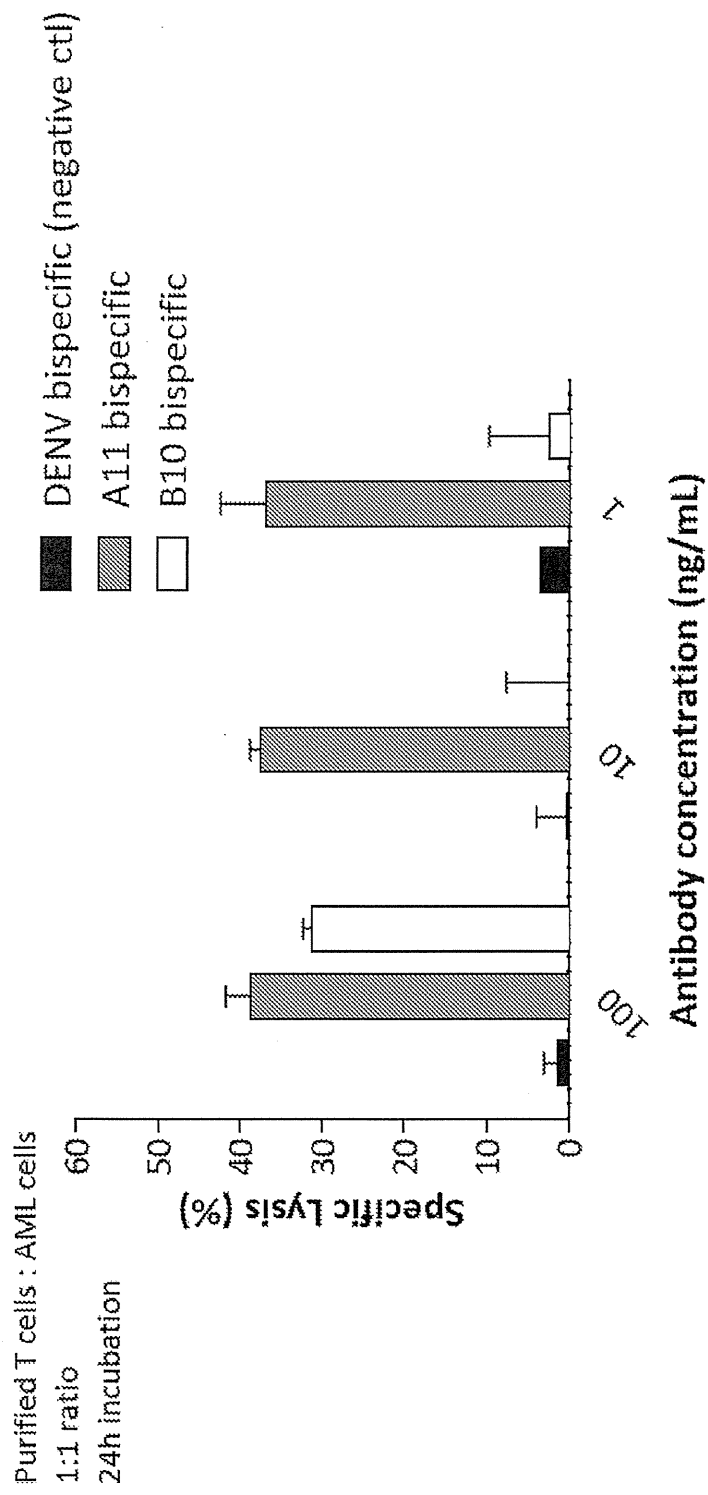


Figure 15

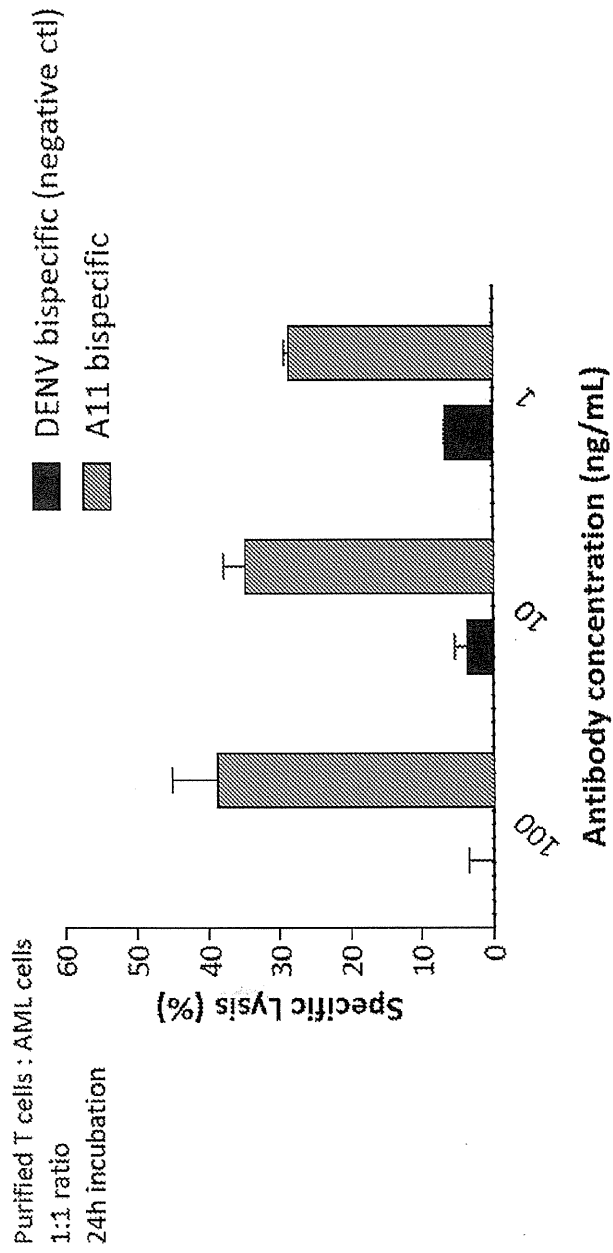
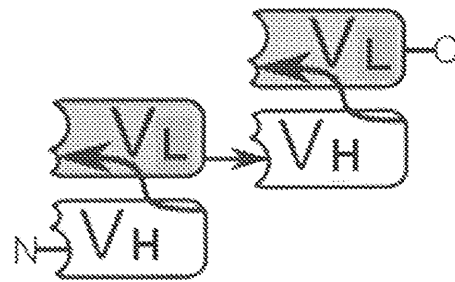


Figure 16



tandem di-scFv

Figure 17