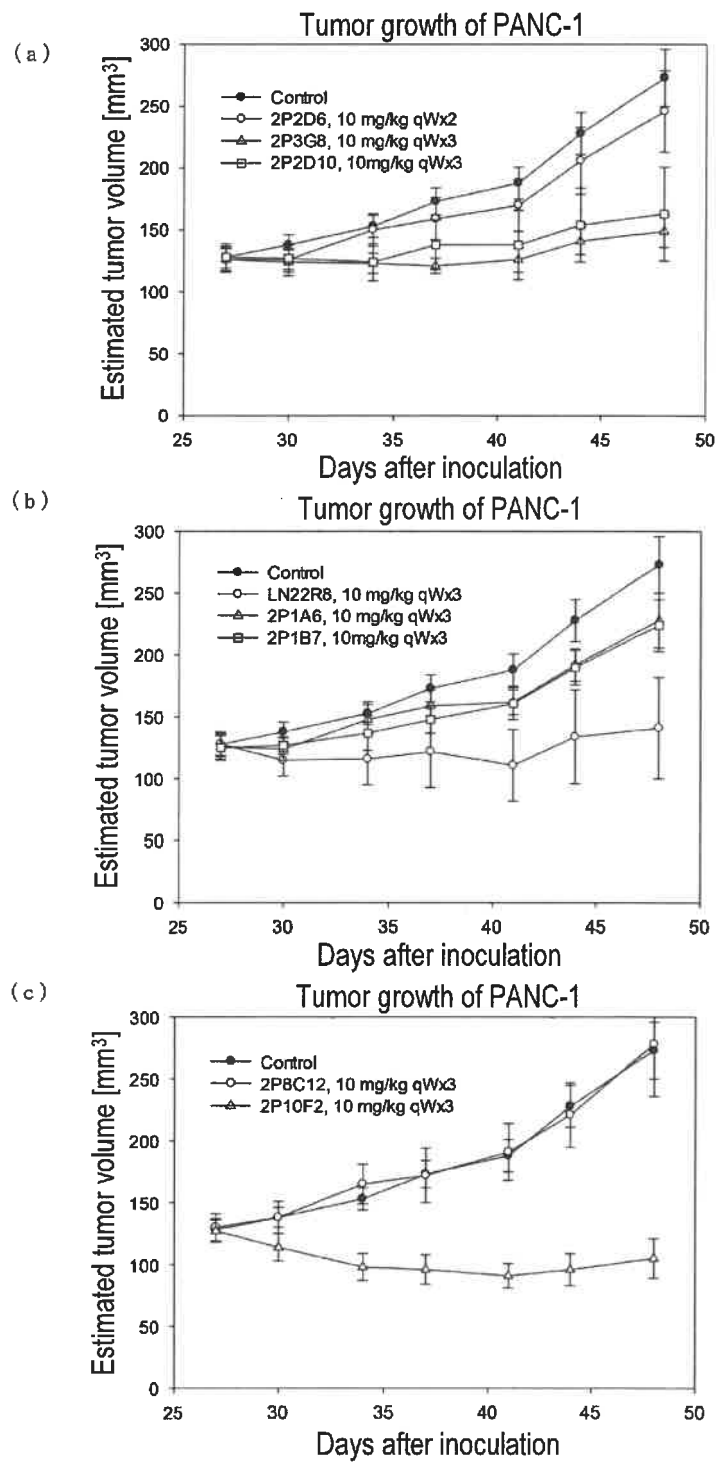
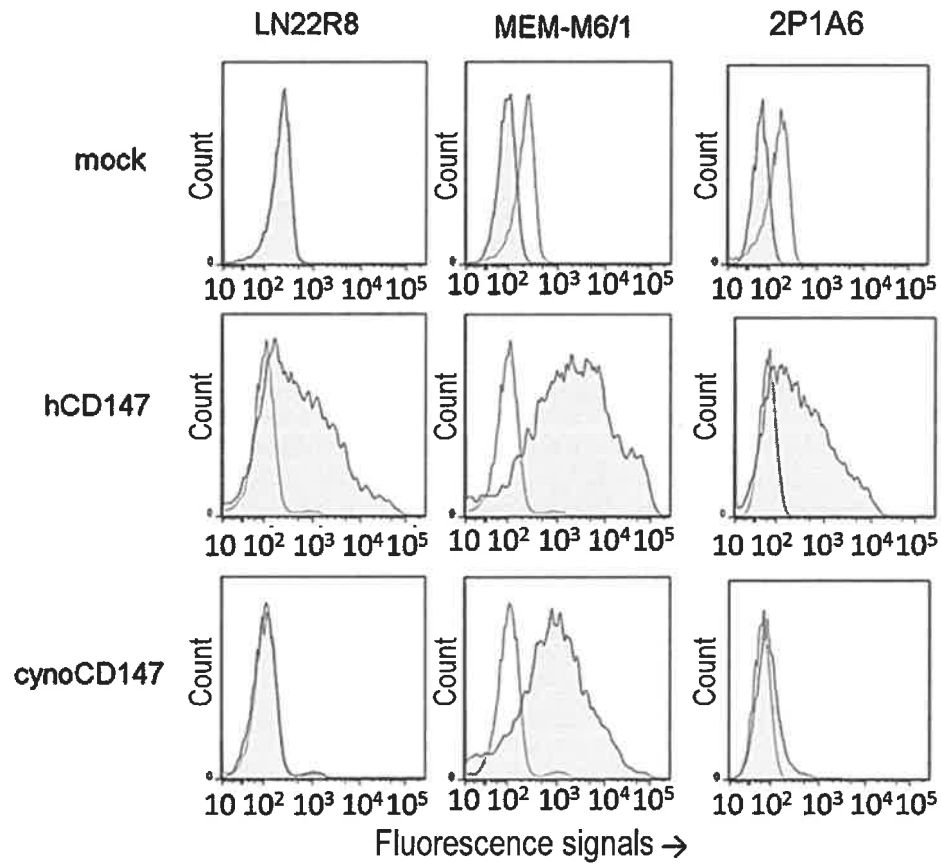


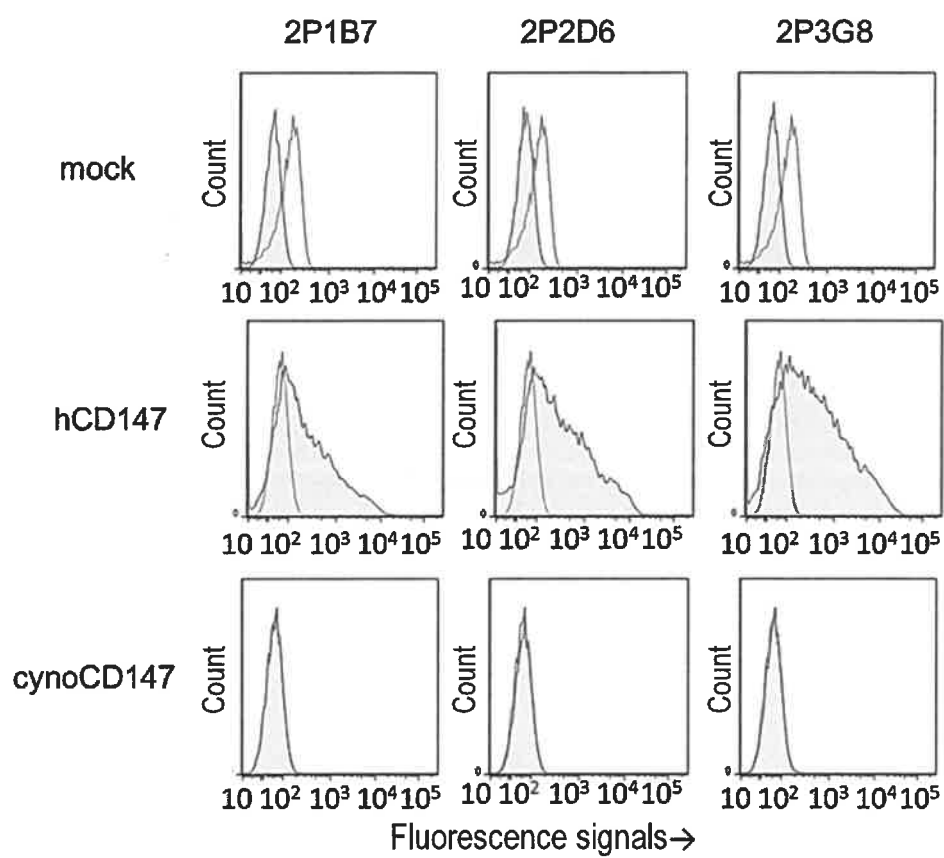
[Figure 1]



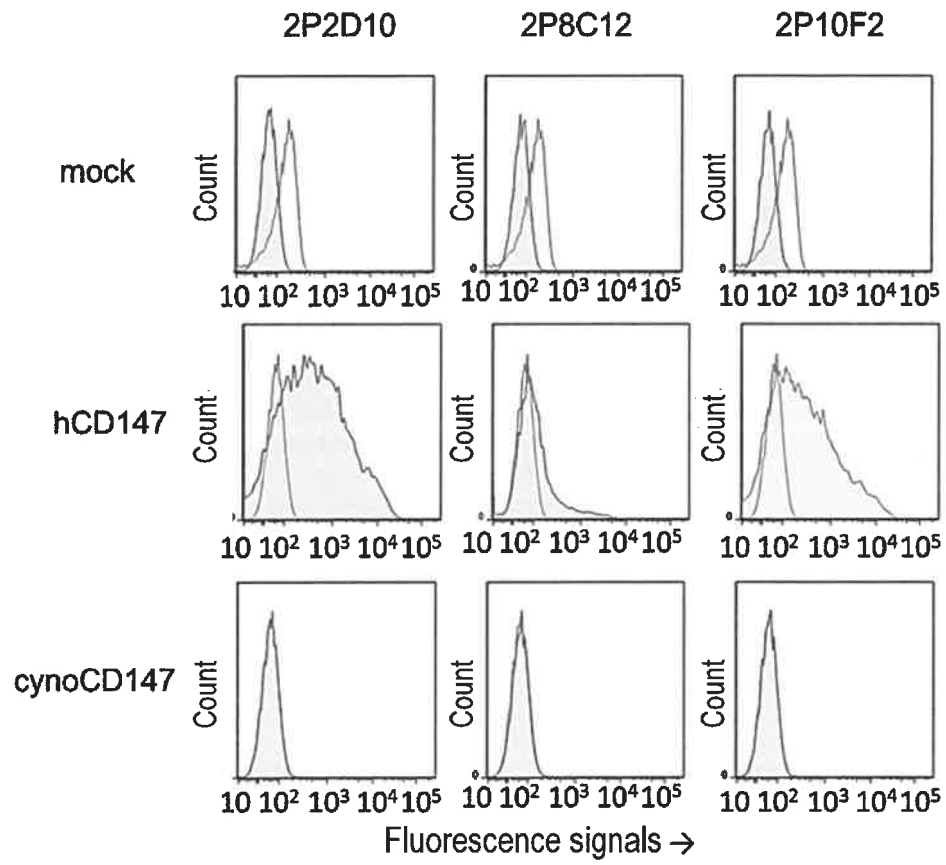
[Figure 2-1]



[Figure 2-2]



[Figure 2-3]



[Figure 3]

Score	Expect	Method	Identities	Positives	Gaps
705 bits(1820)	0.0	Compositional matrix adjust.	339/389(87%)	359/389(92%)	4/389(1%)
cynoCD147	1	MAATFVLLGLALLGAHGASGAAGFVQAPLSQQRWVGGSVELHCEAVGSPVPEIQWVFE			
hCD147v1	1	MAA LFVLLG ALLG HGASGAAGFVQAPLSQQRWVGGSVELHCEAVGSPVPEIQWVFE			
		MAAALFVLLGFALLGTHGASGAAGFVQAPLSQQRWVGGSVELHCEAVGSPVPEIQWVFE			
cynoCD147	61	HGPNDTCSQLWDGARLDRVHIHATYHQHAASTISIDTLAEEDTGTYECRASNDPDRNHLI			
hCD147v1	61	QGNPTCSQLWDGARLDRVHIHATYHQHAASTISIDTLAEEDTGTYECRASNDPDRNHLI			
cynoCD147	121	RAPRVKRWRAQAQAVLVLEPGTVSTSVENIGSKLLTCSLNDSSSTVIGHRWLKGAVLKE			
hCD147v1	121	RAPRVKRWRAQAQAVLVLEPGTVI+VE++GSKLLTCSLNDSSSTVIGHRWLKGAVLKE			
		RAPRVKRWRAQAQAVLVLEPGTVETIVEDLGSKLLTCSLNDSSSTVIGHRWLKGAVLKE			
cynoCD147	181	DILPGQKIDFEVDSDDLGEYSCVFLPEPTGRADIQLDALLSGAPRVKAVKSSEHVSSEGE			
hCD147v1	181	DALPGQKTEFKVDSDDQNGEYSCVFLPEPTGRADIQLDALLSGAPRVKAVKSSEHVSSEGE			
cynoCD147	241	TAVLCKSESLPPVTIMWYKIITDSGDQVIVNGSQRRFFVSSSQGRSERIENLNMEADP			
hCD147v1	237	TAMLCCKSESLPPVTIMWYKIITDSGDQVIVNGSQRRFFVSSSQGRSERIENLNMEADP			
cynoCD147	301	GKYACNGTSEEGIDQATVTLRVRSHHAALWPFLGIVAEVLVLTIIIFIYEKRRKRPEDVLD			
hCD147v1	297	GQYRCNGTSEKGSDDQAITLRVRSHHAALWPFLGIVAEVLVLTIIIFIYEKRRKRPEDVLD			
cynoCD147	361	DDAGSAPLKSTGQHINDKGGKVRQNRSS			
hCD147v1	357	DDAGSAPLKSGQHNDKGGKVRQNRSS			

[Figure 4-1]

SEQ ID NO: 7: Nucleotide sequence of LN22R8 light chain variable region

GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGCGGCAAGTCTGGAAATT
AGTGGTTTCTTAAGTTGGCTTCAGCAGAAACAGATGGAACATTAAACGCCTGATCTACGCCGCATCCATTTAGATTCTGGTGTG
CCAAAAGGTTCAAGTGGCAGTAGGCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGCAGACTATTAC
TGTCTACAATATGCTAGTTATCCGTGGACGTTGGTGGAGGCACCAAGCTGGAATCAAACGG

SEQ ID NO: 8: Amino acid sequence of LN22R8 light chain variable region (each CDR is underlined)

DIQMTQSPSSLSASLGERVSLTCRASLEISGFLSWLQQKPDGTIKRLIYAASILDSGVPKRFGSRSGSDYSLTSSLESEDFADYY
CLQYASYPWTFGGGKLEIKR

SEQ ID NO: 11: Amino acid sequence of CDRL1 of LN22R8

RASLEISGFLS

SEQ ID NO: 12: Amino acid sequence of CDRL2 of LN22R8

AASILDS

SEQ ID NO: 13: Amino acid sequence of CDRL3 of LN22R8

LQYASYPWT

[Figure 4-2]

SEQ ID NO: 9: Nucleotide sequence of LN22R8 heavy chain variable region

CAGATCCAGTTGGTGCAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGGTATACCTTC
ACAAACTATGGAATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCA
ACATATGCTGATGACTTCAAGGGACGTTTGCCTTCTCTTTGAAACCTCTGCCAGCACTGCCTATTTGCAGATCAACAACCTCAAA
AATGAGGACACGGCTACATATTTCTGTGCAAGAGGGGGGTATGGTAACACGGGCGGGGCTATGGACTACTGGGTCAAGGTACC
TCAGTCACCGTCTCCTCA

SEQ ID NO: 10: Amino acid sequence of LN22R8 heavy chain variable region (each CDR is underlined)

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLK
NEDTATYFCARGGYGNYGAGAMDYWGQTSVTVSS

SEQ ID NO: 14: Amino acid sequence of CDRH1 of LN22R8

GYTFNYGMN

SEQ ID NO: 15: Amino acid sequence of CDRH2 of LN22R8

WINTYTGEPT

SEQ ID NO: 16: Amino acid sequence of CDRH3 of LN22R8

GGYGNYGAGAMDY

[Figure 5-1]

SEQ ID NO: 17: Nucleotide sequence of 2P10F2 light chain variable region
 GACATCCAGATGACACAGTCTCCAGCTTCCTGTCTGCATCTCTGGGAGAACTGTCTCCATCGAATGTCTTGAAGTGAGGGCATT
 TCCAATAGTTTAGCGTGGTATCAGCAGAAGCCAGGAAATCTCTCAGCTCCTGATCTATGGTGCAAGTAGCTTGAAGACGGGGTC
 CCATCACGGTTCAGTGGCAGTGGATCTGGCACAGTATTCTCTCAAGATCAGCGGCATGCAACCTGAAGATGAAGGGTTTATTAC
 TGTCAACAGGGTTACAAGTATCATTACGTTCCGGCTCAGGGACGAAGTTGAAATAAACGG

SEQ ID NO: 18: Amino acid sequence of 2P10F2 light chain variable region (each CDR is underlined)
 DIQMTQSPASLSASLGETVSIECLASEGISNSLAWYQQKPKSPOLLIYGASSLQDGVPSRFSGSGSGTQYSLKISGMQPEDEGVYY
 CQQGYKYPFTFGSGTKLEIKR

SEQ ID NO: 21: Amino acid sequence of CDRL1 of 2P10F2
 LASEGISNSLA

SEQ ID NO: 22: Amino acid sequence of CDRL2 of 2P10F2
 GASSLQD

SEQ ID NO: 23: Amino acid sequence of CDRL3 of 2P10F2
 QQGYKYPFT

[Figure 5-2]

SEQ ID NO: 19: Nucleotide sequence of 2P10F2 heavy chain variable region
 GAGGTGCAGCTTCAGGAGTCAGGACCTGGCCTTGTGAAACCCCTCACAGTCACTCTCCCTCACCTGTTCTGTCACTGGTTACTCCATC
 ACTAGTAATTACTGGGGCTGGATCCGGAAGTTCCAGGAAATAAAATGGAGTGGATGGGATGCATAACCTACAGTGGTGGCACTAGC
 TACAACCCATCTCTCAAAGTGAATCTCATTACTAGAGACACATCAAAGAATCAGTTCTTCTGCAGTTGAACCTGTAACTACT
 GAGGACACAGCCACATATTACTGTGCAAGTTCCTATACCAAGTGGTGACGTCGATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCC
 TCA

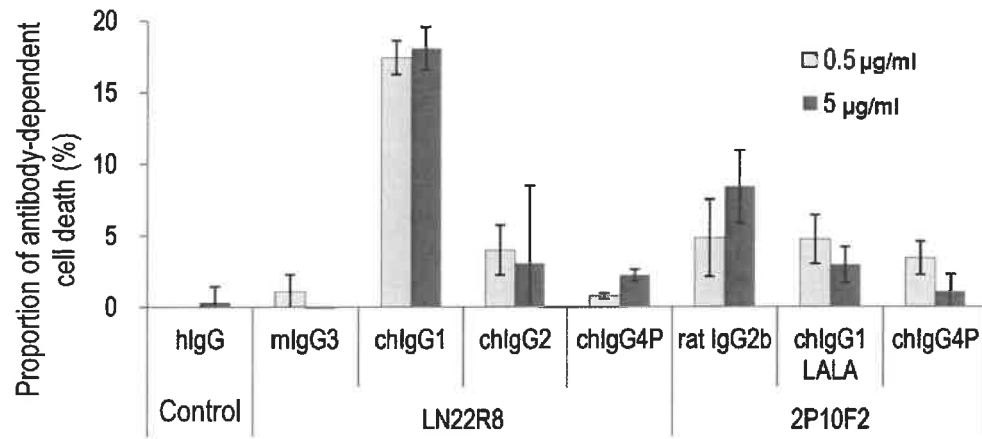
SEQ ID NO: 20: Amino acid sequence of 2P10F2 heavy chain variable region (each CDR is underlined)
 EVQLQESGPGLVKPSQSLSLTCSVTGYSITSNYWGWIHKFPGNKMEWMGCITYSGGTSYNPSLKSRIISITRDTSKNQFFLQLNSVTT
 EDTATYYCASSYTSGDVDYWGQGVMTVSS

SEQ ID NO: 24: Amino acid sequence of CDRH1 of 2P10F2
 GYSITSNYWG

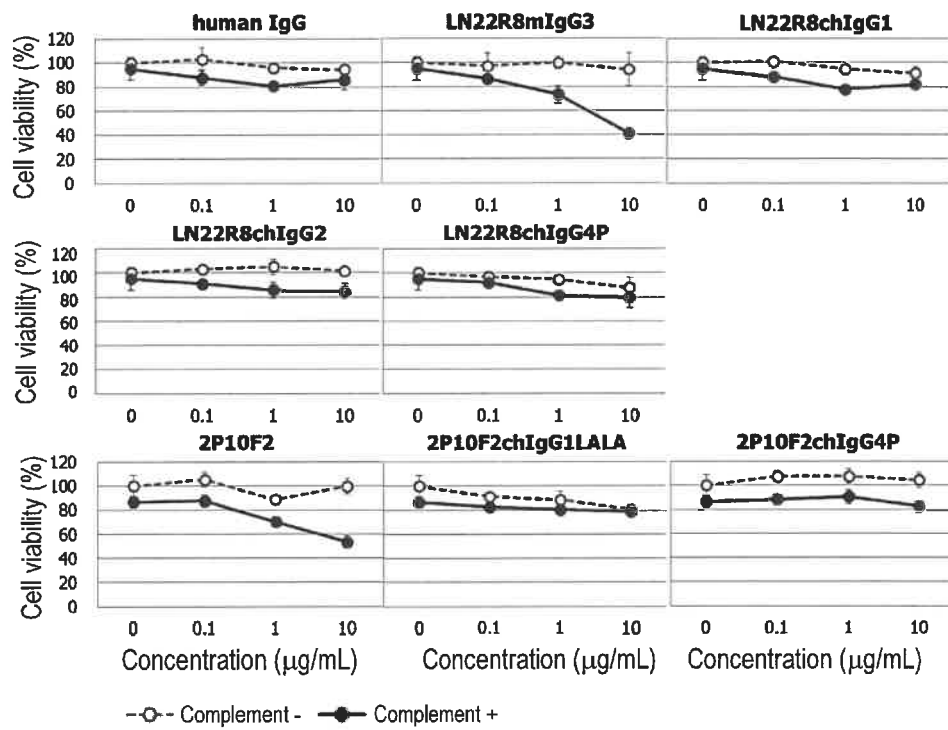
SEQ ID NO: 25: Amino acid sequence of CDRH2 of 2P10F2
 CITYSGGTS

SEQ ID NO: 26: Amino acid sequence of CDRH3 of 2P10F2
 SYTSGDVDY

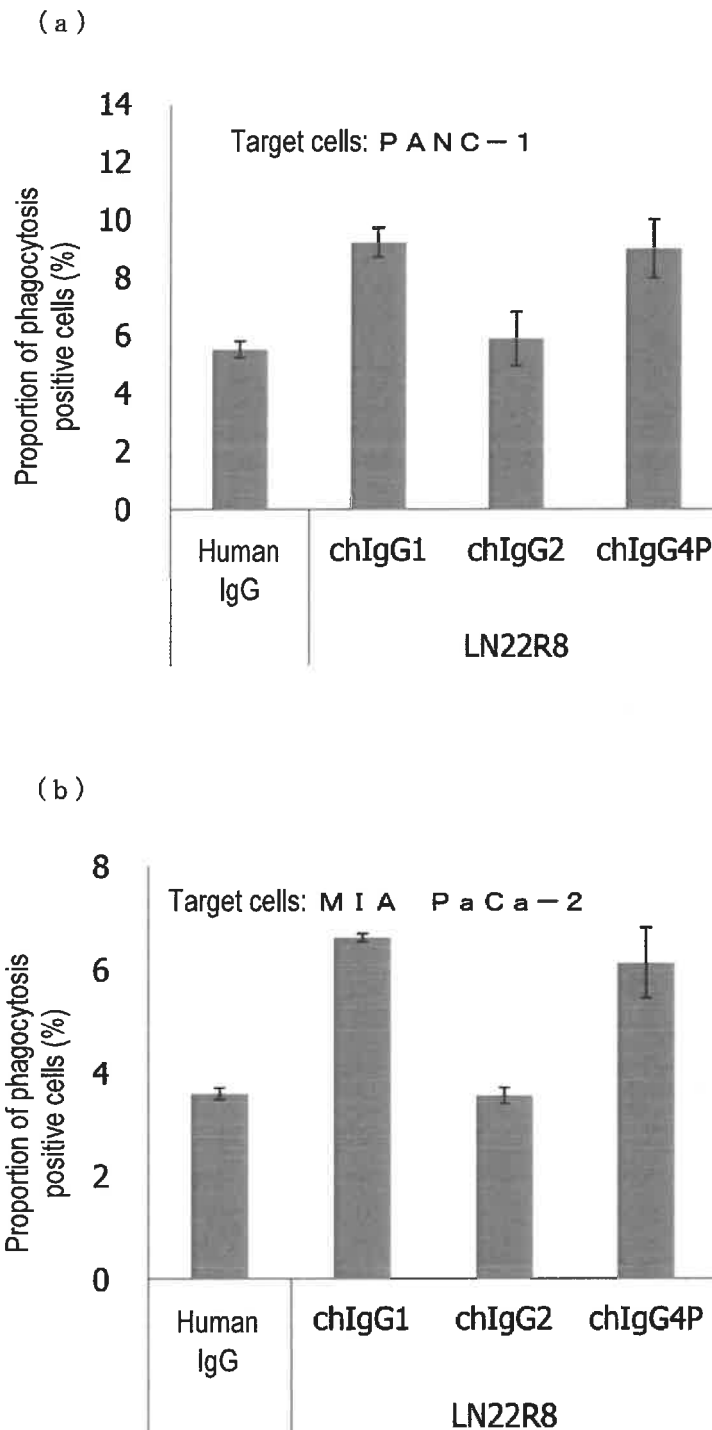
[Figure 6]



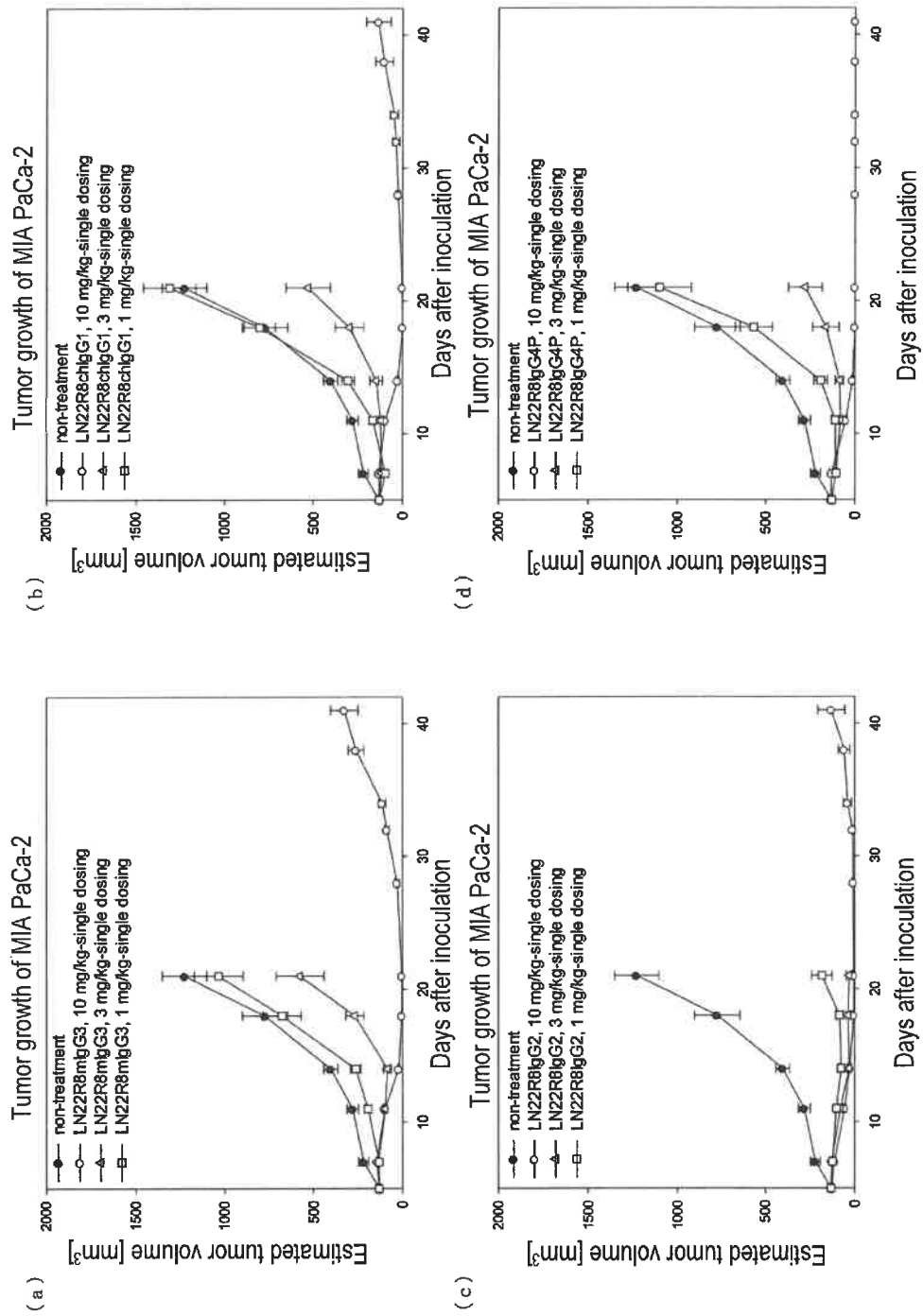
[Figure 7]



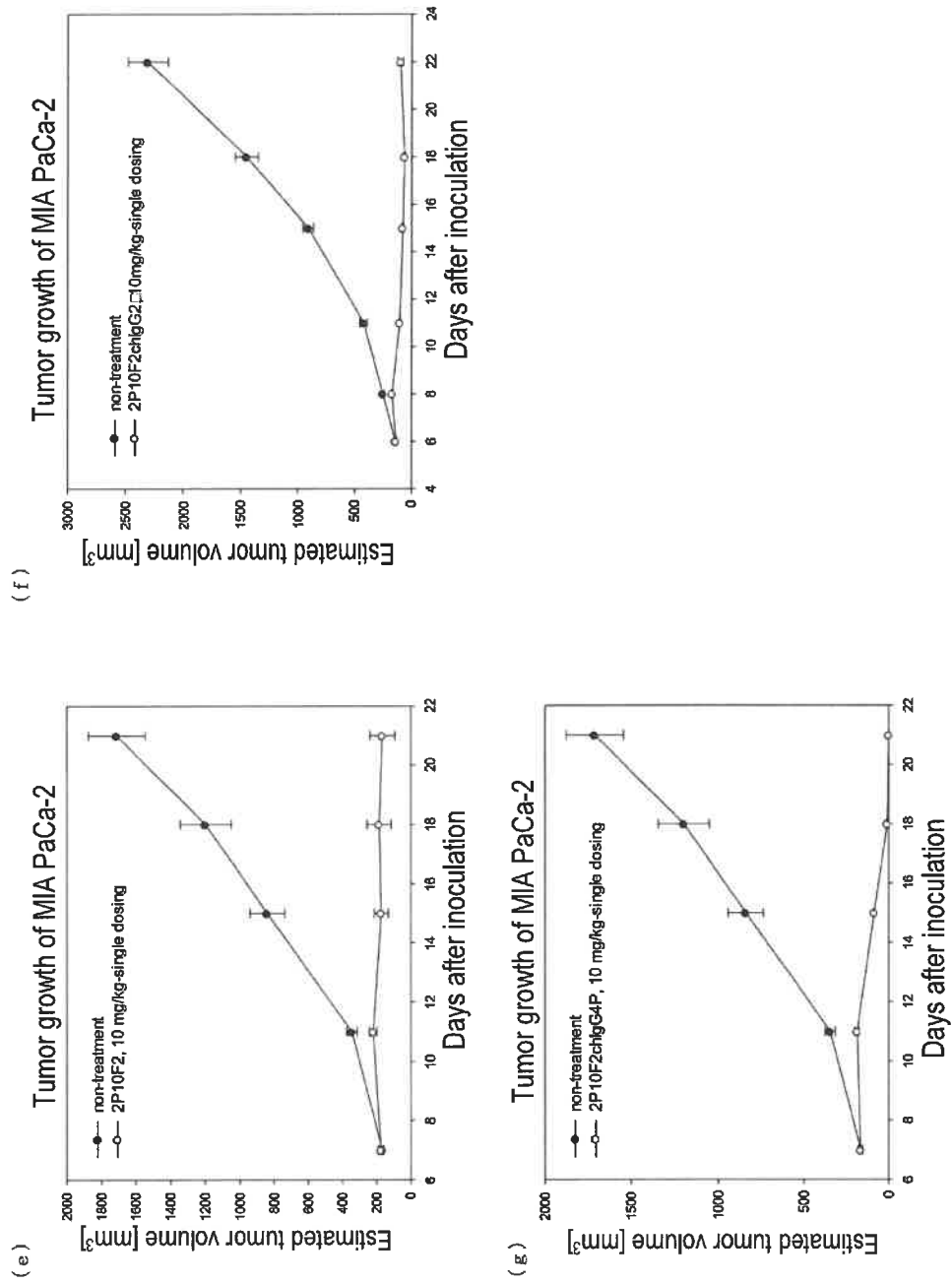
[Figure 8]



[Figure 9-1]

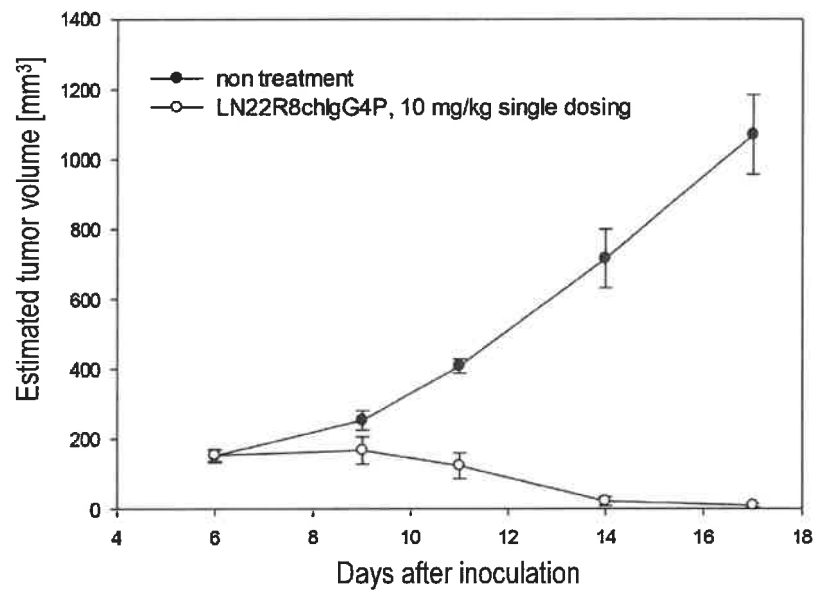


[Figure 9-2]

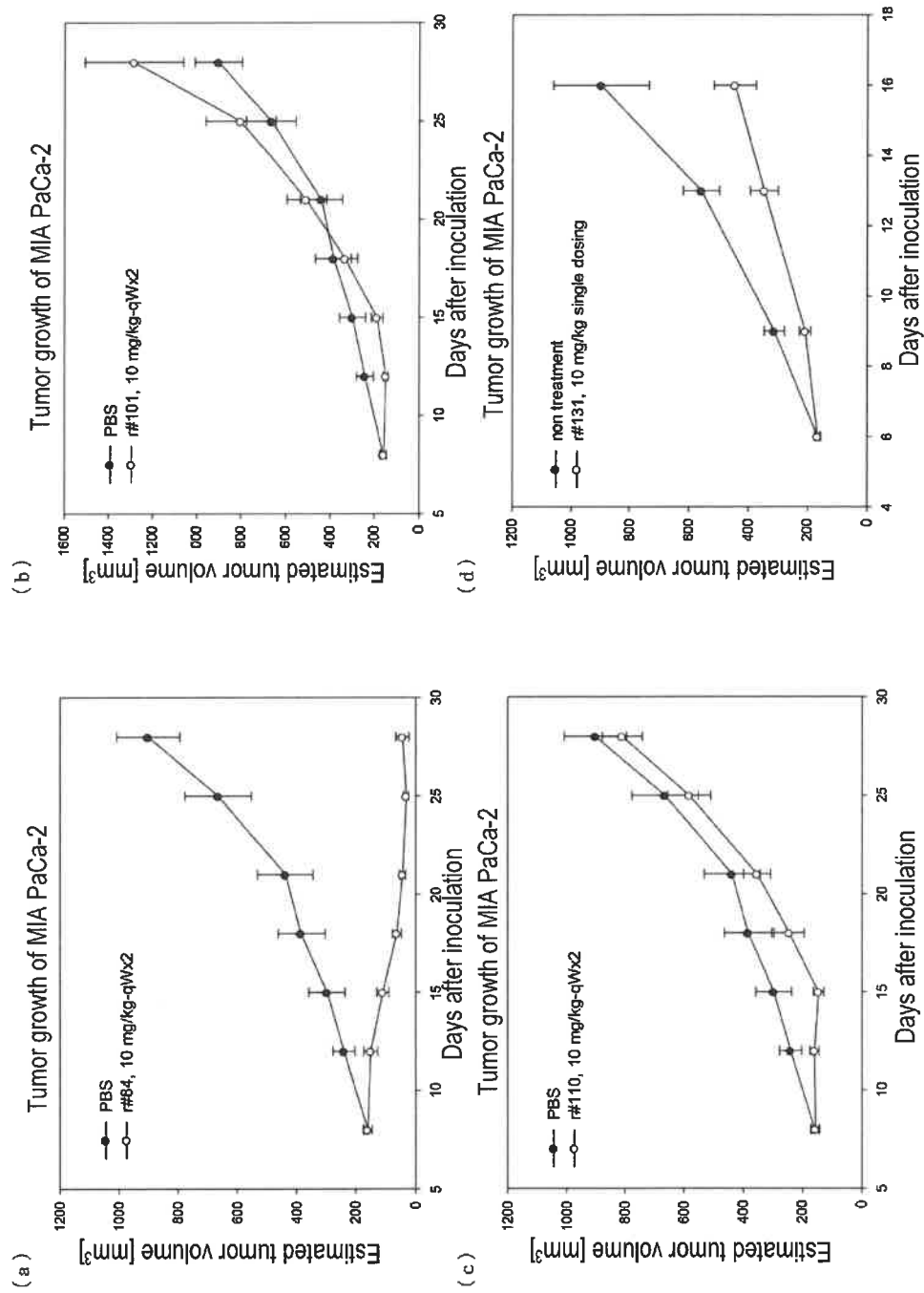


[Figure 10]

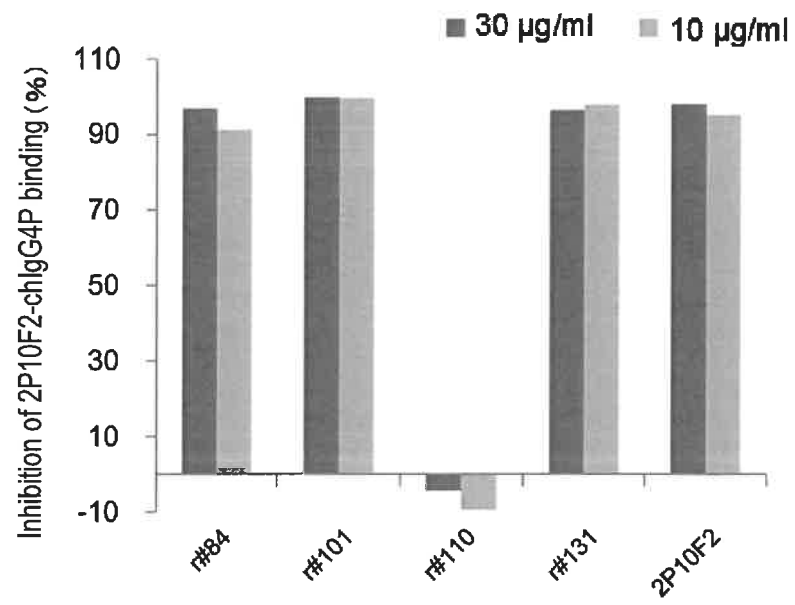
Tumor growth of MIA PaCa-2 in NOG mice



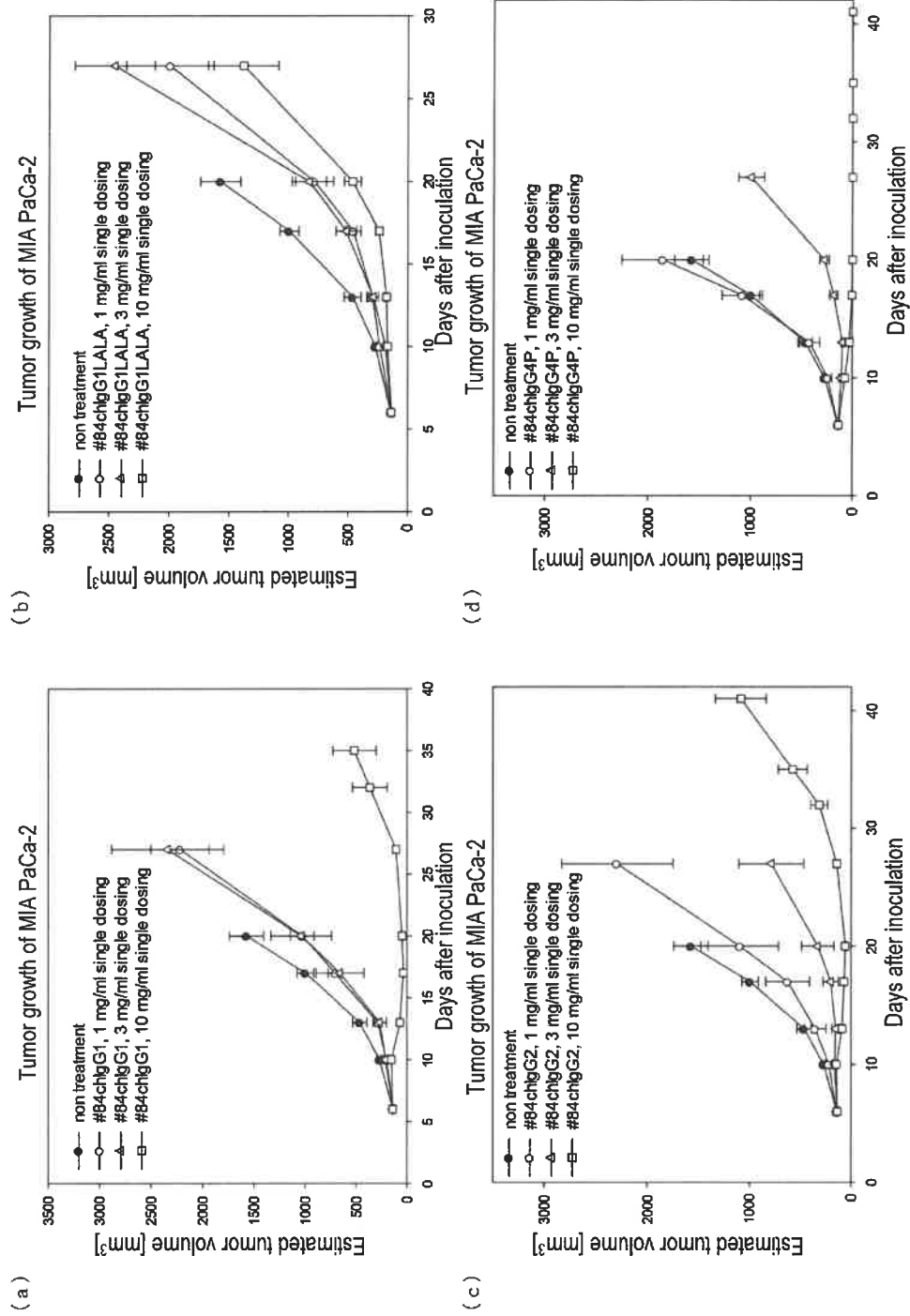
[Figure 11]



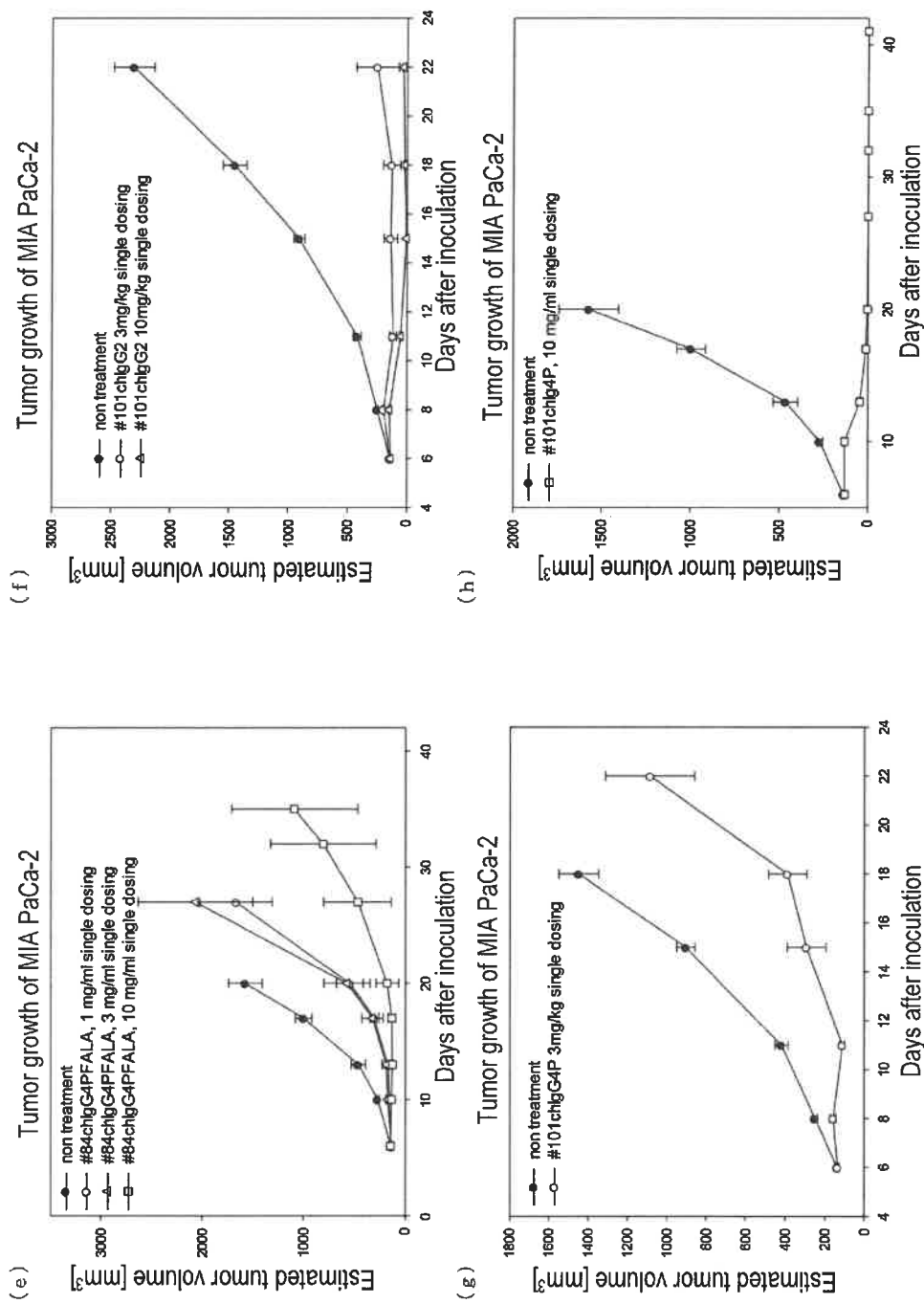
[Figure 12]



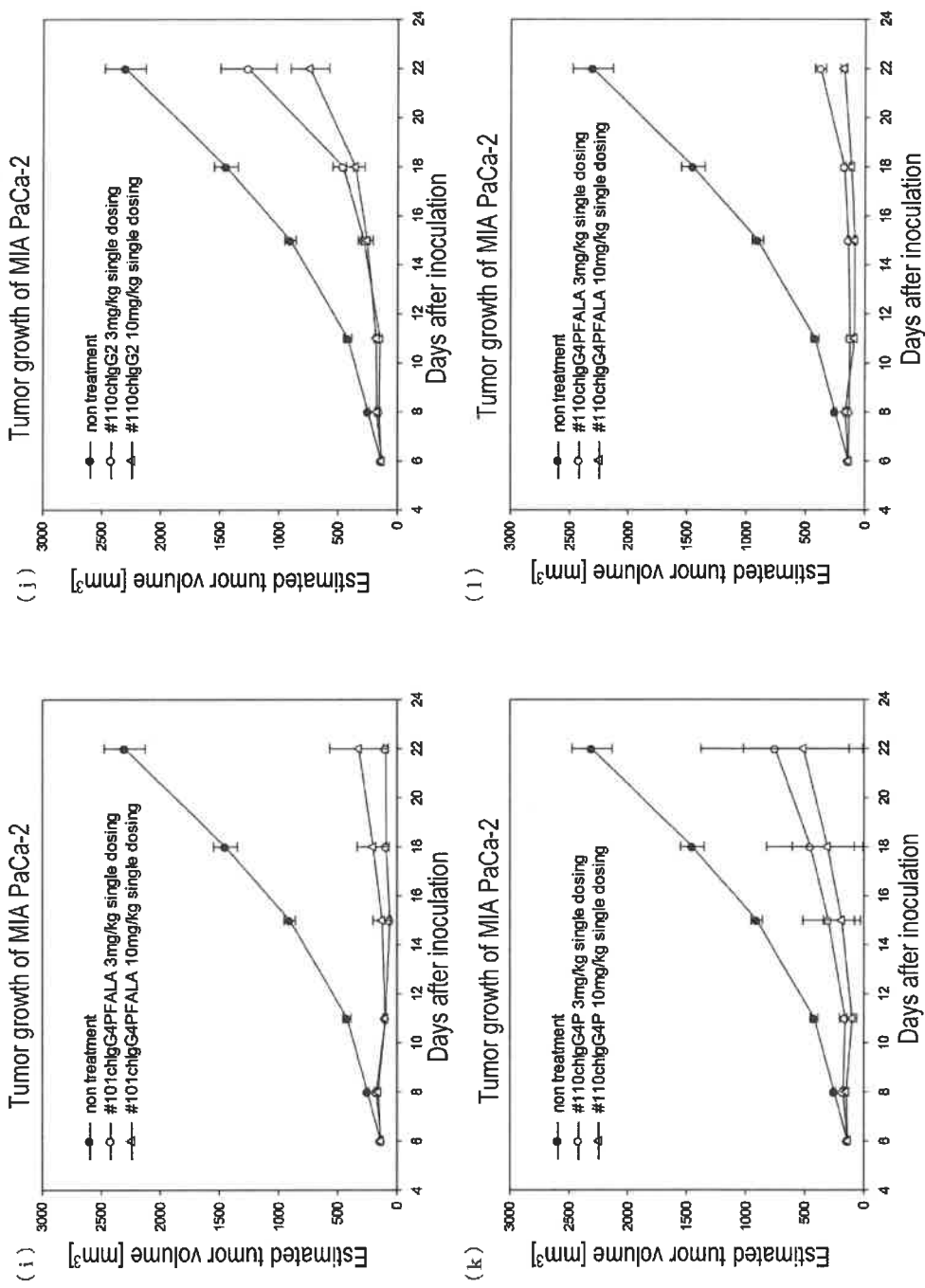
[Figure 13-1]



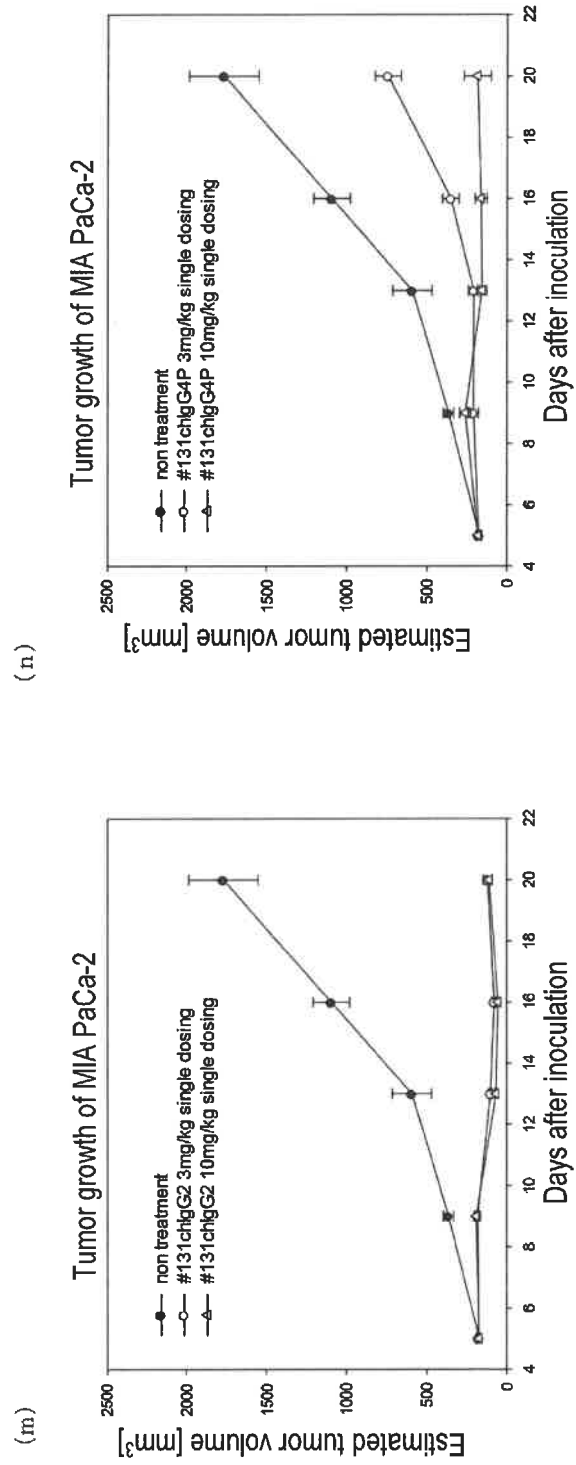
[Figure 13-2]



[Figure 13-3]



[Figure 13-4]



[Figure 14]

(a) Design of #84H1h variable region

```

rat_CD147_#84 HC 1 EVQLVESGGGLVQPGRSLKLSCAASGFTFSNYMMAWVRQAPKKGLEWVATITTSGSRPYY 60
#84H1h          1 .....G...R.....G.....S..... 60

rat_CD147_#84 HC 61 PDSVKGRFTISRDNKSSLYLQMNSLKSEDTATYYCARHIYYDGYPFAYWGQGLVTVS 120
#84H1h          61 A.....S.NT.....RA...V..... 120

rat_CD147_#84 HC 121 S 121
#84H1h          121 . 121

```

(b) Design of #84L2h variable region

```

rat_CD147_#84 LC 1 DVQMTQSPSYLAASPGESVSIKASKSISNNLAWYQEKPGKANKLLIHSGSTLQSGTPS 60
#84L2h          1 .....S.S..V.DR.T.T.....Q..... 60

rat_CD147_#84 LC 61 RFSGSGSGTDFTLTIRSLFEDFAVYYCQQYNEYPLTFGSGTKLEIKR 108
#84L2h          61 .....S..QP....T.....Q...V.... 108

```

[Figure 15]

(a) Design of #101H1h variable region

```

rat_CD147_#101 HC 1 EVQLVESDGGGLVQPGRSLKLSCAASGFTFSNYMMAWVRQAPTKGLEWVATISYDGSNTYY 60
#101H1h          1 .....G.....R.....G..... 60

rat_CD147_#101 HC 61 RDSVKGRFTISRDNKSTLYLQMDSLRSGDTATYYCARFYNNYYFDYWGQGVMTVSS 118
#101H1h          61 .....S.....N...A...V.....TL..... 118

```

(b) Design of #101L2h variable region

```

rat_CD147_#101 LC 1 DIQMTQSPSLLSASVGGRLTLNCKASQNLKYLAWYQQKLGEAPKLLIDNANSLQTGIPS 60
#101L2h          1 .....S.....D.V.I.....P.K..... 60

rat_CD147_#101 LC 61 RFSGSGSGTDFTLTISLQPEDVATYFCQQYSGSYTFGAGTKLELKR 108
#101L2h          61 .....F.....Q...V.I.... 108

```

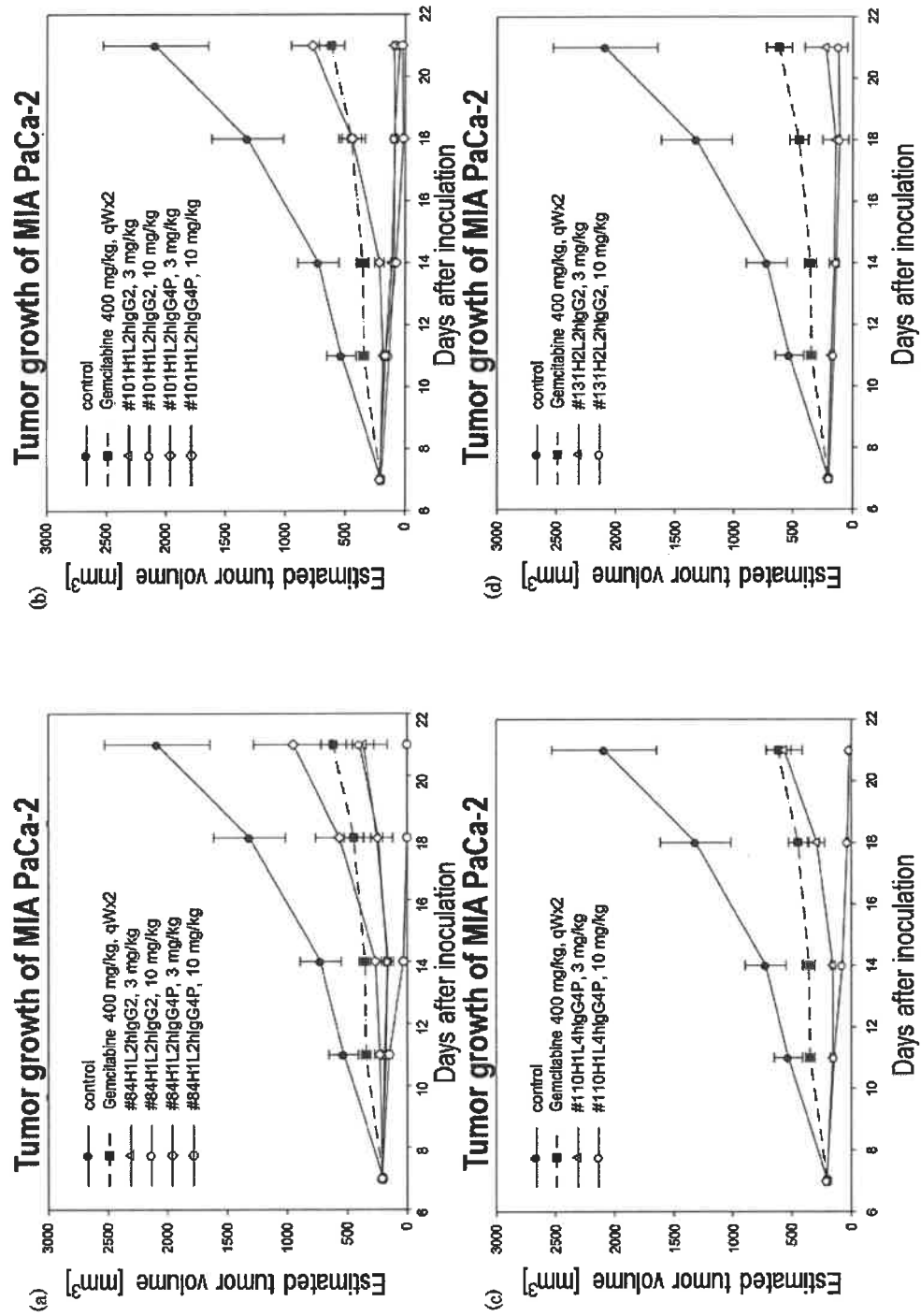
[Figure 16]

(a) Design of #110H1h variable region			
rat_CD147_#110 HC	1	QVQLQQSGAELVKPGSSVKISCKASGYTFTSDFMHWIKQQPGNGLEWIGWIYPGDGDTEY	60
#110H1h	1	...V...VK...A...V...VR.A..Q...M.....	60
rat_CD147_#110 HC	61	NQKFNGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARGRGYVMDAWGQGASVTVSS	117
#110H1h	61	...Q.RV...R.T.I...E..R.R.D.T...Y.....TT.....	117
(b) Design of #110H13h variable region			
rat_CD147_#110 HC	1	QVQLQQSGAELVKPGSSVKISCKASGYTFTSDFMHWIKQQPGNGLEWIGWIYPGDGDTEY	60
#110H13h	1	...V...VK...A...V...VR.A..Q...M.....	60
rat_CD147_#110 HC	61	NQKFNGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARGRGYVMDAWGQGASVTVSS	117
#110H13h	61	A...Q.RV.M.R.T.I...E..R.R.D.T...Y.....TT.....	117
(c) Design of #110L4h variable region			
rat_CD147_#110 LC	1	DIQMTQTPSSMPASLGERVTISCRASQGISNYLNWYQQKPDGTIKPLIYYTSNLQSGVPS	60
#110L4h	1	S...LS..V.D...T.....GKA.....	60
rat_CD147_#110 LC	61	RFSGSGSGTDYSLTISLEPEDFAMVFCQQYDSSPRTFGGGTKLELKR	108
#110L4h	61	T.....Q.....T.....V.I..	108
(d) Design of #110L2h variable region			
rat_CD147_#110 LC	1	DIQMTQTPSSMPASLGERVTISCRASQGISNYLNWYQQKPDGTIKPLIYYTSNLQSGVPS	60
#110L2h	1	S...LS..V.D...T.....GKAP.....	60
rat_CD147_#110 LC	61	RFSGSGSGTDYSLTISLEPEDFAMVFCQQYDSSPRTFGGGTKLELKR	108
#110L2h	61	T.....Q.....T.Y.....V.I..	108
(e) Design of #110L12h variable region			
rat_CD147_#110 LC	1	DIQMTQTPSSMPASLGERVTISCRASQGISNYLNWYQQKPDGTIKPLIYYTSNLQSGVPS	60
#110L12h	1	S...LS..V.D...T.....GKAP.....	60
rat_CD147_#110 LC	61	RFSGSGSGTDYSLTISLEPEDFAMVFCQQYDSSPRTFGGGTKLELKR	108
#110L12h	61	FT.....Q.....T.Y.....V.I..	108

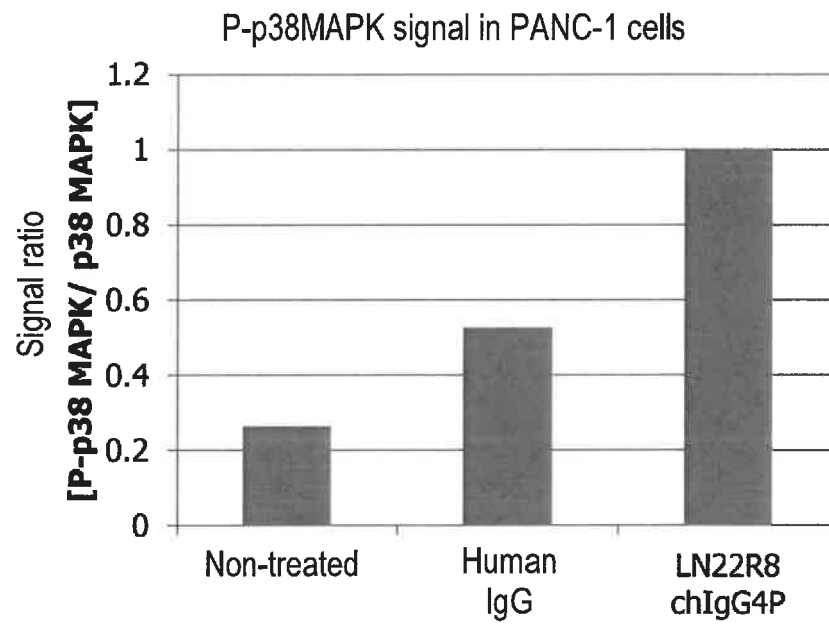
[Figure 17]

(a) Design of #131H2h variable region			
rat_CD147_#131 HC	1	EVQLVESGGGLVQPGSLKLSCKASGFTFNWMTWVRQAPGKGLEWVASITKAGGSTYY	60
#131H2h	1	Q.....V.....R...A.....	60
rat_CD147_#131 HC	61	RDSVKGRFTISRDNASTLYLQMNSLRSEDATYYCTRELGEFYVMDAWGQGASVTVSS	119
#131H2h	61	A.....S.....A.G..V.....TT.....	119
(b) Design of #131L2h variable region			
rat_CD147_#131 LC	1	DVQMTQSPSYLAASPGESVVISCKASKSINTYLAWYQEKPGKTNKLLIYSGSTLQSGTSP	60
#131L2h	1	S..S..V.DR.T.T.....	60
rat_CD147_#131 LC	61	RFSGSGSGTDFTLTIRSLPEDEFAVYYCQQHNEYPFTFGSGTKLEIKR	108
#131L2h	61	S..Q.....T.....Q.....	108

[Figure 18]

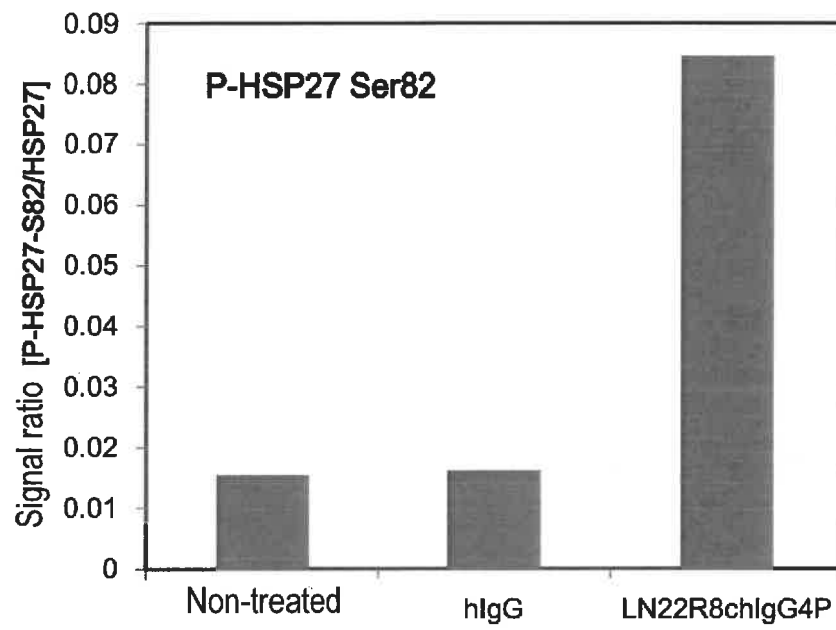


[Figure 19]

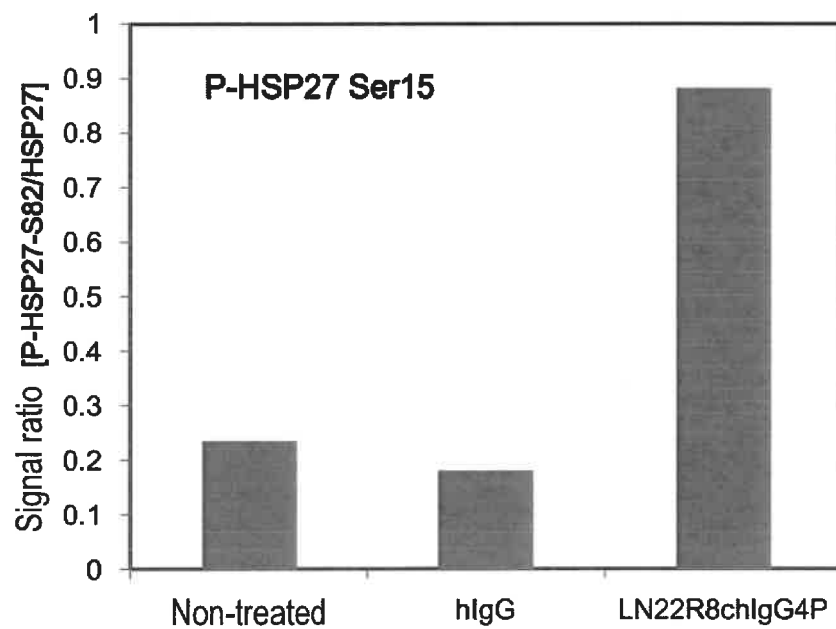


[Figure 20]

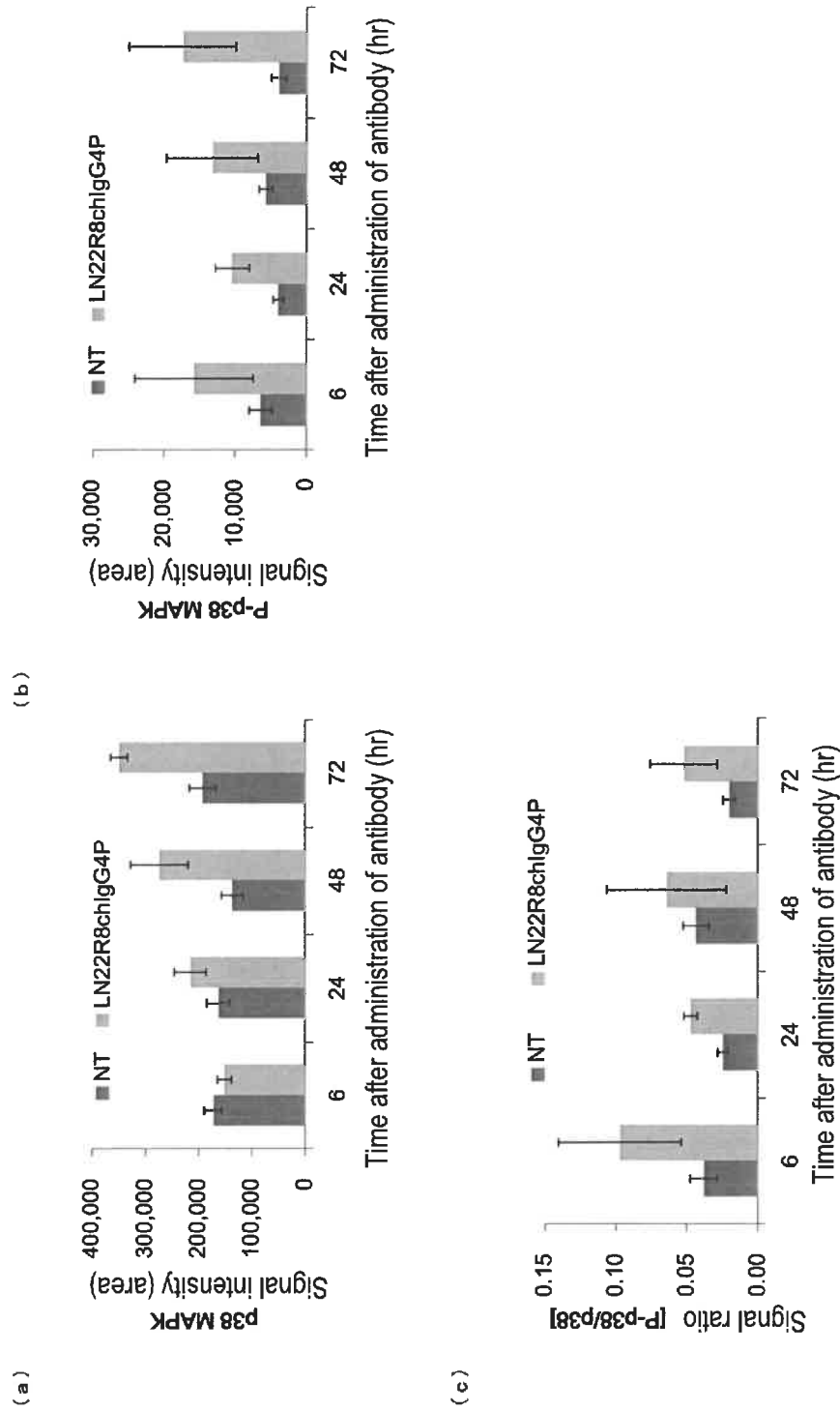
(a)



(b)

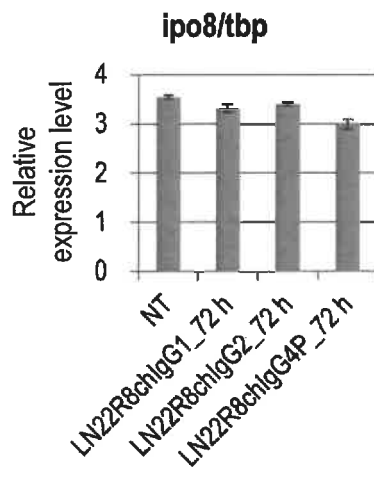


[Figure 21]

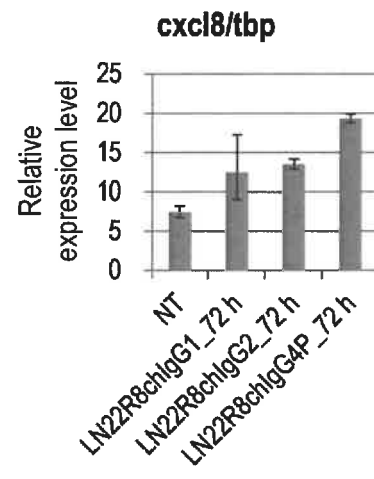


[Figure 22]

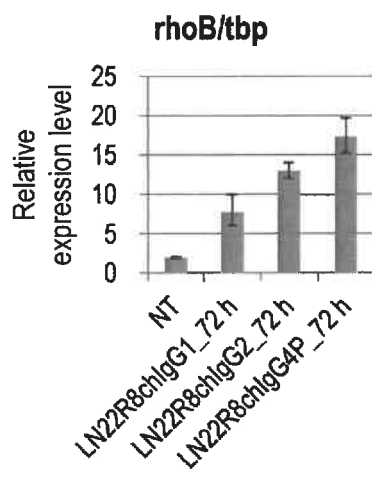
(a)



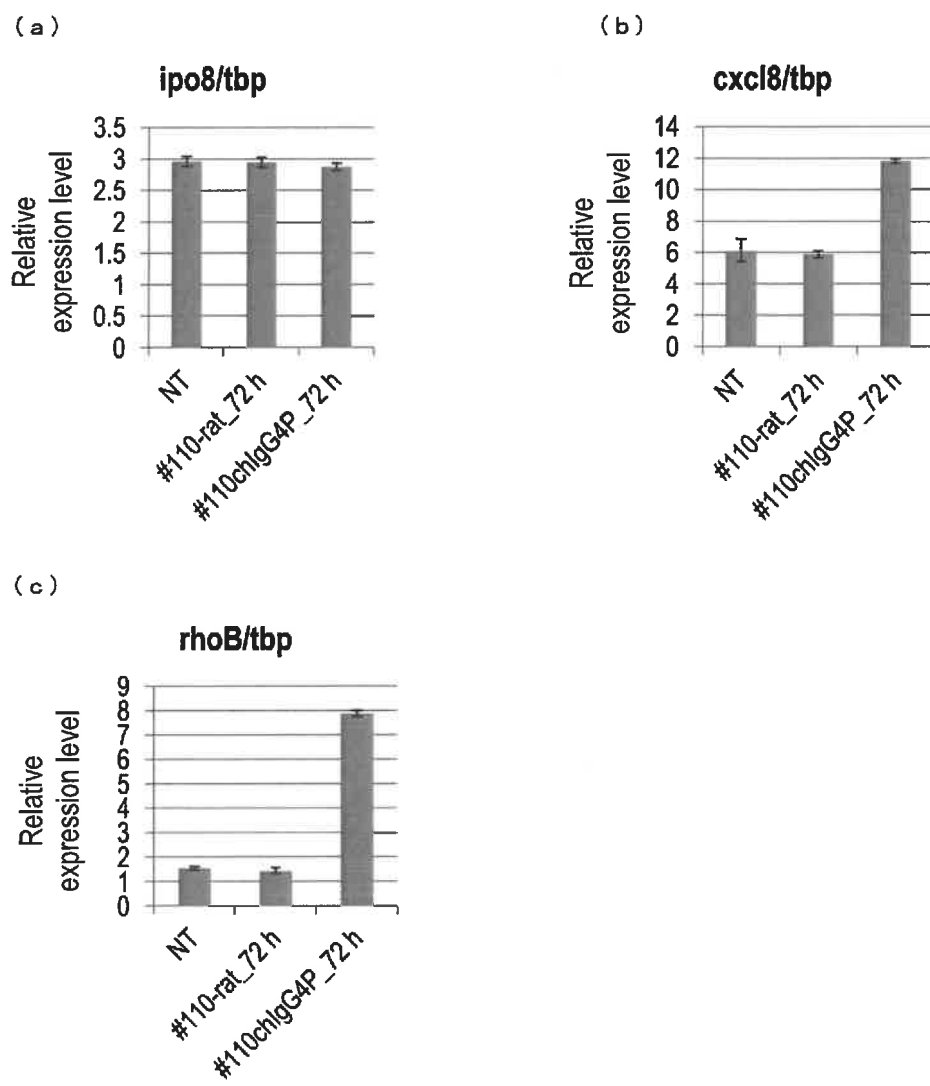
(b)



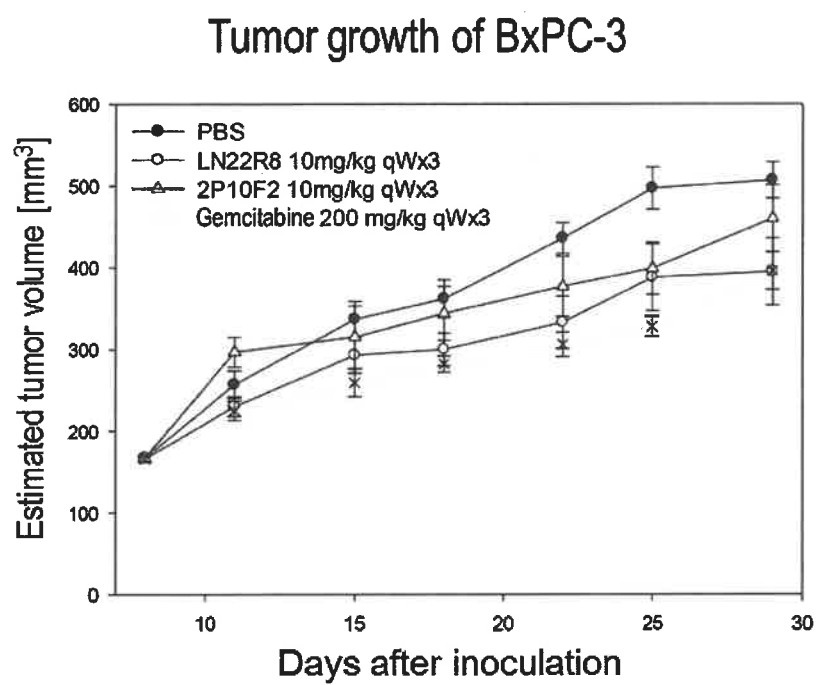
(c)



[Figure 23]

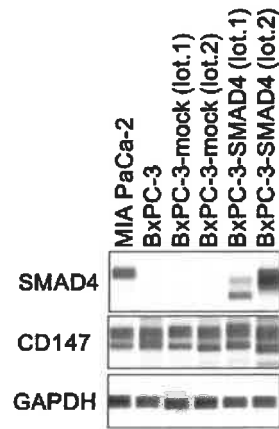


[Figure 24]

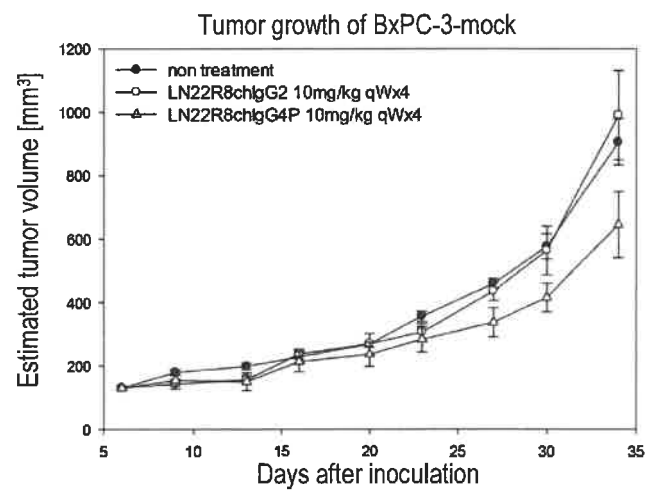


[Figure 25]

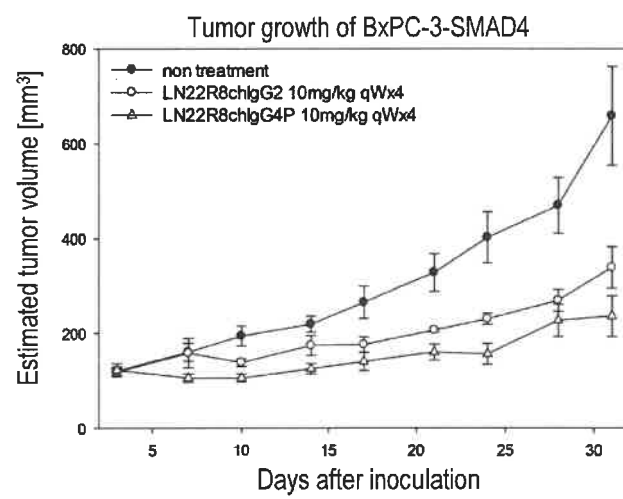
(a)



(b)

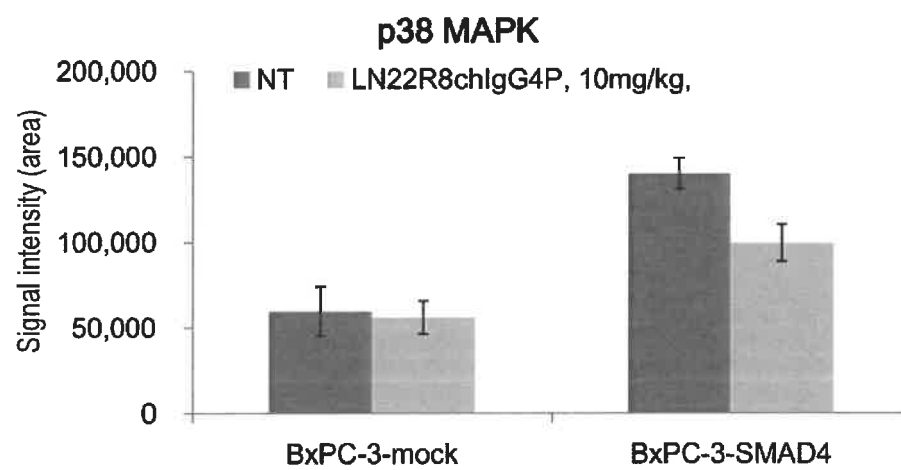


(c)

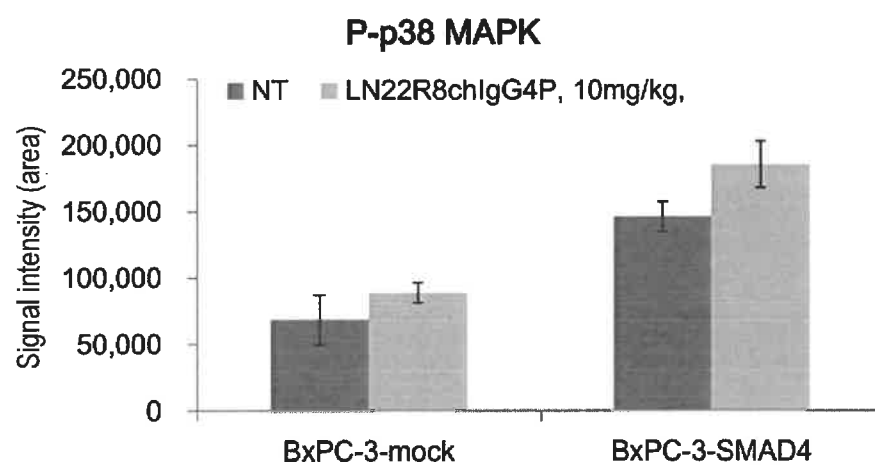


[Figure 26]

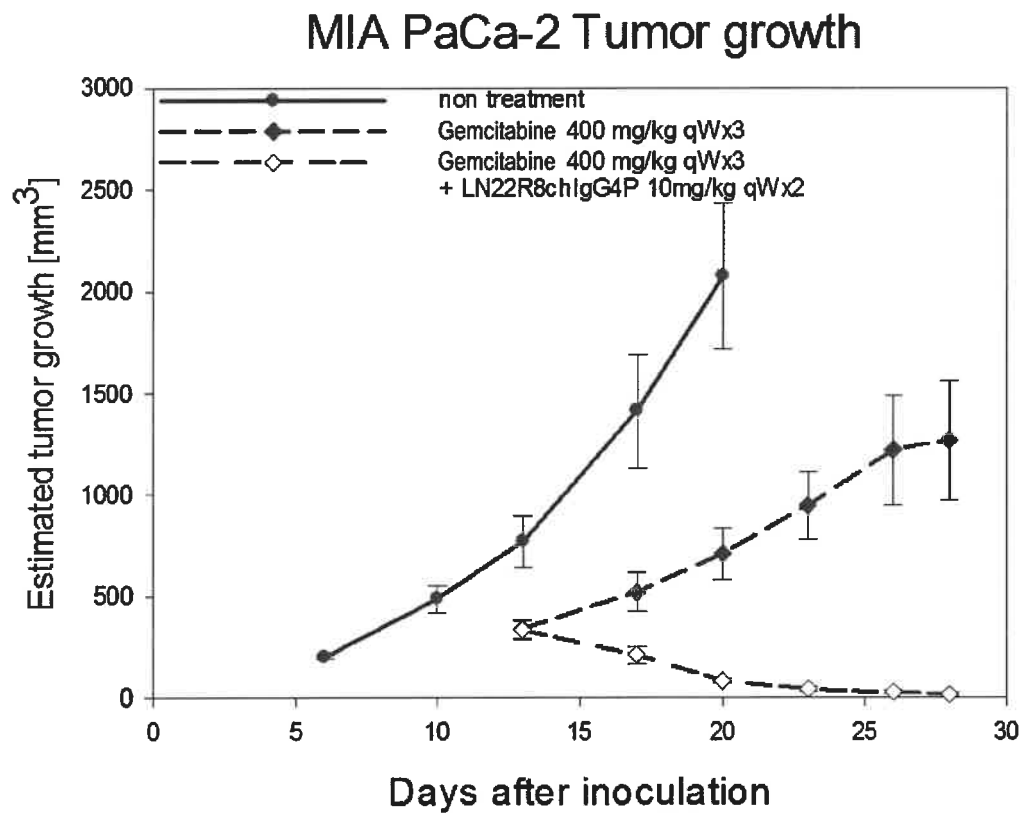
(a)



(b)

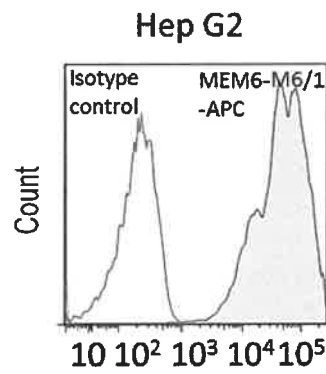


[Figure 27]



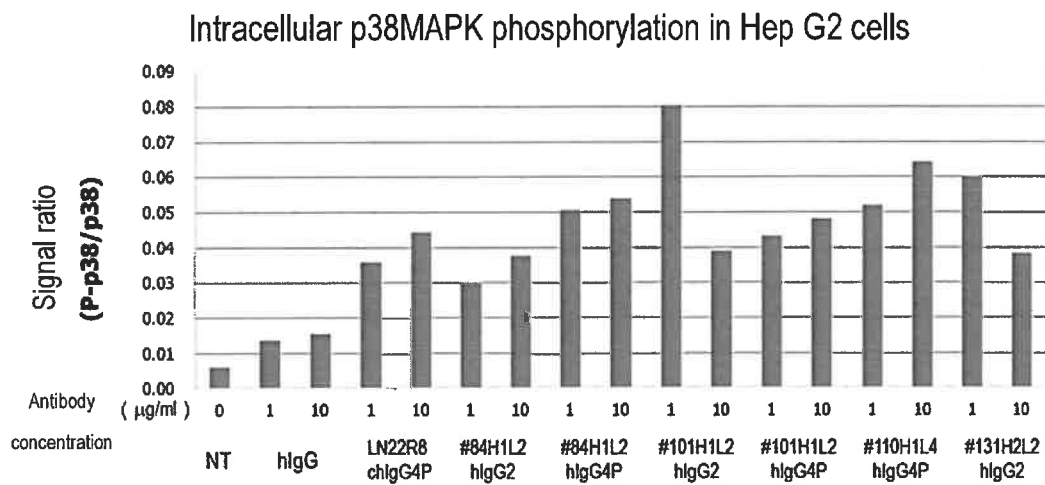
[Figure 28]

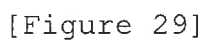
(a)



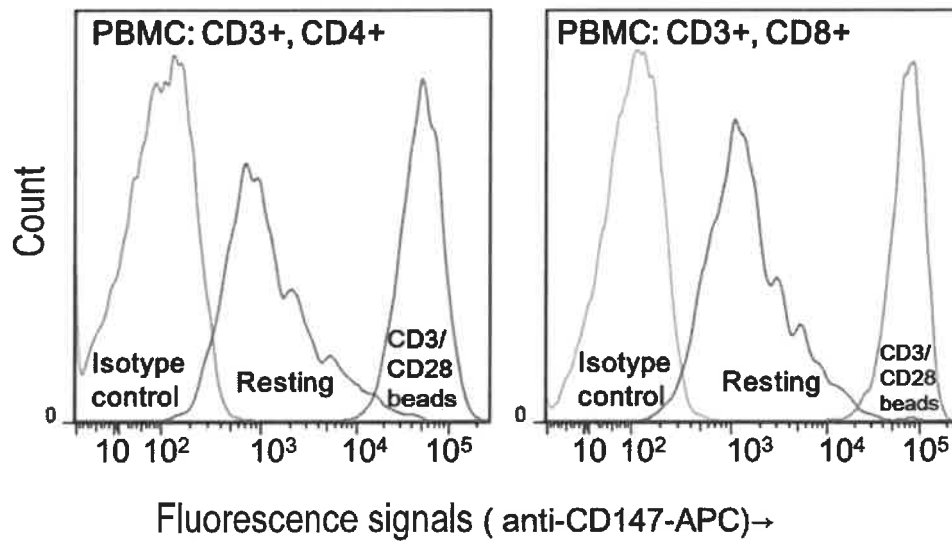
Fluorescence signals →

(b)

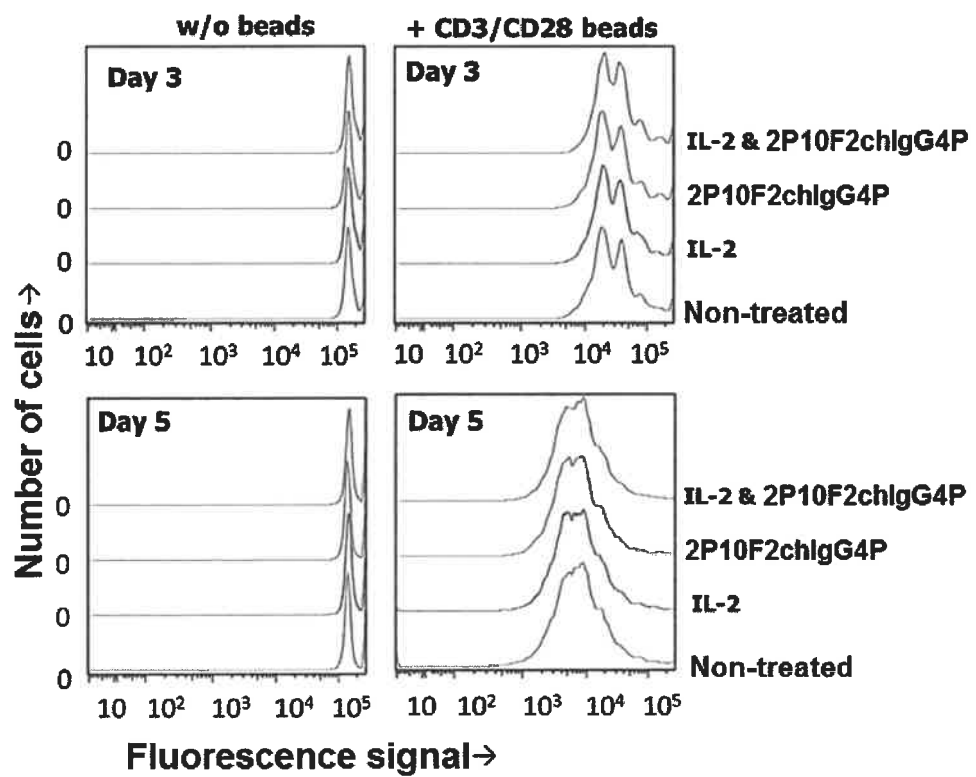




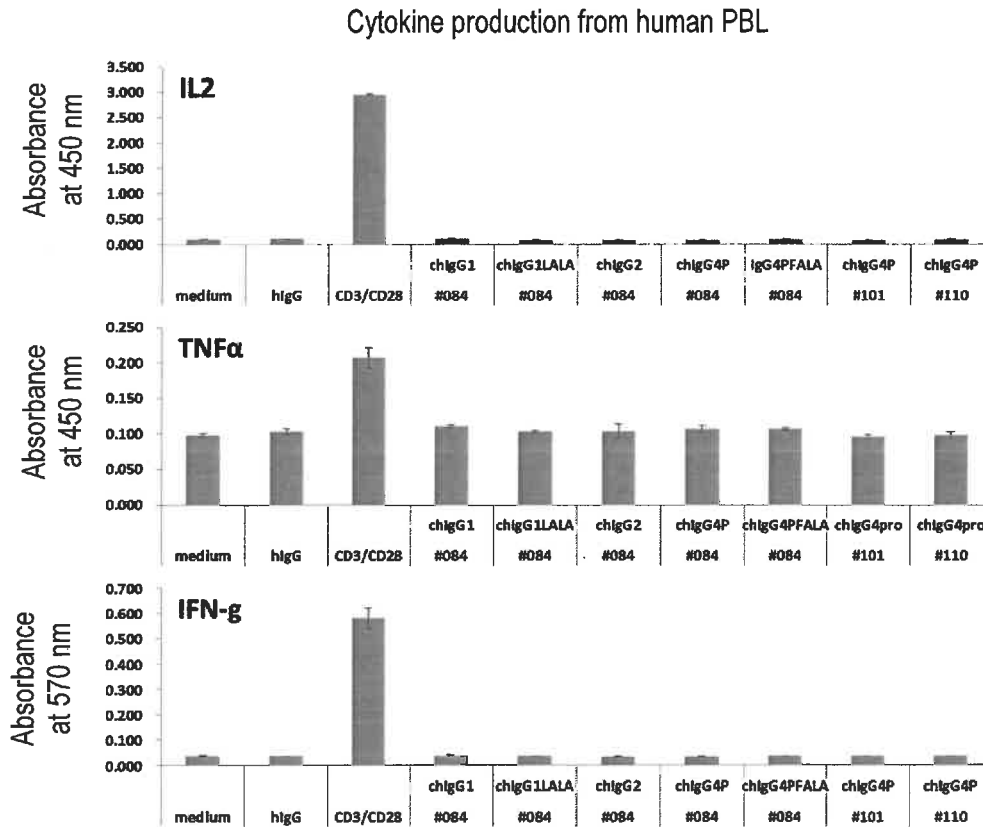
[Figure 30]



[Figure 31]



[Figure 32]



[Figure 33-1]

SEQ ID NO: 48: Nucleotide sequence of rat_CD147_#84 light chain variable region
 GATGTCCAGATGACCCAGTCTCCATCTTATCTTGCTGCGTCTCCTGGAGAAAGTGTTCCATCAGTTGCAAGGCAAGTAAGAGCATTAGCAATAA
 TTTAGCCTGGTATCAGGAGAAACCTGGGAAAGCAAATAAGCTTCTTATTCACCTCTGGGTCAACTTTGCAATCTGGAACCTCCATCGAGTTTCAGTG
 GCAGTGGATCTGGTACAGATTTACGCTCACCATCAGAAGCCTGGAGTTTGAAGATTTTGCAGTCTATTACTGTCAACAGTATAATGAATACCCA
 CTCACGTTCCGTTCTCGGACCAAGCTGGAGATCAAACGG

SEQ ID NO: 49: Amino acid sequence of rat_CD147_#84 light chain variable region (each CDR is underlined)
 DVQMTQSPSYLAASPGESVSISCKASKSISNNLAWYQKPGKANKLLIHSGSTLQSGTPSRFSGSGSGTDFTLTIRSLEFEDFAVYYCQQYNEYPLT
 LTFGSGTKLEIKR

SEQ ID NO: 52: Amino acid sequence of CDRL1 of rat_CD147_#84
 KASKSISNNLA

SEQ ID NO: 53: Amino acid sequence of CDRL2 of rat_CD147_#84
 SGSTLQS

SEQ ID NO: 54: Amino acid sequence of CDRL3 of rat_CD147_#84
 QQYNEYPLT

[Figure 33-2]

SEQ ID NO: 50: Nucleotide sequence of rat_CD147_#84 heavy chain variable region

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTAGTGCAGCCTGGAAGGTCCTGAAACTCTCCTGTGCAGCCTCAGGATTCACCTTCAGTAACTA
TTACATGGCCTGGGTCCGCCAGGCTCCAAAGAAGGGTCTGGAGTGGGTCGCAAGCATTACTACCAGTGGTAGCAGACCTTACTATCCAGACTCCG
TGAAGGCCGATTCACTATCTCCAGAGATAATGCAAAAAGCAGCCTATACCTGCAATGAACAGTCTGAAGTCTGAGGACAGGCCACTTATTAC
TGTGCAAGACATATTTACTATGATGGTTACCCCTTGCTTACTGGGGCCAAGGCACTCTGCTCACTGTCTCTCA

SEQ ID NO: 51: Amino acid sequence of rat_CD147_#84 heavy chain variable region (each CDR is underlined)

EVQLVESGGGLVQPGKSLKLSAASGFTFSNYMAWVRQAPKKGLEWVATITTSGRPYYPDSVKGRFTISRDNKSSLYQMNSLKSEDTATYY
CARHIYYDGYPFAYWGQGLVTVSS

SEQ ID NO: 55: Amino acid sequence of CDRH1 of rat_CD147_#84

GTFSNYMA

SEQ ID NO: 56: Amino acid sequence of CDRH2 of rat_CD147_#84

TITTSGRPY

SEQ ID NO: 57: Amino acid sequence of CDRH3 of rat_CD147_#84

HIYYDGYPFAY

[Figure 34-1]

SEQ ID NO: 58: Nucleotide sequence of rat_CD147_#101 light chain variable region

GAGATCCAGATGACCCAGTCTCCTTCACTCCTGTGCTGCTGTGGGAGGCAGAACTCACTCTCAACTGCAAAGCAAGTCAGAACTCTCTATAAGAA
CTTAGCCTGGTATCAGCAGAAAGCTTGGAGAAGCTCCAAACTCCTGATTGATAATGCAAACAGTTTCAAACGGGCATCCCATCAAGGTTCAAGTG
GCAGTGGATCTGGTACAGATTTCACTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACATATTTCTGCCAGCAGTATTATAGCGGTCG
TACACGTTTGGAGCTGGGACCAAGCTGGAAGTGAACGG

SEQ ID NO: 59: Amino acid sequence of rat_CD147_#101 light chain variable region (each CDR is underlined)

DIQMTQSPSLLSASVGGRIITLNCKASQNLKYNLAWYQKLGAEPLKLLIDNANSLQTGIPSRFSGSGSGTDFTLTISLQPEDVATYFCQQYSGS
YTFGAGTKLELKR

SEQ ID NO: 62: Amino acid sequence of CDRL1 of rat_CD147_#101

KASQNLKYNLA

SEQ ID NO: 63: Amino acid sequence of CDRL2 of rat_CD147_#101

NANSLQT

SEQ ID NO: 64: Amino acid sequence of CDRL3 of rat_CD147_#101

QQYSGSYT

[Figure 34-2]

SEQ ID NO: 60: Nucleotide sequence of rat_CD147_#101 heavy chain variable region

GAGGTGCAGCTGGTGGAGTCTGATGGAGGCTTAGTGCAGCCTGGAAGGTCCTAAACTCTCCTGTGCAGCCTCAGGATTCACCTTCAGTGACTA
TTACATGGCCTGGGTCCGCCAGGCTCCAAAGAGGGGCTGGAGTGGGTCGCAAGCATTAGTTATGATGGTAGTAACACTTACTATCGAGACTCCG
TGAAGGCCGATTCACTATCTCCAGAGATAATGCAAAAAGCAGCCTATACCTGCAATGGACAGTCTGAGGCTCTGGGACAGGCCACTTATTAC
TGTGCAAGATTTACAACAATACTACTTTGATTACTGGGGCCAAGGAGTCATGGTCACAGTCTCCTCA

SEQ ID NO: 61: Amino acid sequence of rat_CD147_#101 heavy chain variable region (each CDR is underlined)

EVQLVESDGLVQPGKSLKLSAASGFTFSDYMAWVRQAPKKGLEWVATISYDGSNTYYRDSVKGRFTISRDNKSTLYQMDSLRSQDTATYY
CARFYNNYYFDYWGGVMVTVSS

SEQ ID NO: 65: Amino acid sequence of CDRH1 of rat_CD147_#101

GTFSFYMA

SEQ ID NO: 66: Amino acid sequence of CDRH2 of rat_CD147_#101

TISYDGSNTY

SEQ ID NO: 67: Amino acid sequence of CDRH3 of rat_CD147_#101

FYNNYYFDY

[Figure 35-1]

SEQ ID NO: 68: Nucleotide sequence of rat_CD147_#110 light chain variable region
 GACATCCAGATGACCCAGACTCCATCCTCCATGCCTGCATCTCTGGGAGAGAGAGTCACCATCAGTTGCAGAGCAAGTCAGGGTATTAGCAATTA
 TCTAAACTGGTATCAGCAGAAACCAGATGGAACGATTAAACCCCTGATCTACTACACATCCAATTTACAATCTGGTGTCCCATCAAGGTTCAAGTG
 GCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAGCCTGGAGCCTGAAGATTTTGAATGTATTCTGCCAACAGTATGATAGTTCTCTCT
 CGGACGTTCCGTGGAGGCACCAAGCTGGAATTGAAACGG

SEQ ID NO: 69: Amino acid sequence of rat_CD147_#110 light chain variable region (each CDR is underlined)
 D1QMTQTPSSMPASLGERVTISCRASQGISNYLNWYQKPDGTIKPLIYYTSNLQSGVPSRFSGSGSGTDYSLTISSELEDFAMVFCQQYDSSP
 RTFGGGTKLELKR

SEQ ID NO: 72: Amino acid sequence of CDRL1 of rat_CD147_#110
 RASQGISNYLN

SEQ ID NO: 73: Amino acid sequence of CDRL2 of rat_CD147_#110
 YTSNLQS

SEQ ID NO: 74: Amino acid sequence of CDRL3 of rat_CD147_#110
 QQYDSSPRT

[Figure 35-2]

SEQ ID NO: 70: Nucleotide sequence of rat_CD147_#110 heavy chain variable region
 CAGGTACAGCTGCAGCAATCTGGGGCTGAACCTGGTGAAGCCTGGGTCTCAGTGAAAATTTCTGCAAGGCTTCTGGCTACACCTTCACCAAGTGA
 CTTTATGCACTGGATAAAACAGCAGCCTGGAAATGGCCTTGAGTGGATTGGGTGGATTATCCTGGAGATGGTGATACAGAGTACAATCAAAAGT
 TCAATGGGAAGGCAACACTCACTGCAGACAAATCCTCCAGCAGCAGCCTATATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTG
 TGTGCAAGGGGACGGGGGTATGTTATGGATGCCTGGGGTCAAGGAGCTTCAGTCACTGTCTCCTCA

SEQ ID NO: 71: Amino acid sequence of rat_CD147_#110 heavy chain variable region (each CDR is underlined)
 QVQLQSGAELVKPGSSVKISCKASGYTFISDFMHWIKQQPGNGLEWIGWIIYPGDGDEYNQKFNKGATLTADKSSSTAYMQLSSLTSEDSAVYF
 CARGRGYVMDAWGGASVTVSS

SEQ ID NO: 75: Amino acid sequence of CDRH1 of rat_CD147_#110
 GYTFISDFMH

SEQ ID NO: 76: Amino acid sequence of CDRH2 of rat_CD147_#110
 WIYPGDGDE

SEQ ID NO: 77: Amino acid sequence of CDRH3 of rat_CD147_#110
 GRGYVMDA

[Figure 36-1]

SEQ ID NO: 78: Nucleotide sequence of rat_CD147_#131 light chain variable region
 GATGTCAGATGACCCAGTCTCCATCTTATCTTGCTGCGTCTCCTGGAGAAAGTGTTCATCAGTTGCAAGGCAAGTAAAGCATTAAACACATA
 CTTAGCCTGGTATCAGGAGAAACCTGGGAAAACGAATAAGCTTCTTATCTACTCTGGGTCAACTTTGCAATCTGGAACCTCCATCGAGATTCAGTG
 GCAGTGGATCTGGTACAGATTTACGCTCACCATCAGAAGCCTGGAGCCTGAAGATTTTGCAGTCTACTACTGTCAACAGCATAATGAATACCCG
 TTCACGTTCCGCTCAGGGACGAAGTTGGAATAAAACGG

SEQ ID NO: 79: Amino acid sequence of rat_CD147_#131 light chain variable region (each CDR is underlined)
 DVQMTQSPSYLAASPGESVSI~~SC~~KASKSINTYLA~~WYQ~~EPKPKTNKLLIYSGSTLQSGTPSRFSGSGSGTDFLTIRSLPEDFAVVY~~CCQ~~HNEY~~P~~
 FTFGSGTKLEIKR

SEQ ID NO: 82: Amino acid sequence of CDRL1 of rat_CD147_#131
 KASKSINTYLA

SEQ ID NO: 83: Amino acid sequence of CDRL2 of rat_CD147_#131
 SGSTLQS

SEQ ID NO: 84: Amino acid sequence of CDRL3 of rat_CD147_#131
 QQHNEYPT

[Figure 36-2]

SEQ ID NO: 80: Nucleotide sequence of rat_CD147_#131 heavy chain variable region

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTAGTGCAGCCTGGAAGGTCTCTGAACTATCCTGTGGAGCCTCTGGATTACATTCAATACTA
CTGGATGACCTGGGTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCATCCATTACTAAAGCTGGTGGTAGCACTTACTATCGAGACTCTG
TGAAGGGCCGATTCACTATCTCCAGAGATAATGCAAAAAGCACCTATATCTGCAAAATGAACAGTCTGAGGTCTGAGGACAGGCCACTTATTAC
TGACAAGAGAACTGGGAGAGTTCTATGTTATGGATGCCTGGGTCAAGGAGCTTCAGTCACTGTCTCCTCA

SEQ ID NO: 81: Amino acid sequence of rat_CD147_#131 heavy chain variable region (each CDR is underlined)

EVQLVESGGGLVQPGSLKLSGASGFTFN^{NYMM}TVVRQAPGKLEWVASITKAGGSTYYRDSVKGRFTISRDNASTLYLQMNSLRSEDATYY
CTRELGEFYVMDA^WGGASVTVSS

SEQ ID NO: 85: Amino acid sequence of CDRH1 of rat_CD147_#131

GFTFN^{NYMM}T

SEQ ID NO: 86: Amino acid sequence of CDRH2 of rat_CD147_#131

SITKAGGSTY

SEQ ID NO: 87: Amino acid sequence of CDRH3 of rat_CD147_#131

ELGEFYVMDA

[Figure 37-1]

SEQ ID NO: 123: Amino acid sequence of #84H1hlgG2 (each CDR is underlined)

MKHLWFFLLLVAPRWVLSEVQLVESGGGLVQPGSLRLSCAASGFTFSN^{YYMA}WVRQAPGKLEWVSTITSGSRPY^YADSVKGRFTISRDN
NTLYLQMNSLR^{AE}DAVYYCARHLY^YYDGY^{PF}AYWGGT^LLVTVSSASTKGPSVF^LAPCSRSTSESTAALGCLVKDY^{FP}PEPVT^{VS}WNSGALTSGV
HTFP^{AV}LQSSGLYSLSSVTV^PSSNFGTQTYTCNV^DHKPSNTKVDKTV^{ER}KCCVECP^{PC}PAPPVAGPSVFL^{FP}PKPDTLMISR^{TP}EVTCV^VVDV
SHEDPEVQ^{FN}WYVDGVEVHNAKTK^PREEQ^{FN}STFRVSVLTVVH^QDWLN^GKEYKCKVSNKGLPAP^IEKTISKTKGQ^{RP}EPQVY^{TL}PPSREEMTKN
QVSLTCLVKGF^YPSDI^AVEWESNG^QPENNYK^TTPMLDS^GSFFLYSKLTVDKSR^WQQGNV^FSCSV^MHEAL^NHNYTQKSLSLSPGK
Signal sequence1-19, Variable region20-140, Constant region141-466

SEQ ID NO: 124: Nucleotide sequence of #84H1hlgG2

ATGAAACACCTGTGGTCTTCTCCTGCTGGTGGCAGCTCCAGATGGGTGCTGAGCGAAGTGCAGCTGGTGAAGTCTGGCGGAGGACTGGTTC
ACCTGGCGGAAGCCTGAGACTGTCTTGTGCCGCCAGCGGCTTACCTTCAGCACTACTATATGGCCTGGGTCGACAGGCCCTGGCAAAGGAC
TTGAATGGGTGTCACCATCACCACAGCGGCGAGAGACCTTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCGGGACAAACAGCAAG
AACACCCGTGTACCTGCAGATGAACAGCCTGAGAGCGGAGGACACCGCGGTGTACTATTGGCCAGACACATCTACTACTAGAGGGCTACCCCTT
CGCCTATTGGGCCAGGGAACACTGGTCACAGTTAGCTCAGCCTCCACCAAGGGCCCTTCCGTGTTCCCTCTGGCCCTTGTAGCCGTTCCACCA
GCGAGTCCACCGCCGCCCTTGGCTGTCTGGTGAAGGACTACTTCCCTGAGCCTGTGACCGTGAGCTGGAACCTCCGGAGCCCTTACCAAGCGCGTG
CACACCTTCCCTGCCGTGCTGCAGTCCAGCGGCCCTTACTCCCTGAGCTCCGTGGTGACCGTGCCCTAGCTCCAACCTTCGGCACCAACCTACAC
CTGTAACGTGGACCACAAGCCTAGCAACACCAAGGTGGACAAGACCGTGGAGCGTAAGTGTGTGTGAGTGTCTCTGCTGCGCCCTCCTG
TGGCCGGACCTTCCGTGTTCTTTCCCTCCTAAGCCTAAGGACACCCCTGATGATCAGCCGTACCCCTGAGGTGACCTGTGTGGTGGTGGACGTG
TCCACAGGAGCCCTGAGGTGCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAAGCCAAAGACCAAGCCTGCTGAGGAGCAATTCACAG
CACCTTCGGTGTGGTGTCCGTGCTTACCGTGGTGCACCAAGACTGGCTGAACGGCAAGGAGTACAAGTGTAAAGGTGAGCAACAAGGGACTTCCTG
CCCTATCGAGAAGACCATCTCCAAGACCAAGGGCCAACTCGTGAGCCTCAAGTGTACACCTTCCCTAGCCGTGAGGAGATGACCAAGAAC
CAAGTGTCCCTTACCTGTCTGTGAAGGGCTTCTACCTAGCGACATCGCCGTGGAGTGGGAGTCCAACGGACAACCTGAGAACAACTACAAGAC
CAGCCCTCCTATGCTTGACAGCGACGGCTCCTTCTCTCTGTACAGCAAGCTGACCGTGGACAAGTCCCGTTGGCAACAAGGCAACGTGTTCAAGCT
GTTCCGTGATGCAGAGGCCCTGCACAACCACTACACCAAAAGAGCCTTCCCTGAGCCCTGGAAAAG

Signal sequence1-57, Variable region58-420, Constant region421-1398

[Figure 37-2]

SEQ ID NO: 125: Amino acid sequence of #84H1hlgG4P (each CDR is underlined)

MKHLWFFLLLVAPRWVLEVLVESGGGLVQPGGSLRLSCAASGFTFSNYMAWVRQAPGKLEWVSTITSGSRPYADSVKGRFTISRDNK
NTLYLQMNSLRAEDTAVYYCARHIYYDGYFPAYWGQGLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTQCNVDHKPSNTKVDKRVESKYGPCCPAPFELGGPSVFLFPPKPKDTLMISRTPEVTCVVD
VSQEDPEVQFNWYDGVVEVHNATKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK
NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFCSVMHEALHNHYTQKLSLSLGK

Signal sequence1-19, Variable region20-140, Constant region141-467

SEQ ID NO: 126: Nucleotide sequence of #84H1hlgG4P

ATGAAACACCTGTGGTCTTCTCCTCCTGCTGGTGGCAGCTCCAGATGGGTGCTGAGCGAAGTGCAGCTGGTGGTCTGGCGGAGGACTGGTTCA
ACCTGGCGGAAGCCTGAGACTGTCTTGTGCCGCCAGCGGCTTACCTTCAGCAACTACTATATGGCCTGGGTCCGACAGGCCCTGGCAAAGGAC
TTGAATGGGTGTCACCATCACCACAGCGGCAGCAGACCTTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACAACAGCAAG
AAGACCCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCGCTGTACTATTGGCCAGACACATCTACTAGCAGCGCTACCCCTT
CGCCTATTGGGGCCAGGGAACACTGGTCACAGTTAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTTCCTCTGGCCCTTGTAGCAGAAAGCACA
GCGAGTCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTCCCGAGCCCGTGACCGTGTCTGGAAGTCTGGCGCTCTGACAAGCGCGTG
CACACCTTCCAGCCGTGCTGCAGAGCAGCGGCTGTACTCTGTCCAGGTCGTGACTGTGCCAGCAGCTCTCTGGGACCAAGACCTACAC
CTGTAACTGGACCAAGCCAGCAACACCAAGGTGGACAAGCGGGTGAATCTAAGTACGGCCCTCCCTGCCCTCCTTGGCCAGCCCTGAAT
TTCTGGCGGAGCCCTCGTGTCTCTGTTCCCGCAAGGCCAAGGACACCCCTGATGATCAGCCGGACCCCGAAGTGACCTGCGTGGTGGTGGAT
GTGTCCAGGAAGATCCGAGGTGCAGTTCAATTGGTACGTGGACGGCTGGAAGTGCACAACGCCAAGACCAAGCCTAGAGAGGAACAGTTCAA
CAGCACCTACCGGGTGGTGTCCGTGCTGACAGTGTGCACAGGACTGGCTGAACGGCAAGAGTACAAGTGAAGGTGTCCAACAGGGCCTGC
CCAGCTCCATCGAGAAACCATCAGCAAGGCCAAGGGCCAGCCCGCGCAACCCAGGTGTACACACTGCCTCCAAGCCAGGAAGAGATGACCAAG
AATCAGGTGTCCCTGACCTGTCTCGTGAAGGCTTCTACCGCTCCGATATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGAGAACAACTACAA
GACCAACCCCGCTGTGCTGGACTCGATGGCTCATTCTTCTGTACAGCAGACTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCA
GCTGCTCGTGTGATGCACAGGGCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGAGCCTGGGCAA

Signal sequence1-57, Variable region58-420, Constant region421-1401

[Figure 37-3]

SEQ ID NO: 127: Amino acid sequence of #84L2h (each CDR is underlined)

MVLQTVFISLLLVISGAYGDVQMTQSPSSLSASVGRVITCKASKSIENNLAWYQOKPGKANKLLIHSGSTLQSGTPSRFSGSGGDFLTIT
SSLQPEDFATYYCQYNEYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQHWKDNLQSGNSQESVTEQDSK
STYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 128: Nucleotide sequence of #84L2h

ATGGTGTGCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCGGTACGGCGACGTTTCAGATGACACAGAGCCCTAGCAGCCTGTC
TGCCAGCGTGGGAGACAGAGTGACCATCACATGCAAGGCCAGCAAGAGCATCAGCAACAACCTGGCCTGGTATCAGCAGAAGCCCGAAAGGCCA
ACAAGCTGCTGATCCACAGCGGAGCAGCACTGCAGTCTGGCAGCCCTAGCAGATTTTCCGGCTCTGGCAGCGGACCGGATTCACCTGACCAT
TCTAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGTACAACGAGTACCCCTCTGACCTTTGGCAGGGCACCAAGGTGGAATCAA
GCCTACGGTGGCGGCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTGTGCTGCTGAATACT
TCTACCCAGAGAGGCCAAGGTGCAGTGAAGGTGGACAACGCCCTGCAGTCCGGGAACCTCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTGAGCAGCACCTGACCTGAGCAAGCCGACTACGAGAAGCACAAGGTGTACGCCCTGCGAGGTGACCCACAGGGCCTGAG
CTCCCCGTCAACAAGAGCTTCAACAGGGGGAGTGT

Signal sequence1-60, Variable region61-384, Constant region385-702

[Figure 38-3]

SEQ ID NO: 133: Amino acid sequence of #101L2h (each CDR is underlined)

MVLTQGVFI SLLLVISGAYGDI QMTQSPSSLSASVGRVITNCKASQNL YKNLAWYQQKPGKAPKLL IDNANSLQTGI PSRFSGSGSGDFTLT I
 SSLQPEDFATYFCQQYYSGSYTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
 STYSLSSLTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
 Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 134: Nucleotide sequence of #101L2h

ATGGTGTGTCAGACCCAGGTGTTTCATCTCCCTGCTGCTGTGGATCTCCGGCCGCTACGGCGATATCCAGATGACACAGAGCCCTAGCAGCCTGTC
 TGCCAGCCTGGGAGATAGAGTGACCATCAACTGCAAGGCCAGCCAGAACCTGTACAAGAACCTGGCCTGGTATCAGCAGAAAGCCGGCAAGGCTC
 CTAAGCTGCTGATCGACAACGCCAACAGCCTGCAGACGGCATTCCACGAGATTTTCTGGCAGCGGCTCCGGCACCATTTCACCTGACCATTA
 TCTAGCCTGCAGCCTGAGGACTTCGCCACCTACTTTTGGCAGCAGTACTACAGCGGCAGCTACACCTTTGGCCAGGGCACCAGGTGGAAATCAA
 GCGTAGCCTGGCGGCCCTCCGTGTTTCATCTTCCCCCTCCGACGAGCAGCTGAAGTCCGGCACCGCCTCCGTGGTGTGCTGCTGAATAACT
 TCTACCCAGAGAGGCCAAGGTGCAGTGGAAAGGTGGACAACGCCCTGCAGTCCGGGAACCTCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGAC
 AGCACCTACAGCCTGAGCAGCACCTGACCTGAGCAAGCCGACTACGAGAAGCACAAGGTGTACGCTCGGAGGTGACCCACCAAGGCGCTGAG
 CTCCCCGTCACCAAGAGCTTCAACAGGGGGAGTGT
 Signal sequence1-60, Variable region61-384, Constant region385-702

[Figure 39-1]

SEQ ID NO: 135: Amino acid sequence of #110H1hlgG4P (each CDR is underlined)

MKHLWFFLLLVAAAPRWLSQVQLVQSGAEVKKPGASVKVSCKASGYTFYTSDFMHWVRQAPGQGLEWMGW IYPGDGDTEYNKFGGRVTLTRDTSI
 STAYMELSRRLSDDTAVYYCARGRGVYMDAWGGGTTVTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
 AVLQSSGLYSLSSVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPPCPAPEFLGGPSVFLFPPKPDLMISRTPEVTCVVVDVSDQ
 DPEVQFNWYVDGGEVHNAKTKPREEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPOVYTLPPSQEEMTKNQVS
 LTCLVKGFYPSDI AVEWESNGOPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTKSLSLSLGK
 Signal sequence1-19, Variable region20-136, Constant region137-463

SEQ ID NO: 136: Nucleotide sequence of #110H1hlgG4P

ATGAAACACCTGTGGTCTTCTCCTCCTGCTGGTGGCAGCTCCAGATGGGTGCTGAGCCAGGTTACGCTGGTTCAGTCTGGGGCCGAAGTGAAGAA
 ACCTGGCGCCTCTGTGAAGGTGCTCCTGCAAGGCCAGCGGCTACACCTTTACCAGCGACTTCATGCACTGGGTCCGACAGGCTCCAGGACAGGGAC
 TTGAATGGATGGGCTGGATCTATCCCGGCGACGGCGACACCGAGTACAACCAAGAAATTCAGGGCAGAGTGACCTGACCAAGACACCAAGATC
 AGCACCGCTACATGGAAGTGAAGCGGCTGAGATCCGATGACACCGCGGTGTACTACTGCGCCAGAGGCAGAGGCTATGTGATGGATGCTTGGGG
 CCAGGGCACCACCGTTACAGTTAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTCCCTCTGGCCCTTGTAGCAGAAGCACCAGCGAGTCTACAG
 CCGCCCTGGGCTGCCTCGTGAAGGACTACTTCCCGAGCCGCTGACCGTGTCCCTGGAAGTCTGGCGCTCTGACAAGCGGCGTGACACCTTTCCA
 GCGGTGCTGCAGAGCAGCGGCTGTACTCTCTGTCCAGCGTGTGACTGTGCCAGCAGCTCTCTGGGCACCAAGACCTACACCTGTAACGTGGA
 CCACAAGCCCAGCAACACCAAGGTGGACAAGCGGCTGGAATCTAAGTACGGCGCTCCCTGCCCTCCTTGCCAGGCCCTGAATTTCTGGGCGGAC
 CCTCCGTGTTCTGTTCCGCCAAAGCCCAAGGACACCTGATGATCAGCCGGACCCCGAAGTGAACCTGCGTGGTGGTGGATGTGCCAGGAA
 GATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGAAGTGCACAACGCCAAGCAAGCCTAGAGAGGAACAGTTCAACAGCACCTACCG
 GGTGGTGTCCGTGCTGACAGTGTGCACCAAGGACTGGCTGAACGGCAAGAGTACAAGTGAAGGTGTCCAACAAGGGCTGCCAGCTCCATCG
 AGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCAACCCAGGTGTACACACTGCCTCCAAGCCAGGAAGAGATGACCAAGAATCAGGTGTCC
 CTGACCTGTCTGTGAAAGGCTTCTACCCCTCGGATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCGGAGAACAACATAAGACACCCGCC
 TGTGCTGGAATCCGATGGCTCATTCTTCTGTACAGCAGACTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTGAGCTGCTCCGTGA
 TGCACGAGGCCCTGCACAACCACTACCCAGAGTCCCTGTCTGAGCCTGGGCAAA
 Signal sequence1-57, Variable region58-408, Constant region409-1389

[Figure 39-2]

SEQ ID NO: 147: Amino acid sequence of #110H13hlgG4P (each CDR is underlined)
 MKHLWFFLLVAAPRWVLSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSDFMHNVRQAPGGGLEWMGWLYPCDGDTEYAKFGQGRVTMTSDTSI
 STAYMELSRLSDDTAVYYCARGRGYYMDAWGGGTTVTYSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSQVHTFP
 AVLQSSGLYSLSSVTVPSSSLGKTYTQNVDPKPSNTKVDKRVESKYGPPCPPPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTVVVDVSQE
 DPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTSKAKGGPREPQVYTLPPSQEEMTKNQVS
 LTCLVKGFYPSDJAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVHHEALHNHYTQKSLSLSLGK
 Signal sequence1-19, Variable region20-136, Constant region137-463

SEQ ID NO: 148: Nucleotide sequence of #110H13hlgG4P
 ATGAACACCTGTGGTCTTCTCCTGCTGCTGGTGGCAGCTCCAGATGGGTGCTGAGCCAGGTTGAGTCTGGTGGCAGGAGTGAAGAA
 ACCTGGCGCTCTGTGAAGGTGTCTGCAAGGCCAGCGGCTACACCTTTACCAGCGACTTCATGCACCTGGTCCGACAGGCTCCAGGACAGGGAC
 TTGAATGGATGGGCTGGATCTATCCCGGCGACGGCGATACAGAGTACGCCAGAAATCCAGGGCAGAGTGACCATGACCAAGACACACAGCATC
 AGCACGGCTAGATGGAAGTGGAGCTGAGATCCGATGACACCGCGGTGTACTACTGCGCCAGAGGCGAGAGGCTATGTATGGATGCTTGGGG
 CCAGGGCACCACCTTACAGTTAGCTCAGCCTCCACCAAGGGCCCTAGCGTGTCCCTCTGGCCCTTGTAGCAGAAAGCACCAGCGATCTACAG
 CGCGCTGGGCTGCTGCTGAAGGACTACTTTCCCGAGCCGCTGACCGTGTCTGGAAGTCTGGCGCTCTGACAAAGCGGCTGCACACCTTTCCA
 GCGCTGCTGCAGAGCAGCGGCTGTACTCTGTCCAGCGTGTGACTGTGCCAGCAGCTCTCTGGGACCAAGACCTACACCTGTAACTGGA
 CCACACGGCTAGACCAAGGTGGACAAGCGGGTGAATCTAAGTACGGCGCTCCTGCGCTCTTGGCCAGCCCTGAATTTCTGGCGGGAC
 CCTCGTGTCTCTCCCCAAAGCCCAAGGACACCTGATGATCAGCGGACCCCGAAGTGACCTGCTGGTGGTGGATGTGTCCAGGAA
 GATCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAAGTGCACAACGCCAAGCCAGCCTAGAGAGGAAACAGTTCAACAGCACCTACCG
 GGTGGTGTCTGCTGACAGTGTCTGACAGGACTGGCTGAACGGCAAGAGTACAAGTGAAGGTGTCCAACAAGGGCTGCCAGCTCCATCG
 AGAAACCATCAGCAAGGCCAAGGGCAGCCCGCGAACCAGGTGTACACACTGCTCCAAGCCAGGAAGAGATGACCAAGAAATCAGGTGTCC
 CTGACCTGTCTGTAAGGCTTCTACCCCTCCGATATCGCGTGGAAATGGGAGAGCAACGGCCAGCCGAGAGCAACTACAAGACACCCGCC
 TGTGCTGGACTCCGATGGCTCATTCTCTGCTGACAGAGCTGACCGTGGCAAGAGCCGGTGGCAGGAAGGCAACGTGTTGAGTGTCTGCTGTA
 TGCACAGGGCTGACCAACCACTACACCCAGAAGTCCCTGTCTGAGCCTGGGCAAA
 Signal sequence1-57, Variable region58-408, Constant region409-1389

[Figure 39-3]

SEQ ID NO: 137: Amino acid sequence of #110L4h (each CDR is underlined)
 MVLQTVFISLLWISGAYGDIQMTQSPSSLSASVGRVTITCRASQGI SNYLNWYQKPKGAIKPLIYYTSLNLSGVPSRFSGSGSDTYLTI
 SSLQPEDFATYFQQYDSSPRIFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKD
 STYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
 Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 138: Nucleotide sequence of #110L4h
 ATGGTGTGACAGCCAGGTGTTGATCTCCCTGCTGCTGTGGATCTCCGGCGGTACGGCGATATCCAGATGACACAGAGCCCTAGCAGCCTGTG
 TGCCAGCGTGGGAGACAGAGTGACCATCACCTGTAGAGCCAGCCAGGCATCAGCAACTACCTGAACTGGTATCAGCAGAAAGCCCGCAAGGCCA
 TGAAGCCCTGATCTACTACACGACCAACCTGCAGAGCGCGTGGCCAGCAGATTTTCTGGCTCTGGCAGCGGACCGACTACACCTGACCAT
 TCTAGCTGACAGCTGAGGACTTGCCACCTACTTTGCCAGAGTACGACAGCAGCCAGAACCTTTGGCGCGGAACAAGGTGGAATCAA
 GCGTACGGTGGCCGCCCTCCGTGTTGATCTTCCCGCCTCCGACGAGCAGCTGAAGTCCGGCAGCGCTCCGTGGTGTGCTGTGAATACT
 TCTACCCAGAGAGGCCAAGGTGCAAGTGGAGTGGACAACGCCCTGCAAGTCCGGGAATCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGAC
 AGCACCTACAGCTGAGCAGCACCTGACCTGAGCAAGCCGACTACGAGAAGCACAAGGTGTACGCTGCGAGGTGACCCACCAAGGCCCTGAG
 CTCGCCGTGACCAAGAGCTTCAACAGGGGGAGTGT
 Signal sequence1-60, Variable region61-384, Constant region385-702

[Figure 39-4]

SEQ ID NO: 149: Amino acid sequence of #110L2h (each CDR is underlined)
 MVLQTVFISLLWISGAYGDIQMTQSPSSLSASVGRVTITCRASQGI SNYLNWYQKPKGAIKPLIYYTSLNLSGVPSRFSGSGSDTYLTI
 SSLQPEDFATYFQQYDSSPRIFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKD
 STYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
 Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 150: Nucleotide sequence of #110L2h
 ATGGTGTGACAGCCAGGTGTTGATCTCCCTGCTGCTGTGGATCTCCGGCGGTACGGCGATATCCAGATGACACAGAGCCCTAGCAGCCTGTG
 TGCCAGCGTGGGAGACAGAGTGACCATCACCTGTAGAGCCAGCCAGGCATCAGCAACTACCTGAACTGGTATCAGCAGAAAGCCCGCAAGGCC
 CTAAGCCTCTGATCTACTACACGACCAACCTGCAGAGCGCGTGGCCAGCAGATTTTCTGGCTCTGGCAGCGGACCGACTACACCTGACCAT
 TCTAGCTGACAGCTGAGGACTTGCCACCTACTACTGCCAGAGTACGACAGCAGCCAGAACATTGGCGGAGGACCAAGGTGGAATCAA
 GCGTACGGTGGCCGCCCTCCGTGTTGATCTTCCCGCCTCCGACGAGCAGCTGAAGTCCGGCAGCGCTCCGTGGTGTGCTGTGAATACT
 TCTACCCAGAGAGGCCAAGGTGCAAGTGGAAAGTGGACAACGCCCTGCAAGTCCGGGAATCCAGGAGAGCGTGACCGAGCAGGACAGCAAGGAC
 AGCACCTACAGCTGAGCAGCACCTGACCTGAGCAAGCCGACTACGAGAAGCACAAGGTGTACGCTGCGAGGTGACCCACCAAGGCCCTGAG
 CTCGCCGTGACCAAGAGCTTCAACAGGGGGAGTGT
 Signal sequence1-60, Variable region61-384, Constant region385-702

[Figure 39-5]

SEQ ID NO: 151: Amino acid sequence of #110L12h (each CDR is underlined)
 MVLQTQVFIISLLWISGAYGDIQNTQSPSSLASVGDRTVITCRASQGIISNYLWYQKPKGAPKPLIYYTSLNLSGVPSRFSGSGSGDTFTLT
 SSLQPEDFATYYCQYDSSPRTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKD
 STYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC
 Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 152: Nucleotide sequence of #110L12h
 ATGGTGTGCAGACCCAGGTGTTCTCTCCCTGCTGCTGTGGATCTCCGGCGCTACGGCGATATCCAGATGACACAGAGCCCTAGCAGCCTGTC
 TGCCAGCGTGGGAGACAGAGTGACCATGACCTGTAGAGCCAGCCAGGGCATCAGCAACTACCTGAAGTGGTATCAGCAGAAAGCCGGCAAGGCC
 CTAAGCCCTGTGATCTACTACACGAGCAACCTGCAGAGCGCGCTGCCAGCAGATTTTCTGGCTCTGGCAGCGGCACCGACTTCACCTGACCAT
 TCTAGCTGCAGCTGAGGACTTCGCCACCTACTACTGCCAGATACGACAGCAGCCCAAGCAATTGGCGGAGGCACCAAGCTGGAATCAA
 GCGTACGGTGGCCGCCCTCCGTGTTCTATCTTCCGCCCTCCGACGACGCTGAAGTCCGGCACCCTCCGTGGTGTGCTGCTGAATAACT
 TCTACCCAGAGAGGCCAAGGTGAGTGAAGGTGGACAACGCCCTGCAGTCCGGGAAGTCCAGGAGAGCGTGACCGAGCAGGACGAAGGAC
 AGCACCTACAGCCTGAGCAGCACCTGACCTGAGCAAGCCGACTACGAGAAGCACAAGGTGTACGGCTGCGAGGTGACCCACCAAGGCCCTGAG
 CTCCCCGTCAACAGAGCTTCAACAGGGGGAGTGT
 Signal sequence1-60, Variable region61-384, Constant region385-702

[Figure 40-1]

SEQ ID NO: 139: Amino acid sequence of #131H2hlgG2 (each CDR is underlined)
 MKHLWFFLLVAAPRIVLSQVLVESGGGVVQGRSLRLSCAASEFTFNINWMTWVRQAPGKLEWVASITKAGGSTYYADSVKGRFTISRDNK
 STLQMNLSRAEGTAVYYCTRELGEFYVMDANGOGTTVTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
 FPAVLQSSGLYSLSSVTVPSNFGTGTQYTCNVDPKPSNTKVDKVERKCCVCPPCAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
 EDPEVDFNMYDGVVEVHNATKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQV
 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKLSLSLSPGK
 Signal sequence1-19, Variable region20-138, Constant region139-464

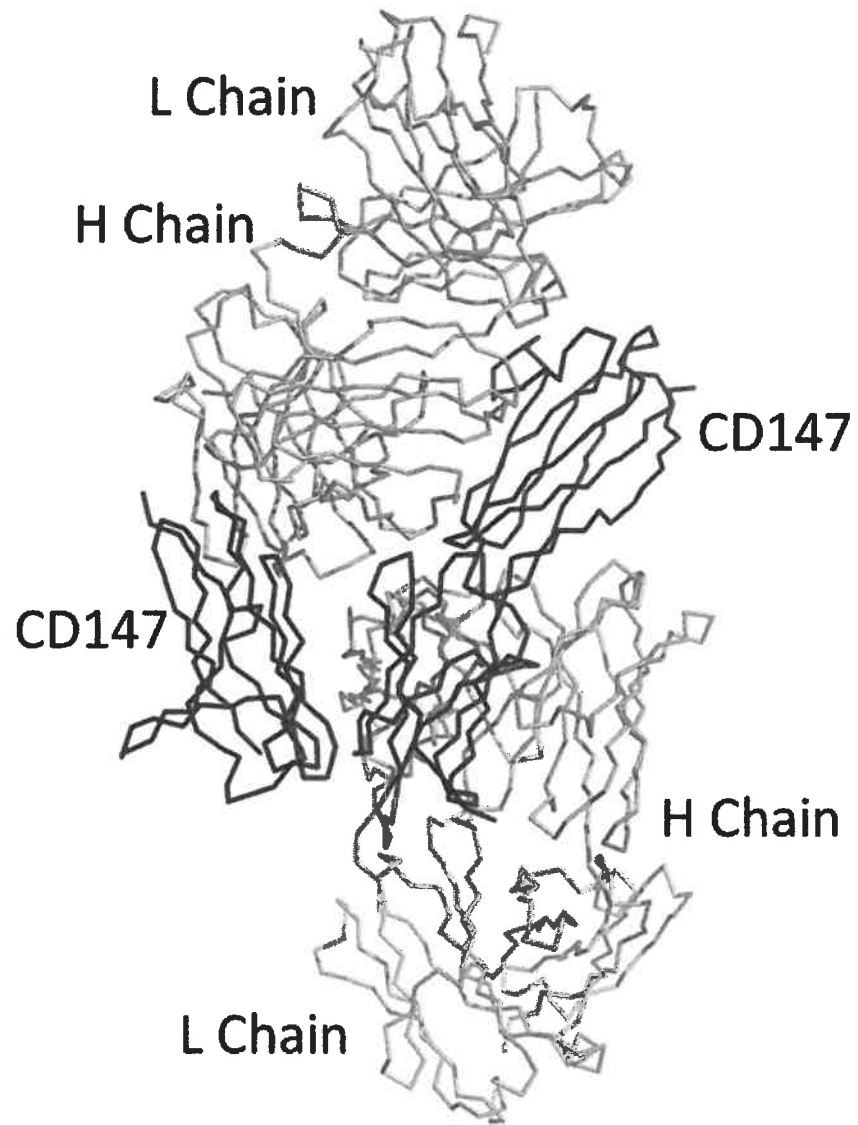
SEQ ID NO: 140: Nucleotide sequence of #131H2hlgG2
 ATGAACACCTGTGGTCTTCTCCTGCTGCTGGCAGCTCCAGATGGGTGCTGAGCCAGGTTACGCTGGTGAATCTGGTGGCGAGGTGGTCA
 GGCTGGCAGATCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCACTTCAACAAGTACTGGATGACCTGGGTCCGACAGGCCCTGGCAAGGAC
 TTGAATGGGTGCCAGCATACCAAGGCTGGCGGCTTACCTACTACGCCGATAGCGTGAAGGGCAGATTACCATCAGCCGGGACAACAGCAAG
 AGCACCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGGCACAGCCGTGTACTACTGTACAAGAGAGCTGGCGAGTTCTACGTGATGGATGC
 CTGGGGCAGGGCACACAGTTACAGTTAGCTCAGCCTCCAGCAAGGGCCCTTCCGTGTTCCCTCTGGCCCTTGTAGCCGTTCACACGAGAGT
 CCACCGCCGCCCTTGGCTGTGTGTGAAGBACTACTTCCCTGAGCCTGTGACCGTGAGCTGGAAGTCCGGAGCCCTACCAAGCGGCTGCACACC
 TTCCCTGCCGTGCTGCAGTCCAGCGGCCCTTACTCCCTGAGCTCCGTGGTGACCGTGCGTACGCTCCAACTTGGGACCCCAAACTACACCTGTAA
 CGTGGACCAAGCCTAGCAACACCAAGGTGGACAAGACCGTGGAGCGTAAGTGTGTGTGGAGTGTCTCCTTGTCTGCCCTCCTGTGGCCG
 GACCTTCGGTGTCTCTTTCCTCCTAAGCCTAAGGACACCTGATGATCAGCCGTACCCCTGAGGTGACCTGTGTGGTGGTGGACGTGTCCAC
 GAGGACCTGAGGTGAGTTCACTGGTACGTGGACGGCTGGAGGTGCACACGCCAAGACCAAGCCTCGTGAGGAGCAATTCAACAGCACCTT
 CCGTGTGGTGTCCGTGCTTACCGTGGTGACCAAGACTGGCTGAACGGCAAGGAGTACAAGTGTAAAGGTGAGCAACAAGGAGACTTCTGCCCTA
 TCGAAGAAGACCATCTCAAGACCAAGGGCAACCTCGTGAGCCTCAAGTGTACACCTTCTCCTAGCCGTGAGGAGATGACCAAGAACCAAGTG
 TCCCTTACCTGTCTGGTGAAGGGCTTCTACCTAGCGACATCGCCGTGGAGTGGAGTCCAAGGGACAACCTGAGAACAACTACAAGACCAACCC
 TCCTATGCTTGACAGCAGCGCTCCTCTCTCTGTACAGCAAGCTGACCGTGGACAAGTCCCGTTGGCAACAAGGCAAGCTGTTACGCTGTTCCG
 TGATGACAGAGGCCCTGCACAACCACTACACCAAAAGAGCCTTCCCTGAGCCCTGGAAAG
 Signal sequence1-57, Variable region58-414, Constant region415-1392

[Figure 40-2]

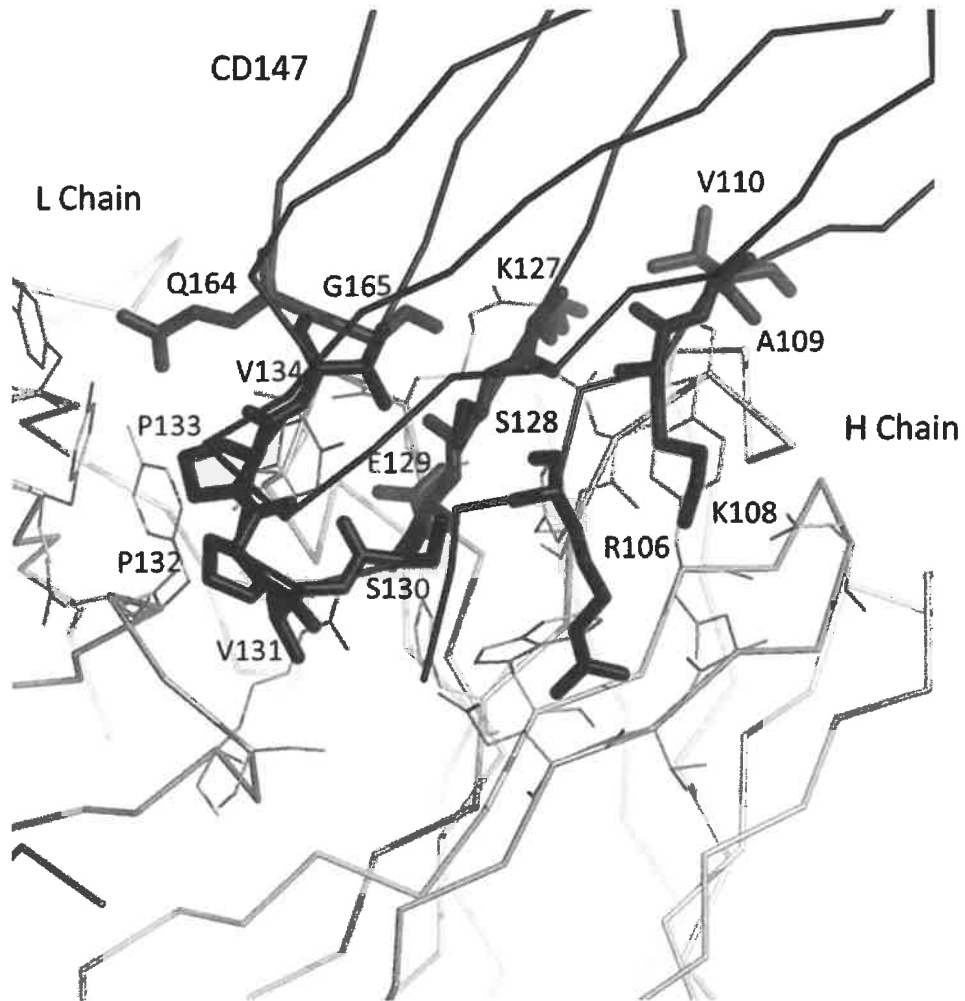
SEQ ID NO: 141: Amino acid sequence of #131L2h (each CDR is underlined)
 MVLQTQVFIISLLWISGAYGDIQNTQSPSSLASVGDRTVITCRASKSINTYLAWYQKPKGKTNKLLIYSGSTLQSGTSPRFSGSGSGDTFTLT
 SSLQPEDFATYYCQHNEYPTTFGGGKLEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKD
 STYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC
 Signal sequence1-20, Variable region21-128, Constant region129-234

SEQ ID NO: 142: Nucleotide sequence of #131L2h
 ATGGTGTGCAGACCCAGGTGTTCTCTCCCTGCTGCTGTGGATCTCCGGCGCTACGGCGACGTTAGATGACACAGAGCCCTAGCAGCCTGTC
 TGCCAGCGTGGGAGACAGAGTGACCATCACATGCAAGGCCAGCAAGAGCATCAACACCTACCTGGCCTGGTATCAAGAGAAAGCCGGCAAGACCA
 ACAAGCTGGTGTGATCTACAGCGGCAGCACACTGCAGAGCGGCACCCCTTCTAGATTTTCCGGCTCTGGCAGCGGCACCGACTTCACCTGACCAT
 TCTAGCTGCAGCTGAGGACTTCGCCACCTACTACTGCCAGGACACAAGAGTACGCCCTTACCTTTGGCCAGGGCACCAGCTGGAATCAA
 GCGTACGGTGGCCGCCCTCCGTGTTCTATCTTCCGCCCTCCGACGACGCTGAAGTCCGGCACCCTCCGTGGTGTGCTGCTGAATAACT
 TCTACCCAGAGAGGCCAAGGTGAGTGAAGGTGGACAACGCCCTGCAGTCCGGGAAGTCCAGGAGAGCGTGACCGAGCAGGACGAAGGAC
 AGCACCTACAGCCTGAGCAGCACCTGACCTGAGCAAAAGCCGACTACGAGAAGCACAAGGTGTACGGCTGCGAGGTGACCCACCAAGGCCCTGAG
 CTCCCCGTCAACAGAGCTTCAACAGGGGGAGTGT
 Signal sequence1-60, Variable region61-384, Constant region385-702

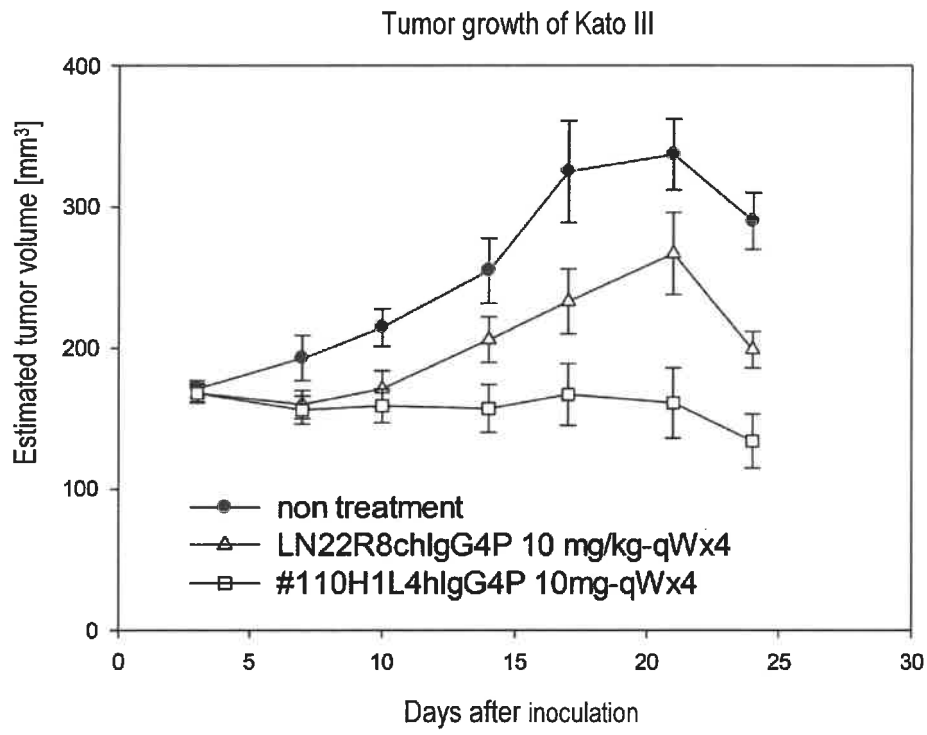
[Figure 41]



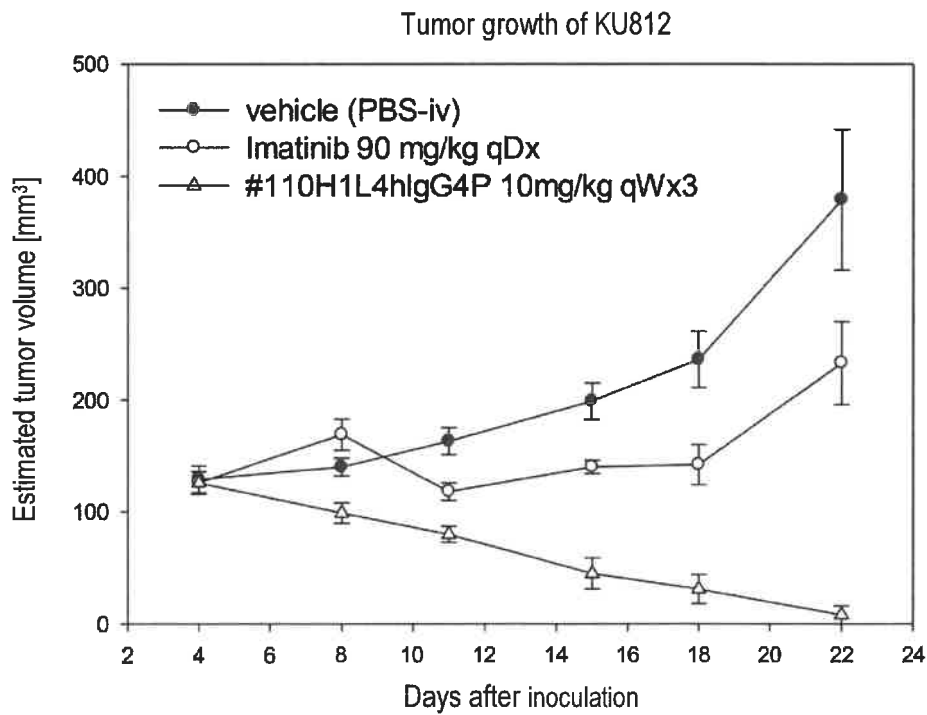
[Figure 42]



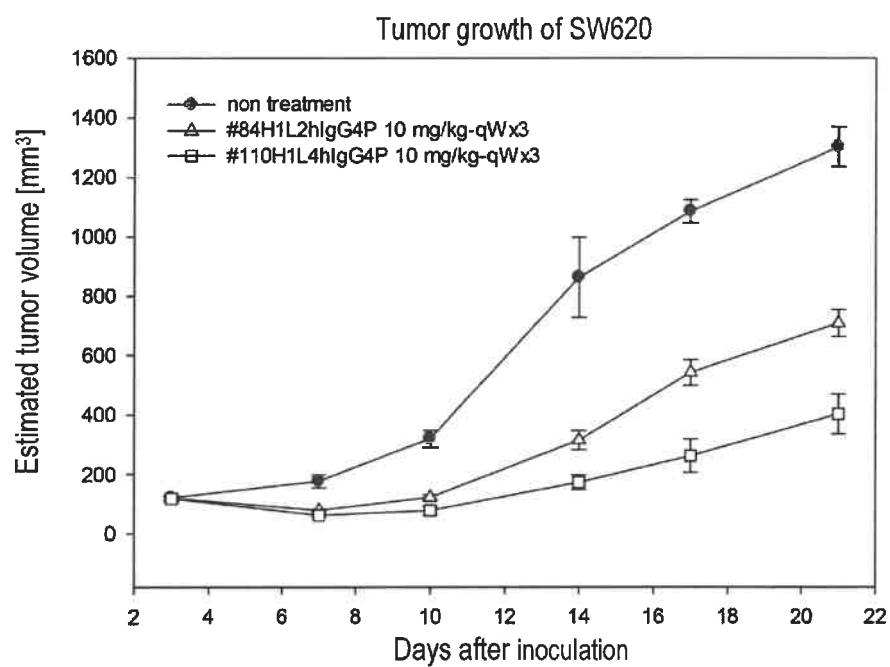
[Figure 43]



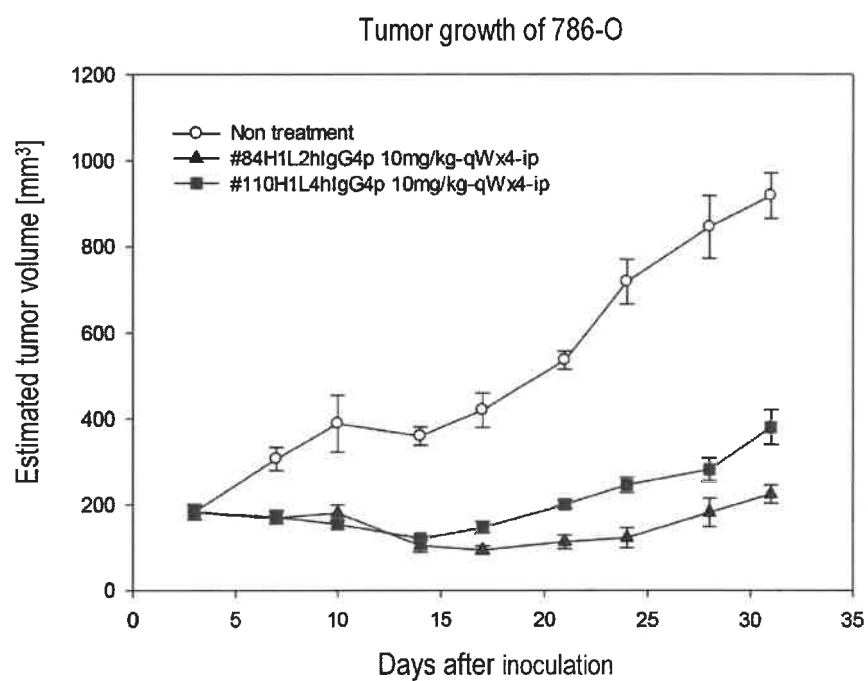
[Figure 44]



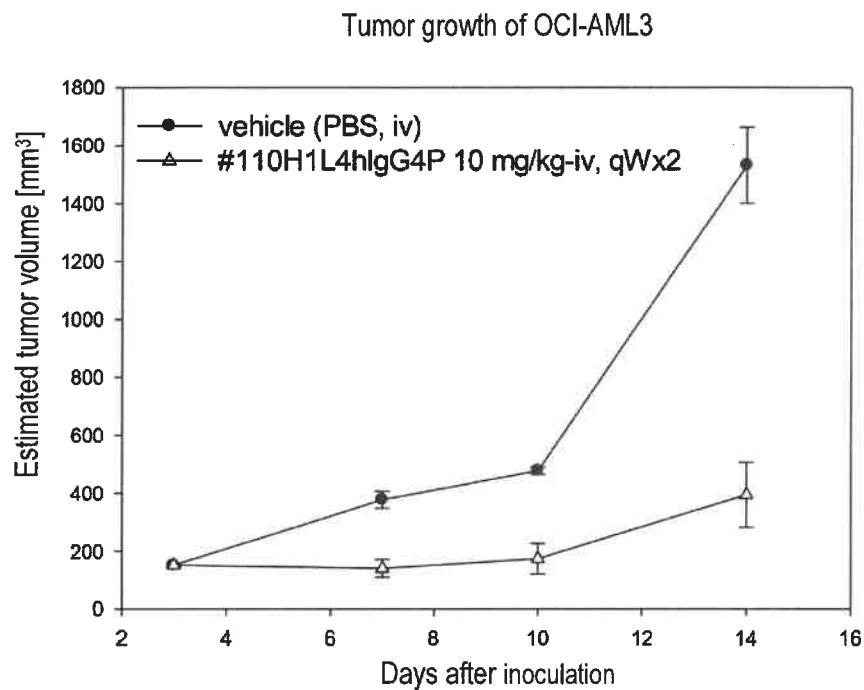
[Figure 45]



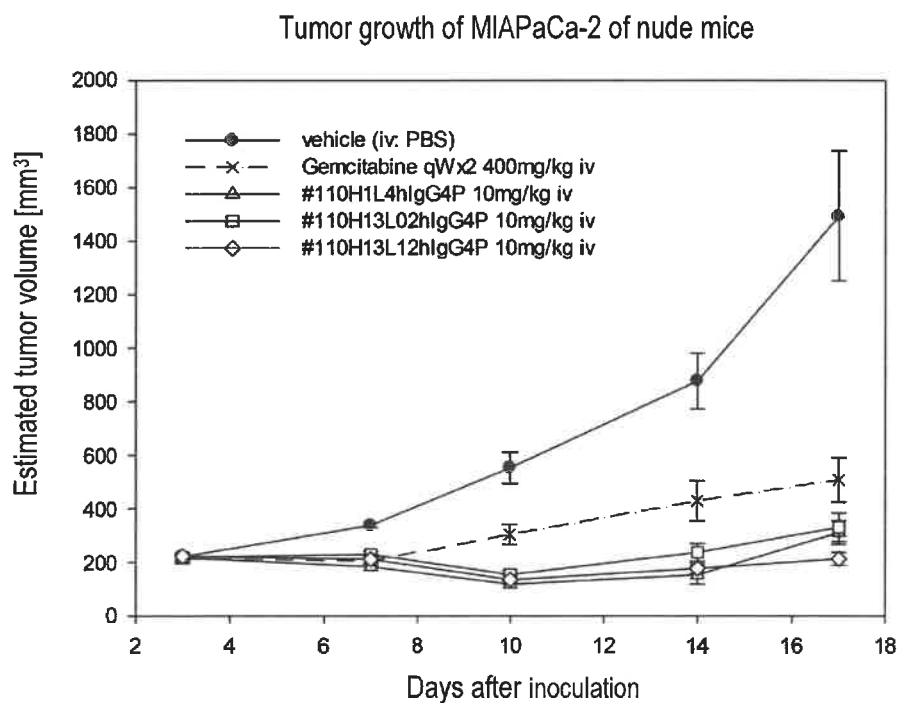
[Figure 46]



[Figure 47]

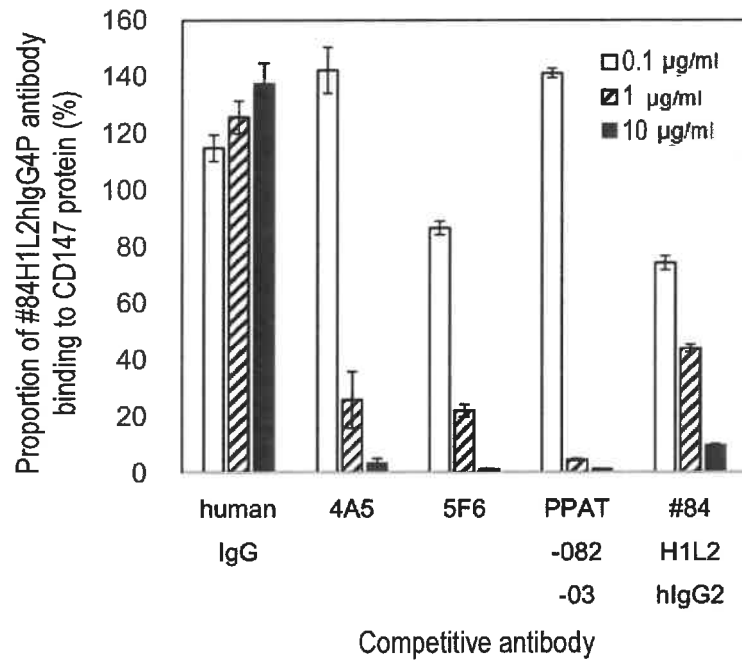


[Figure 48]

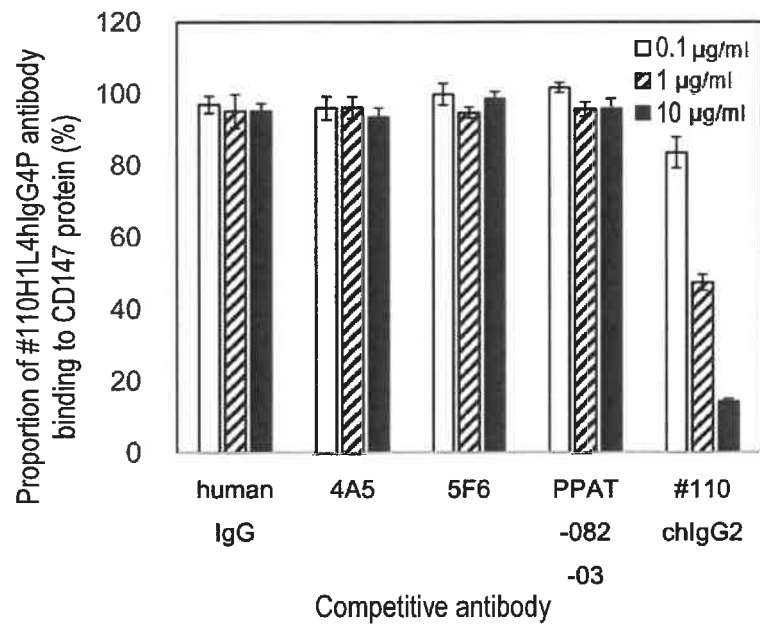


[Figure 49]

(a)

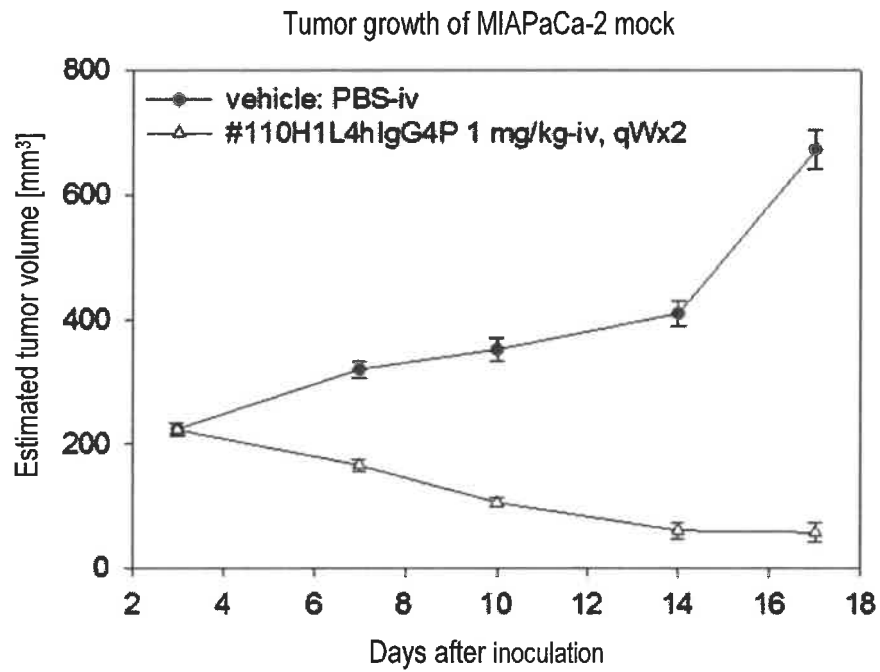


(b)



[Figure 50]

(a)



(b)

