

DRAWINGS

Figure 1

Common Light Chain	SEQ ID No.	Amino Acid Sequence
Variable Region	25	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFLTISLQPEDFATYYCQQS YSTPPTFGQGTKVEIK
Constant Region	29	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACE VTHQGLSPVTKSFNRGEC

Figure 2

Common Light Chain	SEQ ID No.	CDR1	SEQ ID No.	CDR2	SEQ ID No.	CDR3
CDRs	26	RASQSISSYLN	27	AASSLQS	28	QQSYSTPPT

Figure 3

Germline V gene	SEQ ID No.	Amino Acid Sequence
IGHV7-4-1	21	QVQLVQSGSELKKPGASVKVSCASGYTFTSYAMNWVRQ APGQGLEWMGWINTNTGNPTYAQGFTGRFVFLDTSVST AYLQICSLKAEDTAVYYCAR
IGHV3-33	22	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCAR

Figure 4

Alignment between the respective VH of PD1-1 to PD1-5 and IGHV7-4-1/JH6c

	-----FR1-----	-CDR1-	-----FR2-----	-----CDR2-----
IGHV7-4-1 (SEQ ID No. 21)	QVQLVQSGSELKKPGASVKVSCASGYTFT	SYAMN	WVRQAPGQGLEWMG	WINTNTGNPTYAQGFTG
PD1-1 VH (SEQ ID No. 1)	-----Q-----	H-GLH	-----	-L---E---F---
PD1-2 VH (SEQ ID No. 2)	-----Q-V-----	H-GLH	-----	-----
PD1-3 VH (SEQ ID No. 3)	-----M-----	H--LH	-----	-L---E---
PD1-4 VH (SEQ ID No. 4)	-----Q-----	H--LH	-L-----	-L---E---F---
PD1-5 VH (SEQ ID No. 5)	-----Q-----	H--LH	-L-----	-L---E---F---
	-----FR3-----	-----CDR3-----	-----FR4-----	
IGHV7-4-1 (SEQ ID No. 21)	RFVFLDTSVSTAYLQICSLKAEDTAVYYCAR			
D gene (unknown)				
JH6c			HYYYYYMDV	WGKGTTVTSS
PD1-1 VH (SEQ ID No. 1)	-----T-----S-----	GDMVVPTTIWN--HF--	--N--L--	
PD1-2 VH (SEQ ID No. 2)	-----S-----	GDLVVPTTIWN--H--E-	-----L-----	
PD1-3 VH (SEQ ID No. 3)	-----T-----N-----	GDMVVPTTIWN-----	-----	
PD1-4 VH (SEQ ID No. 4)	-----T-----S-----	GDMVVPTTIWN--HF--	--N-----	
PD1-5 VH (SEQ ID No. 5)	-----T-----S-----	GDMVVPTTIWN--HF--	--Q-----	

Figure 5

Clone No.	SEQ ID No.	Amino Acid Sequence
PD1-1	1	QVQLVQSGSELKQPGASVKVSCKASGYTFTHYGLHWVRQAPGQGLEWMGW LNTNTENPTFAQGFTGRFVFLDTSVTTAYLQISSLKAEDTAVYYCARGDMV VPTTIWNYHYHFMVWVGNGTLTVSS
PD1-2	2	QVQLVQSGSELKQPGVSVKVSCKASGYTFTHYGLHWVRQAPGQGLEWMGWI NTNTGNPTYAQGFTGRFVFLDTSVSTAYLQISSLKAEDTAVYYCARGDLVV PTTIWNYHYHMEVWVGKGTTLTVSS
PD1-3	3	QVQLVQSGSELKKPGASVMVSCKASGYTFTHYALHWVRQAPGQGLEWMGW LNTNTENPTFAQGFTGRFVFLDTSVTTAYLQINSLKAEDTAVYYCARGDMV VPTTIWNYYYMDVWVGKGTTLTVSS
PD1-4	4	QVQLVQSGSELKQPGASVKVSCKASGYTFTHYALHWLRQAPGQGLEWMGWL NTNTENPTFAQGFTGRFVFLDTSVTTAYLQISSLKAEDTAVYYCARGDMV VPTTIWNYHYHFMVWVGNGTTLTVSS
PD1-5	5	QVQLVQSGSELKQPGASVKVSCKASGYTFTHYALHWLRQAPGQGLEWMGWL NTNTENPTFAQGFTGRFVFLDTSVTTAYLQISSLKAEDTAVYYCARGDMV VPTTIWNYHYHFMVWVGQGTTLTVSS

Figure 6

Clone No.	SEQ ID No.	CDR1	SEQ ID No.	CDR2	SEQ ID No.	CDR3
PD1-1	6	HYGLH	7	WLNTNTENPTFAQGFTG	8	GDMVPTTIWNYHYHFMV
PD1-2	9	HYGLH	10	WINTNTGNPTYAQGFTG	11	GDLVPTTIWNYHYHMEV
PD1-3	12	HYALH	13	WLNTNTENPTYAQGFTG	14	GDMVPTTIWNYYYMDV
PD1-4	15	HYALH	16	WLNTNTENPTFAQGFTG	17	GDMVPTTIWNYHYHFMV
PD1-5	18	HYALH	19	WLNTNTENPTFAQGFTG	20	GDMVPTTIWNYHYHFMV

Figure 7

Clone No.	SEQ ID No.	Amino Acid Sequence
CD3-2	36	QVQLVQSGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWV AQIWYNARKQEYSDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCT RGTGYNWFDPWGQGTLTVSS

Figure 8

Clone No.	SEQ ID No.	CDR1	SEQ ID No.	CDR2	SEQ ID No.	CDR3
CD3-2	37	SYGMH	38	QIWYNARKQEYSDSVKG	39	GTGYNWFDP

Figure 9

	SEQ ID No.	Amino Acid Sequence
The constant region in heavy chain having the VH of the first arm specifically binding to PD-1	23	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELGRGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTC EVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
The constant region in heavy chain having the VH of the second arm specifically binding to CD3	24	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELGRGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
The constant region in heavy chain having the VH of the first arm specifically binding to PD-1	45	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELGRGPSVFLFP PKPKDTLDISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTC EVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
The constant region in heavy chain having the VH of the second arm specifically binding to CD3	51	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELGRGPSVFLFP PKPKDTLDISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Figure 10

Amino acid sequence of the VH of the 15C3 clone

QVQLVQSGGGVVPGRSLRLSCVASGFTFSSYGMHWVRQAPGKLEWVAAIWYNGRKQDYADSVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAVYYCTRGTYNWFDPPWGQGLTVTVSS

Figure 11

Binding activity to PD-1 of the first arm		
Clone No.	HumanPD-1	Cynomolgus monkey PD-1
	Kd (nmol/L)	Kd (nmol/L)
PD1-1(Bi)	0.6	0.3
PD1-2(Bi)	0.7	0.4
PD1-3(Bi)	3.8	2.0
PD1-4(Bi)	0.9	0.7
PD1-5(Bi)	0.7	0.4
PD1-6(Bi)	0.8	21.8
Binding activity to CD3 of the second arm		
Clone No.	Human CD3 δ /CD3 ϵ	
	Kd (nmol/L)	
CD3-2	19.2	

Figure 12

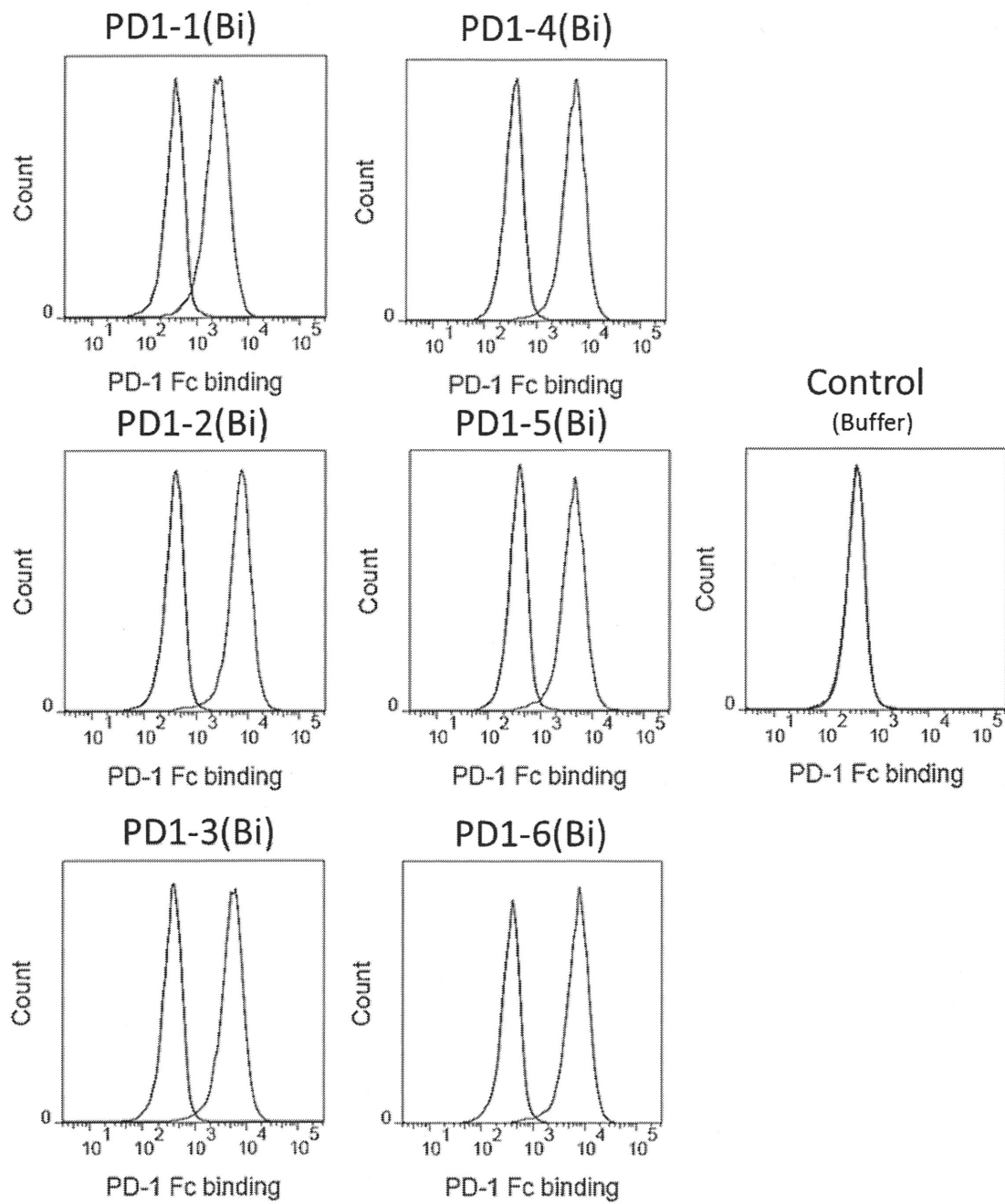


Figure 13

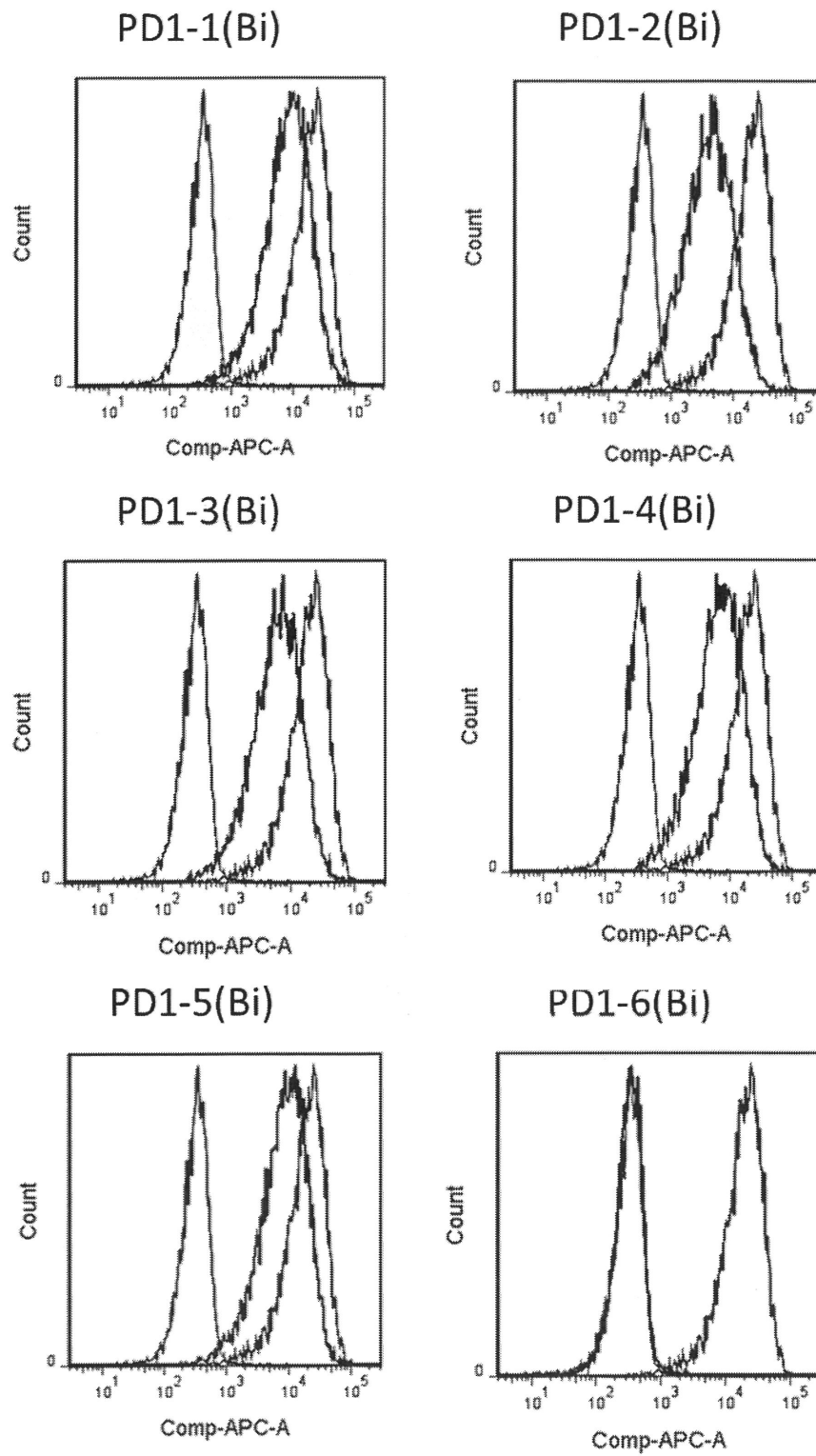


Figure 14

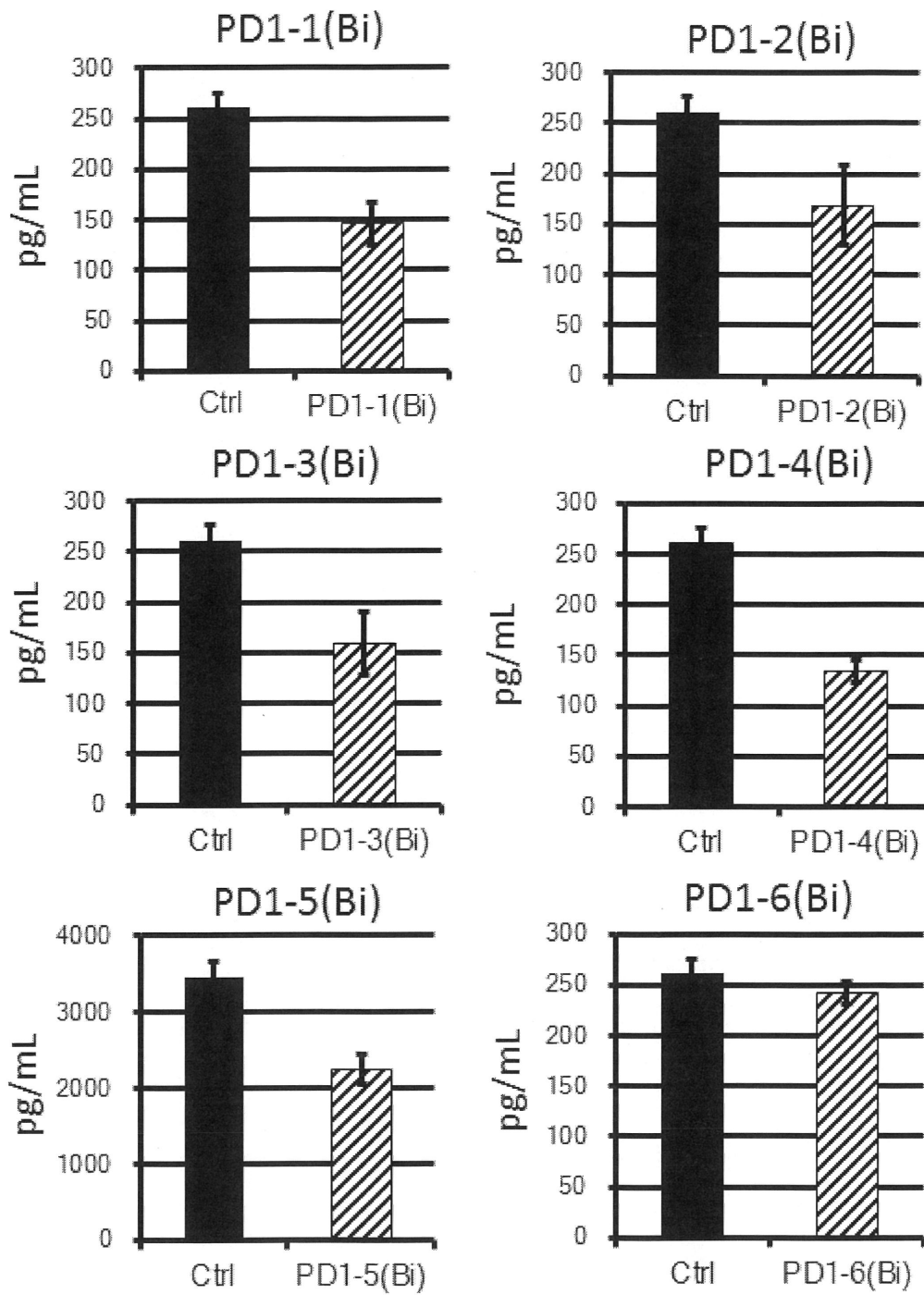


Figure 15

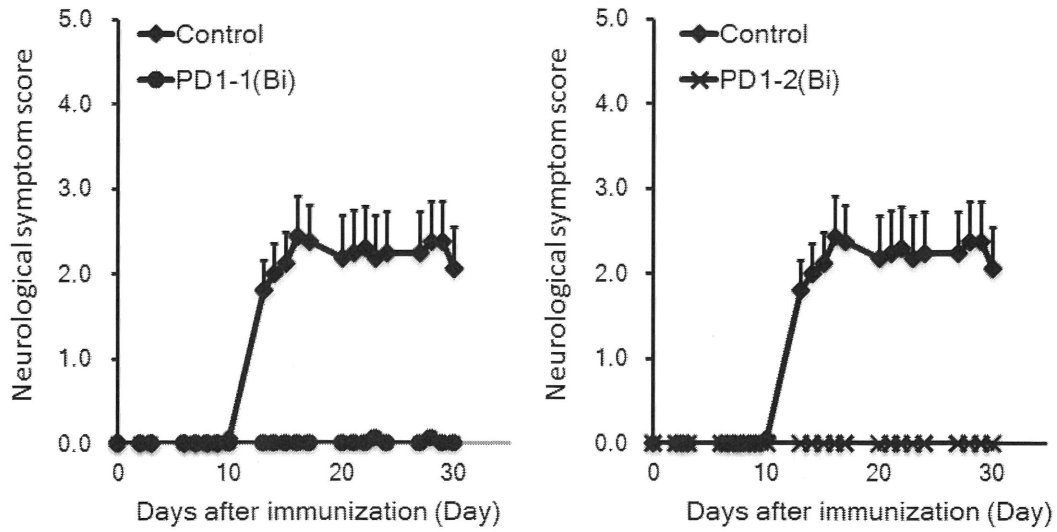


Figure 16

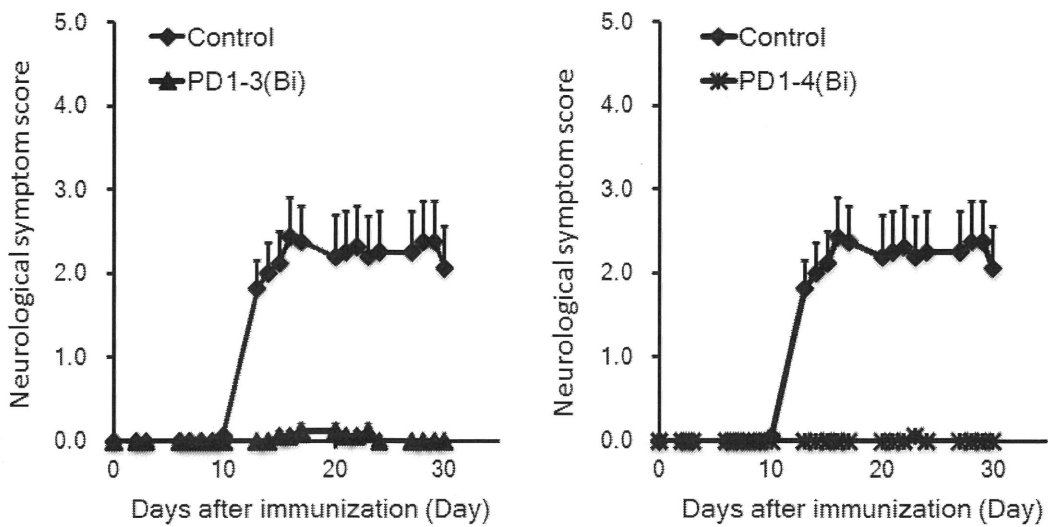


Figure 17

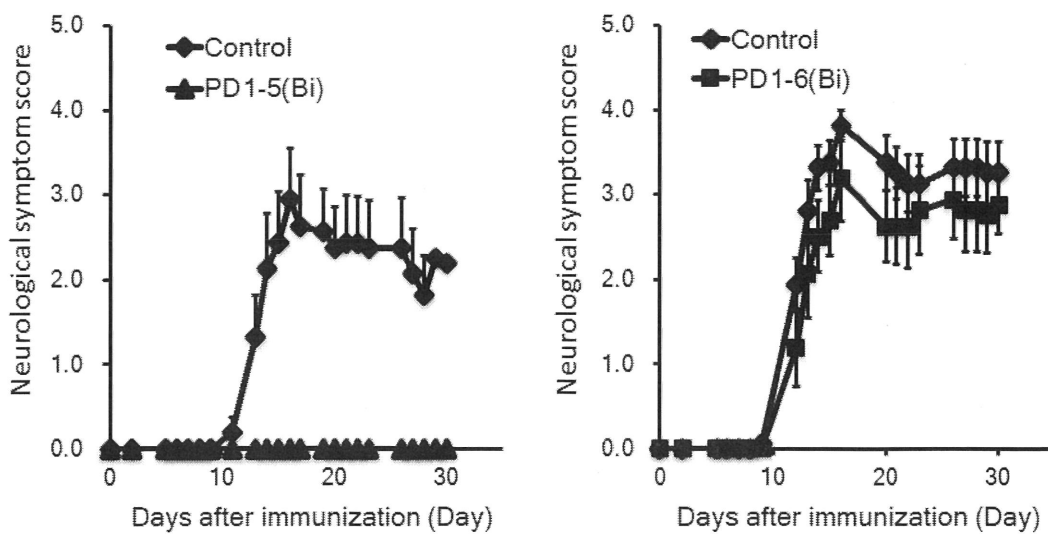


Figure 18

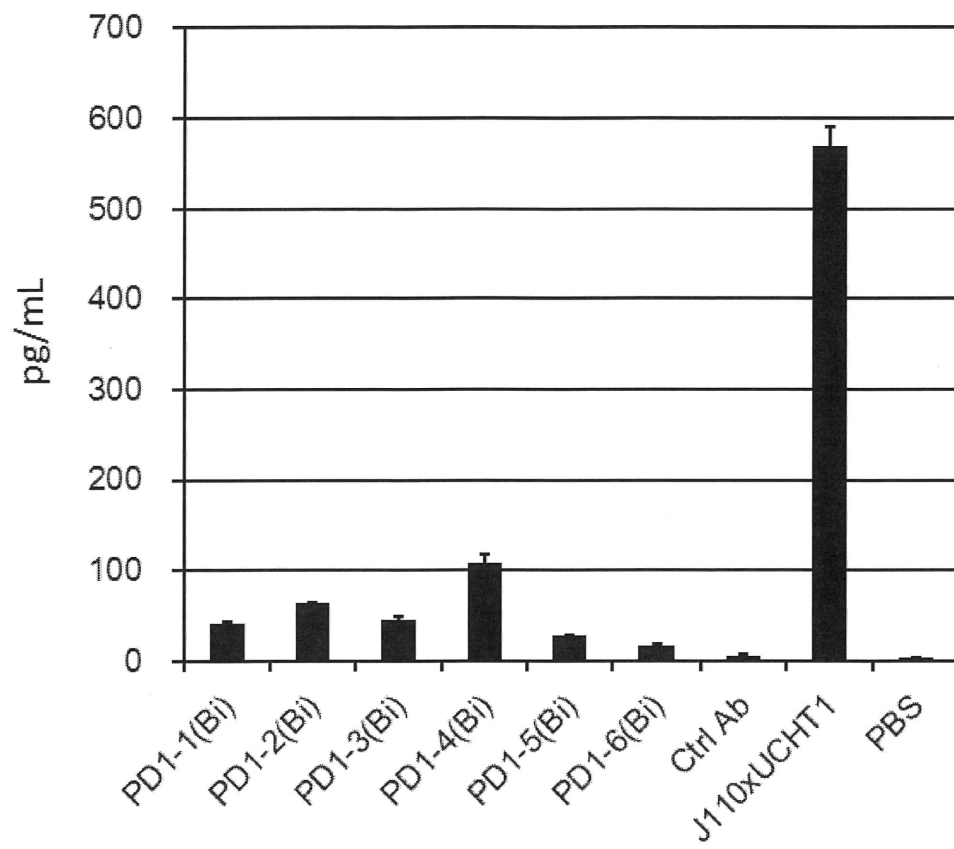


Figure 19

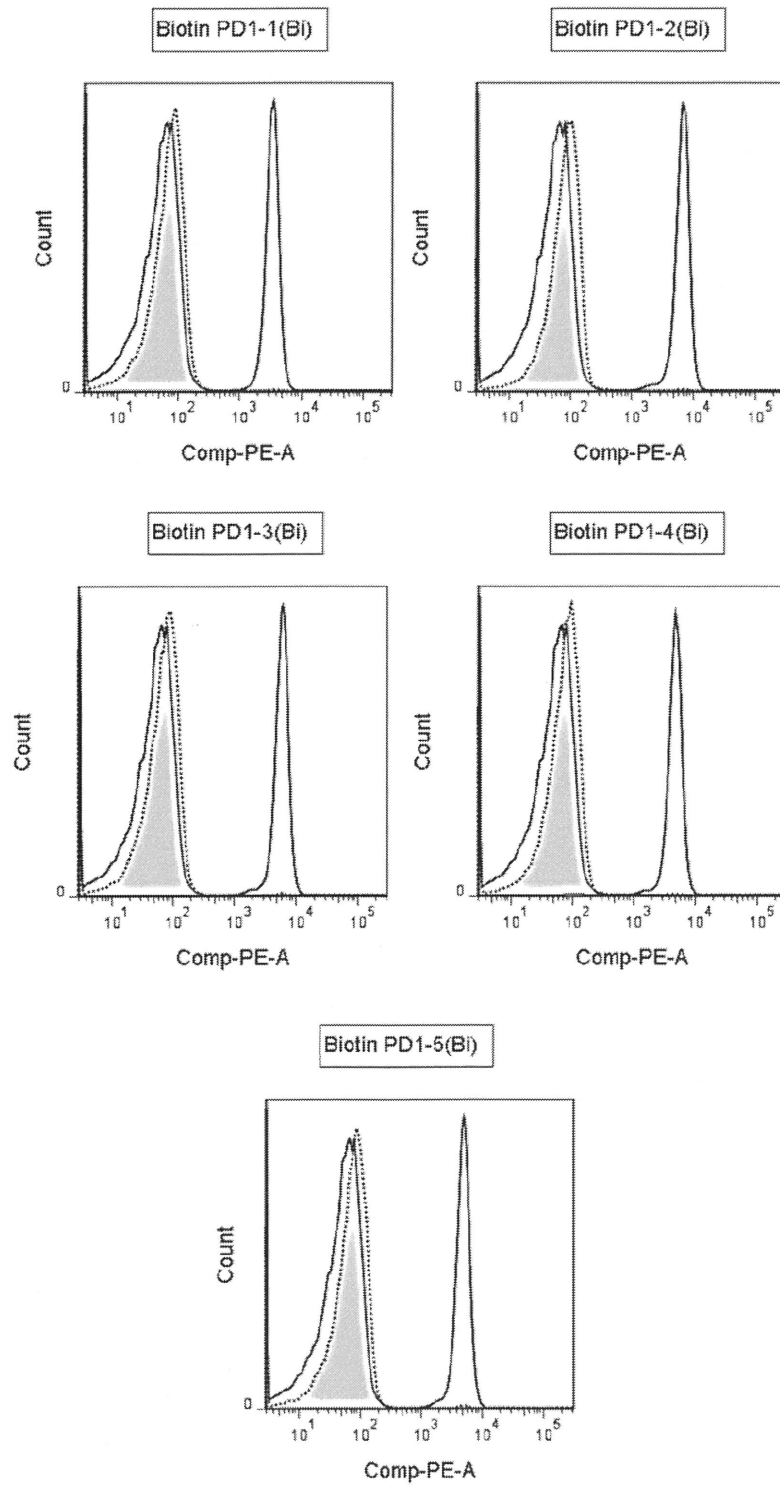


Figure 20

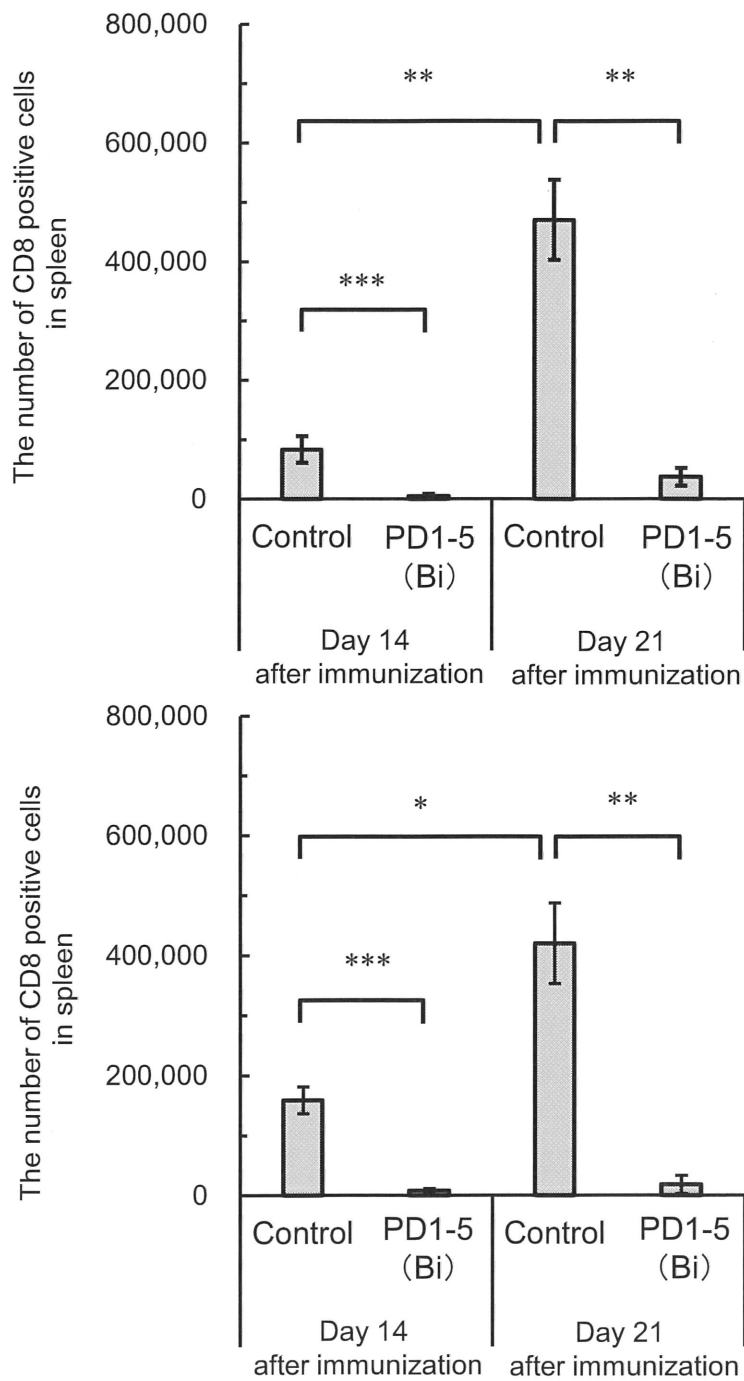


Figure 21

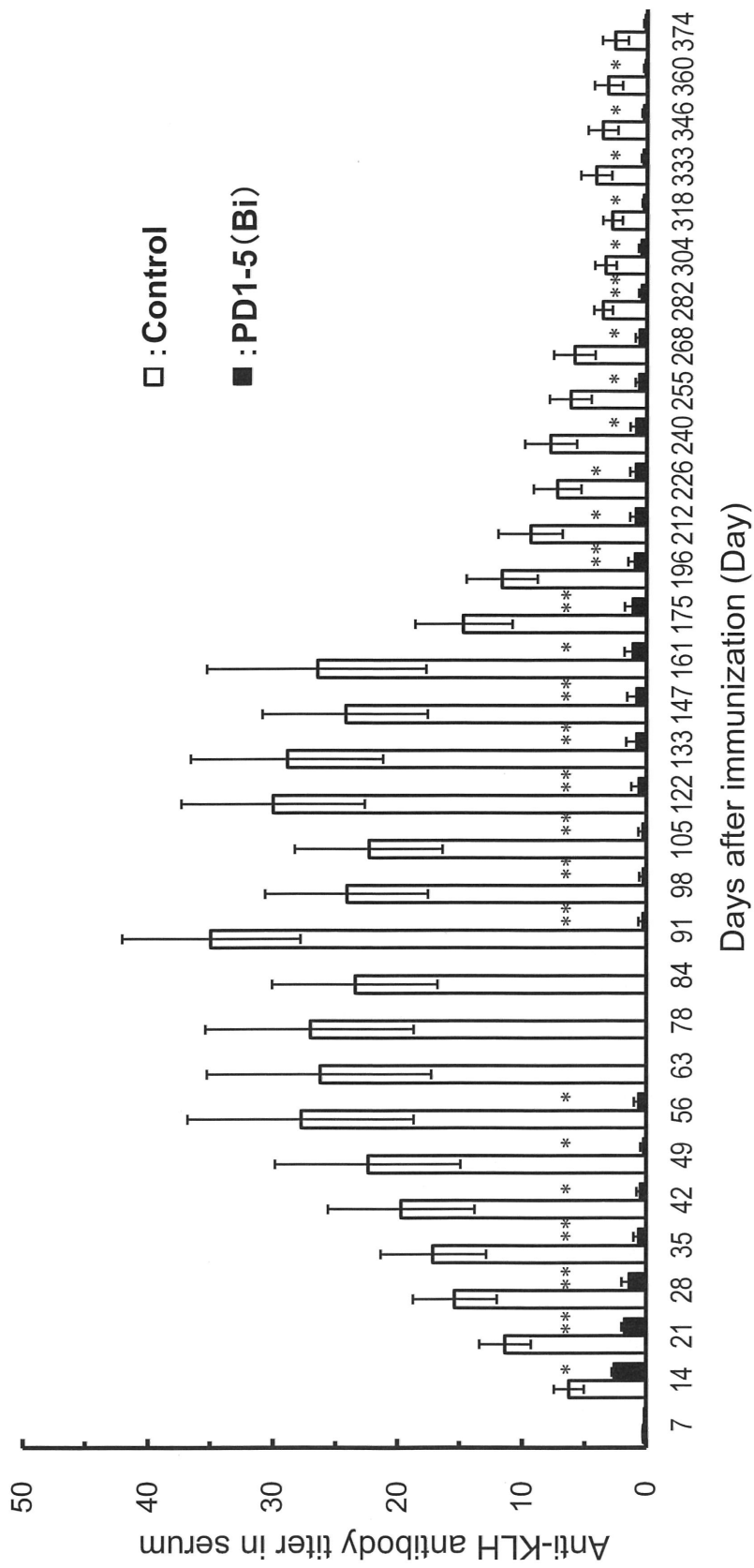


Figure 22

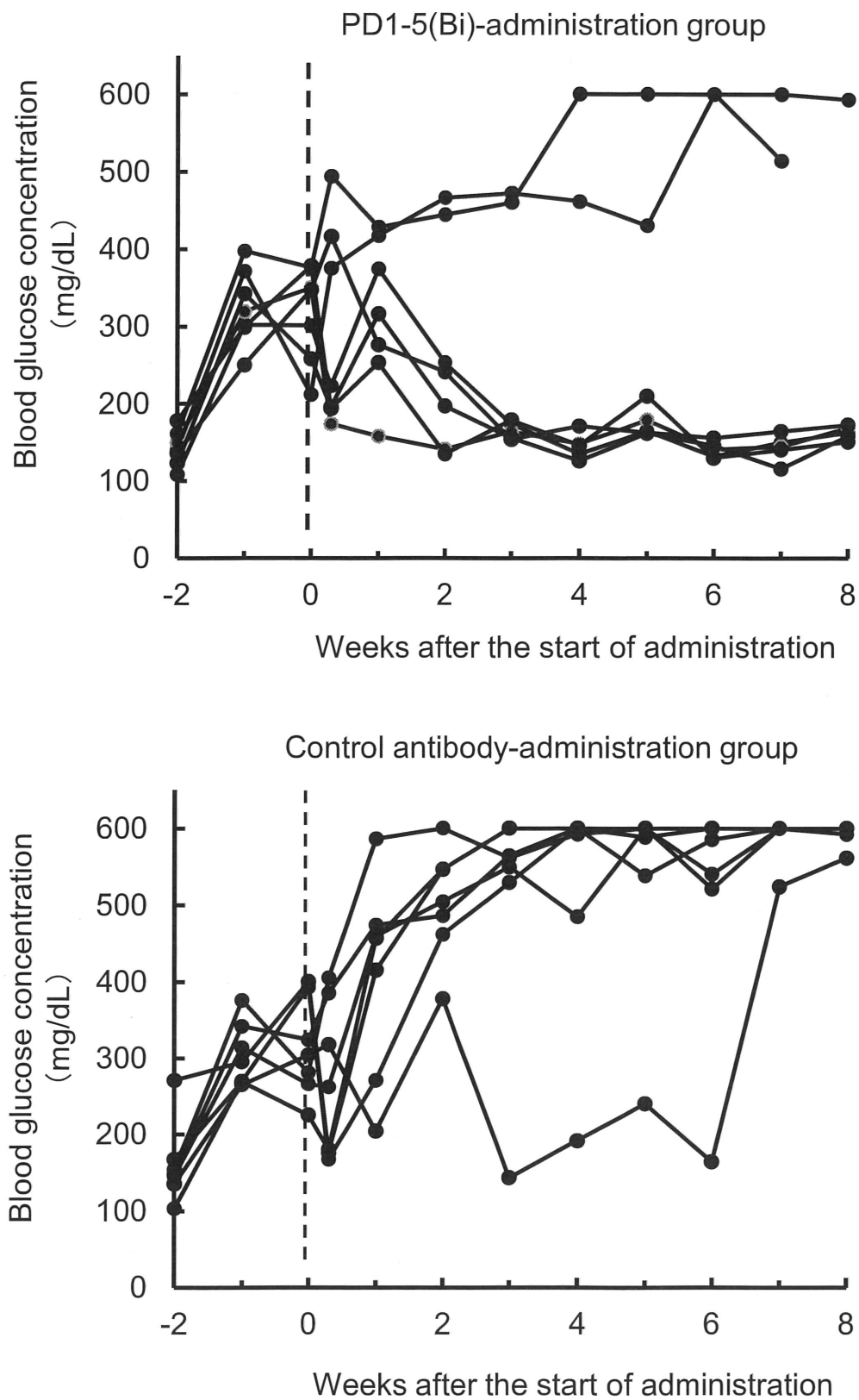


Figure 23

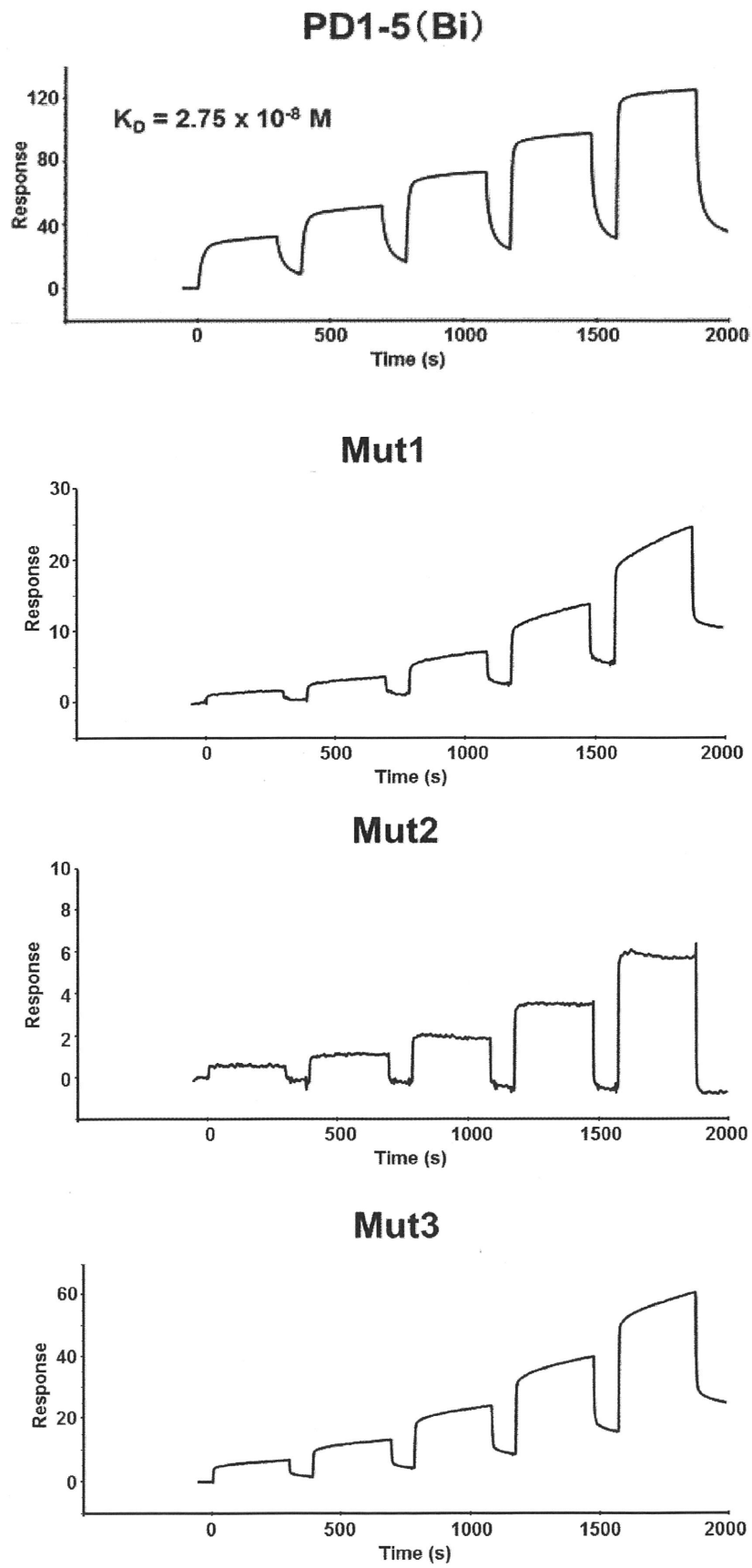


Figure 24

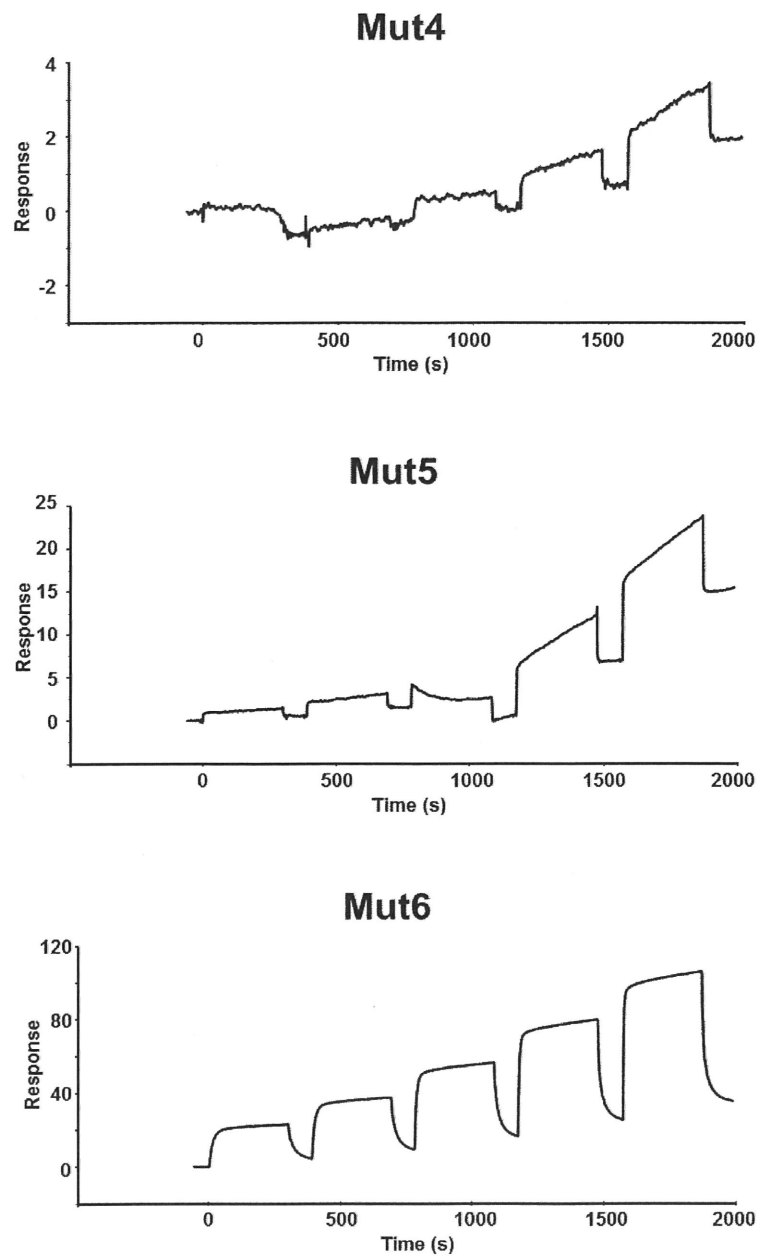


Figure 25

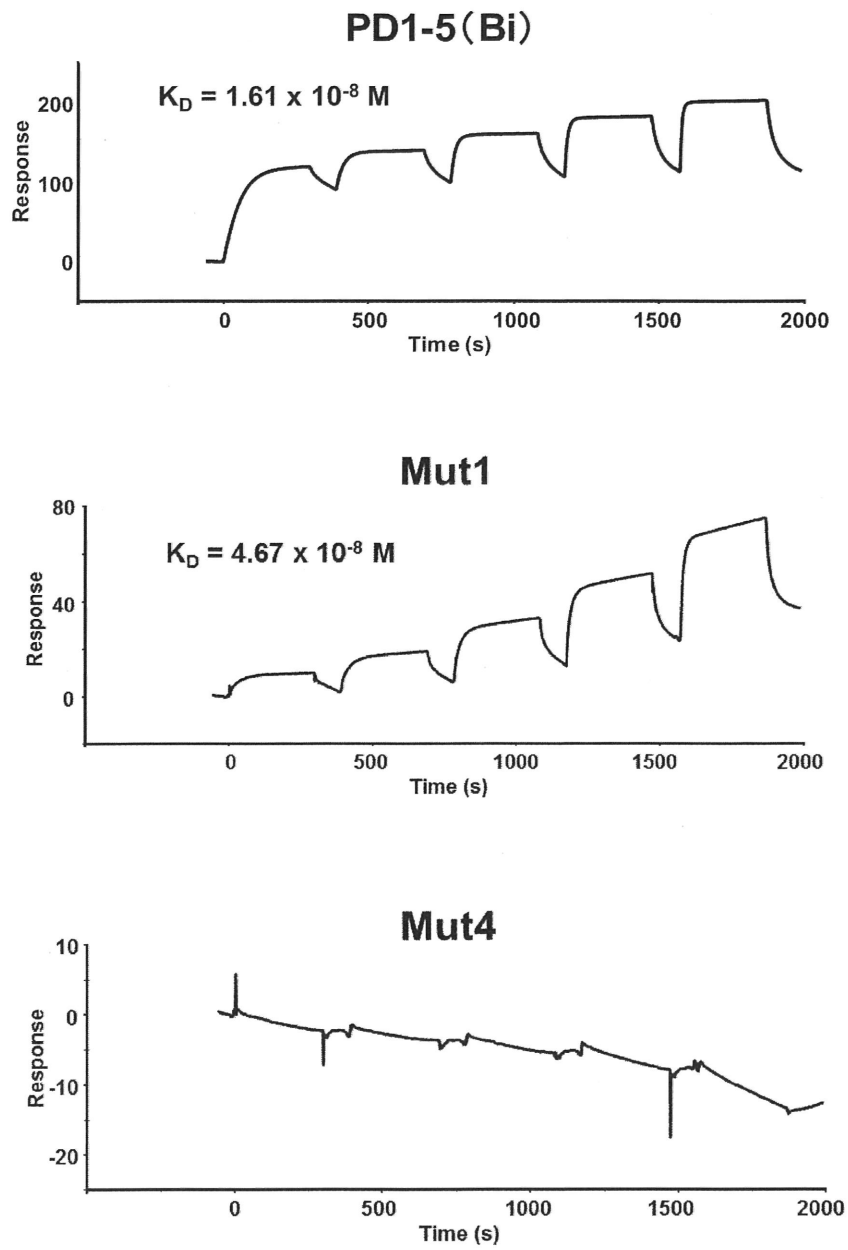


Figure 26

