FIGURES

Figure 1

Common Light Chain	SEQ ID No.	Amino Acid Sequence
Variable Region	25	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQS YSTPPTFGQGTKVEIK
Constant Region	29	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE VTHQGLSSPVTKSFNRGEC

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	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQ APGQGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVST AYLQICSLKAEDTAVYYCAR
IGHV3-33	22	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAR

Figure 4

```
Alignment between each VH of PD1-1 to PD1-5 and IGHV7-4-1/JH6c

                                  ---------------FR1---------------   -CDR1-   ------FR2------   -------CDR2--------
IGHV7-4-1 (SEQ ID No. 21)  |QVQLVQSGSELKKPGASVKVSCKASGYTFT|  |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)  |RFVFSLDTSVSTAYLQICSLKAEDTAVYYCAR
D gene (unknown)
JH6c                                                                  HYYYYYYYMDV|  |WGKGTTVTVSS
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 LNTNTENPTFAQGFTGRFVFSLDTSVTTAYLQISSLKAEDTAVYYCARGDMV VPTTIWNYYHFMDVWGNGTLVTVSS
PD1-2	2	QVQLVQSGSELKQPGVSVKVSCKASGYTFTHYGLHWVRQAPGQGLEWMGWI NTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARGDLVV PTTIWNYYHYMEVWGKGTLVTVSS
PD1-3	3	QVQLVQSGSELKKPGASVMVSCKASGYTFTHYALHWVRQAPGQGLEWMGW LNTNTENPTYAQGFTGRFVFSLDTSVTTAYLQINSLKAEDTAVYYCARGDMV VPTTIWNYYYYMDVWGKGTTVTVSS
PD1-4	4	QVQLVQSGSELKQPGASVKVSCKASGYTFTHYALHWLRQAPGQGLEWMGWL NTNTENPTFAQGFTGRFVFSLDTSVTTAYLQISSLKAEDTAVYYCARGDMVV PTTIWNYYHFMDVWGNGTTVTVSS
PD1-5	5	QVQLVQSGSELKQPGASVKVSCKASGYTFTHYALHWLRQAPGQGLEWMGWL NTNTENPTFAQGFTGRFVFSLDTSVTTAYLQISSLKAEDTAVYYCARGDMVV PTTIWNYYHFMDVWGQGTTVTVSS

Figure 6

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

Figure 7

Clone No.	SEQ ID No.	Amino Acid Sequence
CD3-2	36	QVQLVQSGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWV AQIWYNARKQEYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCT RGTGYNWFDPWGQGTLVTVSS

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
Heavy chain constant region having the VH of the first arm specifically binding to PD-1	23	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP CPAPELGRGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
Heavy chain constant region having the VH of the second arm specifically binding to CD3	24	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP CPAPELGRGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

Figure 10

Amino acid sequence of the VH of the 15C3 clone
QVQLVQSGGGVVQPGRSLRLSCVASGFTFSSYGMHWVRQAPGKGLEWVAAIWYNGRKQDYADSVKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCTRGTGYNWFDPWGQGTLVTVSS

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 CD3δ/CD3ε
	Kd (nmol/L)
CD3-2	19.2

Figure 12

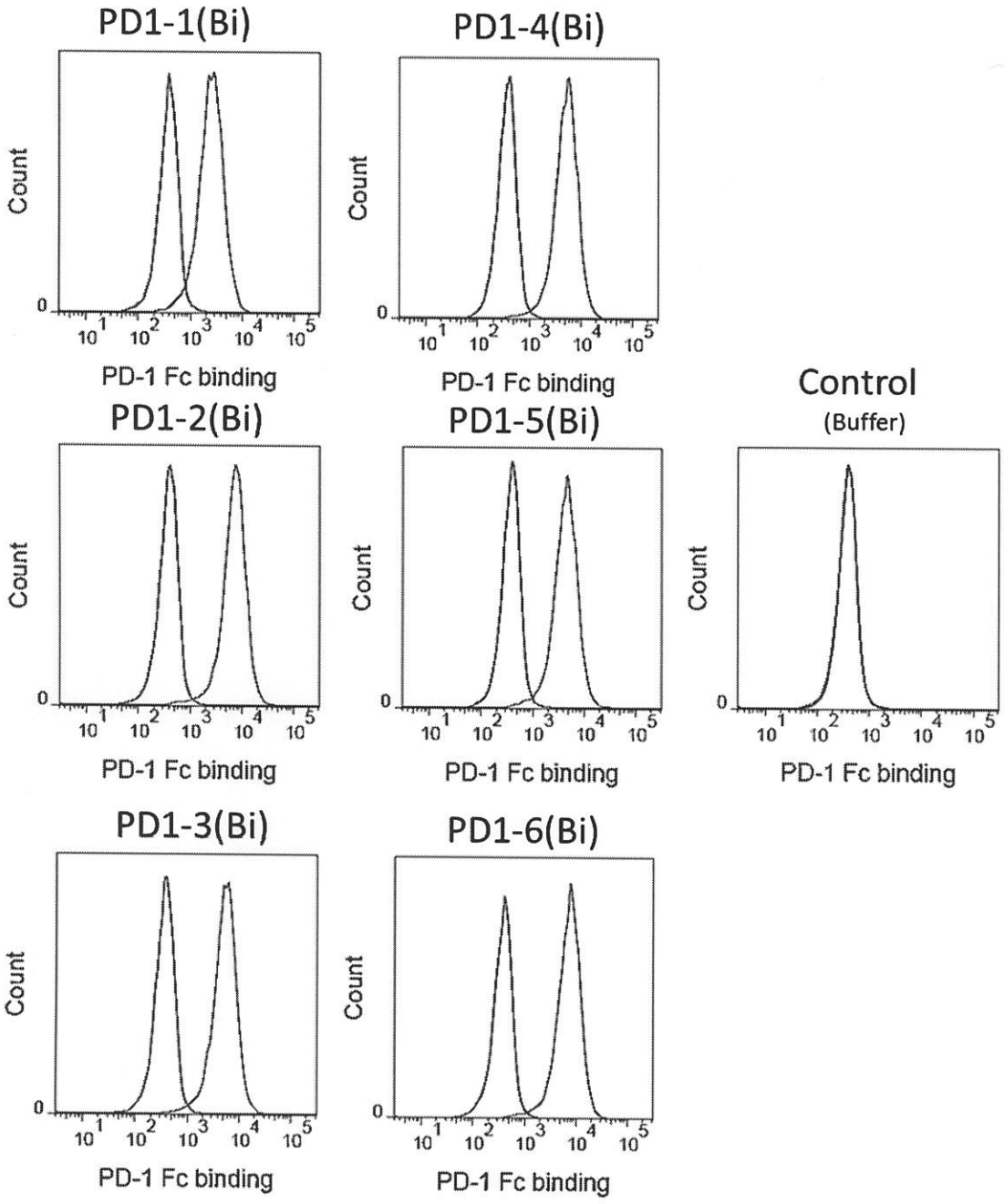

PD1-1(Bi)
PD1-4(Bi)
Control
(Buffer)
PD1-2(Bi)
PD1-5(Bi)
PD1-3(Bi)
PD1-6(Bi)
Count
0
10^1 10^2 10^3 10^4 10^5
PD-1 Fc binding

Figure 13

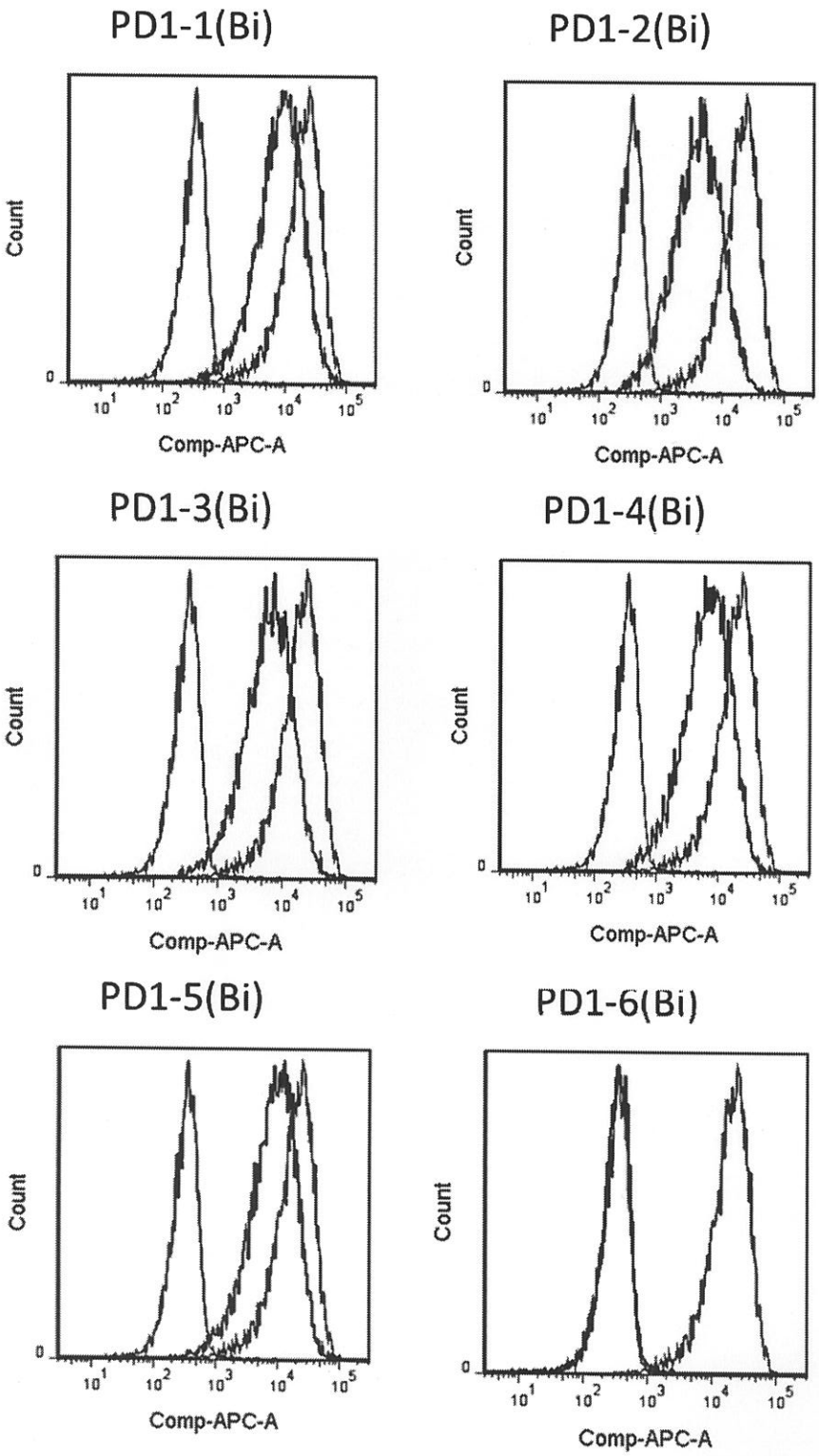

PD1-1(Bi)
PD1-2(Bi)
PD1-3(Bi)
PD1-4(Bi)
PD1-5(Bi)
PD1-6(Bi)
Count
Comp-APC-A
0
10^1
10^2
10^3
10^4
10^5

Figure 14

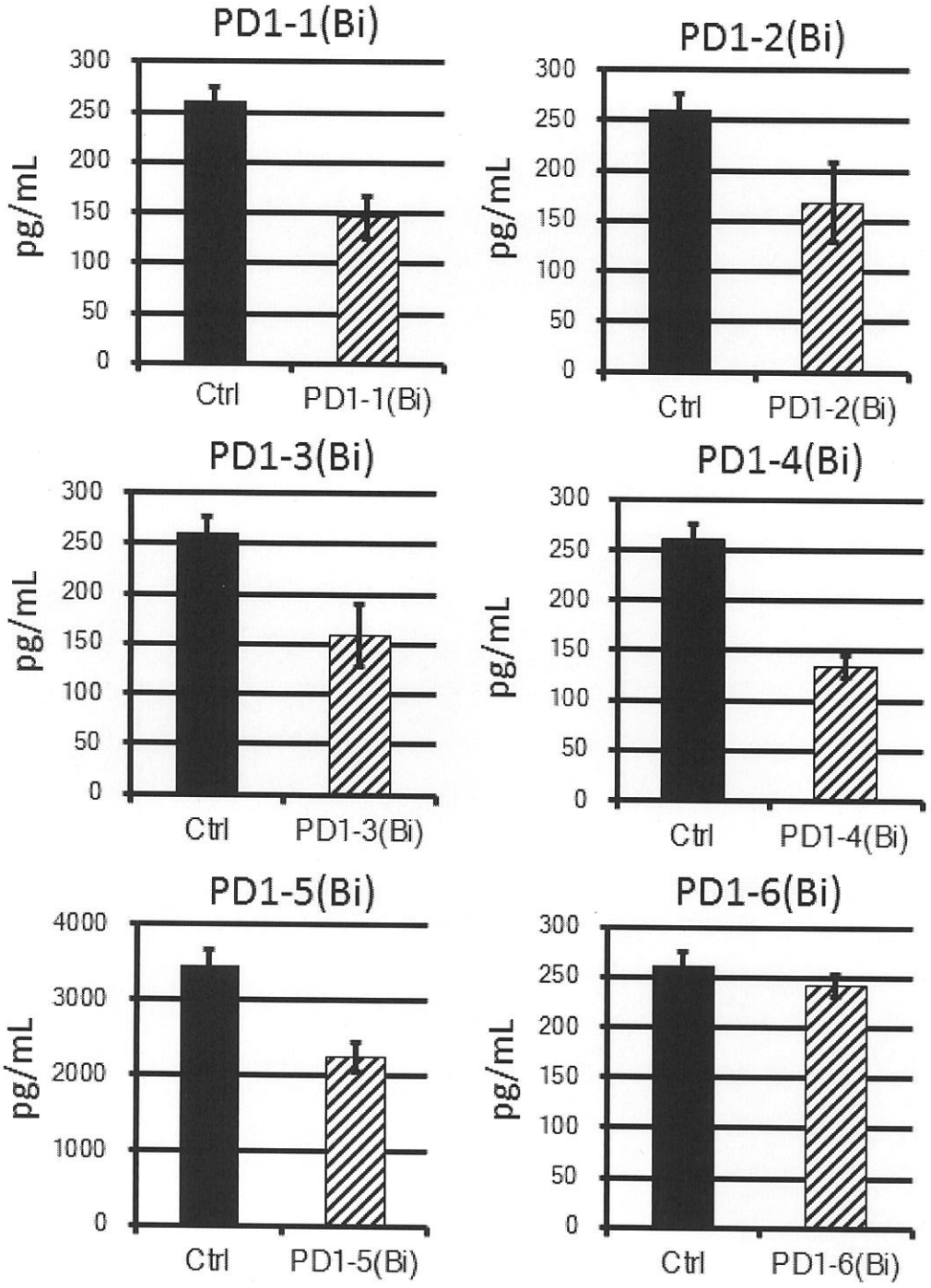

PD1-1(Bi)
pg/mL
300
250
200
150
100
50
0
Ctrl
PD1-1(Bi)
PD1-2(Bi)
pg/mL
300
250
200
150
100
50
0
Ctrl
PD1-2(Bi)
PD1-3(Bi)
pg/mL
300
250
200
150
100
50
0
Ctrl
PD1-3(Bi)
PD1-4(Bi)
pg/mL
300
250
200
150
100
50
0
Ctrl
PD1-4(Bi)
PD1-5(Bi)
pg/mL
4000
3000
2000
1000
0
Ctrl
PD1-5(Bi)
PD1-6(Bi)
pg/mL
300
250
200
150
100
50
0
Ctrl
PD1-6(Bi)

Figure 15

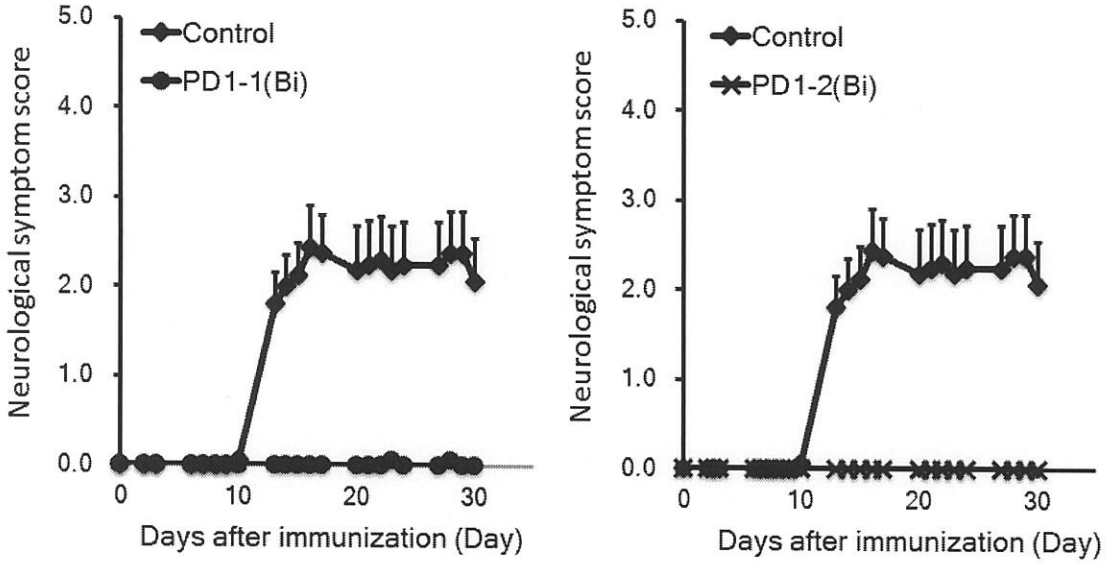


Figure 16

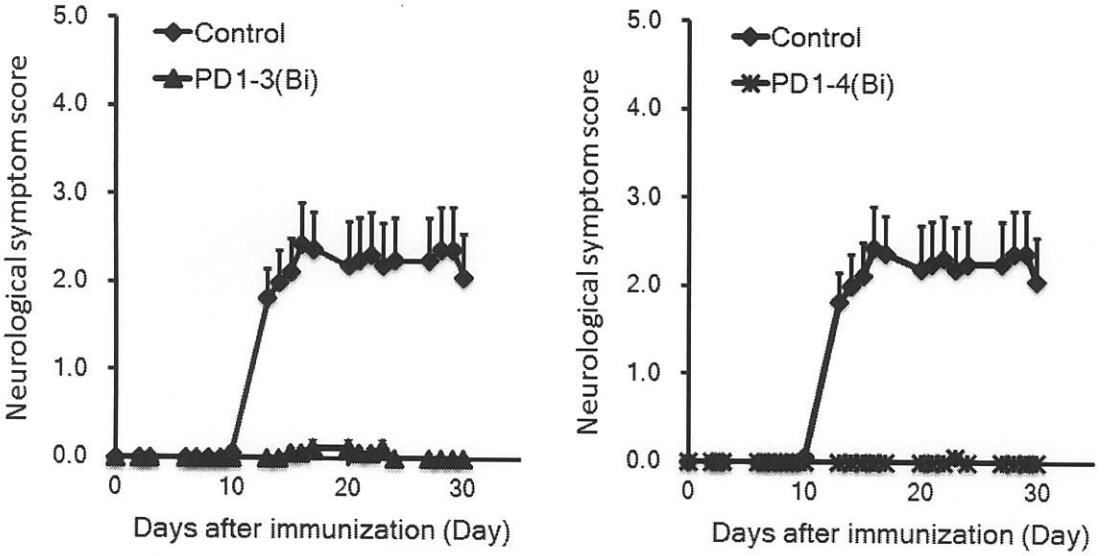


Figure 17

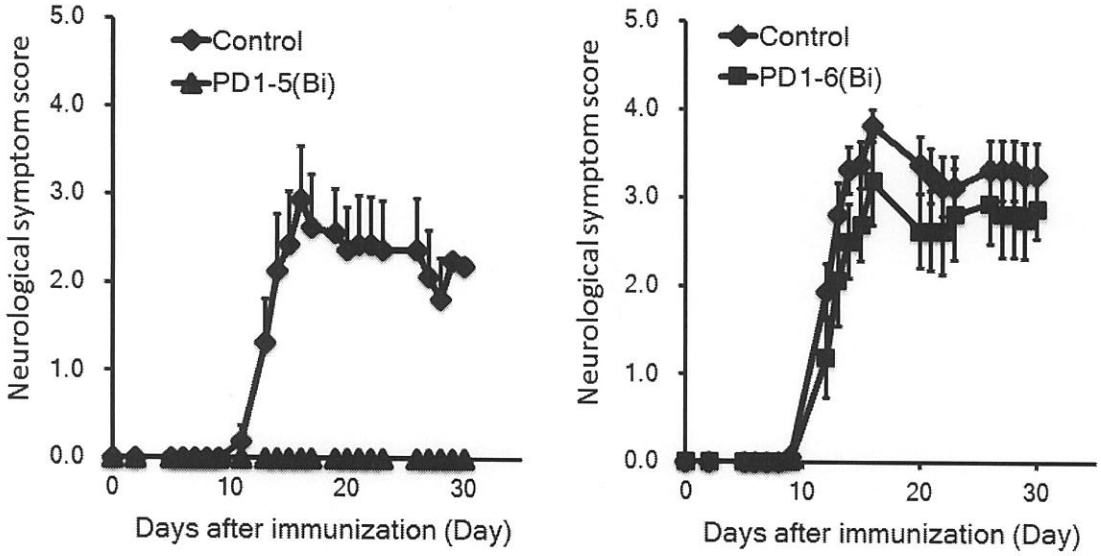


Figure 18

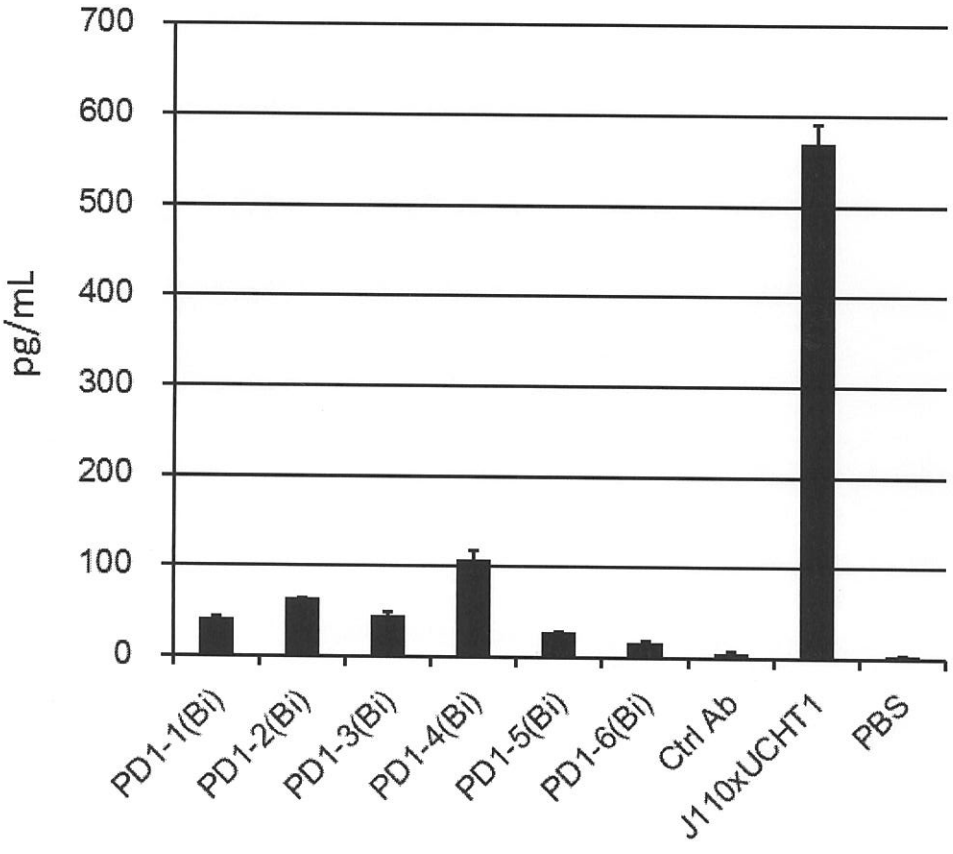
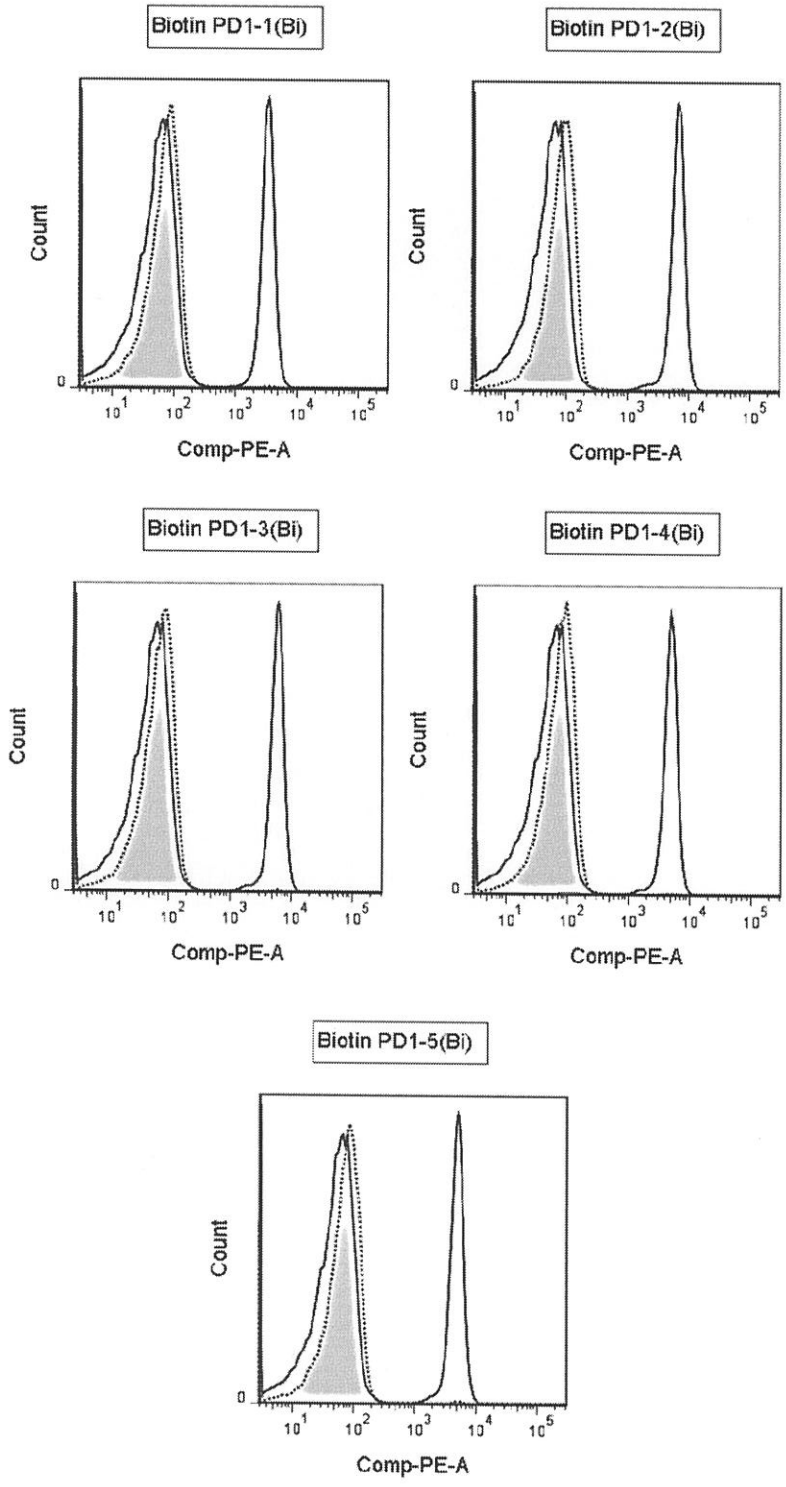


Figure 19


Biotin PD1-1(Bi)
Biotin PD1-2(Bi)
Biotin PD1-3(Bi)
Biotin PD1-4(Bi)
Biotin PD1-5(Bi)
Count
Comp-PE-A
0
10^1
10^2
10^3
10^4
10^5