

**Table 5. Murine PD-L1 mutations and binding data from Wang *et al.* (1) reconciled with murine PD-1/ human PD-L1 complex and human PD-L1 structures**

hPD-L1 interface residues (*) and mutated residues	Murine equivalent	Mutation in ref. 1	Residue location from modeling in ref. 1	Location from crystal structure (this work)	Is any atom within 4 Å of PD-1?	Binding to mPD-1 by FACS	Binding to mPD-1 by ELISA, %	Side chain located in interface, solvent, or buried.	hPD-L1 interface residues (*) and mutated residues
F 19*	same	none	n.r.	N-term	yes	not done	not done	interface	F 19*
T 20*	same	none	n.r.	N-term	yes	not done	not done	interface	T 20*
D 26*	same	none	n.r.	A strand	yes	not done	not done	interface	D 26*
L 27	same	A	A' strand	A' strand	no	++++	100	solvent	L 27
E 31	same	S	A' strand	A' strand	no	++	50	solvent	E 31
S 34	same	Y	B strand	B strand	no	++++	60	solvent	S 34
T 37	same	Y	B strand	B strand	no	++	5	solvent	T 37
D 49	same	S	B/C loop	B/C loop	no	++++	30	solvent	D 49
I 54*	same	none	n.r.	C strand	yes	not done	not done	interface	I 54*
Y 56*	same	S	C strand	C strand	yes	++++	100	interface	Y 56*
E 58	same	S	C strand	C strand	no	+++++	300	solvent	E 58
K 62	E	S	C/C' loop	C/C' loop	no	++++	50	solvent	K 62
Q 66*	same	none	n.r.	C' strand	yes	not done	not done	interface	Q 66*
F 67	same	A	C' strand	C' strand	no	+/-	2	buried	F 67
H 69	A	F	C' strand	C'/C" loop	no	+++++	300	solvent	H 69
E 72	same	S	C' strand	C" "strand"	no	++++	60	solvent	E 72
K 75	same	S	C' /D loop	C" "strand"	no	++++	100	solvent	K 75
K 89	same	S	D strand	D strand	no	++++	60	solvent	K 89
A 98	same	F	E strand	E strand	no	++++	40	solvent	A 98
Q 100	same	S	E strand	E strand	no	++++	100	solvent	Q 100
R 113*	C	Y	F strand	F strand	yes	+++++	300	interface	R 113*
M 115*	I	A	F strand	F strand	yes	+/-	3	interface	M 115*
S 117*	same	Y	F strand	F strand	yes	++++	100	interface	S 117*
A 121*	same	none	n.r.	G strand	yes	not done	not done	interface	A 121*
D 122*	same	none	n.r.	G strand	yes	not done	not done	interface	D 122*
Y 123*	same	none	n.r.	G strand	yes	not done	not done	interface	Y 123*
K 124*	same	S	G strand	G strand	yes	+	3	interface	K 124*
R 125*	same	none	n.r.	G strand	yes	not done	not done	interface	R 125*
I 126	same	A	G strand	G strand	no	-	1.4	buried	I 126
K 129	same	S	G strand	G strand	no	++	35	solvent	K 129

\*Denotes a residue in the interface of the PD-1/PD-L1 complex.

n.r., not reported.

Binding by wildtype mPD-L1 was ++++ by FACS and 100 % by ELISA in Wang *et al.* (1).

1. Wang S, *et al.* (2003) Molecular modeling and functional mapping of B7-H1 and B7-DC uncouple costimulatory function from PD-1 interaction. *J Exp Med* 197:1083–1091.