

Table 4. Murine PD-1 mutations and binding data from Zhang *et al.* (1) reconciled with the PD-1/PD-L1 complex structure

| mPD-1 residue (numbering from this work) | Residue number in ref. 1 | Human equivalent | Mutation from ref. 1 | Location from crystal structures [ref. 1 and this work] | Is any atom within 4 Å of PD-L1? | Binding BIACore, % | Side chain located in interface or solvent | mPD-1 residue (numbering from this work) |
|--|--------------------------|------------------|----------------------|---|----------------------------------|--------------------|--|--|
| D 62 | 29 | S | A | BC loop | no | 115 | solvent | D 62 |
| D 62 | 29 | S | S | BC loop | no | 125 | solvent | D 62 |
| M 64* | 31 | V | A | C strand | yes | 67 | interface | M 64* |
| N 66* | 33 | same | A | C strand | yes | 52 | interface | N 66* |
| N 68* | 35 | Y | none | C strand | yes | not done | interface | N 68* |
| S 73* | 40 | same | none | CC' loop | yes | not done | interface | S 73* |
| N 74* | 41 | same | none | CC' loop | yes | not done | interface | N 74* |
| Q 75* | 42 | same | none | CC' loop | yes | not done | interface | Q 75* |
| T 76* | 43 | same | none | C' strand | yes | not done | interface | T 76* |
| K 78* | 45 | same | A | C' strand | yes | 2 | interface | K 78* |
| N 84 | 51 | E | A | C'C" loop | no | 101 | solvent | N 84 |
| L 86 | 53 | R | A | C" strand | no | 102 | solvent | L 86 |
| Q 88 | 55 | same | S | C" strand | no | 88 | solvent | Q 88 |
| V 90* | 57 | G | A | C"D loop | yes | 87 | interface | V 90* |
| H 107 | 74 | same | S | E strand | no | 96 | solvent | H 107 |
| R 114 | 81 | same | S | EF loop | no | 89 | solvent | R 114 |
| L 122* | 89 | same | none | F strand | yes | not done | interface | L 122* |
| G 124* | 91 | same | none | F strand | yes | not done | interface | G 124* |
| I 126* | 93 | same | A | F strand | yes | 0 | interface | I 126* |
| L 128* | 95 | same | A | F strand/FG loop | yes | 3 | interface | L 128* |
| H 129 | 96 | A | A | FG loop | no | 60 | solvent | H 129 |
| P 130* | 97 | same | A | FG loop | yes | 83 | interface | P 130* |
| K 131* | 98 | same | A | FG loop | yes | 42 | interface | K 131* |
| A 132* | 99 | same | L | FG loop | yes | 121 | interface | A 132* |
| I 134* | 101 | same | A | G strand | yes | 4 | interface | I 134* |
| E 136* | 103 | same | A | G strand | yes | 9 | interface | E 136* |
| D 62/ A 132 | 99/ 29 | same/ S | L/ A | FG loop/ BC loop | yes/ no | 135 | solvent/ interface | D 62/ A 132 |

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

Binding by wildtype mPD-1 was 100% in Zhang *et al.* (1).

1. Zhang X, *et al.* (2004) Structural and functional analysis of the costimulatory receptor programmed death-1. *Immunity* 20:337–347.