

Supplementary information

Investigating the Impact of Asp181 Point Mutations on Interactions between PTP1B and Phosphotyrosine Substrate

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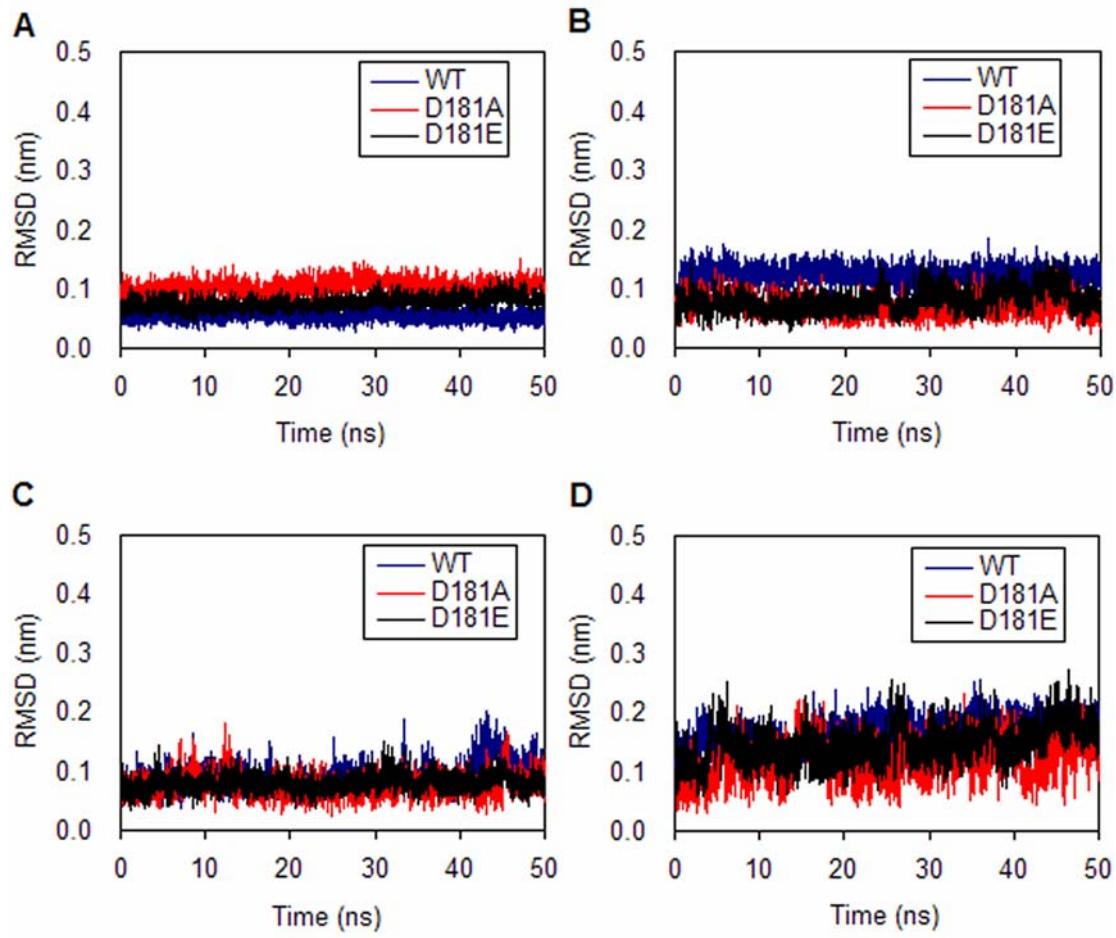


Figure S1 | Comparison of RMSD values in different regions. (A) P loop. (B) WPD loop. (C) Secondary aryl-phosphate-binding site. (D) Other residues in the active site of PTP1B.

Table S1 The analysis of hydrogen bonds between PTP1B and substrate during the last 30 ns MD simulations.

^a Hydrogen bond information dumped for occupancies with dumping schematic of time series (every 60 ps) after each H-bond, key follows: “ ” 0-5%; “.” 5-20%; “-” 20-40%; “o”: 40-60%; “x”: 60-80%; “*”: 80-95%; “@”: 95-100%

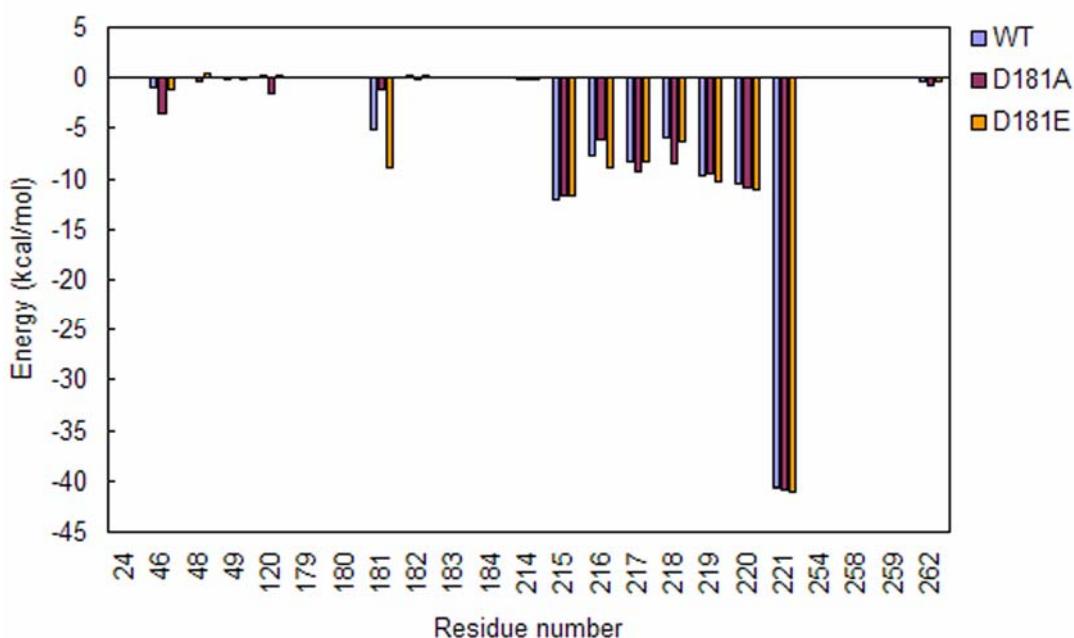


Figure S2 | The average of electrostatic interaction energies between substrate and residues in the active site of PTP1B.

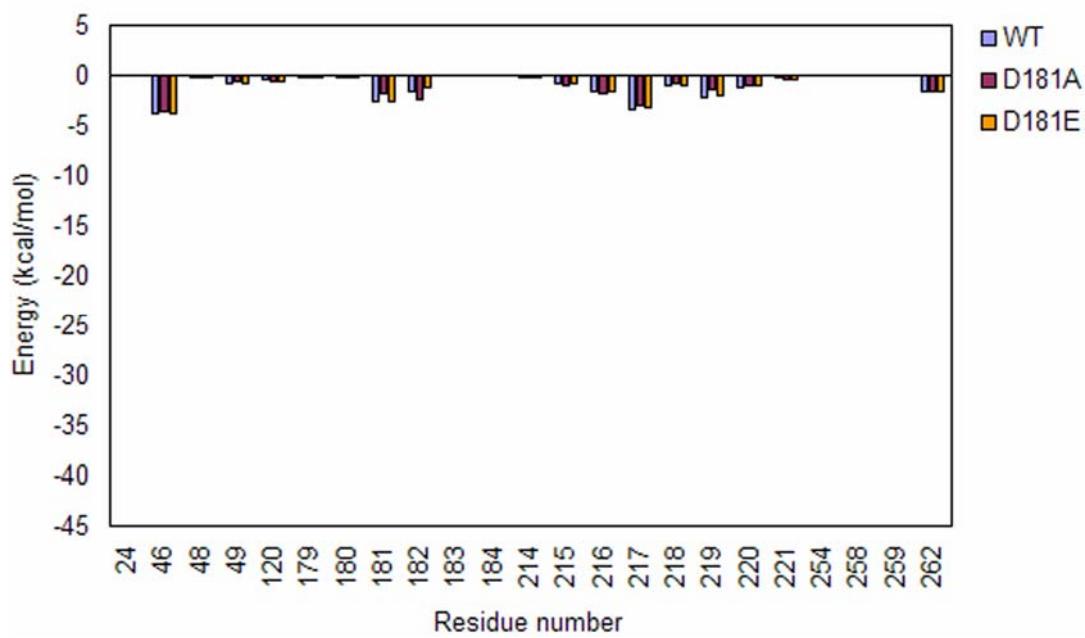


Figure S3 | The average of van der Waals interaction energies between substrate and residues in the active site of PTP1B.