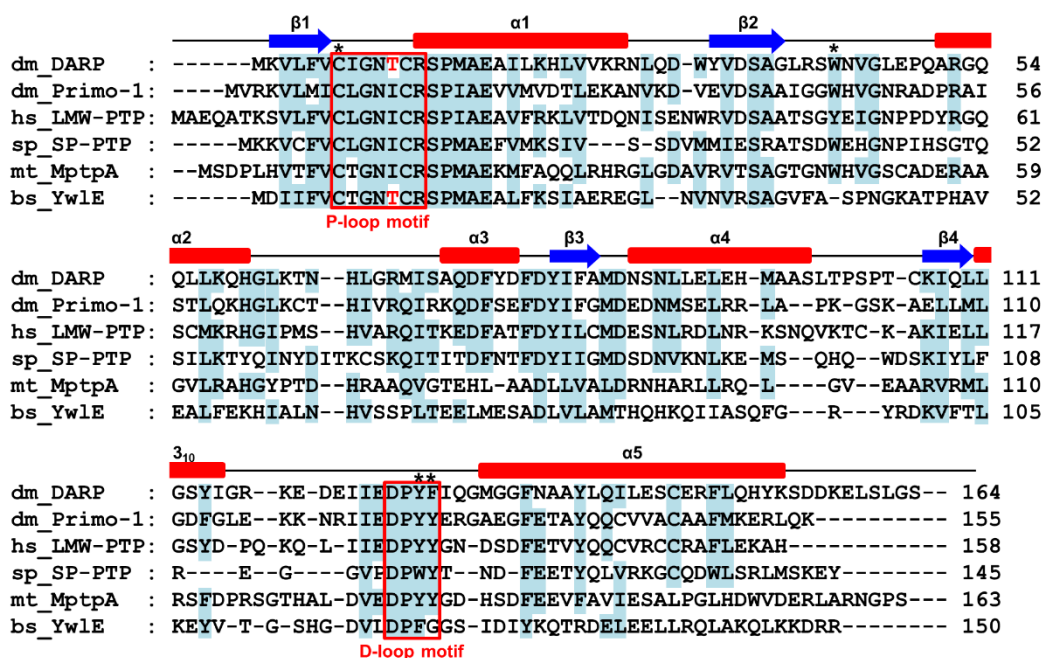


Supplementary Fig. S1. Structural analysis of DARP and Primo-1. (A) Structure and sequence alignment of the $\alpha 4$ $\beta 4$ region of DARP (navy) and Primo-1 (orange). (B) The $2F_o - F_c$ electron density omit map. The phosphate ion and HEPES molecule located at the center of the catalytic pockets of DARP and Primo-1 are contoured at 3.0σ (left) and 1.0σ (right), respectively. (C) Structurally comparison of the catalytic pockets between the indicated phosphatase proteins. Catalytic site-bound molecules and key residues are shown in stick representations and labeled. All the figures were drawn by PyMOL.



Supplementary Fig. S2. Sequence alignment. The sequences of DARP, Primo-1, and for LMW-PTPs are aligned. The secondary structure elements of DARP are shown above the sequences. Conserved residues are shaded in cyan. The P-loop and D-loop motif residues are highlighted by red rectangles. Asterisks denote the catalytic cysteine residues (Cys7 in DARP and Cys9 in Primo-1) and the three bulky aromatic residues in the catalytic pocket region (Trp43, Tyr127, and Phe128 in DARP and Trp45, Tyr126, and Tyr127 in Primo-1). dm, *D. melanogaster*; hs, *Homo sapiens*; sp, *S. pyogenes*; mt, *Mycobacterium tuberculosis*; bs, *B. subtilis*.