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**Structure of Human Protein Tyrosine Phosphatase Receptor Type O (PTPRO) with Bound Phosphate Ions in the Active Site.** Desigan Kumaran, Subramanyam Swaminathan, Biology Dept., Brookhaven National Laboratory, Upton, NY 11973, USA

Receptor-type tyrosine-protein phosphatase O isoform (PTPRO) is selected as one of the protein structure initiative II (PSI-II) target by NYSGRG ([www.nysgrc.org](http://www.nysgrc.org)). PTPRO is a tumor suppressor candidate and dephosphorylates tyrosine phosphate. It encodes as a single intracellular catalytic domain with a characteristic signature motif (H/V)C(5X)R(S/T). Here, we report the crystal structure of PTPRO, the first structure of this family from *Homo sapiens* at 2.2 Å resolution. PTPRO associates as a homo-dimer in the crystal structure via a NCS two-fold. Two phosphate ions were located in the active site. One of the phosphate ions is bound in the cleft formed by the p-loop residues and interacts with the active site residues Cys225, Arg231 and Asp191. Interestingly, another phosphate ion was located at a distance of 8 Å from the first phosphate ion and interacts with the C-terminal his-tag of a symmetry related molecule. The binding environment of phosphate ion with the his-tag mimics the substrate binding. The correlation between the structure and function will be presented.

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