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Crystal structure and functional analysis of the surE protein identify a novel phosphatase family

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The genome sequencing has revealed a large number of proteins of unknown or little characterized functions that have been well conserved during evolution. It remains a great challenge to decipher the molecular and physiological functions of these proteins. One example of the evolutionarily conserved protein family with little understood function is the surE family. Homologs of the *Escherichia coli* surE gene are present in many eubacteria and archaea. In order to obtain possible clues to the function of the surE proteins, we initiated the structure determination of the surE homolog in *T. maritima*. It comprises 247 amino acid residues and the amino acid sequence is 39% identical to that of *E. coli*. The structure reveals a novel active site around a bound metal ion. This information, together with the result from the complementation study on the homologous yeast gene *PHO2*, prompted us to investigate metal ion-dependent phosphatase activities. We demonstrate that the surE protein exhibits a divalent metal ion-dependent phosphatase activity, which is inhibited by vanadate or tungstate. In the vanadate- and tungstate-complexed structures, the inhibitors bind adjacent to the divalent metal ion. Our structural and functional analyses identify the surE proteins as a novel family of metal ion-dependent phosphatase.