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Towards Understanding the Structure and Function of a Conserved Hypothetical Protein SA1388 from *Staphylococcus aureus*. Hong Zhang¹, Xuejun Zhang¹, Kumar Singh¹, Darek Martynowski¹, Lisa Linch^{1,2}, Nick Grishin^{1,2} ¹Dept. of Biochemistry and ²Howard Hughes Medical Inst., Univ. of Texas Southwestern Medical Center, Dallas, TX 75390.

SA1388 from *S. aureus* is a bifunctional protein, containing an apparent enzymatic domain that belongs to a large conserved protein family, COG0327, in the COG protein database, and a PII-like domain inserted in the middle of the COG0327 domain. While the function of COG0327 is currently unknown, the PII-like domain is likely to perform certain signaling function as inferred by its remote homology to the nitrogen-regulatory PII protein. The crystal structure of full length SA1388 was solved by the selenomethionine MAD phasing method and was refined to 2.0Å resolution. The structure revealed a hexameric quaternary arrangement primarily through trimerization of the PII-like domains and dimerization of the COG0327 domains. The active site of the COG0327 domain revealed a two metal center and the metal identity has been determined to be Zn by ICP- atomic emission spectroscopy. Furthermore, additional density in the active site is observed representing an intrinsic ligand directly coordinated to both metal ions. The identification of this ligand is likely to provide key information regarding the function of this conserved protein.