Poster Presentation

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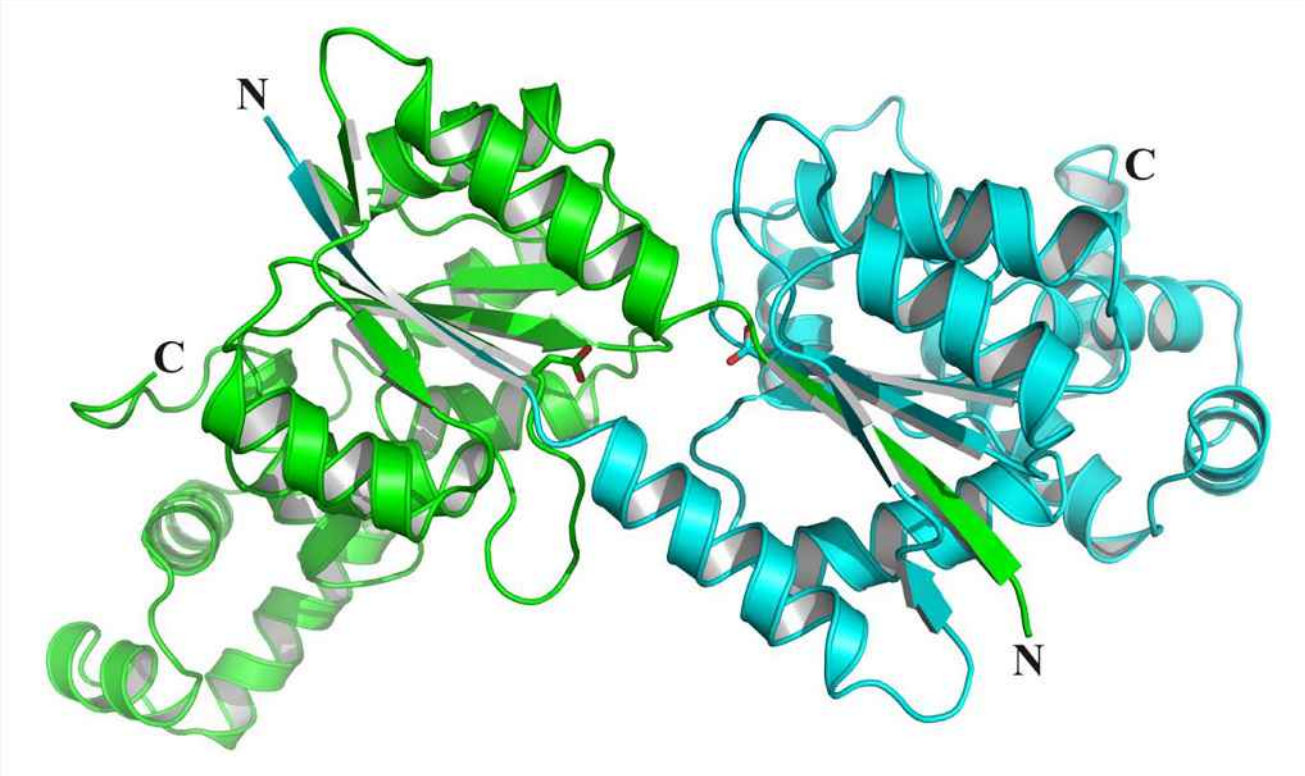
Crystal structure of the response regulator VraR from Staphylococcus aureus

C. Lee[1,2], C. Liu[3,4], W. Chang[3], W. Jeng[1,2,3,4]

[1]Center for Bioscience and Biotechnology, National Cheng Kung University, Tainan, Taiwan, [2]Department of Biochemistry and Molecular Biology, National Cheng Kung University, Tainan, Taiwan, [3]Core Facilities for Protein Structural Analysis, Academia Sinica, Taipei, Taiwan, [4]School of Medical Laboratory Science and Biotechnology, Taipei Medical University, Taipei, Taiwan

*Staphylococcus aureus*is one of the major causes of nosocomial infections today. Infections caused by *S. aureus* are a growing cause of concern owning to the widespread development of multiple antibiotic-resistant strains, particularly methicillin and vancomycin-intermediate resistant strains (MRSA and VISA). The VraSR two component system is reported to be highly related to the development of vancomycin resistance of *S. aureus*. VraS is a membrane-bound sensor histidine kinase that received the signal stimulation from environment to regulate the phosphorylation status of its cognate response regulator protein VraR to control target genes transcription to result in the development of vancomycin resistance of *S. aureus*. Here, we report the crystal structure of unphosphorylated VraR from *S. aureus* in a dimeric form at 1.8 Å resolution. The crystals of VraR belong to the monoclinic space group C2 containing two protein molecules as a dimer in the asymmetric unit. The first β-strand at N-terminal end of each VraR subunit was inserted into the other subunit to form an intertwining dimer structure. Finally, according to previous reports and our crystal structure, we propose a regulation model for VraR. The feedback control of *vra* SR operon would be the unphosphorylated dimeric VraR rather than the unphosphorylated monomeric VraR.

[1] *Belcheva A. and Golemi-Kotra D., "A close-up view of the VraSR two-component system - A mediator of Staphylococcus aureus response to cell wall damage", J Biol Chem, Vol. 283, No. 18, (2008), pp 12354-12364.,* ***[2]*** *Leonard P. G., Golemi-Kotra D. and Stock, A. M., "Phosphorylation-dependent conformational changes and domain rearrangements in Staphylococcus aureus VraR activation", Proc Natl Acad Sci USA, Vol. 110, No. 21, (2013), pp 8525-8530.*



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