

## Poster Presentation

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### *Structure of STM3169, a tripartite ATP-independent periplasmic transporter*

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Substrate-binding proteins (SBPs) form a group of proteins that are commonly related to membrane protein complexes for transport or cell signal transduction. SBPs are comprised of prokaryotic ATP-binding cassette (ABC)-transporters, prokaryotic tripartite ATP-independent periplasmic (TRAP)-transporters, prokaryotic two-component regulatory systems, eukaryotic guanylatecyclase-atrial natriuretic peptide receptors, G-protein coupled receptors (GPCRs) and ligand-gated ion channels (Berntsson et al., 2010). The TRAP transporters are less known as compared with ABC transporters but are ubiquitous in prokaryotes. The TRAP transporters are important elements of solute uptake systems in prokaryotes. These transporters contain two membrane protein components, predicted to have four and twelve transmembrane helices, respectively. In the TRAP transporters of DctP-type, substrate recognition is mediated through a well-conserved and specific arginine/carboxylate interaction in the SBP (Mulligan et al., 2011). Here we have determined the crystal structure of the TRAP transporter from *Salmonella entericaserovarTyphimurium*. Unexpectedly, this structure shows that various ligands can bind to the TRAP transporters. It provides insights into substrate binding mechanism in the TRAP transporter system.

[1] R.P. Berntsson, S.H. Smits, L. Schmitt, D.J. Slotboom, and B. Poolman, *FEMS Microbiol. Rev.*, 2010, 584, 2606-2617, [2] C. Mulligan, M. Fischer, and G.H. Thomas, *FEBS Lett.*, 2011, 35, 68-86

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