Crystal structure of the pyoverdin outer membrane receptor FpvA from *Pseudomonas aeruginosa*. Cobessi D., Célia H., Folschweiler N., Schalk I., Abdallah M. & Pattus F. *Départment Récepteurs et Protéines Membranaires, UPR9050 CNRS, Ecole Supérieure de Biotechnologie de Strasbourg, Boulevard Sébastien Brant, 67410 Illkirch, France*. Email: cobessi@esbs.u-strasbg.fr

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When grown under iron-deficient conditions, many bacteria synthesize and release into the environment iron chelators termed siderophores. In the host it is expected that siderophores sequester iron from iron-containing molecules such as transferrin and deliver iron to the microbial cell. In general, the first step of entry of ferric siderophores into Gram negative bacteria is mediated by specific outer membrane receptors. 3 x-ray structures of the outer membrane ferric siderophore receptors from *E. coli* have been reported. This transport into the periplasm requires the cytoplasmic proton motive force and an energy transduction complex which includes the cytoplasmic membrane proteins TonB, ExbB and ExbD [1]. *P. aeruginosa* is an opportunistic human pathogen which infects injured, immunodificient, or ortherwise compromised patients. Under iron-limited conditions, the bacterium secretes a major siderophore called pyoverdin (PaA). PaA seems to play an important role in infection by competing with transferrin for iron in order to overcome the iron-withholding mechanism present in mammals. Previous *in vitro* and *in vivo* studies have shown that pyoverdin mediated iron uptake through its outer membrane receptor FpvA occurs through a novel mechanism different from the uptake mediated by ferrichrome in *E. coli*. FpvA is able to bind both iron free PaA and ferric-PaA and the normal state of the FpvA receptor under iron limitation seems to be the FpvA-PaA complex. During iron uptake, the extracellular ferric-PaA displaces the bound PaA on the FpvA receptor [2]. We over-expressed and purified FpvA (MM: 86245) from *P. aeruginosa* in its siderophore-bound (FpvA-PaA) and in its ligand-free (FpvA) forms. We crystallized the different forms of the receptor. We are currently building a first atomic model of FpvA-PaA at 3.6 Å resolution from a dataset collected using crystals of a SeMet substituted FpvA-PaA. The current free-R and R factors are now below 30 %. Three molecules related by a non crystallographic 3-fold axis are in the asymmetric unit. The FpvA-PaA model contains 684 residues and the pyoverdin. The structure can be divided in two domains. The N-terminal part of the structure called cork-domain contains 146 residues. It fills the second domain composed of 538 residues which is a β-barrel of 22 antiparallel transmembrane strands. The siderophore is bound on the extracellular side of the receptor where the loops connecting the β-strands are larger than the ones situated in the periplasm. This structure is the first of an *in vivo* loaded siderophore receptor and also the first TonB-receptor structure from another bacterium than *E. coli.*

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[2] Schalk, I.J., Abdallah, M.A. and Pattus, F. (2002). *Biochem. Soc. Trans*., **30**, 702-705.