X-ray crystallographic structure of Pst1, a novel porin from *Providencia stuartii*

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*Providencia stuartii* is an opportunistic pathogen involved in community-acquired as well as hospital-acquired infectious diseases. Clinical strains of *P. stuartii* are mostly isolated from urinary tract infections of patients and, in fewer cases, from respiratory and skin infections. *P. stuartii* is reported as one of the most resistant species in the family of *Enterobacteriaceae*.

Recently, Tran et al. have identified a non-specific porin in the outer membrane of *P. stuartii*, Pst1, which shares 50% homology with the well-known porin OmpF from *Escherichia coli*. Preliminary results suggest an interesting role for Pst1 in the regulation of antibiotic translocation, and a possible explanation for the intrinsic resistance of *P. stuartii* strain against imipenem treatment. A more detailed understanding of the translocation and resistance mechanisms requires, however, the atomic resolution structure of the protein. We will present the x-ray-crystallographic structure of Pst1 at 2.9 Å resolution (Nasrallah et al., manuscript in preparation) and discuss the conformational changes and charge substitutions observed with regard to OmpF.