

# ***SFB 35 Colloquia in Membrane Transport***

Medical University Vienna, Institute of Physiology,

Schwarzspanierstraße 17, 1090 Vienna, „**Kleiner Hörsaal Physio**“, 1st floor (right side)

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**Friday 17.11.2017 14:00 s.t.**

**Host: Thomas Stockner**

## **Konstantinos Beis**

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## ***"Structural basis for the transport of antibacterial peptides across bacterial membranes"***

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### **Konstantinos Beis**

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Bacteria under nutrient starvation produce antibacterial peptides that target closely related species for survival. These peptides can be either lytic or non-lytic. Lytic peptides disrupt the membrane that results in nutrient loss whereas non-lytic peptides hijack membrane bound receptors for internalisation. The lasso peptide MccJ25 is an interesting class of non-lytic peptide that can be used as novel antimicrobial. MccJ25 is also toxic to the producing bacteria, which utilise the ABC transporter MccJ to transport it out of the cell and provide them with resistance. Once it has been secreted it hijacks the outer membrane siderophore receptor FhuA and inner membrane transporter SbmA for internalisation inside the target cell. Inside the cell it targets the RNA polymerase. My lab is interested to elucidate the structure and function of these transporters. We have determined the crystal structure of the ABC transporter MccJ in distinct conformations. The structures are in novel conformations, apo inward-occluded and nucleotide-bound outward occluded that have allowed us to refine the mechanism of antibacterial peptide ABC transporters. Our functional data in proteoliposomes show that MccJ25 is specific to MccJ and not to other antibacterial peptides or drugs. We are also investigating which portion of the peptide is important for recognition by NMR and non-denaturing mass spectrometry. We have also determined the structure of the siderophore receptor FhuA in complex with MccJ25. MccJ25 mimics the binding mode of the natural siderophore substrate. The structure has allowed us to identify a key hydrogen bond that is essential to induce a transport event. In addition, these data provide new avenues for the design of novel antibacterials to fight bacterial multi drug resistance.