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**Structure of Functional *Staphylococcus aureus* $\alpha$-Hemolysin Channels in Tethered Bilayer Lipid Membranes.** FRANK HEINRICH[1], Carnegie Mellon University, GINTARAS VALINCIUS, Institute of Biochemistry, Vilnius, DUNCAN J. MCGILLIVRAY[2], Carnegie Mellon University, JOSEPH W.F. ROBERTSON, NIST Electronics and Electrical Engineering Lab., ILJA IGNATJEV, Institute of Biochemistry, Vilnius, JOHN J. KASIANOWICZ, NIST Electronics and Electrical Engineering Lab., MATHIAS LOESCHE[3], Carnegie Mellon University — We demonstrate the functional reconstitution of the *Staphylococcus aureus* $\alpha$-hemolysin channel in membranes tethered to gold. Electrical impedance spectroscopy measurements show that the pores have essentially the same properties as those formed in free-standing bilayer lipid membranes. Neutron reflectometry (NR) provides high-resolution structural information on the interaction between the channel and the disordered membrane, and validates predictions based on the channel x-ray crystal structure. NR also shows that the proximity of the solid interface does not affect the molecular architecture of the protein-membrane complex. The results suggest that this technique could be used to elucidate molecular details about the association of other proteins with membranes. It also may provide structural information on domain organization and stimuli-responsive reorganization for transmembrane proteins in membrane mimics.

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