北京大学物理化学学术报告

# Computational design of multi-pass transmembrane proteins


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## Abstract:

**The computational design of transmembrane proteins with more than one membrane-spanning region remains a major challenge. I will talk about the design of transmembrane monomers, homodimers, trimers, and tetramers with 76 to 215 residue subunits containing two to four membrane-spanning regions and up to 860 total residues that adopt the target oligomerization state in detergent solution. The designed proteins localize to the plasma membrane in bacteria and in mammalian cells, and magnetic tweezer unfolding experiments in the membrane indicate that they are very stable. Crystal structures of the designed dimer and tetramer—a rocket-shaped structure with a wide cytoplasmic base that funnels into eight transmembrane helices—are very close to the design models. Our results pave the way for the design of multispan membrane proteins with new functions. I will also talk about our effort to design functional transmembrane proteins.**


## Biography

**B.S. in Biological Science, University of Science and Technology of China, Hefei, China, 2009.**

**Ph.D. in Biochemistry &Structural Biology, Tsinghua University, Beijing, China, 2014.**

**2015.1 - Now (Postdoctoral research) Focused on computational protein design, especially computational design of transmembrane proteins and small protein/peptide binders to proteins. Research conducted in Prof. David Baker's Lab at University of Washington, under the mentorship of Prof. David Baker and Prof. Williams Catterall.**

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