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Tackling membrane protein structure and function using solution NMR method

By

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Abstract

The transmembrane (TM) anchors of cell surface proteins have been one of the 'blind spots' in structural biology because they are generally very hydrophobic, sometimes dynamic, and thus difficult targets for structural characterization. A plethora of examples show these membrane anchors are not merely anchors but can multimerize specifically to activate signaling receptors on the cell surface or to stabilize envelope proteins in viruses. Through a series of studies of the TM domains (TMDs) of immune receptors and viral membrane proteins, we have established a robust protocol for determining atomic-resolution structures of TM oligomers by NMR in bicelles that closely mimic a lipid bilayer. Our protocol overcomes hurdles typically encountered by structural biology techniques such as X-ray crystallography and cryo-electron microscopy (cryo-EM) when studying small TMDs. Using the new method, we solved the first transmembrane trimer structures of FAS, HIV1 envelope protein, SARS-COV2, etc. Based on the structures, we screened small molecule drug targeting on membrane adjacent regions to inhibit virus infection.

Biography

Qingshan (Bill) Fu, Professor, Principle Investigator. Received Ph.D. degree in Biochemistry and Molecular Biology from Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences in 2010. From January 2011 to December 2018, Bill worked as a Postdoc in James Chou Lab in Harvard Medical School. Using solution NMR method solved the first transmembrane trimer structure of TNFR family receptors. Solved the structures of membrane adjacent region of HIV1 Envelope-protein. January 2019 to September 2021, Bill was assigned the Instructor's position and worked on HIV Envelope protein, SARS-COV2 spike protein, and screening for drugs to inhibit virus infection. Now, Bill works as a Principle Investigator in Shanghai Institute of Materia Medica.

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ALL ARE WELCOME

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