IS02-2 **Function-related Dynamics of Membrane Proteins**

○ Ichio SHIMADA[1]
[1]Grad. Sch. Pharm. Sci., The Univ. of Tokyo

Membrane proteins, including G protein coupled receptors and ion channels, play fundamental roles in physiological processes and are target proteins for drug development. For better understanding of the functions, not only precise static three-dimensional structures determined by X-ray crystallography and cryo-electron microscopy methodologies, but also dynamical nature are required. NMR (nuclear magnetic resonance spectroscopy) provides us information about membrane proteins dynamics, including conformation equilibrium related to functions. However, it is frequently difficult to obtain information about the membrane protein dynamics related to the functions, due to the molecular weight limitation in NMR. We have recently developed novel NMR methods for characterizing protein dynamics utilizing multiple quantum relaxation rates of side-chain methyl groups, which can be sensitively observed in high molecular weight proteins. In this paper, we will show our recent results of function-related dynamics of membrane proteins.[1)]

1. GPCR drug discovery: integrating solution NMR data with crystal and cryo-EM structures, Ichio Shimada*, Takumi Ueda, Yutaka Kofuku, Matthew T. Eddy, and Kurt Wüthrich*, ***Nat. Rev. Drug Discov.*** (2018) DOI: 10.1038/nrd.2018.180.