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Small-angle neutron and X-ray scattering reveal conformational changes in rhodopsin activation UTSAB R. SHRESTHA, DEBSINDHU BHOWMIK, Wayne State University, MI, SUCHITRHANGA M.C.D. PERERA, UDEEP CHAWLA, ANDREY V. STRUTS, University of Arizona, AZ, VITO GRAZIONO, Brookhaven National Laboratory, NY, SAI VENKATESH PINGALI, WILLIAM T. HELLER, SHUO QIAN, Oak Ridge National Laboratory, TN, MICHAEL F. BROWN, University of Arizona, AZ, XIANG-QIANG CHU, Wayne State University, MI — Understanding G-protein-coupled receptor (GPCR) activation plays a crucial role in the development of novel improved molecular drugs. During photo-activation, the retinal chromophore of the visual GPCR rhodopsin isomerizes from 11-cis to all-trans conformation, yielding an equilibrium between inactive Meta-I and active Meta-II states. The principal goals of this work are to address whether the activation of rhodopsin leads to a single state or a conformational ensemble, and how protein organizational structure changes with detergent environment in solution. We use both small-angle neutron scattering (SANS) and small-angle X-ray scattering (SAXS) techniques to answer the above questions. For the first time we observe the change in protein conformational ensemble upon photo-activation by SANS with contrast variation, which enables the separate study of the protein structure within the detergent assembly. In addition, SAXS study of protein structure within detergent assembly suggests that the detergent molecules form a belt of monolayer (micelle) around protein with different geometrical shapes to keep the protein in folded state.

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