Structure of Adenylyl Cyclase 5 in Complex with Gβγ Offers Insights into *ADCY5*-Related Dyskinesia

Yu-Chen Yen¹, Yong Li², Chun-Liang Chen¹, Thomas Klose³, Val J Watts⁴, Carmen W Dessauer², and John J. G. Tesmer^{1,4}

Affiliations:

¹Department of Biological Sciences, Purdue University, West Lafayette, IN, USA

²Department Integrative Biology and Pharmacology, McGovern Medical School, University of Texas Health Science Center, Houston, TX, USA

³Purdue CryoEM Facility, Suite 171, Hockmeyer Hall for Structural Biology, Purdue University, West Lafayette, IN, USA

⁴Department of Molecular Pharmacology and Medicinal Chemistry, Purdue University, West Lafayette, IN, USA

Abstract

The nine different membrane-anchored adenylyl cyclase isoforms (AC1-9) in mammals are stimulated by the heterotrimeric G protein $G\alpha_s$, but their response to $G\beta\gamma$ regulation is isoform-specific. For example, AC5 is conditionally activated by $G\beta\gamma$. Here, we report the 7 Å cryo-EM structures of ligand-free AC5 in complex with $G\beta\gamma$ and of a dimeric form of AC5 that could be involved in its regulation. $G\beta\gamma$ binds to a coiled-coil domain that links the AC transmembrane region to its catalytic core as well as to a region that is known to be a hub for isoform-specific regulation. We confirmed the $G\beta\gamma$ interaction using both purified proteins and cell-based assays. The interface with $G\beta\gamma$ involves AC5 residues that are the sites of gain-of-function mutations in humans suffering from dyskinesia, indicating that the observed interaction is important for motor function. A molecular mechanism wherein $G\beta\gamma$ either prevents dimerization of AC5 or allosterically modulates the coiled-coil domain, and hence the catalytic core, is proposed. Because our mechanistic understanding of how individual AC isoform-specific drug development.