

Abstract

Adenylyl cyclases (ACs) are a family of enzymes that catalyze the conversion of ATP into secondary messenger, cAMP that can go on to do further downstream signaling events. AC5 is one of the AC family membrane-bound members¹. AC5 knock-out and inhibition showed improvement in cardiovascular diseases^{2,3}. AC5 is regulated by both $G\alpha_s$ and $G\alpha_i$, which are $G\alpha$ stimulatory and $G\alpha$ inhibitory subunits respectively⁴. We know a lot about general AC- $G\alpha_s$ complex⁵, but we don't have much information about the AC5 regulation mechanisms by $G\alpha_i$. Moreover, there has not been any resolved structure for full-length AC5. As a matter of fact, the only AC that has a full-length resolved structure is AC9, which was only published in 2019⁶.

The aim of this project is to obtain a structure of AC5- $G\alpha_i$ complex in order to understand the AC5 regulation mechanisms, as well as conformational changes that differentiate between the active vs inactive forms of AC5. We purified $G\alpha_i$ myristoylated and unmyristoylated, and performed a co-immunoprecipitation with AC5. We showed inhibition of AC5 by both entities if they are GTP-activated compared to GDP-bound myristoylated $G\alpha_i$. We have also tried to perform cryo-EM analysis for the obtained complex, but the grids showed protein aggregates, and a few particles that are not enough for obtaining a high-resolution map.

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