

Structural evidence for “Intermediate” along the activation pathway of Heterotrimeric G-proteins



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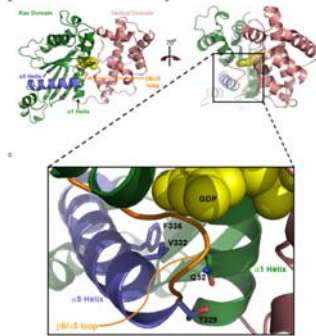
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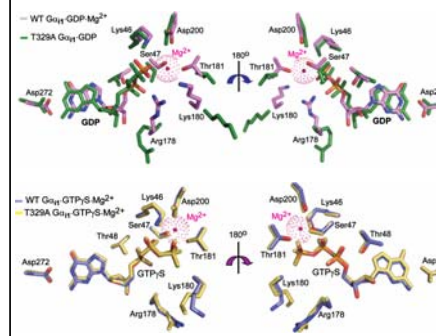
Abstract

Heptahelical G protein-coupled receptors (GPCRs) couple to heterotrimeric G proteins to relay extracellular signals to intracellular signaling networks, but the molecular mechanism underlying GDP release by the G protein α -subunit is not well understood. Amino acid substitutions in the conserved $\alpha 5$ helix of G_i, which extends from the C-terminal region to the nucleotide-binding pocket, cause dramatic increases in basal (receptor-independent) GDP release rates. For example mutant G α_{i1} -T329A shows an 18-fold increase in basal GDP release rate, and when expressed in culture it causes a significant decrease in forskolin-stimulated cAMP accumulation. The crystal structure of G α_{i1} -T329A-GDP shows substantial conformational rearrangement of the switch I region and additional striking alterations of side chains lining the catalytic pocket that disrupt the Mg²⁺ coordination sphere and dislodge bound Mg²⁺. We propose a “sequential release” mechanism whereby a transient conformational change in the $\alpha 5$ helix alters switch I to induce GDP release. Interestingly, this mechanistic model for heterotrimeric G protein activation is similar to that suggested for the activation of the plant small G protein Rop4 by RopGEF8.

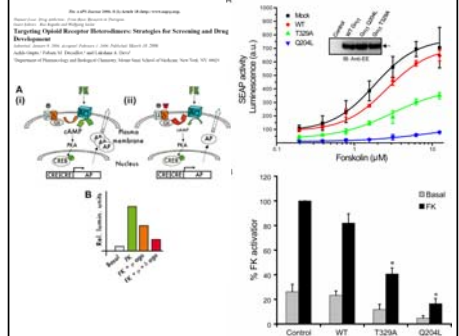
$\alpha 5$ helix point mutants



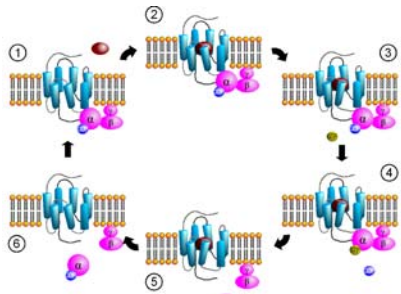
Changes in the Catalytic Pocket



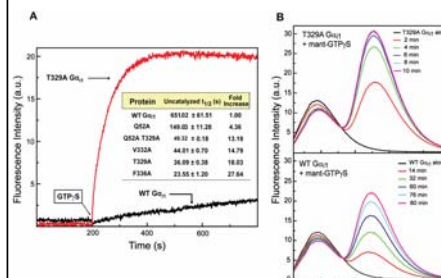
In vivo activity of the mutant



Activation cycle

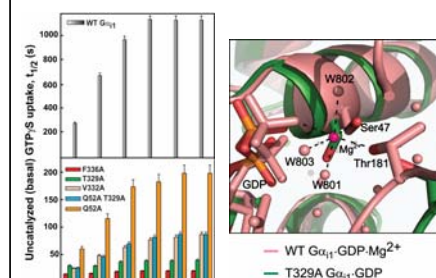


Monitoring Activation

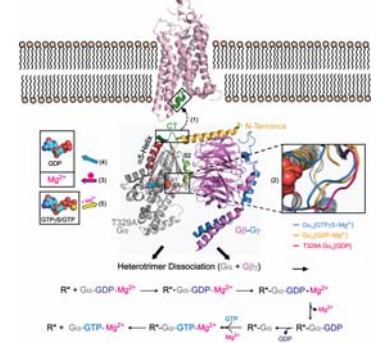


Basal rates of activation much faster for the mutant

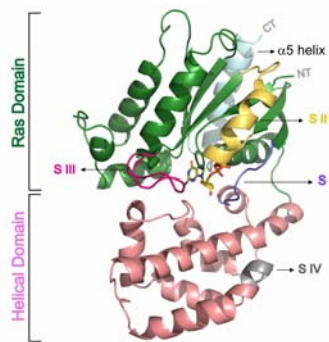
Loss of Mg²⁺ & Catalytic Waters



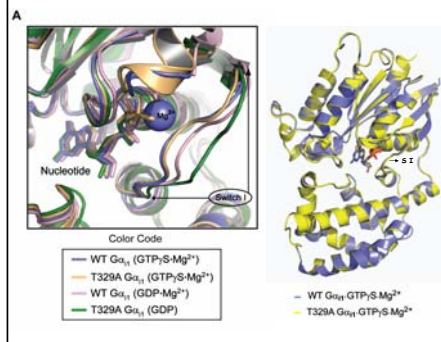
A “Sequential-release” model for activation



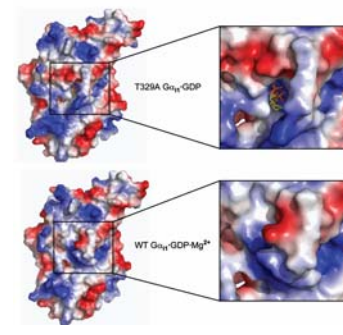
Structure of G protein α -subunit



Changes in Switch I conformation



Electrostatic Potential Surface



References

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