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Probing functional interfaces of rod PDE γ -subunit using scanning fluorescent labeling

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Abstract

In the dark, the activity of the rod cGMP phosphodiesterase (PDE) catalytic α - and β -subunits ($P\alpha\beta$) is inhibited by two γ -subunits ($P\gamma$). On light stimulation of the photoreceptor cells, the GTP-bound α -subunit of visual G-protein transducin ($G_{ta}GTP$) displaces the $P\gamma$ -subunits from their inhibitory sites on $P\alpha\beta$, leading to the effector enzyme activation. We designed a number of $P\gamma$ mutants, each with a single cysteine residue evenly distributed at a different position along the $P\gamma$ polypeptide chain. These cysteine residues served as sites for the introduction of the environmentally sensitive fluorescent probe, 3-(bromoacetyl)-7-diethyl aminocoumarin (BC). Analysis of the interactions of $P\alpha\beta$ and G_{ta} with the fluorescently labeled $P\gamma$ mutants suggests two distinct functional interfaces of $P\gamma$. The $P\alpha\beta/P\gamma$ interface is formed essentially by the C-terminus of $P\gamma$ and by the N-terminal portion of the $P\gamma$ polycationic region, $P\gamma$ -24-45, whereas the $P\gamma/G_{ta}$ interface includes the C-terminal portion of $P\gamma$ -24-45 and the region surrounding $P\gamma$ Cys68. Such functional organization of $P\gamma$ may represent an important element for the PDE activation mechanism during transduction of visual signals.