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Crystal structure of a dynamin GTPase domain in both nucleotide-free and GDP-bound forms

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Dynamins form a family of multidomain GTPases involved in endocytosis, vesicle trafficking and maintenance of mitochondrial morphology. In contrast to the classical switch GTPases, a force generating function has been suggested for dynamins. Here we report the 2.3Å crystal structure of the nucleotide-free and GDP-bound GTPase domain of *Dictyostelium discoideum* dynamin A. The GTPase domain is the most highly conserved region among dynamins. The globular structure consists contains the G-protein core fold, which is extended from a six-stranded β-sheet to an eight-stranded one by a 55 amino acid insertion. This topologically unique insertion distinguishes dynamins from other subfamilies of GTP-binding proteins. An additional N-terminal helix interacts with the C-terminal helix of the GTPase domain, forming a hydrophobic groove, which could be occupied by C-terminal parts of dynamin not present in our construct. The lack of major conformational changes between the nucleotide-free and the GDP-bound state indicate that mechanochemical rearrangements in dynamin must occur during GTP-binding, GTP-hydrolysis or phosphate release and are not linked to loss of GDP.