Research & Design Phase Model Summary

Laconia High School SMART Team

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Recent Research Reveals Possible Dimer Structure of Human MiD51

PDB: 4NXU

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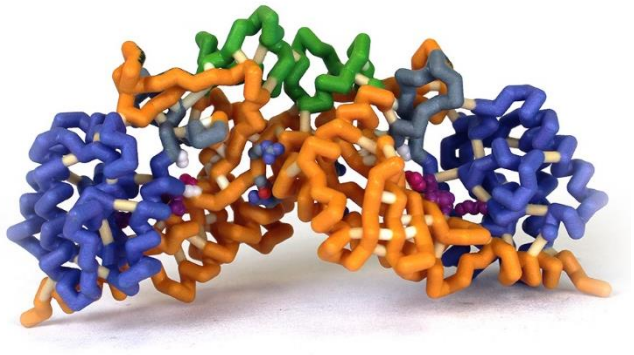

Format: Alpha carbon backbone

RP: Zcorp with plaster

Description: Disruption of Mitochondrial Dynamics Protein of 51 kDa (MiD51) has been linked to neurological diseases, such as Parkinson's, Alzheimer's, and Huntington's disease. MiD51 recruits Dynamin Related Protein 1 (Drp1) from the cytosol to bring about mitochondrial fission. MiD51 belongs to the nucleotidyltransferase fold superfamily of proteins. MiD51 also interacts with ligands ADP and GDP. MiD51 is a globular protein anchored on the mitochondrial outer membrane, and is organized into three domains; a disordered domain, an N-terminal domain containing a binding pocket for ADP/GDP and a recruitment region for Drp1, and a C-terminal domain. The soluble N- and C-terminal structured domains of MiD51 contain 11 alpha helices, 9 beta sheets, and 335 amino acid residues. Residues 215-251 make up the Drp1 recruitment region (beta 3, beta 4, alpha 4). ADP and GDP ligands are present, but research shows that Drp1 recruitment occurs in humans whether ligands are present or not. Human dimeric MiD51 has never been crystallized, but is believed to exist based on the dimeric crystal structure of the mouse homolog. This is further supported by SAXS data collection and modeling. Modeling suggests that R169, R182, and D183 are important for mediating dimer formation. The Laconia High School SMART (Students Modeling A Research Topic) Team modeled MiD51 using 3D printing technology to investigate structure-function relationships. MiD51 research is important because if the structure of the protein and its function of mitochondrial fission could be understood, it could possibly be used to prevent and treat neurological diseases in the future.

Specific Model Information:

Amino acid side chains involved:

- ARG 182, ASP 183, ARG 169 = CPK. Monomer-monomer interface residues.
- GLN 203 = Magenta. GDP binding.
- ARG 342, LYS 368, HIS 201, SER 189 = Purple. ADP binding.
- SER187, Ser340 = White. H bond with ADP and GDP.

Highlighted protein structures:

- C terminal domains are colored orange
- N terminal domains are colored cyan
- DRR is colored green
- Linker domain colored grey

Supporting Features:

- Struts are colored wheat
- H bonds colored Ivory

CBM SMART Teams Website:
http://cbm.msoe.edu/smartTeams/smartTeamsLocal.php