

Low Molecular Weight Phosphatases: Coevolved residues and a Mutation Database

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Abstract

The Low Molecular Weight Phosphatase fold protein family has importance in various eukaryotic and prokaryotic cellular signalling networks. Its proteins influence various diseases such as cancer, diabetes and tuberculosis. Many enzymatic functions are displayed by this protein family, the most important being the dephosphorylation of Tyrosines, Arginines, Ribulosamines and Erythrulosamines, and the reduction of the Arsenate ion to Arsenite. Multiple characterizations, structures and site-directed mutagenesis related to this protein family exist up to this date. In this work, we aimed to describe the biological functions related to the correlated and anticorrelated residue sets extracted from the Pfam database Multiple Sequence Alignment for this family. We found a clear pattern of residues related to the Tyrosine Phosphatase and Arsenate Reductase classes in the network and describe here new possible important positions to be explored in future experimental studies.

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