ESRF

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Shifts: 6	**Local contact(s)**: Dr. B.Shepard	

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Report:

The Crystal Structure of Diadenosine Tetraphosphate Hydrolase from *Caenorhabditis elegans* in Free and Binary Complex Forms

Structure **10 (4)** 589-600, 2002.

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Abstract

The crystal structure of *C. elegans* Ap_4A hydrolase has been determined for the free enzyme and a binary complex at 2.0 Å and 1.8 Å, respectively. Ap_4A hydrolase has a key role in regulating the intracellular Ap_4A levels and hence potentially the cellular response to metabolic stress and/or differentiation and apoptosis via the Ap_3A/Ap_4A ratio. The structures reveal that the enzyme has the mixed / fold of the Nudix family and also show how the enzyme binds and locates its substrate with respect to the catalytic machinery of the Nudix motif. These results suggest how the enzyme can catalyze the hydrolysis of a range of related dinucleoside tetraphosphate, but not triphosphate, compounds through precise orientation of key elements of the substrate.