

**Experiment title:**

Crystal structural analysis of Dhh1p, a DEAD-box helicase involved in mRNA decay

Experiment**number:**

MX-364

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Report:

The regulation of mRNA decay plays an important role in control of gene expression. Decapping is a key step in the mRNA decay pathway because it induces degradation of the mRNA, and thus it is subject to numerous control inputs. A crucial step in the decapping of eukaryotic mRNAs is the exiting of translation and the assembly of an mRNP state that targets the mRNA for decapping. Dhh1p, a member of the DEAD-box family of RNA helicase, has been found to function in moving mRNAs from translation to the non-translating pool of mRNAs, which are concentrated in specific subcellular sites of mRNA decapping and degradation referred to as P-bodies. In order to investigate the functional role of Dhh1 in mRNA decay, and how it interacts with RNA and utilizes energy of ATP hydrolysis to drive mRNAs from translation to non-translating state, we crystallized the yeast Dhh1p with truncations of the N- and C-terminal extensions.

Diffraction data were collected to 2.1 Å resolution on a 200*150*25 μm³ bromide derivative crystal. Crystals belong to space group P2₁ (a=48.21 Å, b=80.41 Å, c=54.82 Å, α=90°, β=100.57°, γ=90°) with one molecule per asymmetric unit. The structure was solved by MAD phasing and refined to an R-factor of 20% and a free R-factor of 23.4%. Functional characterization of Dhh1p is in progress.