Poster Presentation

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Crystal structure of human cytosolic aspartyl-tRNA synthetase

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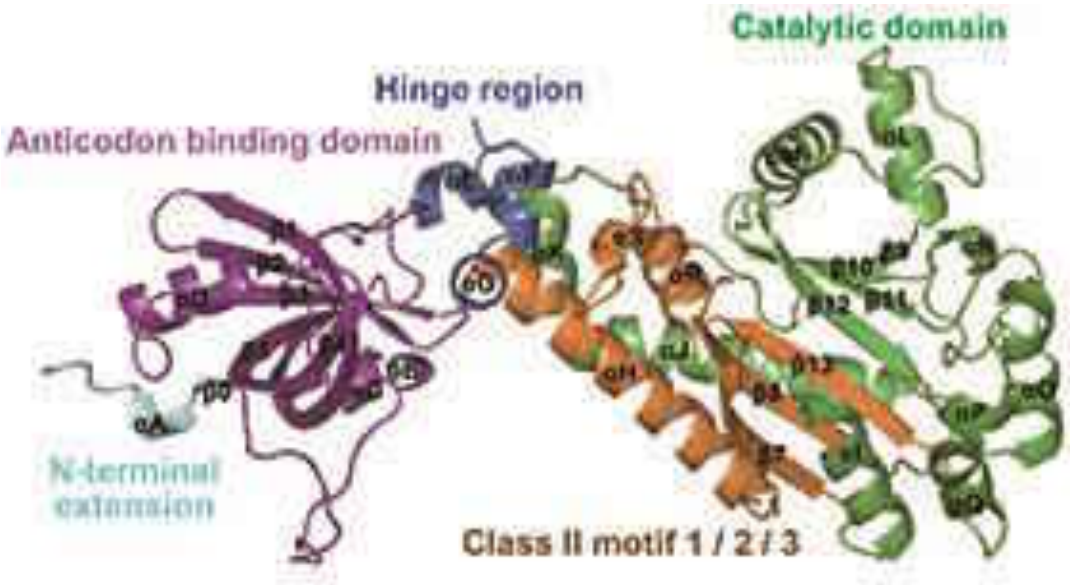
Human cytosolic aspartyl-tRNA synthetase (DRS) catalyzes the attachment of the amino acid aspartic acid to its cognate tRNA and it is a component of the multi-tRNA synthetase complex (MSC) which has been known to be involved in unexpected signaling pathways. Here, we report the crystal structure of DRS at 2.25 Å resolution. DRS is a homodimer with a dimer interface 3,750.5 Å² which comprises of 16.6% of the monomeric surface area. Our structure reveals the C-terminal end of the N-helix which is considered as a unique addition in DRS, and its conformation further supports the switching model of the N-helix for the transfer of tRNAAsp to elongation factor 1α. From our analyses of the crystal structure and post-translational modification of DRS, we suggest that the phosphorylation of Ser146 provokes the separation of DRS from the MSC and provides the binding site for an interaction partner with unforeseen functions.

[1] *KR. Kim, SH. Park, et al, Proteins, 2013, 81, 1840-6*



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