

## Publication

### A structural model for the DEAD box helicase YxiN in solution : localization of the RNA-binding domain

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DEAD box proteins consist of a common helicase core, formed by two globular RecA domains that are separated by a cleft. The helicase core acts as a nucleotide-dependent switch that alternates between open and closed conformations during the catalytic cycle of duplex separation, thereby providing basic helicase activity. Flanking domains can direct the helicase core to a specific RNA substrate by mediating high affinity or high specificity RNA binding. In addition, they may position RNA for the helicase core, or may directly contribute to unwinding. While structures of different helicase cores have been determined previously, little is known about the orientation of flanking domains relative to the helicase core. YxiN is a DEAD box protein that consists of a helicase core and a C-terminal RNA binding domain (RBD) that mediates specific binding to hairpin 92 in 23S rRNA. To provide a framework for understanding the functional cooperation of the YxiN helicase core and the RBD, we mapped the orientation of the RBD in single molecule FRET experiments. We present a model for the global conformation of YxiN in which the RBD lies above a slightly concave patch that is formed by flexible loops on the surface of the C-terminal RecA domain. The orientation of the RBD is different from the orientations of flanking domains in the *T. thermophilus* DEAD box protein Hera and in *S. cerevisiae* Mss116p, in-line with different functions of these DEAD box proteins and of their RBDs. Interestingly, the corresponding patch on the C-terminal RecA domain that is covered by the YxiN RBD is also part of the interface between the translation factors eIF4A and eIF4G. Possibly, this region constitutes an adaptable interface that generally allows for the interaction of the helicase core with additional domains or interacting factors.

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