

BIOLOGICAL CHEMISTRY

*Founded in 1877 by Felix Hoppe-Seyler as
Zeitschrift für Physiologische Chemie*

Felix Hoppe-Seyler (1825–1895) was a pioneer of biochemistry, remembered not only for his discovery of hemoglobin and his contributions to the chemical characterization of many other biological compounds and processes but also for having been the mentor of Friedrich Miescher and Albrecht Kossel. In his preface to the first issue of *Zeitschrift für Physiologische Chemie*, Felix Hoppe-Seyler coined the term *Biochemistry* ('Biochemie') for the then newly emerging discipline.



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COVER ILLUSTRATION

On the cover a superposition of the DEAD-box helicases YxiN and Hera on the C-terminal RecA domain (RecA_C) of their helicase cores is shown. The RNA-binding domain (RBD) of YxiN (blue, right) lies on the opposite side of the helicase core (orange/black) compared to the Hera RBD (cyan, left). In their review article on pp. 849–865 in this issue, Rudolph and Klostermeier summarize and discuss the mechanistic details of RNA binding and unwinding by DEAD-box proteins and the possible roles of ancillary domains or interaction partners in these processes.

The model of full-length YxiN bound to a ribosomal RNA fragment was generated by superposition of the RBDs of a model for full-length YxiN [Karow and Klostermeier, *J. Mol. Biol.* 402 (2010), pp. 629–637] and the crystal structure of the RBD in complex with RNA [Hardin et al., *J. Mol. Biol.* 402 (2010), pp. 412–427; PDB-ID 3moj]. The model for the full-length Hera dimer was constructed from the structures comprising (1) RecA_C and the dimerization domain [DD; Klostermeier and Rudolph, *Nucleic Acids Res.* 37 (2009), pp. 421–430; PDB-ID 3eas], (2) RecA_C, the DD, and the RBD [Rudolph and Klostermeier, *RNA* 15 (2009), pp. 1993–2001; PDB-ID 3i32], and (3) the RBD in complex with RNA [Steimer et al., *Nucleic Acids Res.* 41 (2013), pp. 6259–6272; PDB-ID 4i67], and (4) from a homology model for the closed helicase core, generated with the Vasa structure in complex with RNA and the non-hydrolyzable ATP analog ADPNP [Sengoku et al., *Cell* 125 (2006), pp. 287–300; PDB-ID 2db3] as a template. YxiN core: orange; YxiN RBD: blue; ribosomal RNA: yellow; Hera core: black, second protomer in gray, Hera RBD: cyan.



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