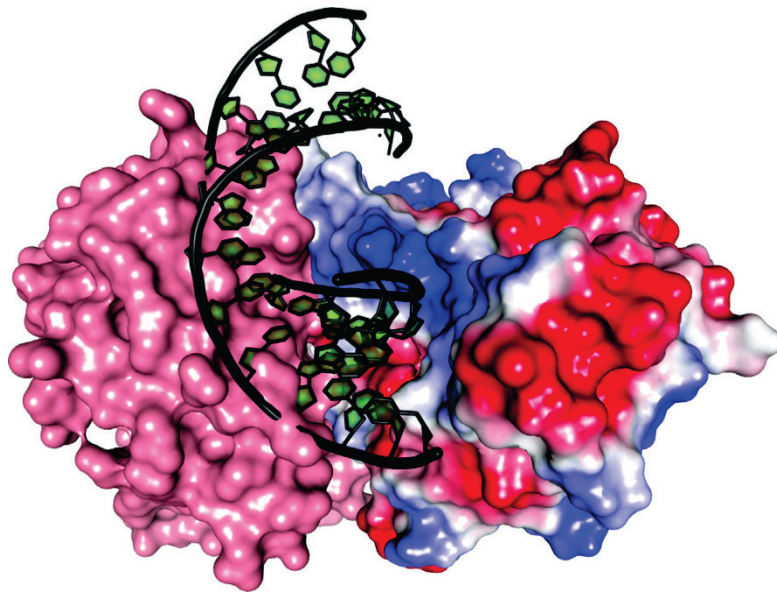


Supplementary Figures

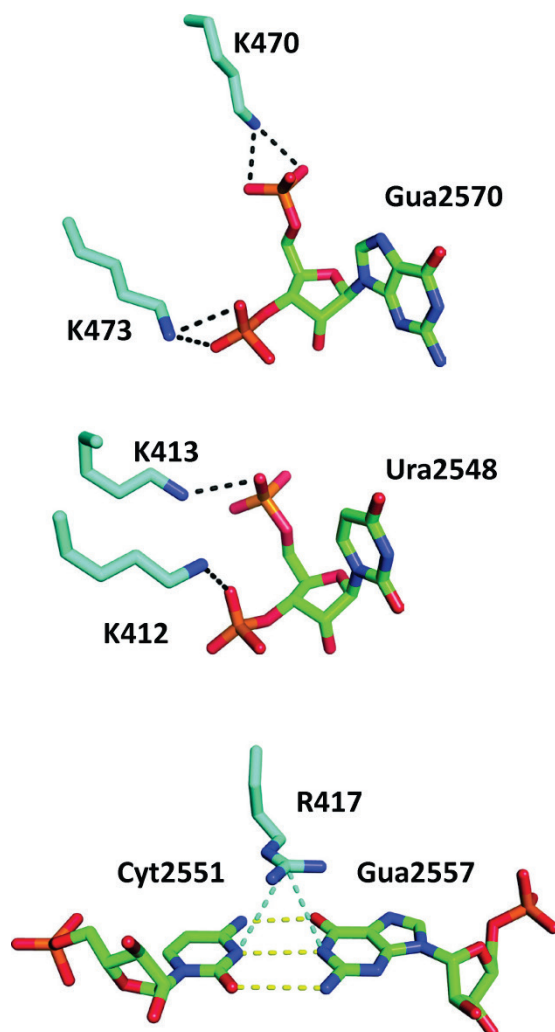
M.G. Rudolph & D. Klostermeier, When core competence is not enough: Functional interplay of the DEAD-box helicase core with ancillary domains and auxiliary factors in RNA binding and unwinding

Supplementary Figure 1: **Mss116 RecA_C bound to a 14mer RNA duplex.**



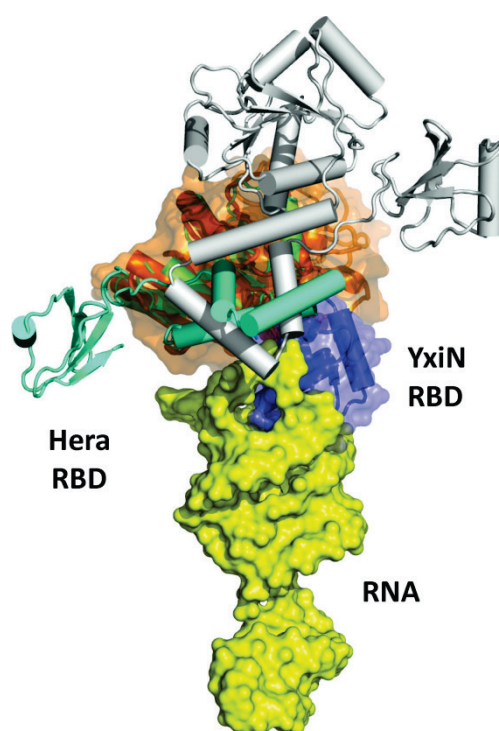
Structure of an Mss116 fragment comprising RecA_C and the CTE in complex with a 14 bp dsRNA (black) {Mallam, 2012 #3172} (PDB-ID 4db2). The RecA_C and the CTE are shown in surface representation, colored according to the electrostatic potential. The RNA duplex binds to a positively charged area of RecA_C. The position of RecA_N in the closed conformation of the helicase core is indicated in surface representation (salmon). The position of the dsRNA (black) is not compatible with the position of RecA_N, pointing to structural rearrangements of the RNA upon closure of the helicase core.

Supplementary Figure 2: **RNA binding to the YxiN RBD.**



Interactions of YxiN with individual nucleotides outside the loop of hairpin 92. Neither of the interactions is base-specific. Gua 2570 is located in the stem of helix 90, close to the bulge. Ura2548 is part of the stem of hairpin 92, and the Cyt2551-Gua2557 pair is the first base pair of helix 92, adjacent to the loop region. Hydrogen bonds are indicated as black and yellow dashed lines, van der Waals interactions as blue dashed lines.

Supplementary Figure 3: **Comparison of the RBD position relative to the core in YxiN and Hera.**



Superposition of the model for the YxiN/RNA complex (see Figure 4A, main text) and the structure of Hera (RecA_C, DD and RBD {Rudolph, 2009 #2241}, PDB-ID 3i32) on RecA_C. The RecA_C of the Hera protomer colored in cyan was used for the superposition. YxiN core: orange; YxiN RBD: blue; ribosomal RNA: yellow surface representation; Hera protomers: gray/cyan. The different positions of the YxiN and Hera RBDs relative to the helicase core are indicated.