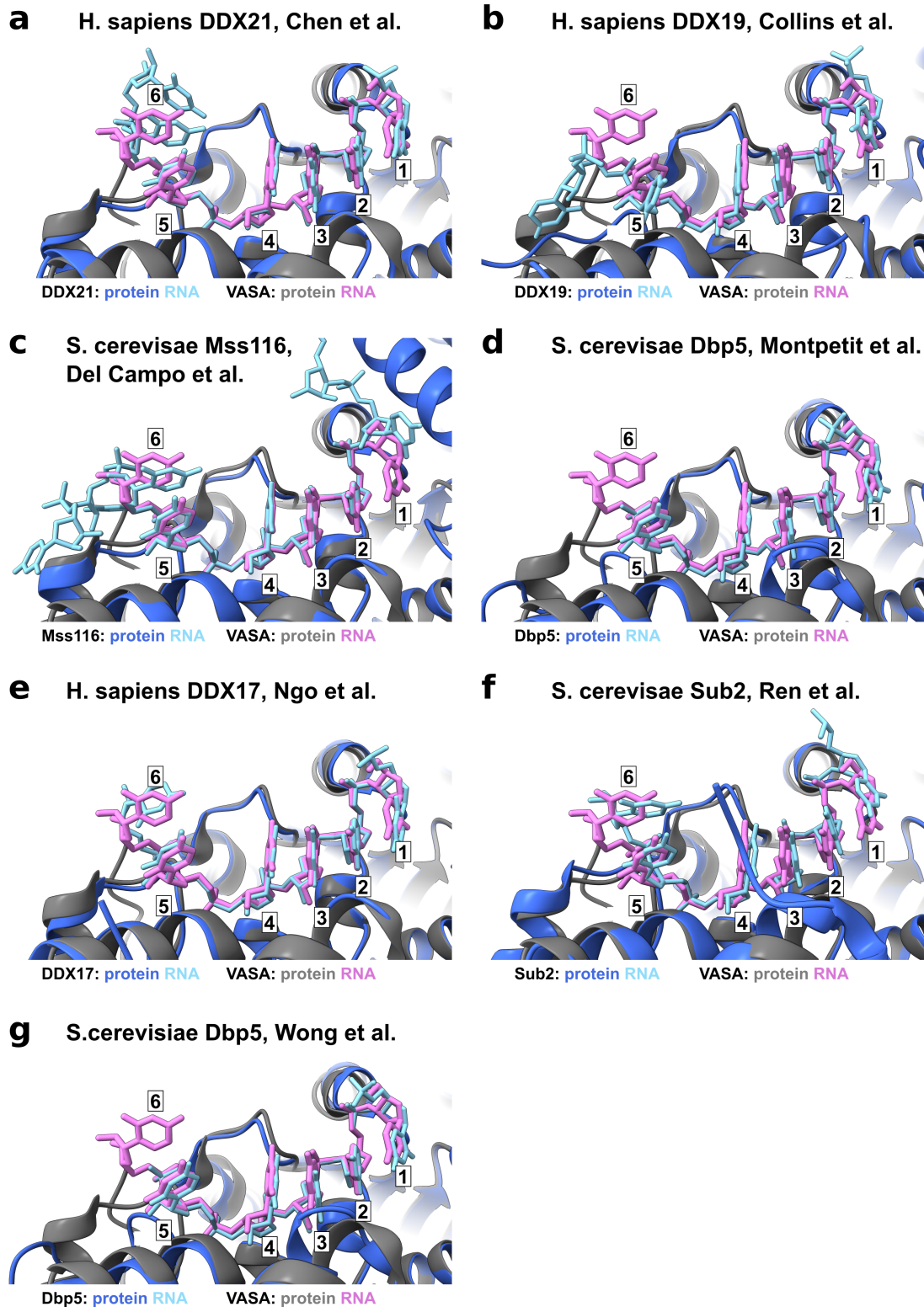




Supplementary Fig. 1: Published structures of ssRNA product-bound DEAD-box helicases in the closed-conformation reveal a highly conserved binding mode.

Close-up of the active site of the helicase core bound to ssRNA. Shown are comparisons between the structure of the DEAD-box helicase VASA from *D. melanogaster* with the structures of (a) *H. sapiens* DDX21 (Chen et al., 2020), (b) *H. sapiens* DDX19 (Collins et al., 2009), (c) *S. cerevisiae*

Mss116 (Del Campo and Lambowitz, 2009), (d) *S. cerevisiae* Dbp5 (Montpetit et al., 2011), (e) *H. sapiens* DDX17 (Ngo et al., 2019), (f) *S. cerevisiae* Sub2 (Ren et al., 2017) and *S. cerevisiae* Dbp5 (Wong et al., 2016). The VASA helicase and the bound ssRNA are shown in grey and pink. The other helicases and bound ssRNAs are colored dark and light blue. The nucleotides that interact with the active site are numbered 1-6. Basically identical conformations are observed for nt 1-5 and the phosphate group of nt 6, whereas the conformation of the ribose and base of nt 6 are less well conserved.