Supplemental material accompanying

THE DExD/H-BOX RNA HELICASE DDX19 IS REGULATED BY AN α-HELICAL SWITCH

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TABLE S1. DDX19 crystal structures: Data collection and refinement statistics.
Values for the highest resolution shell are shown in parentheses.

Structure	apo enzyme	RNA complex
Ligand	ADP	ADPNP
PDB entry	3EWS	3G0H
Beamline	BL14-2	ID-29
Wavelength (Å)	0.91841	0.97931
Space group	$P2_1$	$P2_12_12_1$
Cell dimensions		
a, *b*, *c* (Å)	81.6, 47.6, 124,7	41.6, 81.1, 124.7
β (°)	90.0, 95.4, 90.0	90.0, 90.0, 90.0
Resolution (Å)	20.0 - 2.7 (2.8-2.7)	30.0-2.7 (2.8-2.7)
R_{merge} §	0.067 (0.40)	0.145 (0.55)
I / (σI)	14.5 (4.3)	9.1 (2.5)
Completeness (%)	99.1 (99.5)	99.3 (99.7)
Redundancy	4.7 (4.9)	3.3 (3.2)
Refinement		
Resolution (Å)	19.9 – 2.7	29.6 – 2.7
R_{work} † / R_{free} ‡	0.188/0.260	0.220/0.275
No. atoms		
Protein	6428	3225
Ligands	54	163
Water	26	-
B-factors (Å^2)		
Protein	70.0	13.8
Ligands	46.5	26.5
Water	42.8	-
R.m.s deviations		
Bond lengths (Å)	0.004	0.007
Bond angles (°)	0.77	1.1
Ramachandran plot		
Favored (%)	96	96.8
Additionally allowed (%)	4	3.2

§ $R_{merge} = \Sigma_i | I_i - \langle I \rangle | / \Sigma \langle I \rangle$, where I is an individual intensity measurement and $\langle I \rangle$ is the average intensity for this reflection with summation over all data.
† R_{work} is defined as $\Sigma || F_{obs} | - | F_{calc} || / \Sigma | F_{obs} |$, where F_{obs} and F_{calc} are observed and calculated structure-factor amplitudes, respectively.
‡ R_{free} is the R factor for the test set (5-10 % of the data).

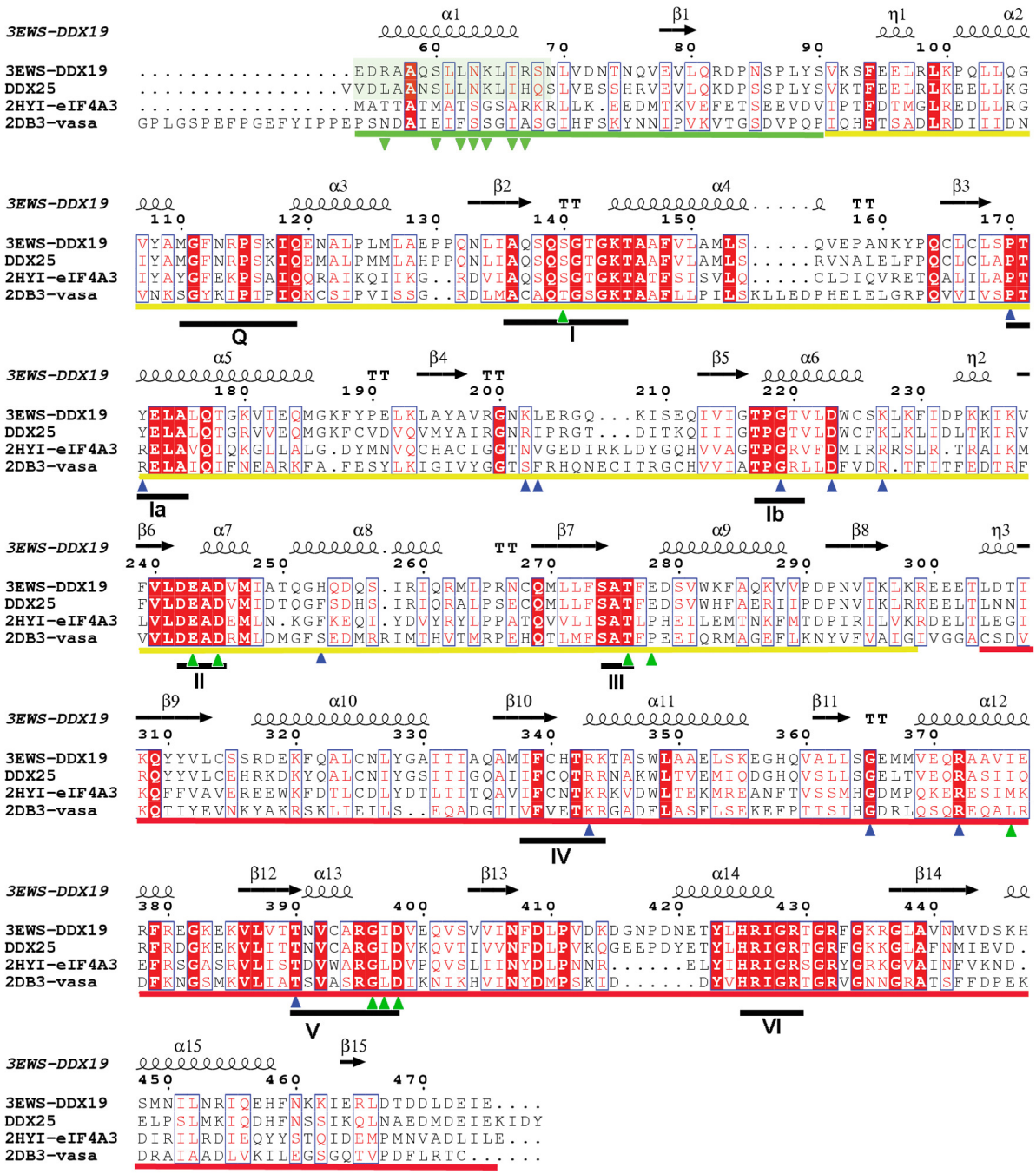

FIGURE S1. Comparison of DDX19 with other DEAD-box helicases. Sequence alignment of human DDX19, DDX25, DDX48, and *Drosophila* Vasa. The conserved domains and motifs are indicated below the alignment (1). The cleft insertion helix α1 is emphasized in light green. Residues that interact with the cleft-inserted helix are indicated by green upward arrowheads, and helix α1 residues that interact with those residues in other parts of the protein are indicated by green downward arrowheads. RNA interacting residues are indicated by blue arrowheads.

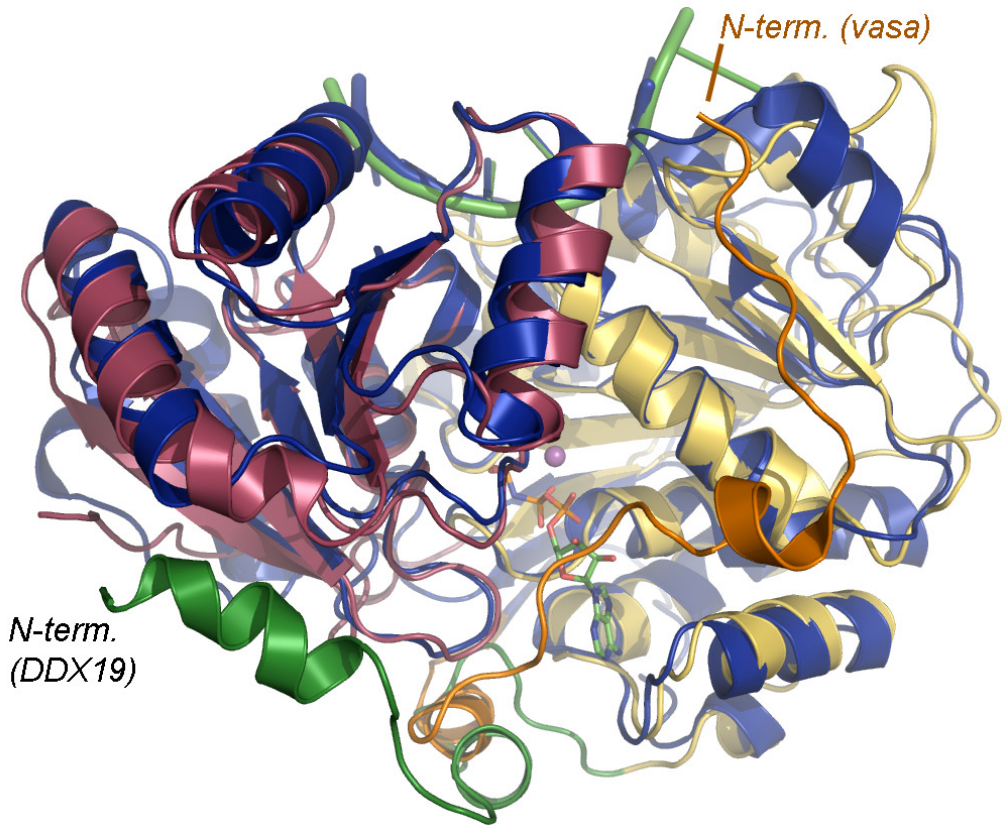

FIGURE S2. Superposition of the DDX19 (pdb entry 3G0H) and Vasa RNA complexes (2DB3). DDX19 is shown in red (conserved domain-1) and yellow (conserved domain-2) with the poly(U) ssRNA in green and the N-terminal helix (indicated) in green. Vasa is shown in blue, with the poly(U) ssRNA in blue and the N-terminal helix (indicated) in gold.

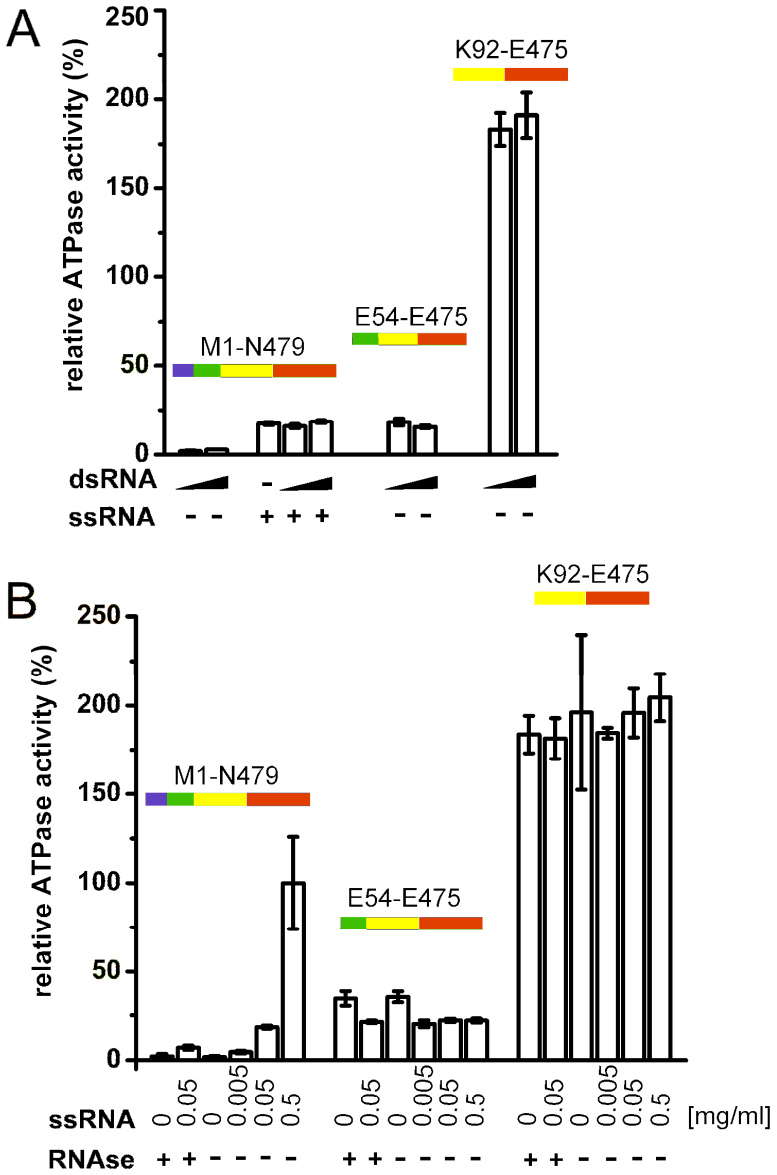

FIGURE S3. ATPase activities of DDX19 proteins used in this study. *A*, influence of double stranded RNA on the ATPase rates of DDX19. Left, full-length protein: Rates measured (from left to right) with 0.05 and 0.5 mg/ml dsRNA, and in the simultaneous presence of 0.05 mg/ml ssRNA and 0, 0.005 and 0.5 mg/ml dsRNA. Center, E^{54} – E^{475}: Rates measured (from left to right) with 0.05 and 0.5 mg/ml dsRNA. Right, K^{92} – E^{475}: Rates measured (from left to right) with 0.05 and 0.5 mg/ml dsRNA *B*, ATPase rates in the presence of varying amounts of ssRNA. Results are those shown in Fig. 2*B* of the main text, but with the addition of RNAse-treated controls. The concentration of ssRNA present is indicated for each column. As in the main text, all activities are relative to the value measured for full-length DDX19 in the presence of 0.5 mg/ml ssRNA (0.77 ± 0.2 min^{-1}).

References

1. Cordin, O., Banroques, J., Tanner, N. K., and Linder, P. (2006) *Gene* **367**, 17-37