

Supporting Information Text S6:  
AATPase supplementary figures

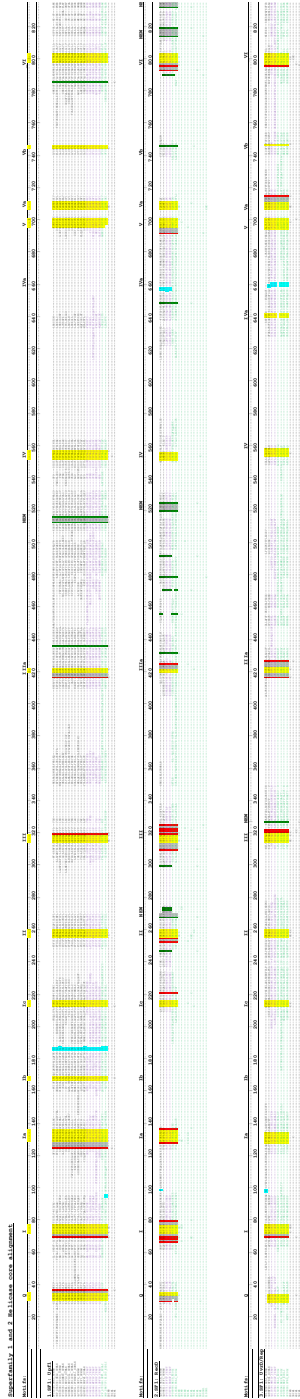


Figure 1: **AATPase: alignment and co-evolution of motifs in the SF1 family.**

Alignments and motif extensions for SF1 helicases families. Alignments are given in (Fairman-Williams et al. 2010). Each known motif is reported in yellow; red positions are co-evolved positions that are used to identify extensions of known motifs; green positions are co-evolved positions that lie distant from known motifs and that, when grouped together (with an allowed distance of  $\leq 5$  positions), form newly identified motifs. In grey, positions belonging to a new motif or to an extension of a known motif. Below each alignment, distinguished lines describe positions (denoted X) belonging to different co-evolving networks. Note that large insertions are removed from the alignment. These sections are marked by cyan highlights of the number of deleted residues.

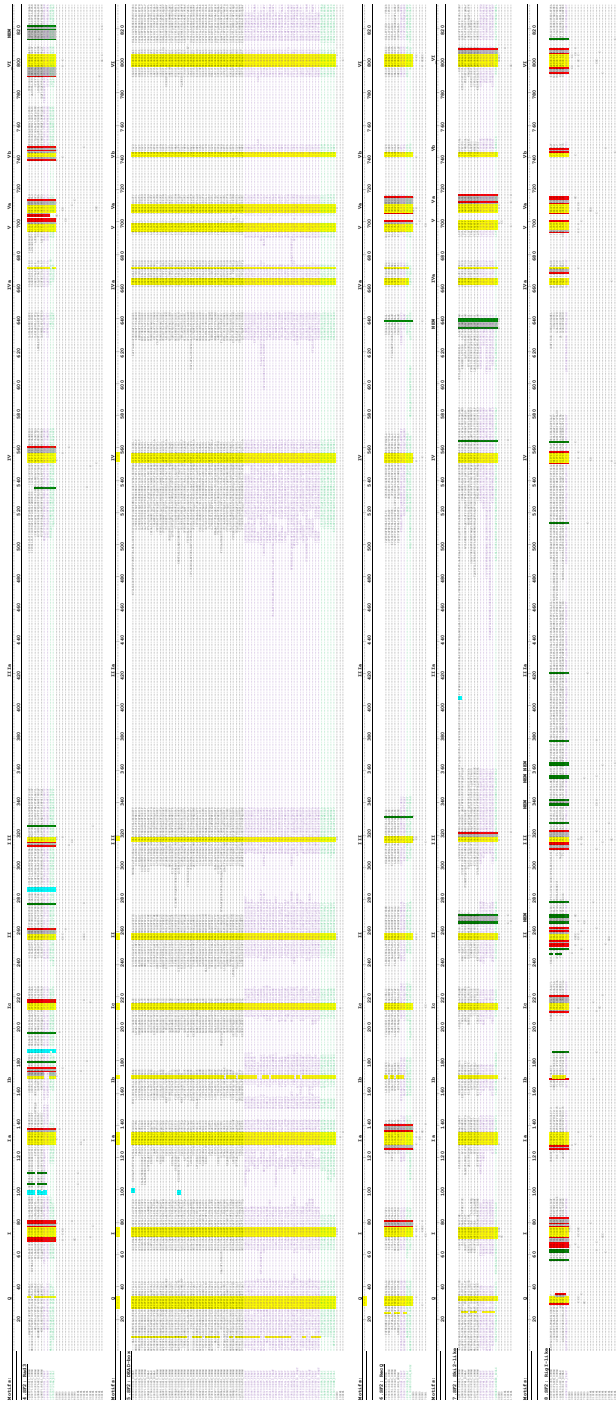


Figure 2: **AATPase: alignment and co-evolution of motifs in the SF2 family, part 1.** Alignments and motif extensions for SF2 helicases families. Legend as in Fig. 1-Text S6.

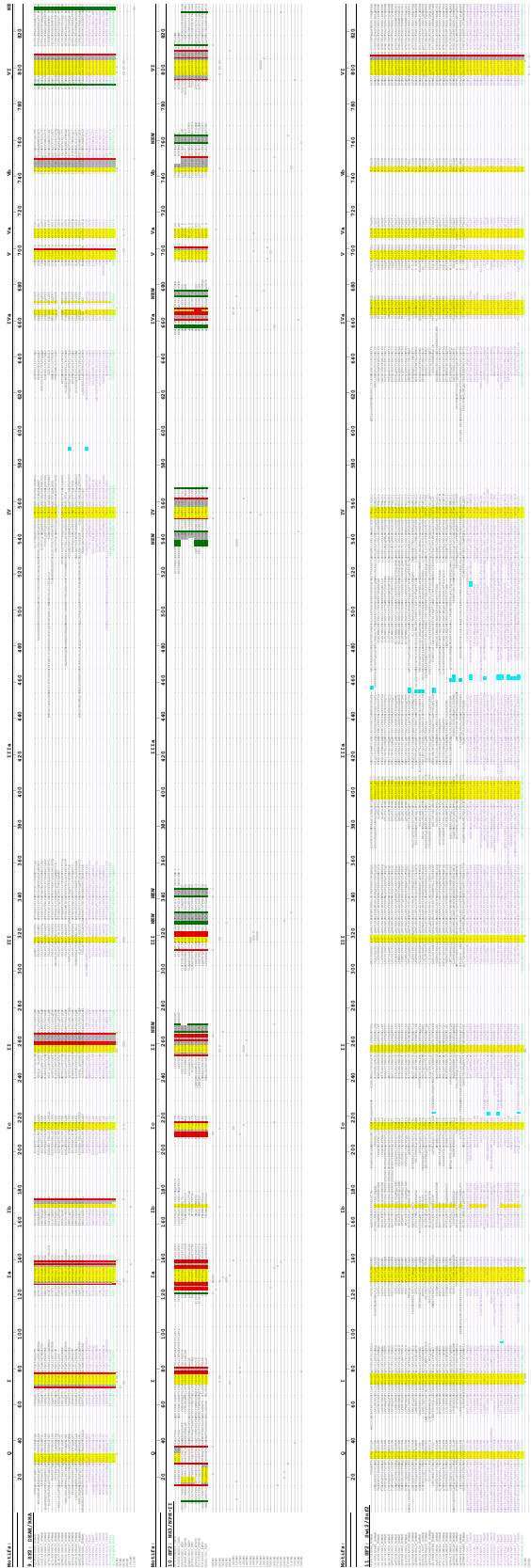


Figure 3: **AATPase: alignment and co-evolution of motifs in the SF2 family, part 2.**  
 Figure 2-Text S6, continued.

SF	Family	Q	I	IA	IB	IC	II
SF1	Upf1						
SF1	RecD						
SF1	UvrD/Rep						
SF2	Rad3						
SF2	DEAD-box						
SF2	RecQ						
SF2	Ski2-like						
SF2	Riq1-like						
SF2	DEAH/REA						
SF2	NS3-NPH-II						
SF2	Swi2/Snf2						

Figure 4: AATPase: logos of protein sequence motifs, part 1.

Extension of known motifs identified for SF1 and SF2 helicase families in (Fairman-Williams et al. 2010) and new motifs. Columns in the table correspond to motifs (the name of a known motif is reported on the top; NEW indicates that the motif is predicted by co-evolution signals) and rows correspond to distinguished families (class and family names are reported). Co-evolving residues are labelled by a star and extended residues by a square. Nine motifs are new. For motif localisation along the sequence, refer to Figs 2 and 3-Text S6. Logos are realized with the package WebLogo (Crooks GE, Hon G, Chandonia JM, Brenner SE, WebLogo: A sequence logo generator, *Genome Research*, 14:1188–1190, 2004).

SF	Family	NEW	III	NEW	NEW	NEW	IIIA	NEW
SF1	Upf1							
SF1	RecD							
SF1	UvrD/Rep							
SF2	Rad3							
SF2	DEAD-box							
SF2	RecQ							
SF2	Ski2-like							
SF2	Riq1-like							
SF2	DEAH/REA							
SF2	NS3-NPH-II							
SF2	Sm12/Smf2							

Figure 5: AATPase: logs of protein sequence motifs, part 2.

Figure 4-Text S6 continued.
























SF	Family	IV	NEW	IVA	NEW	V	VA
SF1	Upf1						
SF1	RecD						
SF1	UvrD/Rep						
SF2	Rad3						
SF2	DEAD-box						
SF2	RecQ						
SF2	SkI2-like						
SF2	RigI-like						
SF2	DEAH/REA						
SF2	NS3-NPH-III						
SF2	Swi2/Snf2						

Figure 6: AATPase: logs of protein sequence motifs, part 3.

Figure 4-Text S6 continued.

SF	Family	VB	NEW	VI	NEW	NEW
SF1	Upf1					
SF1	RecD					
SF1	UvrD/Rep					
SF2	Rad3					
SF2	DEAD-box					
SF2	RecQ					
SF2	Ski2-like					
SF2	RigI-like					
SF2	DEAH/REA					
SF2	NS3-NPH-II					
SF2	Swi2/Snf2					

Figure 7: AATPase: logos of protein sequence motifs, part 4.

Figure 4-Text S6 continued.