

**Table S1. Cues Influencing the Regulation of Snf2-Related ATPases**

<b>Substrate</b>	<b>Example</b>	<b>References</b>
Transcriptional activation domains	The Swi1 and Snf5 subunits of SWI/SNF interact with acidic transcriptional activation domains. Similarly, steroid hormone receptors with human SWI/SNF.	(Burd and Archer, 2013; Prochasson et al., 2003; Yudkovsky et al., 1999)
Basal transcription factors	Mot1 ATPases include HEAT repeats directing specificity to TBP.	(Wollmann et al., 2011)
RNA Polymerase elongation factors	Chd1 interacts with the Rtf1 subunit of the Paf1 elongation complex.	(Simic et al., 2003)
Transcriptional repressors	The yeast Isw2 complex interacts with the repressor Ume6.	(Goldmark et al., 2000)
Histones	The activity of ISWI enzymes is regulated by an epitope in the histone H4 tail.	(Hamiche et al., 2001)
Post-translational modifications	In many cases folds with the potential to recognise histone modifications are present e.g. Bromo, Chromo, PHD, CUE, Macro domains.	(Clapier and Cairns, 2009)
Histone variants	The Swc2 and Swr1 subunits of the Swr1 complex interact specifically with H2AZ-H2B histone dimers.	(Wu et al., 2009)
Histone chaperones	The association of the ATRX complex with the histone chaperone DAAX confers specificity for H3.3.	(Law et al., 2010; Lewis et al., 2010)
DNA	The RSC3 subunit of the yeast RSC complex shows specificity in its binding to DNA. Non specific DNA binding domains within other remodeling enzymes may direct them to DNA adjacent to nucleosomes.	(Badis et al., 2008)
DNA structure	The HARP2 domains of SMARCAL1 target this enzyme to branched DNA structures.	(Betous et al., 2012)

## Supplemental References

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