Journal of Biomolecular NMR (2006) 36:5

Letter to the Editor

NMR assignment of the SRI domain of human Set2/HYPB

DOI 10.1007/s10858-005-4690-8

The Set2 histone methyltransferase from *Saccharomyces cerevisiae* binds the phospho-CTD of elongating RNA polymerase II during transcription elongation via a novel Set2-Rpb1-interacting (SRI) domain located at its C-terminus (Kizer et al., 2005). Deletion of the SRI domain disrupts histone H3 K36 methylation *in vivo*, highlighting the important role of the SRI domain in coupling histone methylation to transcription elongation. The SRI domain binds specifically to Ser2 and Ser5 doubly phosphorylated CTDs with a minimum of two hepta-peptide repeats; it is unrelated to any previously characterized phosphoCTD binding domains, and is uniquely conserved within the Set2 family of methyltransferases, including the human ortholog (hSet2) – the huntingtin yeast partner B (HYPB) protein (Faber et al., 1998). Here we report the near complete resonance assignment of the SRI domain of hSet2/HYPB. The majority of the backbone resonances, except for the N-terminal three residues and T50, and 94% of the sidechain resonances were assigned. BMRB deposit with accession number 6834.

References: Faber et al. (1998) *Hum. Mol. Genet.*, **7**, 1463–1474; Kizer et al. (2005) *Mol. Cell Biol.*, **25**, 3305–3316

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