

Deciphering the molecular mechanisms of chromatin recognition by ATAD2B

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Preliminary Results:

Figure 1. Analytical SEC elution profile full-length ATAD2B. Overlay of absorbance traces (A280) from ATAD2B, GST-ATAD2B, and protein standards mix.

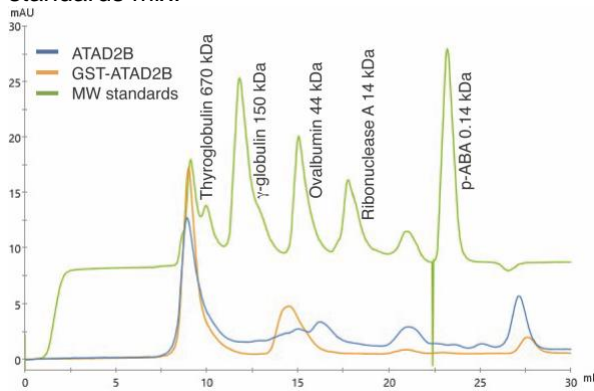


Figure 2. Pull-down assays with GST-ATAD2B full-length protein and acetylated histone H4. SDS-PAGE gel of GST-ATAD2B protein (MW 149 kDa, top arrow) bound to Glutathione Agarose and incubated with the purified recombinant *H. sapiens* histone H4 acetylated at lysine 5, 8, 12, and 16 (H4Kac, MW~11 kDa). Controls: histone H3, histone H4, and GST-ATAD2B alone.

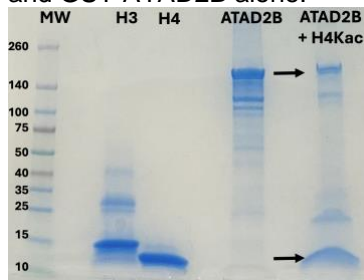


Figure 3. CryoEM images taken of ATAD2B on a 300 kV TFS Titan Krios at the NCCAT. A. A raw micrograph of full-length GST-ATAD2B. B. Representative 2D class averages of the GST-ATAD2B complex processed with CryoSPARC.

