

Preliminary Results:

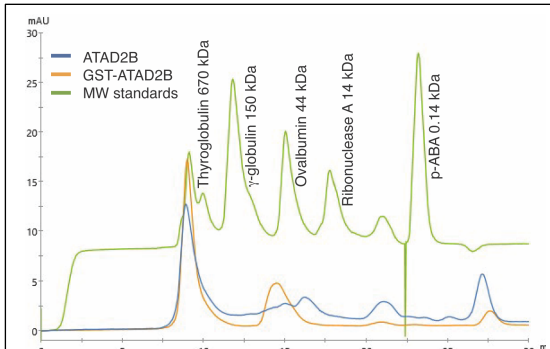


Figure 1. Analytical SEC elution profile of full-length ATAD2B. Overlay of absorbance traces (A280) from ATAD2B, GST-ATAD2B, and protein standards mix.

Figure 2. Pull-down assays with GST-ATAD2B full-length protein and histone H3-H4 tetramer. SDS-PAGE gel of GST-ATAD2B protein (MW 149 kDa, top arrow) bound to Glutathione Agarose and incubated with the purified recombinant *X. laevis* histone H3-H4 tetramer (MW 15.3 and 11.2 kDa).

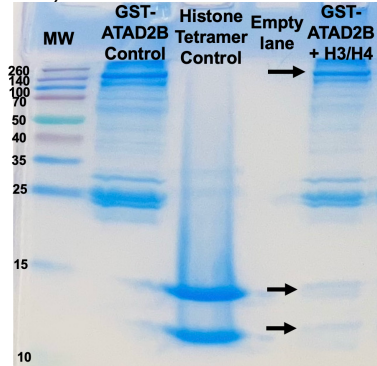


Figure 3. Cryo-EM images taken of ATAD2B on a 300 kV TFS Titan Krios at the NCCAT. A. A raw micrograph of full-length GST-ATAD2B. B. Representative 2D class averages of the GST-ATAD2B complex processed with CryoSPARC.

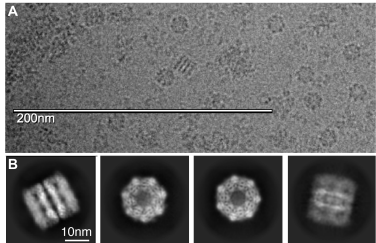


Figure 4. dCypher nucleosome binding assay of PfBDP1 with recombinant nucleosome core particles (NCPs) containing unmodified or acetylated H4 histones.

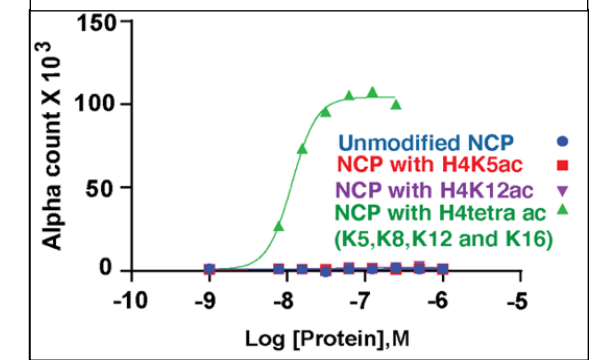


Table 1. Binding affinities of full-length PfBDP1 and PfBDP1-BRDs with histone ligands measured by ITC.

Histone Peptide (1-24)	PfBDP1 Full length (1-488) K_D (μ M)	PfBDP1-BRD (303-488) K_D (μ M)	PfBDP1-BRD (333-456) K_D (μ M)
Unmodified H4	No binding	No binding	No binding
H4K5acK8ac	100 \pm 5.30	1510 \pm 168	No binding
H4K5acK12ac	214 \pm 14.8	621 \pm 28.3	No binding
H4K5acK8acK12acK16ac	48.8 \pm 3.63	173 \pm 11.3	No binding

Figure 5. (A) SDS-PAGE gel of purified full-length PfBDP1. (B) Analytical SEC of full-length PfBDP1 with protein standards.

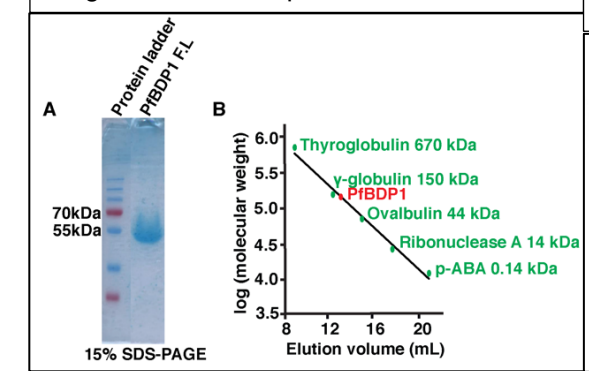


Figure 6. SDS-PAGE gel of the purified GST-CECR2 protein (residues 4-538).

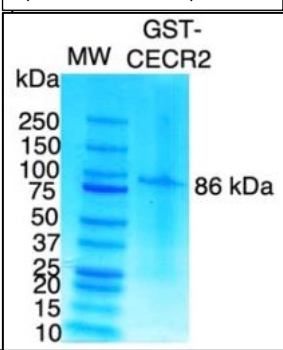


Figure 7. dCypher nucleosome binding assay of the CECR2 bromodomain with recombinant nucleosome core particles (NCPs) containing unmodified or acetylated H4 histones.

