

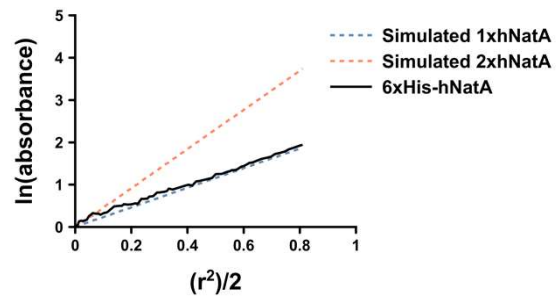
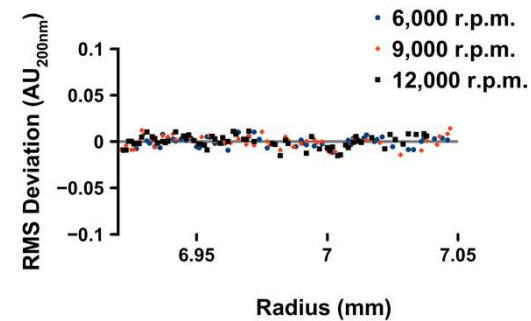
A**B**

Figure S1, Related to Figure 1. Sedimentation Equilibrium of human NatA.

(A) Log plot of sedimentation equilibrium experiments a sedimentation experiment showing theoretical monomer (blue) and theoretical dimer (red) slopes of hNatA ($OD_{A280}=0.8$) at 12,000 rpm (black).

(B) The corresponding residuals for all three speeds associated with A.

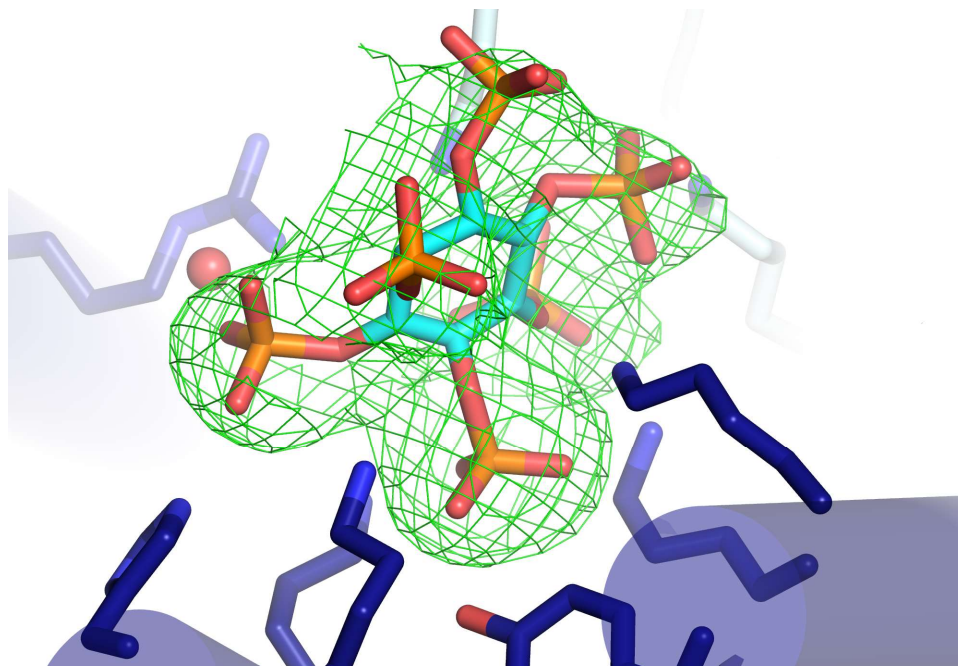


Figure S2, Related to Figure 1. IP₆ F_o-F_c Map.
Human NatA-bound IP₆ density contoured to 3.5σ (shown in green).

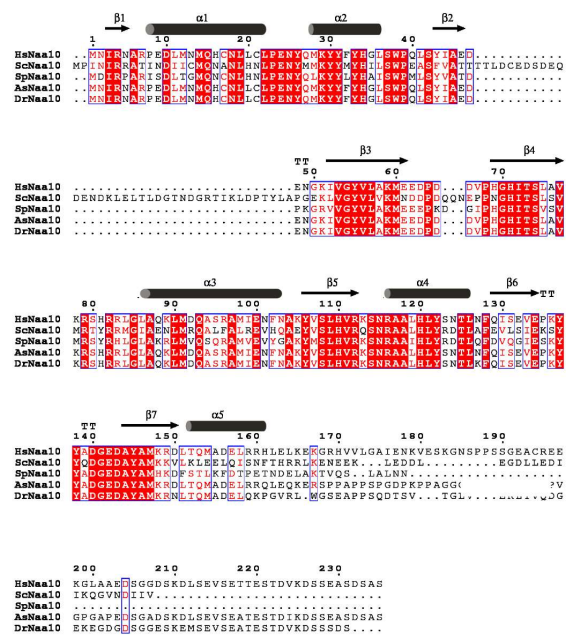


Figure S4, Related to Figure 1. Alignment of Naa10 Homologues. Sequence alignment of Naa10 homologues from *H. sapiens* (Hs); *S. cerevisiae* (Sc); *S. pombe* (Sp); *A. sinensis* (As); and *D. rerio* subunit b (Dr). The dashed line indicates the truncation construct used for all experimental studies.

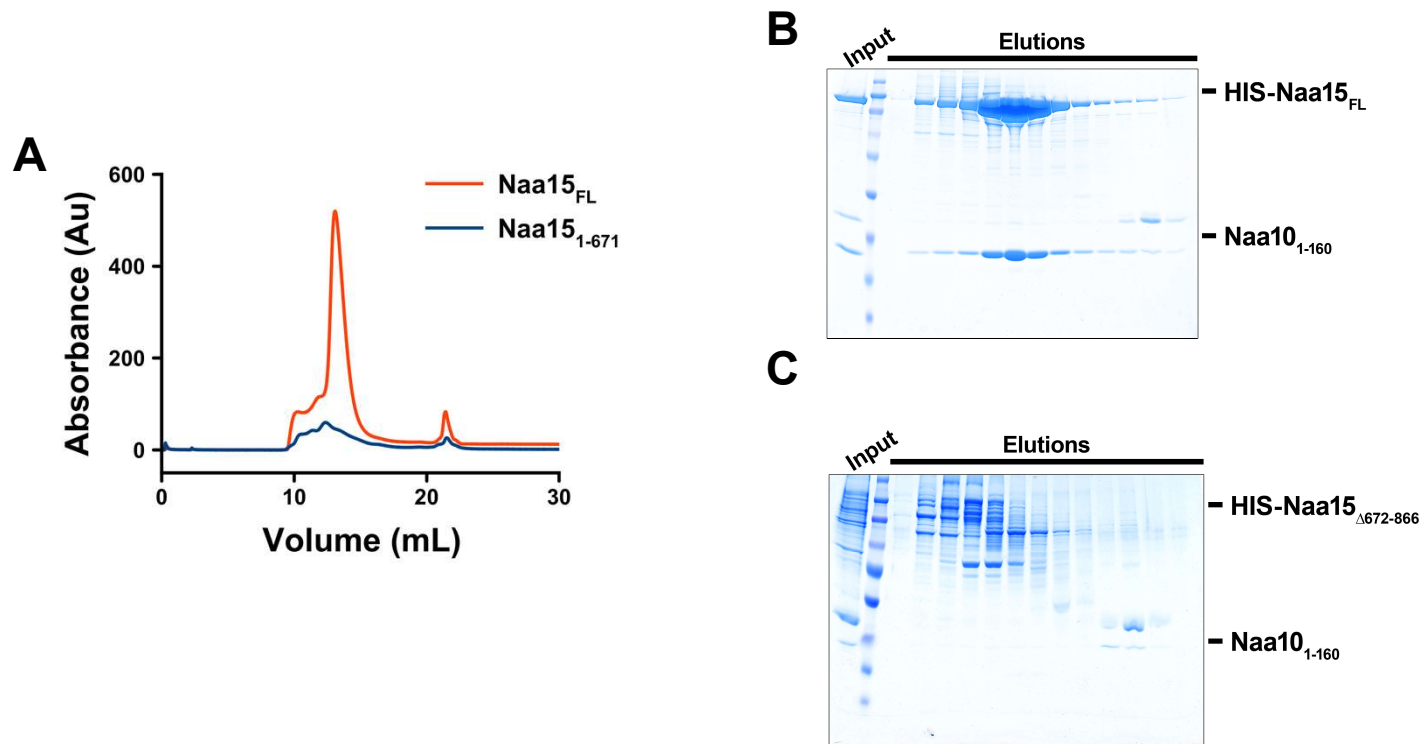


Figure S5, Related to Figure 1. C-terminal Truncation of Naa15 Abrogates NatA Binary Complex Formation.

(A) S200 gel filtration chromatogram.

(B) Corresponding SDS-PAGE gel to the trace of HIS-Naa15_{FL}/Naa10₁₋₁₆₀ complex (red) for A.

(C) Corresponding SDS-PAGE gel to the trace of HIS-Naa15_{Δ672-866}/Naa10₁₋₁₆₀ complex (blue) for A.