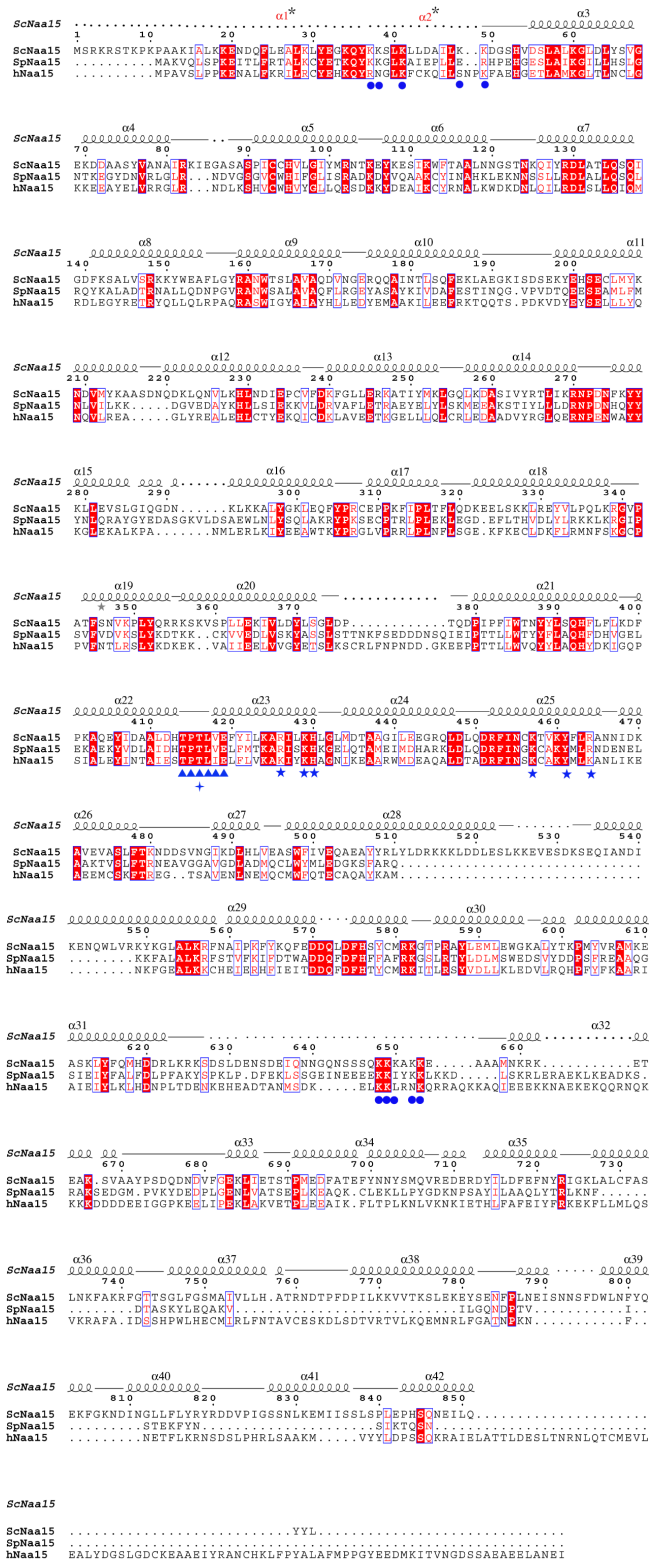


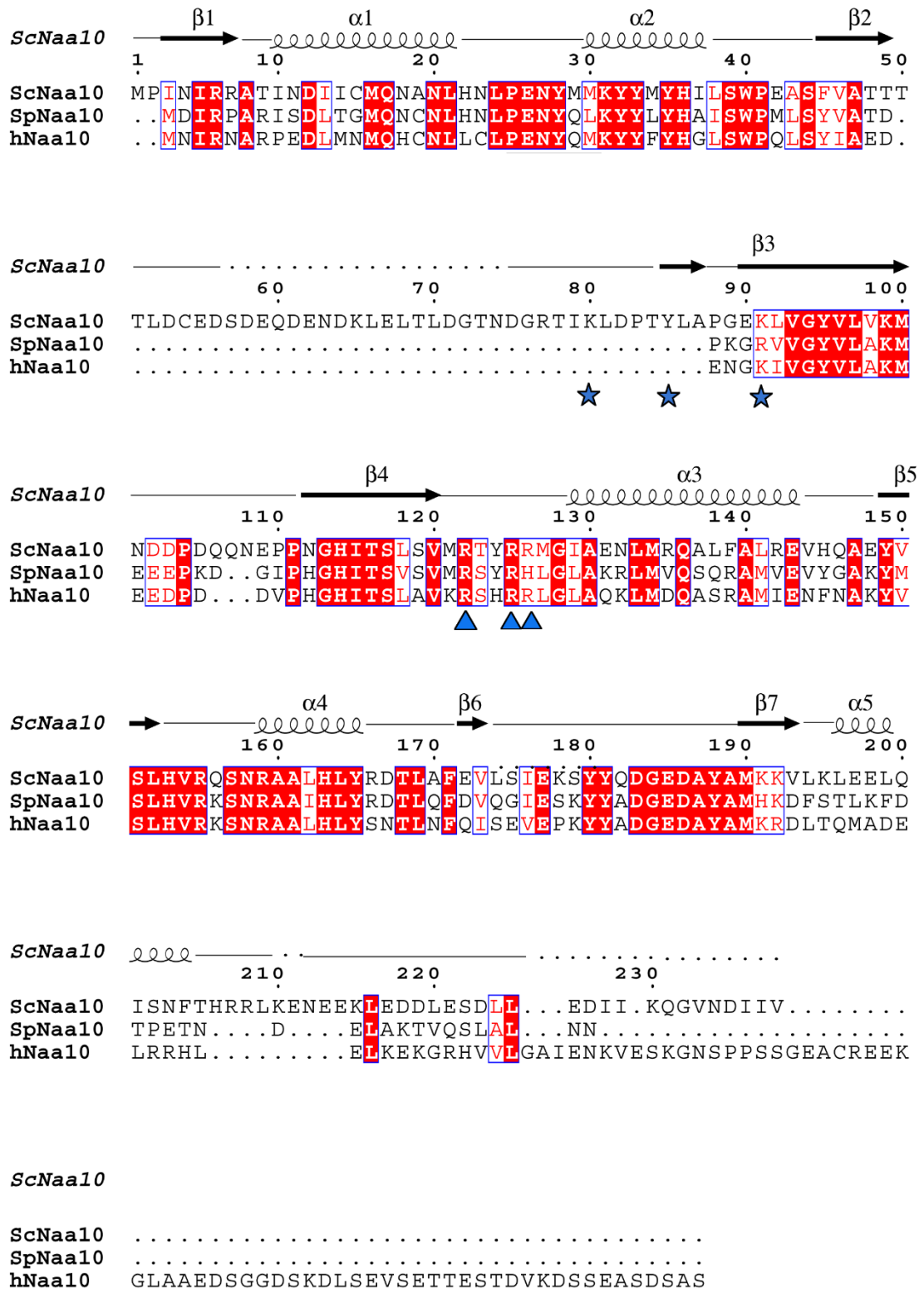
## **Supplemental Information**

### **Structure and mechanism of acetylation by the N-terminal dual enzyme NatA/Naa50 complex**

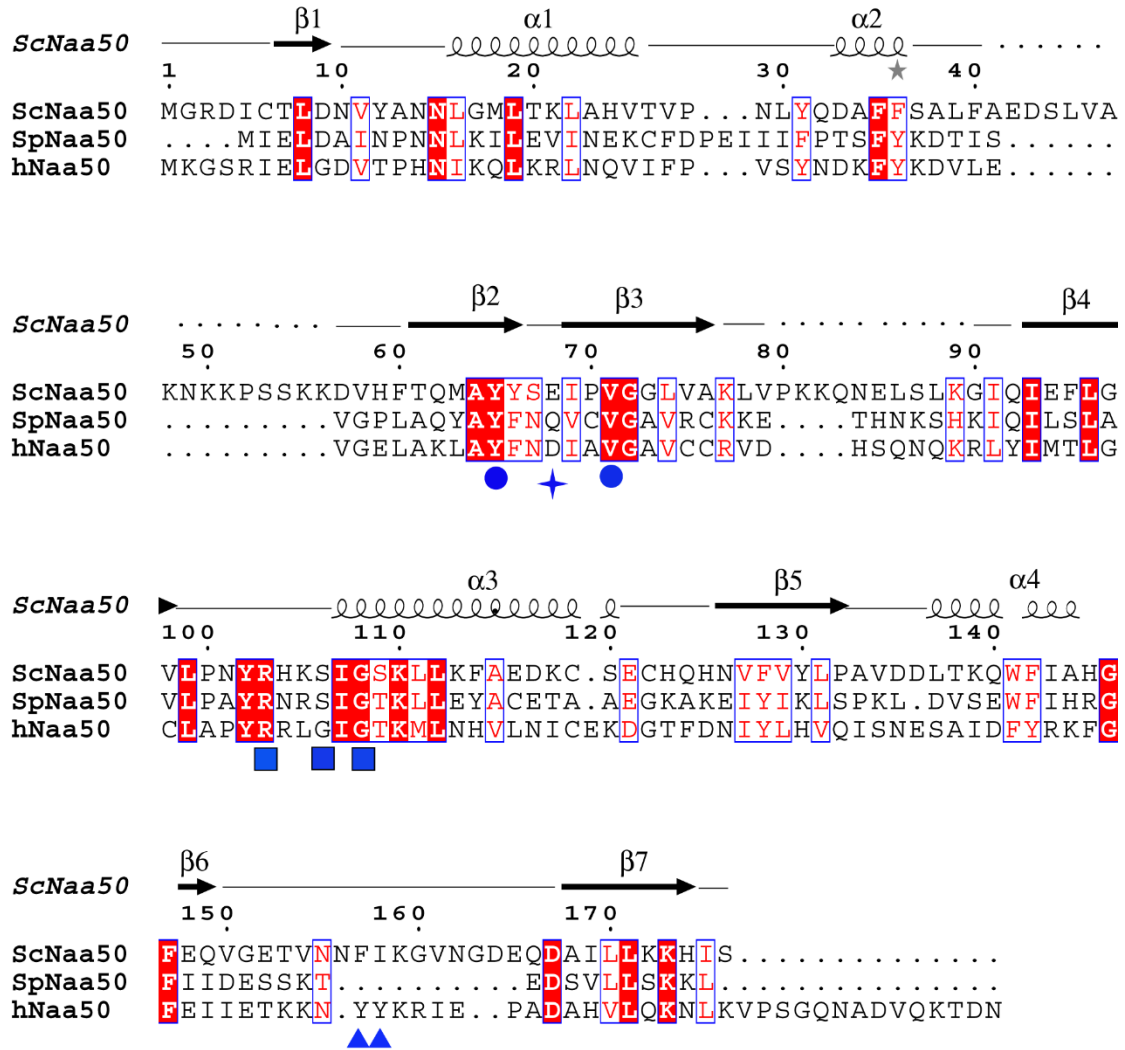
Sunbin Deng, Robert S. Magin, Xuepeng Wei, Buyan Pan, E. James Petersson, Ronen Marmorstein



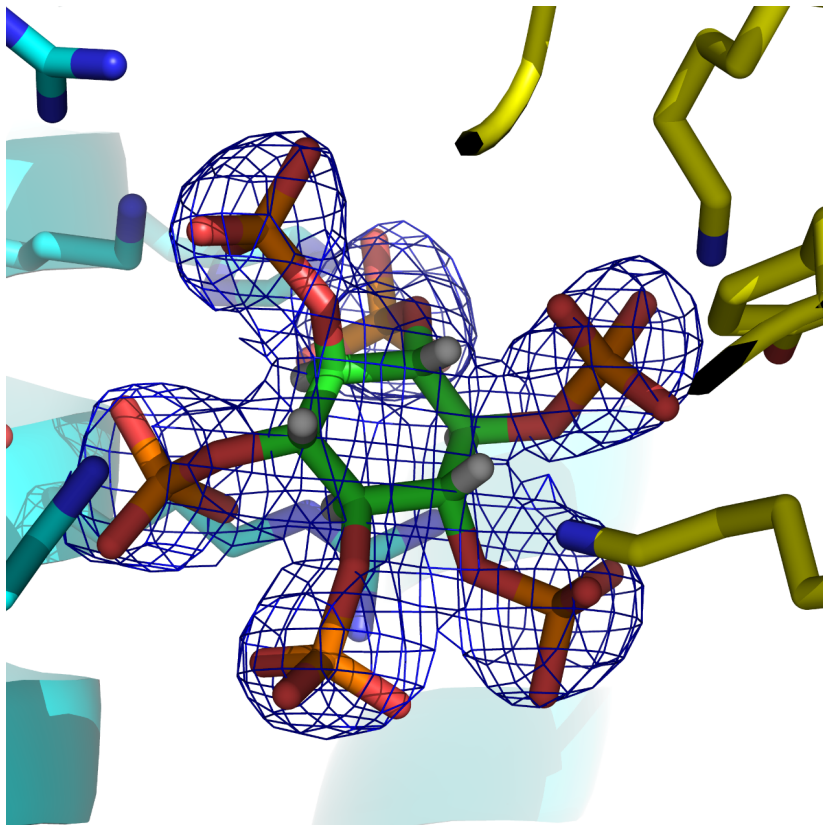
**Figure S1. Related to Figure 2.** Sequence alignment of Naa15 homologues from *S. cerevisiae* (Sc), *S. pombe* (Sp) and *H. sapiens* (h). ★, threonine residue in TY mutants; ▲, TPTLXE motif for Naa50 binding; ★, residues binding IP6. ●, residues involving in ribosome association. The dotted lines indicate regions disordered and not resolved



**Figure S2. Related to Figure 2.** Sequence alignment of Naa10 homologues from *S. cerevisiae* (Sc), *S. pombe* (Sp) and *H. sapiens* (h). ▲, residues contacting Naa50; ★, residues binding IP6.



**Figure S3. Related to Figure 2.** Sequence alignment of Naa50 homologues from *S. cerevisiae* (Sc), *S. pombe* (Sp) and *H. sapiens* (h). ■, potential acetyl CoA binding motif; ●, residues involving NatA binding. ▲, YY motif in NATs for substrates binding



**Figure S4. Related to Figure 2C.** IP<sub>6</sub>2Fo-Fc electron density map of Naa50-bound to IP<sub>6</sub>. The IP<sub>6</sub> electron density is contoured at 3.0  $\sigma$  (shown in blue).