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Supporting information for article:

**Structural and functional investigation of the human snRNP
assembly factor AAR2 in complex with the RNase H-like domain of
PRPF8**

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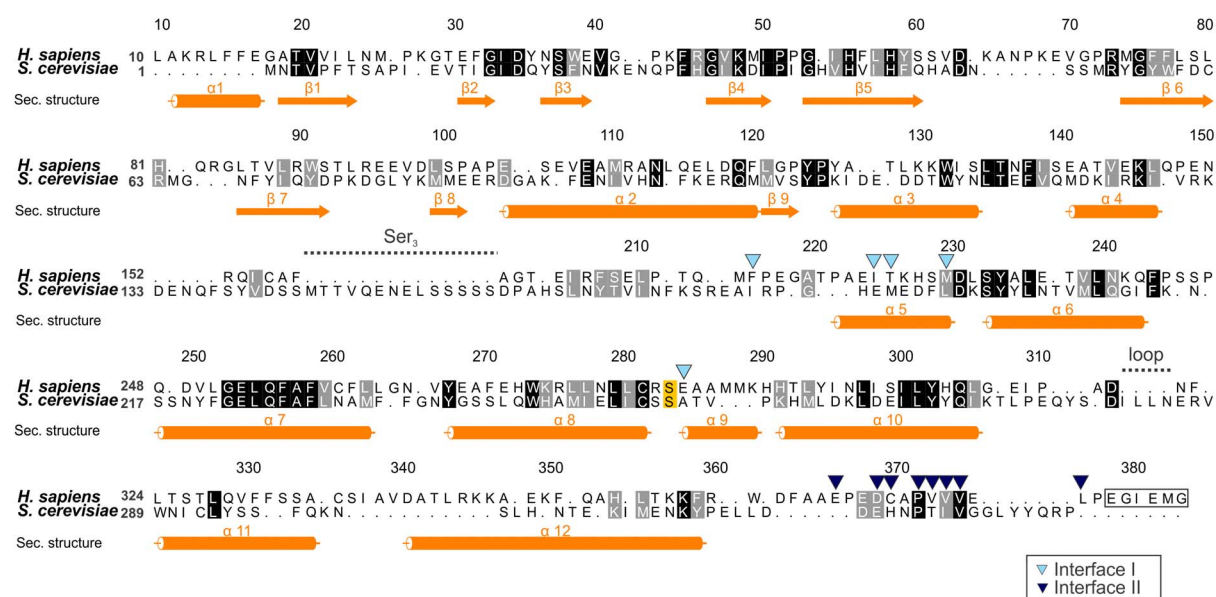


Figure S1 Structure-based alignment of yeast Aarp2 and structured parts of human AAR2. The alignment is based on separate superposition of the Aar2p and AAR2 NTDs, CTDs and C-terminal tails. The alignment was prepared with Chimera¹ and shaded with ALSCRIPT². Identical and similar residues are indicated by black and gray backgrounds, respectively. The numbering above the alignment refers to human AAR2. Secondary structure elements of AAR2^{Δloop} in the AAR2^{Δloop}-PRPF8^{RH} complex structure analyzed with DSSP³ are shown below the alignment. The first ten unstructured residues of AAR2 are not shown in the alignment. Dashed lines indicate residues of AAR2 (not included in the alignment) that were replaced by three serine residues (Ser₃) in AAR2^{Δloop} or residues 286-304 that lacked electron density, also not shown in the alignment (loop). Light blue (Interface I) and dark blue (Interface II) triangles above the alignment indicate residues of AAR2^{Δloop} in contact with PRPF8^{RH}. The last six residues of AAR2^{Δloop} (boxed) also lacked electron density and were not modeled.

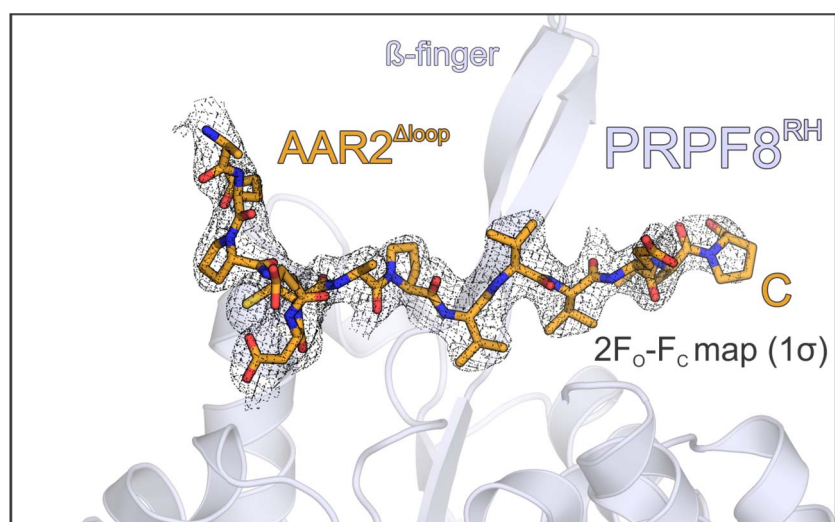


Figure S2 Electron density of the AAR2 C-terminal peptide. 2F_o-F_c electron density around the human AAR2^{Δloop} C-terminal tail (sticks) contoured at the 1 σ level.

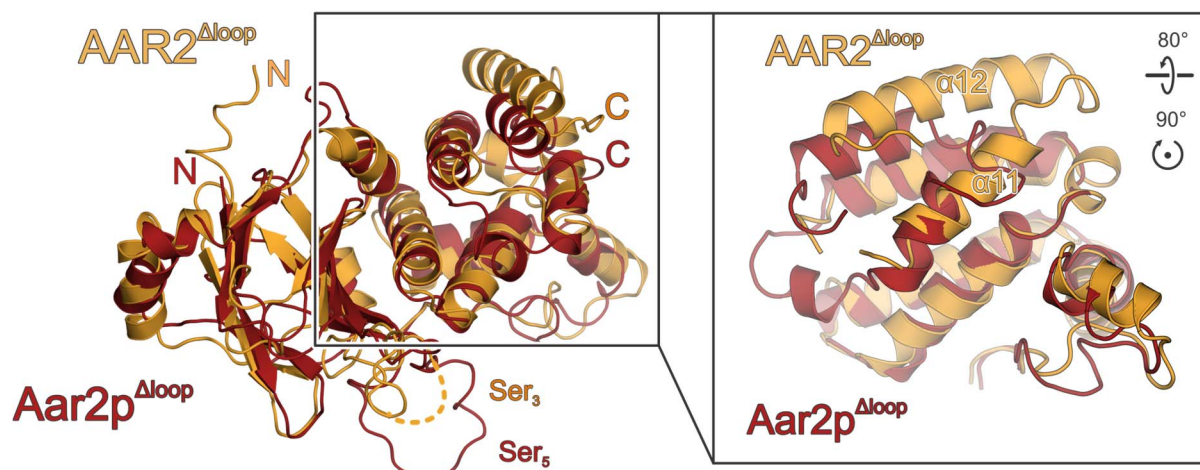


Figure S3 Supplementary Figure S3. Comparison of yeast Aar2p^{Δloop} and human AAR2^{Δloop}.

Superposition of yeast Aar2p^{Δloop} (PDB ID 4ILG) ⁴ and human AAR2^{Δloop}, aligned by their CTDs.

Inset, close-up view of the C-terminal domains showing the extended helices α11 and α12 of AAR2.

SUPPLEMENTARY REFERENCES

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2. Barton, G.J. (1993). Alscript: A tool to format multiple sequence alignments. *Protein Eng. Des. Sel.* 6, 37–40.
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