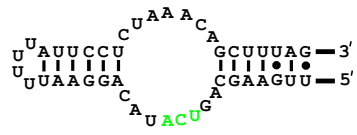
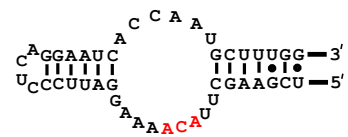
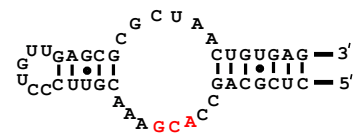
S. cerevisiae RNase MRP



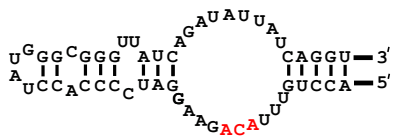
S. pombe RNase MRP



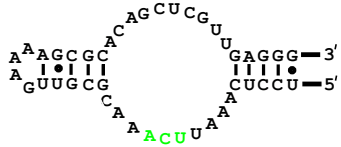
S.kluyveri RNase MRP



C. elegans RNase MRP

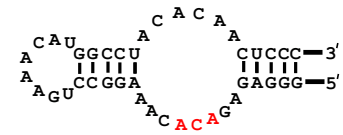


S. cerevisiae RNase P

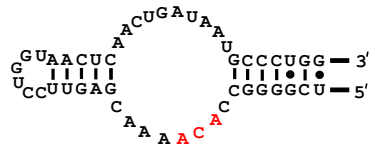


S. pombe RNase P

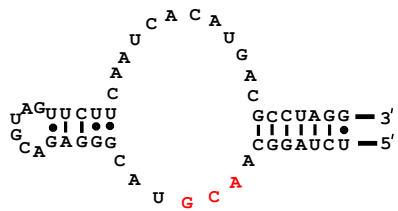
S.kluyveri RNase P



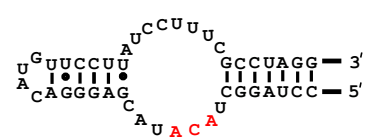
C. elegans RNase P



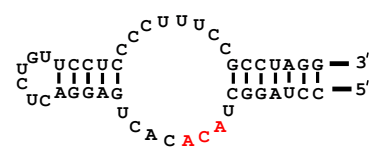
D. melanogaster RNase MRP



X. laevis RNase MRP

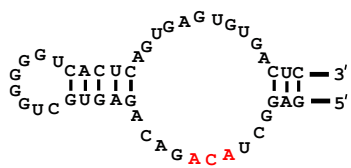


mouse RNase MRP

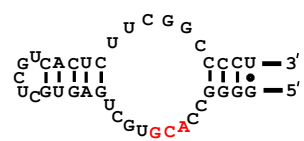


human RNase MRP

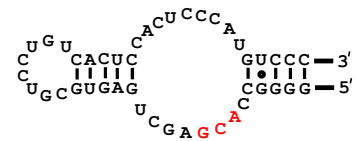
D. melanogaster RNase P



X. laevis RNase P

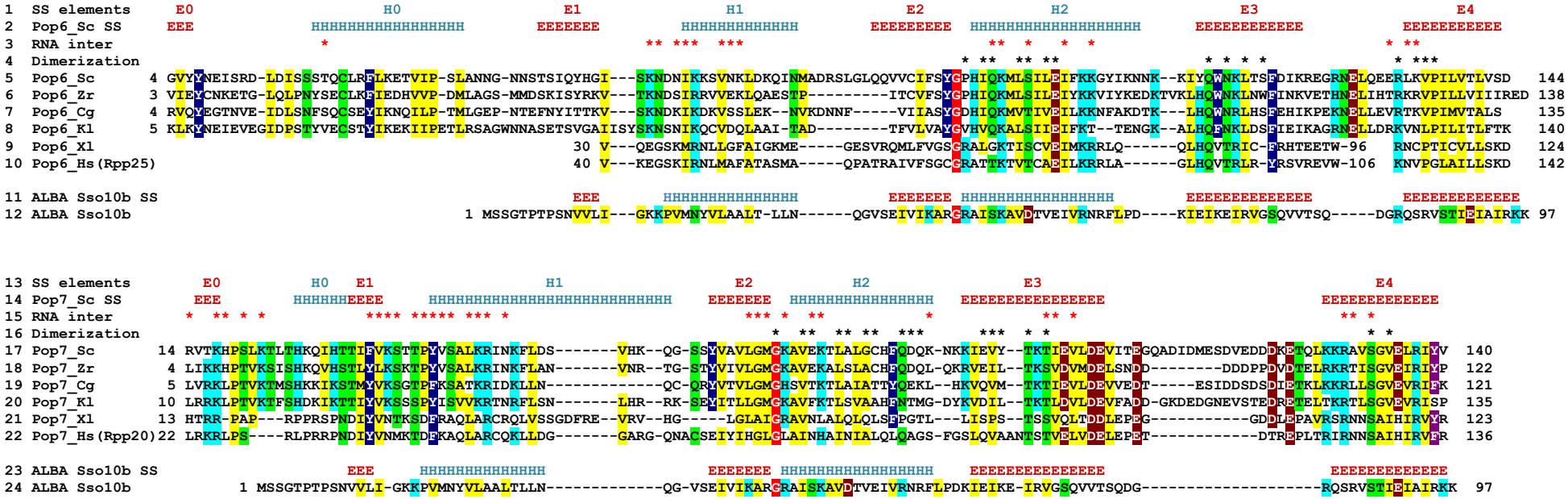


mouse RNase P

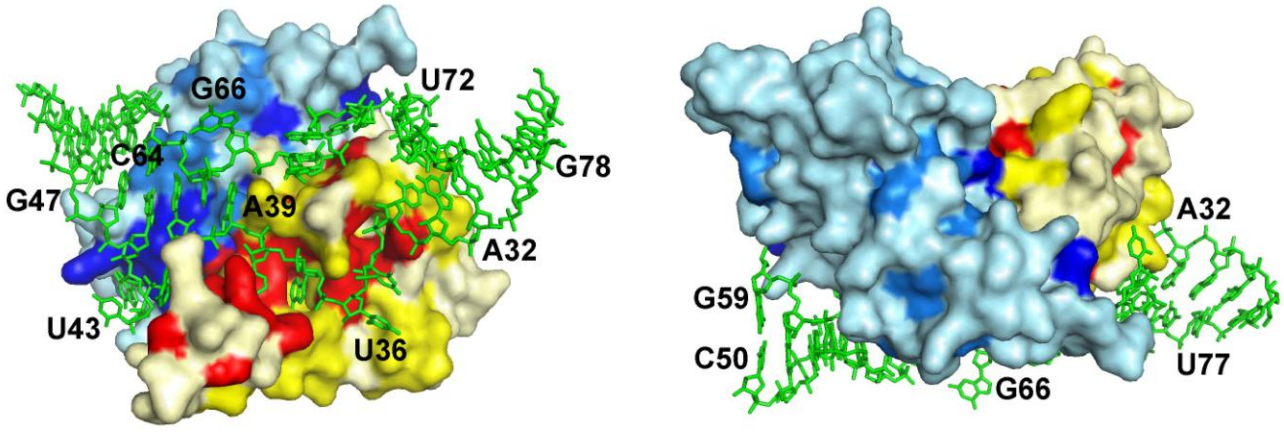


human RNase P

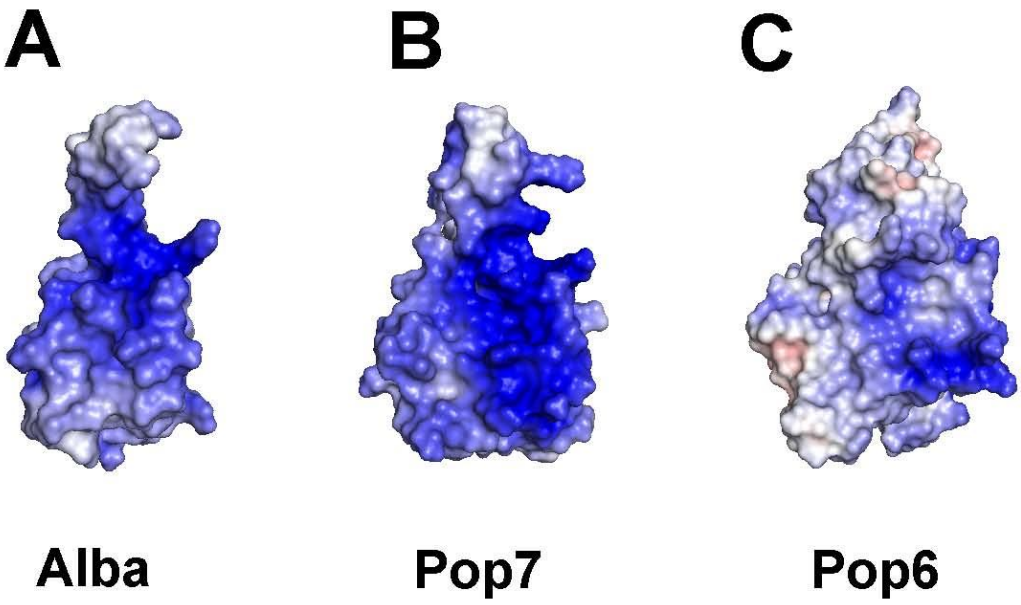
Supplementary Figure S1 Secondary structure diagrams for P3 RNA domains of RNases MRP/P from various eukaryotes. The ACR triad corresponding to A37, C38, A39, which are an integral part of the Pop7 protein fold in *S. cerevisiae* RNase MRP, is shown in red. In *S. pombe*, the ACR triad appears to be replaced by a UCA triad (shown in green). It is not clear whether *S. kluyveri* RNase P possesses an unusually positioned ACA triad (red) or an alternative GCA triad (underlined in orange). The diagrams are based on [Tranguch & Engelke 1993, Ziehler et al. 2001, Li et al. 2002, Piccinelli et al. 2005, Lopez et al. 2009].



Supplementary Figure S2 A structure-guided sequence alignment for Pop6 (lines 1-10) and Pop7 (lines 13-22) versus Alba protein Sso10b (lines 11-12 and 23-24).The alignments are shown for *S. cerevisiae* (Sc, lines 5,17), *Zygosaccharomyces rouxii* (Zr, lines 6, 18), *Candida glabrata* (Cg, lines 7, 19), *Kluyveromyces lactis* (Kl, lines 8, 20), *Xenopus laevis* (Xl, lines 9, 21), and human (Hs, lines 10, 22) proteins. Lines 1,13- secondary structure elements according to the nomenclature from Figure 3; lines 2, 14 - secondary structures of Pop6, Pop7, respectively; lines 11,23- secondary structures of Alba Sso10b (PDB 1h0x). The residues conserved in Pop6 (lines 5-10), Pop7 (lines 17-22) and Alba proteins (line 24) are highlighted as follows: nonpolar aliphatic (GAPVLIM, yellow), aromatic (FYW, dark blue), polar uncharged (STCNQ, green), positively charged (KHR, light blue), negatively charged (DE, brown). The absolutely conserved glycine is highlighted in red. The shown conservation pattern for Alba is based on the alignment of Alba proteins with known structures (PDB ID 1h0x, 1y9x, 1nfj, 1nh9, 2h9u, 2z7c, 2bky, the alignment is not shown). Residues involved in interactions with the P3 domain RNA are marked by red asterisks in lines 3, 15; residues involved in the formation of the Pop6/Pop7 heterodimer are marked by black asterisks in lines 4, 16.



Supplementary Figure S3 Conserved residues mapped to the surface of the Pop6/Pop7 heterodimer. The conservation is shown according to the alignment in Supplementary Figure S2. Non-conserved residues are represented in light blue (Pop6) and light yellow (Pop7); residues conserved in yeast (*S. cerevisiae*, *Z. rouxii*, *C. glabrata*, and *K. lactis*) are shown in blue (Pop6) and yellow (Pop7); residues conserved in all organisms in Supplementary Figure S2 (*S. cerevisiae*, *Z. rouxii*, *C. glabrata*, *K. lactis*, *X. laevis*, and *H. sapience*) are shown in dark blue (Pop6) and red (Pop7). The P3 domain RNA is shown in green.



Supplementary Figure S4 The electrostatic potential of the surface of proteins **(A)** Alba 1hox, **(B)** Pop7, **(C)** Pop6. Positively charged areas are shown in blue, neutral- in white, negatively charged- in red. All proteins are shown in the same orientation.

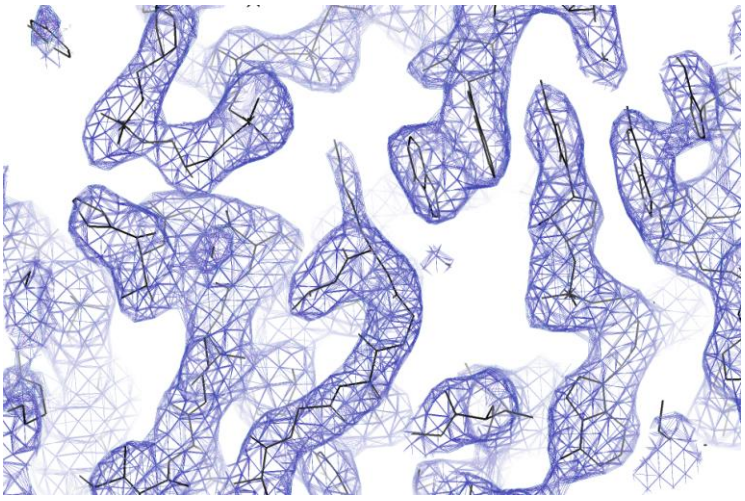
P3 domain upper strand loop

```
                          65 66    67 68 69 70 71 72
RNase MRP   5′- AG-U-AAUAU   -3′
RNase P     5′- AGAUAUUAU   -3′
                72 73 74 75 76 77 78 79 80
```

P3 domain lower strand loop

```
                          35    36 37 38 39 40 41 42 43 44
RNase MRP   5′- U-UACAAAAUG -3′
RNase P     5′- UUUACAGAA-G -3′
                37 38 39 40 41 42 43 44 45   46
```

Supplementary Figure S5 Sequence alignments for the upper and the lower strands of the loop region of the P3 domain RNA from *S. cerevisiae* RNase MRP and RNase P.



Supplementary Figure S6 A sample of a density modified SAD electron density map contoured at the 1.5σ level.