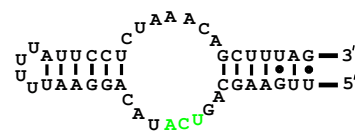
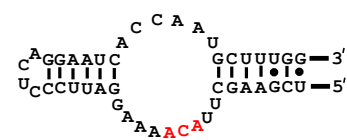


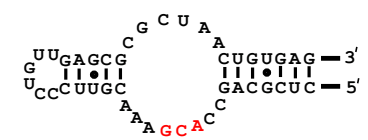
S. cerevisiae RNase MRP



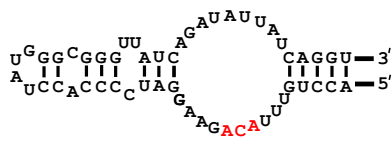
S. pombe RNase MRP



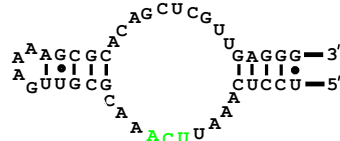
S. kluyveri RNase MRP



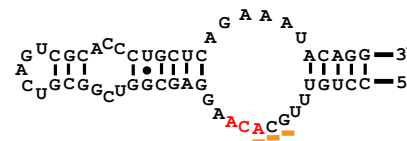
C. elegans RNase MRP



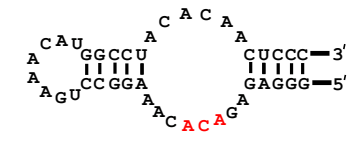
S. cerevisiae RNase P



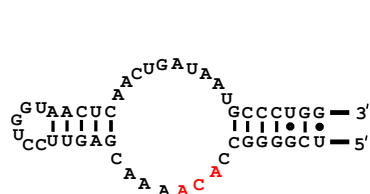
S. pombe RNase P



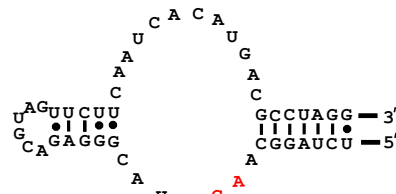
S. kluyveri RNase P



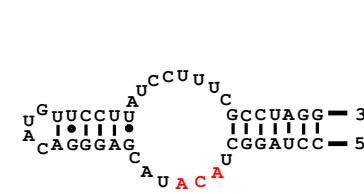
C. elegans RNase P



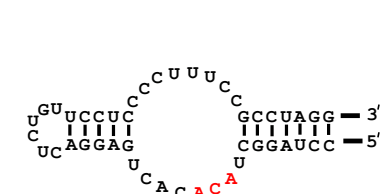
D. melanogaster RNase MRP



X. laevis RNase MRP



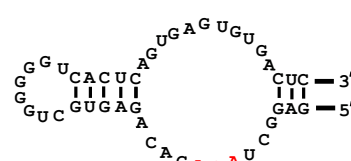
mouse RNase MRP



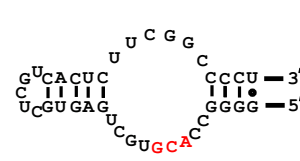
human RNase MRP



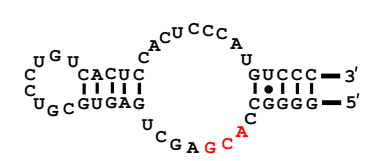
D. melanogaster RNase P



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].

```

1 SS elements      E0          H0          E1          H1          E2          H2          E3          E4
2 Pop6_Sc SS      EEE          HHHHHHHHHHHHHH  EEEEEEE    HHHHHHHHHHHHHH  EEEEEEEEE  HHHHHHHHHHHHHH  EEEEEEEEE
3 RNA inter       *
4 Dimerization    * * * * *
5 Pop6_Sc         4 GVVYNEISRDLDISSTQCLRLGLKETVIP-SLANNG-NNSTSIQYHGI---SKNDNIKKSVNKLKQIIMADRSLGLQVVCFISYCPHIQKMLSILEIFKKGYIKNNK--KIYQWNLKLTSDIKREGRNELQEEERLKVPIILVTLVSD 144
6 Pop6_Zr         3 VIEYCNKETG-LQLPNYSECLKTEEDHVVP-DMLAGS-MMDSKISYRKV---TKNDSIRRVVEKLAQESAP-----ITCVFVSYGPHIQKMLSILEIYKVIYKEDKTVKLHWKLNKNWELINKVETHNELIHTRRKRVPIILVLI IRED 138
7 Pop6_Cg         4 RVQVEGTNVE-IDLSNFSQSEETKKNQILP-TMLGEP-NTEFNYYITTKV---SKNDKIKDKVSSLEK--NVKDNNF-----VITASVGDHIQKMTIVEIILKKNFAKDTK---LHWNLRLHSEHIKPEKNELELVTRKVPIMVTALS 135
8 Pop6_Kl         5 KLVYNEIEVEGIDPSTVYVEESTYIKEKIIIPETLRSAGWNNASETSVGAIIISYSKNSNIKQCVDQLAAI-TAD-----TFVLVAVGVHVKALSIIIEIFKT--TENGL--ALHWENKLDSEIEIKAGRNELLDKRVNLPILITLFTK 140
9 Pop6_Xl         30 V---QEGSKMRNLLGFAIGKME---GESVQRMLFVGSRCRALGKTISCVEIMKRRLQ----QLHGVTRIC-PRHTEETW-96 RNCPTICVLLSKD 124
10 Pop6_Hs (Rpp25) 40 V---KEGSKIRNLMAFATASMA---QPATRAIVFSGCCRATTKTVICAEIILKRRLA----GLHGVTRLR-LRSVREVW-106 KNPVGLAILLSKD 142

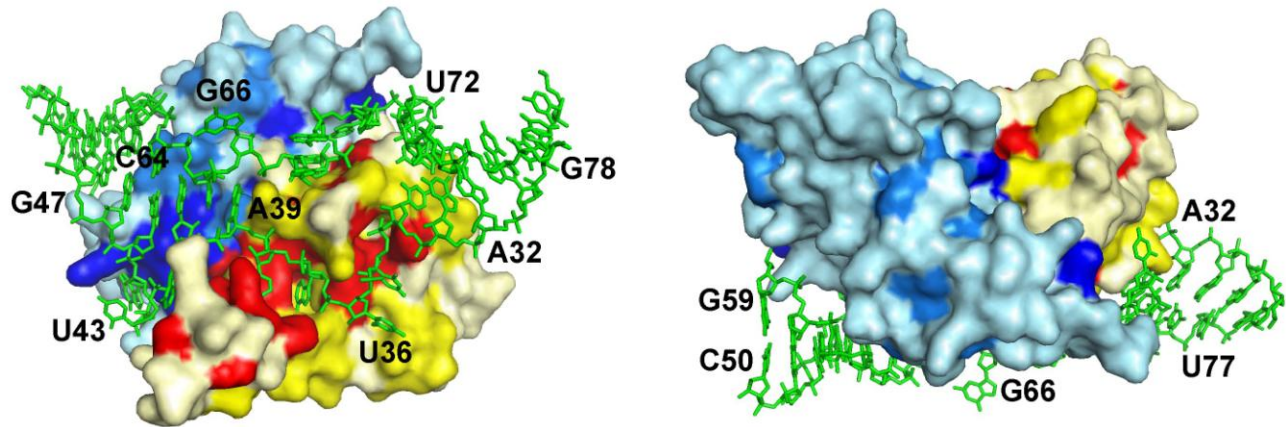
11 ALBA Sso10b SS      EEE          HHHHHHHHHHHHHH  EEEEEEE    HHHHHHHHHHHHHH  EEEEEEEEE  HHHHHHHHHHHHHH  EEEEEEEEE
12 ALBA Sso10b     1 MSSGTTPPSNVVLI--GKKPVMNYVLAALT-LLN-----QGVSIVIKARCRATSKAVDIVEIVRNRFLLPD---KIEIKIIRVGGVQVVSQ-----DGRQSRVSTIEIATRK 97

13 SS elements      E0          H0          E1          H1          E2          H2          E3          E4
14 Pop7_Sc SS      EEE          HHHHHHHHHHHHHH  EEEEEEE    HHHHHHHHHHHHHH  EEEEEEEEE  HHHHHHHHHHHHHH  EEEEEEEEE
15 RNA inter       * * * * *
16 Dimerization    * * * * *
17 Pop7_Sc         14 RVTKHPSLKTLTHKQIHTIIVKSTIPVVSALKRINKFLDS-----VHK--QG-SSVAVVLGMGKAVEKTLALGCHFDQK-NKKIEVY--TKTIEVLDVVIPEGQADIDMESDVEDDKEFTQLKRAVSGVLRIMV 140
18 Pop7_Zr         4 LIKKHPTVKSISHKQVHSTLMLKSKIPVVSALKRINKFLAN-----VNR--TG-STYVIVLGMGKAVEKALSACFODQL-QKRVEIL--TKSVDMOELSND-----DDPPQVDTELKRRTISGVVIRIMP 122
19 Pop7_Cg         5 LVRKLPVKTMSHKKIKSTMVKSCTPEKSATKRIDKLLN-----QC-QRVVTVLGMGHSVTKTLAIAATYQEKL--HKVQVM--TKTIEVLDVVEVDT-----ESIDDSSEIEKTKKRLLSGVVIRTPK 121
20 Pop7_Kl         10 LRRKLPVKTFSHDKIKTIIVKSSSPYISVVKRTRNRLSN-----LHR--RK-SPYITLLGMGKAVFKTISVAAHNTMG-DYKVDIL--TKTLDVLDVVFADD-GKDEGDGNEVSTEDRETELTKRLLSGVVRISP 135
21 Pop7_Xl         13 HTRR-PAP---RPPRSPNDIVVNRKSDPRAQLARCRQLVSSGDFRE--VRV--HG----LGLAICRAVNLALQLQSPGTL---LISPS--TSVQVLTODLEPEG-----GDDEPAVRSNNNSAIHIVR 123
22 Pop7_Hs (Rpp20) 22 LRRKLPV---RLPRRPNDIVVNRKSDPRAQLARCRQLVSSGDFRE--VRV--HG----LGLAICRAVNLALQLQSPGTL---LISPS--TSVQVLTODLEPEG-----GDDEPAVRSNNNSAIHIVR 136

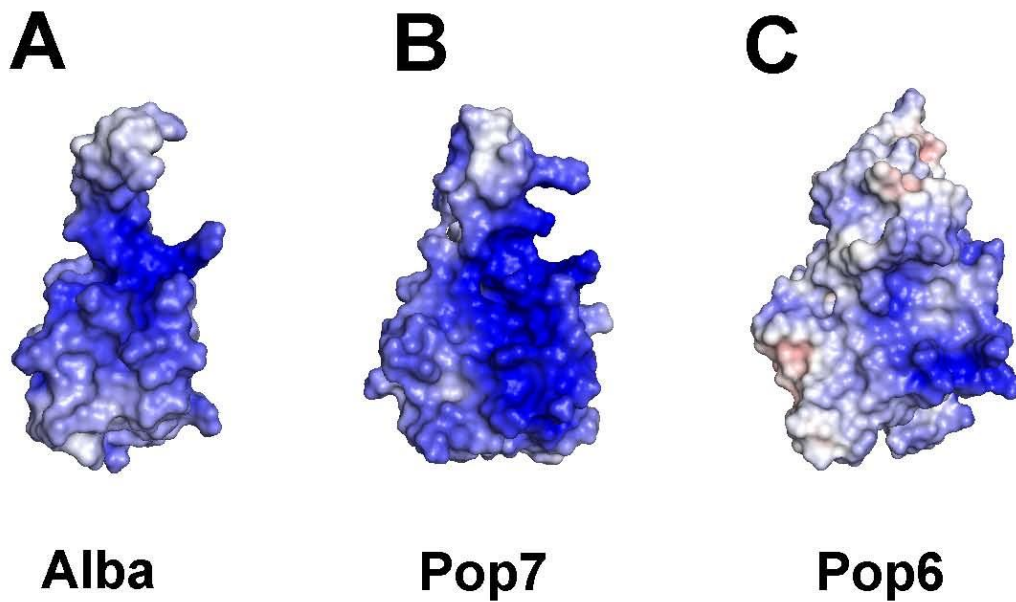
23 ALBA Sso10b SS      EEE          HHHHHHHHHHHHHH  EEEEEEE    HHHHHHHHHHHHHH  EEEEEEEEE  HHHHHHHHHHHHHH  EEEEEEEEE
24 ALBA Sso10b     1 MSSGTTPPSNVVLI--GKKPVMNYVLAALTLLN-----QG-VSEIVIKARCRATSKAVDIVEIVRNRFLLPDKIEIKIIRVGGVQVVSQDG-----DGRQSRVSTIEIATRK 97

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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 (GAPVLM, 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.

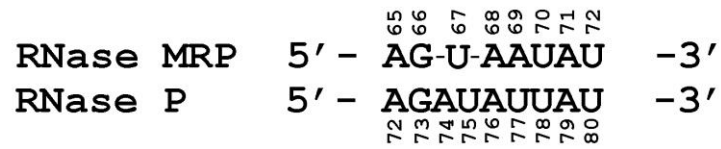


Supplementary Figure S3 Conserved residues mapped to the surface of the Pop6/Pop7 heterodimer. The conservation is shown according to the alignment in Supplementary Figure S2. Non-conserved residues are represented in light blue (Pop6) and light yellow (Pop7); residues conserved in yeast (*S. cerevisiae*, *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.

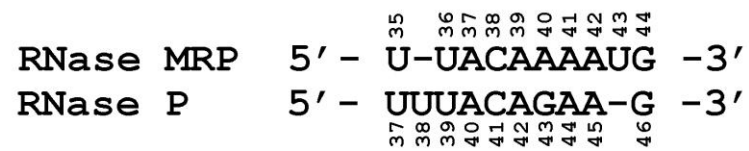


Supplementary Figure S4 The electrostatic potential of the surface of proteins **(A)** Alba 1hox, **(B)** Pop7, **(C)** Pop6. Positively charged areas are shown in blue, neutral- in white, negatively charged- in red. All proteins are shown in the same orientation.

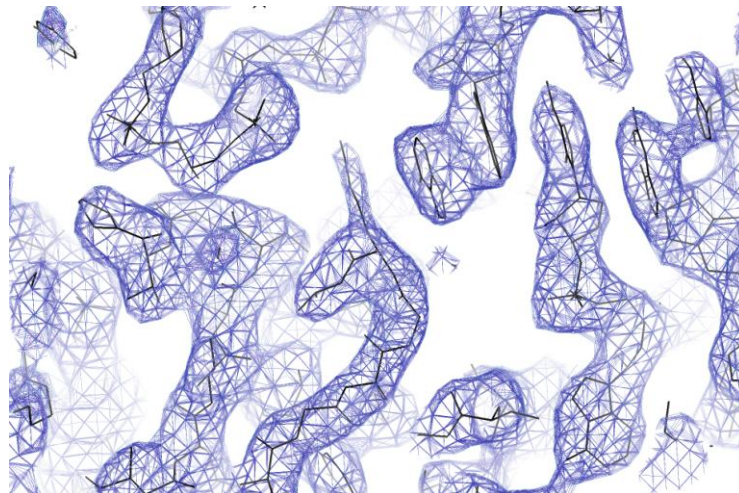
P3 domain upper strand loop



P3 domain lower strand loop



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.