A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation


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The authors inadvertently omitted Woonghee Lee from the list of authors. The corrected author list and affiliations appear above. Revised acknowledgment paragraphs including Woonghee Lee’s funding source and contribution appear below. In addition, the authors noted the omission of details of NMR structure calculation from the Materials and Methods section. The relevant paragraph and the references associated with it are appended below.

The HTML and PDF versions of this article have been corrected. The errors remain only in the print version.

Acknowledgements

We thank C. Leidig, G. Manikas, Y. Matsuo, B. Bradatsch, E. Thomson, and C. Ulbrich for reagents and discussion on the project. We thank R. Kunze for purification of pulse-chased Rpl25; C. Ulbrich and M. Haufe for the genetic analysis; S. Bilén for generation of the ipi3 ts mutants; G. Manikas for cloning of ctRSA4; K. Wild, Y. Ahmed, E. Lenherr, and D. Lupó for support in crystallization and data collection; and J. Kopp and C. Siegmund from the BZH/Cluster of Excellence CellNetworks crystallization platform for protein crystallization. We are grateful to D. Kressler, M. Fromont-Racine, A. Johnson, V. Panse, M. Seedorf, D. Wolf, and M. Remacha for sharing plasmids, strains, and antibodies; to J. Nováček and R. Fiala of the National Center for Biomedical Research (Faculty of Science) Masaryk University for NMR data collection. The CS-Rosetta calculations were carried out on the server at the Biological Magnetic Resonance Bank.

J. Baßler and E. Hurt are supported by grants from Deutsche Forschungsgemeinschaft (DFG; BA2316/1-4, HU363/10-5). E. Barbar and A. Nyarko are supported by the National Institutes of Health (GM 084276). I. Sinning acknowledges support by grants from DFG (FOR967, GRK1188, and SFB638). I. Sinning and E. Hurt are investigators of the cluster of excellence CellNetworks. Financial support from the Access to Research Infrastructures activity in the seventh Framework Program of the European Community (Project number 261863, Bio-NMR) for conducting the research is also acknowledged. C. Barrio-Garcia is a fellow of the Graduiertenkolleg GRK 1721. W. Lee is supported by NIH grant P41GM103399, which funds the National Magnetic Resonance Facility at Madison.

The authors declare no further competing financial interests.


NMR structure calculation

A list of chemical shift assignments and 13C- and 15N-filtered 3D NOESY data were provided as input to PONDEROSA-C/S (Lee et al., 2014), which with its refinement option solved the initial structure. PONDEROSA-C/S incorporates TALOS-N (Shen and Bax, 2013) for the generation of structural restraints from chemical shifts and CYANA (Güntert, 2004) for structure determination. Next, hydrogen bond constraints were generated by predictions from CYANA, TALOS-N, PSIPRED (Buchan et al., 2013), analysis of NOESY spectra and the initial structure. Analysis was aided by use of Ponderosa Analyzer, NMRFAM-SPARKY (Lee et al., 2015) with the Ponderosa plug-in, and PyMOL. Ponderosa Analyzer was used to validate and refine distance and angle constraints and to export these to the Ponderosa Client for protein structure determination.
iterative structure calculations by the Ponderosa Server. Water refinement by XPLOR-NIH (Schwieters et al., 2003) was carried out by the Ponderosa Server. The final structure, as represented by 20 models, was analyzed by the protein structure validation software suite (PSVS; Bhattacharya et al., 2007).

References