***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

This type of analysis is not needed for the present submission.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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We describe the number of particles used in the cryo-EM reconstructions in Figure 1–figure supplement 1 and provide details in Tables 1-3.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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Statistical analysis for the structures is provided in Tables 1-3 and in Figure 1–figure supplements 2-3. For analysis of archaeal and eukaryotic u11 proteins, the analysis is shown in Figure 4–figure supplement 3. Analysis of prior 50S structures is described in the Methods, and is shown in Figure 7–figure supplement 1 and in Figure 8–figure supplement 1. Phylogenetic analyses for u11, bS21 and uL16 are described in the Methods, and data provided in Supplementary Tables 1-2.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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Not applicable.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Maps and model of the 70S ribosome and models used for the analysis in Figure 4–figure supplement 3 are given in the directory <https://drive.google.com/drive/u/0/folders/1fH8UFYnGMK6jNgyfCvwzI_A-viJEi6iq>

All maps and models have now been deposited in the PDB, EMDB and cryo-EM movies in EMPIAR. See the data deposition section of the manuscript.