***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

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The data refinement for the Sfh5 structure is described in detail in the Methods. The pdb validation file is provided as related manuscript and the maps&coordinates file is provided as a Supporting zip file. The UV-vis, EPR and Mossbauer spectroscopy experiments necessarily show representative experiments but the replicate information are described in the Figure legends and the text.

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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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Data are found in the figure legends and in the text (for the Mossbauer experiments)

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* 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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Reported in the Methods and the Figure legends

(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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Not applicable

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* 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
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The pdb for the Sfh5 structure has been deposited in the Protein database. The pdb validation file is provided as related manuscript and the maps&coordinates file is provided as a Supporting zip file. The spectroscopic traces are all source data. The refinement statistics for the crystal structure and the parameters for Mossbauer fitting are tabulated in Tables 1 and in the Supplementary materials.