

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- | | | |
|-------------------------------------|-------------------------------------|--|
| ☐ | ☒ | The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement |
| ☒ | ☐ | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☒ | ☐ | The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ | A description of all covariates tested |
| ☒ | ☐ | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| ☐ | ☒ | A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| ☒ | ☐ | For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| ☒ | ☐ | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| ☒ | ☐ | Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection Leginon 3.3 (legion.org);

Data analysis Refmac5; Parrot; Phaser; Coot 0.8.9; Phenix 1.14-3260; CTFFind 3.1; MotionCorr 1 (with custom patch, available upon request); EMAN 1.81; Relion 1.2 (with custom IHRSR patch, available upon request, current version 1.4); Chimera 1.11.2; EMRinger (<https://fraserlab.com/2015/02/18/EMRinger/>); MatLab (MathWorks)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

CryoEM maps and the associated atomic models have been deposited to EMDB, PDB under the accession numbers EMD-20526/PDB:6PYT (pre-contraction helical trunk), EMD-20643/PDB:6U5B (pre-contraction baseplate), EMD-20646/PDB:6U5H (pre-contraction hub in C3 symmetry), EMD-20644/PDB:6U5F (pre-contraction collar), EMD-20647/PDB:6U5J (post-contraction collar) and EMD-20648/PDB:6U5K (post-contraction baseplate), respectively. X-ray crystal structures have been deposited to PDB under the accession numbers 5CES (PA0618 C-terminal domain), 4S36 (PA0616 C-terminal domain) and 4S37 (full length PA0616). All other data are available from the corresponding authors upon reasonable request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The presented study is of structural biological nature. We averaged huge numbers of particles (See Ext Data Table 1) to reach the stated resolutions, which is then tested and confirmed in the work. For Figure 4f, the phenotypical evaluation of H257F mutant, 200 micrographs were taken for each condition and particles counted. For Ext Data Figure 6, samples were prepared independently three times, 10 micrographs were taken for each of them (b and c), giving us 0 pre-contraction and about 150 post-contraction pyocins for the WT and 0 pre- and about 150 post-contraction pyocins for the mutant analyzed in total. For (d-g), each experiment was repeated three times.
Data exclusions	No data were excluded.
Replication	Ext Data Fig 6: all experiments were repeated three times.
Randomization	The structural determination process is random by nature since the particles are randomly presented to us in solution.
Blinding	The structural determination process is blinded by nature since the particles are presented to us in solution without selection by prior knowledge.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging