

## Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) 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 ( $n$ ) 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  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- 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.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- 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  $d$ , Pearson's  $r$ ), 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

Data analysis

Software used: OriginPro2023, Origin2018, MATLAB R2021b, Digital Micrograph software 2.1.1, Velox v3.0, minimap2, samtools v1.6, bedtools v2.30.0, cryoSPARC v3.3 or 4.1, RELION-3.1, DeepEMhancer v0.13, UCSF Chimera 1.16, ChimeraX 1.5, WinCoot 0.9.8.1, Phenix 1.20.1, APBS 3.4.1, DiscoverMP v2.5.0, GROMACS 2019.6.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Cryo-EM maps and atomic models have been deposited in the Electron Microscopy Data Bank (EMDB) and wwPDB, respectively, with EMDB/PDB accession codes: EMD-17046/8OPA, EMD-17047/8OPB, EMD-17048/8OPC, EMD-17049/8OPD, EMD-17050/8OPE, EMD-17051/8OPF, EMD-17052/8OPG, EMD-17053/8OPH, EMD-17054, EMD-17055, EMD-17056, EMD-17057, EMD-17058, EMD-17059, EMD-17060, EMD-17061, EMD-17062/8OPJ, EMD-17063/8OPK, EMD-17064, EMD-17065, EMD-17066, EMD-17067, EMD-17068, EMD-17069, EMD-17070, EMD-17071, EMD-17072/8OPL, EMD-17073, EMD-17074 and EMD-17075, with corresponding structures and atomic models provided in Table 1 and Supplementary Tables 1 and 2. These links will be released upon publication, with cryoEM maps and corresponding models currently provided on Dryad database (doi:10.5061/dryad.9ghx3ffp2). Validation reports for 11 atomic models are provided in combined PDF form next to Source data file.

Raw cryo-EM datasets have been deposited to the Electron Microscopy Pilot Image Archive (EMPIAR) with accession codes EMPIAR-11545 (EMD-17046/8OPA, EMD-17047/8OPB, EMD-17048/8OPC), EMPIAR-11546 (EMD-17049/8OPD, EMD-17050/8OPE), EMPIAR-11547 (EMD-17052/8OPG), EMPIAR-11548 (EMD-17053/8OPH, EMD-17054, EMD-17055), EMPIAR-11549 (EMD-17062/8OPJ, EMD-17063/8OPK) and EMPIAR-11550 (EMD-17072/8OPL).

RNA nanopore sequencing data have been deposited on European nucleotide archive (ENA) with accession code PRJEB61146.

Source data are provided with this paper as Supplementary Data. Additional data is provided in the Supplementary information file.

## Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	<input type="text" value="n/a (human participants were not included in the study)"/>
Population characteristics	<input type="text" value="n/a"/>
Recruitment	<input type="text" value="n/a"/>
Ethics oversight	<input type="text" value="n/a"/>

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## 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	<input type="text" value="Study included only in vitro studies of purified recombinant proteins expressed in bacteria. We prepared at least two independent biological replicates (in RNA analysis by RNA sequencing, RTqPCR) with three technical measurements (in Thermal stability assay)."/>
Data exclusions	<input type="text" value="No data was excluded."/>
Replication	<input type="text" value="Experiments were performed with different batches of isolated proteins. Their activity and folding was confirmed and compared before including them in further experiments. Number of replications is clearly stated at every experiment shown in the article. All attempts of recreation were successful."/>
Randomization	<input type="text" value="Not applicable, since all the experiments were performed in vitro."/>
Blinding	<input type="text" value="Not applicable, since all the experiments were performed in vitro."/>

## 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	Involvement	Material/System
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Dual use research of concern

### Methods

n/a	Involvement	Method
<input checked="" type="checkbox"/>	<input type="checkbox"/>	ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/>	MRI-based neuroimaging