nature portfolio

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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	Epu v2.6.l.69REL, TEM User interface Titan v6.15.3.5341REL, Digital Micrograph v3.22.1461
Data analysis	MotionCor2, CTFFIND4, cisTEM 1.0.0, RELION 3.0.7, cryoSPARC 2.11, Warp 1.0.7, pyEM v 0.5, Phenix 1.19, Coot 0.9-pre, UCSF Chimera 1.14, UCSF ChimeraX 0.93, xQuest v2.1.1, Image J 1.52p (JAVA l.8.0_172), Tycho NT.6 software (v 1.3.1.868), Jalview (v 2.11.2.1), RStudio (v 2021.09.1), GraphPad PRISM v9.0.

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

The cryo-EM density maps were deposited at the Electron Microscopy Data Bank (EMDB) and the Protein Data Bank (PDB) under the accession codes EMD-14534 (substrate recognition state), EMD-14762 (prehydrolysis state), EMD-14562 (posthydrolysis state), EMD-14583 (bridge-deletion posthydrolysis dimer) and EMD-14554 (product state).
The final coordinates of the protein structures were deposited at the Protein Data Bank (PDB) with the accession codes: PDB 7Z7N (substrate recognition state), PDB 7ZKE (prehydrolysis state), PDB 7Z8S (posthydrolysis state) and PDB 7ZB4 (product state).

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

Life sciences study design

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

Sample size	For cryo-EM, a sufficient number of micrographs was collected to yield adequate reconstructions. For ATPase assays sufficient data points were collected to yield a robust linear fitting.
Data exclusions	For cryo-EM, no data were initially excluded, but only a subset of collected data was used for final reconstructions as detailed in the Methods part and in the cryo-EM data processing schemes in Extended Data Figures 6 and 8.
Replication	The quality of the protein samples was assessed by SDS-PAGE before cryo-EM preparation. Thousands of micrographs were collected with consistent quality represented by the example micrographs in the Extended Data. Biochemical assays (EMSAs and ATPase assays) were carried out in the number of replicates indicated in the text.
Randomization	All data were used in an unbiased way for data analysis and image reconstruction. For cryo-EM, final resolution was estimated by random separation of the data set into two halves to calculate their correlation coefficients.
Blinding	Blinding was not relevant to this study. For cryo-EM, micrographs were initially processed automatically without user interference. In biochemical assays all samples were treated equally.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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