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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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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
\boxtimes	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.
X	A description of all covariates tested
\boxtimes	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)
\boxtimes	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>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\times	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes	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

Unicorn (Cytiva Life Sciences, v6.4), Digital Micrograph (Gatan, 2.10.1282.0), Leginon (v3.3 and v3.4), Scanlt Software (Thermo Scientific, v6.1).

Data analysis

Relion (v3.1), MotionCor2 (v2), CTFFind4 (v4), cryoSPARC (v3), Relion (v3.1), 3DFSC (v3.0, remote processing server), ISOLDE (v1.2), ChimeraX (v1.3), Coot (v0.9.4.1), Phenix (v1.18 and v1.20), RStudio (v1.4.1103, Base R: v4.0.3; packages: "dplyr" (v1.0.9), "drc" (v3.0-1), "ggplot2" (v3.3.5)), Fiji (v2.1.0), Chimera (v1.15), BLAST (v2.13.0, NCBI online portal), MAFFT (v7, EMBL-EBI online portal), Adobe Illustrator CC (v26.0.1).

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 <u>data availability statement</u>. 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 electron microscopy maps generated for this manuscript are available from the EMDB (https://www.ebi.ac.uk/emdb/) at the accession codes listed in

Table 1 of the manuscript (EMDB IDs: EMD-27279, EMD-27280, EMD-27281, EMD-27282, EMD-27283, EMD-27284, EMD-27285, EMD-27286, EMD-27287, EMD-27288, EMD-27289, EMD-27299, EMD-27291, EMD-27293, EMD-27294, EMD-27295). The protein models generated for this manuscript are available from the RCSB PDB (https://www.rcsb.org/) at the accession codes listed in Table 1 of the manuscript (PDB IDs: 8DBC, 8DBD, 8DBE, 8DBF, 8DBG, 8DBH, 8DBI, 8DBI, 8DBI, 8DBN, 8DBN, 8DBN, 8DBO). Protein sequences identified by the NCBI online portal for BLAST (v2.13.0; https://blast.ncbi.nlm.nih.gov/Blast.cgi) were queried on the "non-redundant protein sequences (nr)" database. Source data are provided with this paper.

Human rese	arch parti	cipants				
Policy information about studies involving human research participants and Sex and Gender in Research.						
Reporting on sex	and gender	There were no human research participants in these studies.				
Population chara	cteristics	There were no human research participants in these studies.				
Recruitment		There were no human research participants in these studies.				
Ethics oversight The		There were no human research participants in these studies.				
Note that full informa	lote that full information on the approval of the study protocol must also be provided in the manuscript.					
Field-specific reporting						
		s the best fit for your research. If you are not sure, read the appropriate sections before making your selection.				
\(\sime\) Life sciences	В	ehavioural & social sciences				
For a reference copy of t	the document with	all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>				
Life scier	nces stu	udy design				
All studies must dis	sclose on these	points even when the disclosure is negative.				
Sample size	For negative stain electron microscopy, two to three micrographs from different locations on a single grid were recorded and examined per condition, as is common in the field. The number of micrographs collected and particles included in final cryoEM structures are listed in Data Table 1. Unless otherwise noted, technical replicates of kinetic assays were performed in triplicate or greater, as is standard for the field.					
Data exclusions	As is standard in cryoEM data analysis, particles that did not contribute to high resolution structure determination were excluded during 2D and 3D classification.					
Replication	The number of replicates performed for the biochemical assays are listed in the figure legends.					
Randomization	No grouping was performed in this study.					
Blinding	As no grouping was performed in this study, no blinding was necessary.					
Reportin	g for sr	pecific 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 Methods						
Antibodies						
Eukaryotic	Eukaryotic cell lines					
	Palaeontology and archaeology MRI-based neuroimaging					
Animals and other organisms						
Clinical dat						
Dual use research of concern						