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	SerialEM v4.0
Data analysis	relion v4.0 cryosparc v 3.3 CTFFIND v4.1.13 MotionCor2 v1.5.0 topaz v0.2.5 phenix1.19 wincoot v0.9.4 chimeraX v1.3 ISOLDE1.3 Molprobity EMRinger

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 maps have been deposited in the EMDB under accession codes 34748, 34749, 34750, 34751, 34752, 34753, 34754, 34755, 34756, 34757, 34758, 34760, 34759, 34761, 34763, 34762, 34764, 34765, 34766, 34767, 35373, 34768, 34769, 34770, 34771, 34772, 34773, 34774, 34775, 34776, 34777, 34779, 34780, 34778, 34781, 34782, 34783, 34784, 34785, 34786, 34787, 34788, 34789, and 34790. The atomic models have been deposited in the Protein Data Bank accession codes 8HH1, 8HH2, 8HH3, 8HH4, 8HH5, 8HH6, 8HH7, 8HH8, 8HH9, 8HHA, 8HHB, and 8HHC. The initial model for model building is accessible in PDB under accession number 6N2Y. The data that support the findings of this study are available from the corresponding author upon reasonable request.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	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

Life sciences study design

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

Sample size	The sample size is judged from previous studies using the same sample, and a minimum of 5000 micrographs is sufficient to maintain sufficient resolution after classification.
Data exclusions	Micrograph images were excluded using defocus values calculated by CTFFIND. Bad particle images were excluded by 2D classification and heterogeneous refinement. Some micrograph images were largely out of focus due to acquisition errors and were excluded by the defocus value(8000-25000Å) calculated by CTFFIND.
Replication	At least five independent protein purifications have been performed, including previous studies, and all attempts at replication have been successful.
Randomization	This is not relevant to structural determination using cryo-EM, because no grouping is needed.
Blinding	Blinding is not required because it is based on a random subset of particles.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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