

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 v4.1, Warp v1.0.9

Data analysis cryoSPARC v4.7.0, RELION v5.0, ChimeraX v1.10, LocScale-2.0, AlphaFold2, Phenix v1.20, Namdinator (no version number), Situs v3.8, DomainSeeker (no version number), CryoAtom v1.0.0, FoldSeek (no version number), findMySequence v1.0.12, pyem v0.66, Spectronaut v20.3

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 have been deposited to the EMDB with accession codes: EMD-54838 (composite map), EMD-54839 (consensus map), EMD-54840 (local refinement, PADI6 region), EMD-54841 (local refinement, SCMC region), and EMD-54842 (local refinement, tubulin subcomplex region). The atomic model has been deposited

to the PDB with accession code PDB 9SFP. Mass spectrometry data has been deposited in PRIDE with accession number PXD073451. Previously-published structures used for analysis/comparison include: EMD-16458, PDB 6DPV, PDB 4I4T, PDB 3CLZ, PDB 1FXT, PDB 9FMN, PDB 2DEW, PDB 8H93, and PDB 8X7W.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	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	For cryo-EM processing, no methods were used to predetermine sample size because the final size of the cryo-EM datasets is dependent on what is necessary to obtain reconstructions at sufficient resolution to confidently identify proteins and build an atomic model. The exact number of micrographs/movies collected and particles used are listed in Extended Data Table 1. Mass spectrometry measurements were performed on four (4) independent replicates of ~30 oocytes each.
Data exclusions	Workflows for cryo-EM single particle reconstruction may down-weight or exclude particles.
Replication	The cryo-EM maps reported represent an average of several hundred thousand copies of the molecule of interest (exact particle numbers are given in Extended Data Table 1). Cryo-EM data in this study was collected from two different grids across two separate microscope sessions, with initial screening performed on independent biological preparations. Mass spectrometry measurements were performed on four (4) independent replicates of ~30 oocytes each; all mass spectrometry replicates were successful and yielded similar results.
Randomization	For calculation of Fourier Shell Correlation (FSC) curves used to estimate resolution, particles were randomly split into two half-sets during cryo-EM refinement. For mass spectrometry experiments, oocytes collected from several mice were randomly split into groups of ~30 oocytes each.
Blinding	No blinding was necessary and is not applicable to cryo-EM structure determination since no conditions/experimental treatments were being compared. Furthermore, knowledge of the proteins present within the sample is essential for building an accurate atomic model. Likewise, since conditions were not being compared, no blinding was done for mass spectrometry analysis.

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

Methods

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

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

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Oocytes were obtained from sexually-mature female BALB/cN mice. Ovaries were obtained exclusively from surplus animals sacrificed for other purposes.
Wild animals	The study did not involve wild animals.
Reporting on sex	Oocytes were collected from female animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	No ethical approval or guidance was required because organs were used from surplus animals sacrificed for other purposes.

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

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A