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	Automated cryo-EM data collection was performed using SerialEM.
Data analysis	Cryo-EM daya analysis used CryoSPARC, GisSPA, ChimeraX, Coot and Phenix. Proteomics raw data were processed using Proteome Discoverer software v2.1 (Thermo Scientific).

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 generated in this study have been deposited in the Electron Microscopy Data Bank under accession numbers EMD-76333 (CPL filament map), EMD-76335 (ASU consensus map), EMD-76334 (ASU composite map), EMD-76315 (focused on PADI6 dimers 1–4), EMD-76321 (focused on NLRP5+TLE6 +OOEP+KHDC3), EMD-76322 (focused on NLRP5'+TLE6'+OOEP'+ZBED3), EMD-76323 (focused on NLRP14+UHRF1), EMD-76324 (focused on tubulin), EMD-76325

(focused on NLRP4F), EMD-76326 (focused on FBXW19-SKP1+FBXW21+SKP1), EMD-76327 (focused on UBE2D3+UHRF1RING), EMD-76330 (focused on PADI6 dimer 5), and EMD-76331 (focused on NLRP14'+UHRF1'+UBE2D3'). The corresponding atomic model of CPL ASU has been deposited in the Protein Data Bank under accession number PDB ID: 12DL. The proteomics data generated in this study have been deposited in the PRIDE repository under accession number PXD076290. Source data are provided with this paper.

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	No human participants in this research.
Reporting on race, ethnicity, or other socially relevant groupings	No human participants in this research.
Population characteristics	No human participants in this research.
Recruitment	No human participants in this research.
Ethics oversight	No human participants in this research.

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	No statistical method was used to predetermine sample size. Sample sizes were chosen based on established practice in the field. The number of cryo-EM micrographs and particles for structural determination is provided in Extended Data Fig.2 and Table 1 and 2.
Data exclusions	Low-quality cryo-EM particles were excluded during standard processing steps, including 2D classification to remove junk particles, duplicate removal, 3D classification, and subset curation.
Replication	Multiple rounds of structural refinement were performed, all of which yielded consistent density maps, albeit at varying resolution.
Randomization	Randomization was not relevant to this study, as samples were not assigned to different experimental intervention groups. For cryo-EM processing, particles were computationally classified using established maximum-likelihood procedures implemented in CryoSPARC, and gold-standard refinement was performed using independently refined half datasets for unbiased resolution estimation.
Blinding	Blinding was not relevant to this study, as the experiments did not involve subjective allocation of samples into treatment groups. Cryo-EM data collection, processing, and structural interpretation were performed using established computational workflows and objective reconstruction criteria.

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
☒	☐ Plants

Methods

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	6–8-week-old CD1 mice and 6–12-week-old C57BL/6 mice were used.
Wild animals	This study did not involve wild animals.
Reporting on sex	Only female mice were used in this study, as oocyte collection requires female animals.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All protocols involving mice were approved by the Yale University Institutional Animal Care and Use Committee (approval number 2024-20408). Mice were housed under specific pathogen-free (SPF) conditions with a 12-hour light/dark cycle.

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