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 2.11
Data analysis	CryoSparc 3.2, PyMol 2.4.1, ChimeraX 1.2.5, Rosetta v2021.48-dev61806, Coot 0.9.4, Phenix 1.19.2-4158, CCP4 7.1.011

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

Coordinate files and experimental density maps for the C3-symmetric, and for the C1-symmetric reconstructions were deposited at the PDB and at the EMDB under accession codes 7PUY / EMD-13662 and 7PVD / EMD-13667, respectively. The C3-focused map was deposited to the EMDB under the EMD-13668 accession code.

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 number of repeats in each experiment was maximized with considerations of available reagents, and /or labor but without a prior calculation for the number or desired repeats.
Data exclusions	We did not exclude data from our analysis
Replication	All assays were repeated at least three times to verify reproducibility. We did not observe findings that could not be repeated / reproduced.
Randomization	Not applicable for the assays that were used in this study.
Blinding	Not applicable for the assays that were used in this study.

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

Antibodies

Antibodies used	Anti matriglycan IIH6 antibody (Developmental Studies Hybridoma Bank, Hybridoma Product IIH6 C4, AB_2617216), goat anti-mouse IgM-HRP (Santa Cruz, sc-2973), rabbit anti-Flag polyclonal antibody (Thermo Fisher, PA1-984B), anti-rabbit conjugated HRP IgG (Jackson ImmunoResearch Laboratories, 111-035-003), Anti-Flag beads (Sigma Aldrich, F2426).
Validation	We did not perform independent validation to any of these antibodies.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293F cells (Invitrogen), HEK293T (ATCC), GP2-293 packaging cell line (Clontech)
Authentication	We did not authenticate any of the cell lines used in this study.
Mycoplasma contamination	Mycoplasma contamination was not tested in the cell-lines used for this study.
Commonly misidentified lines (See ICLAC register)	We did not use any commonly misidentified cell line.