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	cryoEM data for structure determination was collected using SerialEM (v.3.6-v.3.8).
Data analysis	cryoSparc(v2.15.0, v3.3.1), Relion (V.3.0.8), cisTEM(1.0.0-beta), Chimera(1.13.1), ChimeraX-1.2.1, ChimeraX-Isolde 1.2.2, PHENIX (v1.20.1-4487-000), MatLab (v.9.11.0)

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 deposition of all cryoEM maps and models is in progress during review. The cryoEM maps presented in this study will be deposited to the Electron Microscopy Data Bank (EMDB). The atomic coordinates of the models will be submitted to the PDB. Accession codes will be included in the final publication. All bacterial strains and plasmids will be available from the corresponding author on a reasonable request.

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 sample size calculation was performed. For cryoEM reconstructions, data was collected in accordance with microscope availability and need to sample side-views (0-60 degree tilts) as judged by changes in resolution/z-stretch of the map.
Data exclusions	Data was excluded as with accepted single particle cryoEM processing pipelines. 2D averages were used to keep or exclude data, followed by 3D classification to further remove low resolution or poorly aligned particles.
Replication	2D lattices were obtained at least twice in negative stain with protein alone and at least four separate times in cryoEM with assembly assisted by a lipid monolayer. MBP-PhuN immunofluorescence sample preparation and imaging was done once.
Randomization	Experimental groups were not allocated and thus no randomization was performed.
Blinding	Investigators were not blinded for any part of the experiments as this is not common practice for the methods applied here.

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	Maltose Binding Protein Epitope Tag Antibody (Rockland Inc. Rabbit Polyclonal, Product # 200-401-385); ThermoFisher Goat Anti-rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor555 (Catalog #A-21429)
Validation	Rockland tested the MBP antibody using western blots, finding that it reacts with all the MBP tagged proteins they tested while not cross-reacting with endogenous proteins from bacterial extracts. The Secondary Antibody has been prepared by Invitrogen using affinity purification to remove cross-reactive species and has been validated with immunofluorescence analysis by Invitrogen; it has also been used extensively in publications (559 references cited by ThermoFisher to date).