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Last updated by author(s): Feb 6, 2024

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	The SerialEM (version 3.8) was used to collect the cryo-EM micrographs.
Data analysis	MotionCor2, Gctf (v1.18), RELION 3.08 and CryoSPARC (v3.2) were used to process cryo-EM single particles. Phenix (version 1.14-3260-000) was used to perform structure refinement. Coot (version 0.8.9.2) was used to perform structure model building. 3DFSC Program Suite (version 3.0) was used to quantify directional resolution and density isotropy of cryoEM maps. UCSF Chimera (version 1.14) was used for structure analysis. UCSF ChimeraX (version 1.3) and PyMOL (version 2.1) were used to prepare figures and videos. BioXTAS RAW (version 1.5.1) and ATSAS (3.0.3) were used to analyze SEC-SAXS data. Prism (version 9.3.1) was used to analyze ATPase activity assay. ImageJ(version 1.54) and Photoshop (version 23.2.2) was used to perform generation of figures for in vivo data. Data Analysis Octet(version 9.0.0.10) was used for data processing and presentation of DNA binding activity assay.

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 and atomic coordinates have been deposited into the Electron Microscopy Data Bank and the Protein Data Bank with the following accession codes: EMD-34025 (PDB:7YQH, Smc5/6-8mer-overall), EMD-34953 (PDB:8HQS, Smc5/6-8mer-head), EMD-37587 (PDB:8WJO, Smc5/6-8mer-arm), EMD-33914 (PDB:7YLM, Smc5/6-8mer-hinge), EMD-35116 (PDB:8I13, Smc5/6-6mer-overall), EMD-37586 (PDB:8WJN, Smc5/6-6mer-head), EMD-35128 (PDB:8I21, Smc5/6-6mer-arm), EMD-37584 (PDB:8WJL, Smc5/6-6mer-hinge), EMD-35187 (PDB:8I4X, Smc5/6-5mer-overall), EMD-35186 (PDB:8I4W, Smc5/6-5mer-head), EMD-35185 (PDB:8I4V, Smc5/6-5mer-arm), EMD-35184 (PDB:8I4U, Smc5/6-5mer-hinge), and EMD-33927 (PDB: 7YMD, Nse1-3-4).
Structures used for structural comparisons/analyses have the following accession codes from the Protein Data Bank:5mg8, 3htk, 7lto, 7ogg, 7tve, 7dg2, 7qcd, 7ogt, 6yvu, and 7nyy. The AlphaFold identifiers used for model building include AF-Q08204-F1 (Smc5), AF-Q12749-F1 (Smc6), AF-Q07913-F1 (Nse1), AF-P38632-F1 (Nse2), AF-Q05541-F1 (Nse3), AF-P43124-F1 (Nse4), AF-Q03718-F1 (Nse5), and AF-P40026-F1 (Nse6).

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	The sample size and statistical method have been described in the figure legends. Typically, three biological duplicates were examined over three independent experiments to ensure the robustness of conclusions.
Data exclusions	No data was excluded.
Replication	For all in vivo experiments, three biological duplicates were examined over three independent experiments to ensure the robustness of conclusions.
Randomization	Not applicable as no groups to be allocated.
Blinding	Not applicable as no groups to be allocated.

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

Antibodies

Antibodies used	Antibodies used were anti-Flag (F1804, Sigma-Aldrich), anti-HA (11867423001, Sigma-Aldrichm), and anti-myc (BE0238, Bio X Cell).
Validation	Validation of all the antibodies were provided on the manufacturers' websites.