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Corresponding author(s): H. Eric Xu

Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☒	☐	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Cryo EM processing: Relion2.1, eman2, EPU, and motioncorr2, Unblur, Ctffind4 MD simulation: Gromacs 5.0.6, and fABMACS (customized)
Data analysis	PyMol, VMD, Chimera, Coot, Phenix, LabVIEW longdistances program, Rosetta, Molprobity, Maestro, MDTraj 1.7.2

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All raw and processed data is avaiable upon request.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The sample size for integrative structure determination was determined from 227,386 particles. For all other experiments, we counted and reported accordingly how many times we performed each experiment.
Data exclusions	No data were excluded from the analysis
Replication	The experimental findings were reliably reproduced
Randomization	No randomization was required for the experiments performed in this study
Blinding	no blinding was required for the experiments performed in this study

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Research animals
☒	☐ Human research participants

Antibodies

Antibodies used	Fab-G50, 1D4-antibody (MA1-722, ThermoFisher), HRR-conjugated anti-FLAG (A8592, Sigma), anti-HA antibody (H3663, Sigma), HRP-conjugated anti-M13 mouse monoclonal antibody (ab50370, Abcam)
Validation	The antobodies were validated by pull-down assay, size exclusion chromatography, ELISA, and Western blot

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	AD293, sf9, HEK293, HEK293S GnTI-
Authentication	None of the cell lines have been authenticated
Mycoplasma contamination	All cell lines were tested negative for mycoplasma constamination
Commonly misidentified lines (See ICLAC register)	No Commonly misidentified cell lines were used

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging