

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 SerialEM v4.0, Legion v3.5, i-control v1.10.4

Data analysis cryoSPARC v3.3.1, RELION v4, Appion v3.4, Phenix v1.19.1-4122, Coot v0.9.8.2, UCSF Chimera v1.14, UCSF ChimeraX V1.2.5, MolProbity v4.5.1, Warp v1.0.9, BBtools v38.98, DISOPREDE3

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](#)

Atomic models determined in this study are available through the Protein Data Bank (PDB) with accession codes: 8EA3 (major configuration), 8EA4 (minor configuration), and 7SVU (TnsBCTD-TnsC-TniQ complex). All cryo-EM reconstructions from this study are available through the EMDB with accession codes:

EMD-27971 (major configuration), EMD-27972 (minor configuration), and EMD-25453 (TnsBCTD-TnsC-TniQ complex). Other atomic models used in this study are available through the PDB, including PDB: 7M99 (ATPyS-bound TnsC helical filament), PDB: 7SVW (TnsB strand-transfer complex), and PDB: 7PLA (sgRNA)

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	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	Sample sizes are reported in the figure legends. To obtain SD values, biological replicates of n=3 were used. For illumina sequencing of the in vitro transposition products, we pooled all the colonies from the antibiotics-selected plates. The number of colonies ranged from 50 to 500 depending on experimental condition.
Data exclusions	No data was excluded.
Replication	All the information related to the replication were included in the figure legends. Both ATP-hydrolysis assays and transposition assays were done in biological triplicates, and all the results showed similar results.
Randomization	For cryo-EM structures, during the 3D refinement processing, all the particles were randomly split into two half sets. For all other experiments, all the data was used in analysis so randomization was not needed.
Blinding	For counting colonies from in vitro transposition assays, each condition was labeled with numbers, and counted by multiple operators without knowing the conditions corresponding to each labeled number. Illumina sequencing was done by operators who do not have knowledge on the system. For ATP hydrolysis assay, each condition was also labeled with numbers, and the experiments and the analysis were done without knowing the condition corresponding to each labels.

Behavioural & social sciences study design

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

Study description	N/A
Research sample	N/A
Sampling strategy	N/A
Data collection	N/A
Timing	N/A
Data exclusions	N/A
Non-participation	N/A

Randomization

N/A

Ecological, evolutionary & environmental sciences study design

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

Study description

N/A

Research sample

N/A

Sampling strategy

N/A

Data collection

N/A

Timing and spatial scale

N/A

Data exclusions

N/A

Reproducibility

N/A

Randomization

N/A

Blinding

N/A

Did the study involve field work?

 Yes No

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

Methods

n/a Involved in the study

- Antibodies
- Eukaryotic cell lines
- Palaeontology and archaeology
- Animals and other organisms
- Clinical data
- Dual use research of concern

n/a Involved in the study

- ChIP-seq
- Flow cytometry
- MRI-based neuroimaging

Antibodies

Antibodies used

N/A

Validation

N/A

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

N/A

Authentication

N/A

Mycoplasma contamination

N/A

Commonly misidentified lines
(See [ICLAC](#) register)

N/A

Palaeontology and Archaeology

Specimen provenance

Specimen deposition

Dating methods

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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

Wild animals

Reporting on sex

Field-collected samples

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration

Study protocol

Data collection

Outcomes

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Public health
<input type="checkbox"/>	<input checked="" type="checkbox"/>	National security
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Crops and/or livestock
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Ecosystems
<input type="checkbox"/>	<input checked="" type="checkbox"/>	Any other significant area

Other impacts

Hazards

For examples of agents subject to oversight, see the United States Government [Policy for Institutional Oversight of Life Sciences Dual Use Research of Concern](#).

Experiments of concern

Does the work involve any of these experiments of concern:

- | | | |
|-------------------------------------|--------------------------|---|
| No | Yes | |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Demonstrate how to render a vaccine ineffective |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enhance the virulence of a pathogen or render a nonpathogen virulent |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Increase transmissibility of a pathogen |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Alter the host range of a pathogen |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enable evasion of diagnostic/detection modalities |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enable the weaponization of a biological agent or toxin |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Any other potentially harmful combination of experiments and agents |

Precautions and benefits

Biosecurity precautions	<input type="text" value="N/A"/>
Biosecurity oversight	<input type="text" value="N/A"/>
Benefits	<input type="text" value="N/A"/>
Communication benefits	<input type="text" value="N/A"/>

ChIP-seq

Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <small>May remain private before publication.</small>	<input type="text" value="For 'Initial submission' or 'Revised version' documents, provide reviewer access links. For your 'Final submission' document, provide a link to the deposited data."/>
Files in database submission	<input type="text" value="Provide a list of all files available in the database submission."/>
Genome browser session <small>(e.g. UCSC)</small>	<input type="text" value="Provide a link to an anonymized genome browser session for 'Initial submission' and 'Revised version' documents only, to enable peer review. Write 'no longer applicable' for 'Final submission' documents."/>

Methodology

Replicates	<input type="text" value="N/A"/>
Sequencing depth	<input type="text" value="N/A"/>
Antibodies	<input type="text" value="N/A"/>
Peak calling parameters	<input type="text" value="N/A"/>
Data quality	<input type="text" value="N/A"/>
Software	<input type="text" value="N/A"/>

Flow Cytometry

Plots

Confirm that:

- The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- All plots are contour plots with outliers or pseudocolor plots.
- A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	N/A
Instrument	N/A
Software	N/A
Cell population abundance	N/A
Gating strategy	N/A

Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	N/A
Design specifications	N/A
Behavioral performance measures	N/A

Acquisition

Imaging type(s)	N/A
Field strength	N/A
Sequence & imaging parameters	N/A
Area of acquisition	N/A
Diffusion MRI	<input type="checkbox"/> Used <input checked="" type="checkbox"/> Not used

Preprocessing

Preprocessing software	N/A
Normalization	N/A
Normalization template	N/A
Noise and artifact removal	N/A
Volume censoring	N/A

Statistical modeling & inference

Model type and settings	N/A
Effect(s) tested	N/A
Specify type of analysis:	<input type="checkbox"/> Whole brain <input type="checkbox"/> ROI-based <input type="checkbox"/> Both
Statistic type for inference (See Eklund et al. 2016)	N/A
Correction	N/A

Models & analysis

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Functional and/or effective connectivity
<input checked="" type="checkbox"/>	<input type="checkbox"/> Graph analysis
<input checked="" type="checkbox"/>	<input type="checkbox"/> Multivariate modeling or predictive analysis