# natureresearch

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## **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 <u>Authors & Referees</u> and the <u>Editorial Policy Checklist</u>.

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FUL	all statistical analyses, commit that the following items are present in the figure legend, table legend, main text, or inlethous section.
n/a	Confirmed
x	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
x	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.
x	A description of all covariates tested
X	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. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
x	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
X	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
x	Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i> ), indicating how they were calculated

Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

### Software and code

Policy information about availability of computer code

Data collection

SerialEM (University of Colorado, USA), TIA (FEI, Eindhoven, Netherlands)

Data analysis

Fiji, IMOD (University of Colorado, USA), Chimera (University of California, San Francisco, USA), Dynamo (University of Basel, Switzerland), Blender (Blender Foundation, Netherlands), MotionCorr2 (University of California, San Francisco, USA), (Relion 3.0 (Medical Research Council, UK), MatLab (Mathworks, USA), Adobe Illustrator (Adobe, USA).

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. 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 <u>data availability statement</u>. 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 data needed to evaluate the conclusions in this paper are presented here or in the Supplementary Information. Structural data is available from the Electron Microscopy Data Bank, accession numbers for electron density maps are EMD-10136, EMD-10137, EMD-10138 and EMD-10138.

### Field-specific reporting

# Life sciences study design

Data exclusions No	o data exclusion
Replication	experiments are reproduced reliably.
Randomization Not	ot applicable.
Blinding	ot applicable.

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	n/a   Involved in the study	
x	Antibodies	ChIP-seq	
x	Eukaryotic cell lines	🗷 🔲 Flow cytometry	
x	Palaeontology	MRI-based neuroimaging	
X	Animals and other organisms		
X	Human research participants		
×	Clinical data		