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For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

☐	☒	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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐	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 <i>Give P values as exact values whenever suitable.</i>
☒	☐	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

Policy information about [availability of computer code](#)

Data analysis MotionCor2 1.4.0, CtfFind4.1.14, EMAN2.3, Relion3.1, DRAFTER V1, MolProbity 4.5, Chimera 1.13.1, UCSF ChimeraX version:1.3.dev202105290025, Phenix 1.19.2-4158, Coot version:0.9.1, crvoSPARC v3.2.0

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.

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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
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Cryo-EM structures and atomic models generated in this study have been deposited in the wwPDB OneDep System under EMD accession codes EMD-33812, EMD-33813, EMD-33814, EMD-33815, EMD-33811, EMD-33816 and PDB ID codes under accession codes 7YG9, 7YGA, 7YGB, 7YGC, 7YGD, 7YGE, respectively. The

models (PDB ID: 7EZ0 and 7EZ2) used in this study are adapted from wwPDB OneDep System. The source data for Supplementary Fig. 1a are provided as a Source Data file.

Human research participants

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Reporting on sex and gender

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Recruitment

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☒	☐ Animals and other organisms
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Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging