nature research

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Last updated by author(s): Jun 14, 2020

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.

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
Data analysis	MotionCor 2, CTFFIND 4, RELION 3.0, UCSF Chimera (version 1.11.2), Resmap (version 1.1.4), COOT (version 0.8.9.1), PHENIX (version 1.16), UCSF Chimerax (version 0.91), Phyre2 (web server), Swiss Model (web server)

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 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

Ten cryoEM maps generated during this study have been deposited in the Electron Microscopy Data Bank (EMDB) and are available under accession numbers EMD-21504 (Icosahedral capsid reconstruction), EMD-21505 (C5 whole virus reconstruction), EMD-21506 (C2 2-fold sub-particle reconstruction), EMD-21507 (C3 3-fold sub-particle reconstruction), EMD-21508 (C5 CATC-absent penton vertex sub-particle reconstruction), EMD-21510 (C1 3-fold sub-particle reconstruction), EMD-21515 (C6 hexon sub-particle reconstruction), EMD-21525 (C1 CATC-binding penton vertex sub-particle reconstruction), EMD-21526 (C5 portal vertex sub-particle reconstruction), and EMD-21527 (C12 portal sub-particle reconstruction). Atomic models corresponding to EMD-21506, EMD-21507, EMD-21508, and EMD-21510 have been deposited in the Protein Data Bank (PDB) and are available under accession number PDB-6W19 (combined). Atomic models corresponding to EMD-21525 and EMD-21526 have been deposited in the Protein Data Bank (PDB) and are available under accession numbers PDB-6W2D and PDB-6W2E, respectively.

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 were estimated on the basis of previous study (DOI 10.1099/vir.0.043265-0).
Data exclusions	None
Replication	Reconstructions are the result of calculations performed on the collected data set. Therefore, all reconstructions are reproducible if the workflow is maintained.
Randomization	During 3D refinements, particles were randomly split into two halves then reconstructed two half maps in order to calculate FSC curves in Fourier space.
Blinding	Blinding is not applied in this study as this study is mainly focusing on structural analyses to multiple obtained cryoEM density maps.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Latent EBV-infected marmoset B cells (B95-8, a gift from George Miller of Yale University)
Authentication	The cell line has not been authenticated.
Mycoplasma contamination	Cell line was not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	Only B95-8 cell line was used in this study. No any commonly misidentified lines were cultured in this study.