

## 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

CryoEM data collection was performed using Thermo-Fisher EPU software

Data analysis

CryoEM data were analysed using the following software: Relion (v.2.1), MotionCor2, GCTF (v.1.06), SPIDER (v.22.10), Phenix (v.1.13), Coot (v.0.8.8), UCSF Chimera (v.1.11.2). SAXS data were processed using DAMMIF, PRIMUS and GNOM within the ATSAS (v. 2.8.3) package, RNA release assay data were processed using GraphPad Prism (v. 7.04).

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

The icosahedral reconstruction of undecorated FCV and the C3-symmetrised reconstruction of FCV-fJAM-A are deposited in the EM databank with accession

numbers EMD-0054 and EMD-0056 respectively. The atomic coordinates for the FCV capsid asymmetric unit (VP1) are deposited in the protein data bank with accession number PDB-6GSH. The atomic coordinates for the FCV-fJAM-A portal vertex (VP1, VP2 and fJAM-A) are deposited in the protein data bank with accession number PDB-6GSI. Motion corrected micrographs of undecorated and fJAM-A labelled FCV (the raw data) are deposited in the EMPIAR data bank with accession numbers EMPIAR-10192 and EMPIAR-10193 respectively. In addition there are raw data associated with Extended Data Figures 7 and 8 that can be made available 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  Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://www.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	Samples size for each cryoEM data set was established as that which was necessary to achieve the desired resolution.
Data exclusions	Data were excluded according to standard protocols for the use of Relion 2.1.
Replication	CryoEM reconstructions were performed using the Gold-standard FSC method. Each data set was randomly divided into two halves and processed independently to generate a reliable resolution measurement prior to merging of all data to produce the final reconstruction.
Randomization	Random assignment of the data to one of two halves is automated in Relion 2.1
Blinding	Processing of the independent data sets is automated in Relion 2.1 - thus blinding is achieved computationally.

## Reporting for specific materials, systems and methods

### Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

### Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging