

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 (<i>n</i>) 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. <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>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Serial EM v3.6 used for cryo-EM data collection.
Data analysis	MotionCor v2.1.2.1, Gctf v1.06, RELION v3, ResMap 1.1.4, UCSF Chimera v1.17, Coot v0.9.8.1, Phenix v1.14, Pymol v3.0.3, ALEX smFRET Analysis V1.10, Typhoon7000, Image J v1.54, Prism 8 v8.3.0, Tanon 5200 Imaging System.

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](#)

EMD-60634, PDB 9LCK.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender There is no related assay in our study.

Reporting on race, ethnicity, or other socially relevant groupings There is no related assay in our study.

Population characteristics There is no related assay in our study.

Recruitment There is no related assay in our study.

Ethics oversight There is no related assay in our study.

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](https://www.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 More than three times protein purifications and Cryo-EM samples screening were performed. For the Cryo-EM data collection, a total of 4,299 micrographs were collected. These data is enough for reconstruction of a high resolution structure. A sample size of 3 was chosen as this value was sufficient to assess the reproducibility of results. So all of functional assays were performed at least 3 times.

Data exclusions Particles were automatically picked. Images which contain contaminations were deselected. During the process of classification and refinement, images of denatured or damaged proteins were removed.

Replication All of the biochemical experiments including protein purification and polymerase activity can be replicated with the same experimental conditions. At least 3 independent experiments have been performed to assess the reproducibility.

Randomization This study is not involved in Animal or clinical trials. Randomization was not performed in this study.

Blinding This study is not involved in Animal or clinical trials. Blinding was not performed in this study.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used Rabbit anti-PB1 Antibody (Catalog # PA5-34914, Invitrogen), used at 1;3000;

Antibodies used	β -Actin (E4D9Z) Mouse mAb (Catalog # 58169S, CST), used at 1:1000. Anti-Rabbit IgG, HRP-linked Antibody (7074S, CST) and Anti-mouse IgG,HRP-linked Antibody (7076S, CST) ,used at 1:3000.
Validation	Rabbit anti-PB1 Antibody (Invitrogen), β -Actin (E4D9Z) Mouse mAb (58169S), Anti-Rabbit IgG, HRP-linked Antibody (7074S) and Anti-mouse IgG,HRP-linked Antibody (7076S) have been validated for use in western blotting, as stated on the invitrogen product page.

Eukaryotic cell lines

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

Cell line source(s)	Two insect cells (SF9 and Hi5 cells, Invitrogen) were used for protein expression using the bac-to-bac expression system.Human embryonic kidney 293T cells (HEK-293T) were using for the polymerase activity.
Authentication	The insect cell lines were purchased from Invitrogen Company and maintained in our lab.The HEK-293T cell line was purchased from ATCC.
Mycoplasma contamination	There are no mycoplasma contamination in these cell lines.
Commonly misidentified lines (See ICLAC register)	No Commonly misidentified lines were used.

Plants

Seed stocks	This study is not involved in Plants. There are no seed stocks in this study.
Novel plant genotypes	This study is not involved in Plants. There are no novel plant genotypes in this study.
Authentication	This study is not involved in Plants. There are no authentication in this study.