

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	EPU 3.3.0
Data analysis	cryoSPARC 4.5.3 EMready 2.0 cryoSPARC Patch Motion Correction Chimera X 1.6 Phenix 1.21-5207 Pymol 3.1.3.1 Coot 0.9.8.5 EL ImageQuant LAS 4000 Proteome Discoverer 2.5 Desmond version 7.2 simulation package PRIME PROPKA3 SEDFIT

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](#)

Atomic coordinates for C1 cpzA3H-VCBC and C2 cpzA3H-VCBC structures were deposited in the Protein Data Bank under accession code 9E9V and 9E93, respectively. Unsharpened cryo-EM density map and half-maps for C1 cpzA3H-VCBC and C2 cpzA3H-VCBC were deposited in the Electron Microscopy Data Bank under accession code 47805 and 47752, respectively. Other structures used in this study include

4n9f [<https://doi.org/10.2210/pdb4n9f/pdb>],
 5z98 [<https://doi.org/10.2210/pdb5z98/pdb>],
 8h0i [<https://doi.org/10.2210/pdb8h0i/pdb>],
 7b5l [<https://doi.org/10.2210/pdb7b5l/pdb>],
 7b5m [<https://doi.org/10.2210/pdb7b5m/pdb>],
 7oni [<https://doi.org/10.2210/pdb7oni/pdb>],
 8fvj [<https://doi.org/10.2210/pdb8fvj/pdb>],
 8fvi [<https://doi.org/10.2210/pdb8fvi/pdb>],
 8cx2 [<https://doi.org/10.2210/pdb8cx2/pdb>],
 8e40 [<https://doi.org/10.2210/pdb8e40/pdb>], and
 6nil [<https://doi.org/10.2210/pdb6nil/pdb>].
 Source Data are provided with this paper.

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

N/A

Reporting on race, ethnicity, or other socially relevant groupings

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

N/A

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

No statistical method was used to predetermine sample size for data collection such as cryo-EM data set, but we retrospectively confirmed that no improvement of obtained result was observed. Therefore, we concluded that the used data size was enough for our research purpose. All attempts at replication were successful.

Data exclusions

No data was excluded from the analyses.

Replication

For an assessment of reproducibility, experimental replication was applied for in-vitro ubiquitination assay and Vif-induced A3H degradation assay (n > 3). We are happy to provide all raw data for the western blotting experiments should they be requested by the editor or reviewers.

Randomization

There is no sample grouping in this study, and, therefore, no randomization was applied.

Blinding

There is no sample grouping in this study, and, therefore, no blinding was applied.

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

anti-DYKDDDDK (FLAG)-tagged mouse monoclonal antibody (mAb) (1:2,000; Fujifilm Wako Pure Chemical Co.; cat #012-22384)
 anti-A3H rabbit polyclonal antibody (1:2,000; Novus Biologicals; cat #NBP1-91682)
 mouse anti-HIV-1 Vif monoclonal antibody (1:1000; Abcam; cat#ab66643)
 rabbit anti- β -tubulin polyclonal antibody (1:2000; Abcam; cat #ab6046)
 goat anti-mouse IgG antibody (1:20,000; Thermo Fisher Scientific)
 goat anti-rabbit IgG antibody (1:20,000; Thermo Fisher Scientific)

Validation

All primary antibodies were validated by the manufacture on their availability, at least, for western blotting application in terms of reactivity, specificity, and stability per lot.

Eukaryotic cell lines

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

Cell line source(s)

HEK293T cells, purchased from ATCC

Authentication

The cell is routinely maintained in our lab. No specific authentication was performed.

Mycoplasma contamination

The cell was tested negative for Mycoplasma contamination by MycoAlert detection kit (Lonza).

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified cells were used in this study.

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.