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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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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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.
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.
X	A description of all covariates tested
\times	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>
X	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
X	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
X	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 <u>statistics for biologists</u> contains articles on many of the points above.
C -	former and and

Software and code

Policy information about <u>availability of computer code</u>

Data analysis cryoSPARC v4.1.2, Phenix v1.20.1, Coot v0.9.8.2, UCSF Chimera v1.16, UCSF ChimeraX v1.5, Topaz v0.2

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

The atomic models have been deposited in the PDB with accession codes: 8FVI (A3H-VCBCC complex) and 8FVJ (VCBCC complex dimer). The cryo-EM maps have been deposited in the EMDB with accession codes: EMD-29488 (A3H-VCBCC complex), EMD-29489 (VCBCC complex dimer), and EMD-29490 (A3H-VCBCCR complex). Raw electron microscopy data files have been deposited in the Electron Microscopy Public Image Archive (EMPIAR) with accession code EMPIAR-11423 (A3H-VCBCCR complex) and EMPIAR-11424 (A3H-VCBCC complex and VCBCC complex dimer). Source data are provided with this paper.

Reporting on sex and gender N/A Population characteristics N/A Recruitment Repeached the study produced in the manuscript. Field—special selection before making your selection. Life sciences Behavioural & social sciences Lorder selection before making your selection. Recruitment discolose on these points even when the discolosure is negative. No mentodose were used that would require any analysis and recruitment and all the current study related to Vif-mediated degradation assay and in vitro obliquitination assay, and single-particle cryo-EM. Vif-mediated degradation assay and in vitro obliquitination assay, and single-particle cryo-EM. Vif-mediated degradation assay and in vitro obliquitination assay were repeated at least three times and all the replicates showed the similar results. All attempts at replication were successful. Randomization The croticin particle images used in the final 3D reconstruction of the cryo-EM analysis were randomly split into two half datasets for the estimation of the coveral res	Human rese	arch parti	cipants			
Population characteristics NVA Recruitment NVA Ethics oversight NVA 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 ror a reference copy of the document with all sections, see nature convidocuments for reporting summary flat pdf Life sciences study design All studies must disclose on these points even when the disclosure is negative. No methods were used that would require a predetermined sample size due to the nature of the current study related to Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM. Vif-mediated degradation assay and in vitro ubiquitination assay were performed independently triplicates. The reproducibility of the triplicates made us confident that pains less was sufficient. The sample size in cryo-EM was considered adequate since the addition of extra data did not improve the 3D reconstruction significantly. Data exclusions No data were excluded from the study. Vif-mediated degradation assay and in vitro ubiquitination assay were repeated at least three times and all the replicates showed the similar results. All attampts at replication were successful. Randomization The protein particle images used in the final 3D reconstruction of the cryo-EM analysis were randomity split into two half datasets for the estimation of the overall resolution by Fourier shell correlation. No other methods were used that would require any randomization electriques due to the nature of the current study related to Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM and no randomization was applied. Blinding There is no allocation of sample groups in Vif-mediated degradation assay, in vitro ubiq	Policy information a	about <u>studies i</u>	nvolving human research participants and Sex and Gender in Research.			
Recruitment N/A Statistics 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 Tot a reference cupy of the document with all sections, see restart econolidocuments/hirrequorines.ammuschlat.adf Life sciences study design All studies must disclose on these points even when the disclosure is negative. No methods were used that would require a predetermined sample size due to the nature of the current study related to Vif-mediated degradation assay, in vitro ubiquitination assay and single-particle cryo-EM. Vif-mediated degradation assay and in vitro ubiquitination of extra data did not improve the 3D reconstruction significantly. Data exclusions No data were excluded from the study. Wif-mediated degradation assay and in vitro ubiquitination assay were repeated at least three times and all the replicates showed the similar results. All attempts at replication were successful. Randomization The protein particle images used in the final 3D reconstruction of the cryo-EM analysis were randomly split into two half datasets for the estimation of the overall resolution by Fourier shell correlation. No other methods were used that would require any and single-particle cryo-EM. There is no allocation of sample groups in Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM and no randomization assay, and single-particle cryo-EM. There is no allocation of sample groups in Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM and no randomization was applied. Blinding There is no allocation of sample groups in this study and no binding was applied. All experiments were conducted in an unblinded way since	Reporting on sex and gender		N/A			
Ethics oversight NA 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 topy of the document with all sections, see nature cont/documents/nc-resorting-summare/lat adf Life sciences study design All studies must disclose on these points even when the disclosure is negative. Sample size No methods were used that would require a predetermined sample size due to the nature of the current study related to VIF-mediated degradation assay, in vitro ubiquitination assay were performed independently triplicates. The reproducibility of the triplicates made us confident that the sample size was sufficient. The sample size in cryo-EM. May considered adequate since the addition of extra data did not improve the 3D reconstruction significantly. Data exclusions No data were excluded from the study. Replication Wif mediated degradation assay and in vitro ubiquitination assay were repeated at least three times and all the replicates showed the similar results. All attempts at replication were successful. Randomization The protein particle images used in the final 3D reconstruction of the cryo-EM analysis were randomly split into two half datasets for the estimation of the overall resolution by Fourier shell correlation. No other methods were used that would require any randomization techniques due to the nature of the current study related to Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM and no trandomization was applied. Blinding There is no allocation of sample groups in this study and no blinding was applied. All experiments were conducted in an unbilinded way since the investigators were involved in the planning, execution and an	Population chara	cteristics	N/A			
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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/hr reporting summary-flat adf Life sciences study design All studies must disclose on these points even when the disclosure is negative. Sample size ☐ No methods were used that would require a predetermined sample size due to the nature of the current study related to Vif-mediated degradation assay in vitro ubiquitination assay were performed independentily triplicates. The reproducibility of the triplicates made us confident that the sample size was sufficient. The sample size in cryo-EM was considered adequate since the addition of extra data did not improve the 3D reconstruction significantly. Data exclusions ☐ No data were excluded from the study. Replication ☐ Vif-mediated degradation assay and in vitro ubiquitination assay were repeated at least three times and all the replicates showed the similar results. All attempts at replication were successful. The protein particle images used in the final 3D reconstruction of the cryo-EM analysis were randomly split into two half datasets for the estimation of the overall resolution by Final 3D reconstruction. No other methods were used that would require any randomization techniques due to the nature of the current study related to Vif-mediated degradation assay, in vitro ubiquitination assay, and single-particle cryo-EM and no randomization was applied. Blinding ☐ There is no allocation of sample groups in this study and no blinding was applied. All experiments were conducted in an unblinded way since the investigators were involved in the planning, execution and analyses of the current study. Reporting for specific materials, experimental systems and methods used in many studies. Here, indicate whethe	Ethics oversight		N/A			
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n/a Involved in the study n/a Involved in the study						
Antibodies ChIP-seq						
		Palaeontology and archaeology MRI-based neuroimaging				
Animals and other organisms Clinical data						
Dual use research of concern	Clinical dat	a				

Antibodies

Antibodies used Monoclonal ANTI-FLAG® M2 antibody (Catalog #F3165, Sigma, 1:3,000)

Monoclonal ANTI-HA antibody (Catalog #H9658, Sigma, 1:3,000) Monoclonal anti-tubulin antibody (Catalog #GT114, GeneTex, 1:5,000)

Monoclonal anti-HIV-1 Vif antibody (National Institutes of Health AIDS Reagent Program #319, 1:2,000)

Cy3-labelled goat-anti-mouse secondary antibody (Catalog #PA43009, GE Healthcare, 1:3,000)

Validation Monoclonal ANTI-FLAG® M2 antibody: https://www.sigmaaldrich.com/US/en/product/sigma/f3165

Monoclonal ANTI-HA antibody: https://www.sigmaaldrich.com/US/en/product/sigma/h9658

Monoclonal anti-tubulin antibody [GT114]: https://www.genetex.com/Product/Detail/alpha-Tubulin-antibody-GT114/GTX628802 Monoclonal anti-HIV-1 Vif antibody: https://www.hivreagentprogram.org/Catalog/HRPMonoclonalAntibodies/ARP-6459.aspx Cy3-labelled goat-anti-mouse secondary antibody: https://www.cytivalifesciences.com/en/us/shop/protein-analysis/blotting-and-

detection/blotting-standards-and-reagents/amersham-ecl-plex-cydye-conjugated-antibodies-p-05749#productsupport

Eukaryotic cell lines

Policy information about <u>cell lines and Sex and Gender in Research</u>

Cell line source(s) 293T (or HEK293T) Cells from ATCC.

Authentication No authentication procedure for the cell line was used.

Mycoplasma contamination No contamination.

Commonly misidentified lines

(See ICLAC register)

No commonly misidentified cell lines were used in this study.