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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 [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 (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	Invitrogen Attune NxT, Operetta High Content Imaging System; FlexStation 3 (Molecular Devices); CFX Connect Real-Time System (Bio-Rad); Illumina HiSeq 2500; FEI Tecnai G2 20 Twin transmission electron microscope; ImmunoSpot® Analyzer; SCIEX Triple Quad 5500+ LC-MS/MS System; TwoMP instrument (Refeyn Ltd, Oxford, UK); Optima AUC analytical ultracentrifuge (Beckman Coulter)
Data analysis	ImageJ v2.0.0; XDS (version January 10, 2022); PHASER; phenix.refine (Phenix version 1.19.2-4158); Molprobit PHENIX program (phenix.mosaic); PyMol v3.0.3 (Schrödinger, LLC); AcquireMP v2.3 (Refeyn Ltd); DiscoverMP v2.3 (Refeyn Ltd); Prism Graphpad v9.0.2; hydropro (version 10) ; FOXTROT and PRIMUS from ATSAS 3.2; RAW 2.3.1; GNOM (version 5.0); CRYSQL (version 2.8.3); DAMMIN (version 5.3); PerkinElmer Harmony high-content analysis software v4.9

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](#)

Coordinates and structure factors have been deposited in the Protein Data Bank under the accession code 9QQV (<https://www.rcsb.org/structure/unreleased/9QQV>). All other relevant data generated in this study are provided in the Supplementary Information/Data and Source Data file.

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

In this study, we did not include any human participants, and did not collect any information.

Reporting on race, ethnicity, or other socially relevant groupings

In this study, we did not include any human participants.

Population characteristics

In this study, we did not include any human participants.

Recruitment

In this study, we did not include any human participants.

Ethics oversight

In this study, we did not include any human participants.

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

The sample size was indicated in the figure legends with n equals to 3 or above (three or more independent biological experiments). No sample size calculation was performed. Sample size (n=3 or above) is chosen based on the standard of the corresponding field.

Data exclusions

No data were excluded.

Replication

Data shown are an average of two or more independent experiments performed in duplicate or triplicate. Similar findings were obtained from all repeats.

Randomization

Male animals used in the study were allocated randomly. Randomization is not relevant to other cell culture-based experiments. The same number of cells were used for the experiments. The experiments were well-controlled and there is no background difference between experimental groups.

Blinding

Since the experimental groups were conducted in parallel with the sample procedures, and data are quantitative, the investigators who conducted the cell culture experiments were not blinded, but the data collection and analysis were performed carefully by two or more different investigators for all the experiments.

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
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

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

Antibodies

Antibodies used	mAb 7D11 (antibody system #RVV13903)
Validation	Commercial primary antibodies were validated by the manufacturers and validation statements are available on the manufacturer's website.

Eukaryotic cell lines

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

Cell line source(s)	BS-C-1 (Cell Bank of the Chinese Academy of Sciences #SCSP-5506), CV-1, HaCaT, SW13, Huh7, Vero E6 (Cell Bank of the Chinese Academy of Sciences, #GNO17), HFF-1 (ATCC #SCRC-1041), U-2 OS (ATCC #HTB-96), BHK-21 (ATCC #CCL-10), HEK 293T (ATCC #CRL-3216), A549 (ATCC #CCL-185), and HeLa (ATCC #CCL-2)
Authentication	None of the cell lines used in the manuscript were authenticated by authors.
Mycoplasma contamination	All cell lines used were tested routinely and free of mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	None.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Male SCID mice aged 4-5 weeks were used to assess the antiviral efficacy. Male ICR mice (4–6 weeks, 18–22 g) were used to determine the pharmacokinetics of the compounds. Male dormice aged 10-12 weeks were used to evaluate the replication of single-cycle viral particles.
Wild animals	No wild animals used.
Reporting on sex	In this study, we just have enough male animals ready for the experiments.
Field-collected samples	No field-collected samples involved.
Ethics oversight	All animal experiments were conducted in accordance with the National Institutes of Health (NIH) Guide for the Care and Use of Laboratory Animals and were approved by the Animal Care and Use Committees of the Changchun Veterinary Research Institute (IACUC approval no. AMMS-11-2023-041).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Plants

Seed stocks	<i>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.</i>
Novel plant genotypes	<i>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.</i>
Authentication	<i>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.</i>

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

Common cell lines were collected from cell culture by using the Trypsin or TrypLE (Thermo).

Instrument

Thermo, Invitrogen Attune NxT.

Software

FlowJo vX.0.7

Cell population abundance

About 0.1 million cells per sample were analyzed. We didn't determine the purity of cells in the relevant experiments in this study.

Gating strategy

Gating was used to eliminate debris and multiplet cells using forward and side scatter parameters (SSC-A/FSC-A). The antibody-bound, or mGreen-positive cells were gated positive based on SSC-A/APC-A or SSC-A/FITC. The staining with isotype control was used as the control of gating.

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.