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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	MALDI-TOF spectrometry data was collected on Bruker Daltonics Compass 1.4 for flexSeries software. HPLC data was collected on LabSolutions Realtime Analysis version 5.81 SP1 software. MS data was collected on Bruker Daltonics Hystar version 3.2 SR4 software. NMR spectroscopy was collected using JNM-AL version 6.0 software. Molecular docking was calculated using Autodock 4.2 and Autodock Vina software version 1.1.2 software. Fluorescence data was collected using SoftMax Pro version 7.0.3 software. Cell imaging data was collected using BZ-X Viewer software. All software packages and code used are commercially or freely available.
Data analysis	MALDI-TOF spectrometry data was analyzed by Bruker Daltonics Compass 1.4 for flexSeries software. HPLC data was analyzed on LabSolutions Postrun Analysis version 5.81 SP1 software. MS data was analyzed on Bruker Daltonics Compass DataAnalysis version 4.2 (Build 383.1). NMR spectroscopy was analyzed using JEOL Delta version 5.0.2 software. Molecular docking was graphically implemented using AutoDockTools version 1.5.6 software. Protein-ligand figure generation was performed using PyMOL version 0.99rc6 and Discovery Studio Visualizer version 17.2.0.16349 software. Fluorescence data was analyzed using SoftMax Pro version 7.0.3 software. Cell imaging data was analyzed using BZ-X Analyzer software. All software packages and code used are commercially or freely available.

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 data that support the plots within this paper and other findings of this study are available from the corresponding author upon reasonable 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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes were chosen based on reproducibility
Data exclusions	No data were excluded from the analysis, unless an obvious error/spillage/fault was encountered during the experiment.
Replication	All experiments were performed in experimental replicates described, where material allowed.
Randomization	For cell imaging studies, data was collected from 3 random locations.
Blinding	There was no blinding

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	SW620, HeLa, A549 cell lines
Authentication	All obtained from RIKEN Cell Bank, where Quality Control includes STR analyses.
Mycoplasma contamination	All obtained from RIKEN Cell Bank, where Quality Control includes tests for Mycoplasma infection.
Commonly misidentified lines (See ICLAC register)	All obtained from RIKEN Cell Bank, where Quality Control includes tests for misidentification via Short Tandem Repeat polymorphism analysis.