

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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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	Protonation states of small molecules were obtained using either Dimorphite-DL 1.2.4 or OpenBabel 3.1.1. Rosetta virtual screening codes developed in this work have been incorporated in the latest version of Rosetta 3.14 at https://github.com/RosettaCommons/rosetta . OpenVS platform codes and scripts are available on Zenodo at https://doi.org/10.5281/zenodo.12988631 and also on GitHub at https://github.com/gfzhou/OpenVS .
Data analysis	Post virtual screening analysis used CSD 2023.3 python api, RDKit 2023.3.3, openbabel 3.1.1, Rosetta 2023.45 and analysis codes included in the OpenVS platform. X-ray diffraction data was automatically processed using xia2 to run DIALS 3.8. All crystallographic data were analyzed using Phenix package version 1.20.1 and COOT version 0.9.8.91. Figures of structural analysis were generated by PyMOL version 2.5.5 and LIGPLOT version 2.0. The BioLayer interferometry (BLI) data were analyzed by the Octet data analysis software version 9.0. Figures of binding analysis were generated with Prism 8 (GraphPad). Figures in the manuscript were rendered using Inkscape 1.3.2.

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](#)

All compounds in this work are available from Enamine. The virtual screening library, Enamine REAL and ZINC22, used in this work is freely available from Enamine (<https://enamine.net/>) or ZINC22 (<https://cartblanche.docking.org/>) respectively. The druglike-centroid library generated in this study is available for download at <https://files.ipd.uw.edu/pub/OpenVS/centroids.tgz> [<https://files.ipd.uw.edu/pub/OpenVS/centroids.tgz>]. The source data for figures and tables in the main text and supplementary information are provided in the Supplementary Information/Source Data file. The crystal structure of the KLHDC2-C29 complex is available from the PDB with accession code: 8UXS [<https://doi.org/10.2210/pdb8UXS/pdb>]. The crystallographic data associated with Fig. 2e is deposited with the PDB. Chemical purity of all the compounds and their LC-MS spectra are available in Supplementary Data 2-3. All other data are available from the authors upon request. 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

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

Life sciences study design

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

Sample size	No sample size calculation was done for the studies described in this manuscript. The sample sizes chosen were based on our previous studies for reproducibility and widely adopted protocols in the field.
Data exclusions	No data were excluded from the analyses.
Replication	All data are representatives of at least two independent experiments. All attempts of replication were successful.
Randomization	Randomization was not required since no animal or humans were involved.

Blinding

Blinding was not required, since no animal or human subjects were involved and no human judgment was involved in generating the data.

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

Eukaryotic cell lines

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

Cell line source(s)	Sf9 (from Life Technologies B825-01) and High Five (from Life Technologies B85502) insect cells were used for recombinant protein production. Stable ion channel-expressing HEK293 cell lines used in electrophysiological experiments were gifted to our laboratory by various collaborators as described in the Methods section.
Authentication	Sf9 (from Life Technologies B825-01) and High Five (from Life Technologies B85502) insect cells have been authenticated by the vendors. No further authentication was performed for commercially available cell lines. All cell lines used in electrophysiological experiments were regularly used and maintained in our laboratory, but not authenticated.
Mycoplasma contamination	Sf9 (from Life Technologies B825-01) and High Five (from Life Technologies B85502) insect cells were not tested for mycoplasma contamination. No mycoplasma contamination was detected using Applied Biological Materials Inc.'s Mycoplasma PCR Detection Kit after cells were treated using Applied Biological Materials Inc.'s MycoAway™ Mycoplasma Elimination kit.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used.

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>