nature portfolio

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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	Tm of proteins were estimated on a QuantStudio 3 Real-Time PCR System (Applied Biosystems) using the QuantStudio Design & Analysis Software v1.5.2. Crystallinity of PET samples were estimated using DSC250 (TA Instruments) with a Trios software (TA Instruments). Bioreactor parameters were followed and controlled using Parallel Bioreactor controller system (Multifors, Infors, Switzerland). Chromoleon software was uesd for acquisition of spectra on High-Performance Liquid Chromatography (HPLC) LC-20AT chromatography system (Shimadzu, Kyoto, Japan) equipped with a ZORBAX extend-c18 column (150 × 4.6 mm, 5 µm, Agilent). Crude enzyme activities were estimated using a microplate reader (BioTek, USA) with a Gen5 v2.04.11 software.
Data analysis	Molecular docking files for ICCG, 3PET and 4PET were generated by the software AutoDockTools 1.56. The config file containing the 3D coordinates of the molecule docking region and the boundaries of the region was generated by pymol 2.0. Autodock vina 1.1.2 was used for molecular docking of ICCG and PET molecular (3PET and 4PET). MD simulations were performed using NAMD 2.12 with the PET force field and the OPLS-AA/M force field, and the PET force field was generated using the online tool LigParGen. Analysis of the trajectory was performed with VMD 1.9.2. The R package bio3d 2.4 was used for clustering MD simulation trajectories, and the R package pheatmap was used for clustering of key residues bound by 3PET. Images of hydrogen bonds, energy analysis and protein structure diagram were generated by R, GraphPad Prism 8 and Chimera X.

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

Data supporting the findings in this study are available within the paper and its Supplementary Information, or are available from the authors upon reasonable request.

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	Not applicable
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable
Population characteristics	Not applicable
Recruitment	Not applicable
Ethics oversight	Not applicable

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	For enzymatical assays with quantitative data, 3 replicates were performed to determine mean and standard deviation and is stated when relevant. For enzymatical assays with Tm assessment, 4 replicates were performed to determine mean and standard deviation and is stated when relevant.
Data exclusions	No data was excluded.
Replication	All experiments with explicit standard deviation (SD) were performed in triplicates or quadruplicates.
Randomization	No data was randomized.
Blinding	For HPLC and DSC analysis, the analytical team who analyze the data were blind to the samples that they were analyzing.

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