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	HKL-3000 (release 708) obtained at http://www.hkl-xray.com/hkl-3000 CCP4 (version 7.0) obtained at https://www.ccp4.ac.uk/
Data analysis	GraphPad Prism (version 9.4.0); coot (Coot 0.9.3 to 0.9.8.8) https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/binaries/; phenix.refine (PHENIX 1.19.1_4122) https://phenix-online.org/; PyMol (version 2.5.4), (https://pymol.org/); Waters MassLynx software V4.1 SCN949; Aimless (imosflm version 7.4.0); ccp4i2 (Version 1.1.0 revision 6539, user interface to CCP4 Program Suite version 9.0.003); ARP-WARP (Version 8.0)

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 data generated during this study are provided within the manuscript, the Supplementary Information and Source Data files. All biological materials are available to qualified researchers upon request. Structure datasets are available in the Protein Data Bank under accession codes 7UBZ [https://www.rcsb.org/structure/7UBZ] and 9CYS [https://www.rcsb.org/structure/9CYS]. Sequences for Tle and Tli are available from Genbank under accession codes WP_013096193.1 [https://www.ncbi.nlm.nih.gov/protein/WP_013096193.1] and WP_013096194.1 [https://www.ncbi.nlm.nih.gov/protein/WP_013096194.1], respectively.

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	No statistical methods were used to determine sample sizes. Sample sizes were chosen according to accepted standards in the field and based on our recently published studies (PMCID:PMC10294671, PMCID: PMC7777165).
Data exclusions	no data were excluded
Replication	All experiments (competition co-cultures, crosslinking and phospholipase activity assays) were performed independently at least three times with similar results.
Randomization	Randomization was not required for this study because for each experiment, all samples were simultaneously treated and analyzed in parallel.
Blinding	All results are based on objective and/or quantitative analyses of primary capture data, with no subjective interpretations. Therefore, blinding was not required for this study.

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

Antibodies

Antibodies used: Custom rabbit polyclonal antisera raised against full-length Tle from Enterobacter cloacae ATCC 13047 was used as the primary antibody at 1:5,000 dilution, and IRDye 800CW goat anti-rabbit IgG (LI-COR, Cat# P/N 925-32211) served as the secondary antibody used at 1:40,000 dilution.

Validation: Polyclonal antibody specificity is demonstrated in Figs. 1a and 3f, where lysates from control cells that do not produce Tle protein are analyzed.

Plants

Seed stocks: not applicable

Novel plant genotypes: not applicable

Authentication: not applicable