

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input checked="" type="checkbox"/>	<input type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of all covariates tested
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input checked="" type="checkbox"/>	<input type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	<input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input checked="" type="checkbox"/>	<input type="checkbox"/> 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	Chromeleon Client v6.80 was used for preparative HPLC and ChemStation Rev. B.04.03-SP2 for HPLC-UV/MS and HPLC-UV operation. Jeol Delta 6.1 and Bruker Topspin 3.5 softwares were used for NMR measurements.
Data analysis	The ProtParam tool of ExPASy was used for calculation of the molecular weight and molar extinction coefficient of enzymes used. ChemStation Rev. B.04.03-SP2 (Agilent) was used for HPLC-UV/MS and HPLC-UV data analysis; Chromeleon Client v6.80 for preparative HPLC data analysis. MestReNova 16.0 (Mestrelab Research, S.L.) and JASON v3.1 (Jeol) were used for NMR spectra interpretation. SigmaPlot v10.0 was used for nonlinear fitting of initial rate data. AlphaFold DB was used for structural prediction and Pymol v4.6 for structural analysis of proteins.

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 relevant data are reported in the manuscript and in the associated Supplementary Information. All data are available from the corresponding author upon request. There is no restriction on data availability. Sequence information on proteins used within this study is available on the UniProt database (<https://www.uniprot.org/>). UGT84A49, UGT84A119, UGT72D1 and UGT72D7 are registered under accession numbers Q2V6K1 [<https://www.uniprot.org/uniprotkb/Q2V6K1/entry>], A0A2N9FYZ7 [<https://www.uniprot.org/uniprotkb/A0A2N9FYZ7/entry>], Q9ZU72 [<https://www.uniprot.org/uniprotkb/Q9ZU72/entry>] and A0A067GVI4 [<https://www.uniprot.org/uniprotkb/A0A067GVI4/entry>], 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	<input type="text" value="N/A"/>
Reporting on race, ethnicity, or other socially relevant groupings	<input type="text" value="N/A"/>
Population characteristics	<input type="text" value="N/A"/>
Recruitment	<input type="text" value="N/A"/>
Ethics oversight	<input type="text" value="N/A"/>

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	<input type="text" value="The study was performed with purified enzymes. The sample size 'n' is given in each experiment. Kinetic measurements were conducted in three individual experiments. The n= employed is the standard for biochemical protein characterization."/>
Data exclusions	<input type="text" value="No data was excluded from the analysis."/>
Replication	<input type="text" value="Kinetic studies were conducted in three individual experiments. All attempts of replication were successful, leading to the calculation of consistent kinetic parameters."/>
Randomization	<input type="text" value="Randomization is not typically applied in enzyme kinetics determinations/biocatalysis assays."/>
Blinding	<input type="text" value="Blinding is not typically applied in enzyme kinetics determinations/biocatalysis assays."/>

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	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input 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	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging