

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 NOVA Autolab 1.10.0, GPES 4.9

Data analysis Microsoft Excel 2016, Graphpad Prism 8, Byonic (ProteinMetrics v4.3), UCSF Motioncor 1.0.4, CTFFIND 4.1.8, Relion 3.1.2, crYOLO 1.7.6, cryoSPARC 3.0.1 and 3.3.2, gautomatch V 0.53, ChimeraX 1.3, Phenix 1.17, AlphaFold 2.1.1, Origin 8, Qsoas 3.0, Coot 0.92, Pymol 2.4.1, pyem v0.5, CAVER 3.0, EasySpin v.6.0.0-dev47, XDS 20230630, CCP4 8.0.012v, Clustal algorithm

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](#)

CryoEM maps and atomic models, and X-ray crystallographic models and structure factors generated in this paper have been deposited in the Protein Data Bank (accession code 8UEM, 8UDS) and the Electron Microscopy Data Bank (accession code EMD-42164). AlphaFold2 models and Source Data are provided with this

paper. All the data generated in this study is available within the main text, the Supplementary Information file; source data are provided in the Source Data file. Data is also available from the corresponding authors upon request. Raw data for the mass spectrometry experiments associated with Figure 3 and Extended Data Figure 7 the paper can be found at [10.5281/zenodo.14189372](https://doi.org/10.5281/zenodo.14189372).

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	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	After a series of optimization experiments a sample size of at least 3 independent repeats was performed.
Data exclusions	A series of optimization experiments were conducted for enzyme assays, prior to the final generation of the final data presented in the manuscript. The data from these optimization experiments were not included in the final manuscript, however, they are consistent with the presented data.
Replication	After a series of optimization experiments at least 3 independent repeats were performed, all attempts at replication were successful.
Randomization	In this study we characterized a single purified enzyme (Carbon Monoxide Dehydrogenase) using a range of techniques. As a single enzyme sample was analysed randomization is not applicable to this study
Blinding	In this study we characterized a single purified enzyme (Carbon Monoxide Dehydrogenase) using a range of techniques. As a single enzyme sample was analysed blinding is not applicable to 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
<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	Involved 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

Plants

Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A