

eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or the [ARRIVE guidelines](#) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

When applicable (Fig 4B; Fig 5B, C, D, E; Fig 6A-D; Fig 1 - figure supplement 1E; Fig 4 - figure supplement 4B and 4C), the exact sample size for each experimental condition is given as a discrete number in the figure legends. We consider this sample size is sufficient because 1/activity measurements are based on continuous monitoring of NADH oxidation, resulting in accurate measurements of the ATP hydrolysis rate as compared with end-point measurements and 2/the values obtained for a given condition are similar to each other

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Replicates should be considered as technical replicates in the sense that the data plotted for a given condition are independent measurements of the same purification. However, Δ NC and Δ C were, for instance, purified several times with similar results. All attempts were included as replicates to plot data displayed in the relevant figures and the reproducibility between the various measurements is illustrated by errors bars (standard deviation) and scatter plots. No data were excluded to plot results. Fig 1 - figure supplement 1E is the result of three independent replicates (independent membrane preparation and purification).

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Whenever applicable, statistical tests used to interpret differences between groups are identified in the figure legends, along with exact p-values. Individual data points are shown for $n < 10$

(For large

datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

No group allocation was performed in this study as the present study is not a clinical research trial and does not deal with human or animal experimental subjects.

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

Source data files have been provided for: Fig 4B; Fig 5B, C, D, E; Fig 6A-D; Fig 1 - figure supplement 1E; Fig 4 - figure supplement 3B; Fig 4 - figure supplement 4; Fig 5 - figure supplement 1C; Fig 6 - figure supplement 1; Fig 6 - figure supplement 2B. Moreover, full raw unedited gels or blots and figures with uncropped gels or blots with the relevant bands clearly labelled have been provided