***eLife’s* transparent reporting form**

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**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:

All sample sizes, replicates and statistical methods are stated in the figure legends. Sample sizes and numbers of replicates were sufficient and standard (>3 experiments, each in triplicate or quadruplicate as appropriate. No sample size computation was necessary. They were all biochemical assays; no animals or human subjects were used.

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* 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
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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All information on biological and technical replicates, the number of independent repeats and the number of replicates within each experiment, is clearly stated in the figure legends. No outliers that were not clearly due to defined experimental errors / technical problems were excluded.

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* 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.

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Data is typically presented as average (mean) ± SEM as indicated in all figure legends and in the materials and methods section Statistical Analysis. Many representations are as bar graphs, which I believe is the most effective form for the data presented. Numbers of replicates are indicated as a range and are always three or more. Whenever a specific EC50 or IC50 value is highlighted in the text the number of replicates *n* is given. Numbers of replicates and exact P values are also given in supplementary tables and data sheets co-submitted with the manuscript.

(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

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None of that is applicable for this manuscript.

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

Two data files, with all raw data for the transport experiments and for the drug sensitivity data, respectively, will be uploaded with the submission. They will have the raw data, numbers of replicates, averages, SEM and P values, and where applicable the percentage change from relevant controls.