***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
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* 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:

Number of participants was determined by availability of sufficient samples for proteomics and acetylomics.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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**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
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This study is a repeated-measures design. There was no group allocation.

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* 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:

Source data for the proteome and acetylome in Figures 2-7 and S1-S4 has been uploaded to PRIDE with the dataset identifier PXD023084, **Username:** [reviewer\_pxd023084@ebi.ac.uk](mailto:reviewer_pxd023084@ebi.ac.uk), **Password:** qjQ6K7vW.