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

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* 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:

State of the art SILAC immmunoprecipitation (IP) experiment with subsequent MS analysis are routinely done in triplicates (indicated in the corresponding legends)

State of the art SILAC RNAi experiments with subsequent MS analysis are routinely done in triplicates (indicated in the corresponding legends)

**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
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The SILAC IP MS analyses shown in Fig. 3B (TbPam16/TbPam18) were done in triplicates. This is indicated in the corresponding legends.

The new SILAC IP MS analysis shown in Fig. 6 – supplement 1 (ACAD) was done in triplicates. This is indicated in the corresponding legends.

The SILAC RNAi MS analysis shown Fig. 9 and Fig. 9 – figure supplement 1 was performed in triplicates. This is indicated in the corresponding legends.

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* Statistical analysis methods should be described and justified
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* 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)
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The statistics used for the bioinformatic analysis shown in Fig. 1, Fig. 1 - figure supplement 1, Fig. 1 - and figure supplement 2 are described in the corresponding figure legends as well as in the Material and Methods sections “Protein similarity network analysis”, “Assembly of diplomenid transcriptomes” and “Phylogenetic analysis”

The SILAC IP MS analyses shown in Fig. 3B (TbPam16/TbPam18) were done in triplicates. This is indicated in the corresponding legends and the Material and Methods section LC-MS and data analysis.

The new SILAC IP MS analysis shown in Fig. 6 – supplement 1 (ACAD) was done in triplicates. This is indicated in the corresponding legends and the Material and Methods section LC-MS and data analysis.

The standard statistical analysis applied to the SILAC RNAi MS data shown Fig. 9 and Fig. 9 – figure supplement 1 was done in triplicates. This is indicated in the corresponding legends and the Material and Methods section LC-MS and data analysis.

(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.)

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* 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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Does not apply to neither the bioinformatic analysis nor to the pulldown experiment

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