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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:

No explicit power analysis was used to estimate appropriate sample size. The number of experimental repeats were commensurate with standards in the field and past work from the lab.

**Replicates**

* You should report how often each experiment was performed
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* 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)

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• Capture of in vitro translated proteins by GST fusions (Fig. 3A, 3B, 3\_S1A, 3\_S1B, 4A, 5A): experiments were repeated between one and five times, most experiments were repeated three times. The results of each individual experiment are plotted as gray data points in the graph and the number of experimental replicates can be deducted by visual inspection of the figures.

• Yeast Two Hybrid (Fig. 3C, 3D, 3\_S1C, 5B, 5\_S1A): Each experiment was repeated at least twice. The number of experimental repeats is indicated in the figure legends.

• Capture of pure BBSome by GST fusions (Fig. 7A): experiments were repeated at least 3 times. This is indicated in the figure legend.

**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.

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(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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* 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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Maps and coordinate uploaded. Fig. 1B and 2.