***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

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* You should report how often each experiment was performed
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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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• 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.

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* Statistical analysis methods should be described and justified
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* 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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* 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
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