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On the cover, the authors have applied a novel algorithm to two recently generated, large scale physical interaction datasets in Saccharomyces cerevisiae that quantitatively report through a purification enrichment score on the relative likelihood of each protein-protein interaction. Hierarchical clustering of the combined dataset presents an accurate view of the in vivo physical interactome for budding yeast. For details, see the article by Collins et al., pages 439–450.

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