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## Budding interactome

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Functional genomics aims to turn genomic information into a comprehensive understanding of the workings of the cell at the molecular level. It is assumed that extensive knowledge of the interactions between proteins will contribute significantly to this goal. In the Early Edition of *Proceedings of the National Academy of Sciences*, Ito *et al.* describe the results of a comprehensive high-throughput screen to identify all the protein-protein interactions (the 'interactome') in the budding yeast *Saccharomyces cerevisiae*. They used the yeast two-hybrid approach to screen 'bait' proteins representing the entire 6000 proteins encoded by the yeast genome. They identified 4,549 interactions between 3,278 proteins. Among the interactions are subnetworks implicated in distinct biological events, such as spindle-pole-body function, autophagy and vesicular transport. Less than 20% of these interactions overlap with those identified in an independent screen, emphasizing the experimental limitations of the methodology and the difficulty in obtaining fully comprehensive datasets.

## References

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