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Gastric interactions

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Large numbers of protein-protein interactions have been mapped for yeast and worms, and now in the January 11 Nature, Rain *et al*. present the first large set of interactions for a prokaryote (*Nature* 2001, **409:**211-215). The two-hybrid screen of 261 proteins from the gastric pathogen *Heliobacter pylori* against a library of genome-encoded polypeptides revealed 1,200 putative interactions. Screening against a library allows the identification of interacting domains, and reduces the rate of false negatives encountered in classical pair-wise screens. A strong selection protocol reduces the number of false positives. Rain *et al*. also use a probability score to compute the likelihood that a given two-hybrid result is a consequence of background noise, and use some of the identified interactions to assign various proteins to particular biological pathways.

References

1. A comprehensive analysis of protein-protein interactions in Saccharomyces cerevisiae.

2. Protein interaction mapping in C. elegans using proteins involved in vulval development.

3. *Nature*, [http://www.nature.com/nature/]