S1 | **A literature derived network for yeast.** A yeast protein network was derived applying IE approaches to all abstracts that are stored in MEDLINE, using both a statistical co-occurence method [1] and an NLP-based one [2]. Functional associations that were derived from co-occurrence are shown in shades of gray according to the level of confidence that was achieved. The NLP method extracts four types of relations: stable physical interactions (green), regulation of expression (red), phosphorylation (dark blue), and dephosphorylation (light blue). The proteins (circles) are coloured according to their functional annotation: (co-)regulators of expression (red), kinases and cyclins (dark blue), phosphatases (light blue), and other proteins (gray). Protein names are written inside the circles.

1. von Mering, C. *et al.* STRING: Known and predicted protein–protein associations, integrated and transferred across organisms. *Nucleic Acids Res.* **33**, D433–D437 (2005).
2. Saric, J., Jensen, L. J., Ouzounova, R., Rojas, I. & Bork, P. Extraction of regulatory gene/protein networks from Medline. *Bioinformatics* July 26 2005 (2005). (doi:10.1093/bioinformatics/bti597).