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9. Ulrich Guldener, Martin Munsterkotter, Matthias Oesterheld, Philipp Pagel, Andreas Ruepp, Hans-Werner Mewes, and Volker Stumpflen. MPact: the MIPS protein interaction resource on yeast. *Nucleic Acids Res*, 34(Database issue):436–441, Jan 2006.
10. T Ideker, V Thorsson, J A Ranish, R Christmas, J Buhler, J K Eng, R Bumgarner, D R Goodlett, R Aebersold, and L Hood. Integrated genomic and proteomic analyses of a systematically perturbed metabolic network. *Science*, 292(5518):929–934, May 2001.
11. Ker-Chau Li. Genome-wide coexpression dynamics: theory and application. *Proc Natl Acad Sci U S A*, 99(26):16875–16880, Dec 2002.
12. Nicholas M Luscombe, M Madan Babu, Haiyuan Yu, Michael Snyder, Sarah A Teichmann, and Mark Gerstein. Genomic analysis of regulatory network dynamics reveals large topological changes. *Nature*, 431(7006):308–312, Sep 2004.
13. A Nabetani, T Koujin, C Tsutsumi, T Haraguchi, and Y Hiraoka. A conserved protein, Nuf2, is implicated in connecting the centromere to the spindle during chromosome segregation: a link between the kinetochore function and the spindle checkpoint. *Chromosoma*, 110(5):322–334, Sep 2001.
14. Joshua O'Madadhain, Jon Hutchins, and Padhraic Smyth. Prediction and ranking algorithms for event-based network data. *SIGKDD Explorations*, 7(2):23–30, 2005.
15. Christos A. Ouzounis and Peter D. Karp. Global Properties of the Metabolic Map of *Escherichia coli*. *Genome Res.*, 10(4):568–576, 2000.
16. Susanne Prinz, Iliana Avila-Campillo, Christine Aldridge, Ajitha Srinivasan, Krassen Dimitrov, Andrew F Siegel, and Timothy Galitski. Control of yeast filamentous-form growth by modules in an integrated molecular network. *Genome Res*, 14(3):380–390, Mar 2004. Comparative Study.
17. Alexander W. Rives and Timothy Galitski. Modular organization of cellular networks. *Proceedings of the National Academy of Sciences*, 100(3):1128–1133, 2003.
18. Quansong Ruan, Debojyoti Dutta, Michael S Schwalbach, Joshua A Steele, Jed A Fuhrman, and Fengzhu Sun. Local similarity analysis reveals unique associations among marine bacterioplankton species and environmental factors. *Bioinformatics*, 22(20):2532–2538, Oct 2006.
19. Victor Spirin and Leonid A. Mirny. Protein complexes and functional modules in molecular networks. *Proceedings of the National Academy of Sciences*, 100(21):12123–12128, 2003.
20. Chris Stark, Bobby-Joe Breitkreutz, Teresa Reguly, Lorrie Boucher, Ashton Breitkreutz, and Mike Tyers. BioGRID: a general repository for interaction datasets. *Nucleic Acids Res*, 34(Database issue):535–539, Jan 2006.
21. Jimeng Sun, Christos Faloutsos, Spiros Papadimitriou, and Philip S. Yu. Graphscope: parameter-free mining of large time-evolving graphs. In *KDD*, pages 687–696, 2007.
22. Chayant Tantipathananandh, Tanya Berger-Wolf, and David Kempe. A framework for community identification in dynamic social networks. In *KDD*, pages 717–726, 2007.
23. D. Thieffry, A. Huerta, E. Perez-Rueda, and J. Collado-Vides. From specific gene regulation to genomic networks: A global analysis of transcriptional regulation in *Escherichia coli*, 1998.
24. Jessica D Tytell and Peter K Sorger. Analysis of kinesin motor function at budding yeast kinetochores. *J Cell Biol*, 172(6):861–874, Mar 2006.
25. Christian von Mering, Roland Krause, Berend Snel, Michael Cornell, Stephen G Oliver, Stanley Fields, and Peer Bork. Comparative assessment of large-scale data sets of protein-protein interactions. *Nature*, 417(6887):399–403, May 2002. Comparative Study.