On the Cover: The interactome, a complete map of all protein-protein interactions, is an invaluable tool for systems biology. As an appetizer for those awaiting the results from high-throughput experimental approaches, an interactome was predicted for the Arabidopsis (Arabidopsis thaliana) genome by identifying pairs of orthologs that interact in yeast, Drosophila, humans, and Caenorhabditis elegans. In this illustration, each circle represents an Arabidopsis protein. The color of the circle is the subcellular localization from the SUBA database, for example, dark blue = nucleus and yellow = vacuole (see article for full list). Where two proteins are connected by a line, there is a predicted interaction. The thickness of the line represents the confidence value, while the line color is the degree of gene coexpression (red = highly coexpressed, yellow = weakly). An interactome of 19,979 interactions was made for 3,617 conserved Arabidopsis proteins, and is available online at the Bio-Array Resource for Arabidopsis functional genomics and can be downloaded from The Arabidopsis Information Resource. Shown on the cover are interactions for 918 proteins where subcellular localization was known. (Illustration courtesy of Matt Geisler.)

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