



**FIGURE 1.** Network map of protein–protein interactions identified by two-hybrid and mass spectrometry-based technologies (Hazbun et al. 2003). Proteins are represented by colored circles. The underlined proteins were used as Gal4 BD-fusions in two-hybrid screens to identify positives, as well as being affinity-tagged and purified before being subjected to mass spectrometry to identify copurifying proteins. The solid lines represent interactions identified by two-hybrid, and the dashed ovals encircle proteins purified with the underlined protein within that oval. The protein–protein interactions observed by mass spectrometry involved proteins predominantly functioning in DNA repair, suggesting these unknown proteins are part of a novel DNA repair complex. In contrast, the function of interacting proteins identified by two-hybrid included DNA repair and other processes that may be more transiently associated with these novel DNA repair complexes. These other processes are functionally grouped by color and labeled with the process. The gray protein (Arl1) is likely a false positive, since it is involved in vesicle-mediated transport.

*Protein–Protein Interactions: A Molecular Cloning Manual*, 2nd Ed., © 2005 by Cold Spring Harbor Laboratory Press, Chapter 37, Figure 1.