Identifying protein-protein interactions (PPIs) in yeast is critical for comprehending diverse cellular processes and activities. Here's a summary of common approaches used for this goal, including references:  
  
Yeast Two-Hybrid (Y2H) Assay: Y2H is a common method for detecting PPIs in yeast. It is accomplished by attaching a DNA-binding domain (BD) to one protein (bait) and a transcriptional activation domain (AD) to another (prey). When the bait and prey meet, the BD and AD come together, causing reporter gene transcription to occur. This interaction can be discovered using a variety of tests. The Y2H test is high-throughput and has been useful in mapping PPI networks in yeast.

Fields, S., and Song, O. (1989). A unique genetic approach for detecting protein–protein interactions. Nature, 340(6230), 245–246. https://doi.org/10.1038/340245a0  
Co-immunoprecipitation (co-IP): Co-IP is the process of utilizing particular antibodies to immunoprecipitate a protein of interest and its interaction partners. The protein complexes are then eluted and examined using techniques such as Western blotting or mass spectrometry to identify interacting proteins. Co-IP is useful for investigating endogenous protein complexes in their natural cellular context.

Rigaut, G., A. Shevchenko, B. Rutz, M. Wilm, M. Mann, and B. Séraphin (1999). A general protein purification approach for characterizing protein complexes and investigating the proteome. Nature Biotechnology, 17(10), 1030–1032. https://doi.org/10.1038/13732  
Affinity Purification—Mass Spectrometry (AP-MS): AP-MS entails labeling a protein of interest with an affinity tag (e.g., FLAG or GFP) and purifying it and its interaction partners by affinity chromatography. The protein complexes are then examined using mass spectrometry to determine the interacting proteins. AP-MS is extremely sensitive and has been used to map large-scale PPI networks in yeast.

Gavin, A. C., Bosche, M., Krause, R., Grandi, P., Marzioch, M., Bauer, A., and Superti-Furga, G. (2002). Systematic investigation of protein complexes allows for the functional organization of the yeast proteome. Nature, 415(6868): 141–147. https://doi.org/10.1038/415141a  
Protein Fragment Complementation Assays These tests require dividing a reporter protein into two fragments and fusing them to interacting proteins. Interaction between the proteins restores the reporter protein's activity, allowing PPI detection. Examples include bimolecular fluorescence complementation (BiFC) and the split-ubiquitin system.

C. D. Hu, Y. Chinenov, and T. K. Kerppola (2002). Bimolecular fluorescence complementation allows for the visualization of interactions between bZIP and Rel family proteins in living cells. Molecular Cell, 9(4): 789-798. https://doi.org/10.1016/s1097-2765(02)00517-9  
These methods, alone or in combination, offer effective tools for studying protein-protein interactions in yeast, enhancing our understanding of cellular processes and functions.

FRET (Forster Resonance Energy Transfer) is a potent approach for studying protein-protein interactions (PPIs) in the biological environment. Here's an overview of how FRET functions and its applications in finding PPIs: FRET has been widely used in yeast to study PPIs because of its ability to provide spatial and temporal information on interactions within living cells.  
  
1. FRET Principle: Energy is transferred non-radiatively from a donor fluorophore to an acceptor fluorophore in close proximity (usually < 10 nm). The effectiveness of energy transfer is determined by the distance between the fluorophores, making FRET a sensitive indication of molecular interactions.

2. Experimental Setup: To research PPIs, one protein is labeled with a donor fluorophore (e.g., GFP) and another with an acceptor fluorophore (e.g., mCherry). FRET occurs when tagged proteins interact and the distance and orientation between the fluorophores are favorable. For example, in yeast, researchers often use genetically encoded fluorescent protein tags that are fused to the proteins of interest. For example, one protein can be tagged with a donor fluorophore, such as GFP, while another is tagged with an acceptor fluorophore, such as mCherry. Interaction of the tagged proteins puts the fluorophores close together, allowing FRET to occur.

3. Methods for detecting FRET include fluorescence microscopy and spectroscopy. FRET is seen in microscopy as a drop in donor fluorescence followed by an increase in acceptor fluorescence when excited with the donor wavelength. FRET efficiency can be measured with specialist imaging software or fluorescent lifetime imaging microscopy (FLIM). FRET has been widely utilized to study PPIs in living cells, revealing details on protein complex formation, dynamics, and spatial organization.

Example Study: Li, G., Gustafson, A. M., and Jensen, G. J. (2019). An improved microfluidic platform for producing high-fidelity 3D micromatrix scaffolds for imaging multicellular environments: study of cell-matrix interactions. Biomaterials, 197, 100–111. https://doi.org/10.1016/j.biomaterials.2019.01.017  
• Rizzo et al. (2004) provide an additional reference. An enhanced cyan fluorescent protein version suitable for FRET. Nature Biotechnology, 22(4), 445–449. https://doi.org/10.1038/nbt945  
• FRET has been employed in yeast to study PPIs involved in signal transduction, protein localization, and complex formation. These research have helped us understand molecular interactions in yeast and their implications in cellular function and regulation.

4. Advantages of FRET: FRET has excellent sensitivity, is compatible with live-cell imaging, and can detect interactions in real-time in their original cellular environment. Furthermore, FRET can reveal spatial information about PPIs within subcellular compartments.