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Protein Interaction Network in E-C Coupling

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Identification of the network of molecular interactions in excitation-contraction (E-C) coupling is the first step toward understanding complex dynamics and mechanisms. Current research for creating the network model in E-C coupling can be described as the construction of protein bank, the identification of protein-protein interactions and the structure determination. First, the protein bank of primary target proteins was constructed by the efficient protein-producing method. The purified proteins serve as a source for analyzing protein-protein interactions in E-C coupling and discovering new proteins that associate with or are regulated by the primary target proteins. Second, the identification of protein-protein interactions was carried out using the analytical techniques such as Isothermal Titration Calorimetry (ITC), Surface Plasmon Resonance (SPR) and GST pull-down assay. Known protein-protein interactions will be further clarified and novel protein-protein interactions will be identified by these analytical methods. Third, the complex structures of interacting molecules are determined using 3D structure modeling and X-ray crystallography. Knowledge of the 3D structure is essential for interpreting the structural mechanism proteins interact with their target molecules. X-ray crystallography is useful method to determine the 3D structure. Due to the limitation of structure determination by X-ray crystallography, 3D structure modeling also is used to identify best matches between two molecules that bind to each other by the simulation of interacting surfaces and free energy minimization at the domain level. Protein interacting network in E-C coupling was made by using computer modeling and X-ray crystallography, together with the experimental analysis. Network model can help to understand the integrated function of E-C coupling and suggest new interpretation for E-C coupling network.