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## Recent advances in protein-protein interaction prediction: experimental and computational methods.

[Jessulat M<sup>1</sup>](#), [Pitre S](#), [Gui Y](#), [Hooshyar M](#), [Omidi K](#), [Samanfar B](#), [Tan le H](#), [Alamgir M](#), [Green J](#), [Dehne F](#), [Golshani A](#).

### Author information

### Abstract

**INTRODUCTION:** Proteins within the cell act as part of complex networks, which allow pathways and processes to function. Therefore, understanding how proteins interact is a significant area of current research.

**AREAS COVERED:** This review aims to present an overview of key experimental techniques (yeast two-hybrid, tandem affinity purification and protein microarrays) used to discover protein-protein interactions (PPIs), as well as to briefly discuss certain computational methods for predicting protein interactions based on gene localization, phylogenetic information, 3D structural modeling or primary protein sequence data. Due to the large-scale applicability of primary sequence-based methods, the authors have chosen to focus on this strategy for our review. There is an emphasis on a recent algorithm called Protein Interaction Prediction Engine (PIPE) that can predict global PPIs. The readers will discover recent advances both in the practical determination of protein interaction and the strategies that are available to attempt to anticipate interactions without the time and costs of experimental work.

**EXPERT OPINION:** Global PPI maps can help understand the biology of complex diseases and facilitate the identification of novel drug target sites. This study describes different techniques used for PPI prediction that we believe will significantly impact the development of the field in a new future. We expect to see a growing number of similar techniques capable of large-scale PPI predictions.

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