

# MoVIN server: Motif Validation of Interaction Networks

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## Motivation

Protein-protein interactions are at the basis of most cellular processes and crucial for many bio-technological applications. During the last few years the development of high-throughput technologies has produced several large-scale protein-interaction data sets for various organisms and many interaction databases have been created by data-mining techniques. It is well known that interactions can be mediated by the presence of specific features, such as motifs, patches and domains. Even if many efforts are underway to elucidate the role of these features in the regulation of interaction networks, very little is known about them on a genome scale.

Data-integration and computational methods can be used to assign a confidence level to specific interactions or datasets and to obtain information about the molecular basis that regulate such interactions.

## Methods

The MoVIN web server is a new bioinformatics resource for the analysis and validation of protein interaction networks. It combines yeast protein interaction data with other biological resources - such as sequences, process and component ontologies, domains and structures - to construct a high-confidence interaction set by identifying similar features in protein groups sharing a common interaction partner. Such results are presented to the user with an integrated graphical interface that offers the possibility of exploring the interaction network and to access many biological-relevant data computed by the server or present in other databases.

## Results

To assess the usefulness of our server, we analysed the presence of similar linear motifs, functions, localization and domains in many different interaction datasets.

We observed a statistically significant presence of such features with respect to random datasets and found that these information are consistent but non redundant.

Our study shows that the analysis of shared motifs in protein interaction networks can be a valuable method to investigate the properties of interacting proteins and to provide information that can be effectively integrated with other sources. As more experimental interaction data become available, this method will be a useful tool to gain a wider and more precise picture of the interactome.

**Availability:** <http://arianna.bio.uniroma1.it/MOVIN>

**Image:** <http://arianna.bio.uniroma1.it/MOVIN/paper.php>

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