

Interaction Graph Validator a New Type of Relation Database for Protein-Protein Interaction mapping by Mass Spectrometry-Based.

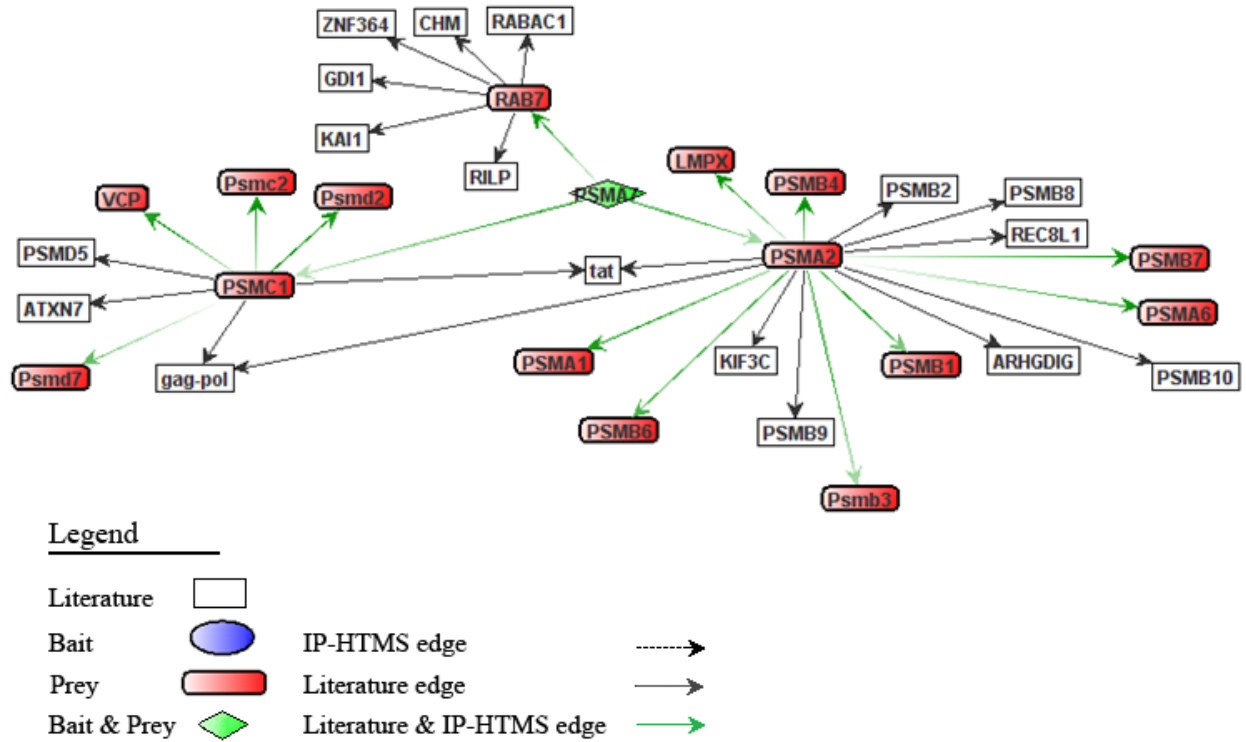
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Mapping protein-protein interaction is a valuable tool to understand protein function and therefore have a better comprehension of human diseases. Large-scale human protein interaction networks have been constructed using different approach such as yeast two hybrid, Mass Spectrometry (MS), literature and orthology.¹ High throughput MS based protein interaction mapping (IP-HTMS) have been reported in yeast, human and other species. Although the results are reported as interaction, in reality they are either direct interaction or association (i.e. interacts with an interactor of the bait). Currently, this information is added to public database which are only designed to handle direct association. We present here an interactive bioinformatics web tool called Interaction Graph Validator (IGV) and a new type of protein-protein relation database using mass spectrometry-based approach that can differentiate interactors versus likely associations. This database is created from two combine approaches, one from the literature search that was manually curated and the other from the IP-HTMS data. IGV includes a protein search tool to query and browse the database. When a query is performed the IGV program creates recursively two networks from the database that we called literature network and IP-HTMS network. The distance between the root of the network and the last child is a maximum of two. Then IGV overlaps the two networks to create an IP-HTMS validated network. IGV also includes a graphic interactive tool to visualize the graph and to navigate on the network. In the figure 1 we can see the network of the search of the protein PSMA7. This example illustrates the power of the IGV method. Three proteins that are known to be directly interacting with PSMA7 are observed. However, the majority of the prey proteins observed with PSMA7 are not direct interactors of PSMA7, but instead are associated to PSMA7 by direct interactions with PSMA2 and PSMC1. Conventional protein interaction databases would have miss annotated the PSMA7 prey proteins. This is a systemic and serious issue for any IP-HTMS datasets. Fortunately, the IGV not only validate the IP-HTMS as direct interactors or association but also can rapidly highlight the novel interactors with the bait protein. The IGV application will be available at the <http://www.oisb.ca> web site.

Figure 1: Overlaps of the literature network and the IP-HTMS network of the protein PSMA7. The preys surrounded by the bait are not shown.



1) Matthias E. Futschik, Gautam Chaurasia and Hanspeter Herzel, Comparison of human protein-protein interaction maps. *Bioinformatics* 23(5):605-611