Protein Interaction Network Analysis and Visualization of *Synechocystis* sp. PCC 6803

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Background

The amount of data stored until now in the field of life science is enormously large. So it gets difficult to find the particular information which gives the leading clue for solving a specific experimental problem.
To support the laboratory work, making this amount of data easily understandable and workable is one goal of the CyanoFactory Knowledge Base. Part of this is the analysis and visualization of protein interaction by using graph theoretical approaches.
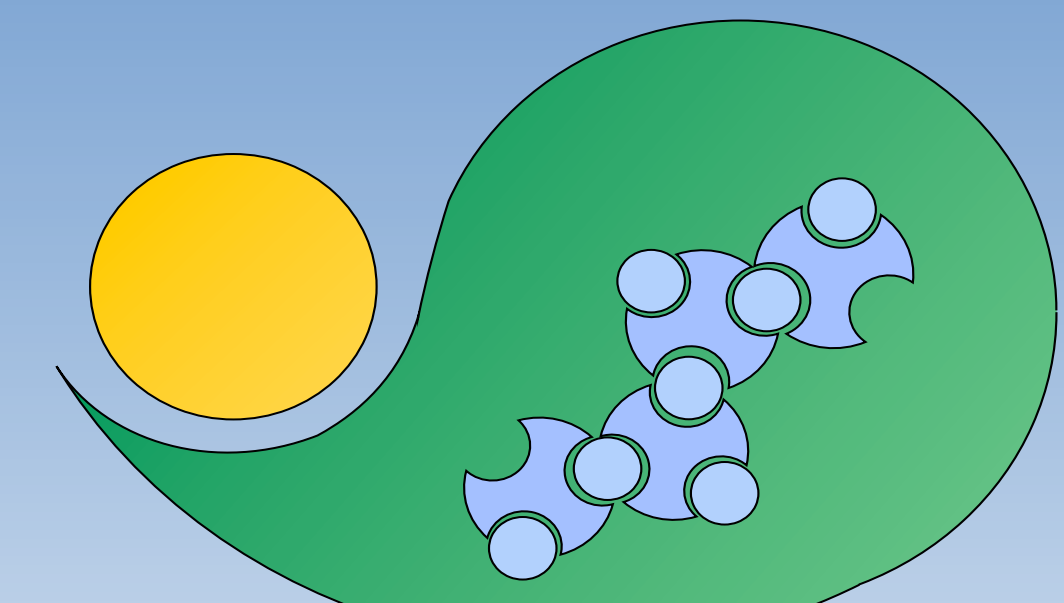
CyanoFactory

Material & Methods
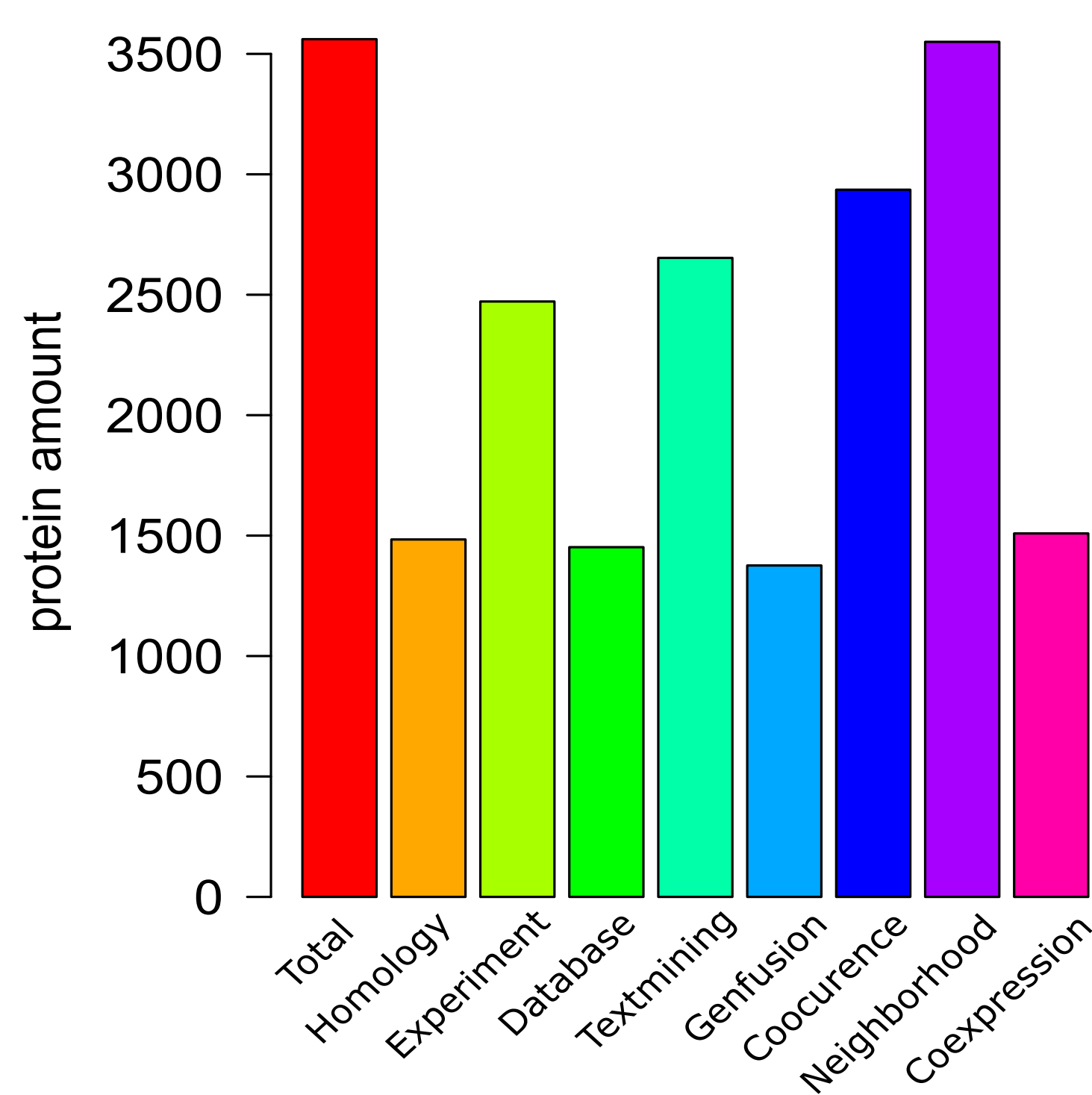
From the STRING[1] and STITCH[2] databases protein-protein and protein-metabolite interactions were extracted. For *Synechocystis* sp. PCC 6803 over 227,000 interactions for more than 3500 proteins were recorded.

The given probability for each protein-protein or protein-metabolite interaction is given. This probability of an interaction differs between the single interaction types. This is caused by the availible experimental information.
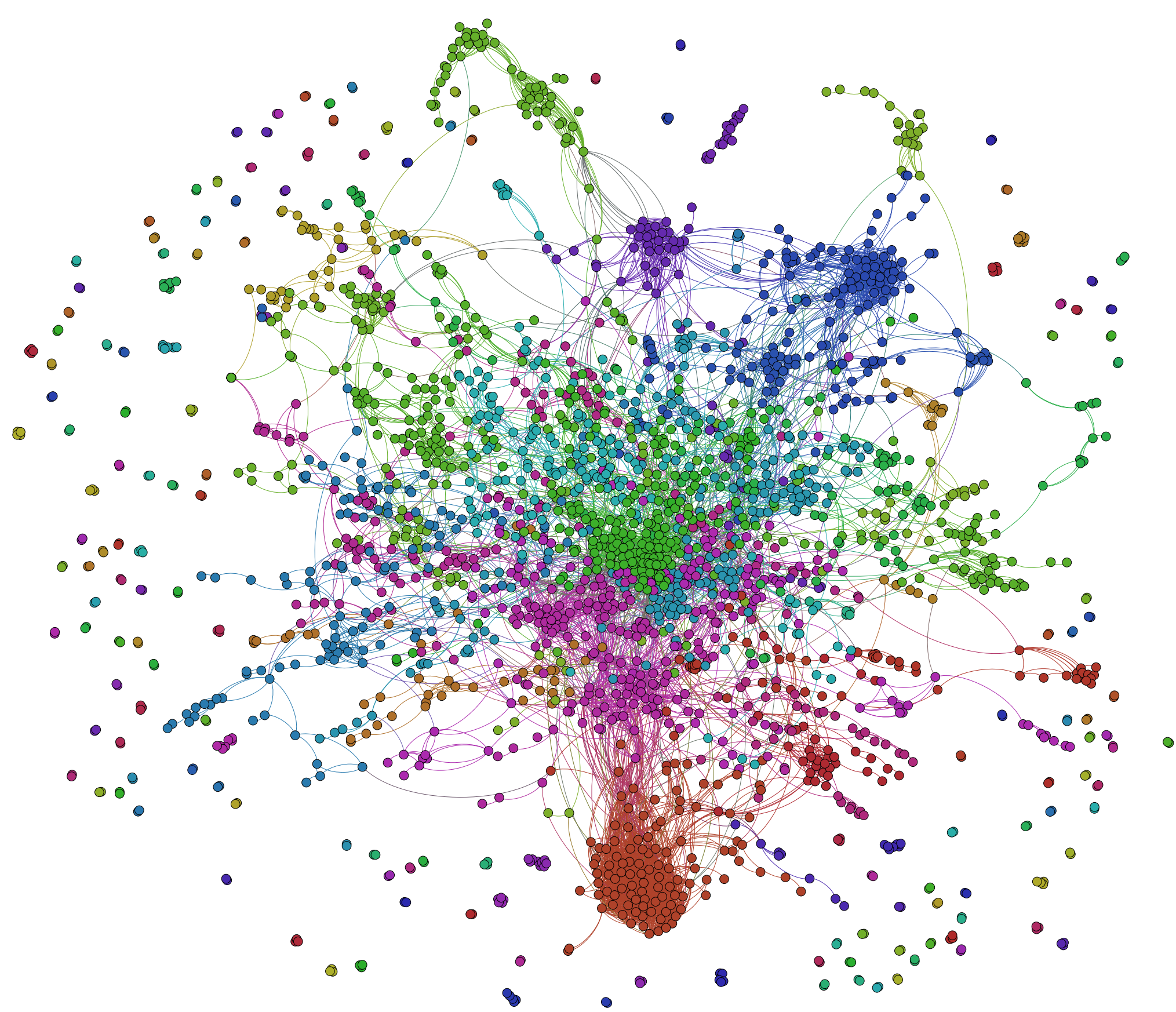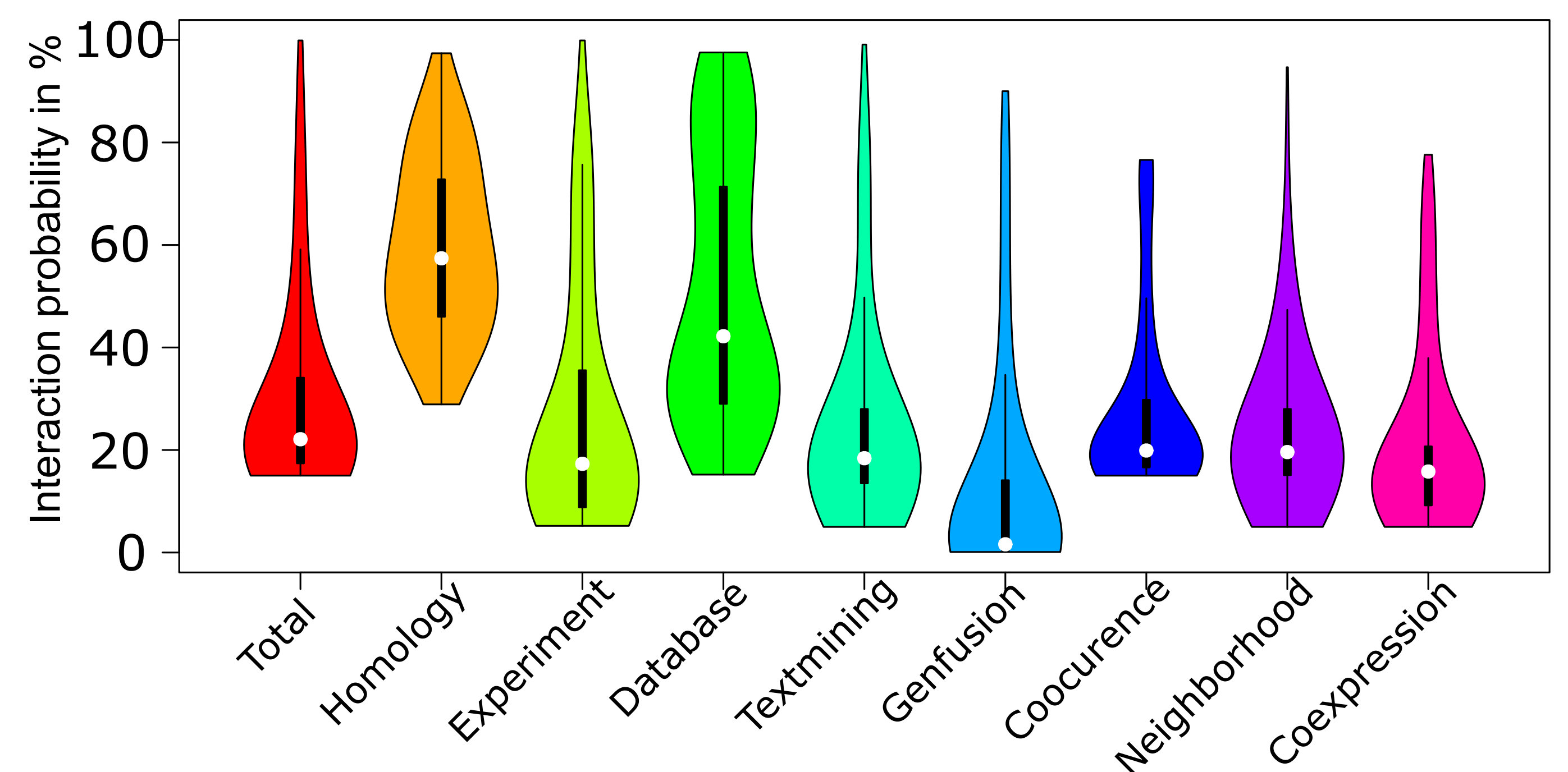
Setting a threshold for the interaction probability creates isolate proteins without any interaction and great cluster of proteins with high interaction probabilities.

Nr. of Interaction-Partner
- selected
- ... 245
- ... 314
- ... 452
- ... 521

Interaction-Score
- ... 20.6%
- ... 40.4%
- ... 80.1%
- ... 99.9%

Results

For a better use of these information the webtool CyanoInteraction was created. With this tool it is possible to visualize specific interactions for an given protein or chemical by filtering the single interaction types.
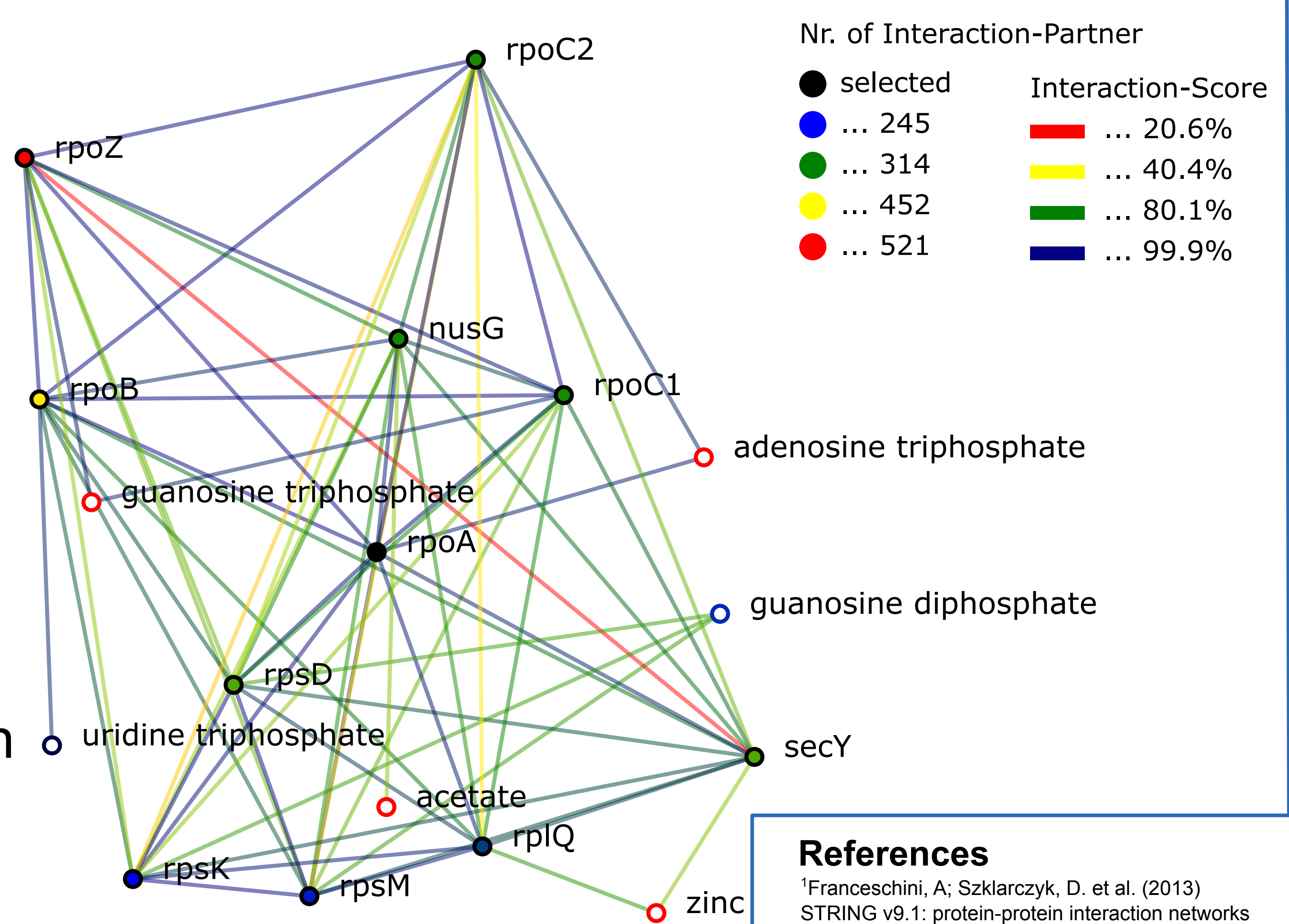
References
[1]Franceschini, A; Szklarczyk, D. et al. (2013) STRING v9.1: protein-protein interaction networks with increased coverage.
Nucleoc acids reasearch Database issue: D808-D815
[2]Kuhn, M.; Szklarczyk, D. et al. (2014) STITCH 4: integration of protein-chemical interactions with user data.
Nucleic acids research Database issue: D401-407