

STRING 8 — a global view on proteins and their functional interactions in 630 organisms

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Motivation

Protein-protein interaction networks are an important ingredient for systems-level understanding of cellular processes. Such networks can be used for filtering and assessing functional genomics data and for providing an intuitive platform for annotating the structural, functional and evolutionary properties of proteins. Exploring the predicted interaction networks can suggest new directions for future experimental research.

Methods

STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) is a database of known and predicted protein-protein interactions. The database contains information from numerous sources, including experimental repositories, computational prediction methods and public text collections. All data is weighted and integrated and a confidence score is calculated for all protein interactions. The results of the various computational predictions can be inspected in different designated views. String can be accessed in two modes: Protein-mode and COG-mode. In the COG-mode, the predicted interactions are propagated to proteins in other organisms for which interaction has been described by inference of orthology.

Results

String is freely accessible and is regularly updated; the latest version 8.0 contains information on 2.5 millions proteins from 630 species. The STRING database and web resource is available at <http://string-db.org/>.

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