

SH3-Hunter: discovery of SH3 domain interaction sites in proteins.

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Motivation

Identifying interacting partners of a given protein is a crucial step towards the discovery of its function. Often proteins communicate by means of protein recognition modules (PRMs), i.e. well conserved domains characterized by a specific function and interacting with short peptides. The SH3 domain family is one of the most representative PRMs, having a pivotal role in intracellular signal transduction and being widely involved in pathologies such as cancer and AIDS.

Methods

SH3-Hunter is a web server that evaluates which peptide-domain pair represents a possible interaction pair and produces as output a list of significant SH3-domain interaction sites for each query protein. Each proposed interaction site is associated to a propensity score and sensitivity and precision levels for the prediction. The server prediction capability is based on a neural network model integrating high-throughput pep-spot data with structural information extracted from known SH3-peptide complexes.

Results

Users can submit one or more sequences, or even a list of peptides as possible interactors of one or more SH3 domains. The input sequences can be processed in simple or advanced mode. In simple mode, a list of inferred interactions is proposed with the whole list of SH3 domains available (see <http://cbm.bio.uniroma2.it/SH3-Hunter/help.html>). Otherwise, a fine selection of test domains can be prepared. The output consists of a list of significant domain-peptide pairs that the predictor recognizes as reliable interacting pairs.

Availability: <http://cbm.bio.uniroma2.it/SH3-Hunter>

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