HOTSPOT WIZARD 3.0: AUTOMATED DESIGN OF SITE-SPECIFIC MUTATIONS AND SMART LIBRARIES

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Key Words: activity, stability, specificity, single-point mutants, smart libraries

HotSpot Wizard is an interactive web server for prediction of amino acid residues suitable for mutagenesis and construction of libraries of mutants with modified activity, specificity or stability [1]. Positions suitable for mutagenesis are evaluated based on protein structure using a combination of structural, functional and evolutionary information obtained from 7 internet databases and 22 computational tools [2]. The application was designed with an emphasis on an easy usage without the necessity of advanced knowledge of the studied system. This is the reason for the setting of all default values of the parameters based on the extensive analysis to appropriately represent a wide spectrum of input data. Four different strategies are automatically evaluated for every protein structure. Analysis of the results is being run directly in the web interface, which provides user-friendly visualization tool. Moreover, HotSpot Wizard provides a module for the design of a construction of protein mutant library with the support of an automatic detection of suitable target amino acids and corresponding degenerative codons. There are several new features for the version 3.0 to be released early 2018. Stability of single-point or multiple-point mutant can be predicted using the Rosetta scoring function [3]. Users can newly enter also protein sequence as the input for calculation. Then searching for structures or models in the databases of experimental structures or depositories of homology models is performed. The users can also run homology modelling using the programs Modeller [4] and I-Tasser [5]. The current version of the application is freely available for academic users at http://loschmidt.chemi.muni.cz/hotspotwizard.

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