

CSFinder (Cleavage Site Finder): A Web-based Software for Identifying Potential Cleavage Site of Protein Based on 3D Structure

Niloofar Shirvanizadeh, Seyed Shahriar Arab*

Department of Biophysics, Faculty of Biological Sciences, Tarbiat Modares University, Tehran, IRAN

*sh.arab@modares.ac.ir

Abstract: The techniques using site specific proteases are employed for several purposes in biotechnology. The most frequent application is to provide a ‘tag’ which will aid the purification of the protein of interest. Although these enzymes are quite specific for cleavage at the inserted cleavage site, proteolysis can frequently occur at other site(s) of the proteins. It is necessary to know the potential cleavage site of proteases in protein using affinity label [1]. There are various bioinformatics tools for prediction of the potential cleavage site of proteins such as Peptide Cutter [2]. They normally use protein sequence for prediction. Some of these specific cleavage sites are located in the core of folded form of protein. Site-specific peptidases can cleave the exposed cleavage site of folded protein. CSFinder as an interactive interface assists users by prediction of potential cleavage site. User can enter the structure of protein of interest by either uploading PDB file or entering PDB code. CSFinder calculate the surface accessibility of each residue, the exposed sequences check with a database of sequence patterns for different proteases. User can select the desire peptidase(s) from the list exist in the input page. CSFinder gives the name of the proteases which have cleavage site in the exposed region of protein in matter of seconds. CSFinder is freely available at URL:

<http://bioinf.modares.ac.ir/software/CSFinder>.

Keywords: Bioinformatics tool; Cleavage site; Tertiary structure

References

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- [2] Elisabeth Gasteiger et al, “The Proteomics Protocols Handbook”, Humana Press, 2005.