



生物信息学研究中心

Center of Bioinformatics

学术报告

题目： PROSPERous: an integrative tool to rank and predict protease substrate cleavage sites by multiple scoring function

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Abstract: The ability to catalytically cleave protein substrates after synthesis is fundamental for all forms of life. Accordingly, site-specific proteolysis is one of the most important post-translational modifications. The key to understanding the physiological role of a protease is to identify its natural substrate(s). Knowledge of the substrate specificity of a protease can dramatically improve our ability to predict its target protein substrates, but this information must be utilized in an effective manner by in silico approaches in order to efficiently identify protein substrates. To address this problem, we present PROSPERous, which is an integrative tool for in silico prediction of protease substrates and their cleavage sites from amino acid sequences. PROSPERous is primarily based on amino acid weights derived from amino acid occurrences and utilizes a variety of scoring functions to score, predict and rank potential cleavage sites of proteases. For proteases with known amino acid specificity, PROSPERous provides a convenient, pre-prepared tool for use in identifying protein substrates for the enzymes. In comparison with two state-of-the-art prediction tools, PoPS and SitePrediction, it achieves a greater accuracy and coverage. It is a powerful tool for substrate identification in protease systems biology that complements the prediction by other current tools.