Computational strategies towards improved protein function prophecy of xylanases from thermomyces lanuginosus

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Abstrak

This brief reports on the interplay of an amino-acid mutation towards substrate which could lead to enhanced effects on mutant. These effects need to be given consideration in the engineering processes of protein stability and further exploration of such learning are required to provide novel indication for selection of an enzymes. There are very few reports showing such stable, energy efficient model towards improved protein function prediction screening in-silico structure based mutagenesis of xylanases from Thermomyces lanuginosus