Short Communication

iMedPub Journals
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Insights in Enzyme Research

2022
Vol 6. No. 2

Computational Resources and Techniques in Enzyme Research

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Abstract

Heterogeneous and ever-expanding biological data requires proportional growth in both computing power, as well as data storage, to collate, manage, analyze, and predict its function. Computational researchers have created various databases and software, or web servers that can be used to predict functional relationships among proteins and/or enzymes, which is especially relevant in the field of metabolic engineering. Bioinformatics techniques are being used in the field of metagenomics to find novel enzyme molecules. Structures of enzymes are predicted by homology-based or ab initio methods. Furthermore, selectivity and stability of engineered enzymes are monitored, improved, and verified by molecular simulations techniques. Here, we describe varied approaches and methodologies that are being employed for predicting the structure-function relationship of enzymes that can save time and costs in wet lab experiments

Received: February 12, 2022; **Accepted:** February 18, 2022; **Published:** February 28, 2022

Biography

He is a senior research fellow at the Institute of Nuclear medicine and Allied Sciences, India. He is in the third year of her Ph.D. and is a holder of DST-INSPIRE fellowship. He has qualified UGC NET exam twice. The Anoushka Khanna is a senior research fellow at the Institute of Nuclear medicine and Allied Sciences, India. He is in the third year of her Ph.D. and is a holder of DST-INSPIRE fellowship. He has qualified UGC NET exam twice. He is a senior research fellow at the Institute of Nuclear medicine and Allied Sciences, India. He is in the third year of her Ph.D. and is a holder of DST-INSPIRE fellowship. He has qualified UGC NET exam twice.

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