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Eukaryotic secretome prediction and knowledge-base development

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Eukaryotic cells make many thousands of different proteins. Synthesized proteins in the cell are transported to different subcellular locations to play their biological roles, a process called protein sorting or targeting. Some of these proteins are secreted outside of the cell, i. e. the extracellular space or matrix. These secreted proteins are collectively called "secretome". Secretomes consist of extracellular enzymes, signal molecules, and structure proteins. Computational prediction and experimental validation of protein subcellular locations are essential for functional classification of proteins. We recently evaluated several bioinformatics tools and developed computational protocols for accurate prediction of secretomes for eukaryotes. Secretome knowledge-bases for fungi and plants are developed. With the complete data available for plants and fungi and associated web-based tools, these secretome knowledge-bases will be valuable resources for exploring the potential applications of secreted proteins.

Biography

Xiang Jia Min, Ph. D., Assistant Professor in the Department of Biological Sciences at Youngstown State University, holds a Ph. D. degree from the University of Hawaii and a Master of Software Systems degree from the University of British Columbia. His primary areas of scientific expertise include functional genomics and bioinformatics. His recent research interests focus on development of bioinformatics tools and databases related to sequence analysis, molecular evolution, and secretomes. He has published more than 20 research articles and implemented some widely used software tools and databases including OrfPredictor, TargetIdentifier, and FunSecKB.

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