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Human and animal secretomes: Current status and prospects

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Secreted proteins are an essential part of an organism's proteome. These proteins play important biological roles in regulation of growth and development in multicellular eukaryotes. These secreted proteins are collectively called "secretome". Secretomes consist of extracellular enzymes, signal molecules, and structure proteins. Computational prediction and experimental identification of secreted proteins are essential for functional and structural classification of these proteins. A secretome consists of two groups of secreted proteins: (1) classical secreted proteins which have a secretory signal peptide in N-terminus, and (2) nonclassical, leadless secreted proteins which do not have a secretory signal peptide. To distinguish these two groups of secreted proteins, we surveyed the manually curated secreted proteins of human and animals in the Swiss-Prot data set of UniProtKB. We also evaluated several bioinformatics tools, including recently released SignalP 4.0, and developed a computational protocol for accurate prediction of secretomes for human and animals. A secretome knowledge-base for human and animals is under construction and is expected to serve as a valuable resource for exploring the potential applications of secreted proteins as biomarkers in medicine.

Biography

Xiang Jia Min, Ph. D., is an Assistant Professor in the Department of Biological Sciences at Youngstown State University. His primary areas of scientific expertise include functional genomics and bioinformatics. He has published 30 research articles and implemented some widely used software tools and databases including OrfPredictor, TargetIdentifier, ASFinder, FunSecKB, and PlantSecKB. He is a member of Editorial Board of the Journal of Proteomics & Bioinformatics, Journal of Data Mining in Genomics & Proteomics.

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