

Daisuke Kihara *Editor*

Protein Function Prediction for Omics Era

 Springer

Protein Function Prediction For Omics Era Author Daisuke Kihara Oct 2011

Daisuke Kihara



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Protein Function Prediction for Omics Era Daisuke Kihara, 2011-04-19 Gene function annotation has been a central question in molecular biology. The importance of computational function prediction is increasing because more and more large scale biological data including genome sequences, protein structures, protein-protein interaction data, microarray expression data, and mass spectrometry data are awaiting biological interpretation. Traditionally, when a genome is sequenced, function annotation of genes is done by homology search methods such as BLAST or FASTA. However, since these methods are developed before the genomics era, conventional use of them is not necessarily most suitable for analyzing a large scale data. Therefore, we observe emerging development of computational gene function prediction methods which are targeted to analyze large scale data and also those which use such omics data as additional source of function prediction. In this book, we overview this emerging exciting field. The authors have been selected from 1) those who develop novel purely computational methods, 2) those who develop function prediction methods which use omics data, 3) those who maintain and update data base of function annotation of particular model organisms. *E. coli* which are frequently referred. *Protein Function Prediction*

Lukasz Kurgan, Daisuke Kihara, 2025-09-02 This fully updated volume explores a wide array of new and state of the art tools and resources for protein function prediction. Beginning with in depth overviews of essential underlying computational techniques such as machine learning, multi task learning, protein language models, and deep learning, the book continues by covering specific tools for protein function prediction ranging from gene ontology term predictions to the predictions of binding sites, protein localization, and solubility, signal peptides, intrinsic disorder, and intrinsically disordered binding regions, as well as presenting databases that address protein moonlighting and protein binding. Written for the highly successful *Methods in Molecular Biology* series, chapters include introductions to their respective topics, step by step instructions on how to use software and web resources, use cases, and tips on troubleshooting and avoiding known pitfalls. Authoritative and up to date, *Protein Function Prediction: Methods and Protocols*, Second Edition helps readers to understand and appreciate this vibrant and growing research area and guides in the quest to identify and use the best computational methods and resources for their projects. **New Approaches of Protein Function Prediction from Protein Interaction Networks**

Jingyu Hou, 2017-01-13 *New Approaches of Protein Function Prediction from Protein Interaction Networks* contains the critical aspects of PPI network based protein function prediction including semantically assessing the reliability of PPI data, measuring the functional similarity between proteins, dynamically selecting prediction domains, predicting functions, and establishing corresponding prediction frameworks. Functional annotation of proteins is vital to biological and clinical research and other applications due to the important roles proteins play in various biological processes. Although the functions of some proteins have been annotated via biological experiments, there are still many proteins whose functions are yet to be annotated due to the limitations of existing methods and the high cost of experiments. To overcome experimental

limitations this book helps users understand the computational approaches that have been rapidly developed for protein function prediction Provides innovative approaches and new developments targeting key issues in protein function prediction Presents heuristic ideas for further research in this challenging area **Protein Function Prediction** Burkhard Rost,2008

Protein Function Prediction Jan Oliver Korbel,2005 **Protein Structure Prediction** Daisuke Kihara,2016-08-23

Protein Structure Prediction Third Edition expands on previous editions by focusing on software and web servers With new chapters that provide instructions on how to use a computational method with examples of prediction by the method Written in the highly successful Methods in Molecular Biology series format chapters include introductions to their respective topics lists of the necessary materials step by step readily reproducible protocols and key tips on troubleshooting and avoiding known pitfalls Authoritative and cutting edge Protein Structure Prediction Third Edition provides diverse methods detailing the expansion of the computational protein structure prediction field

Whispering the Techniques of Language: An Mental Quest through **Protein Function Prediction For Omics Era Author Daisuke Kihara Oct 2011**

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