

1. Record Nr.	UNINA9910298287603321
Autore	Pazos Florencio
Titolo	Practical Protein Bioinformatics // by Florencio Pazos, Mónica Chagoyen
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2015
ISBN	3-319-12727-6
Edizione	[1st ed. 2015.]
Descrizione fisica	1 online resource (111 p.)
Disciplina	570 572/.6 610
Soggetti	Proteins Medicine Chemistry, Organic Protein Science Biomedicine, general Organic Chemistry
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Sequences -- Structures -- Systems.
Sommario/riassunto	This book describes more than 60 web-accessible computational tools for protein analysis and is totally practical, with detailed explanations on how to use these tools and interpret their results and minimal mentions to their theoretical basis (only when that is required for making a better use of them). It covers a wide range of tools for dealing with different aspects of proteins, from their sequences, to their three-dimensional structures, and the biological networks they are immersed in. The selection of tools is based on the experience of the authors that lead a protein bioinformatics facility in a large research centre, with the additional constraint that the tools should be accessible through standard web browsers without requiring the local installation of specific software, command-line tools, etc. The web tools covered include those aimed to retrieve protein information, look for similar proteins, generate pair-wise and multiple sequence alignments of

protein sequences, work with protein domains and motifs, study the phylogeny of a family of proteins, retrieve, manipulate and visualize protein three-dimensional structures, predict protein structural features as well as whole three-dimensional structures, extract biological information from protein structures, summarize large protein sets, study protein interaction and metabolic networks, etc. The book is associated to a dynamic web site that will reflect changes in the web addresses of the tools, updates of these, etc. It also contains QR codes that can be scanned with any device to direct its browser to the tool web site. This monograph will be most valuable for researchers in experimental labs without specific knowledge on bioinformatics or computing.
