

Publication

Automated protein modelling-the proteome in 3D

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

ID 156381

Author(s) Peitsch, M C; Schwede, T; Guex, N

Author(s) at UniBasel [Schwede, Torsten](#) ;

Year 2000

Title Automated protein modelling-the proteome in 3D

Journal Pharmacogenomics

Volume 1

Number 3

Pages / Article-Number 257-66

Functional analysis of the proteins discovered in fully sequenced genomes represent the next major challenge of life science research. Computational methods play an increasingly important role in this activity. Among them, comparative protein modelling will play a major role in this challenge, especially in the light of the Structural Genomics programmes about to be started around the world. In recent years, much progress has been made in automating these methods, enabling the production of models for genome scale problems. In this review we discuss how protein models can be applied to functional analysis, as well as some of the current issues and limitations inherent to these methods.

edoc-URL <http://edoc.unibas.ch/dok/A5259358>

Full Text on edoc No;

Digital Object Identifier DOI 10.1517/14622416.1.3.257

PubMed ID <http://www.ncbi.nlm.nih.gov/pubmed/11256577>

ISI-Number MEDLINE:11256577

Document type (ISI) Journal Article, Review