Functional Genomics

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Unipept

A platform for metaproteomics data analysis with a focus on interactive data visualizations

Unipept, developed at Ghent University, is an open source web application designed for metaproteomics data analysis with a focus on interactive data visualisations. The platform is powered by an index containing all UniProt entries, a tweaked version of the NCBI taxonomy and a custom lowest common ancestor algorithm. This combination enables a lightning fast biodiversity analysis of large and complex metaproteome samples. Next to these core functions, Unipept also has a tool for selecting unique peptides for targeted proteomics and for comparing genomes based on peptide similarity.
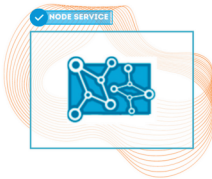
Tabloid Proteome

A database of protein association networks representing a broad scale of biological associations between pairs of proteins that go beyond direct protein interactions

Tabloid Proteome, developed at Ghent University, is a database of protein association networks generated using publically available mass spectrometry based experiments in PRIDE. These associations represent a broad scala of biological associations between pairs of proteins that goes well beyond mere binary protein interactions.

In addition to the collection of co-occurring protein pairs, Tabloid Proteome also links to their biological relation in existing knowledgebases. Moreover, pathway links from Reactome, protein-protein interactions from IntAct and BioGRID, protein complexes from CORUM, and paralog information from Ensembl are also superimposed. Functional annotation is provided by disease information from DisGeNET, and Gene Ontology annotations.
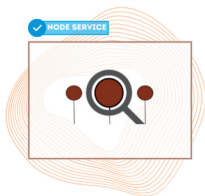
Scop3P

A Comprehensive resource of human phosphosites within their full context

Scop3P provides a unique and powerful resource to explore and understand the impact of phospho-sites on human protein structure and function, and can thus serve as a springboard for researchers seeking to analyse and interpret a given phosphosite or phosphoprotein in a structural, biophysical, and biological context.

The resource re-uses public domain data from a variety of leading international resources, including UniProtKB and PDB, but also uses reprocessed mass spectrometry-based phospho-proteomics data from PRIDE/ProteomExchange, which is in turn globally collected and thus wholly international-driven. Scop3P is developed at Ghent University.

MS2PIP

A tool to predict peptide fragment ion intensities for mass spectrometry-based proteomics data

MS2PIP Server, developed at Ghent University, accurately predicts peptide fragment ion intensities for mass spectrometry-based proteomics data. It employs the XGBoost machine learning algorithm and is accessible through a RESTful API.

The tool enables researchers to make use of MS²PIP, regardless of their computational experience. It is the only peak intensity prediction server that can predict peak intensities for multiple fragmentation methods, instruments and labelling techniques. MS2PIP Server has been used as the benchmark for comparison of other recently published tools for the prediction of MS² peak intensities.

DynaMine

A tool to predict backbone dynamics from a single protein sequence

DynaMine is a fast predictor of protein backbone dynamics using only sequence information as input. It is able to accurately distinguish regions of different structural organisation within proteins, such as folded domains and disordered linkers of different sizes. Additionally, DynaMine can identify disordered regions within proteins with an accuracy comparable to the most sophisticated existing disorder predictors. This high performance is achieved without depending on prior disorder knowledge or three-dimensional structural information, which makes it a unique approach in the field. DynaMine is developed at the Interuniversity Institute of Bioinformatics in Brussels (IB)².

QCQuan

A webtool for automated quality control and statistical analysis of protein expression following labeled mass spectrometry experiments

QCQuan is a webtool for automated quality control and statistical analysis of protein expression following labelled mass spectrometry experiments. The tool is focused on differential expression analysis generated by isobaric labelling experiments. Flat text files from maxQuant, Proteome Discoverer or any other tools can be uploaded for a post-identification analysis. In this process, the user is offered very few options to modify the workflow in order to enhance comparable outcomes from different proteomic experiments. QCQuan is developed at the University of Hasselt in collaboration with VITO.

ELIXIR Belgium is the national node of ELIXIR, the intergovernmental organization that brings together life science resources from across Europe, supporting life science research and its translation to medicine, environment, the bio-industries, and society. The research infrastructure provides platforms and guidance for research data management and reproducible data analysis, and offers domain specific services for Plant and Biodiversity, Human health and COVID-19 research. ELIXIR Belgium also provides data related training and workshops.

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