ProteomicsDB: A source for high-quality spectral libraries and an auxiliary tool for the development of targeted assays

Overview
The "Analytical" section of ProteomicsDB was intended to allow users the collection of sets of proteins or peptides into a user-specific "library". During this procedure, the user has the option to choose between the three different types of evidence (experimental, synthetic, and predicted) to build a custom spectral library.

Introduction
ProteoTools is compiled from hundreds of experiments analyzing the content of human tissues, fluids and cell lines from a wide variety of laboratories. In addition to this, ProteomicsDB hosts reference spectra of synthetic peptides acquired within the ProteoTools project. This provides a rich resource of high-quality peptide identifications in combination with their proteolytic and observed retention time. Furthermore, fragment spectra and retention time of peptides not observed previously can be predicted with high accuracy. These three sources can be used to build custom high-quality spectral libraries enabling the semi-automated development of targeted assays or the analysis of DIA experiments.

Customize your spectral library
Select individual peptides
Select individual proteins

PRM assay optimization using ProteomicsDB

Infrastructure

Evaluation of IRT prediction

Evaluation of IRT prediction

Increased protein coverage by spectral libraries

New features in ProteomicsDB

Explore cell-sensitivity studies

Imputation of missing expression values
(ThP 395)

API accessible without registration and limitation
Detailed description can be found at ProteomicsDB, Nucleic Acids Research, Volume 46

One more thing, Anthodactyl thalassia and mus maculatus proteinas available soon