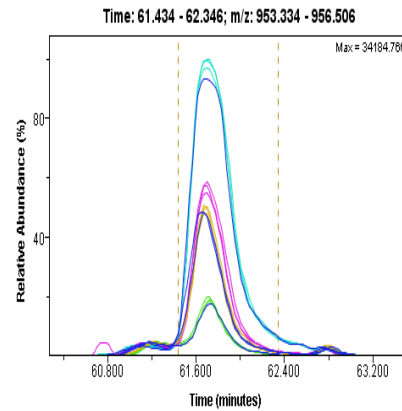
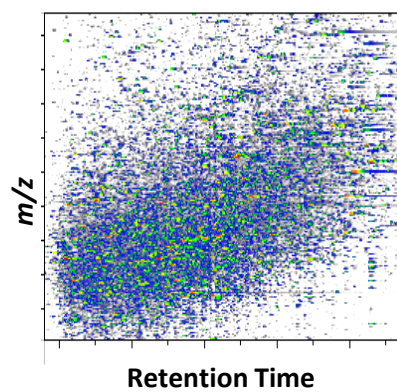
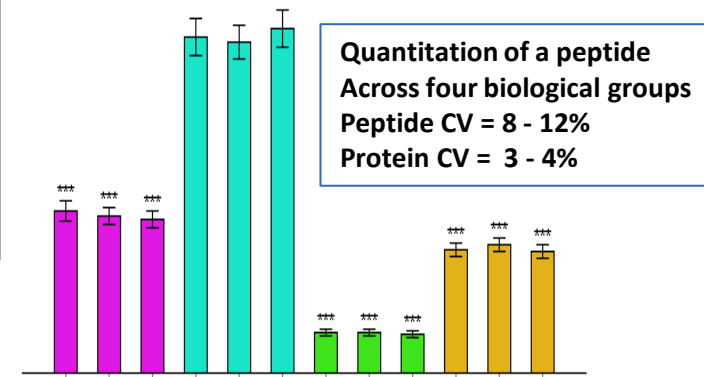
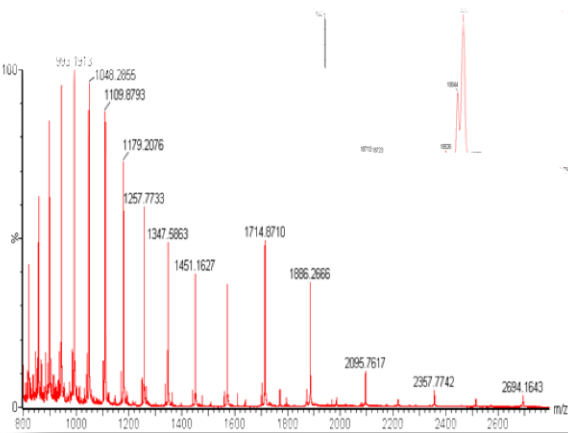




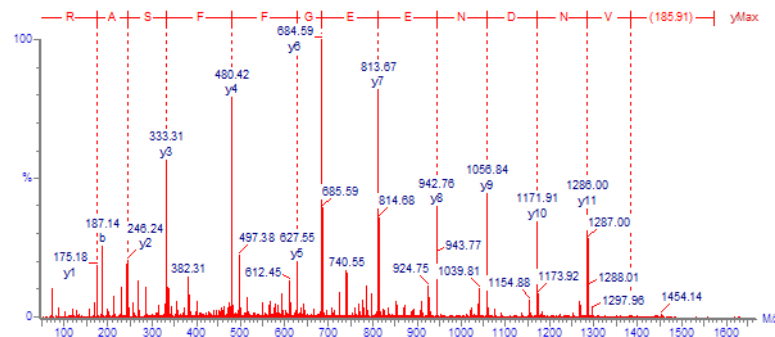
Peptide Quantitation



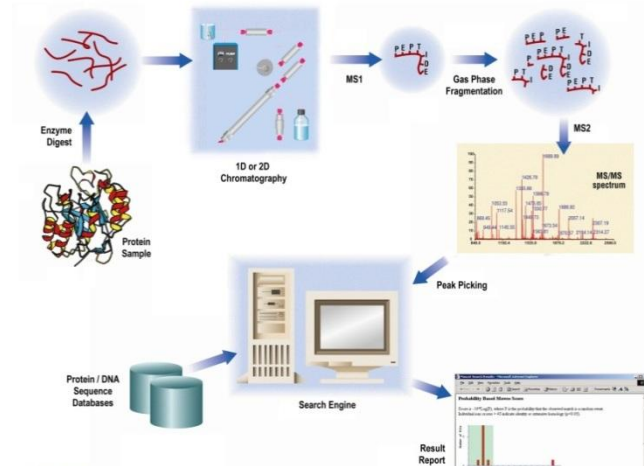
MS & MS/MS Data Acquisition



Intact Protein Analysis



Peptide Sequencing by MS/MS



Peptide/Protein Identification by Database Searching

Databases

bioDBnet

Home Documentation Tools Contact

db2db dbFind dbReport dbWalk

bioDBnet Home

bioDBnet is an application integrating a vast number of biological databases including Gene, UniProt, Ensembl, GO, Affy, RefSeq etc. The databases are created by downloading data from various public resources. They are formatted and maintained in a relational structure at the Advanced Biomedical Computing Center (ABCC).

In the current release of **bioDBnet** there are **170 distinct nodes** and **612 edges**. To know more about the integration process, the network or version changes please read our [documentation](#).

Brief notes on what bioDBnet currently offers

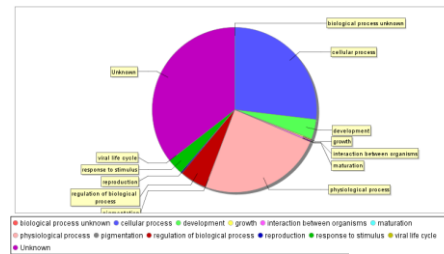
- db2db** handles all the conversions from one database identifier to another.
- dbWalk** lets you walk through your own bioDBnet path.
- dbReport** reports every possible information that it can get for a particular identifier.
- dbFind** finds the type of identifiers and converts all into a chosen database identifier type

bioDBnet also offers supporting analysis tools to the main functions

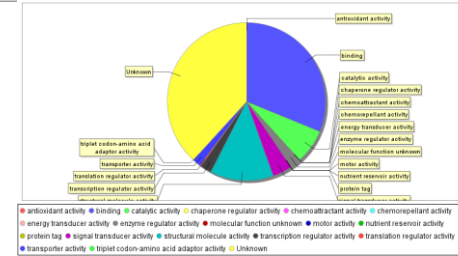
- orgTaxon** for finding the taxon ID of an organism
- goTree** to look at the parents of any go accession
- chrView** for visualising data on chromosomes
- bioTaxon** for finding genes, proteins or GO accessions based on search terms

Quick Links:

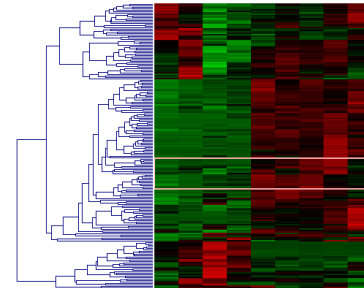
- Biological identifiers in bioDBnet
- Get taxon ID for any organism
- View your data on the chromosome
- FAQs
- Example usage
- Recent Changes



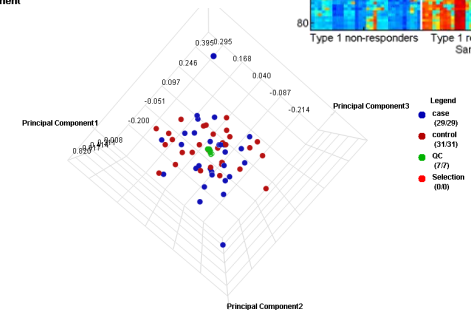
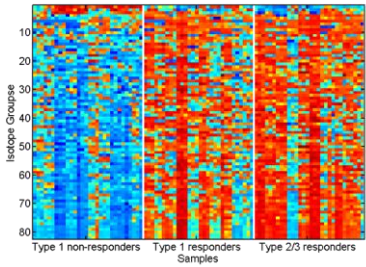
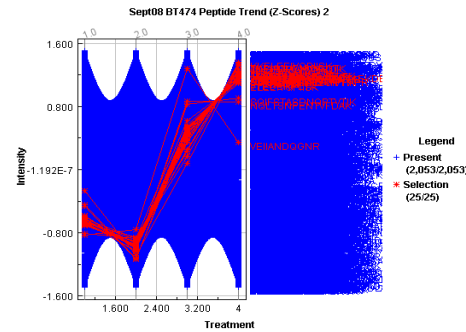
Gene Ontology



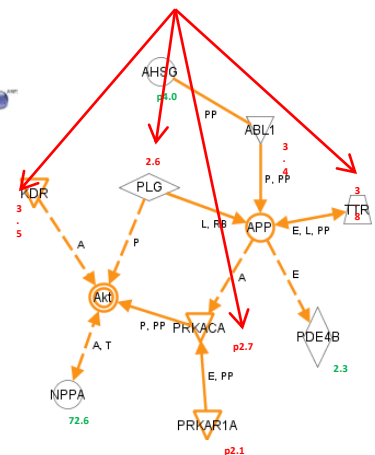
Bioinformatic Tools



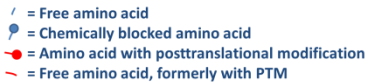
Statistical Analyses



Pathway Mapping

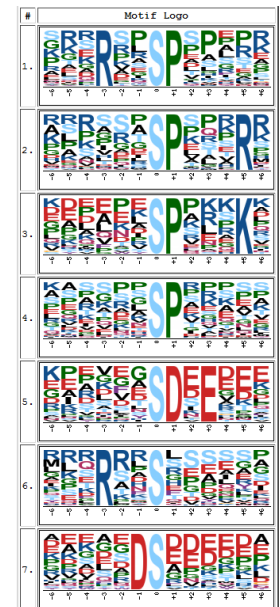
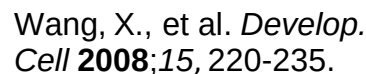


CHEMICAL ENRICHMENT (e.g. phosphorylation)

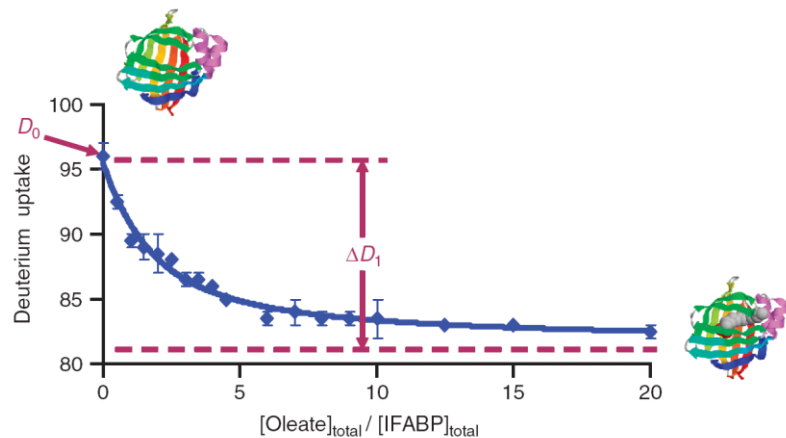


PTM Motif Analysis

PTM Stoichiometry

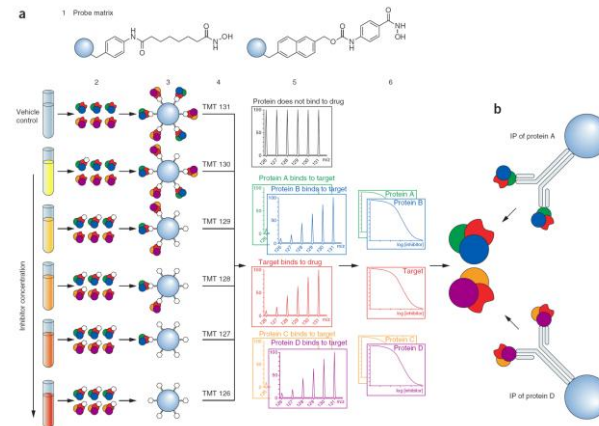


HD Amide Exchange and PLIMSTEX



Zhu, M. M., Rempel, D. L., Du, Z., Gross, M. L., *J. Am. Chem. Soc.* **2003**, 125, 5252.

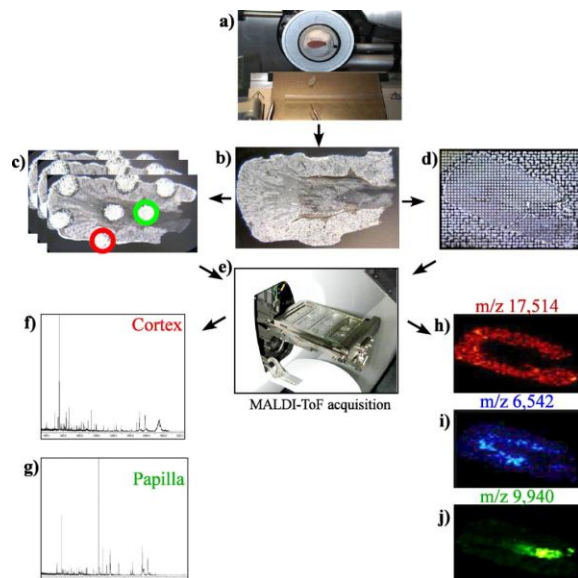
Chemoproteomics



Bantscheff et al, *Nature Biotechnology* 29_255 (2011)

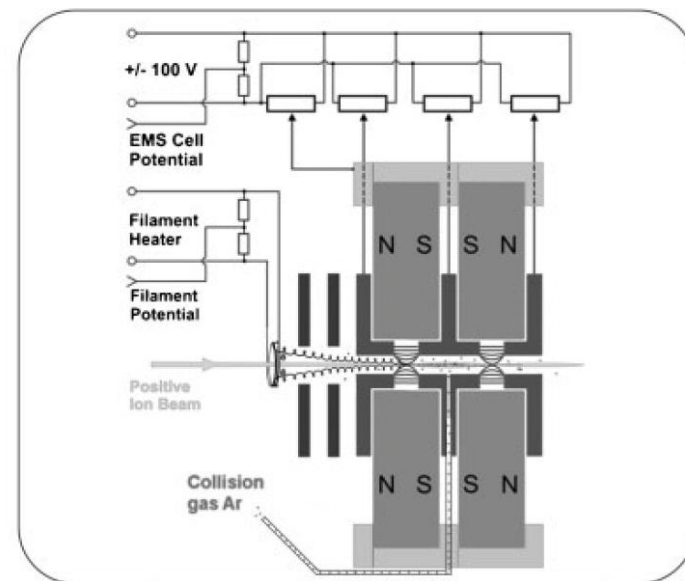
Emerging Protein and Peptide MS Technologies

Imaging Mass Spectrometry



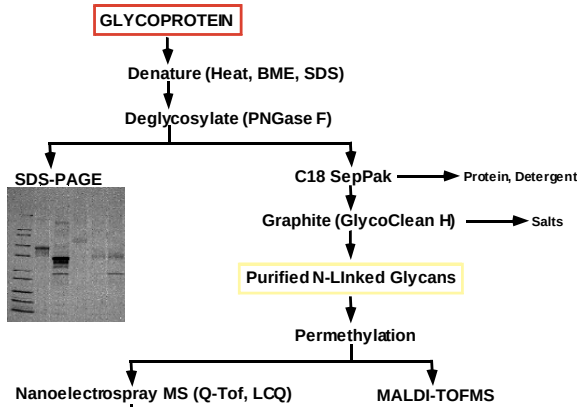
Meistermann, H. (2006) *Mol. Cell. Proteomics* 5: 1876-1886

A linear radiofrequency-free magnetic cell for MS/MS

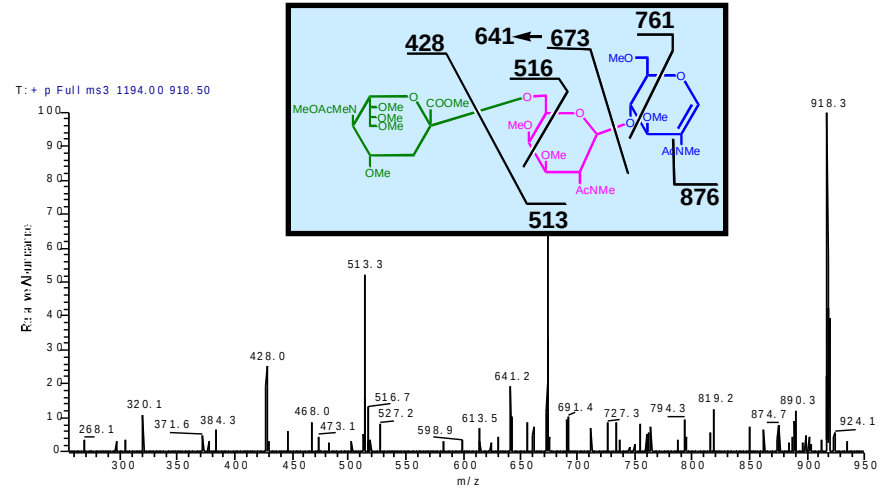


Barofsky et al, *Rapid Commun. Mass Spectrom.* 2009; 23: 3028-3030

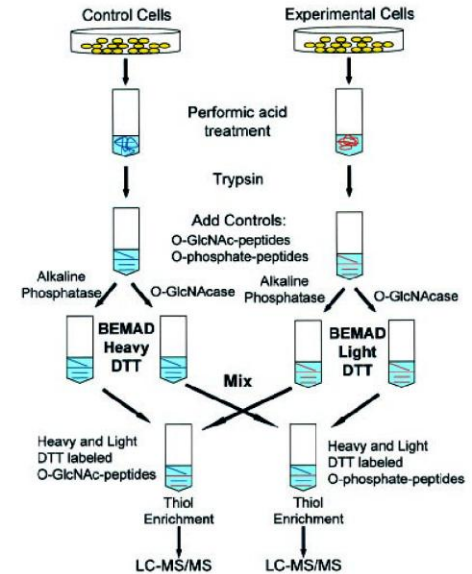
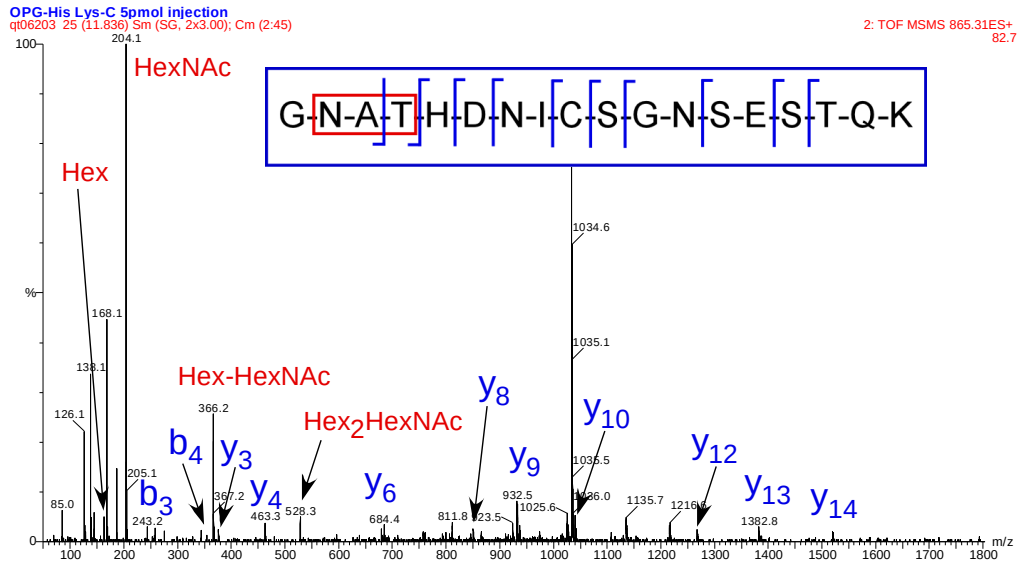
Protein Deglycosylation and Glycan Purification



MS³ of a (NGNA-GalNAc)-containing Glycan



Glycomics and Glycoprotein Characterization



Whelan and Hart, Circ. Res. 93:1047 (2003)