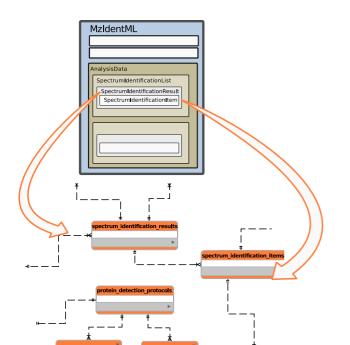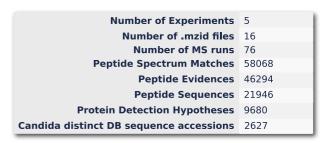Proteopathogen2.0, a database and web tool to store and display proteomics identification results in the MzIdentML standard format

Proteopathogen2.0 is a database-backed web application on shotgun Proteomics experiments addressed at the study of Candida albicans and other fungal pathogens and their interaction with the host. It follows the idea first implemented in the original version of Proteopathogen, proteopathogen.dacya.ucm.es (Vialas et al. 2009, Proteomics)

Number of Experiments	5
Number of .mzid files	16
Number of MS runs	76
Peptide Spectrum Matches	58068
Peptide Evidences	46294
Peptide Sequences	21946
Protein Detection Hypotheses	9680
Candida distinct DB sequence accessions	2627

* Check **Mayu FDR analysis** for different FDR cut offs

***Candida albicans* as a model organism to study fungal pathogens and their interaction with the host**

The opportunistic pathogenic fungus *Candida albicans*, under usual circumstances, is a harmless resident commensal in human mucous membranes of a large percentage of the population. However, taking advantage of weakened host immune defenses, for instance in immunocompromised cancer or AIDS patients, it may switch to its pathogenic status, overproliferating and becoming thus the main etiological agent of candidiasis, one of the most prevalent and costly types of fungal