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PD2 process - A bioinformatics tool for facilitating proteomics data functional interpretation: A quest for biological relevance

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PD2 process is a web-based tool implemented in PHP, JavaScript and Perl for facilitating the functional interpretation of proteomics data. Through a modular approach this tool assists the processing of comparative proteomics, pull-down and phosphoproteomics experiments results. It provides and interactive environment where the researcher can visualize and/or compare sets of quantitative data as well as protein functional information for post-translational modifications, subcellular localization, gene ontologies, etc., The tool also provides links to several biological databases to somehow centralize the information available in these resources. In conclusion, PD2Process constitutes an alternative for storing, visualizing and analyzing proteomics data that focus on the functional description of the identified/quantified proteins and in the case of phosphoproteomics of the identified phosphosites.

Biography

Samy Otero González is close to complete his studies on Informatics Engineering next year at the Polytechnic University José Antonio Echeverría (CUJAE). He developed a passion for Bioinformatics when working as a Chemical technician in the Center for Genetic Engineering and Biotechnology (CIGB, 2002-2014). So he decided to work on his thesis at CIGB's Systems Biology department in close collaboration with the logistic department at CIMAB.

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