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STORING, REPORTING AND COMPARING PROTEOMICS EXPERIMENTS USING THE MIAPE GENERATOR TOOL

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Standardization of experimental proteomics protocols is one of the main objectives of the National Institute for Proteomics (ProteoRed). Several multicentric experiments as well as several participations in ABRF Proteomics Research Group (PRG) studies have been coordinated by ProteoRed with the purpose of comparing both results and experimental protocols applied to obtain these results. From these studies, we obtain conclusions that help to establish the best approach for a certain proteomic problem and to improve the application of new techniques to new proteomics challenges. However, the comparison between different experiments is not a trivial task if there is not a consensus data format.

The Human Proteome Organization's Proteomics Standards Initiative (HUPO PSI) is actively developing XML interchange formats to allow both the exchange and storage of such data, and also guidance modules (Minimum Information About a Proteomics Experiment. MIAPE), to report the use of proteomics techniques in electrophoresis and mass spectrometry-based experiments. ProteoRed has incorporated such reporting standards in the multicentric activities mentioned above, using MIAPE guidelines to report the experiments and therefore, facilitating the comparison between them.

With the aim of helping the implementation of such standard, we have developed a tool freely accessible through the ProteoRed web application at http://www.proteored.org, that generates and stores MIAPE compliant reports, that is, containing the minimum information required to report a proteomics experiment, both MIAPE Gel Electrophoresis (from sample to gel image acquisition), Gel Informatics (analysis of gel image), Mass Spectrometry (from sample to peak list generation) and MIAPE Spectrometry Informatics (analysis of these peak lists) experiments.

The "MIAPE generator tool" also allows to compare different stored MIAPE compliant reports, therefore, to compare different proteomics experiments, providing specific information about the same aspect from different experiments in a single table.

Several important proteomics journals are already asking for some minimal information required to publish a paper, based in the HUPO-PSI MIAPE guidelines. For that reason, using this tool, ProteoRed wants to provide to their costumers a MIAPE compliant report attached to the results as a new service quality label.