A PLATFORM-INDEPENDENT SYSTEM TO REMOVE CONTAMINANTS FROM PMF PEAK LISTS

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Peptide-mass fingerprinting (PMF), is the easiest and fastest method that can be used as a first screening to identify proteins. In this situation, previously purified proteins are digested in-gel by specific cleavage agents (either enzymatic or chemical) to produce a mixture of peptides, which are analyzed by mass spectrometry – frequently Matrix-Assisted Laser Desorption Ionization (MALDI). During the experimental procedures, contaminants can be introduced in the sample averting its identification. The objective of the work is to present an application in PHP that eliminates the contaminant masses from the list of peptide masses, increasing the possibilities of protein identification. The advantages of this method of contaminants elimination include the fact that it is platform and location independent, extending the access to any user of the world. Moreover, it has the possibility of insertion in a processing pipeline so that automated proteomics solutions can benefit from this software. Data can be automatically submitted from peak picking software to this software that, in its turn, can run in background and send the results to protein identification search engines. This software is open source, allowing user customization. In this work we present a simple system capable of detecting and removing contaminant peaks from MS sample data and with proven ability to increase identification scores, although powerful enough to be implemented in proteomics pipelines.