

OMSS@IJM: A WEB-BASED PROTEOMICS DATABASE SEARCH ENGINE WITH EXTENDED CAPABILITIES TO ADDRESS THE IDENTIFICATION OF DISEASE-RELATED PROTEIN DEGRADATION PRODUCTS

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A major issue in clinical proteomics is the characterization of biomarkers, often resulting from the proteolytic cleavage of cellular proteins in organ and/or disease specific processes^[1,2,3]. Actually no web-based search engine address the search and identification of biomarkers from MS/MS. We therefore developed a web service that focused on this important emerging domain of biomarker identification, OMSS@IJM, taking advantage of the attractive features of the open-source algorithm OMSSA^[4]. Our web server allows the user to search a fragmentation spectrum for identification when non-specific cleavage is suspected. To reach this goal, we developed a set of software packages that produced and compiled databases corresponding to a given mass (expressed as MH⁺) entered by the user, together with the MSMS fragmentation spectrum, but without specifying any protein cleavage chemistry.

We also implemented tools allowing the user to 1) analyze large datafiles by extending the size limitation (or number of spectra) restriction, 2) upload and search a private database in Fasta format, and 3) edit and search any non-standard modification of the amino-acids residues.

As a demonstrative example of the OMSS@IJM functionalities, we identified from LC-MS/MS data the monomeric form of ubiquitin as a molecular marker of hepatocellular carcinoma. Our web server has been tested and used since 10 months by the « Mass Spectrometry Core Facility » group of Jacques Monod Institute, and by the Anatomic-pathology Lab from Beaujon Hospital. It has also been used during a one-week master 2 course on proteomics.

Key words: Proteomics, Biomarker identification, Mass Spectrometry, OMSSA

URL: <http://ytat2.ijm.univ-paris-diderot.fr/omssa/index.html>

This website is free and open to all users and there is no login requirement.

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