

MS-Decipher: a user-friendly proteome database search software with an emphasis on deciphering the spectra of O-linked glycopeptides

Abstract: The interpretation of mass spectrometry (MS) data is a key step in proteomics analysis, and the identification of glycosylation, one of the post-translational modifications (PTMs), is essential for understanding the biological functions in living systems. In order to simplify the analysis of proteomic data sets, especially O-glycoproteomic data sets, we provide a user-friendly proteomics database search platform, MS-Decipher, to identify peptides from MS data. Two scoring schemes can be used for peptide matching. As for the result validation step, there are also more than one method for users to choose. In addition, a special search mode we developed before, O-search, is presented to search O-glycopeptides for the O-glycoproteomic analysis. It was found that MS-Decipher performed well in peptide search and O-glycopeptide search compared with traditional database search software. What's more, MS-Decipher has a user-friendly graphical user interface, making it easy to operate. Data and result files in multiple formats can be used for search and validation steps. MS-Decipher is implemented in Java and can be used across platforms. MS-Decipher is free for academic use.

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