

Introducing *mmSearch*

Advanced Protein Database Search Software

MassMatrix's *mmSearch* is a cutting-edge protein database search software designed to revolutionize the identification of peptides and proteins from tandem mass spectrometry (MS/MS) data.

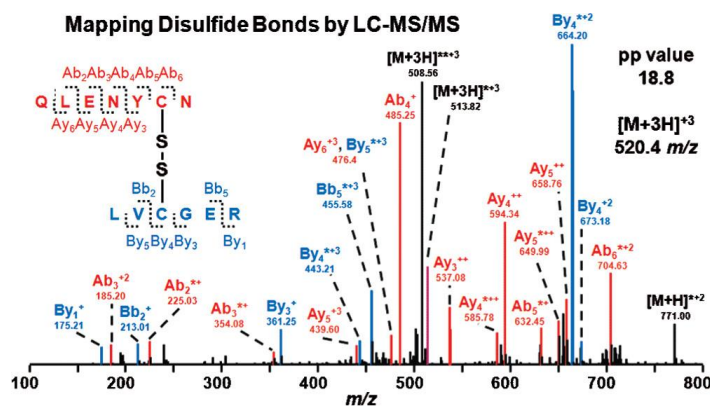
mmSearch utilizes a mass accuracy sensitive probabilistic scoring model to match tandem mass spectra with theoretical peptide sequences derived from a comprehensive protein database.

Our innovative approach ensures higher sensitivity and specificity in peptide identification, outperforming traditional search algorithms, especially in datasets with high mass accuracy.

Key Advantages of *mmSearch*

- Superior sensitivity and specificity, with a false positive rate of just 2%.
- Unique capability to identify peptides and proteins, including those with disulfide bonds, without the need for chemical reduction or derivatization.

- Intuitive probability-based statistical scoring model that accurately assesses the significance of peptide and protein matches.



MassMatrix, Inc. is a Data Analytics and Bioinformatics Software company that specializes in developing custom solutions to complex biodata analysis problems.

We invite you to join our technical advisor team to develop the best platform for sequencing and characterization of therapeutics.

The Science Behind MassMatrix

1. Xu H, Freitas MA. MassMatrix: a database search program for rapid characterization of proteins and peptides from tandem mass spectrometry data. *Proteomics*. 2009 Mar;9(6):1548-55. doi: 10.1002/pmic.200700322. PMID: 19235167; PMCID: PMC2759086.
2. Xu H, Hsu PH, Zhang L, Tsai MD, Freitas MA. Database search algorithm for identification of intact cross-links in proteins and peptides using tandem mass spectrometry. *J Proteome Res*. 2010 Jul 2;9(7):3384-93. doi: 10.1021/pr100369y. PMID: 20469931; PMCID: PMC4141472.
3. Xu H, Zhang L, Freitas MA. Identification and characterization of disulfide bonds in proteins and peptides from tandem MS data by use of the MassMatrix MS/MS search engine. *J Proteome Res*. 2008 Jan;7(1):138-44. doi:10.1021/pr070363z. Epub 2007 Dec 12. PMID: 18072732; PMCID: PMC2749473.

Learn more about how we can help with your data and analysis workflows:

Contact us at www.massmatrix.bio. Email to sales@massmatrix.bio.