

पेटेंट कार्यालय
शासकीय जर्नल

**OFFICIAL JOURNAL
OF
THE PATENT OFFICE**

निर्गमन सं. 02/2024

ISSUE NO. 02/2024

शुक्रवार

FRIDAY

दिनांक: 12/01/2024

DATE: 12/01/2024

पेटेंट कार्यालय का एक प्रकाशन
PUBLICATION OF THE PATENT OFFICE



(12) PATENT APPLICATION PUBLICATION

(19) INDIA

(22) Date of filing of Application :15/12/2023

(21) Application No. **202341085951** A

(43) Publication Date : 12/01/2024

(54) Title of the invention : METHOD AND SYSTEM FOR ANALYSIS OF PROTEINS USING MASS SPECTROMETRY

(51) International classification :G01N0033680000, H01J0049000000, G01N0030720000, H01J0049040000, G01N0027622000

(86) International Application No :NA
Filing Date :NA

(87) International Publication No : NA

(61) Patent of Addition to Application Number :NA
Filing Date :NA

(62) Divisional to Application Number :NA
Filing Date :NA

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(57) Abstract :

METHOD AND SYSTEM FOR ANALYSIS OF PROTEINS USING MASS SPECTROMETRY ABSTRACT The present invention relates to a method and system for the analysis of proteins using mass spectrometry. The method involves introducing a protein sample into a mass spectrometer system, ionizing the proteins within the sample, separating the resulting protein ions based on their mass-to-charge ratio using a mass analyzer, detecting the separated protein ions to obtain mass spectra, and analyzing the mass spectra to identify and quantify the proteins present in the sample. Additional features include pre-processing of mass spectra, peak detection, deconvolution of overlapping peaks, and correlation with a protein database for enhanced accuracy in protein identification. The system comprises modules for sample introduction, ionization, mass analysis, detection, and analysis, offering a comprehensive solution for protein analysis. Further refinements involve tandem mass spectrometry, automated sample handling, ion mobility spectrometry, and machine learning algorithms, contributing to improved efficiency, sensitivity, and reliability in protein analysis.

No. of Pages : 18 No. of Claims : 9