Accepted Manuscript

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PII: S0924-2244(17)30718-5

DOI: 10.1016/j.tifs.2018.04.008

Reference: TIFS 2211

To appear in: *Trends in Food Science & Technology*

Received Date: 5 November 2017

Revised Date: 21 April 2018

Accepted Date: 24 April 2018

Please cite this article as: Andjelković, U., Josić, D., Mass spectrometry based proteomics as foodomics tool in research and assurance of food quality and safety, *Trends in Food Science & Technology* (2018), doi: 10.1016/j.tifs.2018.04.008.

Mass spectrometry based proteomics as foodomics tool in research and assurance of food quality and safety

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ABSTRACT

Background: As a comprehensive discipline that studies food and nutrition, foodomics requires reliable qualitative and quantitative information about the food proteome component in order to extract new, integrative information from the complex multivariable space of omics. This information is necessary to achieve a higher level of understanding of processes in food science and technology, consequently new functions of food and improved markers of food quality and safety and transform the concept of food safety.

Scope and Approach: We are presenting mass spectrometry (MS) based proteomic approaches that are being utilized in different proteomic studies, not necessarily only in the field of foodomics. Current analytical capabilities of MS-based proteomics together with sample preparation procedures and quantification strategies, and recent technical developments were presented.

Key Findings and Conclusions: MS-based proteomics enables the analysis of different aspects of proteins and provides a variety of approaches for reliable quantification of individual proteins and/or food proteome. This is a complex field and its successful implementation requires a