

Foodstuffs - Detection of food allergens by liquid chromatography - mass spectrometry (LC-MS) methods
- General considerations

EESTI STANDARDI EESSÕNA

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English Version

Foodstuffs - Detection of food allergens by liquid
chromatography - mass spectrometry (LC-MS) methods -
General considerations

Produits alimentaires - Détection des allergènes
alimentaires par des méthodes de chromatographie en
phase liquide couplée à la spectrométrie de masse (CL-
SM) - Considérations générales

Lebensmittel - Nachweis von Lebensmittelallergenen
mit flüssigkeitschromatographisch-
massenspektrometrischen (LC-MS) Verfahren -
Allgemeine Betrachtungen

This European Standard was approved by CEN on 22 May 2022.

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European foreword

This document (EN 17644:2022) has been prepared by Technical Committee CEN/TC 275 “Food analysis - Horizontal methods”, the secretariat of which is held by DIN.

This European Standard shall be given the status of a national standard, either by publication of an identical text or by endorsement, at the latest by January 2023, and conflicting national standards shall be withdrawn at the latest by January 2023.

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Introduction

Specific peptides or groups of peptides deriving from specific proteins can serve as markers for the presence of food or food ingredients provoking allergic reactions. This document describes the procedure for the development of qualitative and/or quantitative mass spectrometry-based methods for the determination of protein-derived peptides as markers for potentially allergenic food ingredients or constituents by analysing the protein/s extracted from a sample. Appropriate procedures for the extraction of the targeted proteins are an essential part of each method. This document describes general considerations for the application of liquid chromatography mass spectrometry-based methods in qualitative or quantitative targeted analysis of specific peptides (derived from specific proteins) that are representative for a food allergen. The document includes recommendations for method validation and for the conversion of the analytical results to units of mg protein/kg food.

1 Scope

This document establishes an overall framework covering qualitative and quantitative methods for the determination of food allergens and allergenic ingredients using mass spectrometry-based methods for the determination of specific peptides/proteins. This document provides general guidelines and performance criteria applicable to this methodology. Guidelines, minimum requirements and performance criteria laid down in this document are intended to ensure that comparable and reproducible results are obtained by different analysts, instrumentation and laboratories.

2 Normative references

The following documents are referred to in the text in such a way that some or all of their content constitutes requirements of this document. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies.

EN 15842, *Foodstuffs - Detection of food allergens - General considerations and validation of methods*

3 Terms and definitions

For the purposes of this document, the terms and definitions given in EN 15842 and the following apply.

ISO and IEC maintain terminological databases for use in standardization at the following addresses:

- IEC Electropedia: available at <https://www.electropedia.org/>
- ISO Online browsing platform: available at <https://www.iso.org/obp>

3.1

high-performance liquid chromatography-mass spectrometry

HPLC-MS

analytical chemistry technique that combines the separation capabilities of high-performance liquid chromatography with the detection capabilities of mass spectrometry (MS)

Note 1 to entry: The abbreviation LC-MS is also used.

3.2

tandem mass spectrometry

MS/MS

MS²

sequential combination of two mass analyses

Note 1 to entry: Different mass spectrometer instrument types exist, combining different principles of mass detection, e.g. quadrupole, time-of-flight, ion trap, Fourier-Transform mass spectrometer.

3.3

multi-stage mass spectrometry

MSⁿ

sequential combination of more than two mass analyses