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Profiling of modified nucleosides from ribonucleic acid digestion by supercritical fluid chromatography coupled to high resolution mass spectrometry

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Highlights

- A SFC-HRMS method development for nucleosides profiling is fully described using a commercial standard mixture
- Estimated LOD and LOQ are compatible with biological samples
- Digested tRNA of *E. coli* is used to validate the SFC-HRMS method
- SFC-HRMS results are complementary to the classical LC-HRMS ones

Abstract: A method based on supercritical fluid chromatography coupled to high resolution mass spectrometry for the profiling of canonical and modified nucleosides was optimized, and compared to classical reverse-phase liquid chromatography in terms of separation, number of detected modified nucleosides and sensitivity. Limits of detection and quantification were measured using statistical method and quantifications of twelve nucleosides of a tRNA digest from *E. coli* are in good agreement with previously reported

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