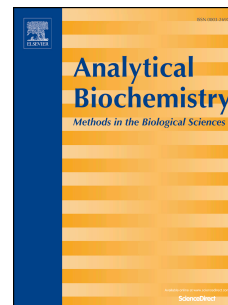


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Quantification of proteins by data independent acquisition: Performance assessment of the Hi3 methodology

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**Quantification of proteins by data independent acquisition: performance assessment of the Hi3 methodology.**

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**Short title:** MS investigation of protein mixture composition

**Abstract**

Proteomics greatly benefited from the development of mass spectrometry. Over the last years, data-independent acquisitions increased in popularity in an effort to provide routine label free quantitative information. In this report, the performance of the Hi3 label free method was assessed based on the analysis of a plasma-derived protein mixture. The following parameters of the method (CVs) were determined: repeatability 13.8%, intermediate precision 27.6%, bias 32.3% and linearity observed over 3 orders of magnitude. Finally an accuracy of 42.5% corresponding to a confidence interval within 2 fold the expected protein abundance should be a good approximation of the method performance.

**Keywords**

Hi3; label free; blood plasma; Cohn fractionation; MS<sup>E</sup>

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