

Application Highlight

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Filter-Aided Sample Preparation (FASP) with Vivacon® 500

In 2009 the group around Matthias Mann, at the Max Planck Institute for Biochemistry, Department of Proteomics and Signaltransduction, Martinsried (Germany), published a new method for the preparation of peptide samples using ultrafiltration devices. This new procedure, termed Filter-Aided Sample Preparation (FASP)¹ allows gel-free processing of biological samples solubilized with detergents for proteomic analysis by mass spectrometry. In FASP, detergents are removed by ultrafiltration and after protein digestion, peptides are separated from undigested material.

The effectiveness of different filtration devices for analysis of proteomes and glycoproteomes was compared. Horizontal ultrafiltration devices including Vivacon® filtration units with nominal molecular weight cut-offs (MWCOs) of 30 and 50 kDa were found to be suitable for FASP².

FASP has become a very popular method in proteomics workflows, as it is fast, easy and highly reproducible. Furthermore, this technique has found many new applications in proteomics, including quantification of nucleic acids to estimate cell number, protein derivatization to support peptide fractionation, and modification of the detergents used to enable partial protein extractions^{3,4}.



References

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