Filter Aided Sample Preparation (FASP) with Vivacon® 500

In 2009 the group around Matthias Mann, Max Planck Institute for Biochemistry, Department of Proteomics and Signaltransduction, Martinsried in Germany published the new FASP method using ultrafiltration devices and founded the sample preparation name Filter Aided Sample Preparation (FASP)[1]. The FASP method 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 glyco-proteomes was compared. Horizontal ultra-filtration devices as Vivacon® filtration units with nominal molecular weight cut-offs of 30 kDa and 50 kDa were found to be suitable for FASP[2].

FASP is becoming a very popular method as it is fast, easy and highly reproducible and is finding many new applications in the proteomics sector[3].

[1] Wiśniewski JR, Zougman A, Nagaraj N, Mann M. Universal sample preparation method for proteome analysis (2009). Nat Methods. 6(5):359-62.

[2] Jacek R. Wiśniewski, Dorota F. Zielinska and Matthias Mann (2010). Anal Biochem Dec 14, 2010

[3] Ivan Matic, Ellis G. Jaffray, Senga K. Oxenham, Michael J. Groves, Christopher Barratt, Sudhir Tauro, Nicola R. Stanley-Wall, and Ron Hay J. Proteome Res., Just Accepted Manuscript
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