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„Food mill“ for proteins – new method improves protein analysis considerably

Until now, extracting as many proteins as possible from biological samples has required a combination of several methods. Scientists at the Max Planck Institute of Biochemistry have now developed a new universally employable sample preparation method that combines the advantages of the usual methods and allows an unprecedented depth of proteome coverage.

Proteins play an important role in the machinery of life, they determine cell structure and participate in all cell mechanisms. Thus protein analysis is crucial for elucidating cell processes. However, prior to their analysis by mass spectrometry, proteins must be extracted from the given sample and digested into smaller pieces (peptides). So far, a combination of different methods was necessary in order to obtain as many proteins as possible – and even then some proteins remained poorly accessible: “For membrane proteins for example we have been searching for a suitable method for the last ten years”, says Professor Jacek Wiśniewski (Max Planck Institute of Biochemistry). Now the scientist and his colleagues in the research department “Proteomics and Signal Transduction” (led by Professor Matthias Mann) report a significant breakthrough: They have developed the first method to extract proteins from biological materials that can be used universally. The so-called FASP (filter aided sample preparation) is a new filtration technique that combines the advantages of the previous methods: robustness against impurities on the one hand and better automatization possibilities on the other hand.

Using FASP, the proteins are first extracted by a strong detergent. Thereafter as the proteins are “glued” to the detergent they then need to be removed from the sample. This is achieved by the new filtration device - here the detergents are removed by urea, while the bulky proteins remain in the filter. “After this, the filter functions similarly to a food mill, such as where apples for example can be sieved”, explains Wiśniewski. Whilst still in the filter the proteins are “digested” by enzymes into smaller peptides, which can then pass through the filter, while impurities are retained. Pure peptides are eluted and – importantly - the protein yield is excellent, as Wiśniewski's experiments prove. “The method is not only interesting from the point of view of membrane proteins, but now it is possible to examine all proteins, whatever their properties, using this one method only, also facilitating interpretation of results considerably”, points out Wiśniewski. Up to now, the scientists have already identified more than 7000 proteins from human tissue using this new method.



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J.R. Wiśniewski, A. Zougman, N. Nagarjuna, M.Mann: Universal sample preparation method for proteome analysis. Nature Methods advanced online publication 19 April 2009.
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Further Information:

<http://www.biochem.mpg.de/mann>

<http://www.nature.com/nmeth/journal/vaop/ncurrent/abs/nmeth.1322.html>

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