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INVITED LECTURE - The use of nuclear analytical techniques in the identification and investigation of metal- and metalloid-containing proteins

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Most metals and metalloids present in biological materials are bound to proteins where they have essential tasks as part of the catalytic centers of enzymes or as structural components. It has been estimated that in the biosphere a multitude of these compounds exists but so far relatively few of them have been detected. Since in most cases the presence of a metal or metalloid in a protein cannot be recognized from its genetic code, specific methods for the identification of novel metal- and metallo-containing proteins and the investigation of their characteristics have to be applied. The information obtained in this way helps elucidate the biological functions of trace elements and is thus of great interest in many fields of the life sciences.

As the properties of most of these compounds are not yet known, initial information on their presence in tissues or cells can only be obtained by protein separation and determination of the element contents in the isolated fractions. For these investigations gel electrophoretic separation procedures have been combined with radiotracer techniques and nuclear analytical methods which allow surface scanning such as proton-induced X-ray emission or synchrotron radiation X-ray fluorescence. In the analysis of several trace elements in purified proteins or protein subunits, which are usually isolated in only very small amounts, neutron activation analysis has been successfully applied. The identification of a novel metalloprotein is then achieved by analysis of the amino acid sequence of the purified protein using MALDI-MS of the peptide fragments, mRNA determination and cDNA synthesis. In this overview the applications of nuclear analytical methods in this field of research and their advantages and disadvantages are discussed with the help of some examples.

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