

High Resolution ICP-MS trace element analysis of proteins fractions obtained from size exclusion high pressure chromatography of human cerebrospinal fluid

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The central nervous system is surrounded by cerebrospinal fluid (CSF). CSF provides a biological matrix for trace element analysis reflecting the living brain. A method to study the protein binding pattern of trace elements in human CSF is described. Proteins in CSF-samples were separated according to size by Size Exclusion Chromatography combined with High Pressure Liquid Chromatography (SEC-HPLC). A size exclusion column, Superdex 75 (10/300GL, Tricorn), and HPLC system (Hewlett Packard, series 1050) with quaternary pump, degasser, manual injector (100 µl loop) and a UV-detector (254 nm) was used for the separation of proteins in the CSF samples. Pump speed was set at 0.750 ml/min, and fractions were collected for 40 min. The column was calibrated to separate proteins in the range 6-70 kDa. Fractions were then analysed off-line using High Resolution Induction Coupled Mass Spectrometry (HR-ICP-MS) to determine trace element composition. We were able to measure more than 10 elements of clinical chemistry interest in the CSF fractions. Results will be presented for Cd, Mn, Fe, Pb, Cu and Zn. HR-ICP-MS has technically very low detection limits and the technique is particularly useful for multi-element determinations in small samples of biological material with low concentrations of trace elements. It is vital that the eluents of the HPLC is tolerated by the plasma and the inlet system of the mass spectrometer. SE-HPLC uses non-denaturing mobile phase at physiological pH which stabilizes the original metalloprotein complexes and is well tolerated by the HR-ICP-MS system. No sample preconcentration was needed for this method.