MS characterization of apheresis samples from rheumatoid arthritis patients for the improvement of immunoadsorption therapy - a pilot study.

Kienbaum M, Koy C, Montgomery HV, Drynda S, Lorenz P, Illges H, Tanaka K, Kekow J, Guthke R, Thiesen HJ, Glocker MO (2009) MS characterization of apheresis samples from rheumatoid arthritis patients for the improvement of immunoadsorption therapy - a pilot study. *Proteomics Clin Appl* 3(7), 797-809.

Details

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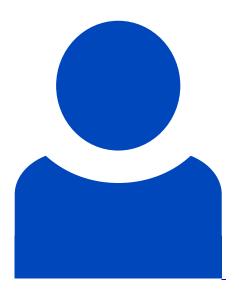
Abstract

Identification of proteins from apheresis samples was performed by both SDS-PAGE and 2-D gel separation of eluted proteins from staphylococcal protein A-based immunoadsorption columns (Prosorba(®)) followed by MS peptide mass fingerprinting and MS/MS peptide sequencing on a MALDI QIT TOF mass spectrometer. MS/MS peptide sequencing was performed in conjunction with a micro reversed phase HPLC configured with an online MALDI plate-spotting device. Apheresis treatment had been performed in three patients with longstanding therapy refractory rheumatoid arthritis. 2-D gels displayed ca. 500 spots representing proteins that were eluted from the Prosorba(®) columns. From 54 gels, a total of 1256 protein spots had been picked and yielded in the identification of 56 non-redundant proteins without counting isoforms. Proteins from the eluates belong to five major groups comprising (i) immunoglobulins (IgG, IgA, IgM heavy and light chains; about 40% of the spots), (ii) proteins involved in coagulation, (iii) HDL/LDL-associated

Beteiligte Forschungseinheiten

Microbiome Dynamics Gianni Panagiotou Mehr erfahren

Leibniz-HKI-Autor*innen



Reinhard Guthke

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