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CHARACTERIZATION OF PEPTIDES AND PROTEINS IN THERAPEUTIC HUMAN SERUM ALBUMIN

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Human serum albumin (HSA) is the most abundant plasma protein, with described ligand-binding and transport properties, antioxidant functions, and enzymatic activities. Commercial HSA is indicated for re-establishing and maintaining circulatory volume in situations resulting from traumatic shock, surgery or blood loss. [1] HSA is also used in extracorporeal liver support devices that performs blood dialysis against this protein. [2] Therapeutic HSA accounts for 14 % of the global market volume for plasma products.

Although therapeutic HSA has been used for more than 50 years, the composition of the commercial product remains unclear. Characterization of its composition is, however, crucial in order to understand its therapeutic effects and adverse reactions, as well as the mechanisms involved in different albumin therapies.

Here, we present the results from an exhaustive analysis of therapeutic human serum albumin composition using proteomic approaches. Low abundant proteins and peptides in these samples were concentrated using a strong anion exchange (SAX) resin (ion exchanger MARS, Gambro, Lund, Sweden). The absorbed material was eluted with stepwise gradient of ammonium trifluoroacetate and the resulting fraction analyzed by MDLC-MS/MS using an LTQ ion trap.

Besides albumin, a total of 1467 peptides corresponding to 102 proteins were identified with a false discovery rate of 1%. Relative to the human plasma proteome (www.plasmaproteomedatabase.org), the collection of proteins identified was apparently enriched on proteins involved in immunity and defense and transport (www.panther.org).

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