

[Get Access](#)[Share](#)[Export](#)

Journal of Chromatography B

Volume 1095, 15 September 2018, Pages 87-93

Characterization of Human Serum Albumin isoforms by ion exchange chromatography coupled on-line to native mass spectrometry

Y. Leblanc, N. Bihoreau, G. Chevreux  

 **Show more**

<https://doi.org/10.1016/j.jchromb.2018.07.014>

[Get rights and content](#)

Highlights

- IEX coupled to native MS was used for HSA isoforms characterization.
- HSA charge variants were efficiently separated by IEX with volatile salts.
- Cleaved, oxidized and glycated forms of HSA were monitored in a single analysis.
- High affinity Cu(II) binding to HSA was monitored at the isoform level.

Abstract

Human Serum Albumin is the most abundant protein of the **plasma** and displays a wide range of non-oncotic properties such as **antioxidant** activity, distribution in tissues and organs of binding molecules and clearance of **toxic compounds**. **Albumin** is susceptible to numerous **post-translational modifications** and particularly related to its free **thiol** group at Cys₃₄ which is the main circulating **scavenger** of **reactive oxygen species**. The characterization of these modifications is of high interest for the diagnosis and treatment of patients with liver diseases and for the structural integrity assessment of albumin as a **therapeutic protein**.

In this study, an ion exchange chromatographic method coupled on-line to native mass spectrometry was developed in order to bridge an effective charge variants [separation method](#) with a powerful identification technique for a detailed characterization of albumin isoforms. The chromatographic performance of the method allows the separation of 9 different isoforms that were on-line characterized by MS as oxidized, glycosylated, deamidated and N/C-terminal truncated forms. The method is also able to detect Cu(II) ions binding to the [N-terminal](#) site of the protein which is an important antioxidant feature of albumin. Finally, the method showed preliminary good performance parameters in term of linearity, precision and sensitivity for characterization of purified albumin as well as albumin from raw plasma for clinical and pharmaceutical purposes.

[< Previous](#)[Next >](#)

Abbreviations

HSA, Human Serum Albumin; RT, retention time; MS, mass spectrometry; IEX, ion exchange chromatography; FcRn, neonatal Fc receptor

Keywords

Mass spectrometry; Ion exchange chromatography; Oxidation; Charge variants; Human Serum Albumin

[Recommended articles](#)[Citing articles \(0\)](#)

© 2018 Elsevier B.V. All rights reserved.

ELSEVIER [About ScienceDirect](#) [Remote access](#) [Shopping cart](#) [Contact and support](#)
[Terms and conditions](#) [Privacy policy](#)

We use cookies to help provide and enhance our service and tailor content and ads. By continuing you agree to the [use of cookies](#).

Copyright © 2018 Elsevier B.V. or its licensors or contributors. ScienceDirect® is a registered trademark of Elsevier B.V.

 RELX Group™