



toxins



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Venom Proteomics and Transcriptomics

Guest Editors:

Prof. Dr. Edwin A. De Pauw

Mass Spectrometry Laboratory (MSLab), MolSys Research Unit, University of Liège (ULiège), Allée du six août 11, 4000 Liège, Belgium

Prof. Dr. Loïc Quinton

Laboratory of Mass Spectrometry - MolSys Research Unit, Allée du six Aout 11 - Quartier Agora - B4000 -Liège 1 - Belgium

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closed (31 January 2020)

Message from the Guest Editors

The deep analysis of venoms is receiving growing interest supported by important advances in sequencing methods, both at the nucleic acid and at the proteins/peptide level. The final toxins present in venoms can be characterized in detail, from their primary structure to their 3D fold. The level of detail that can be reached using mass spectrometry with only tiny amounts of sample opens new ways to characterize single organism toxins and to differentiate venoms from similar species of different geographical origin. The emphasis of this Special Issue will be on papers in which the methodological advances bring real breakthroughs and in which the complementarity of the approaches show a significant added value. Promising separation methods such as capillary electrophoresis and ion mobility are desired, as well as the 2D molecular mapping of venom glands by mass spectrometry imaging.



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Special Issue



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Prof. Dr. Jay Fox

Department of Microbiology,
University of Virginia,
Charlottesville, VA, USA

Message from the Editor-in-Chief

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Contact Us

Toxins Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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