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MASS SPECTROMETRY IN PEPTIDOMICS ANALYSIS: BIOCLUSTERS REGISTRATION IN SAMPLES OF RAT PITUITARY

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A modern trend of the biochemistry is studying of peptides, the understanding of the biological effects of which long time had a rather limited scope. Peptides, most of which are synthesized in the cells of the nervous system, referred to as regulatory molecules that control many physiological processes, such as pain and analgesia, thermoregulation, digestion, sleep, reproduction, learning, emotional reactions, etc.

The effectiveness of the methods of mass spectrometry (FAB, ESI, MALDI, TOF-PDMS, etc.) for the study of proteins and peptides proved long-term studies. Our studies have shown that TOF-PDMS (time-of-flight plasma desorption mass spectrometry) is one of the most informative methods, including peptidomics analysis.

The aim of this study was to explore the possibilities of multicomponent analysis of peptide extracts obtained from rat pituitary tissue by the method of plasma-desorption mass spectrometry with ionization by fission fragments of 252Cf (TOF-PDMS).

Established that the conditions of sample preparation for TOF-PDMS-analysis significantly affect the efficiency of intermolecular interactions in the solid-phase sample, and thus the formation of heteroclusters ions in the gas phase. The successful application of the method may be with the optimization and the standardization of sample preparation steps based on the problems of definition. TOF-PDMS can be successfully used as an analytical method for the screening of synthetic analogs of natural peptides.