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Journal of Chromatography B, 803 (2004) 1–2
JOURNAL OF CHROMATOGRAPHY B
www.elsevier.com/locate/chromb

Preface

Peptide separation and analysis

In view of the growing importance of biopharmaceuticals and biomarkers based on proteins and peptides, this special issue highlights recent separation and analytical technologies for the characterization of (poly-) peptides. In the post-genome era, many research groups now focus on 'proteomics' to search for new diagnostic tools or to elucidate new therapeutic targets. The analysis of a proteome of an organism, tissue, body fluid, or a single cell is—due to technological necessities—always associated with the analysis of protein-derived peptides. Besides the analysis of large proteins, peptides themselves are known to regulate most physiological processes, thereby acting as, e.g. growth and differentiation factors, neurotransmitters, or regulating protease function as corresponding inhibitors. There has been a rapid expansion in the use of peptides as drugs over the last decade, and this is likely to continue. Prominent examples on the market include insulin, erythropoietin, glucagon-like peptide-1, granulocyte colony-stimulating factor, or bone morphogenic peptides acting in such important therapeutic areas as diabetes, renal failure, cancer, or bone fracture healing. Therefore, the first chapter of this special issue is dedicated to the relevance of natural peptides and their pharmaceutical potential. Comprehensive review articles and regular papers present an impressive and complex overview giving relevant examples for endogenous peptides and methodological approaches.

The development of a peptide for therapeutic purposes requires appropriate detection assays for monitoring pharmacological and pharmacokinetic features of the drug (candidate). In this context, there is a growing need for high performance separation and selective detection technologies. The rapidly growing importance of peptides and their potential clinical application as therapeutic agents or diagnostic markers is closely related to the enormous technical progress of analytical instrumentation within the last two decades. In particular, recent developments in mass spectrometry (MS) and the improvement of electronic databases establish the broad range of bioanalytical applications. Therefore, nearly all articles published in this special issue are concerned with MS applications and the resulting benefit. Modern mass spectrometric equipment is of high sensitivity and selectivity allowing the detection and identification of trace amounts of analytes. Nano-scale devices for sample delivery systems enable investigations of small volumes much less than 1 μl. Furthermore, mass analyzers of a tandem-MS design are used for peptide fragmentation necessary for unambiguous sequence analysis and therefore substance identification. Improved algorithms for MS-raw data processing, high-speed computer hardware and a steadily growing extension of public sequence databases accessible on-line make reliable peptide and protein analysis both possible and easy. The award of the Nobel Prize in Chemistry in 2002 to the mass spectrometry pioneers John B. Fenn and Koichi Tanaka reflects the trendsetting and substantial importance of MS-related techniques for the scientific community and progress in life science.

Besides the improved MS detection possibilities, sample separation has also made its progress in high-performance liquid chromatography (HPLC) columns and capillaries of smallest diameters or robust instrument setups for capillary electrophoresis (CE). The high resolution of LC and CE enables advanced separation of the peptide analyte from crude natural samples. Therefore, these high resolution separation techniques combined with highly sensitive and selective MS detection methods consequently represent milestone technologies in life science research. Some review articles in this special issue highlight this importance from different points of view. In particular, the quantitation of peptidic analytes essential in pharmaceutical development and for scientific concepts based on the differential display approach takes advantage of these high performance techniques. We focus on this in the second chapter.

Bearing these aspects in mind, we created this special issue dealing with modern aspects and techniques of peptide separation and analysis, also including examples of the scientific background for systematical investigations of natural peptide sources.

Therefore, the chapters presented herein comprise regular articles and reviews concerning (i) natural peptides and their pharmaceutical relevance, (ii) quantification of peptides, and (iii) special technical progress in peptide characterization and comparative analysis.

We believe that this special issue on 'Peptide separation and analysis' is timely and fits well in the scope of the *Journal of Chromatography B—Biomedical Sciences and Applications*. It has been our sincere pleasure to work with and to learn from the many esteemed contributors to this issue. Our special thanks are extended to the many scientists

1570-0232/$ – see front matter
doi:10.1016/j.jchromb.2003.11.010

who have graciously served as reviewers for these articles and whose suggestions have been the basis for success of this compilation. Finally, we would like to thank the editors of the *Journal of Chromatography B* for giving us the opportunity to prepare this special issue.

Harald John received his Ph.D. degree in analytical chemistry in 1998 from the Westfälische Wilhelms University of Münster (Germany) for the development of chromatographic and immunological methods for the quantification of prostaglandins and related fatty acids. During his subsequent post-doctoral time at the Lower Saxony Institute for Peptide Research (Hannover, Germany) until the end of 1999, he worked with special focus on endogenous polypeptides related to angiogenesis and anti-cancer research. Since 2000 he has been Head of the Division of Analytical Peptide Chemistry of IPF PharmaCeuticals GmbH (IPF) in Hannover. His laboratory characterizes and identifies natural and synthetic regulatory peptides mainly discovered at IPF. Besides chromatographic, capillary electrophoretic and immunological methods, the instrumental focus is on mass spectrometric techniques like MALDI-TOF-MS and ESI-MS. His particular interest is the development of mass spectrometry-based methods for the quantification of physiologically relevant peptides of biological origins applied to pharmacokinetic and stability studies.

Ludger Ständker received his Ph.D. in biochemistry for the isolation and characterization of naturally anti-integrin peptides from the University of Hannover in 1996, and received a research award for these studies from the German Society for Thrombosis and Hemostasis Research (GTH). He continued working in the field of peptide biochemistry with a focus on chromatographic procedures for isolation of bioactive peptides from natural sources and analysis of their post-translational modifications. Since 1998 he has been Head of the Division of Preparative Peptide Chemistry at IPF PharmaCeuticals GmbH in Hannover, where he is responsible for the establishment of natural peptides libraries and several bioscreening programs to identify new drug targets for, e.g. osteoporosis and viral infectious diseases. In 2003, he qualified as a professor in biochemistry at Hannover Medical School (MHH). Recently, he obtained the German AIDS Award 2003 from the German AIDS Society (DAIG) for the discovery and development of a potent anti-HIV peptide isolated from human blood filtrate. Since 2002 he has been a member of the Editorial Board of the *Journal of Chromatography B.*

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