

## **ANALYSIS OF MONOCLONAL ANTIBODIES BY CAPILLARY ELECTROPHORESIS**

### **(Summary)**

Monoclonal antibodies (mAbs) are without doubt one of the fastest-growing therapeutics, although their full potential is yet to be discovered. The number of approved mAbs in Europe is over 100 and rising exponentially. Using mAbs in therapy has actually led to breakthroughs in some diseases thought to be incurable or difficult to treat.

mAbs are subject to considerable heterogeneity due to production, processing and/or storage. Given their highly complex structure, state-of-the-art mAb analysis requires the use of a number of orthogonal, complementary analytical techniques. Gathering information obtained from these analytical methods, one can identify the structure of the therapeutic protein, identify sources of variability and assess the likely therapeutic impact of it.

Among the myriad of analytical techniques suitable for mAb characterization, capillary electrophoretic (CE) methods have gathered widespread attention in the last 20 years. Due to their simplicity, cost-effectiveness, high-efficacy and high-throughput, CE techniques have quickly become benchmarks of mAb analysis.

This book is intended to provide a brief, general picture of mAbs, including information regarding their origin, structure, production technology, and different regulatory aspects, but also to present in a detailed manner the mAbs authorized in Europe.

The second part of the book presents some general aspects of CE, including its theoretical background, how to prevent protein-wall interaction and modes to suppress the EOF. Moreover it presents the most widely applied CE techniques with their advantages and disadvantages, technical requirements and a selected list of publications using the particular CE method for the analysis of mAbs. Findings presented herein indicate that capillary zone electrophoresis (CZE), capillary gel electrophoresis (CGE), capillary isoelectric focusing (cIEF and icIEF) can be successfully applied in the characterization of size- and charge heterogeneity of mAbs, regardless of the level of analysis. CE-MS hyphenation on the other hand has proved to be a major advantage and a versatile tool for peptide mapping, primary amino-acid sequencing, stability testing, glycosylation, sialylation and diamidation analyses.