

## **Abstract for the 2<sup>nd</sup> Conference on Bio-Medical Instrumentation and related Engineering and Physical Sciences (BIOMEPE)**

**M. Kontogiorgis<sup>2</sup>, G. Leontidis<sup>2</sup>, B. Spyropoulos<sup>1</sup>**, An overview of the trends in Next generation Nucleic Acid and Protein Sequencing.

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Numerous Next Generation Technologies for both, Nucleic Acid and Protein sequencing are being developed. The present paper is attempting to predict, by reviewing Industrial Property (IP) Documents, the most credible emerging innovative Techniques that could obtain a position, in the presently dominant laboratory platforms, by the end of this decade.

The evaluation of relevant IP-Documents, retrieved by employing the on-line esp@cenet search-engine of the European Patent Office, attempted a mapping of the promising techniques and thus, a market-trend prediction, for the next years.

Concerning Protein sequencing methods about 90 relevant IP-documents, published between the years 1977-2012, have been retrieved and evaluated. Two annual publication-numbers local maxima are displayed, the first (2002) is related to Mass Spectrometry (MS) equipment optimization and the second (2010) seems to be related with the employment of, additional to MS, property-tuned variable-mass labeling. Concerning Nucleic Acids about 700 relevant IP-documents, published between the years 1984-2012 have been retrieved and evaluated. The trend of IP-documents is continuously increasing until an absolute maximum (2010) decreasing then slightly.

Beyond the optimized Sanger, Edman etc. methods, among the most promising Next Generation Sequencing (NGS) methods, are included LASER-linked Polymerase Colony (Polony), Pyrosequencing, upgraded-MS, Shotgun-PCR, Nanopore and Ion Semiconductor Sequencing (ISFET) methods.