International Journal of Drug Research and Technology
Available online at http://www.ijdrt.com

Perspective

MOLECULAR PROTEIN SEQUENCING

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INTRODUCTION

Despite significant advancements over the last decade, methods for identifying proteins have lagged behind those for nucleic acids, which have extraordinarily high sensitivity, dynamic range, and throughput. The ability to directly characterize proteins at the nucleotide level, on the other hand, would address critical biological challenges such as more sensitive medical diagnostics, deeper protein quantification, large-scale measurement, and the discovery of alternate protein isoforms and modifications, as well as pave the way for single-cell proteomics. As a result of this necessity, there has been a push to dramatically improve protein sequencing technology by borrowing ideas from high-throughput nucleic acid sequencing [1].

With a special emphasis on creating feasible single-molecule protein sequencing methods (SMPS). Sequencing by degradation (e.g., mass spectrometry or fluorosequencing), sequencing by transit (e.g., nanopores or quantum tunneling), and sequencing by affinity are the three types of SMPS technology (as in DNA hybridization-based approaches). Proteins are essential components of life. A cell's and organism's protein composition gives crucial information for understanding biological processes and illness. Despite the importance of protein analysis, only a few methods for determining protein sequences are accessible, and even approaches have disadvantages, such as requiring a large volume of sample [2].

DESCRIPTION

Single-molecule approaches would transform proteomics research, allowing for the detection of low-abundance proteins with unprecedented sensitivity and the implementation of single-cell proteomics. Novel single-molecule protein sequencing systems based on fluorescence, tunneling currents, and nanopores have been proposed in recent years [3].

Proteins have a wide range of critical roles in living organisms, therefore all of the new techniques that allow for their precise, rapid, and accurate characterisation at the single-molecule level represent a major advance in proteomics with significant biomedical implications. We highlight current advances in the development of nanopore-based devices for protein sequencing in this study. We begin with a critical examination of the most important technical needs for nanopore protein sequencing, highlighting some new ideas and approaches. Single-molecule approaches would transform proteomics research, allowing for the detection of low-abundance proteins with unprecedented sensitivity and the implementation of single-cell proteomics.

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In cellular characterisation, proteomic analysis can be a major bottleneck. The present paradigm is based mostly on peptide mass spectrometry and affinity reagents (i.e., antibodies), both of which require a priori sample knowledge. An unbiased protein sequencing approach with a dynamic range that spans the entire range of protein concentrations in proteomes would revolutionize proteomics by making it easier to characterize novel gene products and subcellular complexes. Several innovative systems based on single-molecule protein sequencing have been proposed to this purpose. Proteomics is becoming a more potent and important tool in molecular

cell biology. It can be used to determine post-translational changes, as well as in sophisticated functional screens, to identify the components of tiny protein complexes and big organelles [5].

CONCLUSION

Recent improvements in DNA sequencing technologies have transformed biology by delivering extremely precise readings at high throughput and length. Many biological and medicinal applications make advantage of the read data. Protein sequencing methods are not similar to modern DNA sequencing methods, greatly limiting the use of protein data. Several optical protein sequencing approaches based on fluorescent amino acid labeling have recently been proposed. Various methods depend on the measurement of an electrical signal and does not require fluorescent tagging. The terminal amino acid is detected by its distinctive protonation signal in reprotonation-deprotonation protein sequencing, and each amino acid in the peptide is quantified by repeatedly cleaving the terminal amino acids one by one.

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Cite This Article: John P (2022) "Molecular Protein Sequencing" ***International Journal of Drug Research and Technology*** Vol. 11 (2), 1-4.