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Short Communication

Proteomics as Strategy in the Development of Medicinal Drugs

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INTRODUCTION

Proteins are the focus of activity in pharmaceutical and biotechnology companies since they make up the majority of therapeutic targets. The technology used to discover and measure the numerous proteins, protein-protein and protein-nucleic acid interactions within the proteome, as well as the post-translational changes that alter protein activity, is referred to as 'proteomics.' Proteins that bind to the ligand are then considered therapeutic targets. Proteomics is being used by researchers all around the world to achieve a better knowledge of disease pathophysiology, to identify new and effective biomarkers for early illness diagnosis, and to speed up drug development.

Proteomics is widely performed to explore the molecular basis of many diseases and to create new medications with a better understanding of their targets. It is a technology platform that is becoming increasingly used in drug discovery and development. In proteomics, proteins play vital role in determining the biological phenotype of organisms in both healthy and pathological states. The great majority of pharmacological targets against which pharmaceutical drug design processes are launched are proteins. Proteomics provides essential insight into the interrelationships between proteins that occur in health and disease, as well as following drug therapy. It can be used to discover the pathophysiological basis for disease and to investigate the mechanistic basis for therapeutic action and toxicity. Proteomics is also an effective way to find biomarkers that have the potential to improve therapeutic efficacy and safety decision-making based on data produced from the research of important tissues and the development and proper use of biomarkers. Several biotechnologies, including genomics, proteomics, cellular and organic techniques, have been provided to assist the process. It allows scientists to screen a large number of proteins in clinically distinct samples, which aids in the discovery of disease biomarkers, the identification and validation of drug targets, the design of more effective drugs, the assessment of drug efficacy and patient response, and virtually every step in the modern drug discovery process. Proteomics relies heavily on two-dimensional gel electrophoresis and mass spectrometry, however they are not the only technologies available or required. Pathogenic processes, environmental exposure, or pharmacologic responses to a treatment are all examples of biomarkers, which can be evaluated and quantified as indicators for normal health and physiology-related assessments. Proteomics can detect changes in post-translational modifications, cellular trafficking, and even total expression levels that RNA-based expression analyses are unable to detect. Proteome analysis during preclinical or clinical development may lead to the identification of possible markers for therapeutic efficacy prediction. Purified active recombinant proteins make up recombinant protein arrays. These arrays facilitate the discovery of interactions between proteins and other molecules such as proteins, DNA, RNA, and ligands. Computational techniques are being deployed to drastically reduce the time and resource needs of chemical production and biological testing in order to reduce cost and time. These proteins will be used to assist clinical trial research as efficacy or toxicity indicators. Small, drug-like compounds are either bonded to a polymer or exposed to protein chips in the chemical proteomics approach. It can be employed nearly anywhere in the pharmaceutical industry, including target identification and validation, the discovery of efficacy and toxicity biomarkers, and research into drug action mechanisms or chemo-resistance. Proteomic techniques, along with computer tools, can identify the disease's target, allowing the proper medicine to be discovered. Proteins whose levels change in response to medication administration could provide crucial information about therapeutic efficacy and toxicity. The dynamic nature of a cell's (infected) proteome gives sufficient data for researching a disorder at the protein level, yet obtaining all of this data from a cell demands the use of several methodologies and technologies.

CONCLUSION

Drug discovery is a time-consuming and expensive process that employs a wide range of technologies from several domains. The difficulties that proteomics technologies face are vast; their progress will require the advancement of a variety of

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methodologies at the same time. It is critical to concentrate drug-discovery efforts at this level because the majority of medicines work on proteins. Proteomics can help researchers in a variety of ways during the drug discovery and development process. Recent advancements in computer software, as well as the rapidity and sophistication of computer resources, have facilitated the rapid development in this field (better hardware). New pharmacological targets have been discovered thanks to functional genomics and proteomics. Novel targets analysis, disease processes, structure based drug design and discovering the mode of action of lead compounds among them.

REFERENCES

1. Samavarchi-Tehrani P, Samson R, Gingras AC. Proximity dependent biotinylation: key enzymes and adaptation to proteomics approaches. Mol. Cell. Proteom.2020; 19(5):757-773.
2. Lobingier BT, Hüttenhain R, Eichel K, Miller KB, Ting AY, von Zastrow M, e t.al.An approach to spatiotemporally resolve protein interaction networks in living cells. Cell. 2017; 169(2):350-360.
3. Geladaki A, Kočevar Britovšek N, Breckels LM, Smith TS, Vennard OL, Mulvey CM, et.al.Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. Nat Commun. 2019; 10(1):1-5.
4. Pino LK, Searle BC, Huang EL, Noble WS, Hoofnagle AN, MacCoss MJ. Calibration using a single-point external reference material harmonizes quantitative mass spectrometry proteomics data between platforms and laboratories. Anal Chem. 2018; 90(21): 13112-13117.
5. Sokolina K, Kittanakom S, Snider J, Kotlyar M, Maurice P, Gandía J, et.al.Systematic protein–protein interaction mapping for clinically relevant human GPCR s. Mol Syst Biol. 2017; 13(3):918.