Affinity Capture and Separation

From Molecular Interactions to Diagnostic Medical Applications

Norberto A. Guzman, Ph.D., Princeton Biochemicals Inc. Princeton, New Jersey, U.S.A.

Abstract

Proteomics in disease is highly complex due to the dynamic and diverse nature of proteins, considered to have a greater chemical composition and structural function than any other biological active compounds essential for life. Researchers have developed drafts of what is known as the human proteome: the entire set of proteins expressed in the body, to help understand disease, develop diagnostic tools, and accelerate precision medicine.

The human proteome is composed of subproteomes because each cell type has its own unique proteome. Then there are proteoforms, which make up a proteome, and these proteoforms are the protein variants - or forms - produced by a genome. Unlike the human genome, identifying and studying an entire set of expressed proteins in the human body and organism poses a challenge to scientists.

Proteomics techniques to study diseases focus on identifying, quantifying, and mapping protein changes to discover biomarkers, understand mechanisms, and develop therapeutics. Due to the complexity of the proteome, no single technique is adequate for a complete analysis of the constituents. While existing methods provide valuable information, their limitations drive the development of complementary, innovative methods to achieve greater breath of coverage, dynamic range, or specificity of analysis.

Affinity capture techniques exploiting the specific binding between two molecules has been employed for numerous purposes, from selective removal of interfering (over)abundant proteins or enrichment of scarce biomarkers in complex biological samples to mapping the post-translational modifications (PTMs) and protein interactions with other proteins, nucleic acids or biologically active small molecules.

In this seminar, I will discuss affinity capture separation techniques and focus on their unique advantages for the selective enrichment of low-abundance proteins, as biomarkers of diseases, employing antibodies, lectins and aptamers as affinity capture ligands immobilized to a surface and coupled to capillary electrophoresis for separation of bound and eluted proteins and peptides from complex biological samples (plasma, urine, saliva, sputum, tissues). On a final note, I will outline emerging methods that offer significant promise to proteomics research.

https://sciprofiles.com/profile/NORBERTOGUZMAN
https://webmail-oxcs.networksolutionsemail.com/appsuite/api/share/0cb009230ff83303cb6133cff8334e72bf3325e71a435c0e/1/8/MTIz