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Development of Affinity Capture Materials for Protein Structural Analysis

A new device captures specific proteins from complex sources with high purity, enabling simpler structural analysis for applications like high-dilution sampling and viral concentration.

Currently, it is difficult to isolate a protein sample that is pure and maintains its native conformations for structural analysis. Knowing the shape of a protein helps to understand the function and how it interacts with other proteins and nucleotides.

Researchers at Purdue University have developed a material to capture proteins from crude samples that has high affinity for the specified protein and low non-specific binding giving a very low background. This device can be developed into a commercially available grid that can be used in electron microscopy experiments that avoids non-specific binding and gives scientists straightforward analysis of protein structures. Obvious applications include high-dilution sampling, viral concentrations in hospitals, protein function experiments in laboratories, and protein sampling from crude sources.

Advantages:

-High affinity for specific protein

-Low background interference from non-specific proteins

-Protein maintains native conformation

Potential Applications:

-Biotechnology

TRL: 4

Intellectual Property:

Technology ID
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Category
Biotechnology & Life Sciences/Analytical & Diagnostic Instrumentation
Pharmaceuticals/Research Tools & Assays

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Keywords: protein isolation, structural analysis, native conformation, high affinity material, low non-specific binding, electron microscopy grid, high-dilution sampling, viral concentrations, protein function experiments, biotechnology applications