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Automation of High-Performance Micro-Scale Protein Interaction Analyses

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In the post-genome era increasingly greater attention is given to deeper elucidation of gene function. This is particularly the case for the discovery and development of successful disease diagnostics and therapeutics. For example, ever-increasing proteomics-driven searches for diagnostic biomarkers and potential therapeutic targets demonstrate the need for identifying integral functional players within the disease itself. Once a putative biomarker or drug target within a disease process is identified it's proper place and role within the larger disease pathway must be determined, as well as determining the factors that regulate the presence and absence of this presumed functional player within the disease state. Various techniques and sub-techniques for the analysis of protein interactions are typically applied for these determinations, and many suffer from poor performance characteristics – e.g., they are difficult to automate and often labor-intensive, they possess poor enrichment and purification characteristics, they require overly large samples, etc.

A novel micro-scale affinity column technology is described that enables many of the most critical techniques for protein interaction analyses – such as immunoprecipitation (IP), GST pulldowns, coimmunoprecipitation (CoIP) and chromatin immunoprecipitation (ChIP) – to be performed in an easily automated and straightforward manner. The amount of sample required for successful analyses is a fraction of what is typically required, and performance characteristics such as sensitivity and purity are often dramatically improved over standard techniques. The technology can also be integrated directly into existing fluidic automation, thus opening the door to fully automated high-performance protein interaction analyses for 96 samples at a time.