

Austin Brown
CHM 642

Abstract:

Proteomics, the next step after genomics, is the study of the entire set of proteins in a system. Aside from protein identification, features such as abundance, function, structure, and post-translational modifications are examined. One of the difficulties in the field of proteomics is the inability to detect low-abundance proteins (LAPs) in the presence of high-abundance proteins (HAPs). The primary methods developed to address this problem are HAP depletion and LAP enrichment. This presentation will focus on two of these methods, immunoaffinity protein subtraction and peptide ligand libraries, and will include results from various comparison studies.