430d Improvement upon Bioseparation by Altering the Host Genome

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Separating and purifying a desired product from intracellular materials, fermentation broth, or cell culture supernatant is a crucial and challenging component of commercial biochemical engineering since recovery usually comprises a major part of the production cost. Typically, it is common to apply highly selective chromatography step(s) including an affinity-based separation to aid in selectivity and purity considerations. With sufficient proteome information available now we are able to modify the host cell to further increase the efficiencies during chromatography not by enhancing target protein properties, but by altering the nature of the contaminating protein pool.

Since *Escherichia coli* has been used as host for the manufacturing of many recombinant proteins, we recently identified genomic proteins that would coelute and complicate recovery when IMAC (Immobilized Metal Affinity Chromatography) is used as a capture and purification step. This presentation will focus on a characterization of *E. coli* mutants that have a minimized contaminant pool. Specifically, we will present results that include growth characteristics of these IMAC-friendly hosts, expression of recombinant protein (Green Fluorescent Protein), and finally IMAC recovery.