Faster, standardized process development using traceless tag affinity chromatography

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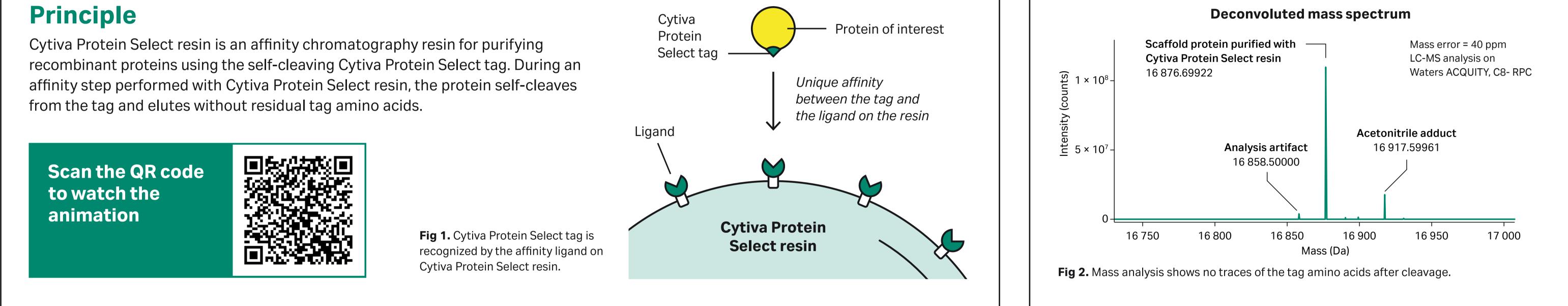
Introduction

Therapeutic proteins must be produced with a very high level of purity, but proteins other than mAbs often don't have an affinity binding partner to facilitate their purification. To be able to standardize and simplify the purification with an affinity step, one strategy has been to add a tag to the recombinant protein. Historically, using a tag has mainly been used for research purposes and not for biotherapeutic purification because tag removal was not traceless, and could generate modifications of the target protein. With Cytiva™ Protein Select™ technology, process development can be standardized with the use of a traceless and self-cleaving tag. This shortens the overall development time while maintaining — or improving — product quality in fewer steps.

Traceless tag cleavage

Below are the results of mass analysis of a scaffold protein purified with Cytiva Protein Select resin and tag. The mass of the purified protein equals the expected mass after cleavage, confirming that the protein is pure and in native state with no traces of the tag amino acids.

Protein	Mass
Protein with tag	22 141 Da
Expected mass after tag removal	16 876 Da
Mass measured after purification with Cytiva Protein Select resin	16 876.7 Da



Standardized, easier, and convenient process development with higher purity

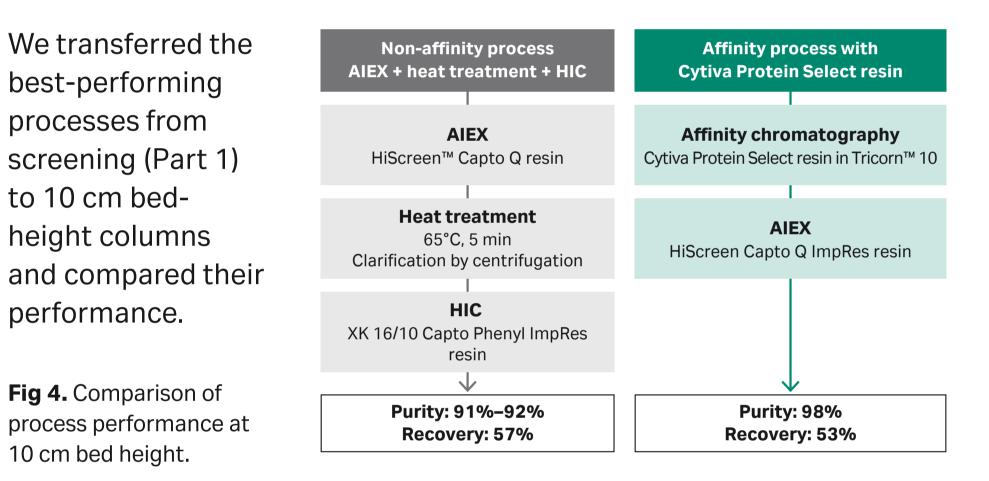
Part 1: Screening for suitable techniques in small-scale, **HiTrap[™] formats**

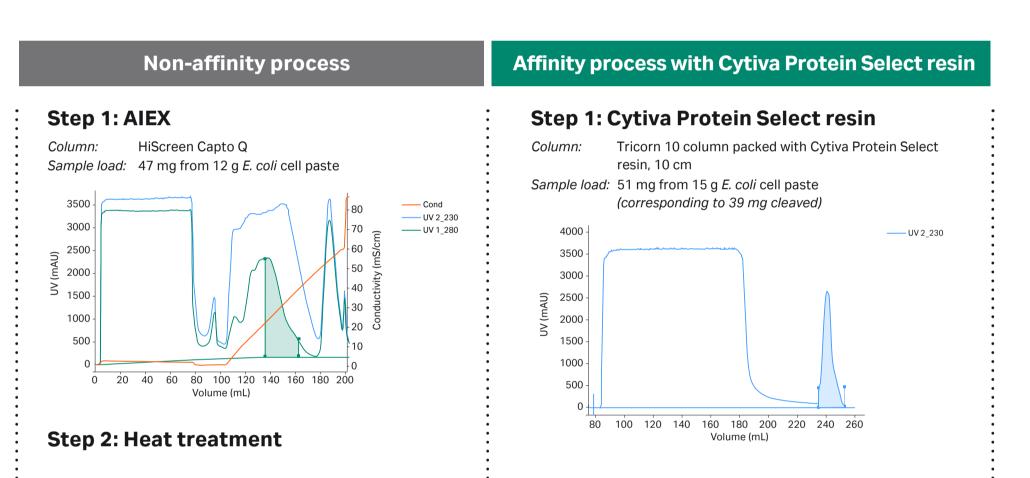
We compared the complexity and time requirements of two approaches for purifying a thermostable scaffold protein expressed in *E. coli*.

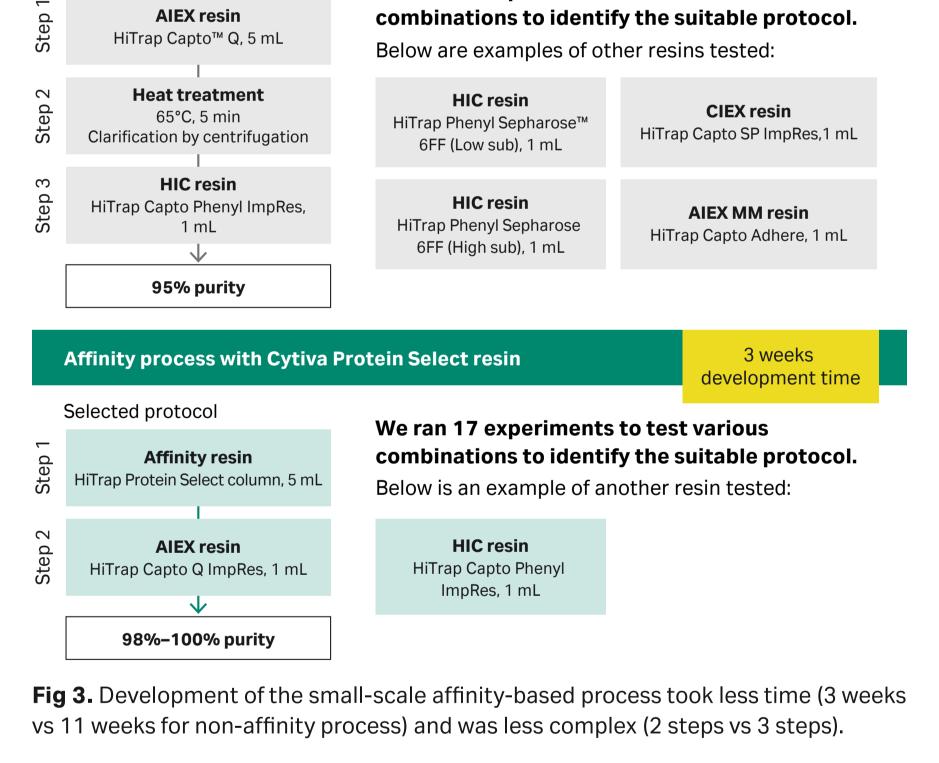
Requirements: purity \ge 95%, recovery \ge 50%

	Non-affinity process		11 weeks development time	
Selected protocol				
		We ran 49 experiments to test various		

Part 2: Process performance (purity and recovery) at 10 cm bed height







AIEX = anion exchange chromatography; CIEX = cation exchange chromatography; HIC = hydrophobic interaction chromatography; MM = mixed mode chromatography

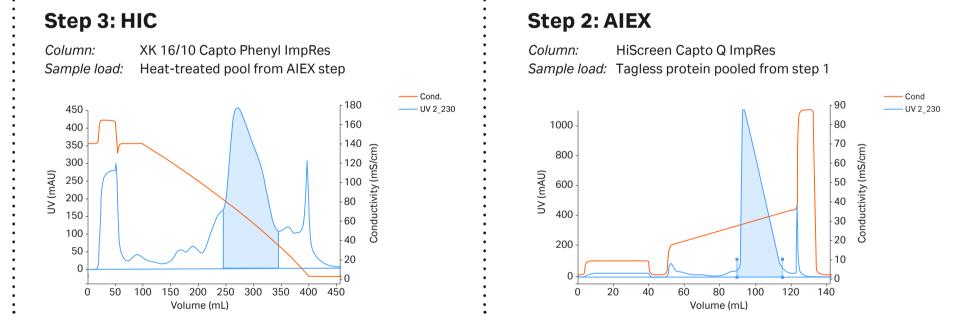


Fig 6. Chromatograms obtained from the different processes.

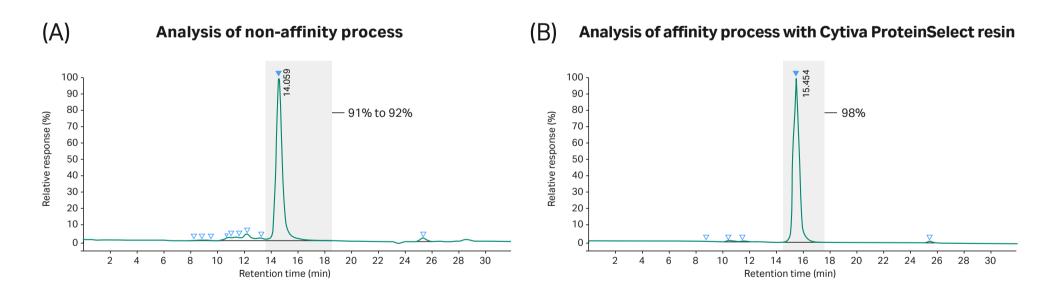


Fig 7. Analytical size exclusion 214 nm on Superdex[™] 75 Increase 10/300 GL column. The nonaffinity process did not produce the required purity, whereas the affinity-based process did.

Facilitating recovery analysis

We used the same protein construct for both processes: we added a 6×His epitope tag upstream of the Cytiva Protein Select tag to facilitate recovery analysis of full-length fusion protein in crude cell extracts.

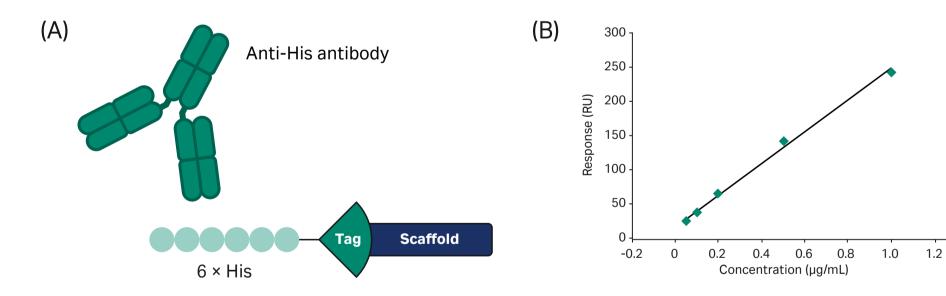


Fig 5. (A) Protein construct with upstream 6×His tag allowing Biacore[™] SPR analysis using anti-His antibodies. (B) Calibration curve using purified fusion protein as standard for recovery calculations.

Reusability, CIP, and regeneration

After each purification, Cytiva Protein Select resin needs cleaning-in-place (CIP) and regeneration to remove cleaved tag, uncleaved protein, and impurities. We tested an *E. coli* homogenate (Fig 8) and a HEK293 feed (Fig 9) containing a protein tagged with Cytiva Protein Select tag together with different CIP solutions on 1 mL columns. Each purification cycle used a single buffer, a cleavage time of 4 h, and regeneration and CIP for 15 min with the respective CIP solution.

Conclusions

Cytiva Protein Select technology standardizes purification of proteins that do not have an affinity binding partner.

Benefits of this technology include:

Processes are easier and faster to develop

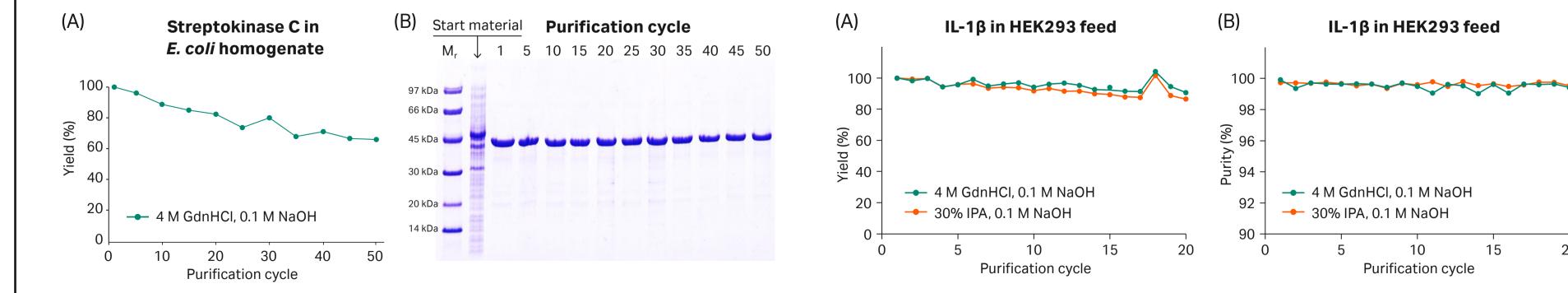
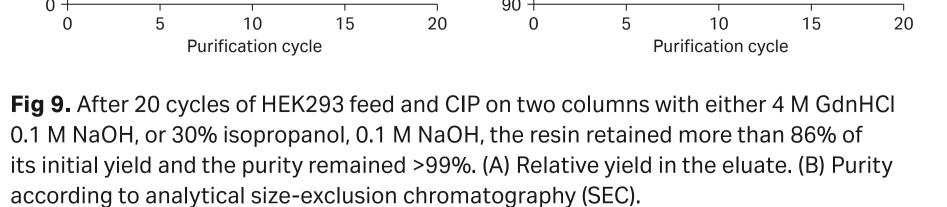
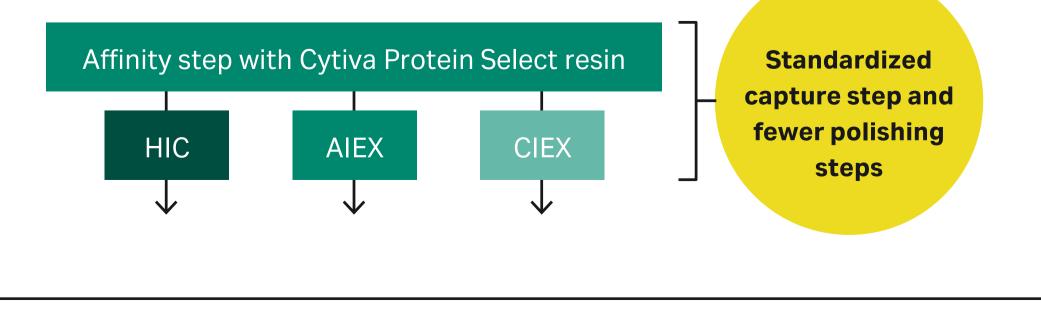


Fig 8. After 50 cycles of E. coli homogenate and CIP with 4 M guanidine HCI (GdnHCI), 0.1 M NaOH, the resin retained more than 65% of its initial yield and the purity remained >91% for all cycles. (A) Relative yield in the eluate. (B) Purity according to SDS-PAGE.



- Higher protein purity, in fewer steps
- Resin reusability





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