Protein Metrics

Advancements in Multi-Protein Quantitation for Chinese Hamster Ovary Proteomics







Figure 1:

that allows analysts to quickly filter and interrogate specific proteins.





Figure 3. Volcano Plot of Protein Abundance Comparison between Fractionation and **Singleshot Conditions.**

(A). The USP1 sample exhibited fold changes ranging from 2 to 4, indicating substantial increase in abundance from singleshot to the fractionation data acquisition condition. (B) In the USP2 sample, most detected proteins exhibited fold changes ranging from -6 to +4, reflecting a much wider variation in abundance of the fractionation than the singleshot acquisition, suggesting that fractionation can enhance detection sensitivity because of ion suppression effects in complex samples.

• Effective for broad biopharma applications, supporting faster and more reliable decision-making.

 Continues to refine proteomic analytics, contributing significantly to process development and regulatory compliance.



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Therapeutics Development & Supply

The authors declare no competing financial interest.