Marín-Vicente C, Calvo E, Rodríguez JM, Villa Del Campo C, Sierra R, Végvári Á, Zubarev RA, Torres M, Vázquez J. A Sample Preparation Procedure for Isobaric Labeling-Based Single-Cell Proteomics. ***Methods Mol Biol***. 2024;2817:33-43. doi: 10.1007/978-1-0716-3934-4_4. Erratum in: Methods Mol Biol. 2024;2817:C1. doi: 10.1007/978-1-0716-3934-4_16. PMID: 38907145.

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Abstract:

Mass spectrometry-based proteomics has traditionally been limited by the amount of input material for analysis. Single-cell proteomics has emerged as a challenging discipline due to the ultra-high sensitivity required. Isobaric labeling-based multiplex strategies with a carrier proteome offer an approach to overcome the sensitivity limitations. Following this as the basic strategy, we show here the general workflow for preparing cells for single-cell mass spectrometry-based proteomics. This protocol can also be applied to manually isolated cells when large cells, such as cardiomyocytes, are difficult to isolate properly with conventional fluorescence-activated cell sorting (FACS) sorter methods.