INTRODUCTION
Mass spectrometry (MS) analysis of biotherapeutic proteins at the intact and subunit level is conducted throughout the product development life cycle. These analyses provide information to confirm sequence integrity and product variations. The increased utility and accessibility of this technology for intact mass analysis has led to widespread use in drug development, clinical sample characterization, and biosimilar molecules. Despite the widespread practice of intact protein mass analysis, experienced MS users are typically required to manage the instrument, operation, data processing, and interpretation. The desire to expand intact mass capability later into development and ultimately into a QC role requires even greater accessibility to non-expert MS users to generate high-quality results produced routinely by experienced analysts.

WORKFLOW SETUP

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