

# Maximizing Productivity by Simplifying Standard Biologics Characterization Workflows



For Research Use Only. Not for use in diagnostic procedures.

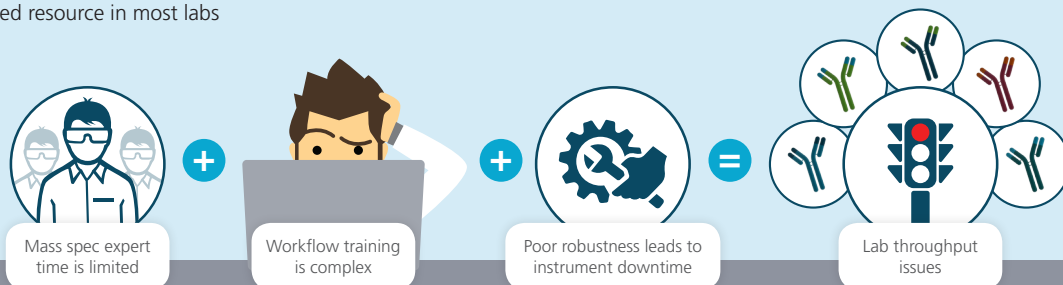
## Overview

There are significant challenges to maintain throughput for biologics characterization, due mainly to the complexity of standard mass spectrometry workflows and poor instrument robustness. **SCIEX offers a simple, compact and robust solution for standard characterization to enable analytical scientists to perform such workflows on a daily basis.**

### Routine biotherapeutic characterization challenges are constant:

- Every biotherapeutic must be well characterized, and data quality must be maintained at a very high standard
- The complexity of characterization workflows often requires the work of mass spectrometry experts, a limited resource in most labs
- Training new scientists to perform standard workflows can be time consuming and negatively impact throughput
- Available LC-MS instrumentation often lacks robustness and ease-of-use; instrument downtime dramatically slows time to results

An easy-to-use, more robust solution for standard characterization workflows can mitigate risk by making itself more accessible to more scientists, and decreasing downtime caused by instrument failures.



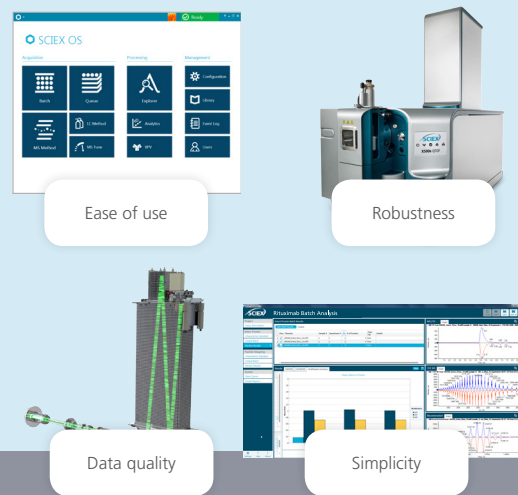
## The SCIEX Approach

Simplification of standard workflows and instrument robustness are the keys to achieving steady-state throughput for biologics characterization. By making high-volume workflows like Intact Mass and Peptide Mapping Analysis accessible to analytical scientists who are not experts in mass spectrometry, reliance upon the limited time of mass spec experts is reduced. Making such workflows easier also speeds training time for new lab members. Lastly, a more robust instrumentation design can dramatically reduce failures and maintenance downtime.

### SCIEX offers the following in the X500B QTOF System:

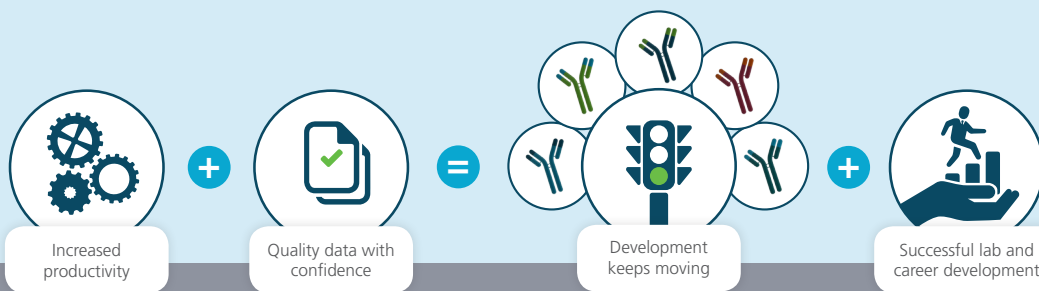
- **Ease of Use:** The intuitive, point-and-click interface of the new SCIEX OS software reduces the need for mass spec expertise in setting up and running characterization methods.
- **Robustness:** The X500B system employs the Turbo V™ Ion Source, well-known for its reliability. In addition, improved front-end optics and easy access to the QJet® Ion Guide means fast and efficient maintenance, increasing total system uptime.
- **Data Quality:** A heated TOF path maintains calibration and mass accuracy over time. This stability helps ensure high quality data on every run.
- **Simplicity:** Automated data processing in BioPharmaView™ Software helps users get to confident answers quickly, rather than just complicated data.

### X500B QTOF Solution



## The Bottom Line

Your lab will be more productive, making the most of the resources you have. You will be confident in the quality of the answers you provide to keep development moving. Most importantly, biologics in development will flow smoothly through your lab, making both the lab and you more successful.



Learn More about simplifying characterization workflows at [sciex.com/X500B](http://sciex.com/X500B)

