



QuiC™

powered by Pulsar

NEXT GENERATION
PROTEOMICS
FACILITY MANAGEMENT

Multi-Level Quality Control Monitoring

INSTRUMENT PERFORMANCE DETERMINES DATA QUALITY

Mass spectrometry-based proteomics enables unique insights into biological mechanisms across a wide variety of samples. The quality of any conclusion from proteomics data critically depends on the quality of the raw data. QuiC allows for instantaneous control of the most important instrument parameters; from the first step in a proteomics experiment, QuiC provides users with a powerful tool to improve the performance of their mass spectrometry facility.

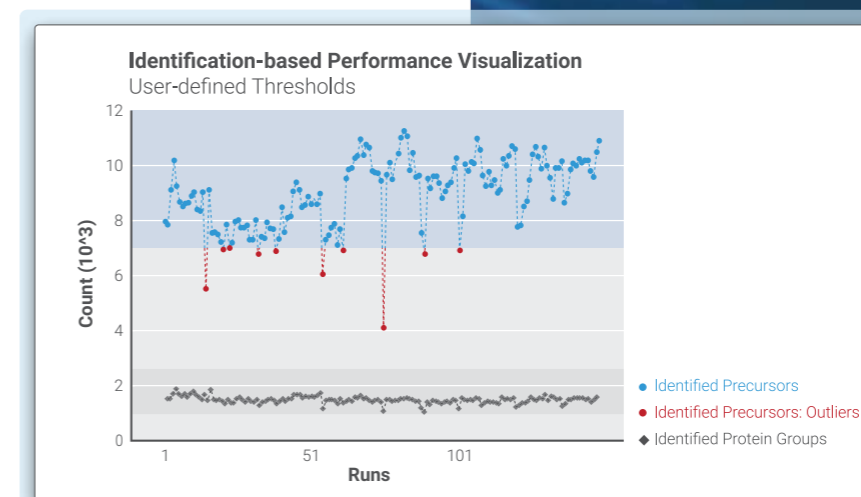
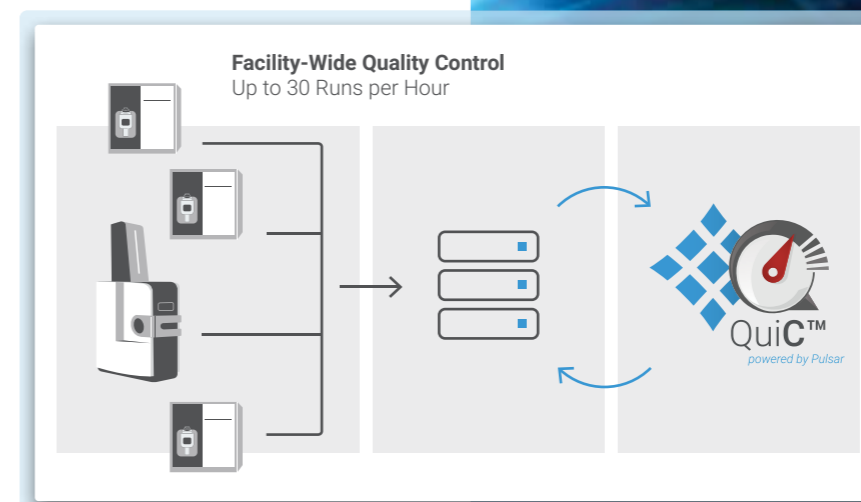
QuiC - Biognosys' quality control (QC) application, has been designed to address QC at its origins by monitoring near-real-time instrument parameters instead of just conducting a post-acquisition data analysis. QuiC can be set up to constantly monitor folders for new measurements, filter them based on user-defined criteria, analyze them, and provide longitudinal readouts on all instruments in a facility.

A wide range of mass spectrometers is supported in four acquisition modes: data-dependent acquisition (DDA), data-independent acquisition (DIA), parallel reaction monitoring (PRM), and multiple reaction monitoring (MRM).

Detailed QC metrics are available for peptides from the Biognosys iRT Kit. For DDA and DIA a background proteome can be specified based on a library or a FASTA file, which can be used to monitor peptide and protein identifications on a high level. Low-level readouts such as MS1 and MS2 scan intensities, peak capacity, and the total ion chromatogram are also available. The data is organized so that users can instantly view the performance of mass spectrometers across an entire facility.

QuiC makes quality control easier and more intuitive than before:

- **Threshold controls:** Set individual thresholds for instrument parameters and view all metrics as a time series or for single runs
- **Full scalability:** Monitor the performance of many instruments and visualize your results quickly
- **QC in complex samples:** Spike the iRT Kit into complex proteomes and search the background proteome using libraries or FASTA files
- **Flexible data sharing:** Share your QC data across your facility or keep it local on instrument PCs
- **Ion mobility (IM) metrics:** Diagnose calibration issues before they affect identification performance



The fastest way to access QC data

All underlying analysis pipelines in QuiC are built for speed and reliability, with support for a wide range of instruments from different vendors. QuiC allows near real-time, centralized monitoring of important metrics from across your MS facility, like peptide and proteins identifications, MS1 and MS2 median intensity, mass accuracy, ion mobility, and many more.

Controlling data quality through predefined parameters

Thresholds can be defined for relevant QC parameters and QuiC immediately flags deviations in the QC runs. This indicates at a glance if troubleshooting is necessary. Smart event tag handling and visualization allow easy tracking of the instrument's maintenance history, making QuiC an ideal tool for facility management.

Supported Instrument Vendors

- Agilent
- Bruker
- SCIEX
- Thermo Scientific
- Waters

Recommended System

- Windows 10 x64
- Intel or AMD CPU with 4 or more cores
- 500 GB of hard drive space or more
- 16 GB of RAM or more

HOW TO GET QUIC

QuiC is designed to work with Biognosys' indexed Retention Time (iRT) Kit and comes free of charge. Our multi-level quality control software is widely used by larger facilities as well as individual researchers to deliver the highest possible mass spectrometer performance. To get your license, please reach out to **order@biognosys.com** or request it via our website.

FIRST CLASS SUPPORT

We are proud to offer you extensive advice and support in order to help you integrate our software and kits into your workflow. Our support team is here to ensure a great user experience.

If you would like to have your own personal meeting with us, please feel free to contact us by emailing **support@biognosys.com**. Our average response time is less than 24 hours.

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that transform science for better lives. We make the proteome actionable to empower research, drug development, and clinical decision-making with our versatile portfolio of mass spectrometry-based proteomics research services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types.

www.biognosys.com