

MassLynx Skyline Interface (MSI)

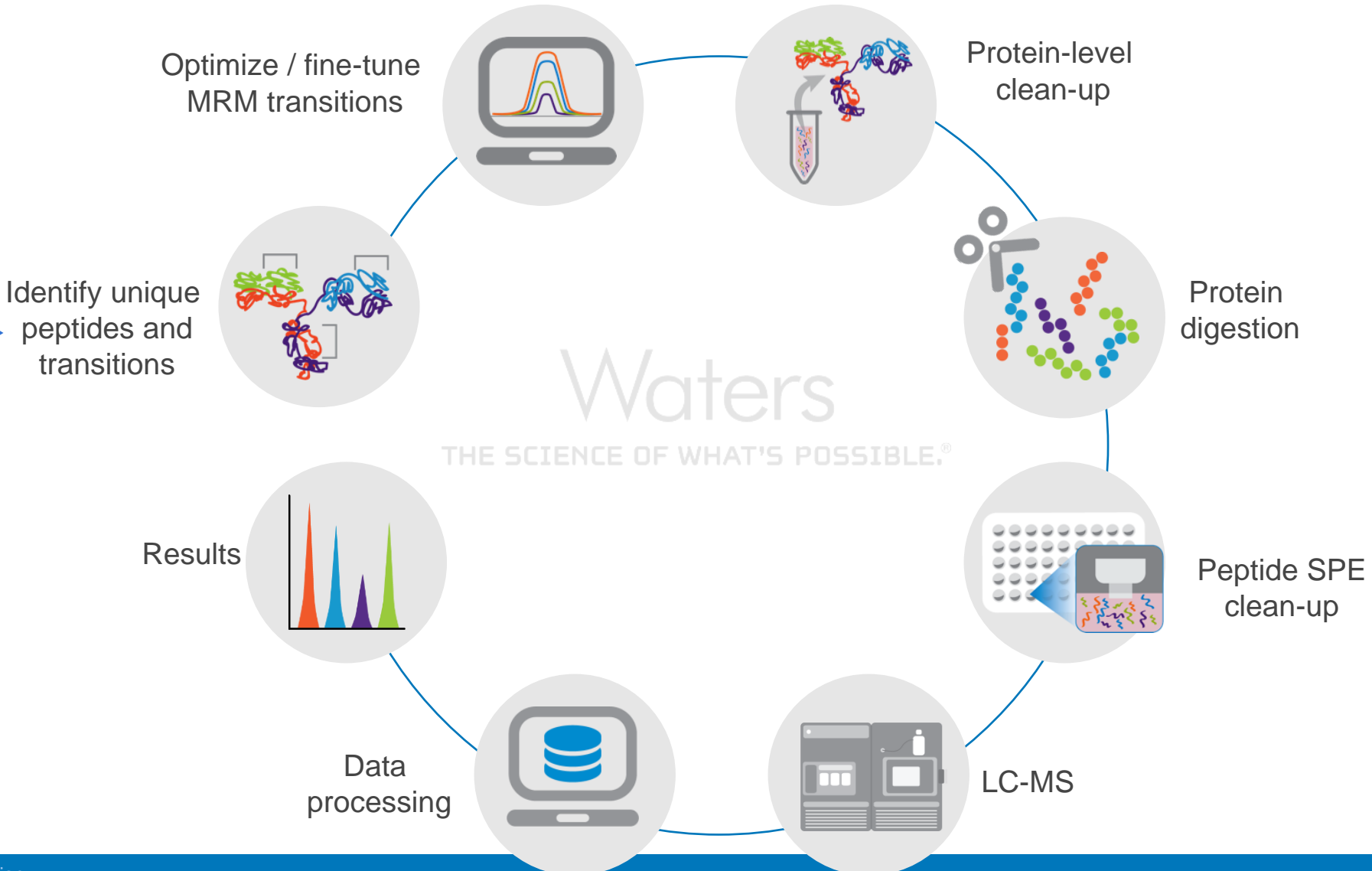
Enabling automated MRM method development for targeted proteomics and peptide bioanalysis workflows.

Nikunj Tanna

*Senior Scientist,
Waters Corporation*

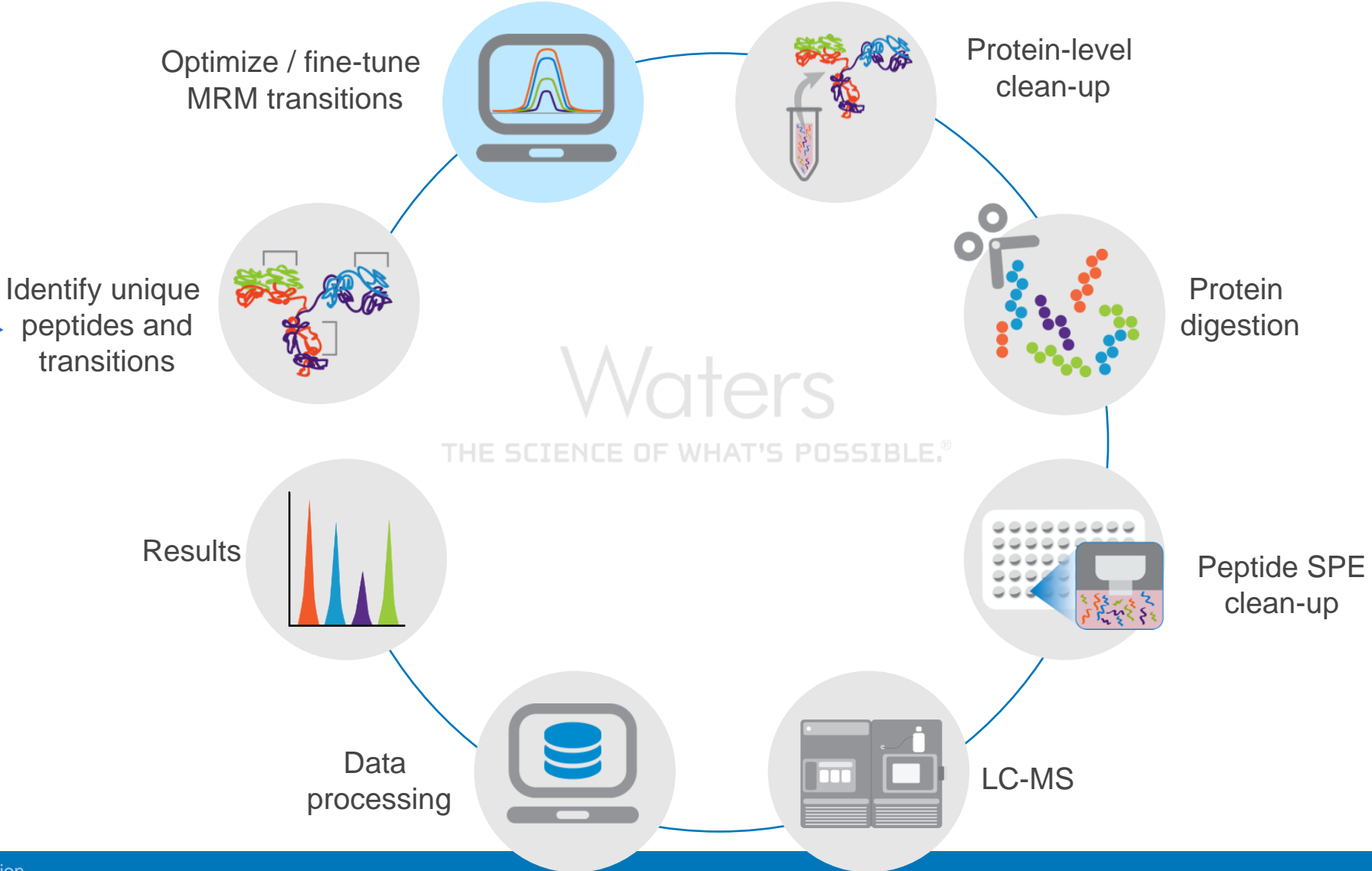
Digested Protein Bioanalysis: *Tandem Quad LC-MS*

WORKFLOW

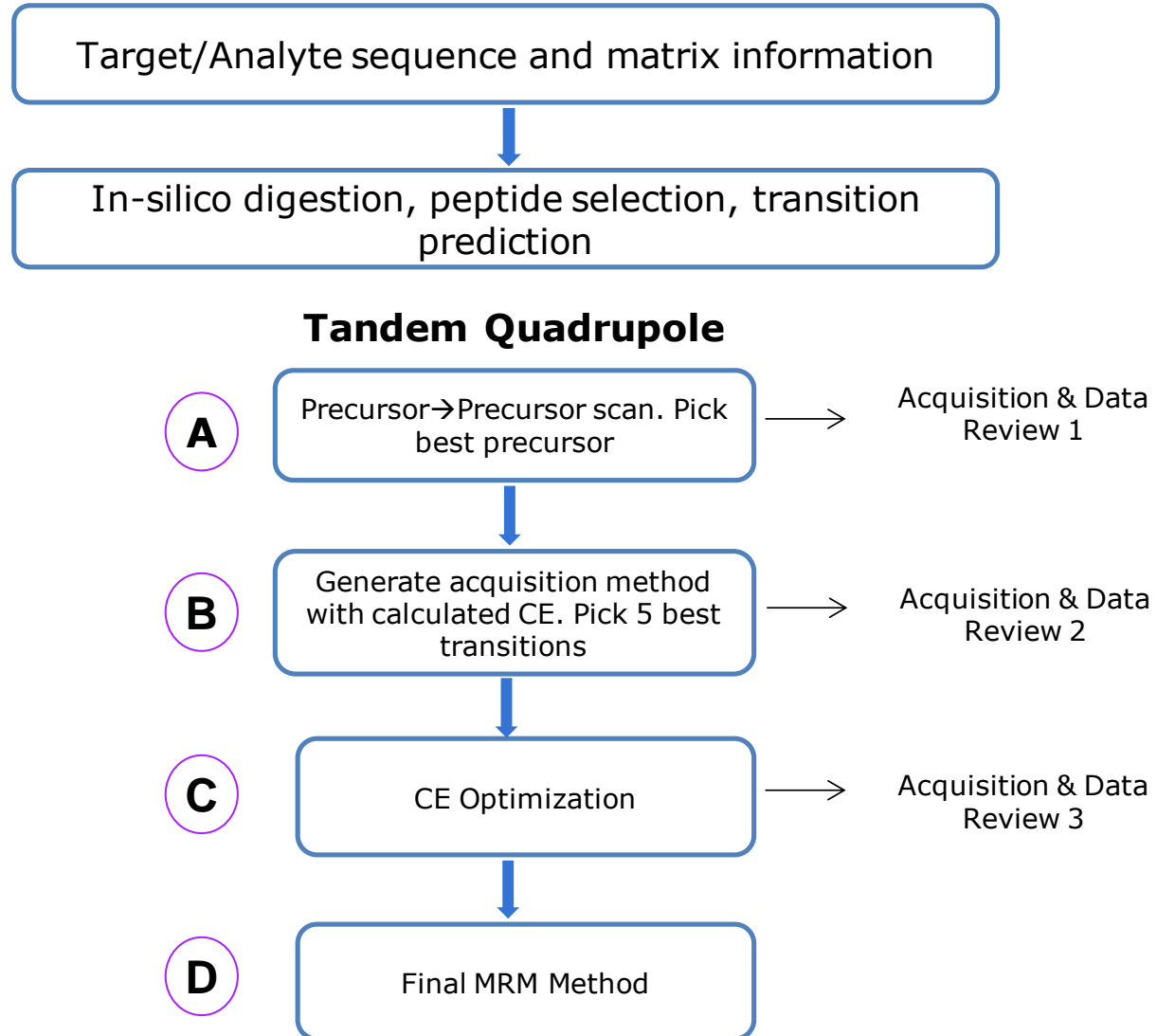


Digested Protein Bioanalysis: *Tandem Quad LC-MS*

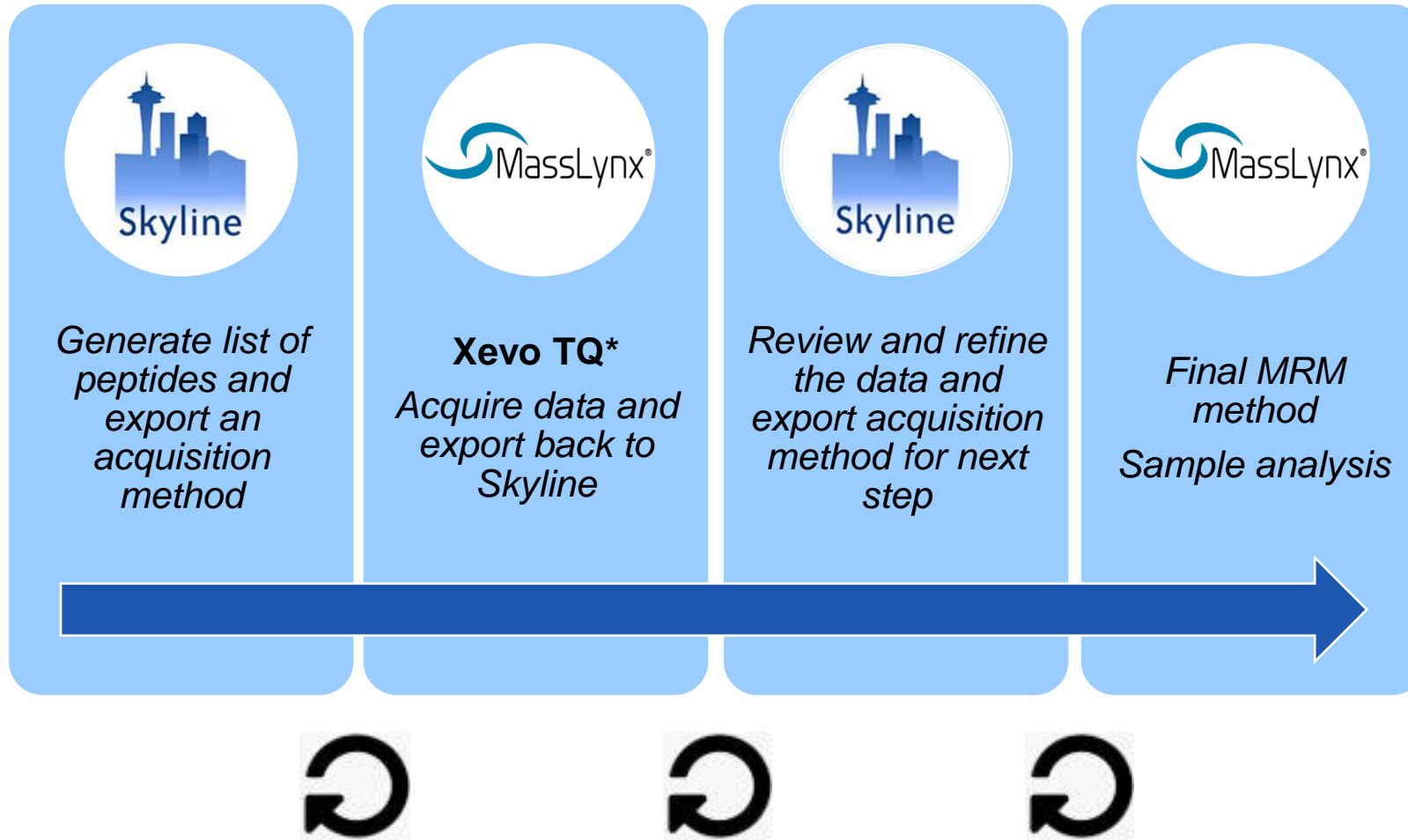
WORKFLOW



Recommended workflow for MRM method development



Previous workflow for Waters customers

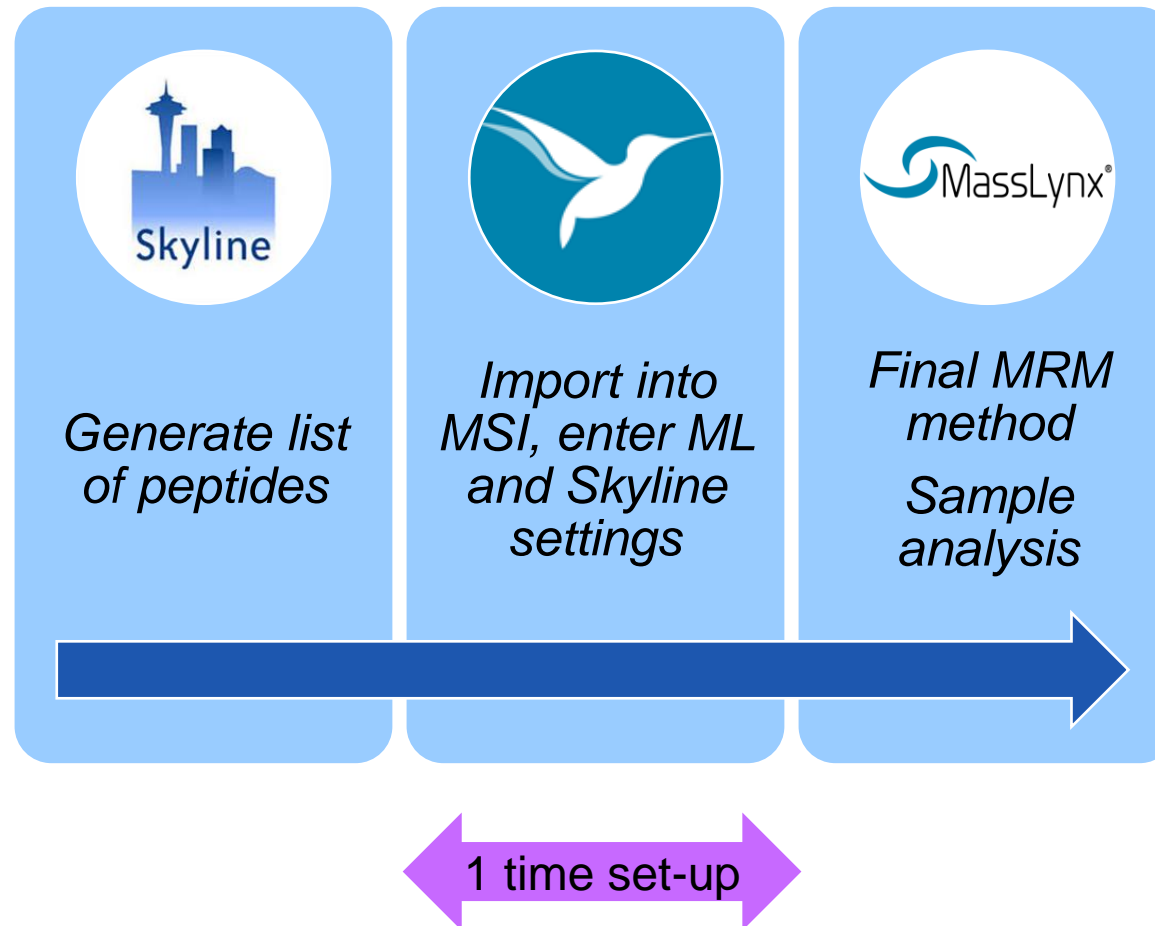


MassLynx Skyline Interface (MSI)

- Introducing the new MassLynx Skyline Interface (MSI)
- Simple, easy, consistent
- Saves time and energy



New workflow for Waters customers



User Interface for MSI

MassLynx Skyline Interface

File View Help

Workflow Type

Workflow: Peptide Bioanalysis Targeted Proteomics

Skyline

Master Document: C:\Users\Administrator\Downloads\MassLynx_Skyline_In ...

Acquisition Template: C:\Users\Administrator\Downloads\MassLynx_Skyline_In ...

Minimum Peak Ratio: 0.01

Number of Peptides per Protein: 3

Number of Transitions per Peptide: 5

MassLynx

Instrument: WatersXevoTQ

Project Folder: C:\MassLynx\BioAnalysis.pro ...

Tune File: C:\MassLynx\BioAnalysis.pro\AcquDB\AcebutololMSMS. ...

Inlet File: C:\MassLynx\SARS CoV2.PRO\ACQUDB\Inlet Method.ftn ...

Sample Location: 1:A,1 ?

Injection Volume (µL): 1

Run Length (min): 4.00

Peak Width (sec): 8.00

Points Per Peak: 10

Max. Transitions: 200

Status

AutoLynx: ● Ready

Skyline Processor: ● Ready

Start Stop

User Interface for MSI

MassLynx Skyline Interface

File View Help

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Max. Transitions: 200

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Start Stop

Select Workflow.

- Peptide bioanalysis to develop a highly sensitive method for therapeutic/biomarker peptides or digested proteins.
- Targeted proteomics is typically chosen in a discovery setting, while trying to generate a targeted methods for proteomics applications.

MassLynx Skyline Interface

File View Help

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Skyline Settings

- Select Skyline Master document containing peptides/proteins of interest
- Provide MS acquisition template which contains an MRM function.
- User selects the # of peptides/protein and # of transitions/peptide needed for the final method

MassLynx Skyline Interface

File View Help

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Start Stop

MassLynx acquisition parameters

- Select project in which the data should be saved
- Select MS Tune
- Select Inlet file
- Define points across peak parameters

MassLynx Skyline Interface

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Status

- Checks if AutoLynx is open and set up correctly
- Checks if the appropriate version of Skyline is installed
- Provides realtime status on the run

- MSI simplifies the user experience for scientists developing MRM methods on tandem quadrupole instruments.
- It ensures similar quality of methods developed across all experience levels
- It saves time and energy for the user and allows them to concentrate on other important aspects of the study
- Available to download now:

https://www.waters.com/waters/en_US/MassLynx-Skyline-Interface-/nav.htm?locale=en_US&cid=135058435