



SpectroMine™  
*powered by Pulsar*

**SpectroMine™ 3**



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## 1 Pulsar Database Search Engine

- Up to 70% faster for immunopeptidomics and many modification searches
- Up to 25% faster for standard searches
- Improved performance for large protein databases (> 2 GB) with Pulsar

## 2 Accurate Quantification

- Improved default settings for quantification
- Improved impurity correction for TMTpro
- Improved turboTMT support
- New MaxLFQ based protein quantification
- New TMTpro 18-plex support

## 3 Comprehensive PTM Analysis

- Site collapse calculations
- Site regulation analysis
- New PTM site report

## 4 Improved Immunopeptidomics support

- Up to 50% faster processing of immunopeptidomics data
- Motif plot visualization for identified n-mers

## 5 Improved Deep-learning Augmentation

- Prediction for ion mobility (1/K0) during library generation
- Improved fragment prediction for unspecific peptides



## 6 New Post Analysis Perspective Features

- Added PCA analysis
- Added custom selection for volcano plots
- New Run based Overview node (Identifications, Peptide Length Distributions, Peptide Motif Plot, and ILQ NA Ratio plot per channel)
- New Summarized Fractions node (Quantifications Overview)
- New PTM Analysis node (PTM Site-based differential analysis plots)

## 7 Improved User Experience and Visualization

- Improved Protein Coverage plot
  - PTM support
  - Peptide tooltip and highlighting
- Detachable perspective and plots for side-by-side visualization
- Improved plot and tree filter selection
- Quick-Action bar for analysis perspective
- Improved warning messages with actionable links
- Improved UI for analysis log

## 8 Improved Report Perspective

- New Summarized Fraction report when analysing a fractionated experiment
- New PTM Site level report when performing PTM localization