ANALYZING TMT PRO 16-PLEX DATA IN PEAKS SOFTWARE

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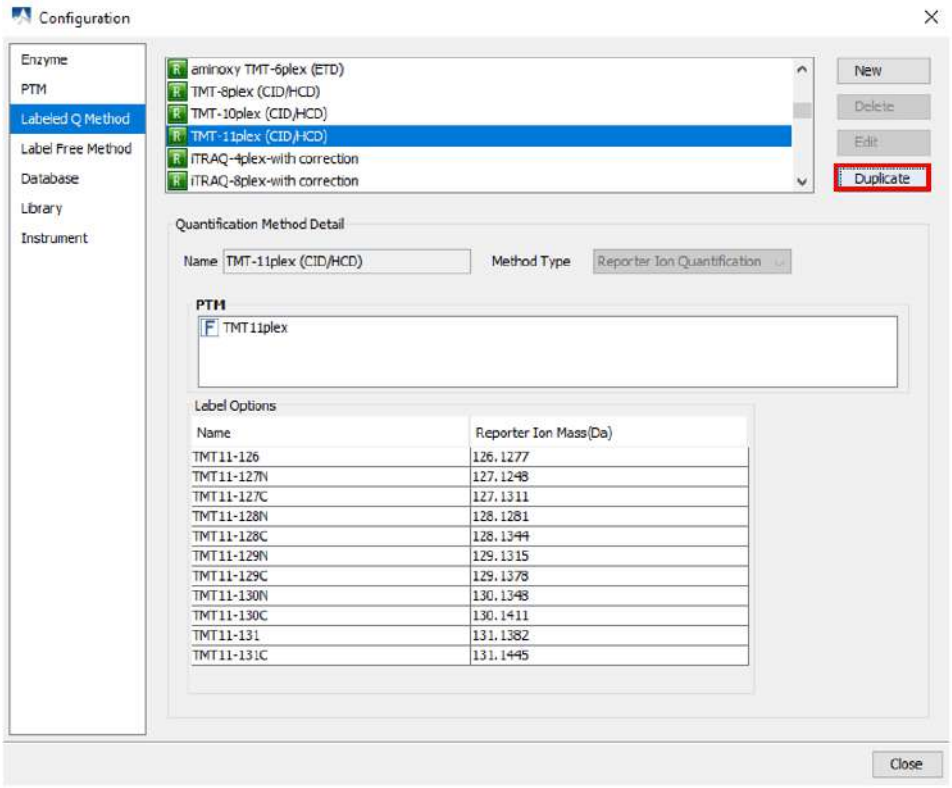
Background

Recently, Thermo Fisher Scientific and Pierce Scientific have released the isobaric TMT Pro 16-plex reagents to allow for the multiplexing of up to 16 samples in the same run. The release of these reagents came after the release of PEAKS X+ and thus we have created this technical note to assist those looking to use these reagents and search their data in one of the PEAKS software suites available.

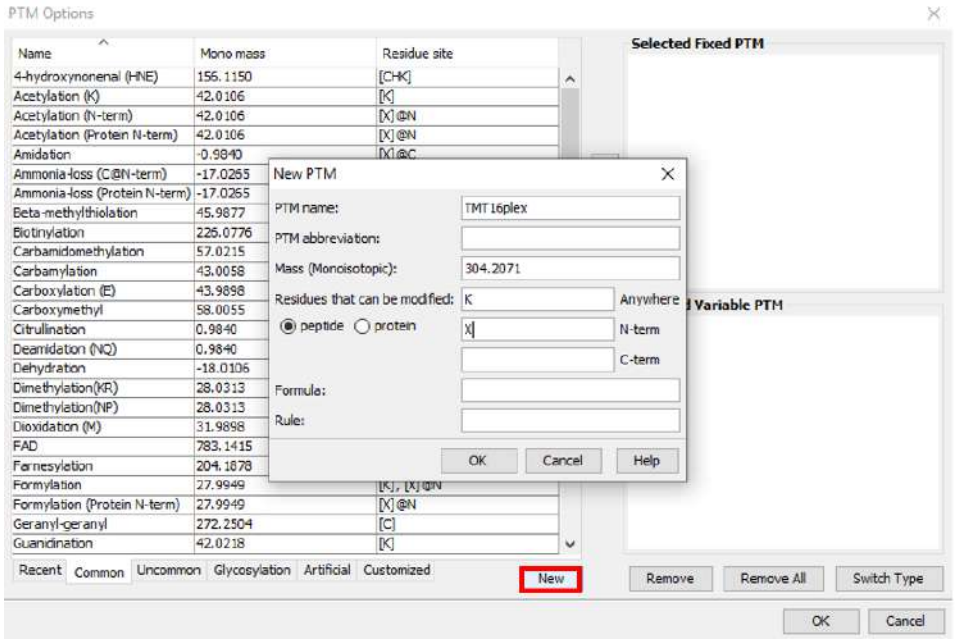
TMT PRO 16-plex Labeled Q Method in PEAKS

To run a TMT16plex analysis in PEAKS, a custom Labeled Q Method and a custom PTM must first be created. To do this, follow the steps below:

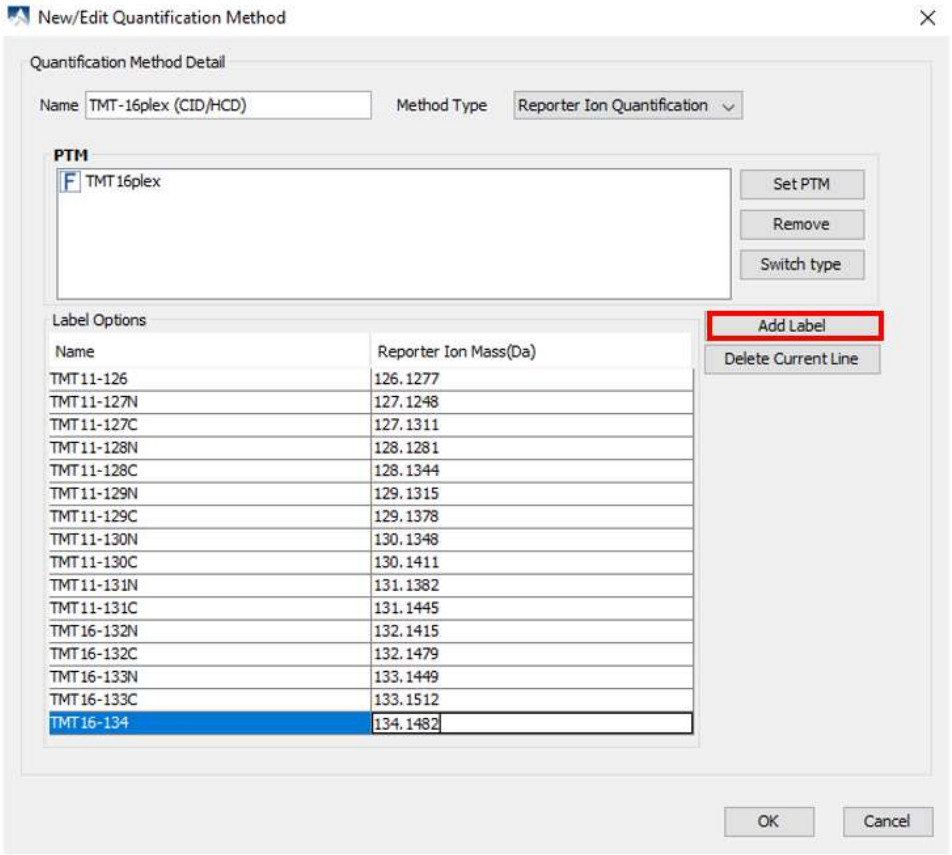
1. Click the Configuration icon and go to the *Labeled Q Method* page. To save time, the built-in TMT11-plex method can be duplicated, renamed, and edited as necessary.



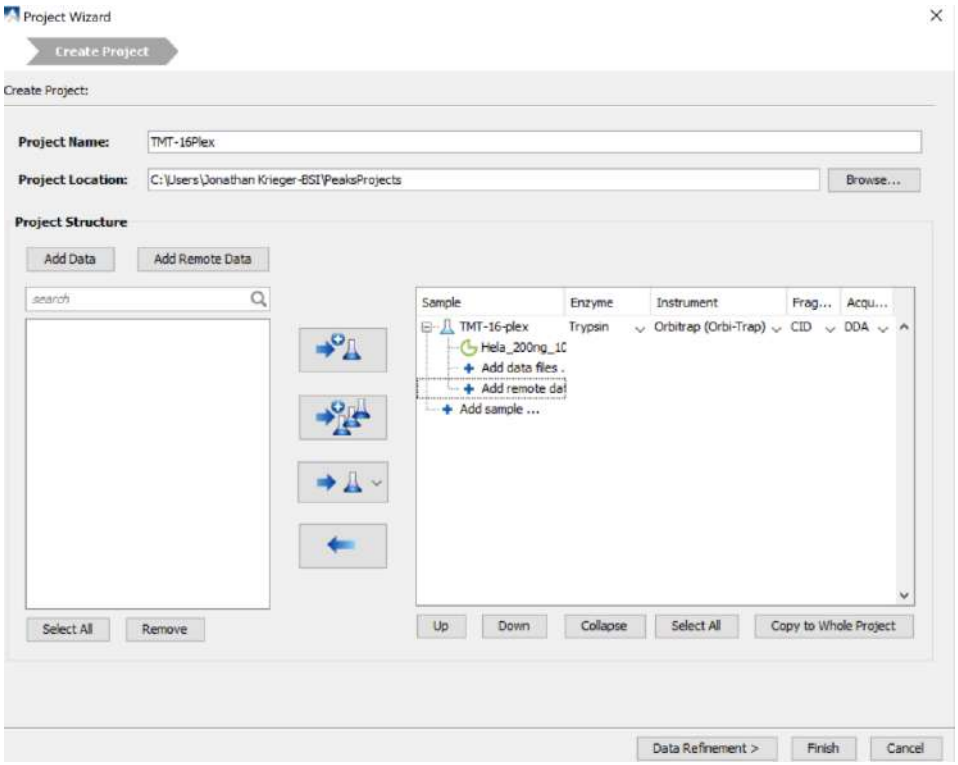
2. Edit the duplicated quantification method by first removing the fixed TMT11plex PTM. Click the **Set PTM** button then **New**, to create a new PTM. Enter the required information and click the **OK** button to save. Under the *Customized* tab, the new PTM will be listed and can be added as a fixed PTM.

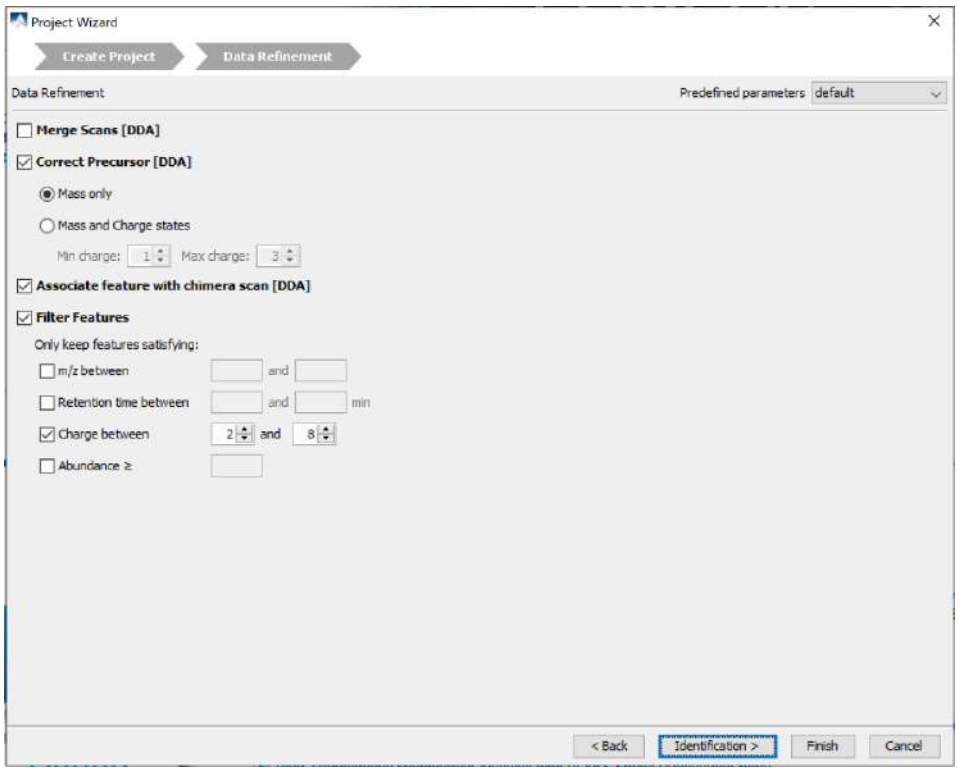


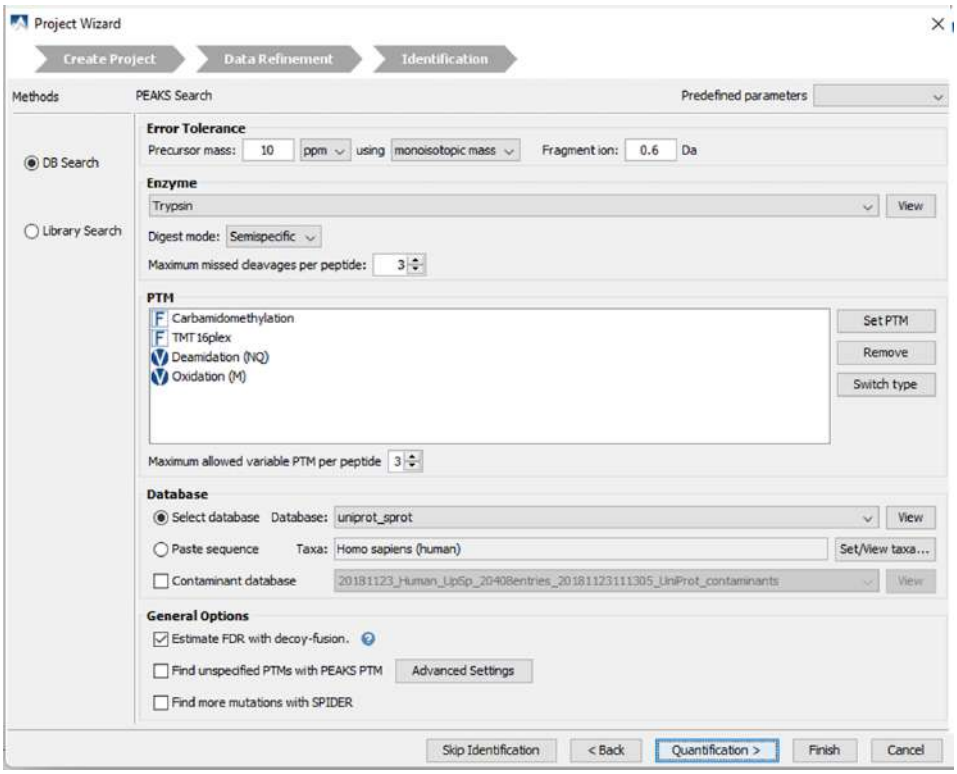
3. Once the PTM is set, click **Add Label** and add the additional TMT16plex labels. Double-click on a line to edit the name or reporter ion mass values. Click **OK** to save.

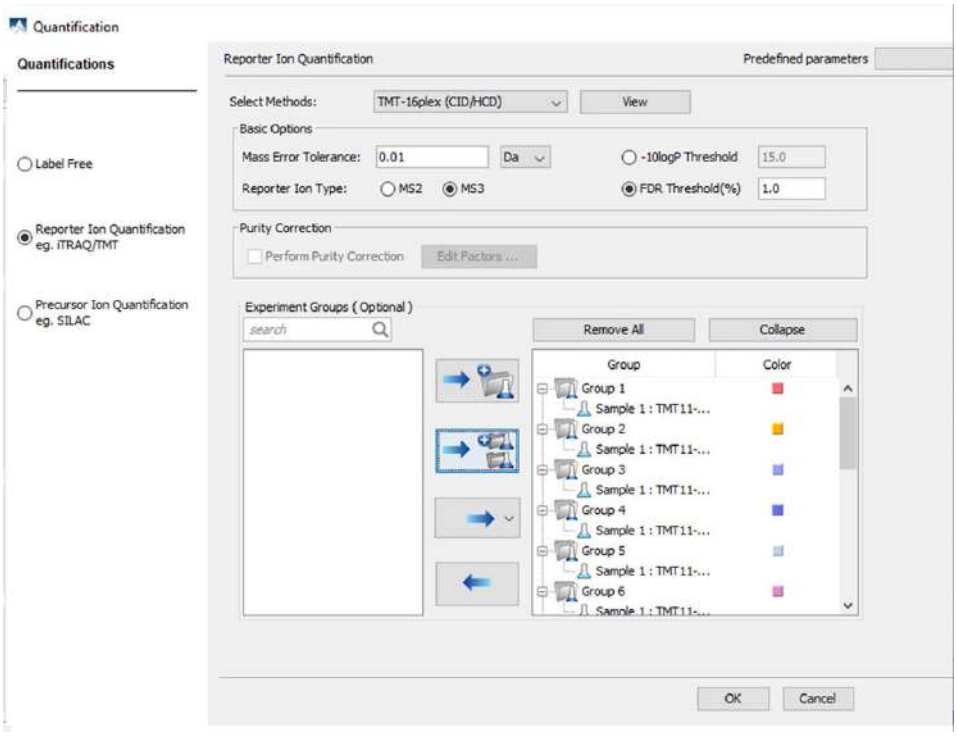


4. For a sample run on an Orbitrap Tribrid mass spectrometer in MS3 mode, the following would be the default settings:









For any questions or inquires related to this technical note, please contact BSI Support.