

TERN 2.2.18 release notes

19-July-2019

Note: This release includes a new procedure file, CT_popupSelector.ipf. When updating, be sure to update any shortcuts in your Igor Procedure Files and User Procedure Files folders, as well as any TERN packed experiment templates (.pxt) you have created.

Also, if you open an older TERN experiment, you will need to open the new procedure manually and recompile.

Reason(s) for release:

1. New .ipf added to handle ToFwerk data files with UMR / HR / UMR + HR data
2. Corrected order of error checking in chrom fitting (moved from step 8 to step 9)
3. Reformatted drop-down tabs for HR ions to make easier to read, and to add a second column to show the exact mass associated with each ion name
4. Re-ordered adjustment controls on chrom fitting tab, ordered into
 - a. Peak searching – values used by TERN to identify candidate peaks for fitting
 - b. Peak fitting – values used by TERN to fit a candidate peak
 - c. Peak vetting – additional tools to reduce excessive mis-identification of candidate peak
5. Quick keys added (p,P) for changing value of “Est. peak width, FWHM” field (see [separate note](#))
6. Additional axis controls added for “Explore Chroms”, “Make/Edit/Add Template” and “Chrom Fitting” tabs
 - a. For Explore and Template tabs, X-axis can be +/- 5% scale with buttons (emulating Igor buttons when modifying axis).
 - b. For Explore tab, individual y-axis button allows toggle between auto-scale and auto-scale from zero
 - c. For Chrom Fitting tab, user can toggle between auto-scale and auto-scale from zero via checkbox in the lower left corner
 - d. For Chrom Fitting tab, y-axis scaling can ignore or observe “other SIC” trace via checkbox
 - e. For Chrom Fitting tab, input box for data display width has been moved from peak fitting mods box to bottom of chrom display panel, as it had no effect on peak fitting