

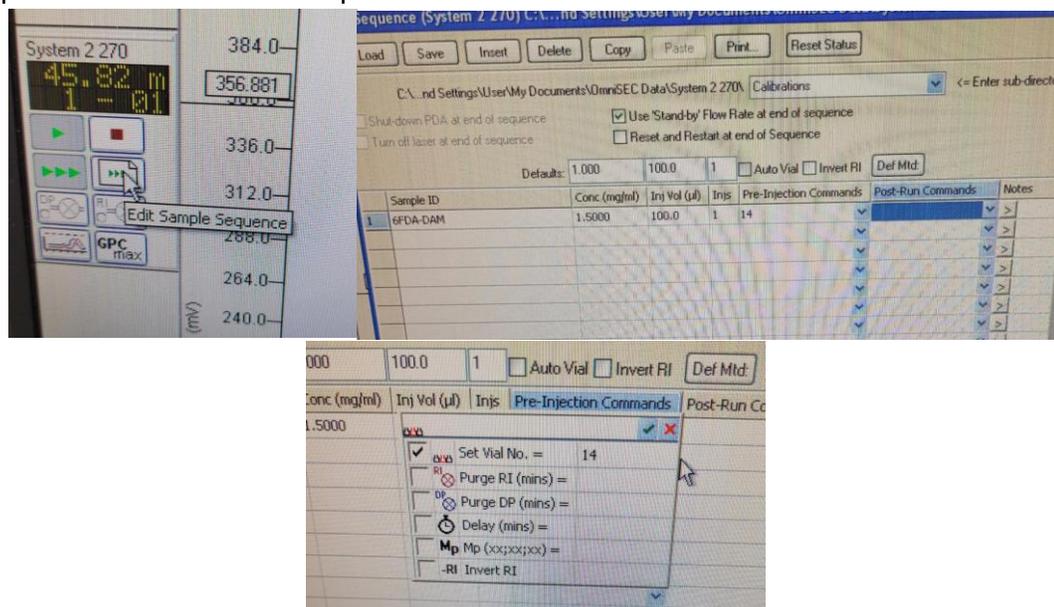
# GPC SOP

## General Info/ Prep

1. THF is used as the mobile phase
2. Samples should be prepared in 1.5 mL GC vials with pre-split septa caps. The solution should be prefiltered with 0.2 micro-meter filter.
3. Click the GPC Max button on the system control panel in the software, input the target flow rate and click apply. To start the system from standby flow, gradually increase the flow rate from 0.1 ml/min to 1 ml/min within 30 minutes.
4. **Before running a sample, place the waste tube into the waste bottle.**
5. When there is no sample running, switch to standby flow rate and place the waste tube into the solvent bottle to recycle the solvent.
6. Record the date when solvent bottle is opened. Do not use solvent that has been opened for longer than 4 months.

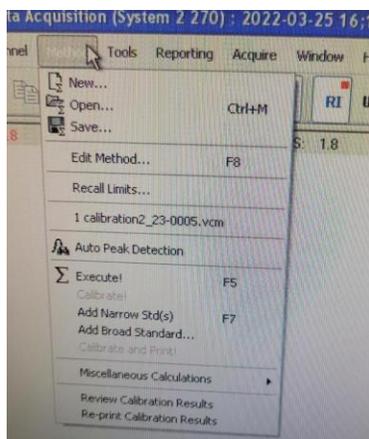
## Collect Chromatograph

1. Place sample into autosampler tray.
2. Open OminSEC software.
3. The panel on left corresponds to the analysis system (RI, TDA, or 270)
4. To do a **single run**, click the single run button and input vial number, running time, and inject volume. Click "OK" to start.
5. To run a **sequence of several samples**, click "edit sequence." Input sample name, sample concentration, vial number and injection volume in the sequence table. Save sequence. Then click "run sequence".



6. To change running time for samples in sequence go to "Acquire">"configer"

- To analyze result after it is collected, open calibration file under “Method”. Select the limits of the peak by right clicking the spectra. Then select the baseline of the peak by right clicking the spectra. Run “execute” to analyze the data under “Method”. The analysis will come up in a new window.



## Calibration

- Prepare a series PS standards with Mn 1200-20000000 by diluting with THF, ~10 ml. Concentrations should approximately as follows:

Sample	Conc	Inj volume
~1000	20	100
~5000	20-15	100
~25000	10-15	100
~50000	3 – 4	100
~100000	3 – 4	100
~200000	2.5 – 5	100

- Run samples in sequence. In the “Post Run commands” set to Add Stds
- After data in collected, open first calibration point data file. Select the limits of the peak by right clicking the spectra. Then select the baseline of the peak by right clicking the spectra.
- To Create a new method go to “Method”>“New”> “Blank”>“Conventional Calibration Homopolymer.” Choose refractive Index and Curve Fit order.
- Double click on top of standard peak.
- Enter MP
- Press F7 to add standard.
- Repeat opening calibration point data files, selecting the limits of the peak by right clicking the spectra, selecting the baseline of the peak by right clicking the spectra, double clicking on top of standard peak, entering MP, and pressing F7 to add standard to each standard data. (Steps 3, 5, 6, and 7 but skipping 4).
- Save the final calibration file with a unique name (Example: FINAL) for later use.