1. Define organizational structure for the processed data
   1. Shared drive
      1. The organization in folders of the processed data quickly becomes arbitrary, so feel free to rearrange and/or put a ton of files together in there if they’re easily searchable.
2. Maxed out values (#SAT) - change to the highest value
3. Subtract out blank spectra ( a representative single blank)
4. Intensity-normalization for all spectra - Make intensity at lambda max equal for all samples
5. Averaging spectra
   1. Spectra should NOT be averaged between plates, only for the triplicate on the same plate.

{lower priority}

1. Difference spectra from normalized - match the concentrations of each of the components!
   1. (peptoid + analyte) - (peptoid only)
   2. (peptoid + analyte) - (analyte only)