HOW TO GET THE MOST OUT OF YOUR MASS SPECTROMETRY ANALYSIS

1. Do your background research BEFORE talking to us.
    - Has anyone successfully studied your types of compounds by mass spectrometry before?
    - What technique did they use? Bring the papers when you come to talk to us.
2. Make sure you TALK to us before submitting a sample for the first time.
3. Give us as much information as possible about your sample. It is crucial that you WRITE IT DOWN on the submission form, so that it is immediately available to the person performing the analysis. We process many samples, so just telling someone is not reliable enough. Some common things we need to know:
    - Approximate concentration of analyte (what you're interested in) in your sample
    - What ELSE is in your sample, besides what you are interested in (buffers, salts, contaminants, other reaction products, starting materials, etc.)
    - Nature of your sample (synthetic reaction mixture, pure protein, protein mixture, peptides, carbohydrates, other small molecules)
4. Before the analysis is performed it is important for you to know what information you expect from the analysis, and appreciate the limitations of the technique used. E.g. it is not feasible to scan the entire mass range from 0 to infinity, and see what is there, for each sample, without having any idea of what you are looking for.
    - We ask for an expected molecular weight, or a mass range of interest.
    - This allows us to focus on the range, and optimize parameters for the detection of the compound of interest.
    - This reduces the ionization suppression of your analyte by other compounds present (which are outside the range).
    - We are also able to select a matrix that will be most suitable to the compound you are looking for. We are able to set up the instrument parameters accordingly e.g. proteins are best ionized in the positive mode, while carbohydrates are generally best in negative mode, etc.
5. If you don't know the concentration of your analyte, and we do not detect it, THAT DOES NOT MEAN THAT IT IS NOT THERE. It could mean that the concentration is too low, or our technique is not suitable to your analyte (e.g. it will not ionize, or decomposes into fragments, and so cannot be detected). It is not possible to troubleshoot or perform method development on a sample like this as it is not scientifically sound.

6. In order to determine whether or not we can see your analyte by the specific technique, and the detection limit, we will need a standard of known concentration. We can develop a method based on the standard, and then apply it to the unknown sample.
7. If your sample requires method development as described above, it is not useful to submit many samples at once, prior to the method development, because this will waste your money and time. It is best to submit a standard to use in method development. Once the method has been developed we can test in on one unknown sample. If the analysis is successful, and you are confident that your results will be meaningful, then you can submit more samples of the same type.