Peptide and Protein Identification

The process of searching mass spectral data for the purpose of peptide and protein identification can roughly be divided into six steps:

* **Step 1: Convert the raw, typically binary, output from the MS instrument into open formats.**
* **Step 2: Process the MS/MS spectra into peak lists.**
* **Step 3: Download the desired sequence database and adapt it to your identification strategy.**
* **Step 4: Search the peak lists against a sequence database using one or more search engines.**
* **Step 5: Identify the peptides and infer the proteins.**
* **Step 6: Validate the detected peptides and proteins.**

**(1) Convert   
Raw Files**

**(3) Generate Database**

**(2) Process MS/MS Spectra**

**(4) Match Peptides   
to Spectra**

**(5) Infer Peptides and  
Proteins**

**(6) Validate Peptides and Proteins**

This tutorial will guide you through these steps, separated into six chapters, and finally provide an introduction to post-translational modifications (PTM) oriented studies:

1. **Database Generation**
2. **Peak List Generation**
3. **Peptide to Spectrum Matching**
4. **Browsing Identification Results**
5. **Peptide and Protein Validation**
6. **PTM Analysis**