1. Web page for MS-Align+ and parameter setting. DONE.

2. Test and compare accuracy and the number of identifications of the new c++ implementation with MS-Align+ 0.7. DONE

3. Test the accuracy of e-values for protein-spectrum-matches that contain one or two PTMs. DONE.

4. Add a new search method for one PTM protein-spectrum-matches filtering (OnePtmFilter). DONE.

5. Add function for identification of merged spectra. DONE.

6. Manual and webpage for releasing (release notes, tutorial). DONE.

7. Test various data sets (at least 3 - 5 data sets). DONE.

8. Add support for database searching using multiple spectra. DONE.

9. Add spectral alignment algorithm based on mass graphs. DONE.

10. Add support for customized fixed PTMs. DONE

11. Add PTM localization and confidence score. DONE

12. Add a function to identify spectra using a pipeline in which spectra that are identified are labelled and ignored in the next round of search. DONE.

13. Release a version of TopFD in TopPIC suite. DONE.

To Do List

1. Add new filtering function for database search using variable PTMs. Two approach: (a) extended protein database with variable PTMs (b) tag based method.(Qiang)

2. Add support for customized databases using three sources: (a) Uniprot, (b) neXtProt, and (c) ProSight [Almost Done].

3. Add scoring function for masses based on intensities.

4. Develop a GUI for visualizing searching result.

5. Restricted version of mass graph alignment (search a band of the search space, which is similar to Fasta).

6. Search top-down spectra against antibody germ line sequences using the mass graph method.

7. Add a scoring function threshold for TopFD.

8. Add multiplexing precursor masses to TopFD and TopPIC.

9. Add TopMG to TopPIC suite.

10. Add GUI to TopMG.

Other

Add visualization of raw data and deconvoluted data.

Antibody de novo sequencing.

Generate mass graphs from RNA-Seq data by SNV calling and Alternative splicing detection.