

# Tools

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## 1. Overview

Provides applicative tools based on JPL.

## 2. QuickMod

[QuickMod](#) is a spectral library search based MSMS data analysis tool, designed to identify modified peptides.

## 3. QuickModViewer

[QuickModViewer](#) is simply a viewer for QuickMod results.

## 4. Deliberator

[Deliberator](#) generates decoy library spectra.

## 5. Liberator

[Liberator](#) generates library spectra.

## 6. MzXMLReIndexer

[MzXMLReIndexer](#) recomputes scan indices of mzXML files.

## 7. Fas2MS

[Fas2MS](#) digests and fragments fasta proteins into annotated MS spectra.

## 8. FastaDecoy

[FastaDecoy](#) generates decoy sequences.

## 9. MassCalc

[MassCalc](#) computes masses for proteins or molecules.

## 10. ProteinDigerster

[ProteinDigerster](#) make the digestion of proteins and compute the isoelectric points and mass

weights of all digested peptides.

### **11. Dig2Mz**

[Dig2Mz](#) make the digestion of proteins and compute the m/z of all digested peptides that passed the charge filters.

### **12. MSDataFilter**

[MSDataFilter](#) read and filter MS data.

### **13. SpextrumConverter**

[SpectrumConverter](#) is not yet implemented.