



MetaboAnalyst 6.0

-- a unified platform for metabolomics data processing,
analysis and interpretation

Peak Annotation [MS2-DDA/DIA]

Module Overview



Database searching for MS2 spectra-based compound identification and results visualization

- ✓ Support single MS2 spectrum searching. This spectrum can be generated by either DDA or DIA;
- ✓ Support MS2 spectra batch searching. The accepted file format can be either MSP (from MS-DIAL) or MGF;
- ✓ Batch searching support at most 20 spectra once at a time. Users can prioritize the spectra;
- ✓ A total of 11 public MS2 reference libraries have been included. Users can choose to use one or more database options for searching;
- ✓ MS2 spectra searching supports direct searching or searching based on neutral loss;
- ✓ MS2 spectrum similarity can be evaluated based on dot-product or spectral entropy method.



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1. Introduction

Background

- MS2 data acquisition could be carried out independently from MS1 in DDA or DIA method.
- MS2 spectra-based compound identification is a commonly used approach for global (untargeted) metabolomics;
- There are multiple public reference libraries curated for metabolomics/exposomics community;

Data Formats

To accommodate application scenario and offer compatibility with MS2 spectra results from other popular tools. There are three formats supported:

- i. Simple text file (m/z and intensity separated by tab);
- ii. MGF file format (standard);
- iii. MSP file format (MS-DIAL);

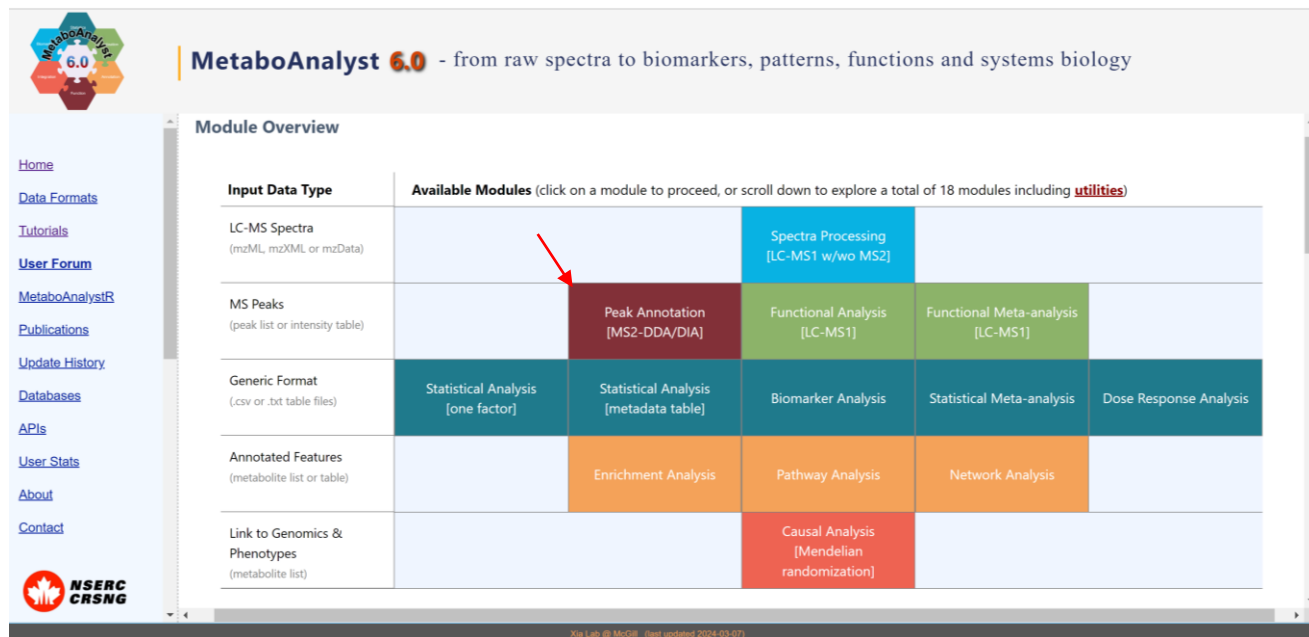
Expected Results

The MS2 spectra/spectrum searching provides results including comprehensive compound identification summary and visualization of the matching pattern:

- i. Compound identification summary table;
- ii. Visualization on MS2 matching pattern and annotation of fragments;

2. Choose the Module

Go to MetaboAnalyst (<https://www.metaboanalyst.ca>), and select the module



The screenshot displays the MetaboAnalyst 6.0 interface. On the left is a navigation sidebar with links: Home, Data Formats, Tutorials, User Forum, MetaboAnalystR, Publications, Update History, Databases, APIs, User Stats, About, and Contact. The main content area is titled 'MetaboAnalyst 6.0 - from raw spectra to biomarkers, patterns, functions and systems biology' and 'Module Overview'. It contains a table mapping input data types to available modules. A red arrow points to the 'Peak Annotation [MS2-DDA/DIA]' module.

Input Data Type	Available Modules (click on a module to proceed, or scroll down to explore a total of 18 modules including utilities)				
LC-MS Spectra (mzML, mzXML or mzData)			Spectra Processing [LC-MS1 w/wo MS2]		
MS Peaks (peak list or intensity table)		Peak Annotation [MS2-DDA/DIA]	Functional Analysis [LC-MS1]	Functional Meta-analysis [LC-MS1]	
Generic Format (.csv or .txt table files)	Statistical Analysis [one factor]	Statistical Analysis [metadata table]	Biomarker Analysis	Statistical Meta-analysis	Dose Response Analysis
Annotated Features (metabolite list or table)		Enrichment Analysis	Pathway Analysis	Network Analysis	
Link to Genomics & Phenotypes (metabolite list)			Causal Analysis [Mendelian randomization]		

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3. MS2 search of single spectrum

3.1 Single spectrum upload

At the first page, user can upload single spectrum or multiple spectra. We used the “**Single Tandem Spectrum**” at this stage.

For single spectrum uploading,

1. It should be a text containing two columns. The first column is m/z values, while the second column is intensity values.
2. The two columns must be separated by tab (not space).
3. It is unnecessary to normalize the intensity values, we will automatically do it.

Please enter your data below

Single Tandem Spectrum Multiple Tandem Spectra

This module is designed to provide an easy tandem MS spectrum annotation functionalities for single MS2 spectrum.

- The input data should be a two-column list, containing m/z and intensity of MS/MS spectrum;
- Two columns should be separated with tab. Each row represents a fragment (e.g. 157.9023 3415);
- m/z of the precursor ion is required;
- Specify the ion mode for the MS/MS spectrum is optional but highly-recommended to improve the accuracy;

135.0802	9.23
147.0807	27.55
149.0965	8.74
153.091	22.39
159.0806	9.47
161.0966	8.84
171.0805	15.77
215.1071	13.62
235.1112	12.59
237.1279	23.62
267.138	11.0
277.1586	27.9
279.1744	77.14
309.1851	30.04
325.1792	20.22
337.1802	100.0
393.21	44.44

Precursor Ion Mass (Da): 393.2072

Precursor Mass Tolerance: 10.0 PPM

Fragment Mass Tolerance: 30.0 PPM

MS/MS Database: HMDB Experimental

Use Neutral Loss: ☐

Ion Mode: Positive

Similarity Method: Dot-product

Try Our Example: ☒

Submit

Click submit to proceed

Parameters for searching,

1. **Precursor Ion Mass** is required, please input the value as precisely as possible;
2. **Tolerance**: both tolerance values are recommended to be optimized based on MS instrument'
3. **MS/MS Databases**: user could customize their database option (see 3.2 for more information);
4. **Use Neutral Loss**: user could optionally use Neutral Loss for database search by use the option. Please note, this is only encouraged for unknown new compound discovery;
5. **Similarity Method**: User could choose traditional way (dot-product) or a new strategy ([spectral entropy](#)).

3.2 MS2 spectra databases

- Users can choose one or multiple MS2 spectra data for searching.
- Different databases contain significantly different number of MS2 spectra records.
- Choose “All Database” will search the entire MS2 spectra database, but it may take significantly longer to complete.

The image shows a search interface for MS2 spectra. On the left is a search form with fields for Precursor Ion Mass (Da), Precursor Mass Tolerance, Fragment Mass Tolerance, MS/MS Database, Use Neutral Loss, Ion Mode, Similarity Method, and a 'Try Our Example' button. The MS/MS Database dropdown is open, showing options: All Database, HMDB Experimental (selected), HMDB Predicted, GNPS, and MINES. A green arrow points from the form to a detailed view of the database options on the right.

It is allowed to customize the database options based on your needs. You could select one or multiple database for MS/MS searching. It is noted that if you selected "All Database", the searching may take a quite long time based on your MS/MS spectrum and server loading. Here is a summary on all database option:

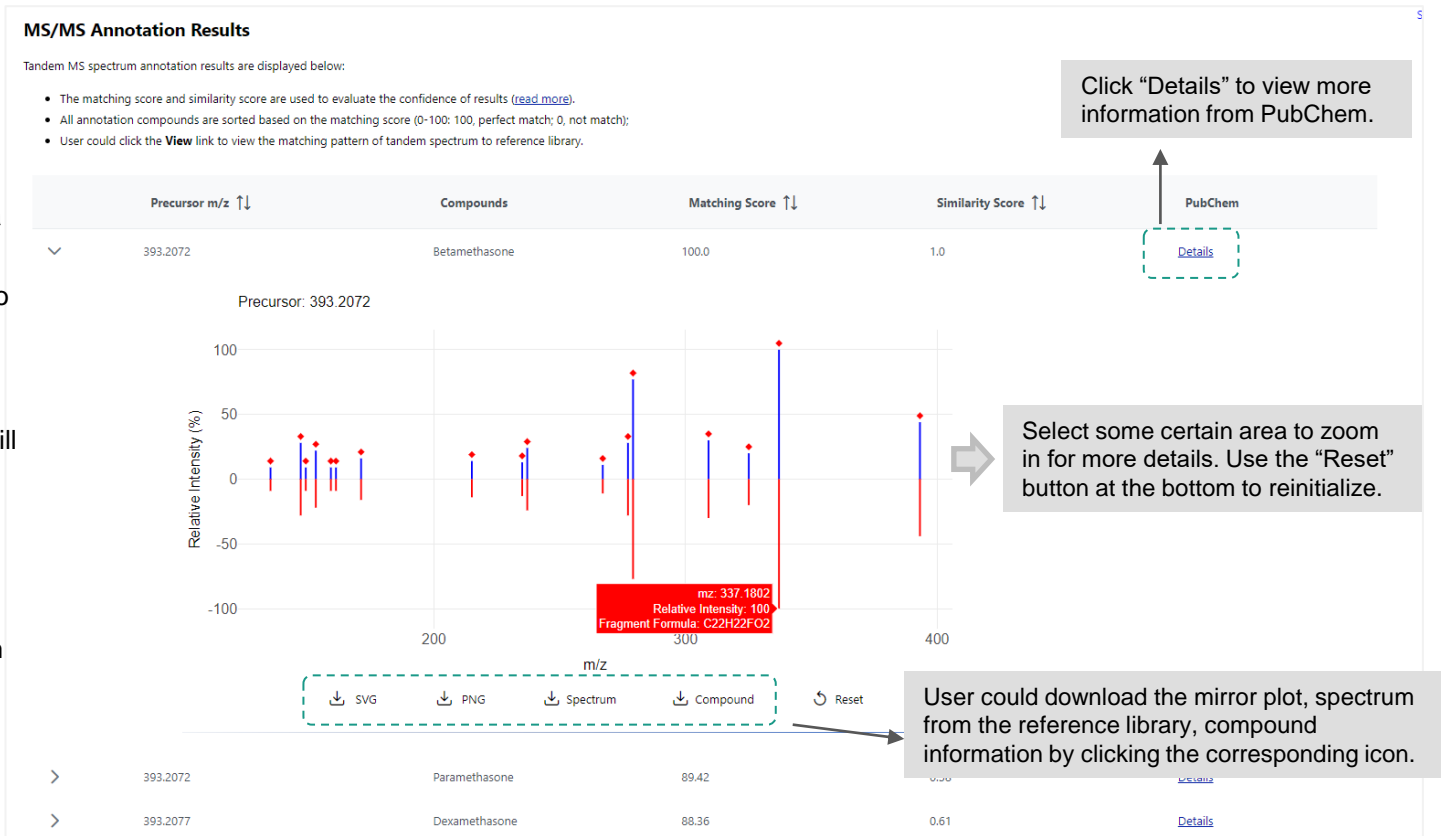
Database	Total Records	Unique Compounds	Version/Date
HMDB Experimental	64711	4049	v5 (Sep 4th 2022)
HMDB Predicted	1786690	204969	v5 (Sep 4th 2022)
GNPS	80802	11852	Aug 30th 2022
MoNA	1545053	614391	Aug 15th 2022
MassBank	90190	16879	Sep 4th 2022
MINES	3009477	537799	Feb 2nd 2023
LipidBlast	1832594	778501	Feb 7th 2023
RIKEN	12771	1231	Sep 7th 2022
ReSpect	4310	691	Sep 7th 2022
VaniyaNP	39937	2681	Sep 4th 2022
MSDIAL	1726174	606878	v4.8 (Sep 11th 2022)
BMDMS	227307	2739	Aug 20th 2022

Mouse hover the help tip to view the detailed information on different database options.

3.3 MS2 spectra searching results

MS2 results explanation,

1. Database search results would be summarized as a table;
2. User could expand a row to visually explore the matching results of a MS2 spectrum;
3. Information of fragments will be automatically displayed when mouse hover the fragment;
4. The top (blue) part are users' input, while the bottom (red) parts are from the reference library;
5. All matched fragments will be marked with red diamond at the top.





4. MS2 spectra batch search

4.1 MSP/MGF spectra upload

“**Multiple Tandem Spectra**” tab can be used to upload multiple spectra once at a time.

Click “**Choose**” button and select msp or mgf file to upload.

These parameters are the same as single tandem spectra (see 3.1 section).

Single Tandem Spectrum **Multiple Tandem Spectra**

This module is designed to provide an easy tandem MS spectrum annotation functionalities for multiple MS2 spectra.

- The input data should be a standard mgf file or msp file generated by [MS-DIAL](#).
- To ensure the searching can be finished in time, at most 20 tandem MS spectra are supported for an individual upload;
- All tandem MS without MS2 spectrum will be excluded;
- The maximum msp file size allowed is **1MB**

Data Format: ☒ MSP ☐ MGF

Data File:

Precursor Mass Tolerance: PPM

Fragment Mass Tolerance: PPM

MS/MS Database:

Use Neutral Loss: ☐

Ion Mode:

Similarity Method:

Try our test data

Data Type: ☒ Whole blood ☐ DDA dataset

Description: This is an example dataset from whole blood dataset. This msp file is generated by MS-DIAL. This dataset is processed by mzMine. The original dataset are generated with data dependant acquisition (DDA) mode.

You can try to download either example from the bottom of the uploading page or Click “**Submit**” button directly to test.

Click submit to proceed

4.2 Spectra Integrity Check

MetaboAnalyst could process your data and do an integrity check. The integrity check results are summarized here.

Public server is limited to search 20 spectra once at a time due to computing constraints.

If your msp/mgf file contains more than 20 spectra, you can Click “**Edit Data**” to customize/prioritize some features (See 4.3), or MetaboAnalyst will include the first 20 spectra.

MSP Spectra Integrity Check:

1. MetaboAnalyst only supports tandem spectra searching on level 2. Other levels will be excluded.
2. To ensure the efficiency of database searching, MetaboAnalyst support at most 20 spectra in an individual search.
3. User could manually edit the precursor ion inclusion list for MS/MS annotation, unless the total number of MS/MS spectra in your msp file is < 20.
4. Searching > 20 MS/MS may take over 1 minute. Please wait patiently once you click **Proceed**.

Data processing information:

Checking data content ...passed.
Your msp file is exported by MS-DIAL
A total of 1872 MS/MS records detected in your data.
A total of 154 non-empty MS/MS spectra found in your data.
Only first 20 tandem spectra will be searched by default!
The m/z range of all precursors in your data is from 70.01316 to 257.9769.
The retention time range of all included precursors in your data is from 0.300231 to 0.5887133.
The minimum number of MS/MS fragments is 8.
The maximum number of MS/MS fragments is 61.
Please use **Edit** button below to manually update the inclusion list for database searching!
Please click **Proceed** button to start database searching.


Edit Data

Proceed

If you want to use the default or you have finished the Editing, click “**Proceed**” button to continue.

4.3 Spectra inclusion for searching

Spectra inclusion editor,

1. Since MetaboAnalyst only support at most 20 spectra searching once at a time, user could manually customize the inclusion list for MS2 database search;
2. By default, the first 20 spectra will be listed into “Include” list to be included for searching;
3. User could move MS2 spectra features between two lists by using the blue moving arrows; 
4. Once the editing is done, Click “**Submit**” button to confirm.

MS/MS Spectral Inclusion List Editor

You can use the panels below to **exclude** particular MS/MS spectra. Note, you must click the **Submit** button to complete data editing. You could only include at most 50 MS/MS spectra for searching once at a time. Data need to be re-calibrated after this step. you will be redirected to the **Sanity Check** page when you click the **Submit** button.

[Edit Inclusion List](#)

Include

109.9893mz@0.300231min
176.9719mz@0.3228013min
82.01434mz@0.5701352min
83.03799mz@0.5701352min
84.96017mz@0.5701352min
88.02363mz@0.5701352min
99.53149mz@0.5701352min
100.0247mz@0.5701352min
111.0393mz@0.5701352min

>

>>

<

<<

Exclude

125.9862mz@0.5887133min
129.02mz@0.5887133min
130.0862mz@0.5887133min
139.0178mz@0.5887133min
143.9967mz@0.5887133min
147.1127mz@0.5887133min
151.0352mz@0.5887133min
152.036mz@0.5887133min
167.0127mz@0.5887133min

Submit










Users could use the searching box to find the MS2 spectra of interests.

All MS2 spectra are labelled based on the information of their precursors.
For example,
147.1127mz@0.5887133min represents the MS2 spectra, and the m/z and retention time of its precursors is 147.1127 and 0.5887133min.

4.4 MS2 spectra batch searching results

MS2 results explanation,

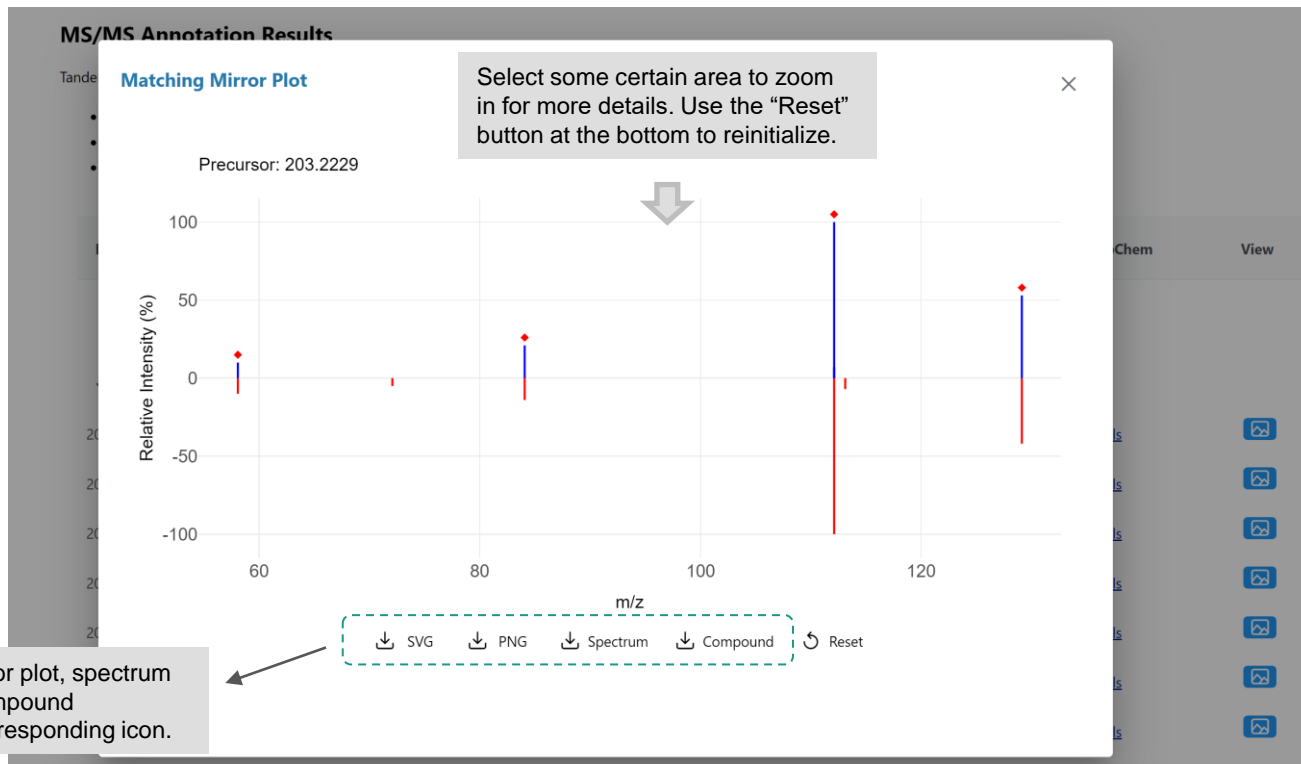
1. Database search results would be summarized as a table;
2. Each row of the table is a MS2 spectra (labelled with their corresponding precursor's information);
3. User could expand a row to check all chemical candidate;
4. Click “**Details**” to see the detailed information of this compound;
5. Click “**View**” icon to visually check the MS2 matching results from the pop-up dialog (see 4.5).

Precursor m/z ↑↓	Compounds	Matching Score ↑↓	Similarity Score ↑↓	PubChem	View
> 123.0404mz@0.5887133min					
> 176.9719mz@0.3228013min					
▼ 203.2229mz@0.5701352min					
203.223	Spermine	85.07	0.99	Details	
203.223	SPERMINE - 40.0 eV	83.25	0.98	Details	
203.223	SPERMINE - 50.0 eV	82.6	0.96	Details	
203.223	SPERMINE	82.03	0.94	Details	
203.223	SPERMINE - 60.0 eV	80.73	0.88	Details	
203.223	SPERMINE - 30.0 eV	78.77	0.8	Details	
203.223	SPERMINE - 70.0 eV	77.51	0.75	Details	
203.223	SPERMINE - 20.0 eV	74.61	0.64	Details	
203.223	N~1~,N~4~-bis(3-aminopropyl)-1,4-butanediamine	55.66	0.09	Details	
> 257.9769mz@0.5701352min					

4.5 MS2 spectra visualization results

MS2 results visualization,

1. Information of fragments will be automatically displayed when mouse hover the fragment;
2. The top (blue) part are users' input, while the bottom (red) parts are from the reference library;
3. All matched fragments will be marked with red diamond at the top.



5. Download Results

MS/MS Annotation Results

Tandem MS spectrum annotation results are displayed below.

- The matching score and similarity score are used to evaluate the confidence of results ([read more](#)).
- All annotation compounds are sorted based on the matching score (0-100; 100, perfect match; 0, not match);
- User could click the **View** link to view the matching pattern of tandem spectrum to reference library.

Precursor m/z ↑↓	Compounds	Matching Score ↑↓	Similarity Score ↑↓	PubChem	View
▼ 123.0404mz@0.5887133min					
123.04	2-methylcyclohexa-2,5-diene-1,4-dione	49.17	0.3		
123.04	Benzoic acid	46.42	0.02		
123.04	Benzeneformic acid	40.47	0.0		
123.04	Benzoic acid	40.47	0.0		
> 176.9719mz@0.3228013min					
> 203.2229mz@0.5701352min					
> 257.9769mz@0.5701352min					

> Download Page

From the bottom of the result page, click “**Download Page**” button to go to the results downloading page.

Details 

Download Results & Start New Journey

Please download the results (tables and images) from the **Results Download** tab below. The **Download.zip** contains all the files in your home directory. You can also generate a **PDF analysis report** using the button. Finally, you can continue to explore other compatible modules using the **Start New Journey** tab.

Results Download

Start New Journey

Generate Report

Download.zip

mirror_plotting_0_123.0404_72.png

Rhistory.R

mirror_plotting_0_203.2229_72.json

mirror_plotting_0_203.2229_72.png

mirror_plotting_0_123.0404_72.json

Logout



In summary

If you have any questions, please read/post into OmicsForum (www.omicsforum.ca)

Or contact us:

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[jeff.xia\[at\]xialab.ca](mailto:jeff.xia@xialab.ca)

- MS2 data acquisition could be carried out independently from MS1.
- Users can input MS2 spectra directly into the module by uploading a single MS2 spectrum or an MSP file containing multiple MS2 spectra.
- For single spectrum searching, users must specify the m/z value of precursors. However, for batch searching based on MSP file, users do not need to specify the precursors' m/z .
- MetaboAnalyst 6.0 public server processes only 20 spectra for each submission. Users can manually prioritize preferred spectra for searching.
- Following this pilot study, users can then download the R command history to annotate all MS2 spectra in the MSP/MFG file locally using the MetaboAnalystR.