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pFind Studio

pTop 1.2 User Guide

Version 1.2.0

pFind Group

2017.12.26

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- Installation steps
- Software registration
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Before software installation

- **Hardware requirements**
  - **2 GB or higher recommended memory**

- **Software requirements**
  - **Windows 7 or above**
  - **Xcalibur (2.1 or above) or MSFileReader**
  - **.NET Framework 4.5 environment**

Installation steps

- **Step 1: Select the installer language(Figure 1). Now it only supports English and Chinese(Simplified).**

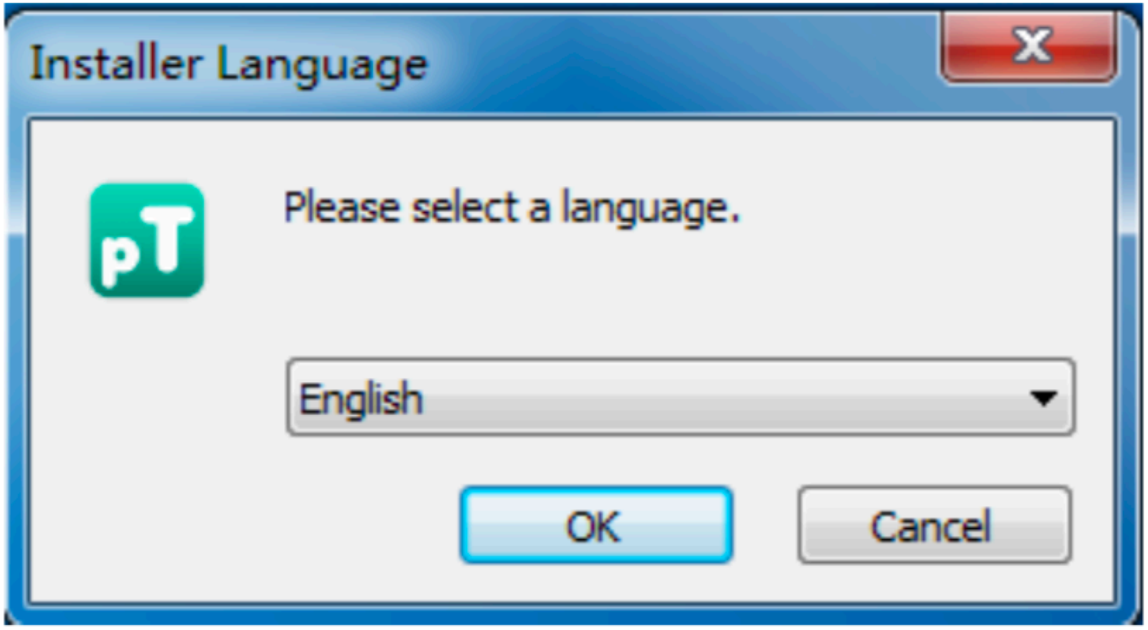


Figure 1. Installer language

Installation steps

- Step 2:Click Next to start the setup.

Figure 2. Welcome to the setup wizard

Installation steps

- Step 3:Choose the install Location. And D drive disk is recommended.

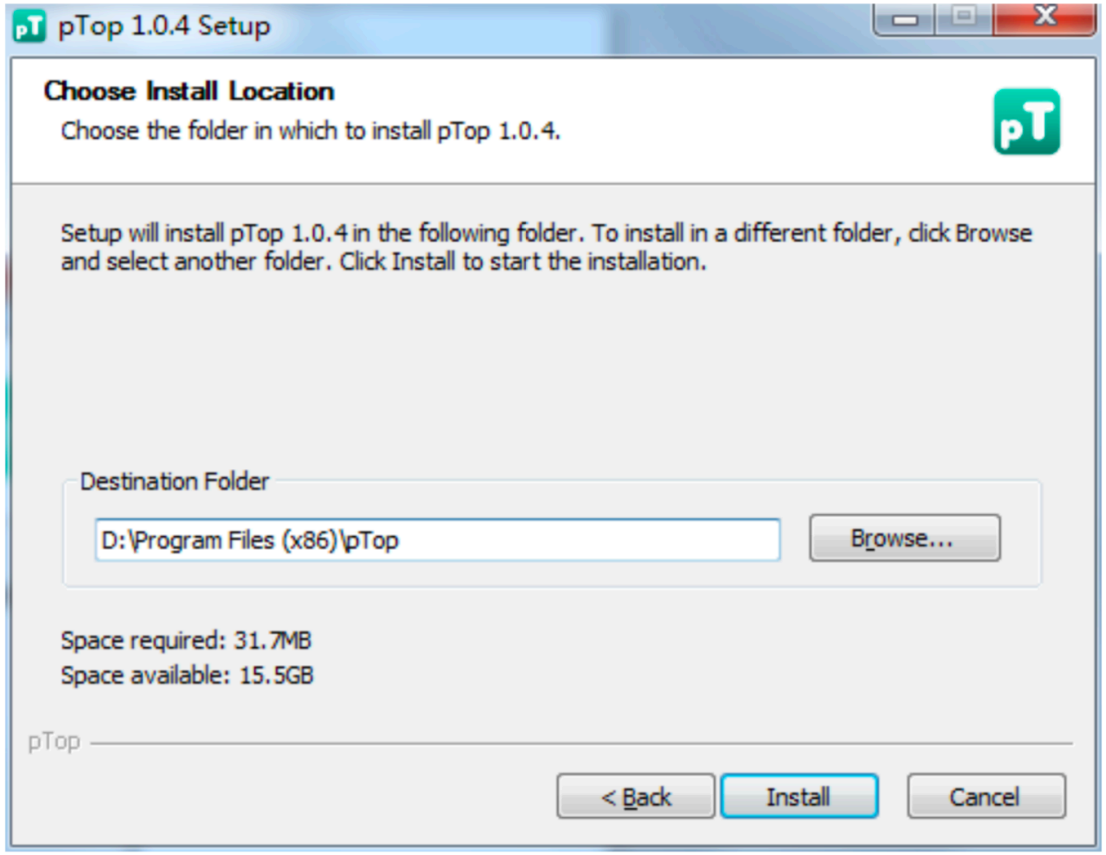


Figure 3. Choose install location

Installation steps

- Step 4: Just wait a few seconds, the Installation will be finished.

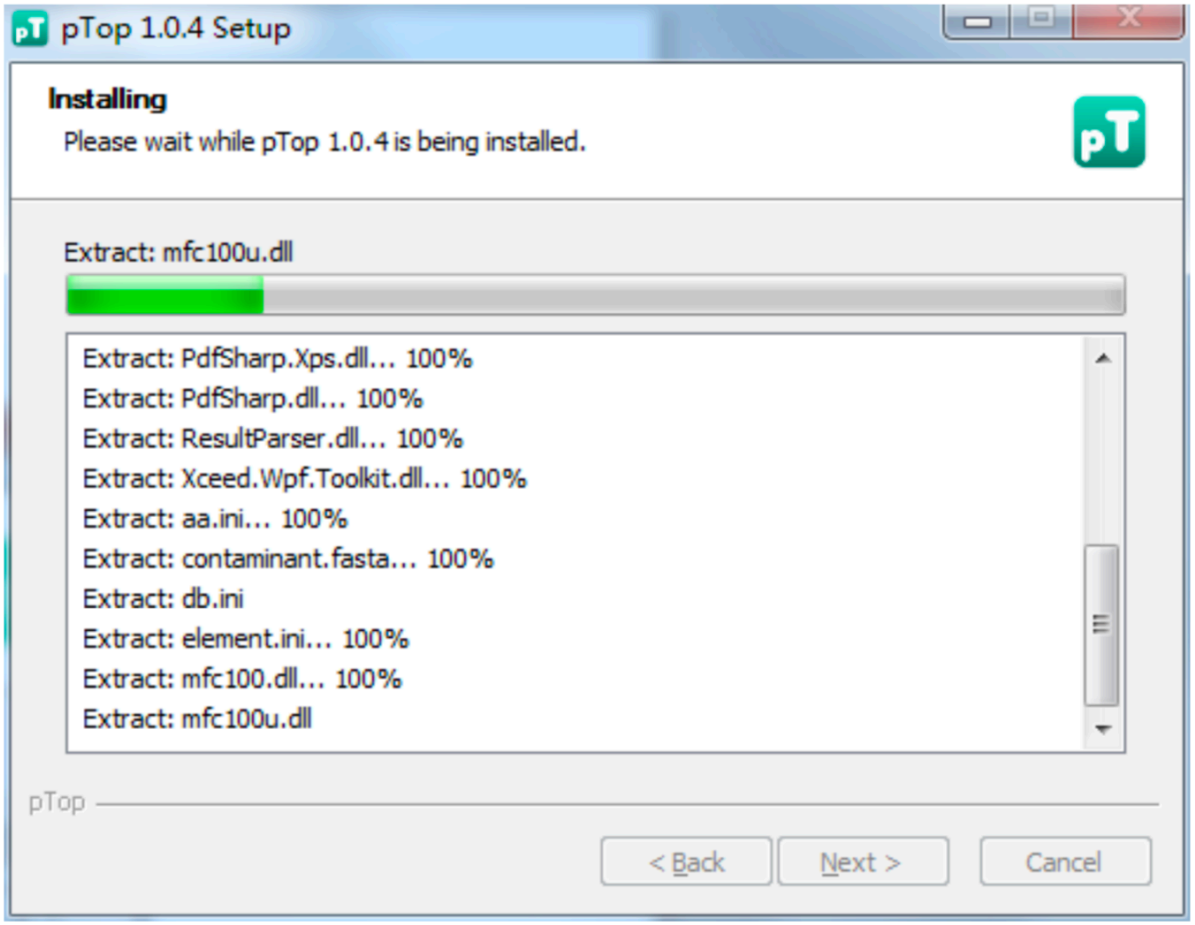


Figure 4. Installing

Installation steps

- Step 5: Finally, you can check the box of run pTop and then click Finish to start pTop.

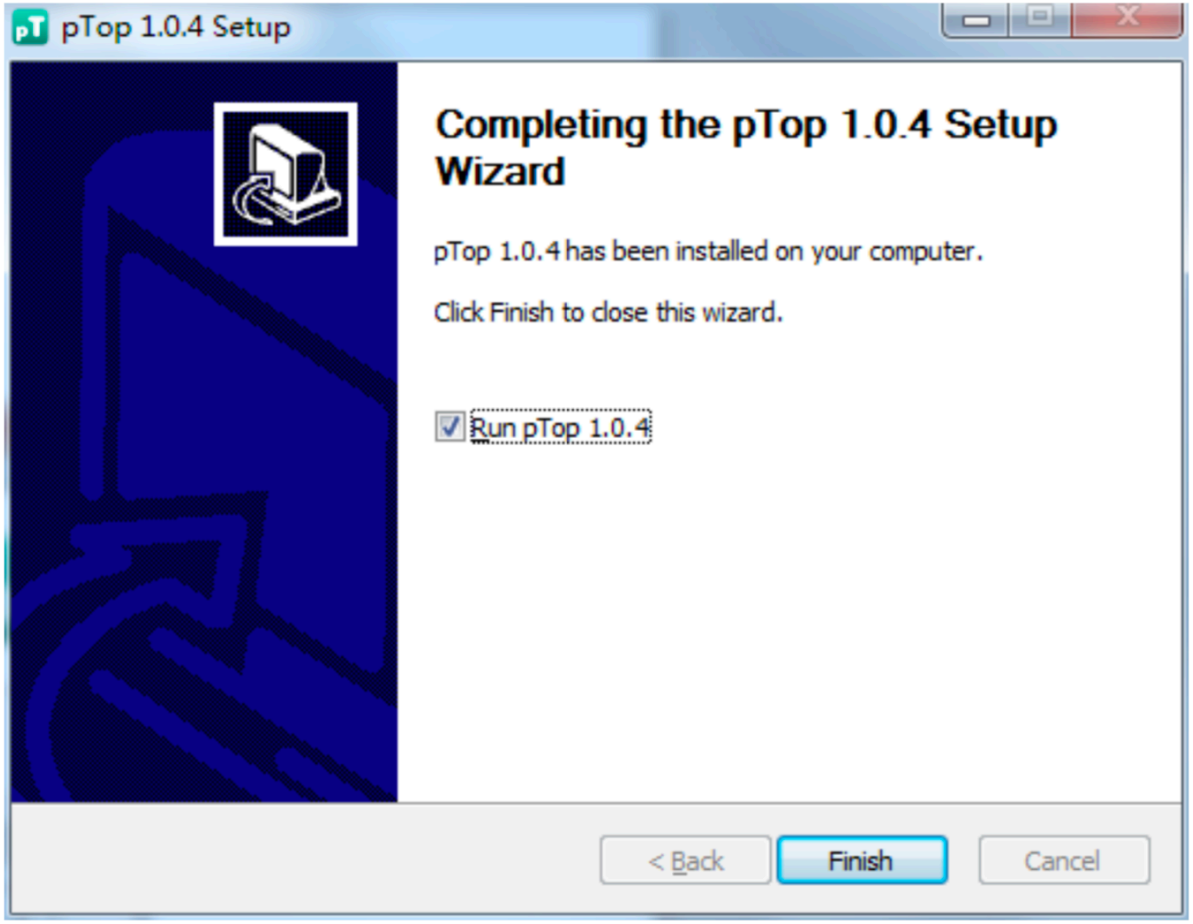
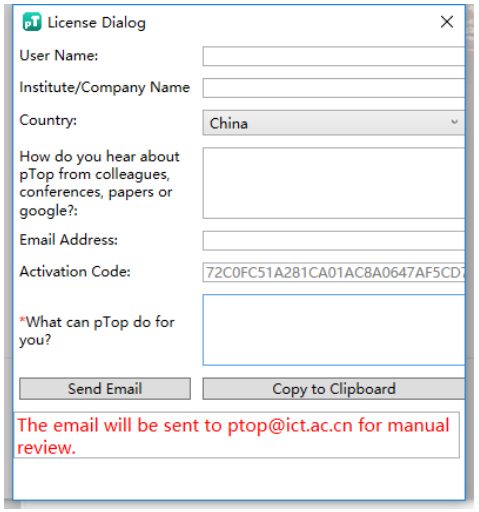


Figure 5. Installation finished

Software registration

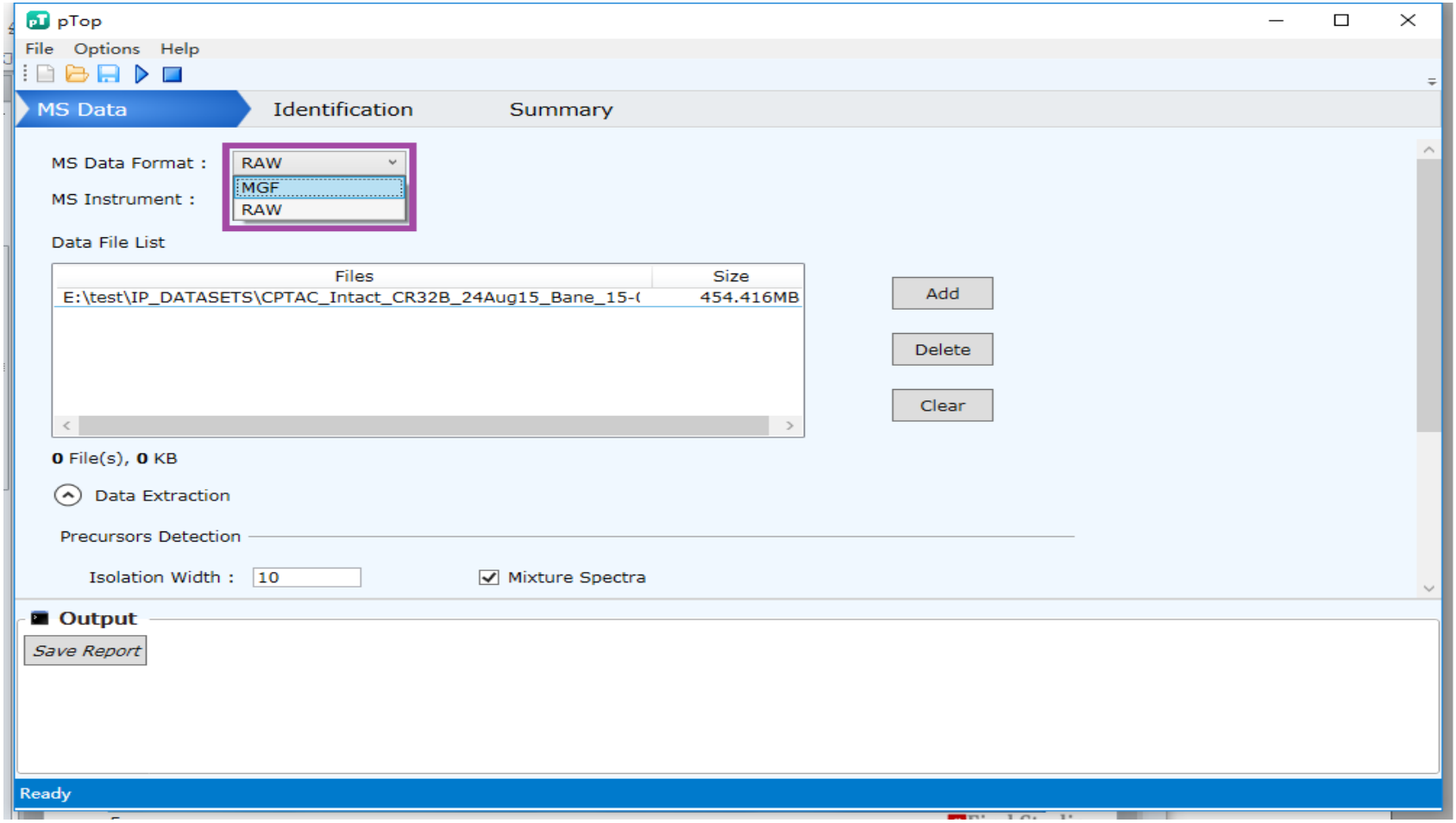
- Click pTop.exe and fill in personal information in the following information panel.



- Send the information to ptop@ict.ac.cn
- Apply for pTop.license.
- Put the pTop.license into pTop installation directory under the \pTop\bin folder.

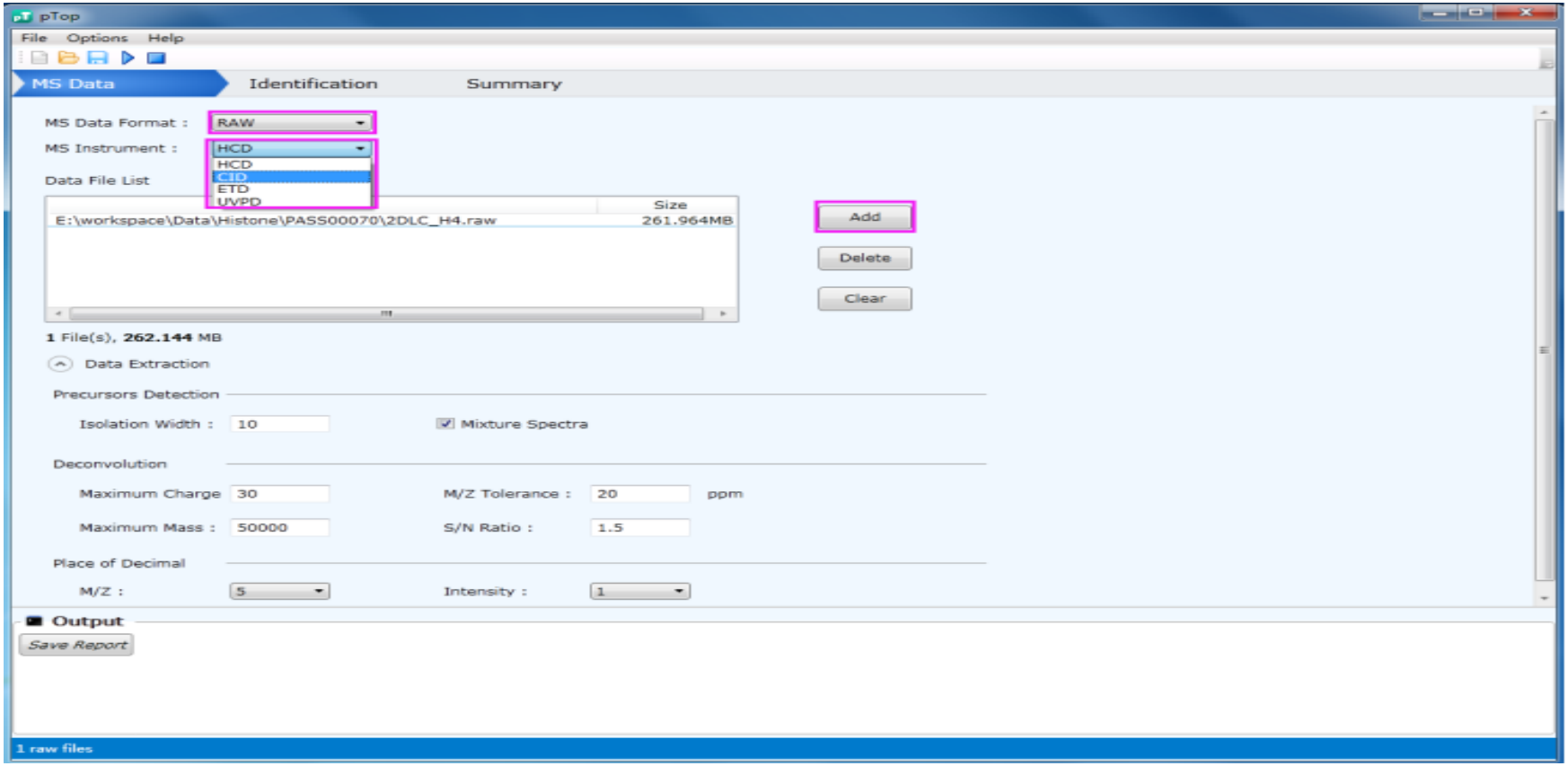
1. Data import and preprocess.

- **MS Data format: following formats are supported by pTop: RAW, MGF and PF.**



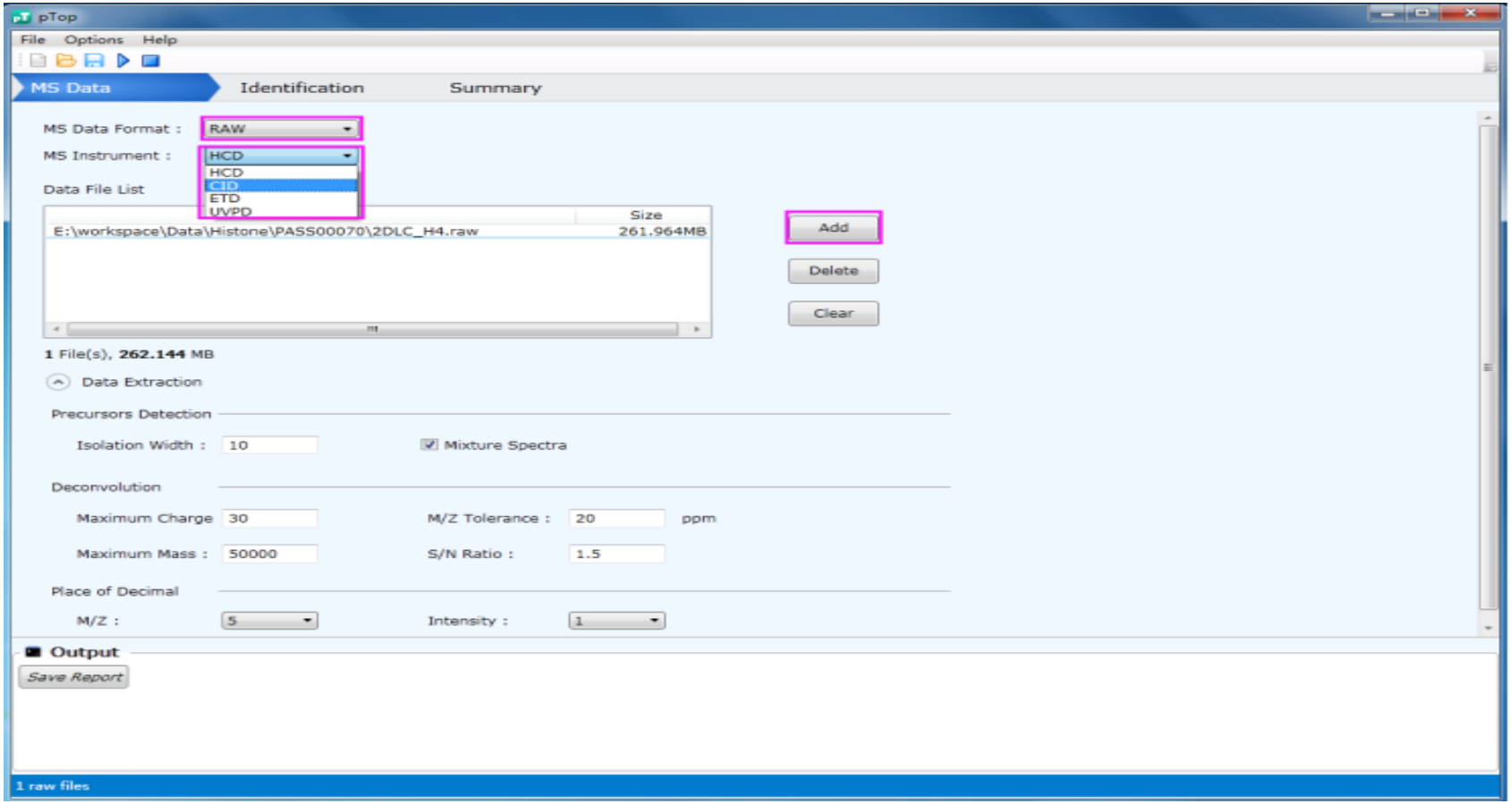
1. Data import and preprocess.

- **MS Instrument determines which fragment ion series will be used for scoring. Now HCD, CID, ETD and UVPD are supported.**



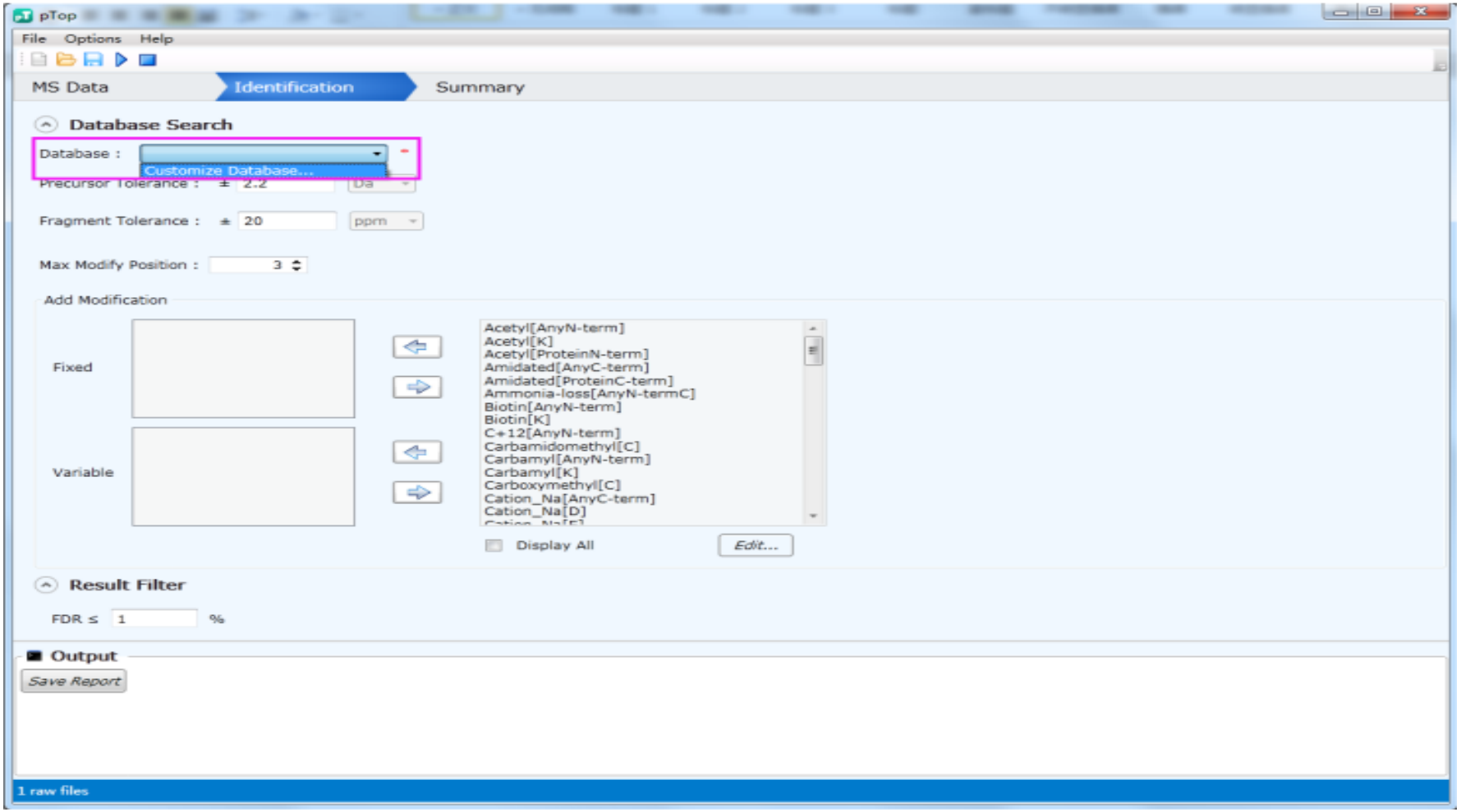
1. Data import and preprocess.

- **Click Add to put the paths of input files in the list, the path or folder containing the tandem mass spectra.**



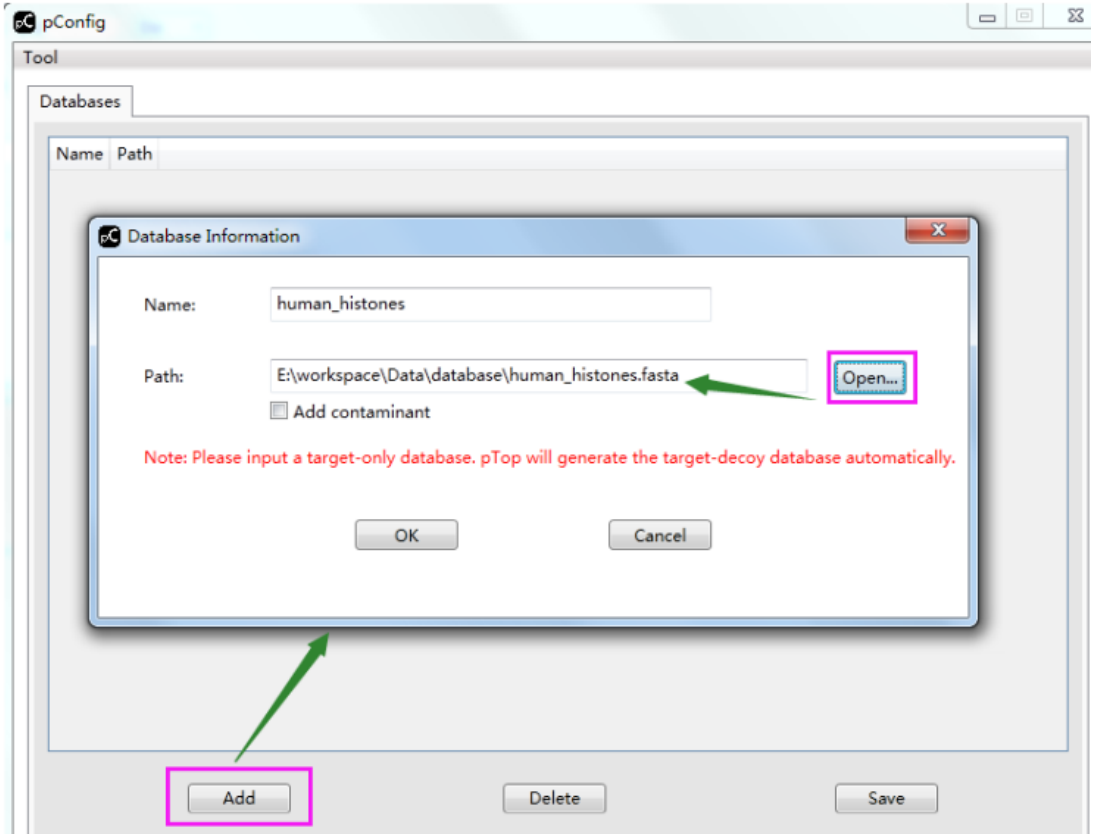
2. Set search parameters

❖ **A) Select and import database.**



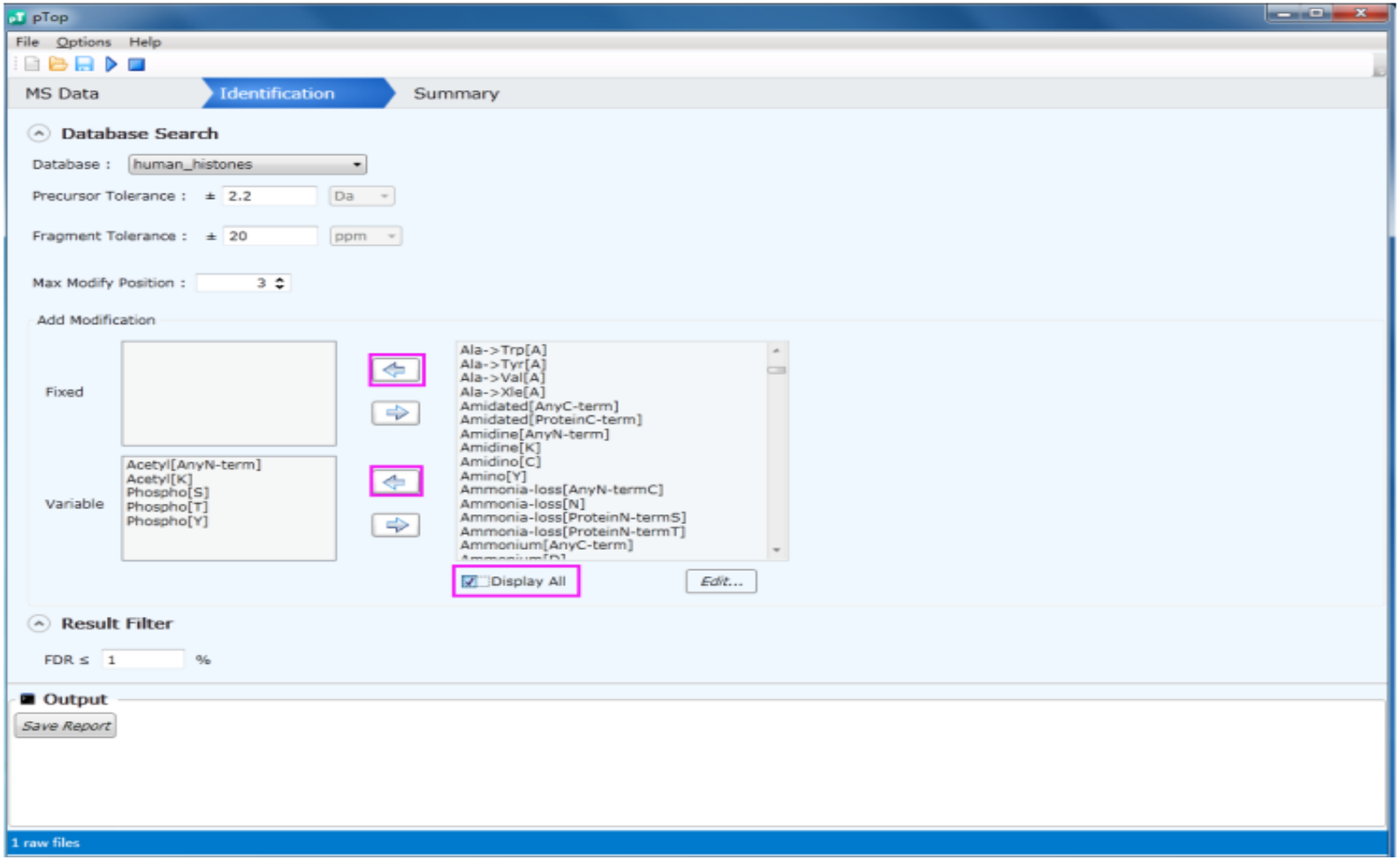
2. Set search parameters

- **A) Select and import database.**
  - **Add contaminated proteins to the database if it doesn't contain them.**



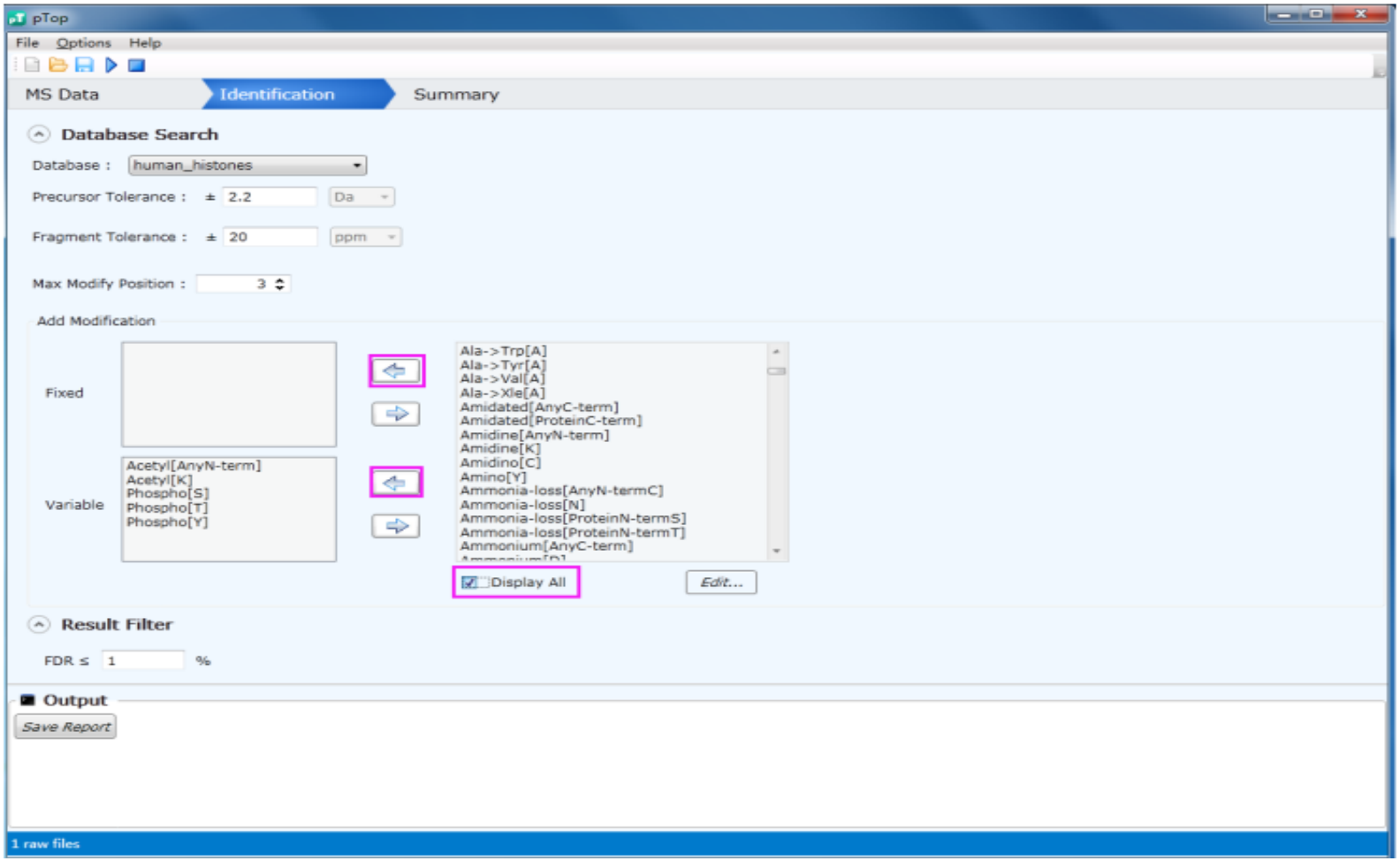
2. Set search parameters

❖ **B) Select the modifications.**



2. Set search parameters

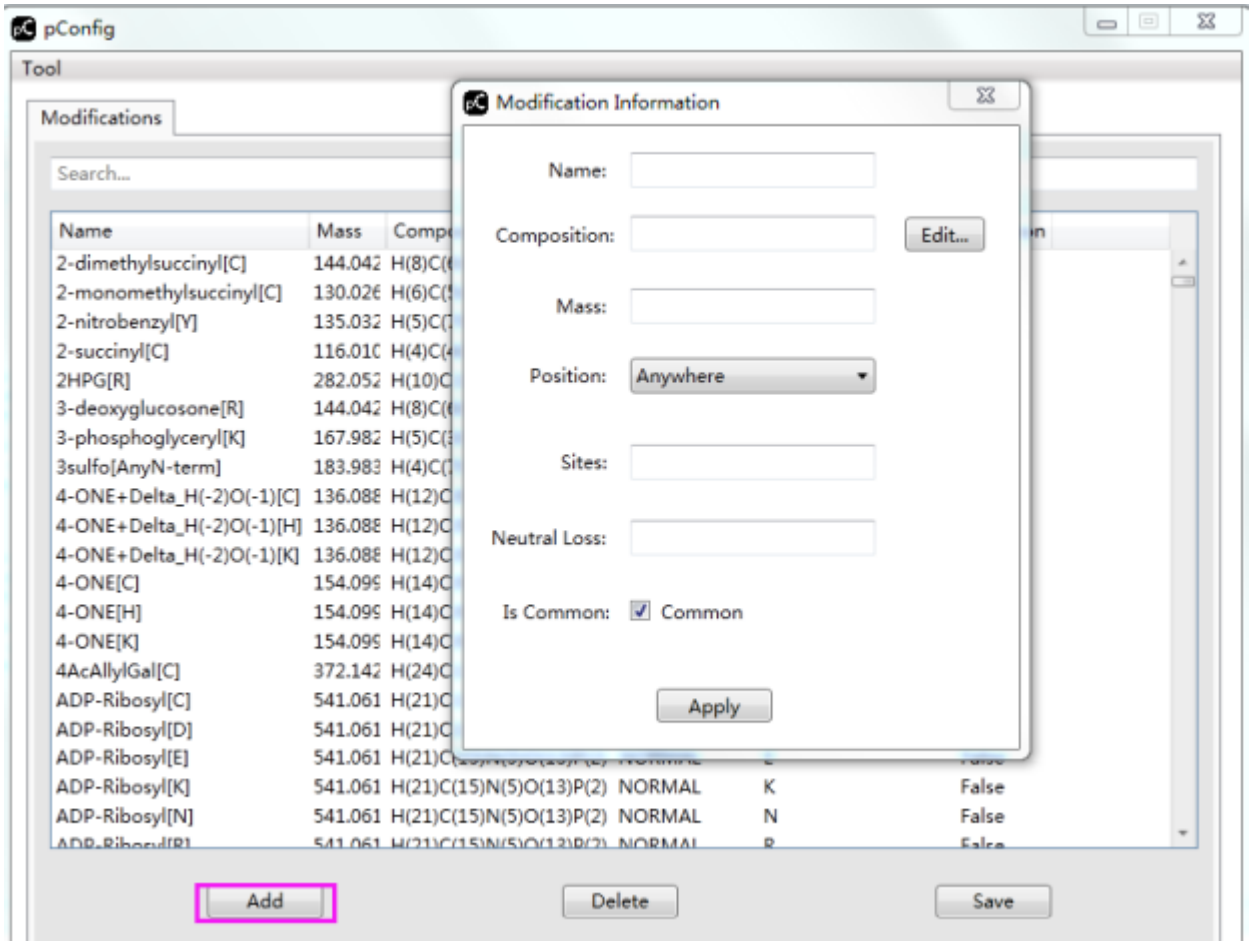
❖ **B) Select the modifications.**



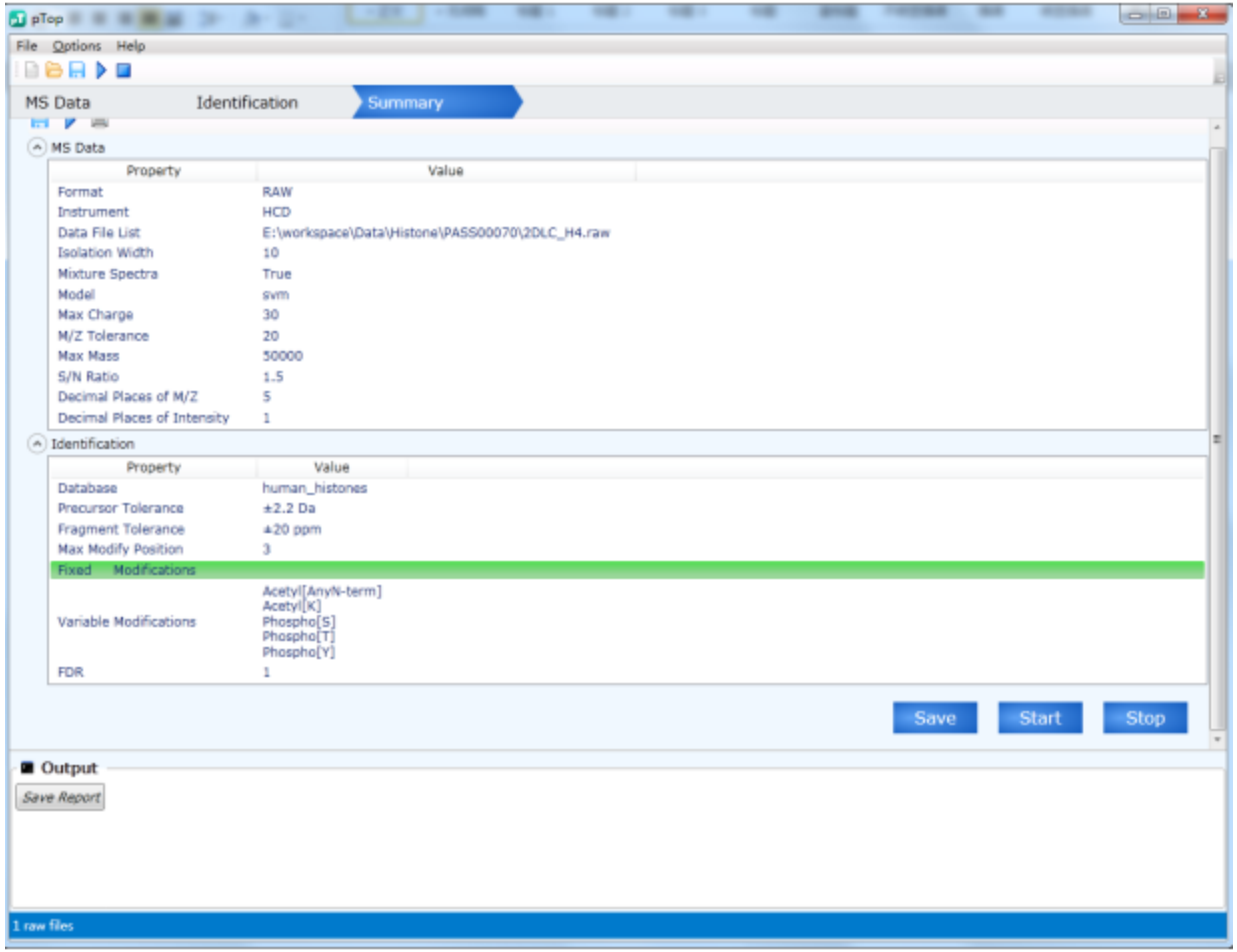
2. Set search parameters

❖ B) Select the modifications.

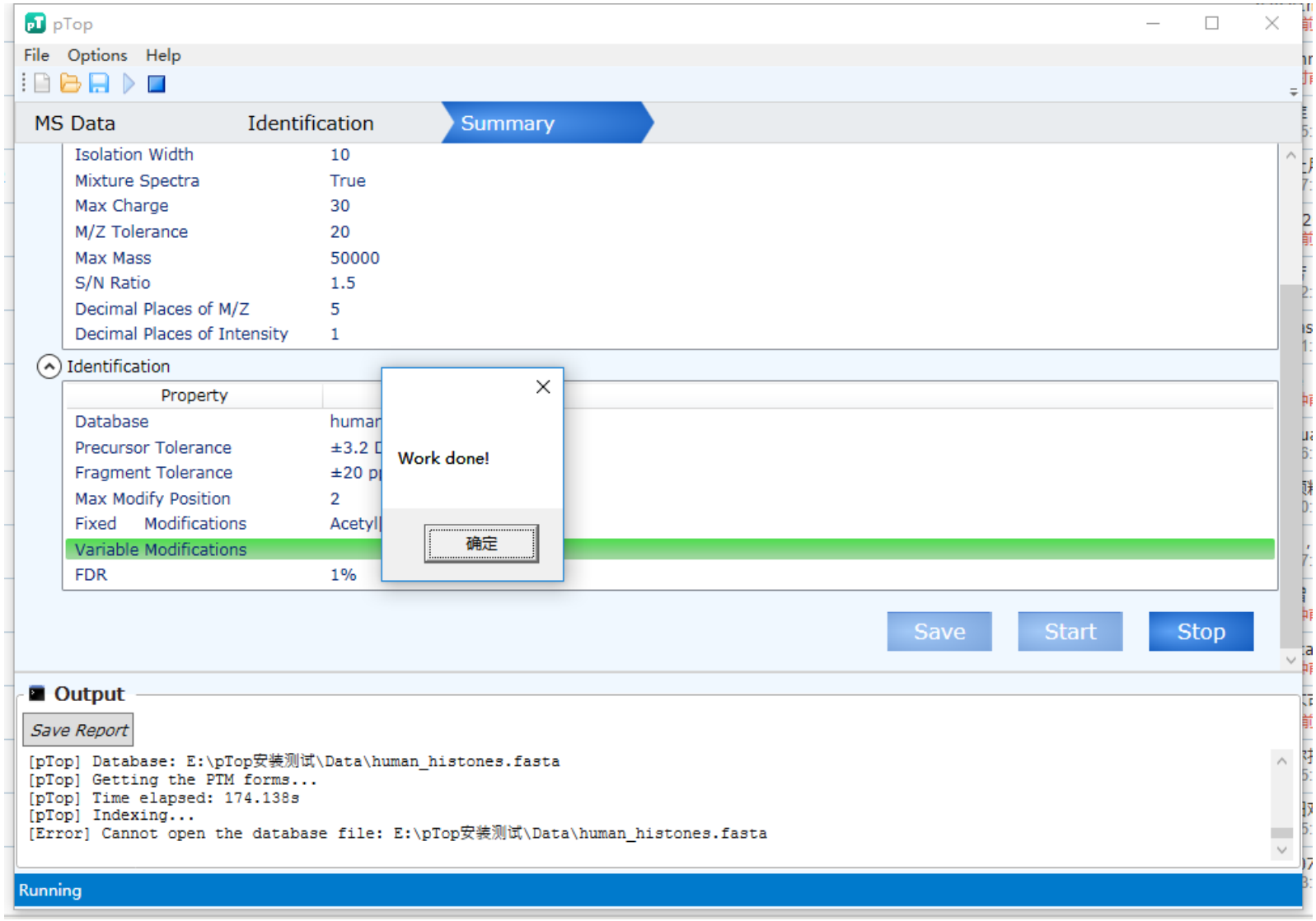
- **You can add a custom modification.**



Searching…


pTop
File Options Help
MS Data
Identification
Summary
MS Data
Property
Value
Format
RAW
Instrument
HCD
Data File List
E:\workspace\Data\Histone\PASS00070\2DLC_H4.raw
Isolation Width
10
Mixture Spectra
True
Model
svm
Max Charge
30
M/Z Tolerance
20
Max Mass
50000
S/N Ratio
1.5
Decimal Places of M/Z
5
Decimal Places of Intensity
1
Identification
Property
Value
Database
human_histones
Precursor Tolerance
±2.2 Da
Fragment Tolerance
±20 ppm
Max Modify Position
3
Fixed Modifications
Variable Modifications
Acetyl[AnyN-term]
Acetyl[K]
Phospho[S]
Phospho[T]
Phospho[Y]
FDR
1
Save
Start
Stop
Output
Save Report
1 raw files

Searching completed



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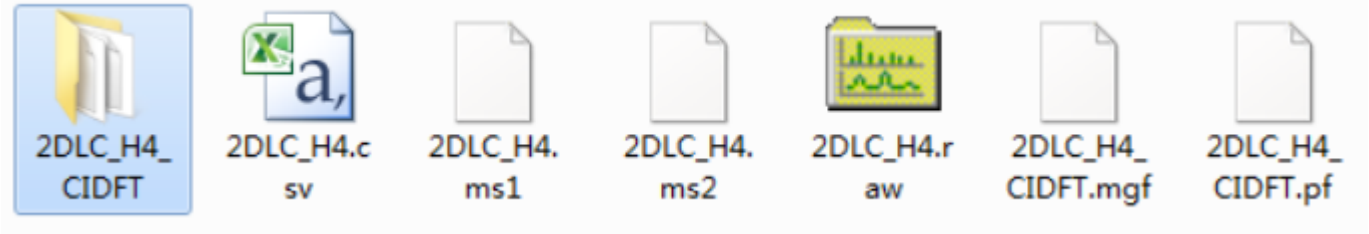
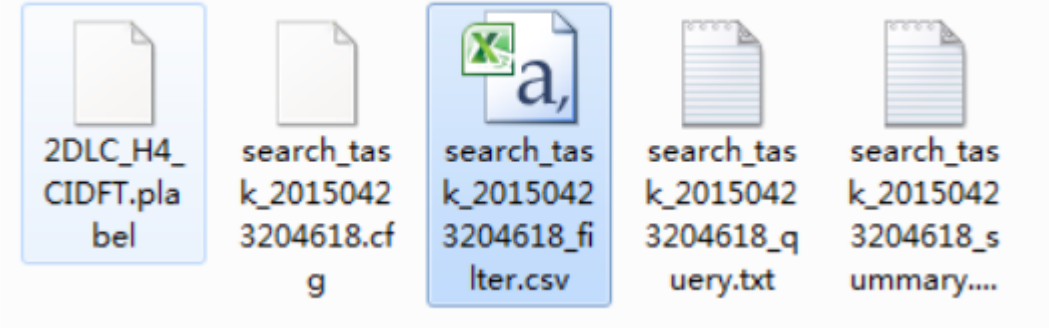
Contents of search results files

- **In the same path of the input data, you can see a folder with the same name of MGF file.**



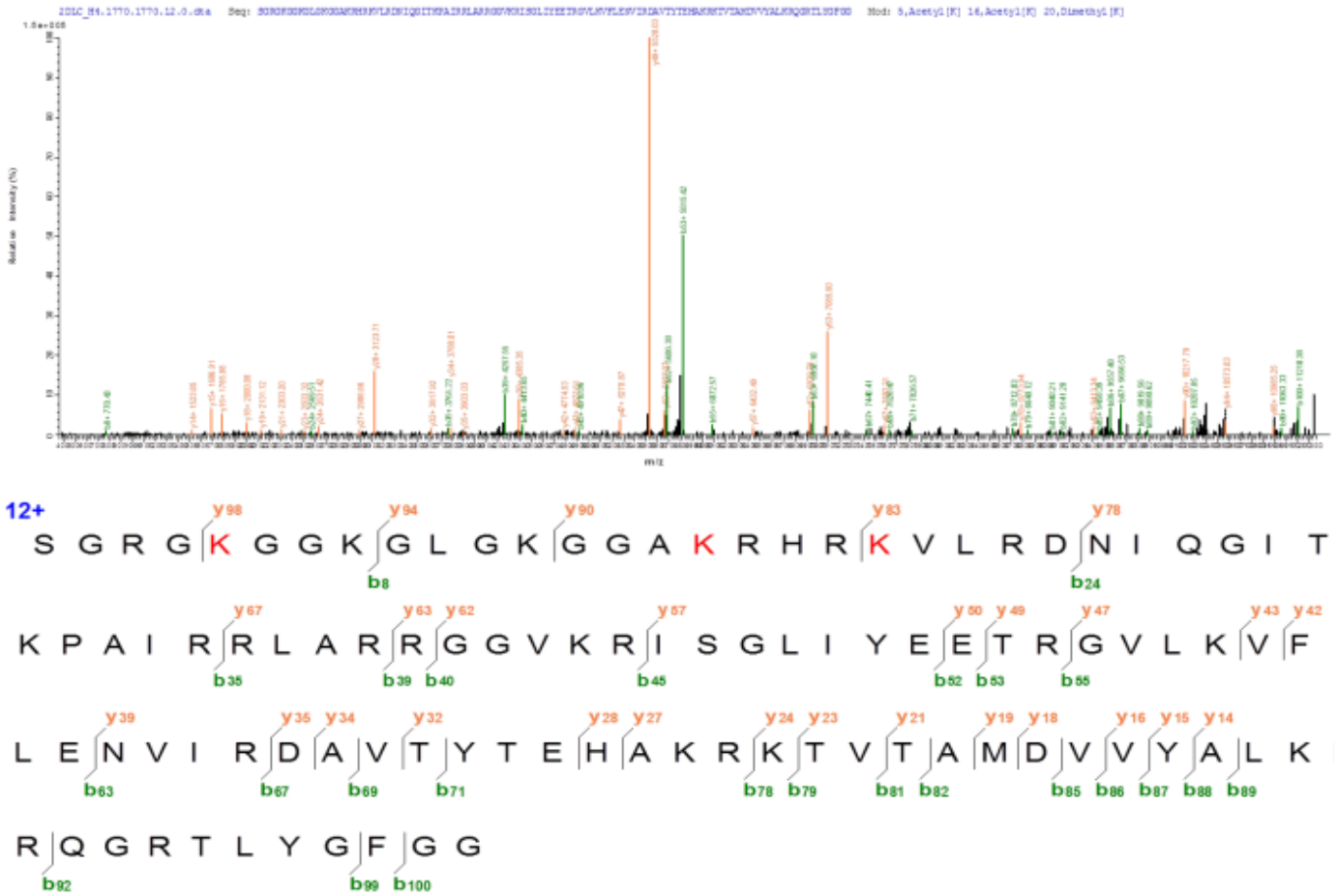
Contents of search results files

- In the folder, there are 5 files for each search. They are .plabel, .cfg, filter.csv, query.txt and summary.txt. And the finally identification reports are list in the filter.csv file.



View search results

- **pLabel: Result statistics**



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- **Thank you for using pTop 1.2!**

- **If you have any questions, please contact ptop@ict.ac.cn or rxsun@ict.ac.cn .**