After the server installation is complete, access the address http://127.0.0.1:8080/MsAlignPlus/.

TopID			н
TopiD Results			
Search Information			
Title			
Spectrum File: Choose File No	file chosen		
Database File Choose File No	file chosen		
Search Arguments			
Fragmentation Method:	FILE		
Protein N-Terminal Variable PTM:	≫ NME	☑ NME and N-Terminal Acetylation	
Parent and Fragment Mass Error Tolerance;		15	РРМ
Cysteine Protecting Group:	NONE		
Decoy:	0		
Cutoff Type:	EVALUE	•	
Cutoff Value:	0.01		
Number of Unexpected PTMs:	2	•	
Max PTM Mass:	1000000		

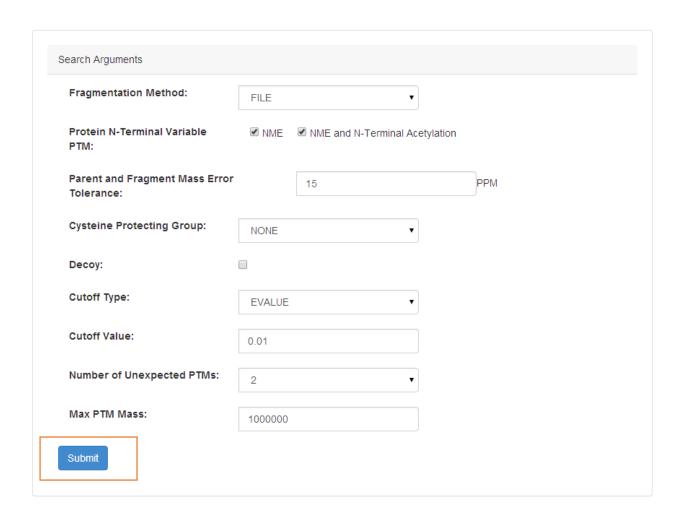
In the following text box, enter the title of the task, and it can not be empty.

Search Infomat	on			

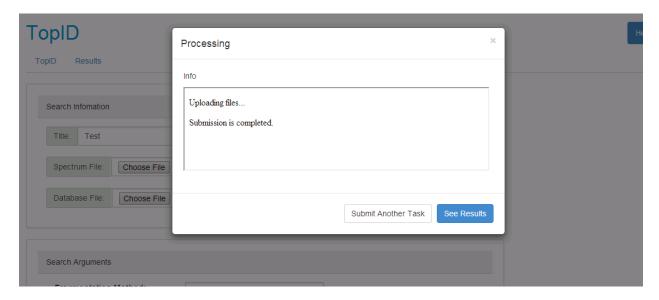
Select the input spectra file and database file in the file box whose name must be end with .msalign and .fasta:

Spectrum File:	Choose File No file chosen
Database File:	Choose File No file chosen

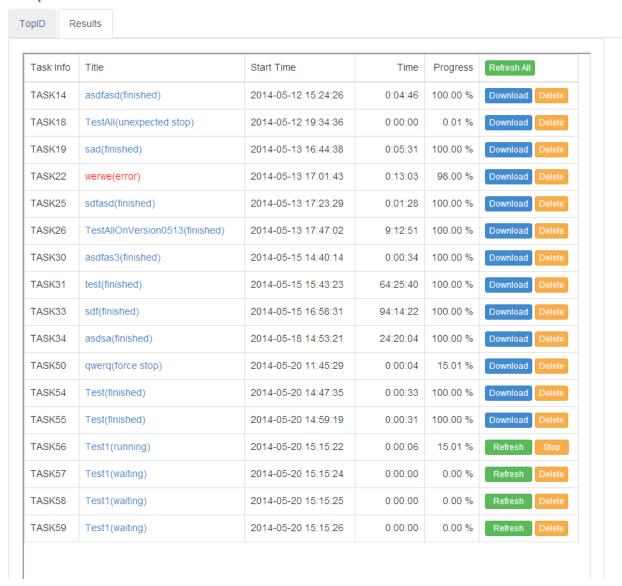
Set the arguments for the search in the following area and then click the button to submit,



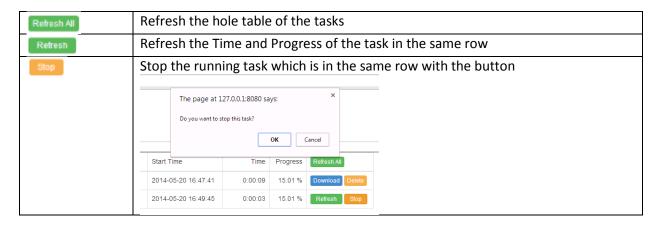
The it will show the window like the following pic if the task is submitted to the task list, Click the button "Submit Another Task" to return and submit another task or click "See Results" to show the task list.

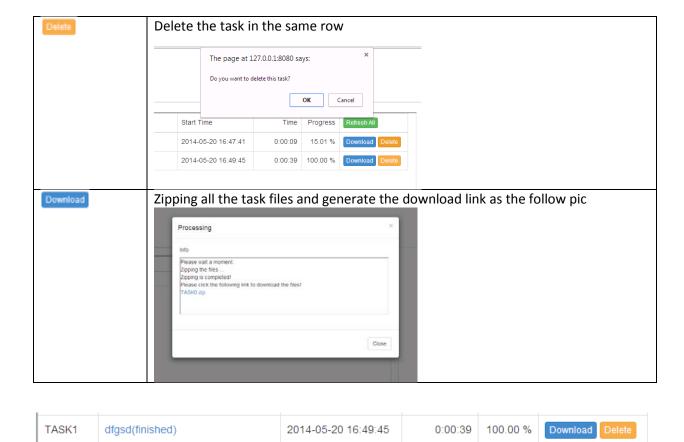


TopID



The function of these buttons in this page is :





If the title of the task ends with (finished), the link of the title would show the result page



1 proteins discovered

The titles with other states would forward to the file list in the task folder, and you can click the log .txt file to find what happened

```
/TASK0
arguments.xml
log.txt
prot.fasta
spectra.geno complete
spectra.ZERO internal
spectra.ZERO prefix
spectra.ZERO prefix
spectra.ZERO SUFFIX
TASK0.zip
```