

1. Data Source

Mascot dat Files Folder

Mascot dat files folder:
F:\target\datfiles_324

Browse

2. Agent Summary Table

Name	Active	Veto	Parameters
Delta threshold	<input checked="" type="checkbox"/>	<input type="checkbox"/>	delta : 10
Homology	<input checked="" type="checkbox"/>	<input type="checkbox"/>	NA
Length	<input checked="" type="checkbox"/>	<input type="checkbox"/>	length : 9
Modification	<input type="checkbox"/>	<input type="checkbox"/>	modification : mox
More Confident Hits	<input checked="" type="checkbox"/>	<input type="checkbox"/>	delta : 0
N Term Acetylation	<input checked="" type="checkbox"/>	<input type="checkbox"/>	NA
Proline Peak	<input checked="" type="checkbox"/>	<input type="checkbox"/>	intensity : 0.4
Protein Accession	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	accession : SHUFFLED
Reporter Ion Agent	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	error : 0.2 ratio : 1.5 reporter_mz_2 : 117.1 reporter_mz_1 : 114.1
Sequence RegExp	<input type="checkbox"/>	<input type="checkbox"/>	regular expression : .*[LI]3.*
Sim Inspects for the deviating reporter ion intensities. Selects when two reporter ions (114.1 , 117.1) have a more then 1.5 fold intesity ratio.			
Start Site	<input checked="" type="checkbox"/>	<input type="checkbox"/>	low : 2 high : 200
SubSequence	<input type="checkbox"/>	<input type="checkbox"/>	Subsequence : TESTPEPTIDE
Suspect Residue	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	sites : R;H
b-ion coverage	<input checked="" type="checkbox"/>	<input type="checkbox"/>	percentage : 0.30
y-ion coverage	<input checked="" type="checkbox"/>	<input type="checkbox"/>	percentage : 0.30

Load Agents

Save Agents

Clear

3. AgentAggregator Selection Table

Best Hit Agent Aggregator

Info

Properties Table

Name	Value
Theshold Score	2

Confidence