

# Mascot tips & tricks

**MASCOT**



## Mascot tips & tricks

1. Automatic exporting of search results
2. Mascot Distiller Viewer
3. Clear out cache files periodically
4. Moving Mascot Server to a new computer
5. Running Mascot Daemon on desktop
6. Turning off summing of scans in Mascot Distiller
7. Use of Virtual Machines for Mascot Servers
8. Site analysis added to export
9. NCBIInr on 32-bit computers
10. Combining CID and ETD data in a single search
11. Webcast training

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013



I am going to cover a mixture of 10 topics today. Some are questions that come up regularly in technical support conversations. There are a couple of new features that I'm going to introduce and, as a bonus feature, I am going to tell you about our online training course.

So lets get started with the first topic, Automatic exporting of search results

## 1. Automatic exporting of search results

### On the fly with

- Mascot Daemon's external tasks

### Export a large set of existing results

- Using a script or a batch file

There are two main ways that you can automate the exporting of search results and I am going to cover two of them.

The first method is designed to export the results immediately after the search has been completed. Either on the computer where Mascot Daemon is installed or on the Mascot Server.

The second method is for exporting a batch of existing search results on the Mascot Server.

## Build an export command line

1. Read the export script help page
  - [http://www.matrixscience.com/help/export\\_help.html](http://www.matrixscience.com/help/export_help.html)
2. Experiment with one result file in the web browser.
3. Record the command line arguments and test.
4. Compare.

Before we can automate the exporting of results we need to determine which format we are going to export too and which fields we are going to export.

I recommend reading the export functions help page to get a better idea of how it works particularly the command line section. Then, experiment with a result file to make sure that all the information you need is included in the output. Record the command line arguments and try running the export on the command line. Compare the exported files from step 2 and 3 to make sure you have all the arguments set correctly.

If that works then you can take the command line arguments and use them in an automated export.

## Build an export command line

In Mascot Server version 2.3 we added a button to display the command line arguments.



### Command line arguments equivalent to current form settings

```
_minpeplen=7 _server_mudpit_switch=999999999 _sigthreshold=0.05 do_export=1
export_format=XML file=./data/F981123.dat pep_calc_mr=1 pep_delta=1 pep_exp_mr=1
pep_exp_mz=1 pep_exp_z=1 pep_expect=1 pep_isbold=1 pep_isunique=1 pep_miss=1
pep_query=1 pep_rank=1 pep_scan_title=1 pep_score=1 pep_seq=1 pep_var_mod=1
peptide_master=1 prot_acc=1 prot_desc=1 prot_hit_num=1 prot_mass=1 prot_matches=1
prot_score=1 protein_master=1 search_master=1 sessionid=richard_222484722070586
show_format=1 show_header=1 show_mods=1 show_params=1
```

Add `export_dat_2.pl` to the beginning of the options and redirect the output to a file with `> ./data/F981123.xml`

**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



It is quite easy to make a mistake and miss out an important argument when you build the list of command line arguments by hand. Because of this we introduced the option to view the command line arguments for an export in Mascot Server 2.3.

To test these arguments add `export_dat_2.pl` to the beginning of the options and redirect the output to a file with the greater than sign

## Build an export command line

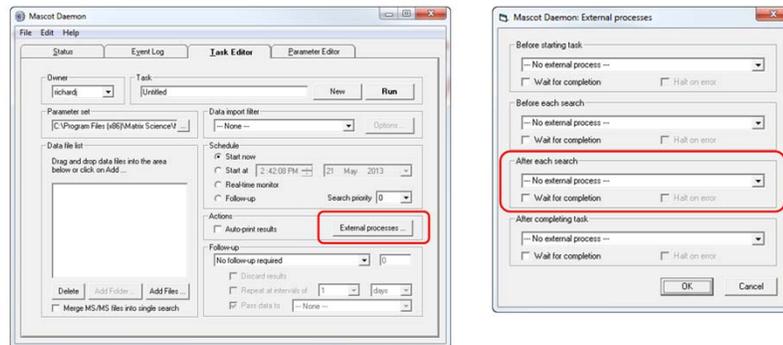
The command line script can output html when called by a CGI process.

Add the following argument to prevent this:

- `generate_file=1`

Here is a top tip: The script should not output the HTML for the interactive download button when executed, but this can happen if it is called from a CGI process. Add the `generate_file=1` argument to prevent this

## Automatic exporting through Mascot Daemon's external tasks



**You will need ActivePerl installed on the Mascot Daemon computer.**

**MASCOT** : Mascot tips & tricks

© Matrix Science 2013

**MATRIX  
SCIENCE**

Let's look at the first method to automate the exports, from the Mascot Daemon external processes.

Mascot Daemon can run an external script or program at a number of different times while processing a task. The most useful time is after each search.

Click on the external processes button and press F1 while the dialog is displayed to find out more information about the external processes feature.

I normally use the Perl programming language for small script and programming tasks but you can use any programming language as long as it accepts command line arguments. If you are going to use Perl then you will need to install ActivePerl from ActiveState on the Mascot Daemon computer.

## Automatic exporting through Mascot Daemon's external tasks

### Preconfigured script

- Set export parameters and format
- Set export location on Mascot Daemon computer

### Set security login credentials

Takes about 100 to 150 lines of code.

Add any custom processing or file renaming

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013



The script or program will contact the Mascot Server through the web interface and it has to be preconfigured with the export arguments and format that you have previously worked out along with a location of where to save the resulting files.

When it runs it needs to know how to handle any Mascot Server or website security that is in place,

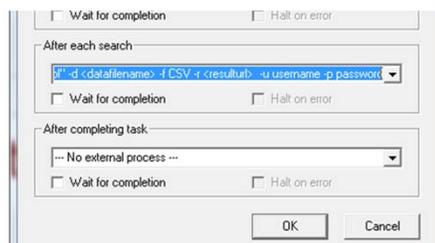
All that can be done in about 100 or so lines of code. We have an example Perl script that you can use as a starting point.

You can also add additional features to the script or program that automate other tasks you normally perform on results such as file renaming and extracting pieces of information for reports.

## Automatic exporting through Mascot Daemon's external tasks

### Configure Mascot Daemon to call the export script

- `perl "C:/Temp/DaemonCGIExport.pl" -d <datafilename> -f CSV -r <resulturl> -u username -p password`



**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



Here I am going to show how to call this script. In the Mascot Daemon external processes dialog box, I fill in the After each search field. There is a character limit on the field so don't make the options too long.

Mascot Daemon supports the use of tokens that are replaced with the actual information at run time. Here I pass the input data file name and the result url to the script along with a user name and password for Mascot security.

When Mascot Daemon runs this command will be run for each search exporting the results to a location of my choosing.

Previous commands can be displayed in the drop down box by Daemon so that they can easily be selected and used again with a new Daemon task.

## Export a large number of old results

### Export with a script or a simple excel sheet.

- Select export conditions
- Build a list of files to export  
file=../data/20060906/F007842.dat
- Use Excel calculations to create a url

The second method of exporting search results is best suited to exporting a batch of results

As before, select the command line arguments for the export. The next step is to build a list in Excel of all the search results we want to export. For example in Mascot Daemon, browse through the result files you want to export. For each one, click on the result link to load the result report in a browser. Copy the last bit of the URL from the browser into Excel, one URL on each row. For example

```
file=../data/20060906/F007842.dat
```

Paste this piece into Excel so that we can create a final URL for the export

	A	B	C	D	E	F	G	H	I	J
1	file=../data/20060906/F007842	file=..	data	20060906	F007842	dat	export_dat_2 pl do_export=1 export_format=XML	report=0 show_format=1 show_header=1 show_params=1 show_mods=1 protein_master=1 prot_acc=1 prot_desc=1 prot_hit_num=1 prot_mass=1 peptide_master=1 pep_exp_mr=1 pep_exp_z=1 pep_calc_mr=1 pep_delta=1 pep_start=1 pep_end=1 pep_miss=1 pep_score=1 pep_expect=1 pep_rank=1 pep_seq=1 pep_var_mod=1	export_dat_2 pl do_export=1 export_format=XML file=../data/20060906/F007842 .dat report=0 show_format=1 show_header=1 show_params=1 show_mods=1 protein_master=1 prot_acc=1 prot_desc=1 prot_hit_num=1 prot_mass=1 peptide_master=1 pep_exp_mr=1 pep_exp_z=1 pep_calc_mr=1 pep_delta=1 pep_start=1 pep_end=1 pep_miss=1 pep_score=1 pep_expect=1 pep_rank=1 pep_seq=1 pep_var_mod=1 > F007842.xml	
	file=../data/20060906/F007843	file=..	data	20060906	F007843	dat	export_dat_2 pl do_export=1 export_format=XML	report=0 show_format=1 show_header=1 show_params=1 show_mods=1 protein_master=1 prot_acc=1 prot_desc=1 prot_hit_num=1 prot_mass=1 peptide_master=1 pep_exp_mr=1 pep_exp_z=1 pep_calc_mr=1 pep_delta=1 pep_start=1 pep_end=1 pep_miss=1 pep_score=1 pep_expect=1 pep_rank=1	export_dat_2 pl do_export=1 export_format=XML file=../data/20060906/F007843 .dat report=0 show_format=1 show_header=1 show_params=1 show_mods=1 protein_master=1 prot_acc=1 prot_desc=1 prot_hit_num=1 prot_mass=1 peptide_master=1 pep_exp_mr=1 pep_exp_z=1 pep_calc_mr=1 pep_delta=1	

**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



I have broken up the result file path so that the filename can be used to construct the output path. I create the final command line by concatenating the arguments and file paths. Copy the command line column.

## Export a large number of old results

### Export with a script or a simple Excel sheet.

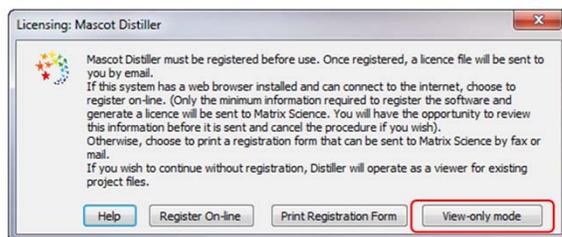
- Select export conditions
- Build a list of files to export
- Use Excel calculations to create a URL
- Copy completed command lines and paste into a text editor
- Save the file in the Mascot cgi folder as mascot\_export.bat
- Execute mascot\_export.bat

And past it into a text file. Save the file in the Mascot cgi folder as mascot\_export.bat. Then, execute the batch file and each of the individual files will be exported in turn and saved to disk.

This is a great way to export hundreds of files from a project in one go.

## 2. Sharing results with Mascot Distiller viewer

**Mascot Distiller can be installed on any computer without a license and used as a viewer**



**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



One often overlooked feature of Mascot Distiller is the read only mode that allows collaborators to view search and quantitation results.

Mascot Distiller can be installed on any computer and, if it is not licensed, view only mode can be activated.

## Sharing results with Mascot Distiller viewer

**For best results you need the search toolbox.  
Share the raw MS data and the Distiller .rov files.**

**The end user can examine the data in greater depth than with a web report.**

- Core labs
- Quantitation
- PTM's

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013

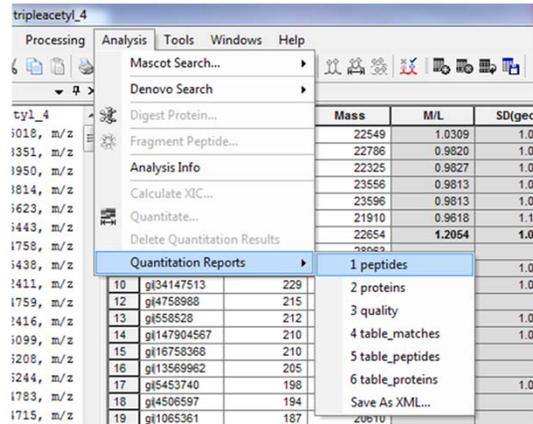


The licensed copy of Distiller used to create the project needs to include the search toolbox so that search results can be imported and saved.

You need to make both the raw MS data and the Mascot Distiller rov file available to the end user. Collaborators do not need access to the Mascot Server as everything is stored in the rov file.

With these files the end user can examine the data in greater depth than by looking at the web-based report. This is particularly useful for core labs distributing results involving quantitation or when you want to inspect hits that are evidence for PTM's

You can still save reports and copy text and images from the file but not change them.



**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



When a project is opened in the read only view mode features that can not be used are grayed out. If you were to look in the Mascot Search and de novo menus all the options would be grayed out and inactive.

You can export quantitation results, as shown here, but not change any of the processing parameters or format options.

### 3. Clear out cache files periodically

#### Mascot Server 2.3 and up caches search results in the data directory

- Windows: C:\inetpub\mascot\data\cache
- Linux: /usr/local/mascot/data/cache

Over time this cache can grow very large

Safe to delete older files

The cache files are recreated as needed

In Mascot Server 2.3 we adding a caching feature to Mascot Server. This makes it a lot quicker to view the search results once the cache has been created. Combined with the protein family report it allows you to view large result sets produced by today's MS instrumentation. However the cache files will grow with time and are a bout a third of the size of the raw results files.

It is safe to delete older cache directories to free up disk space. If you open one of the older reports at a later data the cache files will be recreated.

## 4. Migrating Mascot Server to a new computer

As part of an update or upgrade you may also want to move the Mascot Server to a new computer.

There is a new help page that covers six different scenarios:

- <http://www.matrixscience.com/help/upgrading.html>

There is a new help page that covers six different scenarios: moving, updating, upgrading, or combinations of moving updating and upgrading

If you want to make a trial installation, do not register using your permanent Mascot 2.4 product key. Instead email Matrix Science to request a temporary license key

## Migrating Mascot Server to a new computer

1. Updating Mascot Server to version 2.4 on the current hardware
2. As 1 while migrating to new hardware
3. Upgrading Mascot Server to use additional processors on the current hardware
4. As 3 while migrating to new hardware
5. Converting from a stand alone Mascot Server to a cluster using the current hardware
6. Adding search nodes to an existing cluster

The different scenarios are as follows:

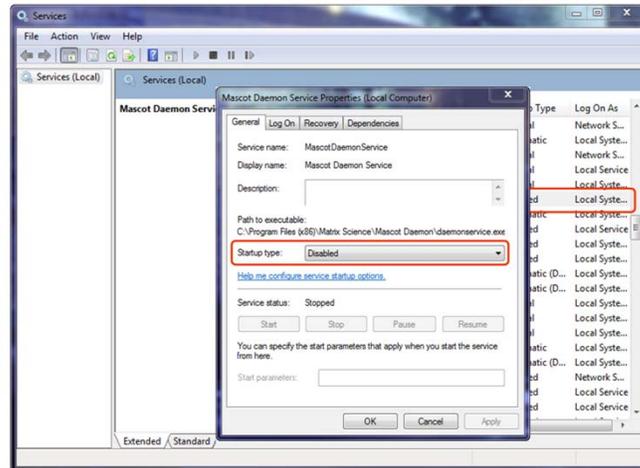
## 5. Running Mascot Daemon on desktop

**Mascot Daemon can be used to batch automate quantitation of individual files**  
**Run Mascot Distiller on the desktop or it may run out of resources**  
**Select the resulting Distiller .rov files in a multi-file project to quickly create large quantitation data sets.**

If you are using Daemon to batch automate Distiller quantitation, you need to run the Daemon service component on the Windows desktop, in the system tray. Otherwise, it may run out of resources. This is particularly important for datasets that used with Mascot Distiller multi-file quantitation.

Batch processing individual files in Daemon is efficient because each project then contains the individual search and quantitation results. To create a multi-file project, select the individual project files in Distiller. This is much faster than creating a multi-file project from the raw files.

## Running Mascot Daemon on desktop



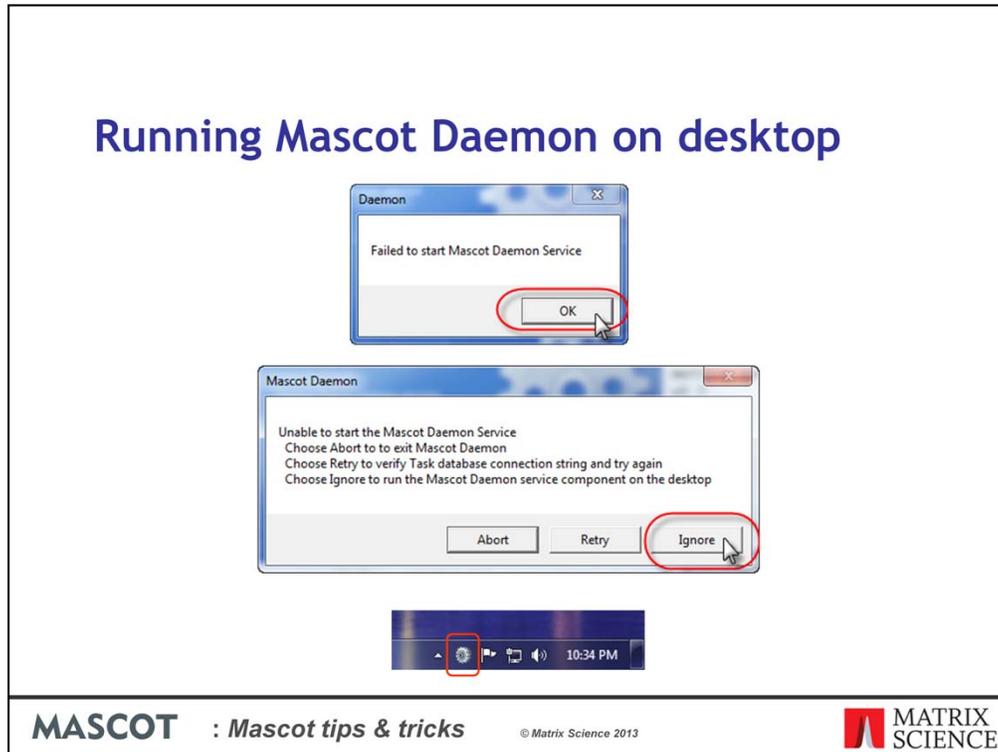
**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



To change the settings for Mascot Distiller go to the Start menu->Settings->Control panels->Administrative tools->Services panel and double click the Mascot Daemon service. Set startup type to Disabled and save the changes.

## Running Mascot Daemon on desktop



When you restart Mascot Daemon it will report that it has failed to start the Mascot Daemon service. Click Ok.

And then choose Ignore to run the Mascot Daemon service from the desktop. You will then see the Mascot Daemon cog icon in the taskbar notification area.

There are two points to note about the change:

Mascot Daemon Service is now running in your user account and will be able to access any network drives that you can normally access making it easy to search data from remote computers.

When you log out of the computer, Mascot Daemon will stop in the middle of what it is doing but will continue a task when restarted.

## 6. How to turn off summing of scans in Mascot Distiller

**Most default .opt file automatically sum scans.**

**For quantitation it is advisable to turn off summing.**

**When analyzing mixed CID/ETD data turn off summing.**

**When analyzing CID/HCD data you might want to keep it turned on.**

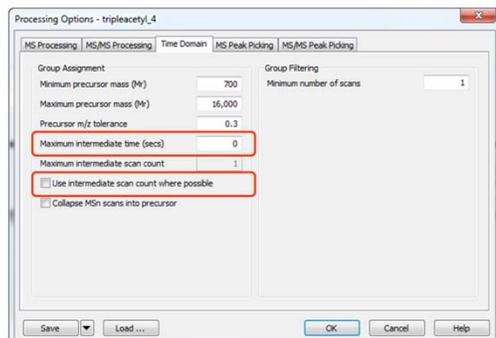
Most of the default processing options or .opt files that ship with Mascot Distiller have scan summing turned on. In some cases, this can improve signal to noise and result in higher scoring matches.

There are other cases where you will want to make sure scan summing is turned off. For example, when analyzing data sets containing alternate CID/ETD.

Alternatively, you might want to keep summing turned on for alternate CID and HCD data.

## How to turn off summing of scans in Mascot Distiller

- Set the maximum intermediate time to 0
- Uncheck the "Use intermediate scan count where possible" check box



**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



You can turn off summing in the Mascot Distiller processing options in the Time Domain tab by Setting Maximum intermediate time (sec) to zero and unchecking the Use intermediate scan count where possible box. Save the changes and use the options to process the data.

## 7. Using Virtual Machines as hosts for Mascot Servers

**We use VM's for testing purposes but we don't advise using them for production systems.**

**The Mascot end user license is for a single installation.**

**A VM has the same hardware requirements as a normal system.**

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013



Questions about running Mascot in a virtual machine are coming up quite a lot in technical support.

At Matrix Science, we use VM's for testing purposes, particularly when testing a new version of the server on different operating systems. However we do not recommend their use for production environments.

The Mascot Server end user license is for a single instance of the software, whether in a VM or in the host OS. If you use a VM you are only licensed to run one instance at a time. The Mascot Server software is locked to the underlying hardware so moving the VM to another host will mean that you need to reregister the license again.

One important thing to remember is that the Mascot Server VM will have the same requirements as a non-VM system. The Mascot Server web site has a help page on PC Hardware for Mascot Servers

## Using Virtual Machines as hosts for Mascot Servers

**By using a VM you are adding an extra layer of software and complexity between the application and the hardware**

**The VM host maybe hosting more than one VM**

**The VM host may have less CPU's and resources than your Mascot Server license**

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013

**MATRIX  
SCIENCE**

One of the reasons why we don't recommend using VM's is because it adds an extra layer of software and complexity between the application and the hardware. This may degrade performance.

The VM host may be running multiple VM's all sharing the same resources. This means that you may be sharing the CPU time with other applications.

It is quite possible to configure a VM to have 2 quad core CPU's, which would be suitable for a 2 CPU Mascot Server license, but then run that image on a computer with fewer cores. This means that your Mascot Server looks like it has suitable hardware but the performance will be less than you might expect.

In general the Mascot Server software license is more expensive than the computer hardware up to about 8 CPU's and if you wish to obtain maximum bang for your buck dedicated hardware is the way to go.

## 7. Exporting Site analysis results

Introduced with Mascot Server version 2.4.0  
in the peptide\_view

Score	Mr(calc)	Delta	Sequence	Site Analysis
83.4	1846.7179	0.1889	DIGSESTEDQAMEDIK	Phospho S4 84.56%
75.8	1846.7179	0.1889	DIGSESTEDQAMEDIK	Phospho S6 14.73%
62.7	1846.7179	0.1889	DIGSESTEDQAMEDIK	Phospho T7 0.72%
26.9	1846.7808	0.1261	KLNSNPENYCESELK	
22.8	1846.7729	0.1339	KMEDSVGCLETAEEVK	
15.5	1846.9230	-0.0161	GAYTIEQHPVLGLEIK	
14.2	1846.7729	0.1339	KMEDSVGCLETAEEVK	
13.9	1846.8754	0.0315	YVKGIYENLPSIDEK	
13.8	1846.8866	0.0202	QLIEAPDPVPSFEVAR	
13.3	1846.9052	0.0016	KIDFSNIAMLFGGVQK	

MASCOT : Title



Site analysis was introduced in Mascot Server 2.4 in the Peptide View report and is based on the score differences between matches with different arrangements of modifications as shown here in this example.

Originally, this information could not be exported, but this has been fixed in Mascot 2.4.1.

## Exporting Site analysis results

### Mascot Server 2.4.01 enables exporting of the site analysis results

unassigned queries  
(peptide matches not assigned to protein hits)

**Query Level Information**

Query title

seq(), comp(), tag(), etc.

Query level search parameters

MS/MS Peak lists

**Raw peptide match data**

Show command line arguments    Export search results

**MASCOT** : Title



To include site analysis, the export needs to include the top ten matches for each query. We have to include the following arguments:

- Query level information
- Raw peptide match data

## Exporting Site analysis results

Export site analysis results to XML, CSV and mzIdentML

CSV in the pep\_var\_mod\_conf column in the last section of the report

pep_score	pep_seq	pep_var_mod	pep_var_mod_pos	pep_var_mod_conf	pep_scan_title
67.78	DGARPDRVTESESGSPEYR	Methyl (DE) [+14.02]	0.000000000X0000000.0	22.20%	29: Sum of 8 sca
66.1	DGARPDRVTESESGSPEYR	Methyl (S) [+14.02]	0.000000000X0000000.0	15.08%	29: Sum of 8 sca
66.1	DGARPDRVTESESGSPEYR	Ser->Thr (S) [+14.02]	0.000000000X0000000.0	15.08%	29: Sum of 8 sca
65.09	DGARPDRVTESESGSPEYR	Methyl (S) [+14.02]	0.000000000X0000000.0	11.95%	29: Sum of 8 sca
65.09	DGARPDRVTESESGSPEYR	Ser->Thr (S) [+14.02]	0.000000000X0000000.0	11.95%	29: Sum of 8 sca
64.2	DGARPDRVTESESGSPEYR	Methyl (DE) [+14.02]	0.000000000X0000000.0	9.73%	29: Sum of 8 sca
64.15	DGARPDRVTESESGSPEYR	Methyl (T) [+14.02]	0.0000000X000000000.0	9.62%	29: Sum of 8 sca
64.15	DGARPDRVTESESGSPEYR	Thr->Asp (T) [+13.98]	0.0000000X000000000.0		29: Sum of 8 sca
57.74	DGARPDRVTESESGSPEYR	Methyl (S) [+14.02]	0.0000000000000X0000.0	2.20%	29: Sum of 8 sca
57.74	DGARPDRVTESESGSPEYR	Ser->Thr (S) [+14.02]	0.0000000000000X0000.0	2.20%	29: Sum of 8 sca
11.31	GEMAYVVSVDGTDNKAYR	Acetyl (N-term)	1.0000000000000000.0		29: Sum of 8 sca

**MASCOT** : Mascot tips & tricks

© Matrix Science 2013



The site analysis information can be exported to the XML, CSV and mzIdentML export formats. In the CSV file the information is reported like this with the site confidence reported with the query level information at the end of the report in the pep\_var\_mod\_conf column.

## 9. NCBIInr on a 32-bit computer

**NCBIInr is >15GB with >24 million entries.**

**Mascot Server on 32-bit OS can run out of resources when compressing or searching NCBIInr.**

**Mascot Server ≤2.2 use 32-bit applications so moving to a 64 bit OS will not help.**

Another support question that is coming up quite a lot at the moment with users of older versions of Mascot Server is the use of NCBIInr on 32-bit operating systems.

NCBIInr has been doubling roughly every 18 months for quite a few years now and is 15GB in size and more than 24 million entries.

Mascot Servers on 32-bit operating systems can run out of resources when compressing or searching NCBIInr. Older versions of Mascot Server, version 2.2 and earlier use 32 bit applications to compress and search so moving them to a 64 bit OS will not help much.

The problem normally presents itself after the database has been updated and the status does not change to “In use”

## NCBIInr on a 32-bit computer

### Fix the database compression by editing mascot.dat, change

- IgnoreDupeAccessions EST\_others  
to  
IgnoreDupeAccessions EST\_others NCBIInr

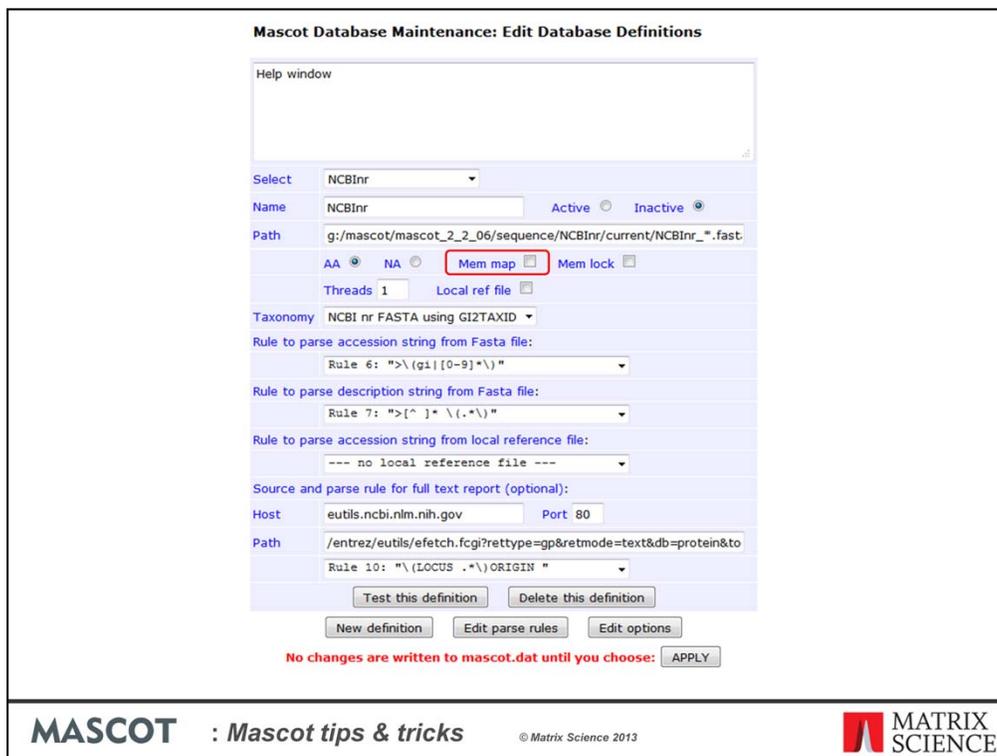
### For older hardware increase MonitorTestTimeout

- From 1200 to 2400 or higher

There are a couple of things we can do to enable Mascot to search NCBIInr on these systems.

First is to edit the mascot.dat file and add NCBIInr to the IgnoreDupeAccessions option. This means that, if there are duplicate accessions in the database, matches will be misreported. NCBIInr has been very reliable, and we are not aware of this ever happening, but we do not recommend adding other very large databases to the IgnoreDupeAccessions directive unless you can verify by other means that there are no duplicate accessions.

For Mascot Server running on older computers the time taken to run the test search can be longer than the default MonitorTestTimeout option. Doubling or tripling this value in mascot.dat may be required.



After making those changes the database will sometimes halt with a “failed to memory map error”. Or, the database reaches “In Use” and you can start searches against it but they crash. If so, you will have to make this additional change: Go to the database definition for NCBIInr and make sure that the “Mem lock” option is unchecked, which it is by default, and uncheck the “Mem map” option and apply the changes. This should enable you to search NCBIInr but both searches and opening of the results files will be a slower than normal.

If you are using an older version of Mascot Server on older hardware it is probably a good time to consider updating both the software and hardware.

## 10. Combining CID and ETD data in a single search

**Create a peak list from data containing alternating CID and ETD data with summing turned off.**

**Search using the new CID+ETD instrument.**

- If your Mascot Server does not have the CID+ETD instrument defined you can add it

It is very easy to search data with mixed CID/ECD or ETD data. First make sure that scan summing is turned off. The results will be clearer to analyze that way. The peak list can contain a mixture of spectra.

When you search the peak list, select a CID+ETD instrument type.

If your Mascot Server does not have a CID+ETD instrument setting you can add it through the configuration editor.

**Mascot Configuration: Instruments**

Instruments							
Ion series	Default	ESI QUAD TOF	CID+ETD	ETD TRAP	MALDI TOF PSD	ESI TRAP	ESI QUAD
1+	X	X	X	X	X	X	X
2+ (precursor>2+)	X	X	X	X		X	X
2+ (precursor>3+)							
immonium					X		
a	X				X		
a <sup>m</sup>	X				X		
a0					X		
b	X	X	X		X	X	X
b <sup>m</sup>	X	X	X		X	X	X
b0		X	X		X	X	X
c			X	X			
x							
y	X	X	X	X	X	X	X
y <sup>m</sup>	X	X	X			X	X
y0		X	X			X	X
z							
yb							
ya							
y must be significant							
y must be highest score							
z+1			X	X			
d							
v							
w			X	X			
z+2			X	X			
Minimum mass							
Max mass	700	700	700	700	700	700	700
		Delete Edit	Delete Edit	Delete Edit	Delete Edit	Delete Edit	Delete Edit

**MASCOT** : Mascot tips & tricks

© Matrix Science 2013

As you can see we take the CID and the EDT entries and combine the ion series that we search in to a new entry.

The CID+EDT instrument will give near identical results to searching each spectra with the relevant CID or ETD instrument type.

Home Mascot database search Products Technical support Training News Blog Contact

Access Mascot Server | Database search help

Mascot database search > Access Mascot Server > MS/MS Ions Search

### MASCOT MS/MS Ions Search

Your name: Richard Jacob Email: richardj@matrixscience.com

Search title:

Database(s): Invertebrates\_EST, Human\_EST, Fungi\_EST, Environmental\_EST, SwissProt

Enzyme: Trypsin

Allow up to: 1 missed cleavages

Quantitation: None

Taxonomy: All entries

Fixed modifications: --- none selected ---

Variable modifications:  Disulfide modifications

Peptide tol. ±: MALDI-TOF-TOF, MALDI-TOF-PSD, ESI-TRAP, ESI-QUAD, ESI-FTICR

Peptide charge: FTMS-ECD, ETD-TRAP, MALDI-QUAD-TOF, MALDI-QIT-TOF, MALDI-HSD

Data file:

Data format: CID+ETD

Instrument: CID+ETD

Decoy:

13C: 0 MS/MS tol. ±: 0.6 Da

Monoisotopic:  Average:

Precursor:  m/z

Error tolerant:

Report top: AUTO hits

Start Search ... Reset Form

**MASCOT** : Mascot tips & tricks © Matrix Science 2013

**MATRIX SCIENCE**

We can select the instrument type from the drop down list of instruments at the time of the search.

That's it! Peptides will be identified with predominately CID ion series or ETD ion series. There may be one or two peaks that match an ion series for the other type of fragmentation but they will have little effect on the score.

## 11. Mascot training



**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013

**MATRIX  
SCIENCE**

At around this time of year we are normally contacted by someone looking for a Mascot training summer camp! Sadly we have to direct them elsewhere. This is the Minnesota Vikings mascot Viktor the Viking who is based here in Minneapolis.

## Webcast Mascot training

**In December 2012 we released the online version of the Mascot training course.**

- Completely free
- No registration
- Hands on exercises for most of the presentations
- Optional short examination for a certificate

[http://www.matrixscience.com/training\\_webcast.html](http://www.matrixscience.com/training_webcast.html)

**MASCOT** : *Mascot tips & tricks*

© Matrix Science 2013



For the last 6 years we have held training courses one or twice a year on the east and west coasts of the States, in London UK and other European and worldwide locations. We realized that it was not always possible for everyone that wanted to attend the course to attend so at the end of last year we released the complete course on our website.

The course is completely free and requires no registration to view it. There are the same exercises that we used in the live training courses and, if you complete the multiple choice exam at the end of the course, you will receive a certificate. The course is available from this link on our public website.

**Mascot Training**

Learn how to get the best out of Matrix Science Mascot software. This course, created by the people who develop and support Mascot, covers every aspect of protein identification and characterisation using Mascot Server, Mascot Daemon, and Mascot Distiller. To access an individual presentation, click on the button below.

We recommend viewing the presentations in order, because they occasionally refer back to material covered earlier. For some presentations, there are web-based practical exercises that will reinforce the most important messages.

<b>1. Introduction</b>	<b>2. Search Parameters</b>
<b>3. Sequence Databases</b>	<b>4. Modifications</b>
<b>5. Scoring &amp; Statistics</b>	<b>6. Very Large Searches</b>
<b>7. Mascot Distiller</b>	<b>8. Sequence Queries</b>
<b>9. Mascot Daemon</b>	<b>10. Quantitation</b>
<b>11. Sequence Database Administration</b>	<b>12. General Mascot Server Administration</b>

**MASCOT** : Mascot tips & tricks © Matrix Science 2013 

The course has the same content as our live course and has been updated for the latest version of Mascot Server.

We cover everything from a basic introduction to bring everyone up to speed, more in depth training on scoring and statistics and specialist subjects like Mascot Server administration.

One nice thing about the course is that you can follow it in your own time

**5. Scoring & Statistics**



**5. Scoring & Statistics**  
Click play to begin the session

**Presenters** **Documents**

**John Cottrell**  
Matrix Science

What is probability based scoring and why is it important. Significance thresholds and expectation values. Target decoy search to estimate false discovery rate. Sensitivity improvement with Percolator.

After watching this presentation, please try the hands-on exercise under Scoring & Statistics

<http://www.matrixscience.com/training/exercises.html>

**MASCOT** : Mascot tips & tricks © Matrix Science 2013 **MATRIX SCIENCE**

Each presentation includes a short Video introduction and audio narration over the slides. You can pause and repeat any slides that interest you.

## 5. Scoring & Statistics

Score	Expect	Delta	Hit	Protein	Peptide			
33	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
32	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
31	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
30	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
29	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
28	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
27	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
26	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
25	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
24	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
23	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
22	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
21	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
20	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
19	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
18	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
17	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
16	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
15	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
14	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
13	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
12	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
11	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
10	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
9	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
8	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
7	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
6	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
5	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
4	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
3	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
2	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR
1	0.00000	1243.3763	1243.3763	0	0	0.00000	1	STYPTDDEGR

- Presenters
- Documents
- Slides and Speaker Notes
- Matrix Science Website
- MCP Guidelines for Publication
- Research Paper: Target-decoy search strategy for increased confidence in large-scale protein...
- Research Paper: Empirical statistical model to estimate the accuracy of peptide identifications...
- Research Paper: Semi-supervised learning for peptide identification from shotgun proteomics datasets

What is probability based scoring and why is it important. Significance thresholds and expectation values. Target decoy search to estimate false discovery rate. Sensitivity improvement with Percolator.

After watching this presentation, please try the hands-on exercise under Scoring & Statistics  
<http://www.matrixscience.com/training/exercises.html>

MASCOT : Scoring & Statistics © 2007-2012 Matrix Science MATRIX SCIENCE

## 5. Scoring & Statistics

MASCOT : Mascot tips & tricks © Matrix Science 2013 MATRIX SCIENCE

Each presentation includes a PDF of the slides and speakers notes plus links to relevant publications and websites

Home Mascot database search Products Technical support Training News Blog

Course outline | Live course | Webcast course

Training > Webcast course > Exercises > MSMS1

## Exercise MSMS1

**Topic**  
Use an error tolerant search to find unusual modifications, sequence variants, and non-specific cleavage.

**Requirements**  
User access to any Mascot server, including the Matrix Science [public web site](#)

**Experimental**  
Perform an automatic error tolerant search of the supplied MGF format peak list against Swiss-Prot with a taxonomy filter of Mammalia. Use Trypsin, 2 missed cleavages, 0.5 Da / 0.5 Da, no modifications, and the ESI-QUAD-TOF instrument.

**Data**  
Right-click this link: [qtof10348.mgf](#), and choose *Save target as* or *Save link as*.

**Tips**  
\* Use the yellow pop-ups to try and decide which modifications or substitutions may have caused the mass deltas

**Questions**

1. Try to explain as many as possible of the additional error tolerant matches
2. Are there any that you cannot explain or do not believe?
3. Which modifications, if any, should have been selected for the first pass search?

Hints | [Search results](#) | [Answers](#)

[Return to list of exercises](#)

---

**MASCOT** : Mascot tips & tricks © Matrix Science 2013 

After many of the lessons there are one or more exercises to put your knowledge into action. There are instructions, links to the data, and a set of questions to answer. If you need it there are hints to help you along and links to the search results and answers.

Home Mascot database search Products Technical support Training News Blog Contact

Course outline | Live course | **Webcast course**

Training > Webcast course > Examination

## Webcast course examination

### Mascot Training Examination

00:58:38

Question 4 of 36 | Multiple Choice | 1

Which of these would speed up an MS/MS search?

- Use a narrower precursor mass tolerance
- Use a narrower fragment mass tolerance
- Select enzyme type None
- Reduce the number of fixed modifications

Search Parameters

MASCOT | ESI/MS

Outline... Submit

**MASCOT** : Mascot tips & tricks © Matrix Science 2013 **MATRIX SCIENCE**

After you have finished the course and exercise take the test to earn a certificate. It is a multiple choice exam and you have an hour to complete it.

Home Mascot database search Products Technical support Training News Blog Contact

Course outline | Live course | **Webcast course**

Training > Webcast course > Examination

## Webcast course examination

### Mascot Training Examination

Result page

Total Questi...	Full Score	Passing Rate	Passing Score	Your Score	Elapsed
36	36	75%	27	31	00:11:55

Congratulations, you passed! You can now create a printable certificate.

Finish

**MASCOT** : Mascot tips & tricks © Matrix Science 2013 **MATRIX SCIENCE**

At the end you can see your score and if you passed



And then print your certificate.

We do hope that you will take the course as it contains a lot of knowledge and information that make you a more proficient user of our software.

## Mascot tips & tricks

1. Automatic exporting of search results
2. Mascot Distiller Viewer
3. Clear out cache files periodically
4. Moving Mascot Server to a new computer
5. Running Mascot Daemon on desktop
6. Turning off summing of scans in Distiller
7. Use of Virtual Machines for Mascot Servers
8. Site analysis added to export
9. NCBI nr on 32-bit computers
10. Combining CID and ETD data in a single search
11. Webcast training

I have covered 11 topics in this mascot tips and tricks presentation and I hope that you all heard something useful for your research.