# READ ME FIRST!

Please read the notes for specific Windows platforms starting on page 3 before following the installation instructions in Chapter 3 of the Installation and Setup Manual. A complete, up-to-date copy of the Installation and Setup Manual can be found on the Mascot installation CD, (manual.pdf).

### **New: Quantitation**

Mascot 2.2 contains all of the infrastructure needed for a wide variety of quantitation experiments.

### **New: Configuration Editor**

Web browser based configuration editor can be used to view and edit quantitation.xml, unimod.xml, and the other Mascot configurations files

**New: Automatic Error Tolerant Searches** 

### **New: Automatic Decoy Database Searches**

#### And lots more

- Mass values are now selected, iteratively, by peak intensity for PMF searches
- A new search parameter to handle cases where the 13C peak was picked without having to open out the mass tolerance.
- A new utility, TS2Mascot, for importing peak lists from an Applied Biosystems 4000 series databases.
- Mascot Daemon has a reduced memory footprint and can now handle raw files and peak lists larger than 2 GB.

### Changes since last release

Details of individual changes since the previous major release of Mascot are listed on page 7 of these notes.

#### Last minute additions to documentation

See page 2

## Last minute additions to documentation

- The installation program creates a file containing configuration settings for Apache 2.x web server. If you use Apache, ensure that ForkForUnixApache in the Options section of mascot.dat is set to 1
- On page 34 of the Installation and Setup Manual, the IIS web server configuration page has a checkbox labelled 'Use SSL/TLS to access this web site'. This checkbox has since been removed. If you want to run Mascot on a secure (https:) IIS server, you must configure IIS for non-SSL (http:) operation, perform the Mascot installation, then switch back to secure mode.
- When performing an upgrade, any text files that have been modified since the last installation are copied to a directory called \_install\_backup. This includes configuration files, Perl scripts, and HTML pages.
- Setup.exe is the Mascot installation program for 32 bit (x86) Windows platforms. Setup64 exe is for 64 bit (x64) Windows platforms. Similarly, there are two installers for ActivePerl, one with x86 in the filename, for 32 bit Windows, and one with x64 in the filename, for 64 bit Windows.
- MSDB has become too large to fit onto the installation CD, and the installer now uses SwissProt as a test database. Additional sequence databases, including MSDB, are supplied on a separate DVD.
- Some third party applications require helper scripts to be installed on the Mascot web server. If Mascot security is enabled, you should be aware that such scripts may create security holes.
- Some compressed sequence database files are now larger than 2 GB. Even with the latest release of wget, (1.10.2), there are bugs that interfere with Time-Stamping. Probably best to update very large databases by hand until these issues are resolved.
- If your web browser is Microsoft Internet Explorer 7, you may find it very difficult to distinguish between normal and bold face type in a Mascot result report. This is a side effect of Clear Type. To fix, in Internet Explorer, click the Tools button, and then click Internet Options. Click the Advanced tab, scroll to the Multimedia section, clear the Always use Clear Type for HTML check box, and then click OK. The changes will take effect the next time you start Internet Explorer.

# Notes for specific Windows Platforms

### Windows NT4

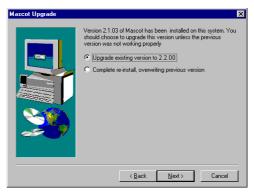
Microsoft ceased to support Windows NT4 in 2004. Mascot 2.2 will be the last Mascot release to support NT4. Now would be a very good time to upgrade to a more recent version of Windows.

If you wish to continue with NT4, the new Mascot installer requires Windows Installer 3, which is not available for Windows NT4. Please email support@matrixscience.com to request a CD with the old installer.

### To upgrade Mascot using the old installer

- 1. Service pack 6 or 6a must be installed
- 2. If your version of Perl is less than 5.6, it must be upgraded. Uninstall Perl, then install Perl 5.8 from the Mascot CD. More details on page 29 of the manual. You may need to update Windows Installer. To do so, change to the unpacked html downloads directory on the Mascot CD, and execute the file InstMsiW.exe
- 3. Ensure that any other users are aware that they will not be able to perform searches while the upgrade is taking place.
- 4. Check that you are logged in with administrator privileges, and execute setup.exe on the Mascot CD
- 5. If anything on the system information page is incorrect, refer to the troubleshooting section of the manual, beginning page 44.
- 6. Choose to upgrade unless the previous version was not working properly, or if you want to install Mascot onto a new drive, or install it into a new Web Server. Note that it is not possible to run both the old and the new version of Mascot on the same system.





- 7. You should leave all options selected unless you understand the system very well, and have customised some Perl scripts or HTML pages. Any additional enzymes that you have added will be unaltered.
- 8. Choose the appropriate option for sequence database installation.
- 9. In Mascot 2.2, modifications are taken from a new XML file, unimod.xml. Your existing mod\_file will be backed up. You will need to add any custom modifications that were in your mod\_file to unimod.xml after the installation has completed using the new, browserbased configuration editor.





**NOTE:** It is not always possible for the installation program to update your own additions and changes in mascot.dat. It is a good idea to compare your mascot.dat file with the latest template file, not.mascot.dat, to judge whether further changes should be made. Mascot.dat entries are fully described in Chapter 6 of the Setup and Installation manual.

# Windows 2000

Service pack 4 must be installed

A clean installation of Windows 2000 SP4 includes Windows Installer 2. It is very likely that the installer will already have been upgraded to version 3 in the course of installing other software packages. If not, you will see a message when you try to install Mascot stating that the installer must be upgraded. For Windows Installer 3.x download details, go to <a href="http://support.microsoft.com/?kbid=893803">http://support.microsoft.com/?kbid=893803</a>

# Windows XP

The latest service pack should be installed

### 64 bit support

XP Professional x64 edition uses IIS 6.0. See the notes about this version of IIS under Windows Server 2003, below.

There are no repositories for 64 bit ActiveState Perl modules. If you plan to use Perl for applications besides Mascot, you may find it more flexible to install 32 bit Perl.

To install Mascot on XP Professional x64 edition, execute setup64.exe instead of setup.exe

### **Windows Firewall**

Remember to open port 80 (HTTP) if you want to access the Mascot server from other computers

### Windows Server 2003

The latest service pack should be installed

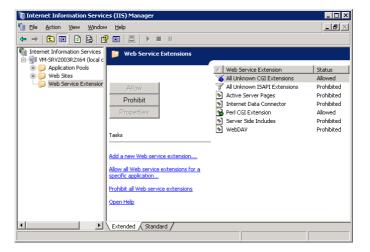
#### **IIS 6.0**

If a search is submitted from a browser and the connection is broken before the search is complete, the search will be killed. The only known workaround is to use Apache 2.x as your web server.

IIS 6 does not serve files with unknown MIME types. Its default list of MIME types does not include XML schema documents. See Microsoft Knowledge Base article Q326965 for the procedure to add \*.XSD to the IIS 6 list of MIME types

http://support.microsoft.com/default.aspx?scid=kb;en-us;326965

After installing Perl, ensure web service extensions for 'Perl CGI' and 'All unknown CGI' are set to allowed



### 64 bit support

There are no repositories for 64 bit ActiveState Perl modules. If you plan to use Perl for applications besides Mascot, you may find it more flexible to install 32 bit Perl.

To install Mascot on a Server 2003 R2 x64 platform, execute setup 64.exe instead of setup.exe.

#### **Windows Firewall**

Remember to open port 80 (HTTP) if you want to access the Mascot server from other computers

### Windows Vista

Microsoft is trying to make Windows Vista more secure than previous Windows platforms. Unfortunately, IIS 7.0 includes security features that interfere with the correct operation of CGI applications such as Mascot. At this time, we have been unable to configure a working Mascot system on IIS 7.0. If you wish to use IIS as your web server, we recommend choosing either Windows XP or Server 2003.

Mascot can be installed on Vista when the web server is Apache. This has been tested with Apache 2.2.4. It is not known whether earlier releases of Apache are also compatible with Vista. The procedure is as follows:

- 1. Do not install IIS
- 2. You must install the following applications as Administrator. It is not sufficient to install as a user with administrator privileges. The easiest way to do this is to open a command window by right clicking the start menu item (under accessories) and choosing 'Run as administrator'. Verify that the title bar says 'Administrator: Command prompt'. Execute the installers by typing their filename in this command prompt and pressing return.
- 3. Download the latest Apache MSI installer from <a href="http://httpd.apache.org/download.cgi">http://httpd.apache.org/download.cgi</a> and install accepting all defaults. At the end of the installation, you will be prompted by Windows firewall. Choose to unblock port 80 (HTTP). Don't be concerned if you see an empty error message at the end of the installation. This is because the installer is unable to start the Apache service.
- 4. Install ActiveState Perl from the Mascot installation CD. Accept all defaults
- 5. Install Mascot
- 6. Copy the Apache configuration settings from the httpd.conf file created in the Mascot config directory and paste them at the end of the Apache httpd.conf file, (in C:\Program Files\Apache Software Foundation\Apache2.2\conf). Save the changes.
- 7. In Windows Explorer, go to the Apache bin directory, (C:\Program Files\Apache Software Foundation\Apache2.2\bin). Right click ApacheMonitor.exe and choose properties. On the compatibility tab, check 'Run this program in compatibility mode for' with 'Windows XP SP2' in the drop-down list, then choose OK.
- 8. Re-start Vista

# Changes since Version 2.1.04

ID	Title
21	select mass values in a peptide mass fingerprint by intensity
335	Report should display errors in the units chosen in the search form
1244	Support for metabolic labeling, e.g. N15
2045	Exclusive (binary) modifications. E.g.ICAT where all Cys in one peptide are heavy or all light.
2046	Limit number of variable mods on a single peptide
2047	Report emPAI Quantitation
2057	Help text needs to describe expectation value threshold
1504	Add table of links to Peptide View report to display reports for other matches
1752	Warning for 'impossible' tags
1777	db_gui.pl doesn't allow multiple wildcards
1803	Database maintenance utility should check limits:  1. Database name > 19 chars  2. Parse rule > 128 chars  3. Any Path > 256 chars  4. Number of threads > 1024
1822	Integrated (automatic) error tolerant search
1828	Add a note about MaxAccessionLen to the varsplic help page
1911	Add a help pages for quantitation
1975	Automatic decoy database search
2035	Would like a "Spoof as " drop down list in the search form for user names and emails
2038	Would like option to export the protein sequence in export utility
2039	Show the precursor neutral loss peak in Peptide View
2061	MudPIT switch point should be ratio of queries to entries, not a fixed number of queries
2070	IT_MODS should be available in local scope of peak list
2078	Daemon fails if peak list > 2GB
2083	Seq tags cannot extend to full length of sequence
2096	Database maintenance test of ref file fails for Celera CDS databases
2098	Help text for error tolerant search needs improving
2109	Give database name with error M422
2111	Mascot Daemon needs to pass through user parameters in follow on searches
2114	Integra Daemon needs sort by options in dialog box to choose search parameter set
2158	Control characters can appear in Mascot email field
2159	Improve memory footprint of Daemon. Need to make intermediate field into disk file
2160	Limit to 4 cores for licensing.
2161	Database maintenance should recommend num threads based on HT or dual core
2162	Change case of database name, db_gui.pl doesn't realise need new _SEQ
2163	In cluster mode, spurious error message about changed service binary file location for service MascotNodeService at each startup. (Case sensitivity problem)
2164	Want option to export the query title from export_dat.pl

1	
	xml output from ms-getseq to speed up retrieval of batches of sequences
	xml output for ms-gettaxonomy to speed up retrieval of batches of queries
	ms-monitor.exe exits with error M00012 if problem with database file permissions
2170	If "ACCESSION" field is specified and the accession is a secondary accession for an entry in db, then it will never be found
	embedded user parameters are not handled properly in cluster mode
2116	Support for ETD/CID mode by allowing allow INSTRUMENT in local scope of spectrum
2121	Modifications syntax needs ResiduesProteinCterm and ResiduesProteinNterm
	Select summary – remove redundant protein check boxes.
2127	Specifying y-ions will make repeat search fail
2129	Add modification position to the custom CSV/XML export script
	Too easy to overwrite existing definition in database maintenance when trying to add new database
2134	Daemon limited to data files < 2 GB
2141	Remove error message from database maintenance about accession too long
	daemon desktop application crashes if try to run task where follow-up task has been deleted
2145	Daemon "repeat at interval" searches not working correctly
	Get duplicate key in results file if there are (legitimate) duplicate analyzerType attributes in mzData
2152	Pass through the mzData accession to the results files
2156	Daemon fails to try guest login
2157	Remove Protein Mass (SEG) from the Mascot ms-ms search form
2172	Need to enable multiple mascot executables co-exist in the same environment in cluster mode
	Masses close to 16 kDa can cause problems
2175	MGF clarification & documentation on Data Format help page
	Misleading error message when using ITOL= in BEGIN IONS
2177	Allow for poor peak detection, picking a C13 peak with accurate mass data (PEP_ISOTOPE_ERROR)
2181	Cluster mode fails to bootstrap if gethostbyname_r fails
2185	To make result file completely self-contained, need to add information for enzyme, taxonomy, quantitation, and modifications
	Daemon status tab can display wrong task label
2187	Finer control of parser params for client.pl xmlresults2 output
2188	ShowSubSets should be a number between 0 and 1 which represents the maximum fraction of the peptide matches in the primary hit that can be missing in the sub-set hit. 1 would be equivalent to Show Sub-sets true, 0 would be equivalent to Show Sub-sets false.
2189	If export includes a "masses" section, XML from export utility may not validate against mascot_search_results_1.xsd if there are fixed mods
2190	Problems with conflicts between variable mods and error-tolerant mods
2192	client.pl should return version numbers for individual binaries.
2194	Crash when submitting a fasta file instead of a peak list
2198	ms_getseq post request for NA sequence with showsequence = true and showlen = false fails to translate
2200	add support for quantitation.xml to ms_status.exe for getparams.pl
2201	Support 64 bit Linux on Intel/AMD
0047	Change lcq_dta_shell.pl to have default Min. Scans / Group of 1
2217	Change icq_dta_shell.pl to have default with. Scans / Gloup of 1

Store part of event log in Integra version of Task DB so that Integra is guaranteed access to remote Daemon event log Daemon will mess up Distilier import if scan numbers are not consecutive in data file.  2230 Add second error graph in peptide view for ppm errors In Daemon, change default setting for "Save Distiller project" to true Database maintenance utility allows & in database name. Should be illegal Daemon gives Run-time error '35601' Element not found on start up if there are multiple tasks which have New in the action_request field 2206 If the date directory is created for a task id, then it doesn't have correct rights 2208 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked 2210 MinPepLenInSearch is being incorrectly applied to PMF 2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00) Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS) File not found error in Daemon if using import filter and task name has trailing space(s) 2213 Add the expectation value to the yellow popup 2215  cq_dta_shell.pl needs to have security login 2228  eseq.pl should give an error when user doesn't have access to a database 2232  Export script falling to escape double quotes in attributes 2238  ms-getseq and ms-gettaxonomy need detailed error info in xml output 2239  ms-getseq and ms-gettaxonomy need detailed error info in xml output 2230  ms-getseq and ms-gettaxonomy need detailed error info in tolerant search of NA database 2231  ms-getseq and ms-gettaxonomy need detailed error info in ror tolerant search of NA database 2232  ms-getseq and ms-gettaxonomy need fetailed error info in xml output 2233  ms-getseq and ms-gettaxonomy need fetailed error info in xml output 2243  ms-getseq and ms-gettaxonomy need fetailed error info in xml output 2254  ms-getta number of ions matched - getNumlonsMatched() 2265  ms-getta number of ions matched - getNumlonsMatched() 2276  ms-getta number of ions matched - getNumlonsMatched() 2277  ms-getta number of	2224	master_results.pl needs to use expectation value instead of 1/probability (to avoid underflow)
2230 Daemon will mess up Distiller import if scan numbers are not consecutive in data file. 2231 Add second error graph in peptide view for ppm errors 2232 In Daemon, change default setting for "Save Distiller project" to true 2232 Daemon gives Run-time error "35601" Element not found on start up if there are multiple tasks which have New in the action, request filed 2236 If the date directory is created for a task id, then it doesn't have correct rights 2238 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked 2240 MinPepLenInSearch is being incorrectly applied to PMF 2241 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00) 2241 Pelip not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS) 2243 File not found error in Daemon if using import filter and task name has trailing space(s) 2244 Add the expectation value to the yellow popup 225 lcq_dta_shell.pl needs to have security login 226 gsteeq.pl should give an error when user doesn't have access to a database 227 protein masses are large negative numbers for error tolerant search of NA database 228 wrong mass values being reported for substitutions found in error tolerant search of NA database 229 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 248 Status screen reports too many processors! 249 Add support for minInternalMass, maxInternalMass to peptide_view.pl 250 XML export should output the number of ions matched - getNumlonsMatched() 251 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 252 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 253 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 254 Add arz Dost for ETD 255 Macd at 21 ons for ETD 255 Macd at 22 ions for ETD 256 Lemms missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all pep	2225	Store part of event log in Integra version of Task DB so that Integra is guaranteed access
2230 Add second error graph in peptide view for ppm errors 2203 In Daemon, change default setting for "Save Distiller project" to true 2204 Database maintenance utility allows & in database name. Should be illegal 2205 Daemon gives Run-time error '35601' Element not found on start up if there are multiple tasks which have New in the action, request field 2206 If the date directory is created for a task id, then it doesn't have correct rights 2208 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked 2210 MinPepLenInSearch is being incorrectly applied to PMF 2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00) 2212 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS) and END IONS) 2213 File not found error in Daemon if using import filter and task name has trailing space(s) 2214 Add the expectation value to the yellow popup 2215 Icl and shell.pl needs to have security login 2226 Export script failing to escape double quotes in attributes 2232 Export script failing to escape double quotes in attributes 2233 Wrong mass values being reported for substitutions found in error tolerant search of NA database 2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 2248 Status screen reports too many processors! 2498 Add support for minInternalMass, maxInternalMass to peptide_view.pl 2502 XML export should output the number of ions matched - getNumlonsMatched() 2603 Was screen reports too many processors! 2604 Add maData format as peak list option for Mascot Distiller import filter in Mascot Daemon gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 2616 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 2617 Add z+2 ions for ETD 2626 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2627 Cannot use the f option or move the data directory if the input file	2227	
2003 In Daemon, change default setting for "Save Distiller project" to true 2004 Database maintenance utility allows & in database name. Should be illegal 2005 Daemon gives Run-time error '35601' Element not found on start up if there are multiple tasks which have New in the action_request field 2006 If the date directory is created for a task id, then it doesn't have correct rights 2008 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked 2010 MinPepLenInSearch is being incorrectly applied to PMF Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00) 2112 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS) 21213 File not found error in Daemon if using import filter and task name has trailing space(s) 21214 Add the expectation value to the yellow popup 2015 [ac_dta_shell.pl needs to have security login] getseq.pl should give an error when user doesn't have access to a database 21232 Export script failing to escape double quotes in attributes 21233 ms-getseq and ms-gettaxonomy need detailed error info in xml output 21237 protein masses are large negative numbers for error tolerant search of NA database 21248 Vrong mass values being reported for substitutions found in error tolerant search of NA database 21249 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 21240 XML export should output the number of ions matched - getNumlonsMatched() 21254 Add support for minInternalMass, maxInternalMass to peptide_view.pl 21255 XML export should output the number of ions matched - getNumlonsMatched() 21264 Database 21275 Add z+2 ions for ETD 21286 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 21265 Data and provided matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT 21261 Small ions score discrepency in error tolerant 21262 Bug 1495 is back. If one mod na		· ·
Database maintenance utility allows & in database name. Should be illegal  2205  Daemon gives Run-time error '35601' Element not found on start up if there are multiple tasks which have New in the action_request field  2206  If the date directory is created for a task id, then it doesn't have correct rights  2208  Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked  2210  MinPepLenInSearch is being incorrectly applied to PMF  2211  Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00)  Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS)  2213  File not found error in Daemon if using import filter and task name has trailing space(s)  2214  Add the expectation value to the yellow popup  2215  Icq_dta_shell.pl needs to have security login  2228  2230  Export script failing to escape double quotes in attributes  2231  2232  Export script failing to escape double quotes in attributes  2233  2234  Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247  10 error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248  2249  Add support for minInternalMass, maxInternalMass to peptide_view.pl  2249  2240  Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255  Mule export should output the number of ions matched - getNumlonsMatched()  2254  Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255  Mule apport for minInternalMass, maxInternalMass to peptide_view.pl  2260  2271  2282  Data file file fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257  Add z+2 ions for ETD  2258  Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268  Cannot use the -f option or move the data directory if the input file is mzData file  2273  Mods string will use characters A-W t		9 1 1 1
Daemon gives Run-time error '35601' Element not found on start up if there are multiple tasks which have New in the action_request field  2006 If the date directory is created for a task id, then it doesn't have correct rights  2008 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked  2101 MinPepLenInSearch is being incorrectly applied to PMF  2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00)  2112 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS)  2113 File not found error in Daemon if using import filter and task name has trailing space(s)  2114 Add the expectation value to the yellow popup  2115 Icq_dta_shell.pl needs to have security login  2126 gets.pell.pl should give an error when user doesn't have access to a database  2127 protein masses are large negative numbers for error tolerant search of NA database  2128 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2129 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2219 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2220 XML export should output the number of ions matched - getNumlonsMatched()  2221 Add and Add and Add and Add Add Add Add Add Add Add Add Add A		1 1
2206 If the date directory is created for a task id, then it doesn't have correct rights 2208 Daemon parameters editor tab; instrument combo box not disabled when MS/MS unchecked 2210 MinPepLenInSearch is being incorrectly applied to PMF 2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00) 2212 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS) 2213 File not found error in Daemon if using import filter and task name has trailing space(s) 2214 Add the expectation value to the yellow popup 2215 [oq_dta_shell.pl needs to have security login 2218 getseq.pl should give an error when user doesn't have access to a database 2229 Export script failing to escape double quotes in attributes 2230 ms-getseq and ms-gettaxonomy need detailed error info in xml output 2231 protein masses are large negative numbers for error tolerant search of NA database 2232 Wrong mass values being reported for substitutions found in error tolerant search of NA database 2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 2248 Status screen reports too many processors! 2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl 2250 XML export should output the number of ions matched - getNumlonsMatched() 2251 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2252 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 2253 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2255 Utems missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT 2260 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2263 Cannot use the -f option or mov		Daemon gives Run-time error '35601' Element not found on start up if there are multiple
unchecked  2210 MinPepLenInSearch is being incorrectly applied to PMF  2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00)  2212 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS)  2213 File not found error in Daemon if using import filter and task name has trailing space(s)  2214 Add the expectation value to the yellow popup  2215   Icq. dta. shell.pl needs to have security login  2231 getseq.pl should give an error when user doesn't have access to a database  2232   Export script failing to escape double quotes in attributes  2233   ms-getseq and ms-gettaxxonomy need detailed error info in xml output  2237 protein masses are large negative numbers for error tolerant search of NA database  2238   Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247   In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248   Status screen reports too many processors!  2249   Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252   XML export should output the number of ions matched - getNumlonsMatched()  2254   Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255   gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256   When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257   Add z+2 ions for ETD    2259   Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261   Small ions score discrepency in error tolerant  2262   Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2263   Cannot use the -f option or move the data directory if the input file is mzData file  2273   Mods string will use characters A-W to support more than 9	2206	
2211 Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00)  2212 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS)  2213 File not found error in Daemon if using import filter and task name has trailing space(s)  2214 Add the expectation value to the yellow popup  2215   Icq_dta_shell.pl needs to have security login  2231 getseq.pl should give an error when user doesn't have access to a database  2232   Export script failing to escape double quotes in attributes  2235 ms-getseq and ms-gettaxonomy need detailed error info in xml output  2237 protein masses are large negative numbers for error tolerant search of NA database  2238   Wrong mass values being reported for substitutions found in error tolerant search of NA database  2249   In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248   Status screen reports too many processors!  2249   Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252   XML export should output the number of ions matched - getNumlonsMatched()  2254   Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255   gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2266   When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2267   Add z+2 ions for ETD  2268   Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261   Small ions score discrepency in error tolerant  2262   Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2263   Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2264   Cannot use the -f option or move the data directory if the input file is mzData file  2273   Mods string will use characters A-W to support more than	2208	
2212 Help not clear about SCANS and RTINSECONDS (Can only go between BEGIN IONS and END IONS) 2213 File not found error in Daemon if using import filter and task name has trailing space(s) 2214 Add the expectation value to the yellow popup 2215 Icq_dta_shell.pl needs to have security login 2231 getseq.pl should give an error when user doesn't have access to a database 2232 Export script failing to escape double quotes in attributes 2235 ms-getseq and ms-gettaxonomy need detailed error info in xml output 2237 protein masses are large negative numbers for error tolerant search of NA database 2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database 2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 2248 Status screen reports too many processors! 2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl 2252 XML export should output the number of ions matched - getNumlonsMatched() 2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 2257 Add z+2 ions for ETD 2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant 2262 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored. 2263 Cannot use the -f option or move the data directory if the input file is mzData file 2264 ms-monitor exits without error with:SubClusterSet 7 14 2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2210	
and END IONS)  2213 File not found error in Daemon if using import filter and task name has trailing space(s)  2214 Add the expectation value to the yellow popup  2215 Icq_dta_shell.pl needs to have security login  2231 getseq.pl should give an error when user doesn't have access to a database  2232 Export script failing to escape double quotes in attributes  2235 ms-getseq and ms-gettaxonomy need detailed error info in xml output  2237 protein masses are large negative numbers for error tolerant search of NA database  2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a  2257 Add z+2 ions for ETD  2259 Item missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge,  2261 all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU,  11T_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2262 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2263 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2264 Cannot use the -f option or move the data directory if the input file is mzData file  2275 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14	2211	Daemon 2.1.04 will not work with Mascot 2.0 (Was OK in 2.1.00)
2214 Add the expectation value to the yellow popup  2215   Icq_dta_shell.pl needs to have security login  2231 getseq.pl should give an error when user doesn't have access to a database  2232   Export script failing to escape double quotes in attributes  2235 ms-getseq and ms-gettaxonomy need detailed error info in xml output  2237 protein masses are large negative numbers for error tolerant search of NA database  2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249   Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252   XML export should output the number of ions matched - getNumlonsMatched()  2254   Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255   gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2266   When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257   Add z+2 ions for ETD  2259   Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261   Small ions score discrepency in error tolerant  2262   Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2263   Cannot use the -f option or move the data directory if the input file is mzData file  2264   Mods string will use characters A-W to support more than 9 mods  2276   ms-monitor exits without error with:SubClusterSet 7 14	2212	
2215   cq_dta_shell.pl needs to have security login 2231   getseq.pl should give an error when user doesn't have access to a database 2232   Export script failing to escape double quotes in attributes 2235   ms-getseq and ms-gettaxonomy need detailed error info in xml output 2237   protein masses are large negative numbers for error tolerant search of NA database 2238   Wrong mass values being reported for substitutions found in error tolerant search of NA database 2247   In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 2248   Status screen reports too many processors! 2249   Add support for minInternalMass, maxInternalMass to peptide_view.pl 2250   XML export should output the number of ions matched - getNumlonsMatched() 2251   Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2255   gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 2256   When multiple fixed mods are specified for same residue or terminus, this should be a 2267   Add z+2 ions for ETD 2259   Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, 2268   all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, 2269   IT_MODS, INSTRUMENT 2260   Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2260   Cannot use the -f option or move the data directory if the input file is mzData file 2273   Mdc string will use characters A-W to support more than 9 mods 2276   ms-monitor exits without error with:SubClusterSet 7 14 2279   add support for unimod_2.xml to ms-status.exe for getparams.pl	2213	File not found error in Daemon if using import filter and task name has trailing space(s)
2231 getseq.pl should give an error when user doesn't have access to a database 2232 Export script failing to escape double quotes in attributes 2235 ms-getseq and ms-gettaxonomy need detailed error info in xml output 2237 protein masses are large negative numbers for error tolerant search of NA database 2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database 2249 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard 2248 Status screen reports too many processors! 2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl 2252 XML export should output the number of ions matched - getNumlonsMatched() 2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation. 2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable 2257 Add z+2 ions for ETD 2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT 2261 Small ions score discrepency in error tolerant 2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored. 2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2267 Cannot use the -f option or move the data directory if the input file is mzData file 2278 Mods string will use characters A-W to support more than 9 mods 2279 ms-monitor exits without error with:SubClusterSet 7 14	2214	Add the expectation value to the yellow popup
Export script failing to escape double quotes in attributes  ms-getseq and ms-gettaxonomy need detailed error info in xml output  protein masses are large negative numbers for error tolerant search of NA database  Wrong mass values being reported for substitutions found in error tolerant search of NA database  1 herror tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2 tatus screen reports too many processors!  2 to septimens protein massor Deptimens mascor Daemon  2 tatus in mascor Daemon protein mascor Daemon  2 tatus in mascor Daemon  2 to screen report detailed for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2 to screen report detailed for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2 to screen report detailed for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2 to screen report detailed for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2 to screen report detailed for same residue or terminus, this should be a fatal error. At the moment, the dupli	2215	lcq_dta_shell.pl needs to have security login
ms-getseq and ms-gettaxonomy need detailed error info in xml output protein masses are large negative numbers for error tolerant search of NA database  2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2266 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, 1T_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant 2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2265 Cannot use the -f option or move the data directory if the input file is mzData file 2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14	2231	getseq.pl should give an error when user doesn't have access to a database
2237 protein masses are large negative numbers for error tolerant search of NA database  2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2262 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2263 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14	2232	Export script failing to escape double quotes in attributes
2238 Wrong mass values being reported for substitutions found in error tolerant search of NA database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2262 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2235	ms-getseq and ms-gettaxonomy need detailed error info in xml output
database  2247 In error tolerant search, need to make it clear in pop-up which matches are ET and which are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2262 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2263 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2237	protein masses are large negative numbers for error tolerant search of NA database
are standard  2248 Status screen reports too many processors!  2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl  2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a  fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  1259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, 1T_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  Mods string will use characters A-W to support more than 9 mods  ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2238	
2249 Add support for minInternalMass, maxInternalMass to peptide_view.pl 2252 XML export should output the number of ions matched - getNumIonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon 2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant 2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored. 2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2268 Cannot use the -f option or move the data directory if the input file is mzData file 2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2247	
2252 XML export should output the number of ions matched - getNumlonsMatched()  2254 Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2256 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl		·
Add mzData format as peak list option for Mascot Distiller import filter in Mascot Daemon  2255 gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.  2266 When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2249	Add support for minInternalMass, maxInternalMass to peptide_view.pl
<ul> <li>gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.</li> <li>When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable</li> <li>Add z+2 ions for ETD</li> <li>ltems missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT</li> <li>Small ions score discrepency in error tolerant</li> <li>Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.</li> <li>Daemon spelling mistake: monisotopic in mascot daemon (parameters page)</li> <li>Cannot use the -f option or move the data directory if the input file is mzData file</li> <li>Mods string will use characters A-W to support more than 9 mods</li> <li>ms-monitor exits without error with:SubClusterSet 7 14</li> <li>add support for unimod_2.xml to ms-status.exe for getparams.pl</li> </ul>	2252	XML export should output the number of ions matched - getNumlonsMatched()
When multiple fixed mods are specified for same residue or terminus, this should be a fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14		·
fatal error. At the moment, the duplicates are converted to variable  2257 Add z+2 ions for ETD  2259 Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2255	gi_taxid_nucl.dmp is too large for Linux. Problem is memory fragmentation.
Items missing from export_dat.pl output: QUANTITATION, query_intensity, query_charge, all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant 2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored. 2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2268 Cannot use the -f option or move the data directory if the input file is mzData file 2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl		fatal error. At the moment, the duplicates are converted to variable
all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU, IT_MODS, INSTRUMENT  2261 Small ions score discrepency in error tolerant  2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl		
2264 Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.  2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page)  2268 Cannot use the -f option or move the data directory if the input file is mzData file  2273 Mods string will use characters A-W to support more than 9 mods  2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2259	all peptide matches for a query. At query level: RTINSECONDS, SCANS, TOL, TOLU,
2266 Daemon spelling mistake: monisotopic in mascot daemon (parameters page) 2268 Cannot use the -f option or move the data directory if the input file is mzData file 2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14 2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2261	Small ions score discrepency in error tolerant
2268 Cannot use the -f option or move the data directory if the input file is mzData file 2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2264	Bug 1495 is back. If one mod name is a sub-string of another, it is ignored.
2273 Mods string will use characters A-W to support more than 9 mods 2276 ms-monitor exits without error with:SubClusterSet 7 14 2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2266	Daemon spelling mistake: monisotopic in mascot daemon (parameters page)
2276 ms-monitor exits without error with:SubClusterSet 7 14  2279 add support for unimod_2.xml to ms-status.exe for getparams.pl	2268	Cannot use the -f option or move the data directory if the input file is mzData file
add support for unimod_2.xml to ms-status.exe for getparams.pl	2273	Mods string will use characters A-W to support more than 9 mods
- 1	2276	ms-monitor exits without error with:SubClusterSet 7 14
2280 Note in Daemon help about mascot.dll memory leak	2279	add support for unimod_2.xml to ms-status.exe for getparams.pl
	2280	Note in Daemon help about mascot.dll memory leak

2281	ms-monitor should create mod_file, substitutions, and masses for third party apps
	implement multiple NL and pep NL for exclusive modification groups (even though they
	are otherwise treated as choice of fixed mods)
	Overflow problems with variable mods and mass values over 9865 Da
2288	Cannot POST searches > 2 GB
2289	protein mass is incorrect when using quantitation if there are exclusive mods
2293	Allow the delimiter for CSV export to be changed
2297	Cannot search more than 1000 sequence tags without adding an ms spectrum
2298	Remove error M000345 (pl) from the category mailed to sysadmin
2299	Add support to Daemon for TS2MASCOT
	peptides with X at different positions are merged in result file. For example, protein1 with a peptide XABCD with the best ion score on WABCD-substitution and protein2 with WACBX with the best score on WACBD-substitution
	browscap.ini updated
	extract_msn -P parameter (MS^n) not working in Daemon
	For ET search, don't try substitutions for a residue that was an X
	File extension of "lastquery.asc.mas" causes weird behaviour on Windows when Access is installed
	Mascot Daemon should write its own version number to event log
	column alignment problem in CSV export
	Misleading error message: M00012 Can't open .unsort for "rb" when there is no peak list
	Scripts must use Parser to access config information from mascot.dat, unimod.xml, enzymes, taxonomy, fragmentation_rules.
2320	Can get very low qmatch and hence score threshold due to MinPepLenInSearch
2321	Add section to update script to create decoy database automatically
2322	http://unxutils.sourceforge.net/ is dead, change links to http://gnuwin32.sourceforge.net/packages.html
2327	error tolerant pop-ups broken when choose suppress pop-ups
2328	increase limit on number of parse rules from 64 to 256
2331	We need to make the following parameters configurable through security session object:  1) maxnumber of variable mods in a standard search  2) maxnumber of variable mods in ET search (old and new)  3) maxnumber of accession strings for old type ET search
2334	SECTASK_MAXJOBPRIORITY not being used anywhere
	Cross-site scripting vulnerability. It is possible to inject rogue scripting code into a submitted search form
2337	Installer will use SwissProt instead of MSDB
	maxnumber of accession strings for old type ET search to be read from security
	Export should include flag for whether match would be bold in summary report
	export_dat.pl not overriding mascot.dat file when RequireBoldRed=1
	Daemon needs to support error tolerant & decoy searches
2367	Remove references to trembl_new
2380	Export for PMF mixture gives invalid csv file
2383	Update Unix installation script to use parser
2398	Improve usage instructions for db_update.pl
2399	ms-monitor passes flags no longer used to load_node.pl