最初にお読みください
Mascot Server version 2.7 for Windows Release Notes

新規インストール

　　新規インストールを行う前に、2頁の「最新の追加情報」に対応する注意点」をご覧ください。インストールDVDにある「Mascot_Server_v2.7_Win_新規インストール手順.pdf」書類にしたがってインストールを進めてください。また、インストールDVDにある「manual.pdf」書類の「3. Installation: Windows」も併せてご覧ください。

アップグレード

　　バージョン2.6からバージョン2.7 にアップグレードする場合は、インストールDVDにある「Mascot_Server_v2.7_Win_アップグレード手順.pdf」書類にしたがってアップグレードを進めてください。また、インストールDVDにある「manual.pdf」の「3. Installation: Windows」も併せてご覧ください。なお、今まで使用していたライセンスファイルはバージョン2.7では使えませんので、弊社が提供するプロダクトキーを使ってバージョン2.7用のライセンスファイルを新規に取得してください。

新規サポート機能

　　インストールDVDにある別紙資料「ver.2.7新機能紹介.pdf」をご覧ください。

バージョン 2.6 からの変更点

　　3頁にバージョン2.6.0 からの変更点をまとめました。なお、この書類以降に追加された内容を含む最新の変更点に関しては、2ページの「最新の追加情報」並びに「http://www.matrixscience.com/mascot_support_v2_7.html」をご覧ください。

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最新の追加情報
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　お客様が作成したPerlスクリプトやサードパーティのプログラムに対するヘルパー・スクリプトがMascotフォルダにインストールされている場合、それらのスクリプトがMASCOT のセキュリティ設定が適用されないセキュリティホールになる可能性があります。MASCOTのセキュリティ機能をご利用の場合はご注意ください。

バージョン 2.6.2 からの変更点

以下の表並びに http://www.matrixscience.com/mascot_support_v2_7.html をご覧ください。また、下記項目の「Description」はメモ書きのような記述内容です。内容が気になる項目の詳細については弊社までお問い合わせください。

ID	Component	Description
4701	Server	Support third column in mgf fragment ion list for charge state
6036	Server	Variable mods permutations limit needs rethink
6289	Server	Can't open for "reading". Error No such file or directory [M00012]
6529	Server	Report decoy stats for proteins as well as peptides
6563	Server	Monitor very slow to start up under Windows when there are a large number of files under data
6762	Server	Cannot have both fixed and variable mods with terminus specificity
6795	Server	Get incorrect deltas if fixed and variable mods have overlapping but not identical specificity
6897	Server	'Silly' search causes crash in cluster mode. OK in standalone mode
10427	Parser	ms_aahelper needs argument to generate mass values for all neutral losses
10714	Parser	Parser error handling is not thread safe
10793	Parser	findPeptides() with FT_PEPTIDE_EXP_MZ and FC_SEARCH_ALL_RANKS returns all ranks with no match
10932	Server	Change to Trypsin if Manual error tolerant run
11283	Server	symlinks are deleted by the installer. For example, if you have set c:¥inetpub¥mascot¥data => d:¥mascot_data
11515	Server	Quantitation checkboxes enabled when related information can not be generated
11802	Parser	Python example script emits "query out of range" errors and crashes
11821	Server	Display long accessions in full
11835	Server	Show ET mod delta in modification counts, refine the yellow popup and allow searching for ET mods by delta
11930	Server	Add a confirmation button for deleting users and groups
12139	Server	When exporting percolated results with retention times enabled, the export form should not try to percolate the results a second time
12148	Server	Add switch to mascot.dat to over-ride asynchronous search submission (batch mode)
12190	Server	Add a checkbox to the MGF export form that outputs spectra in the original order
12326	Parser	Add switch to mascot.dat to over-ride asynchronous search submission (batch mode)
12365	Server	Failing to escape "&" in MS_STATUSXML
12393	Server	SwissProt PMF uses frightening amount of RAM
12397	Server	SVG spectrum graphic scales intensity axis incorrectly when match has reporter ions
12399	Server	SwissProt is not online; pI and sequence coverage are not available.
12420	Server	Inconsistencies in use of lower case letters for collapsed / alternative matches
12482	Daemon	Add a link for the combined search results
12496	Parser	Disallow creating a database whose name differs from an existing one only by case

12504	Server	Cleavage sites in spectrum graphic labelled incorrectly
12515	Server	Add Fasta to export formats
12523	Server	Display the number of active / inactive databases.
12575	Server	Modifying the fasta or msp file results in deletion of the old file
12610	Server	Forward all non-fatal error messages from cluster nodes back to master
12616	Daemon	Prevent submitting a library search as PMF or error tolerant or as average mass
12617	Daemon	Task never completes with certain follow-up settings
12620	Server	Mods defined in a quantitation method are not imported correctly in a spectral library
12633	Server	http://maxquant.org/contaminants.zip is no longer there
12634	Server	Fails to recognise downloaded file is compressed
12646	Server	Roll-up of changes to Manual, release notes, and HTML pages for 2.7
12667	Server	SearchControl very slow to create cache files
12697	Server	Error 587: Inconsistent peptide length : 6 provided, 5 in use
12701	Server	Protein Family Summary should support tag searches
12705	Server	Quantitation module of configuration editor is using old schema
12714	Server	Time to drop extract_msn search form
12730	Daemon	Checkboxes in auto-export dialog all checked on load
12753	Parser	ms_tinycdb openIndexFile uses string comparison on gmt timestamps to check file dates
12768	Server	Need to check at start of search that all query level mods are valid
12769	Server	Database Manager log files (e.g. db_manager.log) use UTC, while other Mascot logs use local time
12770	Server	Reporting of MIME errors in input file not working correctly
12805	Server	Windows installer does not backup fragmentation_rules, but does overwrite it
12806	Server	Crawled MSP file's comment field "File" should use forward slashes on Windows
12811	Server	Top down ET search with one significant first pass sequence shows no matches when trying to display ET results
12812	Server	Windows 8.1 and Windows 10 Start menu does not support sub folders. So, for example, the 'admin' or 'Distiller' folders are not shown.
12813	Daemon	Windows 10 (and possibly 8) Start menu does not appear to have sub folders. So, for example no 'admin' or 'Distiller' folders
12822	Server	If m_queries is higher than SplitNumberOfQueries in PMF, stop the search and warn the user
12834	Server	Export of a library-only search shows default threshold of 0.05 instead of 300
12842	Server	Error when adding frame number to an accession for ms-getseq in post request
12843	Server	Mascot Daemon does not report the top hit for a Spectral library search
12847	Server	Suppress PSMs with complementary deltas in error tolerant searches
12857	Parser	Potential crash when sorting peptides
12860	Parser	willCreateCache adds errors to the ms_mascotresfile object, resulting in duplicates
12863	Parser	Search modification by name with findPeptides returns only one value on Windows
12865	Server	Missing or outdated b00 file should trigger a recompression like other index files
12869	Server	Increase number of download attempts
12875	Daemon	Review string encoding in Daemon when submitting searches as POST requests
12888	Parser	Add a documentation page for the FDR procedure
12890	Server	programming error when filtering on Mr(calc)
12895	Parser	Add a utility function to compare XML files

12899	Server	Result files for searches against a single fasta should not have qX_pX_db lines
12900	Server	Add protein mass and peptide missed cleavages to mzTab output
12902	Parser	Modification statistics for error tolerant search can be highly misleading
12906	Server	Warning: unexpected difference between Mr from result file (1992.829956) and Mr re-calculated from masses (1990.835879425)
12913	Parser	Revert to just saving rank 1 in percolator pip file
12921	Parser	Add PSM and sequences used for ID to proteinHit element of quant XML export
12924	Parser	Peptide summary cache file name is different between master_results and ms-searchcontrol
12933	Server	On monitor start-up, if the reference fasta is incorrectly cased, warn that a similar database exists
12936	Parser	Report of Error tolerant search does not display all matches when None is selected
12937	Parser	Update from SWIG 2.0.12 to SWIG 3.0.12 for ALL languages supported by Parser
12972	Server	Substitution of XBZ is not consistent at either terminus - Erroneous absence of braces in CSeqModifier::chooseNextRes
12977	Parser	Revive MinGW as target platform and compile against ActivePerl/Strawberry Perl 5.26, 5.28, 5.30
12985	Daemon	Should be some easy way to open the parameter set selected in task editor tab in the parameter editor
12987	Daemon	(MDS1016) 5: Nullable object must have a value
12990	Parser	Logging: Improvements for ms_ms_loggingmonitor required including better documentation
12997	Server	Cannot create custom annotation URL for NA database
13003	Server	Isn't numeric in sort error message when crawling and building a SL.
13020	Parser	I don't believe PSM and PepSeq counts for Percolated results
13029	Parser	Add ActivePerl 5.24, 5.26, 5.28, 5.30 build targets on Linux
13032	Server	Cross-link changes in nph-mascot
13033	Parser	.MSP File Format Issues (Was Error message text for ERR_MSP_NIST_MSP_NO_SPECTRA is misleading)
13034	Server	Put all warnings and errors from parsing a spectral library into the compression log
13043	Server	Must click Next twice when copying a database definition
13045	Server	Tooltip on FDR says 'False decoy rate'
13046	Server	Search form changes for intact crosslinking
13058	Server	Remove CMC as mail option
13063	Server	DBM error after installation
13065	Server	Percolator is executed by default for all auto-decoy searches
13075	Server	Need an option to suppress pip file creation
13086	Server	Feature finder outputs z+2 fragments as z+1 fragments
13088	Server	Bug in copying over or replacing PRIDE_Contaminants?
13091	Server	When using DECOY_PROTEIN_RANDOM as DecoyTypeNoEnzyme, no peptide matches in a 5-sequence AA database
13094	Server	Incorrect insertion of forward slash in a file URL if directory doesn't exist
13101	Parser	Add support for Python 3.6
13102	Server	Tag searches should not allow ambiguity codes
13108	Parser	.MSP File Format Issues #2
13109	Server	Error tolerant wierdness with lower case peptide sequences, peptides assigned to the wrong protein and scoring differences
13118	Server	Search for a variable mod in the report, subset protein link is sometimes faulty

13122	Parser	Mascot Server reporters error with ms-ms data when variable reporter ion modifications are selected
13124	Parser	Segfault when caching an iTRAQ 4-plex file with variable mod group
13131	Server	Checkboxes for optional columns become enabled after going back in browser history
13132	Server	Proxy authentication fails for HTTPS requests tunneled through an HTTP proxy
13133	Server	Display crosslinked peptides in Peptide View
13140	Server	New command for ms-status.exe for checking when configuration files have been synched with nodes
13144	Server	Modifications module of configuration Editor needs to support crosslinkers
13149	Server	Search with query level IT_Mods crashes
13154	Server	Add a message to monitor.log to say a node has been started/shut down
13164	Server	Platform-dependent rounding differences in generated spectral library and data exported with export_dat_2.pl
13168	Server	Test harness changes to unimod.xml and unimod_xl.xml
13169	Server	Crash when running a search with less queries than nodes
13172	Server	Remove upper limit on MinPepLenInPeptideSummary
13200	Parser	New ms_peptidesummary constructor parameter: minimum number of significant unique sequences
13208	Server	Format time in a standard way in the stats file
13209	Server	Monitor crashes on linux with an old glibc in a sequence is too long
13221	Server	Still problems if fixed and variable mods have overlapping specificities
13222	Daemon	Limit number of cores or threads Mascot Daemon uses for processing.
13226	Server	In Peptide View, link for lower ranking peptides is missing _minpeplen
13227	Server	Add an ion mobility field to MGF
13230	Parser	ms_mascotresfile::appendResfile() generates lots of XML errors unless used on Mascot Server
13234	Parser	Crosslinking method definition API and class structure
13241	Parser	Description of getMaxPepModArrangements method in the documentation is confusing
13243	Parser	Update unimod.xml to the latest one
13244	Server	Merge master_xl.xml and usermod_xl.xml to unimod_xl.xml
13245	Server	Add crosslinking.xml and crosslinking_1.xsd to the shipper image
13250	Daemon	If the PeakListRoot registry value is invalid, Daemon won't start
13251	Server	Modification statistics depend on setting of 'Max. number of families'
13268	Parser	ms_peptidesummary::isDataCached() returns false for BUGFIX_12740
13272	Server	Display crosslinked peptides in Protein View
13274	Server	Read crosslinking parameters from crosslinking.xml
13275	Server	Read crosslinkers from unimod_xl.xml
13276	Parser	ms_mascotresfile::getMasses() sets electron mass to 0.0 for results files from 1.9 and earlier
13284	Parser	DEFAULT_MINPEPLENINPEPSUMMARY should be 7
13288	Parser	ms_fragment needs a constructor for precursor NL peaks
13295	Server	Pretty print crosslinking method and linker definition
13296	Server	get_params.pl: Output [LINKERS] and [CROSSLINKING] sections
13297	Server	MGF export for mzIdentML should specify correct file name
13298	Server	Suppress or remove lastquery.mgf
13301	Parser	Add flanking residues to the distiller xml MS1 quantitation results export
13310	Parser	Peptide without required fixed mod for Reporter quant incorrectly has quant ratios

13312	Parser	Add new option in ms_mascotoptions for suppressing PIP file creation during the search
13313	Server	New command to ms-status.exe, MS_CROSSLINKINGXML_COMPRESSED
13315	Parser	Review default crosslinking methods in crosslinking.xml
13316	Server	Update SwissProt and PRIDE_Contaminants for the installer
13322	Daemon	Mascot Daemon seq-database field length is to small
13324	Parser	New method ms_mascotresults::getDiscoveredLocalModDeltas(), and output order of getDiscoveredErrTolModDeltas() is ambiguous
13326	Server	Add text to the installer to make it clear that it's easier to use IIS on Windows
13329	Server	ms-config.exe needs to pretty print the crosslinking method
13337	Parser	"The msp file: '%s' contains a spectrum with no peaks" should be a warning, not an error
13351	Server	Matches with scores below 0.001 should not appear as they are 0.00 in the result files
13370	Daemon	Perseus / CSV quantitation export
13372	Server	Report percentage progress when exporting merged results
13383	Server	Add function to client.pl to return quantitation.xml config file
13393	Server	Add a new TMT 16-plex quantitation method
13408	Daemon	Add crosslinking to parameter set
13409	Parser	ms_peptide::getIonsScore() and ms_mascoresults::getIonsScore() return different values with same args.
13411	Server	Basic configuration editor for crosslinking methods
13420	Server	MSPepsearch magically changes CAM -> Carbamidomethyl
13437	Parser	Add Options: DechargeFragmentPeaks
13445	Server	The reference cdb file of a spectral library is not updated when the reference database is updated
13455	Server	Change the default MaxSequenceLen to 80000

何かお困りのことがありましたら support-jp@matrixscience.com （技術サポート）にご連絡ください。

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