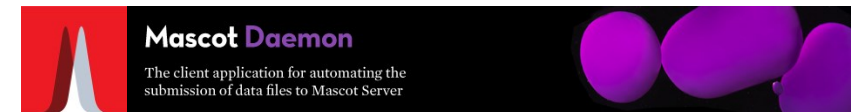
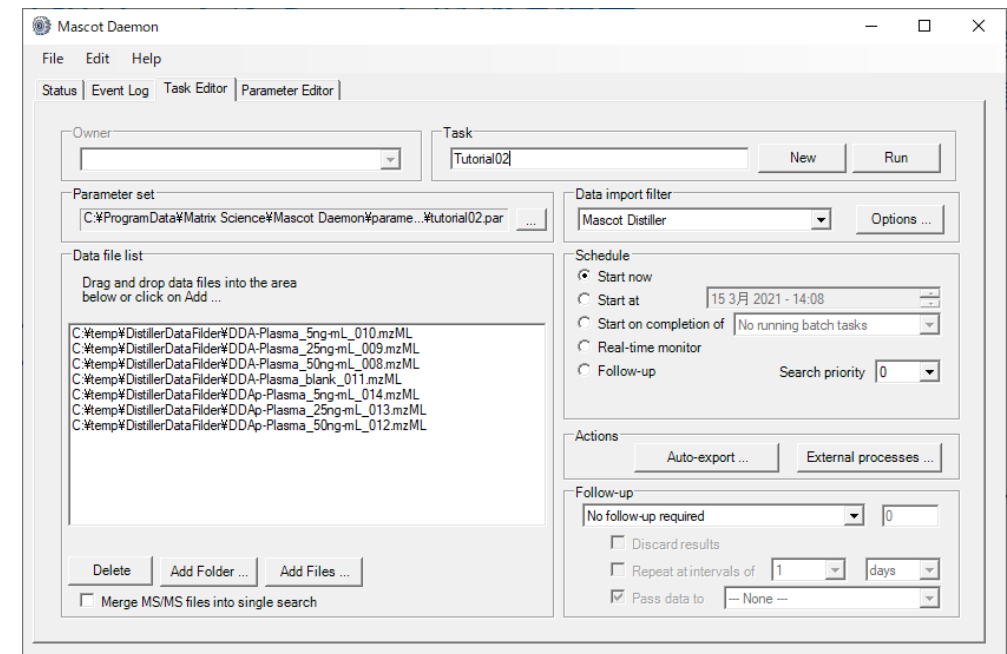


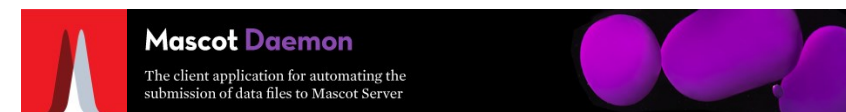
# MASCOT Daemon: 機能



- 複数のデータを同一検索条件で検索実施
- rawデータ変換プログラム (Distiller, ProteoWizard MSconvert)の適用
- データの結合
- CSVファイル出力
- 装置付属のソフトウェアを使わず MASCOT検索が可能



# Daemon の操作手順 : Parameter Editor



Mascot Daemon

File Edit Help

Status | Event Log | Task Editor | **Parameter Editor**

Parameter set  
Filename: C:\ProgramData\Matrix Science\Mas...default.par [New] [Open ...] [Save] [Save As ...]

All Searches

User name <mascot\_user\_full\_name> User email <mascot\_user\_email>

Search title <taskname> (<parameters>), submitted from Daemon on <localhost>

Taxonomy ..... Homo sapiens (human) Report top AUTO hits

Databases SwissProt [Select Databases] Protein mass kDa

Decoy  Enzyme Trypsin

Fixed modifications Carbamidomethyl (C) [Select Modifications] Max. missed cleavages 1

Variable modifications Oxidation (M) Monoisotopic  Average  Peptide charge 2+ and 3+

Peptide tol. ± 0.1 Da # 13C 0

MS/MS

MS/MS Ions search  Data format Mascot generic Instrument Default

Error tolerant search  MS/MS tol. ± 0.1 Da Quantitation None

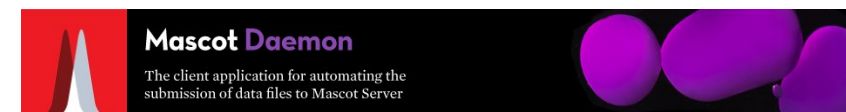
Target PSM FDR 1% Crosslinking None

[1] 「Parameter Editor」タブをクリック

[2] 検索条件を指定

[3] 「Save」または「Save As」ボタンで設定ファイルを保存

# Daemon の操作手順 : Task Editor



The screenshot shows the Mascot Daemon Task Editor window. The interface includes a menu bar (File, Edit, Help), a status bar (Status, Event Log, Task Editor, Parameter Editor), and several main sections: Owner, Task, Parameter set, Data file list, Data import filter, Schedule, Actions, and Follow-up. Red boxes highlight specific elements: the Task Editor tab, the Task name field, the Add Files button, the Run button, and the Data import filter dropdown. Yellow callout boxes provide instructions for each step.

[4] 「Task Editor」タブをクリック

[5] Task名を指定

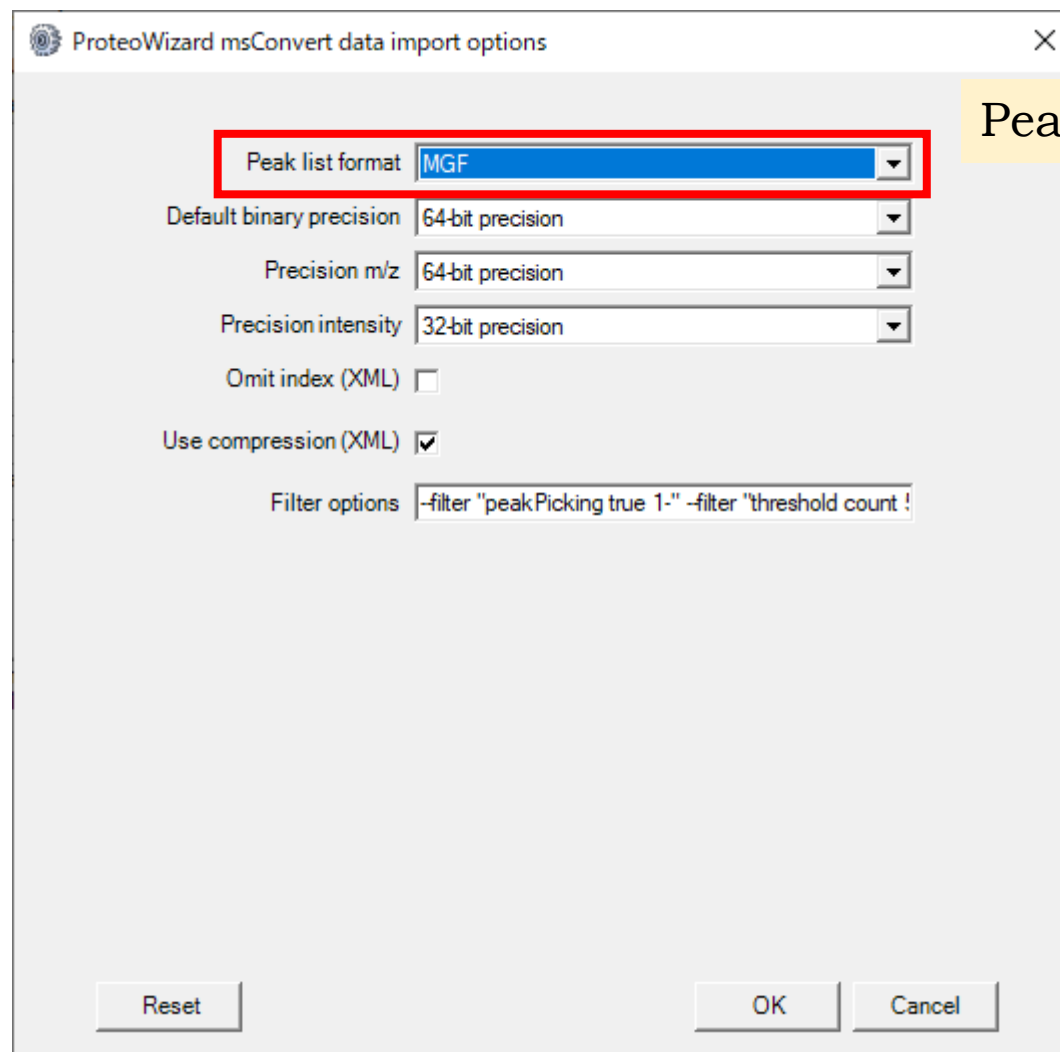
[6] Parameter ファイルを選択

[7] 検索対象となるファイルを選択

[8] \*検索ファイルがrawデータの場合 rawデータを変換するプログラムとそのオプションを指定  
Optionについては次スライドで補足説明

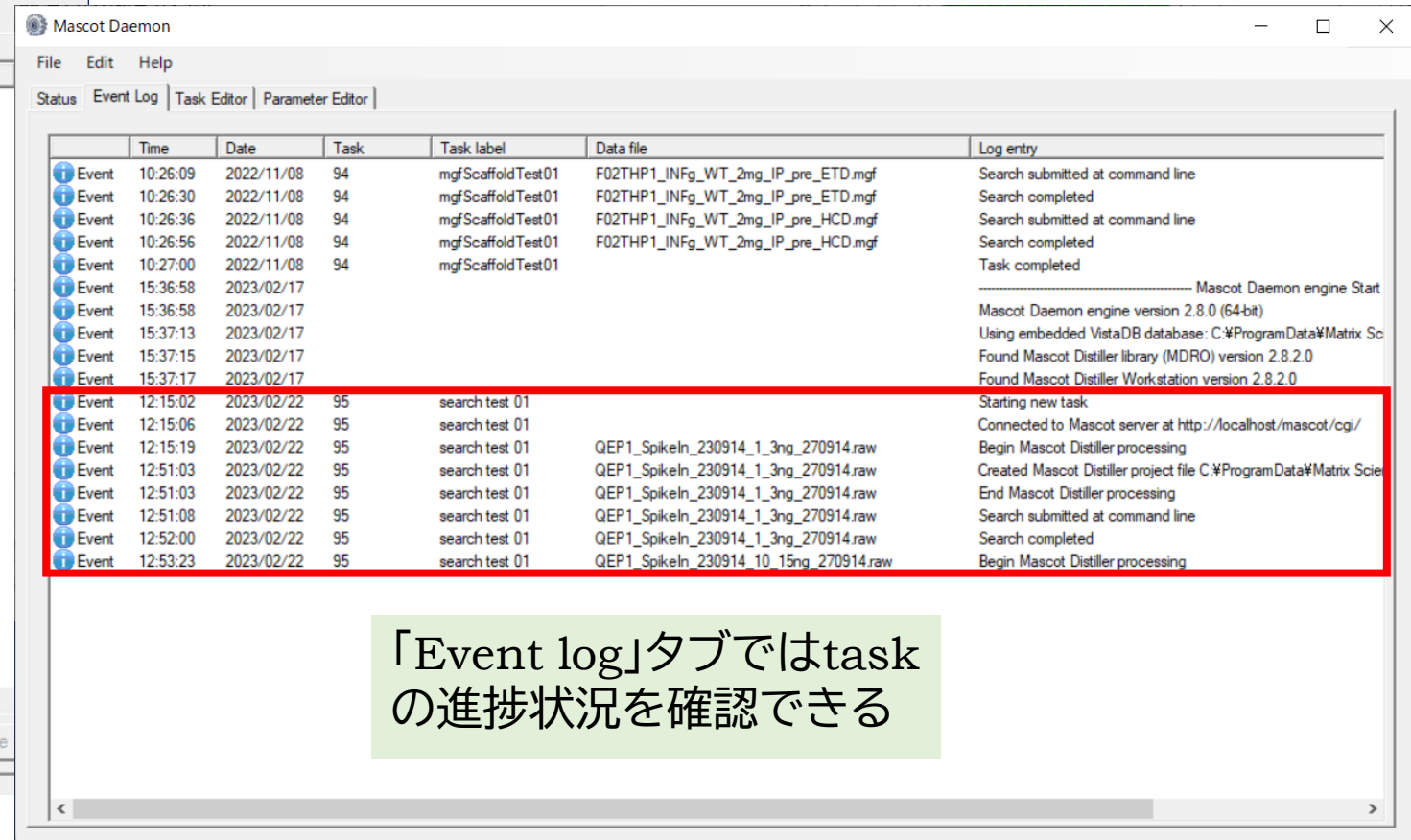
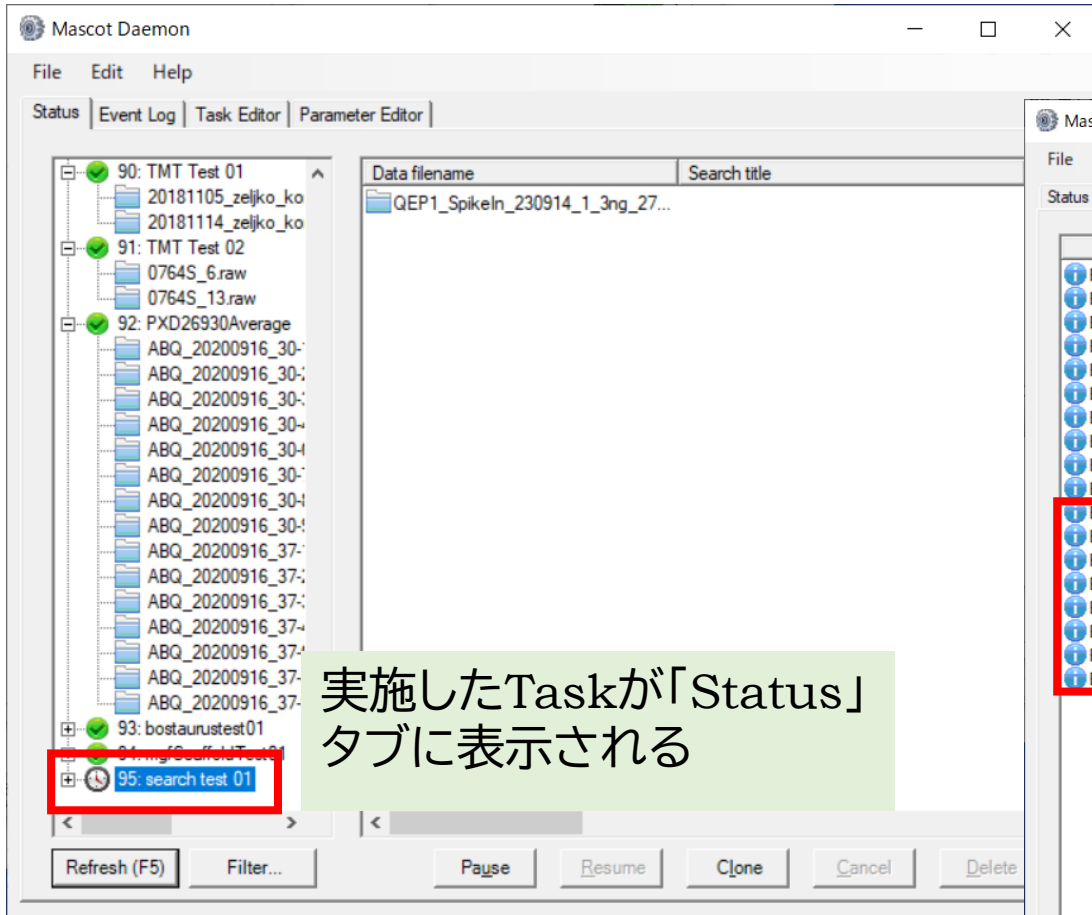
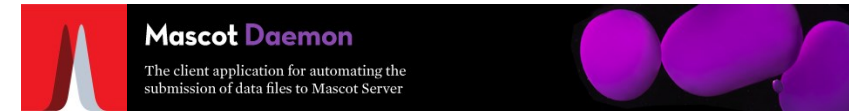
[9] Runボタンを押して検索開始

## 補足説明 : Data import filterのOptionsダイアログ[ProteoWizard MSconvert]

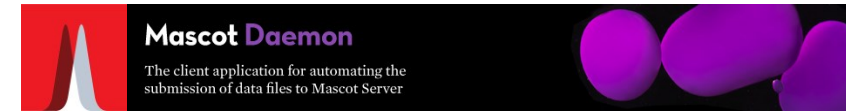


Peak list formatを”MGF”に変更

# Daemon の操作手順：検索待ち



# Daemon の操作手順：検索結果の確認



[11] rawデータのファイル名が記されたフォルダをクリックすると、結果のまとめが表示される

[10] 検索が完了すると、task名の前のマークがとなる。

**MASCOT Search Results**

User :  
E-mail :  
Search title : search test 01 (C:\ProgramData\Matrix Science\Mascot Daemon\parameters\daemondistiller.par), submitted from Daemon on T5820  
MS data file : C:\temp\replicatesDataset\QEP1\_SpikeIn\_230914\_1\_3ng\_270914.raw  
Database : SwissProt\_2022\_02 (567,483 sequences; 204,940,973 residues)  
Taxonomy : Homo sapiens (human) (20,387 sequences)  
Timestamp : 22 Feb 2023 at 03:51:35 GMT

Re-search  All  Non-significant  Unassigned [\[help\]](#) Export As

Not what you expected? Try [\[help\]](#) the select summary.

- Search parameters
- Score distribution
- Modification statistics for all protein families
- Legend

**Protein Family Summary**

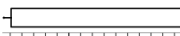
Format Significance threshold p< 0.05 Max. number of families AUTO [\[help\]](#)

[12] result file URL の項目をクリックすると、結果画面が表示される

**Protein families 1-10 (out of 1550)**

10 per page 1 2 3 4 5 6 ... 155 Next Expand all Collapse all

Accession contains Find Clear

1  1 ENOA\_HUMAN 4385 Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV...  
2 ENOB\_HUMAN 1652 Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV...