



We've introduced a number of new features into the forthcoming Mascot Distiller 2.6 release. We'll start by taking a look at the newly added support for Waters MS^E datasets

| )    | Waters MS <sup>E</sup> support      |             | Mascot Distille                             |
|------|-------------------------------------|-------------|---|
| File | View Processing Analysis Tools Help |             |   |
|      | New Project                         | •           | Sciex · 追 遂 谷 Se 智 署 署                      |
|      | New Multi File Project              |             | Bruker +                                    |
| 2    | Open Project                        | Ctrl+O      | Agilent +                                   |
| 2    | Close Project                       |             | Waters >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>> |
|      | Close All                           |             | Shimadzu 🔸 🧳 MassLynx MS^E                  |
| 6    | Save Project                        | Ctrl+S      | Thermo +                                    |
|      | Save Project As                     |             | mzXML                                       |
| 2    | Print                               | Ctrl+P      | mzML  |
|      | Print Preview                       |             | Text  |
|      | Print Setup                         |             |   |
|      |                                     |             |   |
| 1    | ASCOT : Mascot Distiller            | © 2016 Matr | rix Science MATR<br>SCIEN                   |

When you create a new project in Mascot Distiller 2.6 you'll see a new option under the Waters sub-menu – MassLynx MS<sup>\*</sup>E. To create a new MS<sup>\*</sup>E project, simply select this option.

| <b>\$</b> )          |                     | Select Masslynx MS^E data se    | t                | ×            |
|----------------------|---------------------|---------------------------------|------------------|--------------|
| Look in:             | MS^E                |                                 | · 🗿 🤌 📂 🛄 •      |              |
| e.                   | Name                | ^                               | Date modified    | Туре         |
| Provet alares        | 082106_07           | 5_Mix1_Ec_HL_Long_02.raw        | 24/03/2016 08:24 | File folder  |
| Desktop<br>Libraries |                     |                                 |                  |              |
|                      | ٢                   |                                 |                  | >            |
| Network              | File name:          |                                 | ~                | Open         |
| Network              | Files of type:      | All Files (*.*)                 | ¥                | Cancel       |
|                      |                     |                                 |                  | <u>H</u> elp |
| Processing Option    | n default.Wa        | stersMS2E.opt                   | -                |              |
| (A)-IX A, 0.5 pr     | 101, E COI 5 09, 11 | Volue                           | -                |              |
| Creationdate         |                     | 22-Aug-2006-00:54:59            |                  |              |
| Version              |                     | 01.00                           |                  |              |
| Sample name          |                     | Mix 1, 0.5 pmol, E coli 3 ug, H | iigh/L           |              |

And select the MS^E raw data folder in the file dialog.

This allows you to open and process MassLynx MS<sup>E</sup> datasets within Mascot Distiller – including using them for precursor and label free quantitation experiments.

|                           | Processing Option   | ns - 20130214_02_PO1_Sum   |               |
|---------------------------|---|--|---------------|
| MS Processing MS/MS Proce | ssing Time Domain MS Pe   | eak Picking MS/MS Peak Picking   |               |
|                           |   | General Same as MS Peak Picking Apply baseline correction Fit method Vendor: MassLynx Maximum peak iterations per scan   | MS^E ↓<br>500 |
| Vendor Peak Picking Optic | ins   |  |               |
| 1<br>100<br>250<br>0.25   | -bEnableCuda - Enable<br>-chromFWHMMin - FWH<br>-heThresholdCounts - H<br>-leThresholdCounts - Lu<br>-lockMassToleranceAW<br>-lockMassToleranceAW | GPU processing (0 or 1)<br>HM in minutes, calculated if not specified (float > 0)<br>High energy detection threshold (integer > 0)<br>ow energy detection threshold (integer > 0)<br>U - Lock mass error tolerance (float > 0)<br>the external lock spray peak (float > 0) |               |

We're using the Waters libraries to access and deconvolute the MS^E peaklists, while precursor processing is done internally. So if you are setting up MS^E processing options in Mascot Distiller, on the MS/MS Peak Picking settings tab you'll see a new drop down menu for 'Fit method'. This allows you to select the Vendor:MassLynx MS^E fit method instead of the normal Isotope Distribution option.



When we open an MS<sup>E</sup> dataset, this is what the acquisition tree looks like, with a mixture of DIA MS, MS/MS scans along with Calibration scans



We carry out peak detection on the dataset as normal



And the generated peak lists dataset looks like this, with our deconvoluted scans under the precursor.



We can now submit the peaklists to Mascot for a database search just like any other peaklist. One additional minor improvement you can see in this slide is the background highlighting of peptides. When we select a peptide match, such as this one here, it is hightlighted in the Proteins tree in any proteins it matches into.



In addition to this, we can use the extra functionality provided by Mascot Distiller with the processed MS<sup>E</sup> data – for example, the Mascot Distiller Search Toolbox provides a powerful de novo sequencing tool. This dataset is from a species of fungi which is poorly represented in the sequence databases - Here we have an example where the de novo tool has found a good match on one of the MS<sup>E</sup> spectra where the standard database search found no significant matches. A quick BLAST of the denovo sequence result found a match to a sequence from a related species.



One of the biggest advantages of processing the MS<sup>A</sup>E data in Mascot Distiller is that you can now use these datasets for the precursor and label free quantitation protocols supported by the Mascot Distiller quantitation toolbox. Here we have an example of a SILAC MS<sup>A</sup>E quantitation dataset, processed searched and quantified with Mascot Distiller and Mascot Server.





A common problem encountered when carrying out reporter ion quantitation methods, such as TMT or iTRAQ, is that of interfering ion signals in the reporter region. One approach which can be taken to reducing the issue is to reisolate the most abundant ion in the MS/MS spectrum and refragment it – the resulting reporter ion signals in the MS3 signal are then almost exclusively from the target peptide.

| MS3    | Processing Opt         MS Processing MS/MS Processing Time Domain MS Pead         Group Assignment         Minimum precursor mass (Mr)         Decession (Mr)         Precursor m/z tolerance         Maximum intermediate time (secs)         Maximum intermediate scan count         Use intermediate scan count where possible         Group Filtering         Minimum number of scans         Save         Load | ions - pm_diauxic_1       X         rPicking       X         rPicking       Summing         wove reporter ion peaks       scarb         from       to       scarb         Sum identical MS2 scarr types       Sum identical MS2 scars         Sum identical MS2 scarr types       Sum identical MS2 scars         Sum MSn scans into MS2       MS2 scans         OK       Cancel       Help |
|--------|---|---|
| MASCOT | : Mascot Distiller  | © 2016 Matrix Science   |

To support this, we've added new options on the Time Domain section of the Processing Options dialog in Mascot Distiller. Under the 'Group combination' section, if we have 'No summing' selected, we can choose to move the reporter ion peaks from the MS3 scans to the MS2 scans. Alternatively, you can sum the entire MS3 scan into the MS2 scan.



Once we've carried out peak detection, on the peak lists tab we have our MS2 and MS3 scans grouped together. This is the MS/MS scan – notice that it doesn't contain any reporter ions.



And this is the MS3 scan containing the reporter ions. If we click on the grouped scans node



This is the MS/MS scan with the MS3 report ion region merged into it – this is the peaklist that we searched in Mascot. As you may be able to see, this peak list got a very impressive match with a score of 159. Here is the result in Mascot with the quantitation ratios.



In addition to merging MS3 scans into the parent MS/MS scans, Mascot Distiller 2.6 includes options for summing or merging scans together based on scan type.



Some instruments can produce raw data files with multiple different types of scan data for the same precursor in them – a common example of this would be an experiment on a Thermo Orbitrap instrument raw data file containing both CID and HCD scans for the same precursor. Often, you would often want to sum these spectra before carrying out a database search – For example, a common experiment to improve the quality of report ions when using quantitation methods such as iTRAQ or TMT involves carrying out DDA of CID scans on the peptide precursor, and then further fragmenting the same precursor using HCD to get spectral information in the reporter ion region. In this case you'd want to merge the information from the reporter ion information from the HCD scan into the CID scan, and then search the merged peaklist.

| Merg   | Image       C:\ProgramData\Matrix Science\Matrix         MS Processing       MS/MS Processing       Time Domain       MS Peak F         Group Assignment       MS/MS Processing       MS Processing       MS Processing       MS Processing         Maximum precursor mass       (Mr)       700       16,000         Precursor m/z tolerance       0.01       0.01         Maximum intermediate time (secs)       Maximum intermediate scan count       0.01         Use intermediate scan count where possible       Use intermediate scan count where possible       1 | Ascot Di\CID_HCD_reporter.ThermoXcalibur.opt  Ascot Di\CID_HCD_reporter.ThermoXc |
|--------|--|--|
|        | Save V Load  | OK Cancel Help   |
| MASCOT | : Mascot Distiller   | © 2016 Matrix Science MATRIX   |

In Mascot Distiller 2.6 we've introduced the ability to merge different scan types. The options to do this can be found on the Time-Domain tab of the processing options dialog in the Group combination section. If you are interested in only moving reporter ions from one scan-type to another, you can select 'No summing' with the 'Move reporter ion peaks' checkbox checked, as shown here. These processing options would move the reporter ion region specified under the 'single peak picking' region of the MS/MS Peak Picking options from the HCD into the CID scans.

| Merg   | Ing differer<br>Processing Options - C:\ProgramData\W<br>MS Processing MS/MS Processing Time Dor<br>Group Assignment   | nt sc<br>latrix Science\P<br>nain MS Peak F | Aascot Di\CID_HCD_reporter.ThermoXcalibur.opt  |
|--------|--|---|--|
|        | Minimum precursor mass (Mr)<br>Maximum precursor mass (Mr)<br>Precursor m/z tolerance<br>Maximum intermediate time (secs)<br>Maximum intermediate scan count<br>I use intermediate scan count where po | 700<br>16,000<br>0.01<br>0<br>5<br>ssible   | No summing  Move reporter ion peaks from v to v scans Move reporter ion peaks from MS3 to MS2 O Sum identical MS2 scan types |
|        | Group Filtering<br>Minimum number of scans<br>Save V Load  | 1   | CID and HCD MS2 scale  Normalise HCD intensity CID ECD ECD ECD IRMPD ISD PCO Unknown CM CAncel Help                          |
| MASCOT | : Mascot Distiller   |   | © 2016 Matrix Science  |

Previously this could merge complete scans together on the basis of precursor m/z and retention time – now you can also use the scan type.

So you can also sum complete spectra together of any or of specified types, with options for normalising the intensities of the scan type being summed in to the 'parent' scan.



Data taken from http://www.ebi.ac.uk/pride/archive/projects/PXD000503

Once we've carried out peak detection this is what the Peak Lists tree looks like in Distiller, with a Grouped Scans node, under which we have the source scans. This is the CID scan. This is an iTRAQ 8-Plex dataset, and notice that we don't have any peaks in the spectrum below an m/z ratio of about 200. So no reporter ions.



This is the HCD scan. This is where the iTRAQ 8-Plex reporter ions are.



And this is the Grouped Scan with the picked peaks – This contains information from both the HCD and CID scans. I've zoomed in on the report ion region here.



|   | Select Analyst data set   | ×                         |                            |                         | 5                  |             |
|---|---|---------------------------|----------------------------|-------------------------|--------------------|-------------|
| Look in:  | 🕌 Sciex   | Y Q Ø Ø ▷ □ Y             |                            |                         |                    |             |
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| cent places   |   | MS Processing MS/MS Proce | ssing Time Domain MS Peak  | Picking MS/MS Peak Pic  | king               |             |
|   |   |                           |                            | -                       |                    |             |
| Desktop   |   |                           |                            | General                 |                    |             |
|   |   |                           |                            | Same as MS Pea          | k Picking          |             |
| Librarier   |   |                           |                            | Apply baseline o        | orrection          |             |
| Clonences   |   |                           |                            | Tit we then d           |                    |             |
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| This PC   |   |                           |                            | Maximum peak itera      | tions per scan     | 500         |
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| Natural   | File name: 20140119.wff   | Vendor Peak Picking Opdo  | ns                         |                         |                    |             |
| Network   | Files of type: Analyst (*.wiff)   | Value (dick to edit)      | Option Name                |                         |                    |             |
| ocessing Option<br>I)Sample001<br>iield<br>Creationdate<br>Operator | Scfault.ScexAnalyst.opt     API-III.opt     default.ScexAnalyst.opt     QStar.opt     QTapa.opt     qtap.ScexAnalyst.opt     qtap.ScexAnalyst.opt     qtap.sporter.ScexAnalyst.opt     endort.ScexAnalyst.opt     endort.ScexAnalyst.opt | 1999                      | Maximum peaks allowed fo   | r each scan.            |                    |             |

When you create a new project for Sciex .wiff datafiles, you'll see that we've added an additional standard processing options file – vendor. If you select this option, then MS peak detection is carried out by Mascot Distiller, while MS/MS peak picking uses the vendor peak detection. You can select this from the MS/MS peak picking tab on the Processing Options dialog window in Mascot Distiller, so you can switch to using the vendor peak detection for your own, tweaked, processing options.



The big advantage of this is speed – because the vendor peak detection has already been carried out, we're just pulling the values out of the .wiff file. The disadvantage of this is that you cannot of course further tweak the MS/MS peak detection parameters within Mascot Distiller.

As a comparison, I carried out MS/MS peak picking using either Mascot Distiller or the vendor peak picking on the same raw datafile. In both cases, precursor peak detection was carried out by Mascot Distiller. As you can see, using the vendor MS/MS peak detection was considerably faster.



The test dataset I used was a SILAC experiment. Because precursor peak picking and processing was carried out by Mascot Distiller, even though vendor peak picking was used for the MS/MS spectra, we can still carry out SILAC quantitation using Mascot Distiller. So, in the screenshot shown here, we've used Mascot Distiller for precursor peak detection, then used vendor peak detection for the MS/MS spectra. Searched the peaklists in Mascot and carried out SILAC quantitation in Mascot Distiller.





If your raw data files contains different scan types (e.g. CID and ETD scans), then you might want to search the generated peaklists using different ions series depending on the source scan type. Normally, to search CID and ETD scans together, we recommend using a composite CID+ETD instrument definition which contains the ions series for both scan types.

However, the Mascot Generic peaklist format has supports setting the instrument type at the level of each individual MS/MS peaklist. In Mascot Distiller 2.6, on the 'Peak List Format' tab under preferences, you'll find an additional option which allows you to automatically set the INSTRUMENT parameter in the exported peaklists of a selected scan type. For these spectra, when the peaklist is generated, the INSTRUMENT parameter value will override the option selected on the Mascot search form.

Searching the different scan types with the correct instrument definitions can give you better sensitivity – for example, searching this dataset with separate EDT and CID instruments yields a 4.4% increase in the number of significant peptide matches at 1% FDR when compared to searching with the composite instrument definition.



In Mascot 2.6, if you select the MGF or mzData peak list formats, additional structured information about the peak list can be output using the controlled vocabulary defined by the Proteomics Standards Initiative. In the header of an mgf file generated by Distiller 2.6, you'll find these two new labels, DISTILLER SOURCE TYPE and

\_DISTILLER\_INSTRUMENT\_MODEL, which will give the source and instrument model as the PSI:CV term.

In addition, you can include scan type as PSI\_CV terms in the individual scan titles

| Mascot Distille   | r - Preferences -                                     | F1 25-26_5001  |   |                        |
|---|---|--|---|------------------------|
| Seneral Scan TIC M<br>MS/MS Fragmentation Peak List For   | Mascot Search<br>mat                                  | Sequence tag<br>Mass Deltas                                    | g / De Novo<br>Quantitat                              | Digest<br>tion Table   |
| ✓ Single peak list for multiple precursor charges<br>○ Output S/N to peak list in place of area<br>○ Allow multiple precursors per scan | Fragment ior<br>Output a<br>PMF peak list<br>Output a | s in MS/MS peak lists<br>s Mr Output as<br>s<br>s Mr Output as | MH+  Outpu  | ut as m/z<br>ut as m/z |
| GF parameters<br>Processing options in header<br>Allow user parameters<br>Scan range information<br>Output INSTRUMENT=                  | • for   | ▼ scans  | ndude in scan title<br>✔ Raw file path<br>✔ Scan type | >                      |

If you want to include the scan type in the scan titles, go to the 'Peak List Format' tab on the 'Preferences' dialog and ensure that the new 'Scan type' checkbox is checked before you export the peaklist.

| DISTILLER_MDRO_VERSION=2.5.0.243<br>_DISTILLER_ORIGINAL_MDRO_VERSION=2.5.0.0<br>INTERVIEWERSION_MDRO_VERSION=2.5.0.0<br>INTERVIEWERSION=NUMBERGI AND |                                      |
|--|--------------------------------------|
| DISTILLER_INSIGNERI_ROUGENT_AIRSI1000056<br>UNITILER_USE_SINGL_FREUENSUF_FER_FERELISIT<br>DISTILLER_USE_SINFATIO_AS_INTENSITY=0  |                                      |
| _DISTILLER_FRACMENT_IONS_MASS_TYPE=mp/z<br>_DISTILLER_PEPTIDE_IONS_MASS_TYPE=mp+   |                                      |
| BEGIN IONS<br>TITLE=1: Scan 386 (zt=101.368, p=0, c=96, e=1) [D:\MSData\Example datasets\Chalkley_MCP_2005_4_1189_1193\wiff\F1 SuLUCSF.wif<br>PEPMAS=4453.94201 1241<br>CHARGE=24        | <pre>(1) MS:1000133 MS:1000084</pre> |
| SCANS=386<br>RAMSCANS=pd0cy96ex1<br>RINSCONDS=101.368  |                                      |
| 89.03587 0.014532215<br>97.031439 0.0069116147   |                                      |
| 102.06378 0.0067988051<br>107.04769 0.006977926  |                                      |
| 114.07452 0.48558099<br>117.0776 0.0077467478  |                                      |
| 123.02301 0.00/14.0300<br>123.09996 0.058020235<br>124.12047 0.023784212   |                                      |
| 161116VU/ VIVEJUVELE   |                                      |
|  |                                      |
|  |                                      |
| MASCOT : Mascot Distiller © 2016 Matrix Science  | MATRIX<br>SCIENCE                    |

Here we have an example from a peaklist file with the new options included. Here we have the source type and instrument model in PSI:CV terms

And appended to the end of the scan title we have two terms for the scan type, also in PSI:CV





We've made some changes to one hit wonder handling for protein quantitation in Mascot Distiller 2.6. In Mascot Distiller 2.5 or earlier, the number of quantified peptides reported in the protein quantitation information was the total number of quantified matches to the protein sequence, with identical peptide sequences being counted multiple times – so if you had matches to the same peptide sequence at different precursor charge states, that sequence would be counted multiple times. In Mascot Distiller 2.6, we've changed this so that it is now the count of distinct peptide sequences matching to the protein which is reported.

| antita   | ation Table   |  |  |  |   |   |   |  |  |  |
|--|---|--|--|--|---|---|---|--|--|--|
|  | Accession   | Score  | Mass   | M/L  | SD(geo)   |   | H/L   | SD(geo)  |  | Description  |
|  | NMT1_HUMAN  | 187  | 57112  |  |   |   | 0.8725  | 1.2398   | 2  | 2 Glycylpeptide N-tetradecanoyitransferase 1 OS=Homo sapiens GN=NMT1 PE=1  |
|  | SSRA_HUMAN  | 187  | 32216  | 1.4310   | 1.1677  | 2   | 2.0402  | 1.0054   | 2  | 2 Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=  |
|  | DNJA2_HUMAN   | 187  | 46344  | 1.2524   | 1.0273  | 2   | 1.4393  | 1.1691   | 3  | 3 DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV  |
|  | WDFY1_HUM   | 187  | 47320  | 1.1302   | 1.0744  | 2   | 1.5029  | 1.1698   | 2  | 2 WD repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=WDF  |
|  | NPTN_HUMAN  | 187  | 44702  | 0.9985   | 1,1609  | 4   | 1.2151  | 1.0336   |  | 3 Neuroplastin OS+Homo sapiens GN+NPTN PE=1 SV=2   |
|  | SMAP_HUMAN  | 186  | 20378  |  |   |   | 0.9902  | 1.1187   | 2  | 2 Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1   |
|  | BIEA_HUMAN  | 185  | 33693  | 1.1570   | 1.0008  | 2   | 1.1441  | 1.1321   | 3  | 3 Bilverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2   |
|  | LRP10_HUMAN   | 185  | 78027  | 0.6679   | 1.5087  | 2   | 1.2244  | 1.0847   | 2  | 2 Low-density lipoprotein receptor-related protein 10 OS+Homo sapiens GN+LRP   |
|  | NRBP_HUMAN  | 185  | 60378  | 0.8153   | 1,1963  | 3   | 1.0048  | 1.0500   | -  | 3 Nuclear receptor-binding protein OS+Homo sapiens GN+NRBP1 PE+1 SV+1  |
|  | PSMD4_HUMAN   | 184  | 40940  | 1.1684   | 1.0105  | 4   | 1.2834  | 1.1653   |  | 4 26S proteasome non-ATPase regulatory subunit 4 OS+Homo sapiens GN+PSM  |
|  | CNTP1_HUMAN   | 183  | 158220   | 0.9012   | 1.2492  | 2   | 1 0000  | 4 00 30  |  | Contactin-associated protein 1 OS=Homo sapiens GN=CNTNAP1 PE=1 SV=1  |
| + 2<br>+ 3   | GTEDFIVESLDASFR<br>+ GTEDFIVESLDASFR  | X M/L<br>1.<br>1.<br>1.  | 5968 0.107<br>2824 0.194   | х нл.<br>719 2.0<br>464 2.0  | Std.Err<br>1480 0.066<br>1323 0.154   | Frac<br>16 (<br>58 (  | tion Correla<br>0.1928 0.9<br>0.3200 0.9  | tion Intensity<br>696 702995<br>910 52818  | 9<br>1   | arcator Mascot Distiller 2.5   |
| + 2<br>+ 3   | E Sequence<br>+ GTEDFIVESLDASFR<br>+ GTEDFIVESLDASFR<br>tion Table  | X Mu<br>1.<br>1.   | 5968 0.107<br>2824 0.194   | r X H/L<br>719 2 20<br>164 2 20  | Std.Err<br>0480 0.066<br>0323 0.154   | Frac<br>16 ()<br>58 ()  | tion Correla<br>0.1928 0.1<br>0.3200 0.1  | tion Intensity<br>1696 702995<br>1910 52818  | 9<br>1   | Mascot Distiller 2.5   |
| + 2<br>+ 3   | Sequence     GTEDFIVESLDASFR     GTEDFIVESLDASFR     tion Table     Accession   | X Mil  | L Std.En<br>5968 0.107<br>2824 0.194<br>Mass   | т X H/L<br>719 2 20<br>664 2 20<br>М/L   | Std.Err<br>9480 0.068<br>1323 0.154<br>SD(geo)  | Frac<br>16 ()<br>58 ()  | tion Correla<br>0.1928 0.9<br>0.3200 0.9<br>H/L   | tion Intensity<br>1696 702995<br>1910 52818<br>SD(geo)   | Mod<br>9<br>11   | Infrastion<br>Mascot Distiller 2.5   |
| + 2<br>+ 3   | t Sequence<br>GTEDFIVESLDASFR<br>GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NMT1_HUMAN  | x M/1<br>1.<br>1.<br>1.<br>1.<br>1.<br>1.<br>1.<br>1   | Mass<br>57112  | M/L  | Std.Err<br>0480 0.068<br>0323 0.154<br>SD(geo)  | Frac<br>16 ()<br>58 ()  | tion Correla<br>0.1928 0.9<br>0.3200 0.9<br>H/L<br>0.8725   | tion Intensity<br>1696 702995<br>1910 52818<br>SD(geo)<br>1.2398   | Mod<br>9<br>11<br>#<br>2   | strication Mascot Distiller 2.5  Description  Objective II-letradecanoyfrans frage 1 05-Home sagiens GN+INITI PE-1   |
| + 2<br>+ 3   | E Sequence<br>+ GTEDFIVESLDASFR<br>+ GTEDFIVESLDASFR<br>ation Table<br>Accession<br>MMT1_HUMAN<br>SSRA_HUMAN  | X         Mn           Image: Constraint of the second s | Mass<br>57112<br>32246   | т X H/L<br>719 21<br>164 20<br>М/L   | Std.Err<br>0480 0.066<br>0323 0.154<br>SD(geo)  | #   | tion         Correla           0.1928         0.9           0.3200         0.9           H/L         0.8725   | tion Intensity<br>1696 702995<br>1910 52818<br>SD(geo)<br>1.2398   | 9<br>11<br>#<br>2  | Affrection<br>Mascot Distiller 2.5<br>Description<br>Chycybeolde N-letradecancyltransferase 1 05-Homo sapiens GN-INIT I PE-1<br>Translocone-associated protein Suburn days 05-Homo sapiens GH-SURT PE-1  |
| + 2<br>+ 3   | E Sequence<br>+GTEDFIVESLDASFR<br>+GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NMT1_HUMAN<br>SISRA_HUMAN<br>DRUA2_HUMAN  | x Ma   | L Std.Err<br>5968 0.10<br>2824 0.19<br>Mass<br>57112<br>92213<br>40344   | M/L  | SD(geo)<br>1.0273   | #   | tion Correla<br>0.1928 0.9<br>0.3200 0.9<br>H/L 0.8725<br>1.4393  | tion Intensity<br>1696 702995<br>19910 52818<br>SD(geo) 1.2398<br>1.1691   | # 2  | Astronational Mascot Distiller 2.5<br>Description<br>Chycybeptide N-tetradocomytransferase 1 OS-Homo sapiens GH-NUTT PE-1<br>Mana Noncolog subdamily A memory Col-Homo sapiens GH-NUTT PE-1<br>Data Noncolog subdamily A memory Col-Homo sapiens GH-NUTT PE-1<br>Data Noncolog subdamily A memory Col-Homo sapiens GH-NUTT PE-1<br>Data Noncolog subdamily A memory Col-Homo sapiens GH-NUTT PE-1<br>Strategy Subdamily A memory Col-Homo sapiens Strategy Subdamily Su |
| + 2<br>+ 3   | E Sequence<br>+GTEDFIVESLDASFR<br>•GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NMTT_HUMAN<br>ONIA2_HUMAN<br>ONIA2_HUMAN  | x Ma<br>F 1<br>Score<br>187<br>167<br>187<br>187   | Mass 57112 57216 46344 47320   | т X H/L<br>119 2 2.1<br>М/L<br>1.2524<br>1.1302<br>1.1302  | Std.Err<br>0480 0.068<br>0323 0.154<br>SD(geo)<br>1.0273<br>1.0744  | # Frac  | tion         Correla           0.1928         0.9           0.3200         0.9           H/L         0.8725           1.4383         1.5029   | tion Intensity<br>696 702995<br>9910 52818<br>SD(geo) 1.2398<br>1.1691<br>1.1698<br>4.0395   | # 2  | Arrication     Mascot Distiller 2.5     Organization  |
| + 2<br>+ 3   | E Sequence<br>+ GTEDFIVESLDASFR<br>+ GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NMT1_HUMAN<br>DNLA2_HUMAN<br>DVDFY1_HUMAN<br>NVDFY1_HUMAN   | x Ma<br>V 1<br>V 1<br>Score<br>187<br>187<br>187<br>187<br>187   | Mass 57112<br>0224 0.19<br>0224 0.19<br>0224 0.19<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0224<br>0225<br>0225<br>0225<br>0225<br>0225<br>0225<br>0225<br>0225<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>0255<br>025 | r X H/L<br>719 ↓ 2.1<br>464 ↓ 2.1<br>M/L<br>1.2524<br>1.1302<br>0.9985   | Std.Err<br>0480 0.066<br>0323 0.154<br>SD(geo)<br>1.0273<br>1.0744<br>1.1609  | # Prac  | Ition         Correla           0.1928         0.1           0.3200         0.1           H/L         0.8725           1.4393         1.5029           1.2151         0.2151  | tion Intensity<br>1696 702995<br>10 52818<br>5D(geo)<br>1.2398<br>1.1691<br>1.1698<br>1.0336<br>1.4672   | # 2<br>3<br>2<br>3   | Mascot Distiller 2.5     Description     Overviework Internates and the second se  |
| z = 2<br>+ 3                                       | E Sequence<br>+ GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NMT1_HUMAN<br>SSRA_HUMAN<br>ONLA2_HUMAN<br>ONLA2_HUMAN<br>SMAP_HUMAN<br>SMAP_HUMAN   | x Min  | Mass 57112<br>5968 0.10<br>2824 0.19<br>57112<br>52218<br>46344<br>47320<br>44702<br>20378<br>23569  | r X H/L<br>719 ♥ 21<br>464 ♥ 21<br>M/L<br>1.2524<br>1.1302<br>0.9985   | Std.Err<br>0480 0.066<br>0323 0.154<br>SD(geo)<br>1.0273<br>1.0744<br>1.1609  | # 2<br>2<br>4   | tion Correla<br>0.1928 0.0<br>0.3200 0.1<br>H/L 0.8725<br>1.4393<br>1.5029<br>1.2151<br>0.9902  | tion Intensity<br>666 70299<br>1910 52818<br>SD(geo)<br>1.2398<br>1.1698<br>1.0336<br>1.1187<br>4.1231   | #<br>2<br>3<br>2<br>3<br>2<br>2<br>3   | Mascot Distiller 2.5     Discription     Glycybeptde II-tetradecanoyfransferase 1 05-Homo sapiens GN+NUTT PE+1     Tersatoconsassocieted proteins whum 1 gibi 0 doi-Homo sapiens GN-NUTT PE+1     Tersatoconsassocieted proteins under 1 05-Homo sapiens GN-NUTP PE+1     WD repeat and FVVE domain-containip protein 105-Homo sapiens GN-WDFVP     Image and EVVE domain-containip protein 105-Homo sapiens GN-WDFV     Image and EVVE domain-containip protein 105-Homo sapiens     Image and EVVE domain-containip protein 105-Homo sapiens     Image and EVVE domain-containip protein 40-EVVE domain-containip     Image and EVVE domain-containip protein 40-EVVE domain-containip     Image and EVVE domain-containip     Image and EVVE domain-containip     Image and EVVE domain-containip     Image and EVVE d  |
| z + 2<br>+ 3                                       | E Sequence<br>+ GTEDF/VESLDASFR<br>+ GTEDF/VESLDASFR<br>stion Table<br>Accession<br>NUTT_HUMAN<br>SSRA_HUMAN<br>WDFY1_HUMAN<br>WDFY1_HUMAN<br>BKAP_HUMAN<br>BKAP_HUMAN<br>BKAP_HUMAN  | x Ma<br>F 1<br>F 1<br>Score<br>187<br>187<br>187<br>187<br>187<br>187<br>186<br>185<br>185   | Mass<br>5968 0.10<br>2824 0.19<br>Mass<br>57112<br>0224<br>46344<br>47320<br>44702<br>20378<br>33693<br>7002   | M/L<br>1.2524<br>1.1302<br>0.9985<br>1.1570<br>0.0575  | Std.Err<br>0480 0.066<br>0323 0.154<br>SD(geo)<br>1.0273<br>1.0744<br>1.1609<br>1.0008<br>4.0027  | # Prac  | tion         Correla           0.1928         0.1           0.3200         0.1           NIL         0.8725           1.4393         1.5029           1.2161         0.9902           1.1441         1.944  | tion         Intensity           666         702995           9910         52818           SD(geo)         1.2398           1.1691         1.1698           1.0336         1.1187           1.1321         4.047   | #<br>2<br>3<br>2<br>3<br>2<br>3<br>3<br>2<br>3<br>3  | Mascot Distiller 2.5     Description     Coycylogotide II-tetradecanoy/transferase 10 So-Home sagiens GN-NUTT PE-1     TetraMaddeesate/constraints/size/size/size/size/size/size/size/siz  |
| z + 2<br>+ 3                                       | E Sequence<br>- GTEDF/VESLDASFR<br>ation Table<br>Accession<br>NMT1_HUMAN<br>DNA2_HUMAN<br>DDNA2_HUMAN<br>MDPY1_HUM.<br>SMAP_HUMAN<br>LBPD_HUMAN<br>LBPD_HUMAN<br>LDPD_HUMAN  | x Ma   | Mass           57112           V2824           0.19           Mass           57112           V2824           40344           47320           44702           33693           70027           60324   | x         H/L           719         2           464         2           M/L         1.2524           1.1302         0.9985           1.1570         0.6679           0.96579         0.81570   | Std.Err           0480         0.066           0323         0.154           SD(geo)         1.0273           1.0273         1.0744           1.1609         1.0008           1.5007         1.5007           1.5007         1.5007  | Frac         (6           16         (7           68         (10           2         2           2         2           4         2           2         2           2         2           2         2           2         2           2         2           2         2           2         2  | ttion         Correla           0.1928         0.1           0.3200         0.1           NUL         0.8725           1.4333         1.5029           1.2151         0.9902           0.91251         1.2151           0.9002         1.1441           1.2244         1.048                                  | tion         Intensity           4666         702995           100         52818           5D(geo)         1.2398           1.1691         1.1698           1.0047         1.1187           1.1021         1.0047  | Mod<br>9<br>11<br><b>#</b><br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>2<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>2<br>3<br>3<br>2<br>3<br>3<br>2<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3<br>3 | Mascot Distiller 2.5     Description     Gycybeptide II-letradecancytransferase 1.05-Hiom sapiens CNI-III/T1 PE-1     Testaboorsstoorder greater advance 1.05-Hiom sapiens CNI-III/T1 PE-1     Testaboorsstoorder greater advance  |
| z + 2<br>+ 3                                       | E Sequence<br>GTEDF/VESLDASFR<br>IGTEDF/VESLDASFR<br>ation Table<br>Accession<br>IMIT + HUAN<br>SBRA_HUMAN<br>OHA2_HUMAN<br>NDFY + HUAN<br>NDFY + HUAN<br>BEA_HUMAN<br>BEA_HUMAN<br>BEA_HUMAN<br>BEA_HUMAN  | X Mail<br>Score<br>187<br>107<br>187<br>187<br>187<br>187<br>186<br>185<br>185<br>185<br>185   | Mass           57112           52216           4034           47320           44702           20378           33693           760378           40940   | M/L<br>1.2524<br>1.1302<br>0.9985<br>1.1570<br>0.8153<br>1.1571  | Std.Err<br>0480 0.068<br>0323 0.154<br>SD(geo)<br>1.0273<br>1.0744<br>1.1609<br>1.5007<br>1.1963<br>1.5007  | # (68 (10))   | tion         Correla           0.1928         0.1           0.3200         0.1           0.3200         0.1           H/L         0.8725           1.4393         1.5029           1.2151         0.9902           1.1441         1.0048           1.2244         1.0448                                      | ion         Intensity           666         702995           9910         52818           10         52818           1.1691         1.1691           1.1691         1.1691           1.0336         1.1187           1.0047         1.0500           1.9563         1.6533   | Mod<br>9<br>11<br>2<br>3<br>2<br>2<br>3<br>2<br>3<br>3<br>2<br>3<br>3<br>4<br>4  | Mascot Distiller 2.5     Description     Ovcybeptide N-tetradecanoytrans ferase 10 So-Home sapiens GN-NUTT PE-1     Transloces associational good and the same stress of the same s  |
| z + 2<br>+ 3                                       | E Sequence<br>- GTEDFIVESLDASFR<br>ation Table<br>Accession<br>NutT_HUIAN<br>DIA2_HUIAN<br>DIA2_HUIAN<br>DIA2_HUIAN<br>NPTY_HUIAN<br>SMAP_HUIAN<br>SMAP_HUIAN<br>SMAP_HUIAN<br>SMAP_HUIAN<br>CRP2_HUIAN<br>CRP2_HUIAN<br>CRP2_HUIAN<br>CRP2_HUIAN<br>CRP2_HUIAN   | X Ma<br>Score<br>187<br>197<br>187<br>187<br>187<br>187<br>187<br>187<br>187<br>18   | Mass<br>5968 0.10<br>2824 0.19<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57112<br>57216<br>57112<br>57216<br>57112<br>57216<br>57216<br>57512<br>57216<br>57512<br>57216<br>57512<br>57216<br>57512<br>57216<br>57512<br>57216<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57512<br>57526<br>57526<br>57526<br>57526<br>5752<br>57526<br>57526<br>57526<br>5752<br>57526<br>5752<br>57526<br>57526<br>57526<br>5752<br>5752<br>5752<br>57526<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>5752<br>575<br>575   | M/L<br>1 2524<br>1.1302<br>0.9985<br>1.1570<br>0.6679<br>0.8153<br>1.1684<br>0.0679  | Std.Err           0480         0.068           0323         0.154           SD(geo)         1.0273           1.0273         1.0744           1.1609         1.0608           1.5067         1.963           1.0106         1.2493   | Frac           16         (           68         (           2         2           4         2           2         3           4         2  | tion         Correla           0.1928         0.1           0.3200         0.1           MIL         0.8725           0.8725         1.4393           1.5029         1.2151           0.9200         1.1441           1.2244         1.0048           1.2834         1.2834                                   | Intensity           50(geo)           1,2388           1,1691           1,1691           1,1321           1,0360           1,1187           1,1321           1,0500           1,1653   | Mod<br>9<br>11<br>2<br>3<br>2<br>3<br>2<br>3<br>2<br>3<br>4  | Mascot Distiller 2.5     Description     Gycybeptide II-letradocanoyitransferase 1.05-Homo sapiens GH-NUTT PE-T     Handbookanssoedae0-gytransferase 1.05-Homo sapiens GH-NUTT PE-T     Handbookanssoedae0-gytrans Hown Apple Ob-Homo Sapiens GH-NUTP (     Houropistin 0.5-Homo sapiens GH-SUAP PE-1 SV-1     Small acids protein 0.5-Homo sapiens GH-NUAP PE-1 SV-2     Small acids protein Co-Homo sapiens GH-SUAP PE-1 SV-1     Billword in educates A OS-Homo sapiens GH-SUAP PE-1 SV-1     Small acids protein receptor-related protein 10.5-Homo sapiens GH-LIVEP I     Nuclear receptor-holding protein 0.5-Homo sapiens GH-SUAP PE-1 SV-1     Stordsappens GH-SUAP     SV-Homo sapiens GH-SUAP PE-1 SV-1     Stordsappens GH-SUAP     SV-Homo sapiens GH-SUAP     SV-HOM     SV     SV-HOM     SV-HOM     SV-HOM     SV     SV-HOM     SV-HOM     SV  |
| 1 z<br>+ 2<br>+ 3                                  | с Sequence<br>of TEPF/HESLDASFR<br>of TEPF/HESLDASFR<br>toton Table<br>Accession<br>NHT1_HUMAN<br>SSRA_HUMAN<br>WDFY1_HUMAN<br>WDFY1_HUMAN<br>SIAAP_HUMAN<br>SIAAP_HUMAN<br>BEA_HUMAN<br>DRIA_HUMAN<br>CHTP1_HUMAN<br>CHTP1_HUMAN   | X MAI<br>F 1<br>Score<br>187<br>187<br>187<br>187<br>187<br>185<br>185<br>185<br>185<br>185<br>185<br>185<br>183<br>183  | L Std.Er.<br>5668 0.10<br>2824 0.19<br>2824 0.19   | ™         X         HPL           719         ✓         2.           719         ✓         2.           844         ✓         2.           M/L         1.2524         2.           1.1520         0.9685         1.1570           0.6679         0.8153         1.1654           1.1551         1.1556         1.1554    | Std.Err           440         0.066           0223         0.154           5D(geo)         1.0273           1.0744         1.1609           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091           1.0091         1.0091 | #           2           2           2           2           3           4           2           2   | tion Correlation<br>0.1928 0.1<br>0.3200 0.1<br>1.0<br>1.0<br>1.5029<br>1.2151<br>0.9902<br>1.1441<br>1.2244<br>1.048<br>1.2244<br>1.048<br>1.2244  | tion Intensity<br>696 702999<br>910 52818<br>5D(geo) 1298<br>1.2398<br>1.0391<br>1.1691<br>1.1691<br>1.1691<br>1.1336<br>1.1187<br>1.336<br>1.1187<br>1.336<br>1.1297  | Mod<br>99<br>11<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>2<br>2<br>3<br>3<br>4<br>4<br>4  | Mascot Distiller 2.5     Mascot Distiller 2.5     Organization     Or  |
| t 2<br>+ 2<br>+ 3<br>intita                        | с Sequence<br>of TEPF/VESLDASFR<br>of TEPF/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR<br>deterpf/VESLDASFR   | X         Mat           Image: Control of the state | Sed.Er.           5968         0.10           2824         0.19           2824         0.19           4024         0.19           4024         0.19           4024         0.19           4024         0.19           4024         0.20           57112         57212           57212         57212           57212         57212           57212         57212           57212         57212           57213         57212           57214         57212           57215         57212           57215         57212           57212         57212           57212         57212           57212         57212           57212         57212           57212         57212           57213         57212           57214         57212           57215         57212           57216         57212           57217         57212           57217         57212           57217         57212           57217         57212           57217         57212  | X         HuL           719         ∠         21           464         ∠         21           1.2524         ∠         21           1.1570         0.9685         1.1570           0.8153         1.1684         0.9012           1.1576         1.1576         1.1576   | Std.Err           SD(geo)           1.0273           1.0273           1.0744           1.0008           1.0003           1.0003           1.0003  | #           2           2           2           2           3           4           2 | tion         Correlation           0.1928         0.1           0.3200         0.1           ML         0.8725           1.4390         1.5029           1.5029         1.5029           1.2645         0.9902           1.1441         1.244           1.2834         1.2834           1.0325         1.0325 | Intensity           SD(geo)           12388           1.1691           1.689           1.1691           1.1691           1.1691           1.1691           1.1691           1.1691           1.1693           1.1693           1.1694           1.1695           1.2972 | # 22<br>33<br>22<br>33<br>22<br>33<br>4<br>4   | Mascot Distiller 2.5     Oscillation Control Contrel Control Control Control Control Cont  |
| z 2<br>+ 2<br>+ 3<br>entita                        | с Бедчелес<br>отСРЕ/И-ESLDASFR<br>отСРЕ/И-ESLDASFR<br>тоСРЕ/И-ESLDASFR<br>вали - отСРЕ/И-ESLDASFR<br>иссензали<br>онлас, ниман<br>онлас, онласна<br>онлас, ниман<br>онлас, онласна<br>онлас, онласна<br>онлас, онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онласна<br>онл | X         Mat           Image: Control of the state | Stat.Er           5968         0.10           2824         0.19           2824         0.19           2824         0.19           40344         47320           44722         20378           33993         70027           60378         40940           40942         195220           158220         40940           158220         19704           158220         19704           1023         19704           1024         19704  | x         Hu, 1           719         ∠         21           864         ∠         21           M/L         1         2524           1.1502         0.9665         1.1576           0.9655         1.1676         0.9615           1.1676         0.9012         1.1576           ves: 6)         r         X         MU | Std.Err           0480         0.066           0323         0.154           SD(gec)         1.0273           1.0273         1.0744           1.1009         1.0006           1.0006         1.2492           1.0703         1.0703  | Frec           16         (           68         (           2         2           2         2           4         2           2         2           4         2           2         2           4         2           2         2           4         2           2         2           4         2           2         2           4         2           2         2  | Itim         Correlation           0.1928         0.10           0.3200         0.1           MIL         0.8725           1.4359         1.5029           1.4359         1.2154           1.5029         1.141           1.244         1.0048           1.2325         1.0325                                | ion         Intensity           500         702999           9910         52816           500/geo)         1.2398           1.1091         1.1691           1.0696         1.0398           1.1081         1.0647           1.0692         1.0698           1.1693         1.0697           1.0697         1.0697           1.0697         1.2972           1.2972         ation   | # 4 4  | Andread Description     Description     Overybeptide N-tetradecanoyltrans ferase 10 So-Home appiers GN-NUTT PE-1     Tetradocensational Society of the   |
| z 2<br>+ 2<br>+ 3<br>entita<br>cches<br>z 2<br>+ 3 | Eggenese         Eggenese           GTEDF/VESLDASFR         GTEDF/VESLDASFR           GTEDF/VESLDASFR         GTEDF/VESLDASFR           MITT - HUMAN         SSGA_HUMAN           DNIA2_HUMAN         DNIA2_HUMAN           VDF/V_HUL         NPTH_HUMAN           MRD_HUMAN         NPTH_HUMAN           MRD_HUMAN         NRD_HUMAN           CMT2_HUMAN         SGA_HUMAN           CMT0_HUMAN         SGA_HUMAN           CMT0_HUMAN         SGA_HUMAN           CMT2_HUMAN         SGA_HUMAN           CMT2_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           CMT2_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           CMT2_HUMAN         SGA_HUMAN           CMT3_HUMAN         SGA_HUMAN           CMT3_HUMAN         SGA_HUMAN           CMT3_HUMAN         SGA_HUMAN           CMT3_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMAN         SGA_HUMAN           SGA_HUMA   | X         Mail           Image: Control of the state of the stat | Seal.Er.           5968         0.10           5971         2224           0.19         57112           57212         57212  | ×         HuL           719         ✓         21           4644         ✓         21           MAL          24           1.1524         ✓         21           1.1570         0.9685         1.1570           0.8513         1.1576         1.1576           ve: 5)         7         X         1.1444                   | Std.Err           SD(geo)           1.0273           0.154           1.0744           1.0744           1.0703           1.0714           1.0703           1.0703           1.0703           .           Std.Err           0022           0.123  | 5<br>2<br>2<br>2<br>4<br>2<br>3<br>4<br>2<br>2<br>3<br>4<br>5<br>Frace  | tion         Correlation           0.1928         0.1           0.3200         0.1           ML         0.8725           1.4392         1.2151           0.9902         1.4411           1.2244         1.0435           1.2334         1.0325           ction         Correlation                            | intensity           500         Intensity           606         72299           910         52816           12396         12396           1.1691         1.1691           1.1695         1.1695           1.1696         1.1695           1.1697         1.1695           1.1696         1.1695           1.1697         1.1626           1.1697         1.6500           1.1697         1.6501           1.1997         1.6501           1.2972         1.2972  | # 22<br>33<br>22<br>33<br>22<br>33<br>24<br>4<br>4<br>4  | Mascot Distiller 2.5  |

Here we have an example of this from a SILAC dataset – look at hit number 877. In Mascot Distiller 2.5 and earlier, this is reported as a protein ratio with two peptide matches, despite the matches being to the same peptide just at different precursor charge states. In Mascot Distiller 2.6 this is now being treated as a one hit wonder – and because of my settings, the protein ratio isn't being calculated or reported.