Agilent Technologies

Software Status Bulletin

MassHunter Qual MassHunter Qual

Known Problem Report as of Feb 3 2015 3:24PM

Preface

This Software Status Bulletin (SSB) documents all known problems in the software product designated above. The SSB is derived from Known Problem Reports (KPR) which result from user problems that have been classified as documentation problems or software defects. When a KPR is written, an identifying number is assigned to it, and the KPR is added to the next edition of the SSB.

User inputs that have been classified as Enhancement Requests are not documented in the SSB. User problems that have been submitted, but that have not been classified by the time the SSB is generated are not included in the SSB.

How to use the SSB

When you experience a problem with a product, first check this SSB to see if the problem has been reported already, and if there is a temporary workaround available for the problem, or if the problem has already been fixed by a new revision. If the problem is not listed in this SSB then you may wish to report it to the Response Center or to your field support representative.

To determine if your problem is documented in this SSB, first look in the "Keyword Index" section of the SSB. Under each keyword is a listing of one-line descriptions of related KPRs. If any of these sound like yours, locate the KPR # in the "Known Problem Reports" section of the SSB, and read the full KPR. The KPRs in the "Known Problem Reports" section are sorted by KPR #.

There are two sections in the SSB:
Keyword Index: This index is categorized by keyword. For each KPR there is a brief description and a KPR #. A KPR may be associated with more than one keyword.

Known Problem Reports: This section contains KPRs, with all the available information relevant to the problem. KPRs in this section are sorted by KPR #.

KPR#: 5498 Product: MassHunter Qual MassHunter Qual A.01.00

Keyword:

One-line Description:
Peak heights from the general integrator can be affected by peak filter values.

Problem:

If you change the value of the peak area filter (in absolute units of counts) or change to a different type of filter (area percent or peak height), then the height of some peaks reported by the general integrator may change.

If the filter is peak area in counts, the integrator ignores peaks that are too large. All other peak filters are applied to the peak list after the integrator has run but before the peaks are displayed.

The integrator will automatically adjust internal parameters as needed to keep the peak list from becoming too large. These adjustments can cause changes in the reported peak heights. If a peak area filter (in counts) is high enough to limit the number of peaks, no internal adjustments are made. A different peak filter setting may cause internal adjustments to be needed needed, sometimes resulting in different reported peak height values.

Temporary Solution:
n/a

Fix Information:
The RTE algorithm can filter on area but not on height. When you specify height filters, the internal RTE parameters are set to allow any peak area >= 0 (i.e., do not filter), and then the height filter is applied to the results.

KPR#: 9674 Product: MassHunter Qual MassHunter Qual B.01.01

Keyword:

One-line Description:
Peak list row height not saved when list is shown/hidden

Problem:
-display the integration peaks list
-change the row height
-hide the list and display it again.
The row height was not saved.

This also happens with the spectrum peaks list

Temporary Solution:
n/a
Fix Information:
Infragisitics does not 'remember' the row height when saving the table settings. We do not want to disable the feature because the user could change a row height and then want to print the table window report

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KPR#: 9735 Product: MassHunter Qual MassHunter Qual B.01.01

Keyword:

One-line Description:
Error messages in MFE/Cmpd Filter tab are different for same type of error

Problem:
-select the Find by Molecular Feature node and click on Compound Filters tab
-enter "0" into Neutral Losses/Restrict to differences off field. The error message is "0 is not a valid value. Each value in the list must be a list of numbers >0"
-Enter a letter into the same field and the message is: " is not a valid value. Value must be a list of numbers >0"

User prefers the second message, it is more consistent with other error messages in method editor.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 9804 Product: MassHunter Qual MassHunter Qual B.01.01

Keyword:

One-line Description:
File browser in Export dialog points to \layouts\qual

Problem:
-right-click on the integration peak list and select "export"
-in the Export dialog, deselect "Autogenerate filenames"
-click on the browse button next to the destination field.
The Save as dialog points to \Layouts\Qual. At the same time, the default destination path is c:\temp\report.csv
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 10278 Product: MassHunter Qual MassHunter Qual B.01.01

Keyword:

One-line Description:
Error occured during report generation in Qual if TOF Acq software is installed

Problem:
1. Install Qual software (I installed B117.0)
2. Install Analyst (version 1.1 along with the patch for TOF software On Build 9865)
3. Install TOF Acquisition software[A.02.02] (I installed B738.0) [Note: Installation order is important]
4. Run TOF software and close it without performing any operation.
5. Run Qual. Goto File -> Print ->Method Report.

The same error occurs while generating Analysis report.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 10408 Product: MassHunter Qual MassHunter Qual B.01.01

Keyword:

One-line Description:
Not all delimiters should be allowed in Export dialog in Qual

Problem:
-In Export dialog select file type as text / csv
-User can enter any delimiter. User feels that not all delimiters should be allowed. Delimiters like ".." or "8888" (numerical number) will result into wrong export results because it will be same as the numbers that are exported.
Temporary Solution:
Most if the times users will set valid delimiter. In case user enters nuric delimiter by mistak and file is not importable, easy workaround would be to re export file with different delimiter.
Fix Information:
n/a

KPR#: 11734 Product: MassHunter Qual MassHunter Qual B.01.03

Keyword:

One-line Description:
Peak Status no longer available as Peak Label on Chrom Results

Problem:
Peak Status no longer shows in the drop-down list of Peak Labels shown in Tools | Plot Display Options dialog box, Chromatogram tab.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 11930 Product: MassHunter Qual MassHunter Qual B.01.03

Keyword:

One-line Description:
Analysis report printed has ## in the abundance column for peak list tables

Problem:
Analysis report printed has ## in the abundance column for peak list tables.
Temporary Solution:
This behavior is seen only with 120 DPI setting with 96 DPI it works correctly
Fix Information:
n/a

KPR#: 12054 Product: MassHunter Qual MassHunter Qual B.01.03

Keyword:

One-line Description:
Intermediate report directories are not cleared properly in Qual

Problem:
- Clear app settings and run Qual
- Open sulfamix_peak.d data file. Ensure that no node is highlighted in the data navigator.
- Delete all the contents of \reports\temp i.e. intermediate data location.
- Goto File -> Print -> Analysis Report. In the print dialog, check Print Preview checkbox and click

Report is not generated since nothing was highlighted in the treeview and message appears indicating the same. This is correct. Goto intermediate data location.

Temporary report data files created are not cleared. This is incorrect and inconsistent with "Keep intermediate report directories" option setting. Because, even if this check box is unchecked in UI, intermediate directories are not cleared. This problem occurs since; intermediate files get generated even though actual report is not created since, not data was found for report generation.

Temporary Solution:

When reports are successful, then the intermediate files are generated (or not) according to the checkbox accessed via the Tools -> Intermediate Report Files menu item.

When a report is NOT successful, then the intermediate file is not deleted because it DOES help in debugging potential problems, and should have a pretty low impact as it will be relatively rare.

Fix Information:

n/a

KPR#: 12094 Product: MassHunter Qual MassHunter Qual B.01.03

Keyword:

One-line Description:

Qual reports an exception while generating reports if printer is not installed

Problem:

1. Run Qual and open a data file. Goto File -> Print
   -> Analysis Report.
2. Select any non-default printer, check Print Preview checkbox and click .
3. Goto Windows Explorer and delete/remove the selected Printer.
4. Switch back to Qual and repeat step . Verify that deleted printer is still selected in the combo box. Without changing any of the values, click

Temporary Solution:

The user must configure a printer before attempting to print reports.

Fix Information:

n/a

KPR#: 14278 Product: MassHunter Qual MassHunter Qual B.03.00

Keyword:

One-line Description:

RT Match parameter entries do not affect search results

Problem:

The use of RT on spectra does not effect the search results. The RT match is to be used with unknown compound searching where the TargetRT match tolerance window

on the Compound Identification tab is only used during UA to match unknown compound candidates with target compounds. This setting does NOT affect the library match score when performing library matching against spectra versus compound identification.
Temporary Solution:
n/a
Fix Information:
Resovled in Build B.03.00

KPR#: 14294 Product: MassHunter Qual MassHunter Qual B.03.01

Keyword:

One-line Description:
Analysis reports print out in arbitrary order of data files.

Problem:
When a user prints out Analysis Reports for a lot of data files using the option "Separate report per data file" it prints them in an arbitrary order.

If they turn off the option, "Separate report per data file", then it prints them in the order they are listed in the Data Navigator.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14299 Product: MassHunter Qual MassHunter Qual B.04.00

Keyword:

One-line Description:
Some GC chromatograms can causes the MS/MS (GC) integrator to fail and give error message

Problem:
The MS/MS GC integrator is designed for MSMS chromatograms like MRM and cannot processes some GC data signal. When it fails an error message box with stack trace information will appear and the integration will fail. Problem seen in B.03.01 and B.04.
Temporary Solution:
Try using any of the other integrators on GC chromatograms.
Fix Information:
n/a

KPR#: 14305 Product: MassHunter Qual MassHunter Qual B.03.01 SP3

Keyword:

One-line Description:
MFG of some compounds freezes Qual at 69%, need to terminate using the Task Manager

Problem:
Load a large data file with its results and load the results Qual method.

Sort based on Volume, and run MFG on the largest volume compound. In some cases, Qualitative Analysis will freeze.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14310 Product: MassHunter Qual MassHunter Qual B.03.01 SP3

Keyword:

One-line Description:
Peak width is incorrect in the peak table when the peak is manually integrated

Problem:
Peak width in the peak table corresponds the value at half height of the peak, however when you manually integrate any peak, we you get the width at the baseline.

This is due to the fact that manual integration uses the General integrator. For the General integrator the definition of width is the full peak width from start to end.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14312 Product: MassHunter Qual MassHunter Qual B.04.00

Keyword:

One-line Description:
Exporting Graphics doesn't support plot setting

Problem:

In Chromatogram Display Options, plot parameter changed to "Pattern" as the user want to show only "monochrome" in chromatogram.
Chromatogram's display is changed to "monochrome" in the screen.
The user tries to export this screen to metafile by exporting function.
But the graphics in the exported metafile is not "monochrome" instead still a color choromatogram.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14333 Product: MassHunter Qual MassHunter Qual B.04.00

Keyword:

One-line Description:
Define Chromatograms Does Not Contain Complete List of GC Detector Signals

Problem:
In the define chromatograms dialog in the method editor, the complete list of detector signals is not displayed.
Temporary Solution:
By right clicking on the TIC of the data file in the Data Navigator window, the additional signal types can be extracted. Doing this looks in the data file for available signals.
Fix Information:
n/a

KPR#: 14337 Product: MassHunter Qual MassHunter Qual B.03.01

Keyword:

One-line Description:
Product ion scan does not display collision energy for som GC Triple data

Problem:
Data collected on CI mode on GC Triple Quad does not display the collision energy (CID) in product ion spectra. The problem is the result of a negative CID value which is incorrectly placed in the data file by data acquisition. Seen in B.03.01.
Temporary Solution:
None.
Fix Information:
Fixed in B.03.01 SP3.

Also corrected in data acquisition.

KPR#: 14343 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Compound Details View (CDV) - Exception when trying to access the Add/Remove Columns dialog in the 4th level of the Compound ID Results Window

Problem:
In the Compound Details View (CDV), after running MFE + Sequence Match for BioConfirm, and then trying to access the Add/Remove Columns dialog in the 4th level of the Compound ID Results Window, the user is getting the following exception:

Build Configuration: Release
Message: Object reference not set to an instance of an object.
Stack Trace: at Agilent.MassSpectrometry.DataAnalysis.Qualitative.SelectCompoundColumnDialog..ctor(IResultAttributeDefinitions definition)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualForm.AddRemoveColumnsMenuItems_Click(Object sender, ToolClickEventArgs e) in t:\Archer\qual\presentation\AgtQual\QualFormP5ViewMenus.cs:line 5176
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualForm.UltraToolbarsManager1_ToolClick(Object sender, ToolClickEventArgs e) in t:\Archer\qual\presentation\AgtQual\QualFormP6MenuStates.cs:line 2128

Clicking OK on this error message will NOT crash Qual.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14345 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Trying to load a data file in Qual while acquiring will flag an error

Problem:
If a dMRM or tMRM data file is loaded into qual while it is simultaneously being acquired, an exception will be thrown.
Temporary Solution:
n/a

Fix Information:
n/a

KPR#: 14347 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Wizard pages do not display relevant help topics

Problem:
All options in the Wizard menu item do not properly display their relevant help topics when the F1 key is pressed.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14348 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Chemical Data Dictionary Editor tabs do not display the relevant help topics

Problem:
Opening: Sequence -> Chemical Data Dictionary Editor and then pressing F1 will not display that specific tab's relevant help topic.
Instead, the help topic displayed is for the Chemical Data Dictionary Editor dialog box.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14349 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Displaying overlaid MRMs then switching from minutes to scans may cause an error

Problem:
Loading a few MRM files, overlaying them, and then switching from minutes to scans may intermittenly throw an exception.

This error is non fatal and the user may still proceed.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14354 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Diff(ppm) and Diff(mDA) show incorrect values in the MS peaklist when formula generation results are cleared.

Problem:
Generate formula for a spectrum.
Some rows with Diff(ppm) and Diff(mDA) in the MS peak list table there will contain gibberish.
Clearing the spectrum identification results will then result in the MS peak list table containing many rows of "Diff(ppm)" and "Diff(mDA)" filled with gibberish.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14359 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Tab selection in the Maximum Entropy tab of Method Editor -> Find by Protein Deconvolution is out of order

Problem:
1) Method Editor -> Find by Protein Deconvolution and proceed to the Maximum Entropy tab.
2) Whilst using the tab key to change fields, after "Limit to the largest parameter", the tab selection leaves the Method Editor before continuing with the rest of the fields.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14360 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Function: changed value messages are missing in Method Editor > Find Compound by Formula - Options > Results tab.

Problem:
1) Select Find compounds by Formula > Find Compounds by Formula -Options in method explorer
2) Open Results tab.
3) Enable Extract raw spectrum option
4) Enable Clip extracted raw spectra option
5) Select Asymmetric (m/z) from dropdown
6) Enter valid values for both input box (such as 6 and 11)

Changed value blue triangles with a message should be displayed.
Currently, nothing appears there.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14363 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Changing the "Source of formulas to confirm" in the Formula Source tab of FbF - Options also adds a blue triangle to the "Find by Formula - Chromatograms" section in Method Explorer

Problem:
Changing the "Source of Formulas to Confirm" in the Formula Source tab of FbF - Options will also add a blue triangle to the "FbF - Chromatograms" section in the Method Explorer pane.

This does not impact usability.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14365 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
F1 doesn't show help in Isotope Distribution Calculator

Problem:
Pressing F1 in the Isotope Distribution Calculator will not display the help screen.
The user will need to manually mouse to the "Help" menu option.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14366 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Exception occurs in Metlin - Navigator View while repeatedly printing reports over and over for thousands of compounds per data file

Problem:
The following exception will flag in this case:

Program: Agilent MassHunter Workstation Software Qualitative Analysis B.06.00
Build Configuration: Release
Message: Following exception occured while exceuting script -
Error creating window handle.

At-
at System.Windows.Forms.NativeWindow.CreateHandle(CreateParams cp)
at System.Windows.Forms.Control.CreateHandle()
at System.Windows.Forms.Control.get_Handle()
at System.Windows.Forms.Control.CreateGraphicsInternal()
at System.Windows.Forms.Control.CreateGraphics()
at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.WritePlotImageToFile(IAppState appState, ExportedImageType imageType, UIUpdateDisplayPlotControlBase plotControl, Double heightByWidthRatio, String imageFilename)
at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.CreatePlotImageFile(IDataItem plotItem, ExportedImageType imageType, Boolean

overlayPredictionPattern, IRange XZoomRange, Double heightByWidthRatio, Boolean allowZoom)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.WritePlotPairs(IDataItem[] plots, Int32 ItemID)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.WriteCompoundChromatograms(IDataItem plotItem, List`1 cpdChildren, Boolean& hasAllIonsResults)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.WriteCompounds(IDataItem[] compounds)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.GenerateReportSpecialized(IDataItem[] selectedAnalysis)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.GenerateReportAndMapExceptions(IDataItem[] analyses)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.GenerateReport(IDataItem[] selectedAnalysis)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CmdGenerateReport.DoSpecialized()
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualCommandBase.Do()
   at Agilent.MassSpectrometry.CommandModel.CommandHistory.Invoke(ICommand cmd)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.AppManager.Invoke(ICommand cmd)
Stack Trace:
Server stack trace:
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.AppManager.BeginRun(String assemblyPath, QualScriptEnvironment qualScriptEnvironment)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualCommandBase.RunScript(String script, QualScriptParameters scriptParams, ActionItemCollection actions)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualCommandBase.RunScripts(String[] scripts, QualScriptParameters scriptParams, ActionItemCollection actions)
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CmdRunScript.DoSpecialized()
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CmdApply.DoSpecialized()
   at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualCommandBase.Do()
   at Agilent.MassSpectrometry.CommandModel.CommandHistory.Invoke(ICommand cmd)

   at
System.Runtime.Remoting.Messaging.StackBuilderSink._PrivateProcessMessage(IntPt
r md, Object[] args, Object server, Int32 methodPtr, Boolean fExecuteInContext,
Object[]& outArgs)
   at
System.Runtime.Remoting.Messaging.StackBuilderSink.PrivateProcessMessage(Runti
meMethodHandle md, Object[] args, Object server, Int32 methodPtr, Boolean
fExecuteInContext, Object[]& outArgs)
   at
System.Runtime.Remoting.Messaging.StackBuilderSink.AsyncProcessMessage(IMess
age msg, IMessageSink replySink)

Exception rethrown at [0]:
   at System.Runtime.Remoting.Proxies.RealProxy.EndInvokeHelper(Message reqMsg,
Boolean bProxyCase)
   at System.Runtime.Remoting.Proxies.RemotingProxy.Invoke(Object NotUsed,
MessageData& msgData)
   at
Agilent.MassSpectrometry.CommandModel.CommandHistory.InvokeCommand.EndInv
oke(IAsyncResult result)
   at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.AppManager.EndInvoke(IAsyncRes
ult result)
   at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualForm.OnAsyncCallBack(IAsyn
cResult asyncResult)
Message: Error creating window handle.
Stack Trace: at System.Windows.Forms.NativeWindow.CreateHandle(CreateParams
cp)
   at System.Windows.Forms.Control.CreateHandle()
   at System.Windows.Forms.Control.get_Handle()
   at System.Windows.Forms.Control.CreateGraphicsInternal()
   at System.Windows.Forms.Control.CreateGraphics()
   at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.WritePlotIma
geToFile(IAppState appState, ExportedImageType imageType,
UIUpdateDisplayPlotControlBase plotControl, Double heightByWidthRatio, String
imageFilename)
   at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.CreatePlotIm
ageFile(IDataItem plotItem, ExportedImageType imageType, Boolean
overlayPredictionPattern, IRange XZoomRange, Double heightByWidthRatio, Boolean
allowZoom)
   at
Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.WritePlotPair
s(IDataItem[] plots, Int32 ItemID)

at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.WriteCompoundChromatograms(IDataItem plotItem, List`1 cpdChildren, Boolean& hasAllIonsResults)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.WriteCompounds(IDataItem[] compounds)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CompoundReportGenerator.GenerateReportSpecialized(IDataItem[] selectedAnalysis)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.GenerateReportAndMapExceptions(IDataItem[] analyses)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.BaseReportGenerator.GenerateReport(IDataItem[] selectedAnalysis)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.CmdGenerateReport.DoSpecialized()
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualCommandBase.Do()
at Agilent.MassSpectrometry.CommandModel.CommandHistory.Invoke(ICommand cmd)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.AppManager.Invoke(ICommand cmd)

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14367 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Tooltip of Method Explorer is properly updated

Problem:
1) Launch Qual
2) Hover over the Method Explorer pane: it should display the last name of the last method loaded.
3) Open new method and check the tooltip of Method Explorer. The tooltip still displays the previous method's name.

This has no impact on usability.
Temporary Solution:

n/a
Fix Information:
n/a

KPR#: 14368 Product: MassHunter Qual MassHunter Qual B.05.00

Keyword:

One-line Description:
Formula and Mass Calculators do not contain GC/Q-TOF parameters when a GC/Q-TOF method is loaded

Problem:
When a GC/Q-TOF method is loaded, both the mass and formula calculator tools have the "H" selected instead of an electron.
Additionally, the formula calculator has "even electron" selected in "MS ion electron state" instead of "allow both even and odd."
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14369 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
No blue triangles are added to the method editor for search accurate mass library when switching search accurate mass library to search unit mass library

Problem:
Adding a library to the Library selection list in the Search Unit Mass Library > Library Search section will also add a blue triangleto the Search Accurate Mass library line in the Method Explorer.

This has no impact on usability.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14370 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Oligonucleotide reports will contain some cosmetic discrepancies

Problem:
1) Select BioConfirmOligonucleotideCompoundReport.xltx in Common Reporting Options.
2) Load any data file with oligonucleotide results.
3) File -> Print a compound report.

1. The cell borders are missing for all columns after Vol column.
2. The x-axes of EICs and ECCs have overlapping text.

This is cosmetic and has no impact on usability or stability.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14374 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
For targeted MSMS and FBF, repeated calls for extracting complete result set adds an MSMS spectrum

Problem:
1) Open sulfas_PosTargetedMSMS.d
2) Load default.m.
3) Run find compounds by targeted MSMS.
4) Each compound will have a TIC and Product ion scan extracted.
5) Run extract complete result set: a MS scan and Product ion scan is added.
6) Run extract complete result set again: another Product ion scan (same as previous) is added.

This also happens with FbF.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14378 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
EIC Peak List table does not get updated in tandem with compound selection

Problem:
1) Enter 10-20k for the mass range In the Find by Protein Deconvolution method editor.
2) Select TIC and Extract EIC in the results tab.
3) Run Find by Protein Deconvolution for BetaLac.d.
4) Highlight the compounds in the compound list table one at a time.

-The MS Peaks Two table does not always gets updated to correspond to the highlighted compound.

This will not impact usability or stability.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14379 Product: MassHunter Qual MassHunter Qual B.05.00

Keyword:

One-line Description:
MS/MS Formula details disappear when selecting a different "Best" Formula after running Find Compounds by Auto MS/MS and MFG

Problem:
1) Run Find Compounds by Auto MS/MS on "Sulfa-PosESIAutoMSMS-c.d",
2) Run Generate Formula from Compounds.
3) Select Compound 10 with m/z 311.0814 and look at MS/MS Formula Details window, which shows the fragment ion results.
4) Select a different "Best" formula, and the MS/MS Formula Details window will display "No Formula Results for this compound".

Even changing the selection of "Best" back to the correct formula with the highest score will leave this window empty.
Temporary Solution:
The only way to recover the results in MS/MS Formula details is to rerun "Generate Formulas from Compounds".
Fix Information:
n/a

KPR#: 14380 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Annotation does not work properly for a HighE spectrum

Problem:
In the MS Spectrum Results window, annotation does not work properly if the spectrum is a HighE spectrum.

1) Find compounds by formula an an All Ions data file.
2) Add an annotation to the peak at 920 for compound 3 (Crimidine) in the HighE Scan.

- Cannot zoom into the baseline.
- Can add an annotation, but cannot double-click on the annotation to show the annotation dialog box.
- Right-click the annotation; can click the Annotation Properties menu item, but the annotation dialog box is not opened.
- The toolbar buttons are all greyed out.
- The menu items to "Select All Annotations", "Delete Selected Annotations", and "Delete All Annotations" are all greyed out.

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14383 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Qual crashes when Find by Protein Deconvolution is attempted under specific condtions

Problem:
1) Open BioConfirmIntactProtein-default.m method.
2) OpenBetaLac and BGALA data sets.
3) In Find by Protein Deconvolution method editor, select "Pmod" as the algorithm.
4) Enter 10000-150000 in Mass Range field
5) Select Extract EIC and BPC in the Results tab
6) Select "Universal" as integrator in the Find by Protein Deconvolution method editor.
7) Select Actions -> Find by Protein Deconvolution.

This causes Qual to crash.
Temporary Solution:
n/a
Fix Information:

n/a

KPR#: 14384 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
A Compound report after running MFE + MFG contains 3 columns with the identical formula

Problem:
1) Run MFE and then "Generate formulas from compounds"
2) Print the default compound report and the compound list contains three columns with the titles "Formula", "MFG Formula" and "DB Formula", which will all list the same formula (best hit for each compound).
Temporary Solution:
Create a specific report layout for MFE+MFG and only include the appropriate column.
Fix Information:
n/a

KPR#: 14385 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
The "Hide Empty Columns" toolbutton in the Compound List works for the first level, but not the second level

Problem:
The "Hide Empty Columns" toolbutton in the Compound List works for the first level, but not the second level.

This will not impact usabiltiy or stability.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14386 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
If only "Other (CE)" is marked in the User Interface Configuration dialog box, menu

items and method editor sections are not chosen consistently.

Problem:
Mark ONLY "Other (CE)" in the User Interface Configuration dialog box for the separation type.

1) “Find by Targeted MS/MS” algorithm is available in the Method Explorer, but is not listed in the “Find” menu.
2) In the Method Explorer, the only “Identify Compounds” section that is available is “Combine Identification Results”.
However, in the “Compound Automation Steps” section, all of the Compound identification algorithms can be marked.
3) Database Search tabs and the Generate Formulas tabs in the Chromatogram Peak Survey Workflow are also accessible. (but not in the Identify section of the method editor)
4) In the "Identify" menu, the menu item “Search Library for Spectra” is available, but the selected library cannot be changed because those sections are not available in the "Identify" section of the Method Editor.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14387 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
All Ions: ?? appearing on "delete" and "extract complete result set"

Problem:
1) Run All Ions FbF
2) Select a compound
3) Delete All fragment ion EIC objects (Right click delete on treeview)
4) Extract complete result set
5) Delete All fragment ion EICs objects (Right click delete on treeview)
6) Extract complete result set.
7) ?? will appear in the description
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14388 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Exception on generating Compound Report for ForensicsTox Find by Formula analysis

Problem:
When running reports on 1000's of compounds per multiple files, Excel stops and opens the Visual Basic debugger at a formatting statement.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14389 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Compound List column order for BioConfirm Protein Digest is randomly ordered

Problem:
Opening any protein digest file will display compound list columns that are randomly ordered.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14390 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Spectrum not seen on printed report when grid lines are turned on

Problem:
If grid lines are turned on, printing an analysis report for all compounds will not display the spectrum chromatograms in the User Spectra section.
Only the mass labels will be visible.
Temporary Solution:
Turn off grid lines via plot options and then print.
Fix Information:
n/a

KPR#: 14391 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Protein compound report with two data sets may fail

Problem:
1) Open BioConfirmIntactProtein-default.m method.
2) Open BetaLac and BGALA data sets.
3) In Find by Protein Deconvolution method editor Enter 10000-150000 in Mass Range field
4) Select "Use limited m/z range" and "Unspecified" for Isotope width.
5) Select Extract EIC in the Results tab.
6) Select Actions -> Find by Protein Deconvolution.
7) Select File -> Print -> Compound Report.
8) Select All results, and Separate report per data file,
9) Print preview in the Print Comp Rep dialog and click OK.

Only one report gets produced and after that it generates error.

NOTE: This MAY happen sporadically.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14392 Product: MassHunter Qual MassHunter Qual B.05.00 SP1

Keyword:

One-line Description:
When run as a Compound Automation Step, Find Compounds by MRM produces a TIC Scan with NO DATA POINTS

Problem:
This occurs on any MRM or DMRM data file when Find Compounds by MRM is run via Compound Automation.
Temporary Solution:
Run Find Compounds by MRM manually,
Fix Information:
n/a

KPR#: 14393 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Color coding of ions based on Fragment Anotation is still displayed when Fragment Anotation is unchecked

Problem:
Unchecking "Annotate Fragment Specturm Peaks with Formula" in "Method Editor: Generate Formula -> Fragment Formula" will cause the formulas to disappear but leave the ions that match the formulas colored.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14394 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Merged Spectrum ID Results with LibSearch-MFG results - only the highest Lib Score hit has MFG results and Isotope pattern although all are labeled as merged LibSearch-MFG

Problem:
1) Select ranges for the three largets peaks in the TIC
2) Integrate & Extract Spectra -> Over Selected Ranges
3) Highlight spectrum.
4) Search unit mass library NIST11.L or Wiley9th.L for spectra from right-click menu in MS Spectrum Results
5) Run "Generate Formula from Spectrum Peaks"
6) Expand "Best merged hit - MFG results"

Change "best" hit to another merged hit and expand it.
There will be no MFG results.
The MS Spectrum Results now do not include the Isotope Pattern
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14395 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Agile Integrator issue for "All Ions" causes fragments to fail confirmation

Problem:
For any Hi/Lo FV or CE datafile:
-The Agile integrator integrates the main peak in the LOW channel EIC. The peak is not "filled in", but an RT label is assigned and it appears in the Integration Peak list.
-"All ions" is searching for the confirming ions in the first integrated peak's RT range resulting in a failure to confirm the fragment.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14396 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
In CDV with BioConfirm ProteinDigest results - scrolling to the end of the Compound List then back up to last seq. match will cause the cursor to slowly self scroll back to end of list/last compound

Problem:
1) Opn Datafile: enolase-Chip-final.D
2) Load EnolaseMSMS.m if available; if not use BCProteinDigest default method
3) Run MFE - TheEnolase method contains the Enolase sequence
If not available load BSADigest.psq or any available sequence file

4) Run Match Sequence.
5) Switch to CDV (Compound Details View)
6) View->Sequence Coverage Map
7) Proceed to Compound ID Results pane
8) Select another row in Compound List

The Win7 busy icon (turquoise circle) will appear and the cursor will constantly move from row to row endlessly.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14399 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Changing workflows does not work if "Save current method" is checked in the dialog box

Problem:
Normally, when changing workflows, a dialog comes up.
If "Save current method" is checked in that dialog box, no layout change happens.
Temporary Solution:
Unchecking the option allows layout switching.
Fix Information:
n/a

KPR#: 14400 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Fragment formula annotation should show MFG results if best hit is neither Library ID hit nor Manual ID hit for user spectra

Problem:
1) For a user spectra that has a library (and/or manual id) id, MFG, or database search results.
2) Check fragment formula annotation.
3) If the "best" hit is among library id or manual id then FFA (fragment formula annotation) should be executed and the spectra should be colored accordingly
4) However, if the user selects MFG or Dbase ID as "best" hit then peaks that should be labelled with MFG results are not labeled properly (if it is calculated for that spectra).

-Additionally, any Red or Green labeled peaks do not revert to a single color.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14401 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
"Restore to last saved values" from file does not work for Peak absolute height

Problem:
1) Load default.m or any other method
2) Open: Method Editor - Deconvolute (MS): Protein.
3) In the Maximum Entropy tab select "Peak absolute height."
4) Click on the "Restore to last saved values from file" icon in the method editor toolbar.

The radio button will not change back to the "Peak signal-to-noise" parameter.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14402 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
All Ions MS/MS (AIM) - Visualization in the Compound Fragment Spectrum Results window in Compound Details View (CDV) is incorrect

Problem:
a) The default zoom range in the x-axis is currently not limited, for target compounds, to the mass of the highest selected adduct species multiplied by the charge state plus 20.
b) The red isotopic pattern boxes are incorrectly drawn with a factor of 20 too high.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14404 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Layouts in Compound Details View (CDV) and Navigator View (NV) do not save and preserve which PANE is on top if multiple windows are TABBED.

Problem:
1) In Navigator View, have the Compound List and the Peak List tabbed at the top, with the Compound List in front.
2) Save the layout, switch to CDV and back to NV

The Peak List is now in front. After running the MFE algorithm, there are no results in the peak list.

1) In Compound Details View, display the "Overall Chromatogram Results" window tabbed behind the "Compound Chromatogram Results" window.
2) Switch back and forth between CDV and NV will cause the "Overall Chromatogram Results window to come to the front.

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14406 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Occasional exception flags when changing workflows using data files not in the customer's Home path

Problem:
1) Configure User Interface for GC-QTOF
2) Load TOF type file such as MSD_mix_4stds_DG_spl200_03.D
3) Use General or GC-QTOF workflow
4) Run Find by Integration
5) Run a library search with: "demo.L"
6) Save results
7) Configure General Workflow.

- Clicking OK MAY then cause Qual to crash with the following exception:

Date and Time: 8/28/2012 9:55 AM
Program: Agilent MassHunter Workstation Software Qualitative Analysis B.06.00
Build Configuration: Release
Message: Error creating window handle.
Stack Trace: at System.Windows.Forms.NativeWindow.CreateHandle(CreateParams cp)
at System.Windows.Forms.Control.CreateHandle()
at System.Windows.Forms.Control.CreateControl(Boolean fIgnoreVisible)
at System.Windows.Forms.Control.CreateControl()
at System.Windows.Forms.Control.OnVisibleChanged(EventArgs e)
at System.Windows.Forms.Control.OnVisibleChanged(EventArgs e)
at System.Windows.Forms.Form.OnVisibleChanged(EventArgs e)
at System.Windows.Forms.Control.SetVisibleCore(Boolean value)
at System.Windows.Forms.Form.SetVisibleCore(Boolean value)

at System.Windows.Forms.Application.ThreadContext.RunMessageLoopInner(Int32 reason, ApplicationContext context)
at System.Windows.Forms.Application.ThreadContext.RunMessageLoop(Int32 reason, ApplicationContext context)
at System.Windows.Forms.Form.ShowDialog(IWin32Window owner)
at Agilent.MassSpectrometry.DataAnalysis.BaseErrorDialog.ShowException(Exception exception)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.QualForm.OnQualFormThreadExceptionEvent(Object sender, ThreadExceptionEventArgs e)
at System.Windows.Forms.Application.ThreadContext.OnThreadException(Exception t)
at System.Windows.Forms.NativeWindow.Callback(IntPtr hWnd, Int32 msg, IntPtr wparam, IntPtr lparam)
at System.Windows.Forms.UnsafeNativeMethods.DispatchMessageW(MSG& msg)
at System.Windows.Forms.Application.ComponentManager.System.Windows.Forms.UnsafeNativeMethods.IMsoComponentManager.FPushMessageLoop(IntPtr dwComponentID, Int32 reason, Int32 pvLoopData)
at System.Windows.Forms.Application.ThreadContext.RunMessageLoopInner(Int32 reason, ApplicationContext context)
at System.Windows.Forms.Application.ThreadContext.RunMessageLoop(Int32 reason, ApplicationContext context)
at Agilent.MassSpectrometry.DataAnalysis.Qualitative.Program.Main(String[] args)

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14414 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Scrolling anomaly exists in Digest Comparative Analysis window

Problem:
1) Open two digest data files (for example enolase digest).
2) Select Wizards | Compare Digest Files : Find results...
3) Iimport the corresponding sequence file in the Define Match Sequences page.
4) Complete the rest of the wizard and generate results.

In the Comparative analysis window that gets displayed, scroll down Compound Compare List and highlight a row.

The scroll position square jumps up to the top and does not stay at the selected position.

Temporary Solution:

n/a

Fix Information:

n/a

KPR#: 14415 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:

Multiple rows cannot be highlighted in Compound Compare List table

Problem:

1) Open two digest data files (for example enolase digest).
2) Select Wizards | Compare Digest Files : Find results...
3) Iimport the corresponding sequence file in the Define Match Sequences page.
4) Complete the rest of the wizard and generate results.

In the Comparative analysis window that gets displayed, highlight a row in Compound Compare List and use the shift key to highlight multiple rows.
The user is then unable to highlight the multiple rows.

Temporary Solution:

n/a

Fix Information:

n/a

KPR#: 14434 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:

Translated GC MSD ChemStation data gives error “Validation failed ..” when opened in Qual, Can be read in Quant.

Problem:

Some GC MSD ChemStation data files have failed to load into Qual after translation to MassHunter format and give an Error message “Validation failed in time segment #” when opening the file. The files can be opened in Quant. The problem was traced to a defect in the acquired data file collected using the ChemPort driver.

The GCM Translator gives a warning during the translation process.

Temporary Solution:

None

Fix Information:
n/a

KPR#: 14436 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:
Removed NIST98 blocks Qual from seeing newer NIST11 software

Problem:
A system had at one time loaded a copy of NIST98 on the system and later loaded NIST11. Two sets of path and Work Dir were in the Win.ini file. Qual grayed out the "search using NIST MS program" option.
Temporary Solution:
Removethe references to NIST98 corrects the issue.
Fix Information:
n/a

KPR#: 14441 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:
Customer request to be able to calculate "Baseline Drift per hour" for a chromatogram

Problem:
Customer request to be able to calculate "Baseline Drift per hour" for a chromatogram
Temporary Solution:
n/a
Fix Information:
Feature is available in Lab Advisor utility.

KPR#: 14442 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
GC signals are not named correctly in "Chromatogram Extraction " in "Find Compounds by Integration"

Problem:

In "Chromatoragm Extraction" GC signals are listed as GC1, GC2, GC3 etc. They should be named and handled in the same way as LC detector signals i.e. FID1, FID2, FPD1, ECD1, etc.

Temporary Solution:

This handled correctly in Chromatograms -> Extract Chromatograms" from the top level menu. When Other Chromatograms is selected, the FPD1 detector signal in the attached example file is labeled correctly.

Fix Information:

n/a

KPR#: 14443 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:

AutoShow columns confusing :Removed columns come back when a row is selected in the Compound list table.

Problem:

1. Open a digest data file.
2. Load default layout for Protein Digest. Using BioconfirmProteinDigest default method run Find Compounds by MFE.
3. In the Compound list table right click on the column headers and remove a few columns (Cpd, Label or others with data) using Remove Column command.
4. Click on a row to highlight it. The removed columns are put back into the table.

Temporary Solution:

n/a

Fix Information:

n/a

KPR#: 14444 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:

When rerunning "Generate Formulas from Spectra" after changing parameters such that no hits are generated, old results are not cleared

Problem:

When rerunning "Generate Formulas from Spectra" after changing parameters such that no hits are generated, the behavior is different from "Generate Formulas from Compounds". It brings up a message saying that no formulas could be calculated, but it keeps the previous results in the "Spectrum Identification Results Window" up, instead of clearing them out. In case of "Generate Formulas from Compounds" the "Compound Identification Results Window" is cleared.

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14445 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Qual ignores Q-scores as calculated by MFE when set to Large Molecule mode

Problem:
Qual does not use the Q-scores calculated by the MFE algorithm when set to Large Molecule mode. The Q-score column will display all zeros (0) and the Q-score threshold does not impact the number of columns found.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14446 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
When MFE performs Mass Matching without Isotopic Pattern Matching, incorrect score values are given in the Ion Species Table

Problem:
Given an user spectrum where isotopic distributions are not predicable, the MFE algorithm will perform a simpler mass matching without performing isotopic pattern matching. This is expected behavior as no isotopic distributions have been calculated and therefore cannot be pattern matched. However, in the Ion Species table - MFE will populate matching scores of "100" for iso. abundance and iso. spacing rather than "0.0". Also, the overall score is incorrect.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14447 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Universal Integrator is Not Compatible with Find by Formula

Problem:
Data integrated with the Universal Integrator cannot be processed by the Find by Formula algorithm. An unhandled exception error will be thrown when FbF is run.

The Universal integrator is being deprecated and is superseded by the ChemStation, Agile, and Agile 2 integrators.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14448 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
In SIM/Scan data, Qual only displays the time segment delimiters for the SIM data timeline

Problem:
Consider an acquisition method that has 3 scan time segments and 5 SIM time segments. When Qual opens a data file produced by this method, only the SIM group time segment delimiters will be displayed in the TIC. The scan group time segments are not displayed. Scan data is available by EIC extraction or spectral extraction.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14450 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
The pusher offset (not puller offset) value is not displayed in the MSActuals for data acquired on a 6560.

Problem:
The pusher offset (not puller offset) value is not displayed in the View -> MS Actuals panel for data acquired on a 6560.

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14451 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:
When running Find By Deconvolution on a SIM/Scan file, Qual combines both SIM and Scan data in its visualization rather than displaying SIM and Scan separately.

Problem:
When running Find By Deconvolution on a SIM/Scan file, Qual combines both SIM and Scan data in its visualization rather than displaying SIM and Scan separately.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14452 Product: MassHunter Qual MassHunter Qual B.06.00 SP1 Hotfix

Keyword:

One-line Description:
Find by Targeted MSMS fails to find compounds when two time segments are used for the same precursor ion.

Problem:
Find by Targeted MSMS fails to find compounds when two time segments are used for the same precursor ion.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14453 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:
Excel 2013 gives warning on .XLS files

Problem:
When .XLS files are generated by Qual and opened in Excel 2013 - the following error is thrown:

"The file you are trying to open, [filename].xls is in a different format than specified by the file extension. Verify that the file is not corrupted and is from a trusted source before opening the file. Do you want to open the file now?"

If the user responds with "Yes" the file opens.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14454 Product: MassHunter Qual MassHunter Qual B.06.00 SP1

Keyword:

One-line Description:
On Computers without the standard D:\MassHunter\ directory established, an invalid method parameter flag is thrown from the MFE Mass Filters Tab of the Method Editor

Problem:
Under the MFE Mass Filters tab, the default source location points to "D:\MassHunter\PCDL\Default.csv."

On workstations or laptops that do not have a D:\ drive, this will display the "error" exclamation mark even if mass filters are not being used. Adjust the setting in the method to point to the correct location of the default.csv on the C drive.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14455 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Agile integrator does not show base peak m/z

Problem:

If the "Chromatogram Display Options" are set to include "Base Peak m/z," and either the Agile or Agile 2 Integrators are used, Qual will not print the Base Peak m/z on the chromatogram.
Temporary Solution:
Any other integrator (Universal, ChemStation, etc) will label the base peak m/z correctly.
Fix Information:
n/a

KPR#: 14456 Product: MassHunter Qual MassHunter Qual B.06.00

Keyword:

One-line Description:
Subsequent Signal-to-Noise calculations do not update the results table after the first calculation

Problem:
If a Signal-to-Noise calculation has already been performed on a loaded data file, the "Calculate Signal-to-Noise" feature will not replace the already calculated values until "Clear Results" is performed. "Clear Results" must be selected every time the user performs a subsequent Signal-to-Noise calculation for every data file loaded.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14457 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Duplication of product ion scans when switching between Navigator and Compound Detail View will Prevent Molecular Structure Correlator from opening, duplicate entries in PCDL

Problem:
When switching to the Compound Data View then back to the Navigator View, Qual will duplicate any product ion spectra produce by MFE or FbF. If a .CEF file is then exported of this duplicated compound - two problems arise:

1.) Spectrum Mill cannot open this .CEF file.
2.) PCDL will produce duplicate entries in the compound database/library.
Temporary Solution:
Right click and delete the duplicate result before exporting the .CEF file.

Fix Information:
n/a

KPR#: 14458 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Digest list disappears when cancel button is selected

Problem:
With BioConfirm enabled, import a sequence in the Define and Match sequence box and click on Edit to open in sequence editor. Digest the protein and the Digest List window with the Digest List table appears. Click on sequence and select Edit digest reagent. Then add or remove a reagent or change the order of selected reagents and click on cancel. The Digest list then disappears.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14459 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Exception when running FbF with All Ions data file in Formula Confirmation workflow

Problem:
When running Find by Formula on All Ions data in the Formula Confirmation and Sample Purity workflow - one may get an exception fault when "Use Lib Only" is set as the formula source.

Steps to reproduce

1. Open data file and method
2. Switch to Formula Confirmation and Sample Purity workflow. Open MS peaklist 1 window. Select unlinked navigation.
3. Run FbF, Highlight any compound, extract complete result set. Select the FbF spectrum.
4. Switch to “Use lib only” as formula source and ran FbF.

Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14460 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
Selecting a compound in the "Compound Compare List" causes the window to scroll back to the top of the compound list

Problem:
In the Compound Compare List In the Comparative Analysis utility, selecting a compound in the list causes the window displaying the table to scroll back to the top of the list. The compound is selected and highlighted, but the behavior can be disorienting to the user.
Temporary Solution:
Scroll back down to the selected compound in the list. It will be highlighted in blue.
Fix Information:
n/a

KPR#: 14466 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
"Clear Spectrum Results" for MS/MS spectrum or compound does not function as expected

Problem:
1. "Clear Spectrum results" is not available for annotated MS/MS compound spectrum

2. "Clear Spectrum results" does not work properly for annotated MS/MS spectrum, since the results are only cleared from the table but not from the spectrum.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14467 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
The "Min m/z for matching" algorythm does not behave as intended and implemented in Quant.

Problem:
The behavior of the "Min m/z for matching" is not working as needed for matching as implemented in Quant. In Quant, the software looks at both the sample spectrum and the library spectrum and determines the minimum m/z in BOTH spectra which it uses to drive the matching function. The user can increase the m/z via the interface to make it even higher but not make it lower. In Qual, it can be set to a value in the method that is something less that the min seen in both sample and this results in a library spectra resulting in false negatives.
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14468 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
CF and DF values are visible with QQQ MRM data

Problem:
When Qual has QQQ MRM data loaded, the spectrum label will include two values, CF and DF both = 0.000. These values are specific to ion mobility spectrometry and are not relevant to QQQ data.
Temporary Solution:
Ignore the label as the values are meaningless for QQQ data.
Fix Information:
n/a

KPR#: 14469 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
"Integration Off" Event in ChemStation Integrator causes Find by Formula to fail

Problem:
If a user attempts to use the ChemStation integrator while performing any Find by Formula operation - an "Integrator Off" entry in the integrator events table will result in zero compounds found by FbF.
Temporary Solution:
Use any other integrator - or do not turn off the integrator while running FbF with the ChemStation integrator.

Fix Information:
n/a

KPR#: 14470 Product: MassHunter Qual MassHunter Qual B.07.00

Keyword:

One-line Description:
MFE is excluding obvious evidence ions, and thus not correctly choosing the lowest m/z

Problem:
MFE may exclude obvious evidence ions and incorrectly assign the m/z based on an incorrect "lowest mass m/z".
Temporary Solution:
n/a
Fix Information:
n/a

KPR#: 14472 Product: MassHunter Qual MassHunter Qual B.03.00

Keyword:

One-line Description:
Acquisition method report does not work from a GC, GCMS, or GC MS/MS data file

Problem:
Acquisition method report does not work from a GC, GCMS, or GC MS/MS data file
Temporary Solution:
Print acquisition method from the appropriate acquisition application if possible.
Fix Information:
n/a

KPR#: 14473 Product: MassHunter Qual MassHunter Qual B.03.01 SP3

Keyword:

One-line Description:
Carbocation misidentified as [M+H]+ or M*+ but should be M+

Problem:
Carbocation and charged fragments misidentified in MS Formula Results.
Temporary Solution:
n/a
Fix Information:

n/a