

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	All Users	All Modules	X			When opening new data after processing old data and the user did not use IntStd in the regression of the previously opened data, this setting (Do Not Use IS) carries through to the newly-opened data. When opening new data, the Set Global Settings function was not executing first. This bug has been fixed.	7.2.20	2/12/12
2	All Users	HC	X			The 'Save All' function was not working for the Hepatic Clearance module. This bug has been fixed.	7.2.20	2/12/12
1	All Users	All Modules	X			Code meant to affect only the GenChromViewer for the new MetID Exact Mass Import feature was inadvertently interfering with the performance of the other GMSU/QC modules. This bug has been fixed.	7.2.19	2/7/12
1	Thermo Users	GCV	X			The MetID Exact Mass Importer feature needed tweeking.	7.2.18	2/5/12
1	Thermo Users	GCV	X			The MetID Exact Mass Importer feature was incorrectly adding a proton to the exact mass, when in fact the MetID output exact mass has already been corrected for proton. This bug has been fixed.	7.2.17	2/3/12
1	Thermo Users	GCV		X		A feature called 'MetID Exact Mass Importer' has been added added to the Generic Chrom Viewer that will allow users to import exact masses created by Thermo™ MetID™	7.2.16	2/2/12
2	Thermo Users	GCV			X	HT Acquisition users: Users are now able to configure Default Leading Edge Offset and Default Trailing Edge Offset.	7.2.16	2/2/12
3	Thermo Users	GCV			X	The Additional Detector feature has been optimized to make review easier.	7.2.16	2/2/12
4	Thermo Users	GCV			X	Additional settings have been added to the System Suitability feature allowing users to save window size and position and Metrics Plot view, size, and position.	7.2.16	2/2/12
1	All Users	All Modules			X	An archive/restore function has been added to GMSU/QC (Archive/Restore button on Console window). Users can archive data based on date. Users can restore data based on user-selected files.	7.2.15	1/29/12

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	All Users	HC	X			During testing, a normally invisible grid was left visible. The grid is again invisible in 7.2.15.	7.2.15	1/29/12
1	All Users	All Modules	X			The UNC feature was broken in 7.2.10. This bug has been fixed.	7.2.14	1/12/13
1	Thermo Users	All Modules	X			The new support for Rooney Method and Full Scan mass spec had a bug in which an incorrect mass range was recorded for a sample. This bug has been fixed.	7.2.13	1/12/12
1	Thermo Users	All Modules	X			The ppm range portion of the heading of an Int Std chromatogram resulting from a full scan experiment was showing "0.00000 – 0.00000", rather than the actual range. This bug has been fixed.	7.2.12	1/10/12
2	Thermo Users	All Modules			X	Sometimes the mass precision in the filter string embedded in the .raw file does not match the mass precision of the filter string contained in the .pmd file. The algorithm used by GMSU/QC to synchronize the filter string has been optimized.	7.2.12	1/10/12
3	All Users	HC			X	The Hepatic Clearance module Peak Name Set would allow only consistent replicates (e.g. all data points had to be single injections, duplicates, or triplicates, etc.). Users are now allowed to have mixed replicates in the time point set.	7.2.12	1/10/12
1	Thermo Users	GCV	X			Additional Detector window: The Configuration – Retention Time Offset Peak Detection Parameters window was not applying changes to the underlying data. This bug has been fixed.	7.2.11	12/29/11
2	Thermo Users	GCV	X			Additional Detector window: In certain circumstances, GMSU/QC will attempt to save a null value to a database field that is expecting a number. This bug has been fixed.	7.2.11	12/29/11
1	Thermo Users	GCV	X			Additional Detector window: The Threshold value was not populating to all samples when clicking the "=" button as expected. This bug has been fixed.	7.2.10	12/21/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	All Users	All Modules	X			A regression constant feature added in version 7.1.47 causes GMSU/QC to erroneously send an "Entry must be integer" error if the data is Hi Res and there is no Int Std. This bug has been fixed.	7.2.9	12/17/11
2	Thermo Users	GCV	X			HT-Acquisition users: If a .PMD is used that has more than one target cmpd, GMSU/QC may or may not create all expected data sets. This bug has been fixed.	7.2.9	12/17/11
1	All Users	All Modules			X	The Psuedo HT Display feature has been enhanced to be a sizeable floating window that updates when the user chooses a different sample.	7.2.7	12/14/11
2	Thermo Users	GCV			X	The Matrix Chrom Review feature has been enhanced to allow easier chromatographic changes from within the feature.	7.2.7	12/14/11
3	Thermo Users	GCV			X	The Full Scan High Throughput Screening feature will allow users to assign individual libraries to each data file being scanned, rather than one library for all data files.	7.2.7	12/14/11
4	All Users	All Modules	X			When Assigning Transitions and your database has several years of data, GMSU/QC may crash. An ID variable datatype had been set to INTEGER, but should have been set as LONG. This bug has been fixed.	7.2.7	12/14/11
1	Thermo Users	GCV			X	A 'Retention Time Offset Peak Detection' feature has been added to the Additional Detectors feature.	7.2.6	11/13/11
2	Thermo Users	GCV			X	The Additional Detectors feature has been enhanced to allow users to identify peaks using the MS peak as the Relative Retention Time marker.	7.2.6	11/13/11
3	Thermo Users	GCV	X			QQuan users sometimes find that, when the sequence set alternates between positive- and negative-ion internal standards, QQuan will embed the .pmd with the positive-ion information when the negative-ion is needed. GMSU/QC code has been added to assess when this situation occurs and to assign the correct internal standard	7.2.6	11/13/11
1	Thermo Users	All Modules	X			GMSU/QC was not checking to see if the .sld Path contained a backslash (Xcalibur allows paths with and without backslashes). This bug has been fixed.	7.2.4	11/1/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	Thermo Users	All Modules			X	Added a Tailing Factor column to the sample list. Tailing Factor = $(a + b) / 2a * 100$ Reference: <a href="http://www.separations.us.tosohbioscience.com/ServiceSupport/TechSupport/ResourceCenter/ChromatographyCalculations/SystemSuitabilityCalculations.htm#anchor3">http://www.separations.us.tosohbioscience.com/ServiceSupport/TechSupport/ResourceCenter/ChromatographyCalculations/SystemSuitabilityCalculations.htm#anchor3</a> Note: GMSU/QC has added the “* 100” parameter in order to report a more useable number typically in the range of 0.1 to 0.4	7.2.3	10/16/11
1	Thermo Users	GCV	X			When entering Full Scan Rooney Method data, the ‘Set Rooney Ret. Times’ window will crash when attempting to manually enter RTimes or exact masses (rather than pasting from clipboard). This bug has been fixed.	7.2.2	9/21/11
2	Thermo Users	GCV	X			Aria HT Acquisition Users: GMSU/QC would not properly load acquired data when the .sld has 2 or more rows and each .pmd in the row has 2 or more target compounds. This bug has been fixed.	7.2.2	9/21/11
1	Thermo Users	All Modules	X			The ‘Print Chromatogram’ function was not working properly with the new Rooney Full Scan Method data. This bug has been fixed.	7.2.1	9/9/11
1	Thermo Users	GCV		X		The GCV can now display and process data from up to 3 additional detectors. The data may be viewed from Menu – Thermo Tools – Additional Detectors. The additional detectors will all report a %Purity value.	7.2.0	8/29/11
2	Thermo Users	GCV		X		The Rooney Method (different string filters for each sample of a sequence) has been extended to support Full Scan Exact Mass data.	7.2.0	8/29/11
3	All Users	All Modules			X	New command line switches have been added for those who call GMSU/QC from a command line. If interested in calling GMSU/QC from the command line, please contact <a href="mailto:gubbs@gubbsinc.com">gubbs@gubbsinc.com</a> .	7.2.0	8/29/11
4	Thermo Users	GCV			X	Added Int Std Default PNF, ANF, and BW Integration Parameters Configuration Utility Settings	7.2.0	8/29/11
5	Thermo Users	GCV			X	HT Acquisition Users: A ‘pan’ button has been added that allow users to zoom on a certain and ‘pan’ left to right in time increments equal to the zoom window. The button is a horizontal scroll bar located below the Reset button.	7.2.0	8/29/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
6	Thermo Users	GCV Perm PK			X	A Copy-to-Clipboard button (Clip-bd) has been added to the chromatogram pane of these modules.	7.2.0	8/29/11
7	Thermo Users	GCV	X			Aria HT Acquisition Users: when changing an integration parameter, GMSU/QC was identifying peaks outside the defined retention window. This bug has been fixed.	7.2.0	8/29/11
8	Thermo Users	GCV	X			The Full Scan Trace Analysis module would crash if the data file being examined had extremely high signal. This bug has been fixed.	7.2.0	8/29/11
1	All Users	HC			X	In the past, Constants assigned to a data set were not saved – the constants were retrieved from the Global Constant set. Therefore, if Constant values were changed at the Global level and previously-saved data were opened, calculated Clearance values would be changed. Now, Constants are saved with the data set record and will always reflect the Constant values used at the time of data Save.	7.1.52	8/11/11
2	Thermo Users	GCV			X	The Full Scan Trace Analysis Screening feature has been enhanced to allow users to report all found instances of a compound (e.g. isoforms of a peptide digest experiment)	7.1.52	8/11/11
3	ABI Users	HC Perm	X			If a user loads data that has only one transition ion in the experiment (i.e. no Int Std), then GMSU/QC will crash. This bug has been fixed.	7.1.52	8/11/11
4	Thermo Users	All Modules	X			In the following scenario, GMSU/QC will crash: <ul style="list-style-type: none"> <li>• The data is full scan data</li> <li>• The .sld has a .pmd configured in the Processing Method column</li> <li>• The .pmd is not located where the path defines</li> </ul> This bug has been fixed.	7.1.52	8/11/11
5	All Users	HC	X			If the action “Menu – Delete Records” is executed, GMSU/QC crashes. This bug has been fixed.	7.1.52	8/11/11
1	Thermo Users	All Modules	X			Item 1 from 7.1.50 below broke the Matrix Chromatographic Review function. This bug has been fixed.	7.1.51	7/14/11
1	Thermo Users	GCV			X	Users may now configure default values for the Advanced Integration Parameter feature.	7.1.50	7/5/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	Thermo Users	All Modules	X			GMSU will sometimes crash when integration parameters are modified and the System Suitability feature is open. This bug has been fixed.	7.1.50	7/5/11
3	Thermo Users	GCV	X			<p>For HT-A Rapidfire users - In the following scenario, GMSU/QC has a problem:</p> <ol style="list-style-type: none"> <li>1. The number of injections in each .raw file is, for example, 11</li> <li>2. The .sld sequence has a number of rows greater than the number of injections in the .raw file - for example, 16 rows</li> <li>3. In the example scenario, when the user attempts to view the data from the 12<sup>th</sup> dataset (or 13<sup>th</sup>, or 14<sup>th</sup>, etc), the code breaks and doesn't display the expected chromatographic peaks when a sample is chose from the Sample List table.</li> </ol> <p>This bug has been fixed.</p>	7.1.50	7/5/11
4	Thermo Users	GCV	X			Rapidfire users: The Rapidfire processing algorithm has been tweaked to account for minor peak-picking errors.	7.1.50	7/5/11
5	All Users	All Modules	X			A feature addition to the Rooney Method introduced in 7.1.43 broke the Manual Integration function of normal files – when a peak is manually integrated and the sample set has a calibration curve, the peak calculated concentration will not update. This bug has been fixed.	7.1.50	7/5/11
1	Thermo Users	GCV			X	Users of the GCV module now have available Advanced Integration Parameters ('Advanced...' button on the Chromatogram tab). Users involved in High Throughput Acquisition (HT-A), defined as 'acquiring all sequence injections into a single .raw file' sometimes have the need for additional integration parameters in order to achieve optimal peak integration across the entire chromatogram.	7.1.47	6/19/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	All Users	PK Perm GCV			X	Though users are able to set the default Regression Sig Figs parameter in the Configuration Utility, that value is not saved with the data. Therefore, changing of the default Regression Sig Figs would affect how the number of regression constant sig figs displayed in Saved data. For the Permeability Calculator, displayed Papp values would change even for Saved data since intermediate values are calculated using the regression constants displayed at the Sig Fig setting. The Regression Sig Fig value is now saved with the data and can be modified for each data file in the Calibration tab of the respective module	7.1.47	6/19/11
3	Thermo Users	GCV			X	The Full Scan Trace Analysis Screening feature has been enhanced to allow users to force integration of a peak at a user-supplied retention time.	7.1.47	6/19/11
4	Thermo Users	All Modules			X	Especially HT-Acquisition users: The SLD/PMD maker has problems generating a correct .pmd under certain scenarios. If a .pmd has been created that isn't correct (this applies to any form of acquisition), users may assign different or correct string filters as Analyte and/or Int Std using the Menu – Assign Transition Ions feature. In addition, users may use this feature to add additional Analytes to the dataset without having to modify the underlying .pmd.	7.1.47	6/19/11
5	All Users	Perm	X			The Permeability Calculator will calculate an incorrect value for SEM if the number of replicates used to calculate average Papp is less than 3. This bug has been fixed.	7.1.47	6/19/11
6	All Users	GCV	X			If the data set contains less than 36 injections, then the new Matrix Chromatographic Review feature will crash. This bug has been fixed.	7.1.47	6/19/11
7	Thermo Users	All Modules	X			QQuan users: If the the QQuan parent .sld was not acquired to completion, then GMSU/QC would not recognize the parent .sld as a QQuan .sld, resulting in the processing of only one analyte of a multi-analyte compound set. This bug has been fixed.	7.1.47	6/19/11
1	Thermo Users	All Modules			X	Added a new Sample List Column (Aria LC Info) that provides Aria ASProbe and LCSystem information for each sample for those performing Aria HT Acquisition	7.1.46	5/10/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	Thermo Users	All Modules	X			The formula for matching .pmd filter strings with .raw filter strings was tweaked.	7.1.45	5/7/11
1	Thermo Users	GCV			X	For Aria HT Acquisition Users: The SLD/PMD Maker function was creating a .pmd containing all cmpds/transitions acquired in the .raw file. This function has been modified to create only those transitions that have been defined by the user when creating the .pmd.	7.1.43	4/28/11
2	Thermo Users	All Modules			X	When setting the Analyte Retention Time, GMSU/QC would needlessly re-process the Int Std as well (and vice versa). The feature has been enhanced so that only the needed compound gets reprocessed.	7.1.43	4/28/11
3	Thermo Users	GCV			X	For Rooney Method users: a feature has been added (Menu – Retention Time Utilities – Enter Rooney Retention Time Parameters) that allows users to manually enter the expected RT of the .sld subgroups, rather than have GMSU/QC assign the expected RT (which can be erratic when peak signal is weak).	7.1.43	4/28/11
4	Thermo Users	All Modules	X			GMSU/QC has problems processing data that has been acquired with the Xcalibur precision setting set to 3. Functions have been optimized to better adapt to Xcalibur string filters resulting from 3-decimal precision acquisition.	7.1.43	4/28/11
5	All Users	All Modules	X			When manually integrating a peak whose Sample Type is ‘Unknown’, GMSU/QC will needlessly recalculate sample concentrations for the entire sample list. This bug has been fixed.	7.1.43	4/28/11
	All Users	Installer	X			The GMSU/QC installer has not been placing a GMSU/QC icon on the desktop. This bug has been fixed.	7.1.43	4/28/11
1	Thermo Users	GCV			X	New features have been added to the Matrix Chromatographic Review feature, as well as the correction of a small bug.	7.1.41	4/14/11
2	Thermo Users	All Modules			X	New features have been added to the System Suitability feature.	7.1.41	4/14/11
1	Thermo Users	GCV		X		The new Matrix Chromatographic Review feature allows users to review and modify integration parameters (including manually integrate) and print chromatograms in a matrix view of individual chromatograms up 6 rows by 6 columns. Note: This feature is not yet available for HT Acquisition data.	7.1.40	4/4/11

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	All Users	All Modules	X			The GMSU 7.1.37 Installer was packed incorrectly, resulting in an error message during installation and the installer would quit. This bug has been fixed.	7.1.38	2/9/11
2	All Users	All Modules	X			The 'Include in Report – Row Colors' function was not working. This bug has been fixed.	7.1.38	2/9/11
1	All Users	All Modules	X			When clicking the Calibration Tab 'Apply to Chromatography' button, if there were samples with sample type of 'QC', this sample would be incorrectly identified as a Standard. This bug has been fixed.	7.1.37	2/4/11
2	All Users	All Modules	X			If Microsoft® SQL Server is the GMSU/QC database and HT acquisition was performed, then an error occurred if the user attempted to create a Chromatographic Method. This bug has been fixed.	7.1.37	2/4/11
3	All Users	All Modules	X			If Microsoft® SQL Server is the GMSU/QC database, an error occurred if the user attempted to create a new Column Heading set or if an existing Column Heading set was modified. This bug has been fixed.	7.1.37	2/4/11
4	All Users	All Modules	X			Chromatographic Method information is loaded when GMSU/QC is booted. Some time in the past, a debugging set of code was inserted that deleted from memory the Chromatographic Method information when a data set is loaded. This debugging code was not deactivated, resulting in an error if the user attempts to apply a Chromatographic Method to HT acquisition data. This debugging code has been deactivated which resolves the problem.	7.1.37	2/4/11
5	Thermo Users	All Modules	X			When applying a Chromatographic Method to an existing HT acquisition data set, peaks would not be identified if the peak baseline width is unusually wide. The logic for this function has been optimized.	7.1.37	2/4/11
6	All Users	All Modules	X			The De-activate Print Queue window contained a variable whose type was not large enough to handle a large number of records. This bug has been fixed.	7.1.37	2/4/11
1	All Users	All Modules	X			The Assign Transition Ions feature was assigning the incorrect compound name when data is loaded in which there is more than one drug set (Thermo) or .wiff file (ABI) displayed in the 'Choose a file/sample' table, sometimes causing GMSU/QC to crash. This bug has been fixed.	7.1.35	12/05/10

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	All Users	All Modules	X			When viewing HT Acquisition data in the Hep Clearance module, the individual peaks were not centered properly in the displayed chromatogram. This bug has been fixed.	7.1.35	12/05/10
1	All Users	All Modules	X			The new Delete Records function was not deleting all records. This bug has been fixed.	7.1.34	12/02/10
2	Thermo Users	HC	X			In v6.x, a feature was introduced in which the user could save all HC data by simply clicking the Save Results button. That feature was making existing data invisible if the original data is QQuan data (which could be resolved by simply re-loading the data). This bug has been fixed.	7.1.34	12/02/10
1	All Users	HC			X	Added additional units (e.g. ul/min/MillionCells) to the Hep Clearance Module label choices	7.1.32	11/28/10
2	All Users	Perm			X	Added an additional database table (tblPermPapp) to store interim Papp calculations (used to calculate overall Papp values) in order report that data in custom reports	7.1.32	11/28/10
3	All Users	All Modules			X	Added a feature to totally delete one or more records (Menu – Delete Records).	7.1.32	11/28/10
1	Thermo Users	GCV			X	Ion Ratio Evaluation feature added to System Suitability feature.	7.1.31	11/15/10
2	Thermo Users	GCV			X	Enhanced and clarified functionality of the SLD/PMD Maker feature	7.1.31	11/15/10
3	Thermo Users	GCV			X	Added additional functionality to the Full Scan Trace Analysis Screening feature to allow users to import analyte mass and retention time via a spreadsheet/.csv. Also, Custom Report capability was added to this feature.	7.1.31	11/15/10
4	Thermo Users	All Modules			X	Added functionality to account for the new injection time text file format for Biocious (Biotrove) Rapidfire support.	7.1.31	11/15/10
5	Thermo Users	All Modules	X			Corrected a bug in the new Aria HT Acquisition functionality to allow forcing the Analyte Retention Time to synchronize with the Int Std Retention Time.	7.1.31	11/15/10
6	All Users	All Modules	X			The ‘green halo’ feature of the Calibration Curve plot was not functioning. This bug has been fixed.	7.1.31	11/15/10

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
7	All Users	All Modules	X			The Assign Transition Ions feature was not executing properly. This bug has been fixed.	7.1.31	11/15/10
1	All Users	All Modules	X			If an HT Acquisition file is opened accidentally as an LT Acquisition file, the user can rectify the situation by choosing the 'High Throughput Acquisition' option of the Data Acquisition Mode option group. Unfortunately, if the HT file has more than one acquired sample/file, GMSU/QC will not process the additional samples/files. This bug has been fixed	7.1.29	10/10/10
2	Thermo Users	All Modules	X			In some circumstances, if a 2 <sup>nd</sup> .sld is opened during a GMSU/QC session and this 2 <sup>nd</sup> .sld has .pmd's with more than one analyte, the very first analyte sometimes is configured with the incorrect Int Std transition. This bug has been fixed.	7.1.29	10/10/10
1	Thermo Users	All Modules			X	Enhanced Aria HT Acquisition functionality to allow forcing the Analyte Retention Time to synchronize with the Int Std Retention Time.	7.1.27	9/15/10
2	Thermo Users	GCV	X			GMSU/QC will not process Rooney Method data if the acquisition includes summed ions. This bug have been fixed.	7.1.27	9/15/10
1	Thermo Users	GCV			X	Added additional functionality to the Full Scan Trace Analysis module to process CID Orbitrap data. HCD functionality will come soon.	7.1.26	9/15/10
2	Thermo Users	GCV			X	Full Scan Trace Analysis: Added the ability to create a PDF report (requires the installation of Microsoft® Excel 2007 or later).	7.1.26	9/3/10
3	Thermo Users	GCV	X			Full Scan Trace Analysis: The Known Results sort function was hilitating the incorrect row after a sort event. This bug has been fixed.	7.1.26	9/3/10
1	Thermo Users	GCV			X	Full Scan Trace Analysis: Added additional display features	7.1.23	7/16/10
2	Thermo Users	All Modules	X			The Discover Masses module has been optimized to display spectra from samples that have different filter strings	7.1.23	7/16/10
3	Thermo Users	GCV	X			Full Scan Trace Analysis: If the user Updates Results and the Total Intensity display option is chosen, then integrated peak area information is not recorded correctly. This bug has been fixed.	7.1.23	7/16/10

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	Thermo Users	GCV			X	For Aria HT Acquisition users only: The 'Offset peaks' feature has been expanded to allow the user to widen the Aria data acquisition window (rather than simply shift it left or right). In addition, the user can tell GMSU/QC to simply use the Int Stds from the sample to create a retention time method.	7.1.22	7/9/10
1	Thermo Users	GCV	X			The Full Scan Trace Analysis Screening module was not properly configuring a Blank file when using the Browse button in the Blank configuration area. This bug has been fixed.	7.1.21	6/19/10
1	Thermo Users	GCV		X		The Full Scan Trace Analysis Screening module has been further optimized.	7.1.20	6/10/10
2	Thermo Users	All Modules	X			If a .pmd is used that contains more than one filter string and two of the filter strings have identical parent ions but different daughter ions, then GMSU/QC will not display the analyte for the second of the filter strings with identical parent ions. This bug has been fixed.	7.1.20	6/10/10
1	Thermo Users	All Modules	X			Rooney Method Users: When opening data using the 2 <sup>nd</sup> 'Choose Data Access' option and the .sld has only one .pmd, GMSU/QC would not correctly assign transition ions to the Analyte and IntStd. This bug has been fixed.	7.1.18	5/14/10
2	Thermo Users	PK	X			PK plots were not plotting correctly when there was more than one sample for a single time point (such as is common when species is mouse). This bug has been fixed.	7.1.18	5/14/10
1	All Users	HC			X	Standard Deviation error bars have been added to the half-life regression plot in the Excel report	7.1.17	3/9/10
2	Thermo Users	GCV			X	The SLD/PMD maker has been enhanced to act in a more logical manner.	7.1.17	3/9/10
3	Thermo Users	GCV			X	Features have been added to the Full Scan Trace Analysis Screening module	7.1.17	3/9/10
4	Thermo Users	GCV	X			Thermo HT Acquisition users only: If Aria or Rapidfire data is opened without the .cbt or Rapidfire RT text file and the user attempts to change an integration parameter, GMSU/QC will crash. This bug has been fixed.	7.1.17	3/9/10

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
5	Thermo Users	HC	X			In the Detail Section of the Excel report, incorrect values were being shown in the Std Dev column. This bug has been fixed.	7.1.17	3/9/10
6	All Users	All Modules	X			If the number of QCs exceeded then number of Calibr. Stds in the sample list, then GMSU/QC would crash when a Calibr. Std. was excluded. This bug has been fixed.	7.1.17	3/9/10
1	Thermo Users	All Modules	X			Exactive data only: In some scenarios, the Int Std was not being processed. This bug has been fixed.	7.1.16	2/18/10
1	Thermo Users	PK	X			Users are unable to save data. This bug has been fixed.	7.1.14	2/16/10
1	All Users	Config Util	X			When changing the setting 'Use IS as Default Setting' in the Hepatic Clearance category, the user was not being presented with a 'Yes/No' option. This bug has been fixed.	7.1.13	2/5/10
2	All Users	Perm	X			If a Custom Report contained a hidden sheet, the report would not be prepared properly. This bug has been fixed.	7.1.13	2/5/10
1	Thermo Users	GCV			X	The Full Scan Trace Analysis Screening function has been optimized.	7.1.12	2/3/10
2	Thermo Users	All Modules	X			The Autosave function added in 7.1.0 was not functioning properly. This bug has been fixed.	7.1.12	2/3/10
1	Thermo Users	All Modules			X	HT Acquisition users only: The algorithms for detecting peaks in an HT Acquisition data file have been optimized for recognizing missed peaks	7.1.11	1/19/10
1	Thermo Users	HC	X			If assay includes daughter ion summing, then the manual integration and chromatogram redraw functions may not perform as expected. This bug has been fixed	7.1.10	1/13/10
2	Thermo Users	HC	X			If a custom report contains a hidden sheet, then GMSU/QC will crash when attempting to create the report in Excel. This bug has been fixed.	7.1.10	1/13/10
1	All Users	Perm	X			The Calibration Standard Include/Exclude function was not working properly. This bug has been fixed.	7.1.9	1/4/10

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
1	Thermo Users	All Modules	X			The manual integration was still not functioning correctly. This bug has been fixed.	7.1.3	11/17/09
1	Thermo Users	All Modules	X			The color codes of the plots and labels of the Comparative/Discovery Plot feature were not matching. This bug has been fixed.	7.1.3	11/16/09
2	Thermo Users	All Modules	X			A recent feature addition disabled the manual integration function of GMSU/QC. This bug has been fixed.	7.1.3	11/16/09
1	Thermo Users	All Modules		X		XDKOEM 2.1.0.26: The previously-released version of XDKOEM conflicted with the Themo application called QQuan. XDKOEM 2.1.0.26 resolves this conflict.	7.1.2	11/13/09
2	All Users	All Modules		X		Orbitrap users: The 'Discover Masses from TIC' has been activated. This feature allows users to record masses of interest from a full scan Orbitrap file, paste the masses to a spreadsheet for further assignment, and finally enter the masses into the GMSU/QCalc Exact Mass Database.	7.1.2	11/13/09
3	All Users	All Modules			X	Orbitrap users: The following elements have been added to the Comparative/Discovery Plots feature: <ul style="list-style-type: none"> <li>▪ Users may choose to display only samples of type UNKNOWN</li> <li>▪ Users may increase the signal of individual graph lines</li> </ul>	7.1.2	11/13/09
4	All Users	GCV			X	Axes log options are now available to view calibration curves. This feature will be expanded to the other modules soon	7.1.2	11/13/09
5	All Users	PK Perm GCV			X	Report generation code was optimized that allows reports to be generated much more quickly.	7.1.2	11/13/09
6	All Users	HC	X			When Time Point Sets were de-activated in the Configuration Utility, the Time Point Set dropdown box in the Hep Cl module was not filtering out the deactivated sets. This bug has been fixed.	7.1.2	11/13/09
1	All Users	PK Perm GCV	X			When the Analyte textbox displayed in each module is modified by the user, the corresponding Analyte column in the Sample List was not updating to the new value. This bug has been fixed.	7.1.1	11/11/09

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	Thermo Users	GCV	X			Aria HT Acquisition only: If a sequence terminates before completion, then GMSU/QC reports that it cannot process the Aria .cbt file when attempting to process the data. This bug has been fixed.	7.1.1	11/11/09
3	Thermo Users	GCV	X			Aria HT Acquisition only: If a sequence has more than one .raw file, GMSU/QC was recording an incorrect acquisition date for all the files except the first one. This bug has been fixed.	7.1.1	11/11/09
4	All Users	GCV	X			When Time Point Sets were deactivated in the Configuration Utility, the updated status of the Time Point Sets would not be reflected until the Hep Clearance Module was restarted. This bug has been fixed.	7.1.1	11/11/09
1	Thermo Users	All Modules		X		<p>A Configuration Utility feature called 'AutoSave files after review' has been added. If this item is set to 'Yes', then:</p> <ul style="list-style-type: none"> <li>▪ records will be automatically saved when the user moves to another analyte.</li> <li>▪ if the user attempts to Exit or Browse to a new file and there are unsaved analytes associated with the file, the user will be reminded that there are un-saved analytes in the file analyte set</li> </ul> <p>Each module has it's own AutoSave setting.</p>	7.1.0	11/6/09
2	All Users	All Modules		X		<p>A Configuration Utility – Global Category feature called 'User: Use User-specific configuration settings' has been added. If this item is set to 'Yes' and 'User: User-specific directory' is configured with a directory, then an .ini file containing Configuration settings is created at that location for that user. The next time the user opens GMSU/QC, that user's Configuration settings are retrieved from the .ini file rather than the GMSU/QC database.</p> <p>Notes:</p> <ul style="list-style-type: none"> <li>▪ The 'User-specific directory' may be configured on a network allowing users configured in a multi-user environment to access his/her's .ini file from any GMSU/QC installation</li> </ul>	7.1.0	11/6/09
3	All Users	All Modules	X			When opening the Report Generation window from the Menu bar within a module, the current sample selected in the module was not selected in the Report Generation file list if the Report Generation has a default sort setting of anything besides 'Analyte'. This bug has been fixed.	7.1.0	11/6/09

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
4	Thermo Users	PK	X			In some scenarios, the slope of the PK Slope plot was not extending to the length of the plot. This bug has been fixed.	7.1.0	11/6/09
5	Thermo Users	PK Perm GCV	X			GMSU/QC was not reporting QC values even though QC values had been configured in the Processing Method (.pmd). This bug has been fixed.	7.10.	11/6/09
6	ABI Users	HC	X			The HC module was not storing peak height values during a Save action. This bug has been fixed.	7.1.0	11/6/09
1	Thermo Users	HC	X			When the 'ppm Window' value is changed, the chromatogram window X-axis time range is set to 0 – 0.25 min, rather than 0 – [run time] min. This bug has been fixed.	7.0.15	10/7/09
2	Thermo Users	HC	X			If a file is opened that has been saved, the 'ppm Window' dropdown box should be disabled. Currently the dropdownbox is enabled. This bug has been fixed.	7.0.15	10/7/09
3	Thermo Users	HC	X			If a orbitrap data is saved in the Hep Cl module, GMSU/QC crashes the next time you try to open that saved data. This bug has been fixed.	7.0.15	10/7/09
1	Thermo Users	HC	X			Orbitrap data only: The Hep Cl module will crash if Orbitrap data is opened. This bug has been fixed.	7.0.14	9/23/09
1	All Users	All Modules	X			The Assign Transitions feature has been optimized	7.0.13	9/22/09
1	Thermo Users	PK	X			In 7.0.0, a feature was introduced in which PK Peak Name Sets are automatically generated if the Sample ID conforms to a specific naming nomenclature (described in section User Manual 13 Section 28.3.12 or User Manual 14 Section 28.2). The introduction of this feature has caused the existing PK Features options to not execute in certain instances. This bug has been fixed.	7.0.12	9/18/09
1	Thermo Users	All Modules			X	Orbitrap users: When opening a sequence that has no .pmd, the user is presented with the TIC of the .raw files, but the TIC chromatogram was not drawing. Now the TIC chromatogram will draw.	7.0.11	8/14/09

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	Thermo Users	GCV	X			In the System Suitability feature, checking or unchecking the 'RT Differences' checkboxes failed to update the System Suitability window. This bug has been fixed.	7.0.11	8/14/09
3	Thermo Users	All Modules	X			Orbitrap users: When using the Exact Mass Database to assign compounds to acquired data, the Int Std was not being recognized in the quantitative method, even though the chromatograms would draw properly. This bug has been fixed.	7.0.11	8/14/09
1	All Users	All Modules			X	The Path column of the 'Choose a file/sample' table has been right-aligned. That column is now left-aligned.	7.0.8	8/6/09
2	Thermo Users	All Modules	X			The following scenario caused chromatograms to not draw: <ul style="list-style-type: none"> <li>▪ Triplequad HT Acquisition mode is used to acquire data</li> <li>▪ Parent and daughter ion acquisition precision is acquired at 3 decimal places</li> <li>▪ GMSU/QC SLD/PMD Maker feature is used to create the .pmd</li> <li>▪ Data is saved, then re-opened</li> </ul> This bug has been fixed.	7.0.8	8/6/09
3	Thermo Users	All Modules	X			The Peak Width and Signal/Noise functions sometimes resulted in incorrect values. This bug has been fixed.	7.0.8	8/6/09
1	Thermo Users	All Modules			X	Exactive support has been further optimized.	7.0.6	7/19/09
2	All Users	HC	X			If you have been a GMSU/QC user since before v.4.0, when generating a report with v.7.0.0 or newer, GMSU/QC crashes. This bug has been fixed.	7.0.6	7/19/09
3	Thermo Users	GCV	X			For HT Acquisition users only. The incorrect date of acquisition was being recorded for each .raw file. This bug has been fixed.	7.0.6	7/19/09
4	Thermo Users	PK	X			When opening new PK Calculator data, the default Assay Set Name was not being applied. This bug has been fixed.	7.0.6	7/19/09
5	Thermo Users	Setup	X			Beginning with 7.0.0, the GMSU/QC setup failed to create a directory for CopyData.exe. Hence, CopyData.exe was not being installed during GMSU/QC installation. This bug has been fixed.	7.0.6	7/19/09
1	Thermo Users	All Modules		X		Support for Exactive/LTQ orbitrap data has been optimized. Orbitrap data is available in all GMSU/QC modules.	7.0.5	6/23/09

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU/QCalc	Issue Date
				Major	Minor			
2	All Users	Perm GCV PK			X	Users may now paste calibration standard concentrations from the clipboard into the Concentrations table in the Calibration tab	7.0.5	6/23/09
3	Thermo Users	GCV			X	The peak identification routine for Biotrove Rapidfire data has been optimized	7.0.5	6/23/09
4	Thermo Users	GCV			X	The peak identification routine for Thermo Aria data has been optimized	7.0.5	6/23/09
5	All Users	All Modules			X	When data is Saved, the user is prompted with an 'OK' dialog box when the save event is complete. That dialog box has been replaced with a message box that disappears after 0.5 seconds.	7.0.5	6/23/09
6	All Users	Perm GCV PK	X			If a calibration curve has been set to NOT use area ratios, the generated report for that data set will have the calibration plot drawn incorrectly. This bug has been fixed.	7.0.5	6/23/09
7	Thermo Users	PKAUC	X			When using the 'Include Calibr Std' feature to include a calibr standard that has been excluded, GMSU/QC crashes. This bug was introduced in v6.0.20. This bug has been fixed.	7.0.5	6/23/09
8	All Users	GCV	X			The sample list table in the 'Standards' tab was corrupt. It has been repaired.	7.0.5	6/23/09
9	All Users	HC	X			When a new Time Point Set is created, it's default Active setting is set to FALSE. The default Active setting should be TRUE. This bug has been fixed.	7.0.5	6/23/09
1	Thermo Users	All Modules		X		Support for Thermo Orbitrap (Exactive, LTQ) data has been added to all modules	7.0.1	6/14/09
1	Thermo Users	All Modules		X		Support for Xcalibur 2.1 is added	7.0.0	6/9/09

\* Module Legend

- HC: Hepatic Clearance Calculator
- PK: PK Calculator
- Perm: Permeability Calculator
- GCV: Generic Chromatographic Viewer
- TBI: To Be Issued