#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU	Issue Date
				Major	Minor			
1	Thermos Users	Full Scan Trace			X	Added features to Full Scan Screening module to better accommodate users.	8.5.62	10/21/20
1	Thermo Users	All Modules			X	Added functionality to correctly identify filter string when experiment is SIM and all .raw file filter strings are SIM	8.5.61	9/26/20
1	Thermo Users	MassMetaSite	X			If user enters a m/z for IntStd, the IntStd does not apply to the underlying data. This bug has been fixed.	8.5.60	8/4/20
2	Thermo Users	Full Scan Trace	X			Update was not updating the Peak Area column. This bug has been fixed.	8.5.60	8/4/20
1	Thermo Users	GMSU	X			In the Full Scan Screening feature, if the .raw file is very large (e.g. peptide map of ~60 minutes), a time point variable data type will be too small. This bug has been fixed	8.5.59	3/2/20
1	All Users	GMSU		X		All GMSU database updates are now handled by GMSU. UpdateGMSUDatabase.xls has been deprecated.	8.5.58	2/13/20
1	Sciex Users	DAM Creator			X	Modified functionality for Cocktail .dam files	8.5.57	12/10/19
1	Sciex Users	DAM Creator			X	Added functionality for Cocktail .dam files	8.5.56	12/9/19
1	All Users		X			If numAcquisitionTime is null, the Generate Reports grid will stop filling at that record. This bug has been fixed.	8.5.55	11/24/19
1	Thermo Users				X	Added QC Standards in Calibration tab	8.5.54	9/25/19
2	Thermo Users		X			The ‘Discover Masses from TIC’ was not showing mass spectra. This bug has been fixed.	8.5.54	9/25/19
1	All Users	All Modules	X			A function added in 8.5.49 to check the MaxID values caused GMSU to crash if users had a SQL Server database. This bug has been fixed.	8.5.53	9/20/19

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1	Thermo Users	All Modules	X			If data has several experiments (e.g. full scan, hcd, MS2, MS3), a function (GetFullScan) was erroring out, resulting in incorrect assignment of string filter. This bug has been fixed.	8.5.52	9/7/19
1	Sciex Users		X			Peak Area Ratio was not updating when the Peak Area and Peak Height Threshhold fields were modified. This bug has been fixed.	8.5.51	8/27/19
2	All Users				X	Added a function to run every time GMSU is opened to sync tblMaxID values and their respective table primary key equivalents	8.5.51	8/27/19
1	Sciex Users	DAM Creator			X	Tweaked function to be more robust	8.5.50	8/26/19
1	All Users	GVC Report			X	Sometimes the Excel paste function errors out (reported in Win 10 Office 2016 environment). The entire report job is then lost. The paste code has been error trapped to notify user when error occurs and the rest of the report job is continued.	8.5.49	7/30/19
1	Thermo Users	GCV			X	The Additional Detectors feature was tweaked to accommodate different data	8.5.48	7/17/19
1	Sciex Users		X			The HT-A peak identification algorithm was tweaked to be more accurate.	8.5.47	7/10/19
1	All Users	All Modules			X	GMSU is compatible with Win10, the GMSU Installer is ont. The GMSU installer has been modified to be compatible with Win10.	8.5.46	2/11/19
1	All Users	Rapidfire	X			The Rapidfire .rftime logic for the scenario when there is more than one sample (Sciex) or .raw file (Thermo) in the .rftime file (‘Row’ column) had been disabled. This logic has been re-activated.	8.5.45	1/29/19
1	Thermo Users	All Modules	X			The Guassian/Boxcar smoothing type dropdown doesn’t like it when the sequence data is Rooney. This bug has been fixed.`	8.5.44	11/26/18

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2	Thermo Users	All Modules	X			If a peak is manually integrated, the Normalize Y option setting is ignored. This bug has been fixed.	8.5.44	11/26/18
1	Sciex Users	GubbsQMF	X			A round-5 rounding error was found and fixed.	8.5.43	11/7/18
1	Thermo Users		X			If an Exact Mass-containing Rooney sequence has a sample that has no exact mass, GMSU incorrectly categorizes boolIsXactiveTIC = True. This bug has been fixed.	8.5.42	11/6/18
2	Thermo Users		X			The logic for automatically determining Rooney set retention times was incorrect in Function GetRTMaxArea. This bug has been fixed.	8.5.42	11/6/18
1	All Users	Full Scan HT-A	X			If analytes have been added to the dataset, Save will crash for these analytes. This bug has been fixed.	8.5.41	10/30/18
1	Sciex Users	All Modules	X			The Assign Transitions module needed to be tweaked some more when data is Sciex	8.5.40	10/26/18
1	Sciex Users	All Modules	X			The Assign Transitions module needed to be tweaked when data is Sciex	8.5.39	10/26/18
1	Thermo Users	GCV			X	Tweaked HT-A Rapidfire 5-col code	8.5.38	10/23/18
1	Sciex Users	All Modules		X		A feature calls GubbsQMF was introduced that allows users to define the Analyte and IntStd transition ion pairs to be used for each data set	8.5.37	10/10/18
2	Thermo Users	GCV	X			The AutoOpenSpecial Feature installed in 8.5.30 that identified data sets as Open Special has been tweeked.	8.5.37	10/10/18
3	Sciex Users	All Modules	X			For HT-A data, if the 'RT Window' min/max criteria contains more than one peak, GMSU is supposed to report the peak with the largest peak area; instead it was reporting the last peak. This bug has been fixed.	8.5.37	10/10/18
1	Thermo Users	GCV	X			RapidFire HT-A offset feature was incorrectly setting boolAria to TRUE rather than FALSE. This bug has been fixed.	8.5.36	9/5/18

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2	Thermo Users	All Modules	X			The AutoOpenSpecial Feature installed in 8.5.30 is incorrectly identifying data sets as Open Special. This bug has been fixed.	8.5.36	9/5/18
1	Sciex Users	All Modules	X			If a Sciex sample is corrupt and the user attempts to change an integration parameter (no matter which sample is selected), GMSU errors out. This bug has been fixed.	8.5.35	7/4/18
1	All Users	All Modules	X			Default 'Use IS' for calibration curve tab was not activating correctly. This bug has been fixed	8.5.34	6/26/18
1	All Users	All Modules	X			The File Sort function was throwing an error for Perm and PKAUC. This bug has been fixed.	8.5.33	6/4/18
1	Sciex Users	GCV			X	System Suit now supports Sciex data	8.5.32	5/23/18
1	All Users	GVC			X	Modified 3rd party company references	8.5.31	5/21/18
1	All Users	GCV			X	The System Suitability feature has been upgraded to accept Sciex data. Note that the Thermo Ion Ratio function has been disabled in order to accommodate Sciex.	8.5.30	5/9/18
2	Thermo Users	HC	X			HC data were being opened automatically as Open Special. That feature is supposed to ignore HC. This bug has been fixed.	8.5.30	5/9/18
1	All Users	HC	X			The LPR > nn function was reporting the incorrect data. This bug has been fixed.	8.5.29	5/3/18
1	All Users	HC			X	Users are now allowed to exclude all samples from the PK Plot	8.5.28	5/3/18
2	Thermo Users	HC	X			If an .sld has exact mass and species expt info, but is not a Parent/Daughter .sld, the defined Species Experiment does not override the default Species Experiment as it should. This bug has been fixed.	8.5.28	5/3/18

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3	Sciex Users	GCV	X			If the environment is only Sciex and the user attempts to view the System Suitability function, GMSU will crash. This bug has been fixed.	8.5.28	5/3/18
1	Sciex Users	All Modules	X			If a user opens a directory of .wiff files and one of the .wiff files is corrupt, GMSU will crash. This bug has been fixed. Now the user will be prompted about the bad file, then open the rest of the files.	8.5.27	5/1/18
1	Sciex Users	HC			X	If batch.comments contains Species Expt inforamtion, the appropriate Species Experiment will be applied to the data in HC	8.5.26	4/30/18
1	All Users	All Modules		X		In the past, if more than one user is saving data at the same time, there was a probability that a database primary key error would occur, leaving one of the users with an error message. Code has been optimized such that the save command is repeated until the primary key error is not present.	8.5.25	4/30/18
2	Sciex Users	All Modules	X			The code for peak picking in an HT environment was tweaked to be more robust.	8.5.25	4/30/18
1	Thermo Users	GCV	X			The LS-1 Thermo feature needed to be tweaked.	8.5.24	4/18/18
1	Sciex Users	GCV	X			The Leadscape Sciex feature needed to be tweaked.	8.5.23	4/17/18
1	All Users	HC			X	Tweaked HepCl Chrom Method functionality	8.5.22	3/27/18
2	Sciex Users	All Modules	X			Sciex LT data Optimize Sample Number function may report a noise peak if the S/N is low in the Optimize Sample. This bug has been fixed.	8.5.22	3/27/18
1	Sciex Users	LS-1			X	Added functionality to LS-1 import to accept single-stream data.	8.5.21	3/20/18
2	Sciex Users	LS-1			X	Added functionality to LS-1 import to account for imported file with blank rows at the end of it.	8.5.21	3/20/18
1	All Users	All Modules			X	Discover Masses feature was tweaked to perform in a more useful manner.	8.5.20	3/8/18

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2	All Users	HC	X			If the PK plot has no slope, GMSU reports a number in Clint value rather than 0. This bug has been fixed.	8.5.20	3/8/18
1	All Users	All Modules	X			The FileSort function fails to set boolFileSorting back to False when done. This causes first sample of the fgSamples grid to not be prompted to be saved. This bug has been fixed.	8.5.19	2/20/18
2	All Users	All Modules	X			If Configuration Utility – ‘Activate 'Save - Execute Custom Report'’ is True, the ‘If gboolAdd01_01 Then’ code has the possibility of throwing an error because of NULL values in rsAdd_01. This bug has been fixed.	8.5.19	2/20/18
1	Sciex Users	GCV			X	Assay type feature added to LS-1 Sciex Acquisition	8.5.18	2/15/18
2	All Users	HC	X			A code change in v8.5.8 pertaining to HT-A chrom method inadvertently interfered with the ability of the HC to apply the appropriate species experiment to the data. This but has been fixed.	8.5.18	2/15/18
1	Thermo Users	GCV			X	Leadscape-Thermo feature has been tweaked	8.5.17	2/9/18
2	Sciex Users	GCV			X	Leadscape-Sciex feature has been tweaked	8.5.17	2/9/18
1	All Users	GCV			X	Pos/Neg function introduced in 8.5.12 was tweaked.	8.5.16	2/7/18
1	All Users	HC	X			The Sample List window was being shown when it wasn’t supposed to. This bug has been fixed.	8.5.15	2/5/18
1	All Users	GCV			X	Pos/Neg function introduced in 8.5.12 was tweaked.	8.5.14	2/2/18
1	Thermo Users	GCV		X		A Leadscape – Thermo function has been introduced.	8.5.13	1/23/18
2	All Users	Console			X	If the GMSU database is Microsoft Access and the database size is > 800,000, user will be prompted to archive the database	8.5.13	1/23/18
3	Sciex Users	GCV			X	LeadScape - Sciex functionality tweaked.	8.5.13	1/23/18
4	Thermo Users	All Modules	X			If a single full scan sequence has an analyte name, GMSU was not recording the analyte name. This bug has been fixed.	8.5.13	1/23/18

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5	All Users	All Modules	X			If user wishes to copy Sample List, the entire grid can be selected, then cntrl-C to copy. If a column that contains a txtbox is in column 2, the txtbox becomes active when user attempts to select entire grid and the contents of the clipboard is the contents of the txtbox rather than the contents of the Sample List grid.	8.5.13	1/23/18
6	Thermo Users	All Modules	X			If the sequence Processing Method entry contains ".pmd", GMSU will not recognize the pmd. This bug has been fixed.	8.5.13	1/23/18
1	Thermo Users	All Modules		X		Added functionality to pick pos or neg ion filter string depending on the Analyte Name. If Analyte Name includes "Neg_", then a neg ion filter string will be looked for and applied	8.5.12	12/29/17
2	Sciex Users	GCV			X	LeadScape - Sciex functionality tweaked.	8.5.12	12/29/17
3	All Users		X			If users select an integration parameter field while data is saved, then attempts to perform a Save All action, the user will be prompted that the file is saved after every Save Record event. This bug has been fixed.	8.5.12	12/29/17
1	Sciex Users	GCV			X	LeadScape - Sciex functionality tweaked.	8.5.11	12/20/17
1	Sciex Users	GCV		X		Third-party support for Sound Analytics Leadscape Sequence for Sciex data	8.5.10	12/12/17
2	All Users	GCV			X	Added SampleName and SampleID edit boxes to the Sample List grid	8.5.10	12/12/17
3	All Users	GCV, Perm, PK			X	After user manually integrates a peak, cursor focus is set back to the Sample List so that user can continue using the down-arrow key to review data	8.5.10	12/12/17
4	All Users	GCV			X	The Remove Peak button has been added to the Int Std chromatogram	8.5.10	12/12/17
5	All Users	All Modules			X	Previous logic would not populate Analyte column of Sample List if single-analyte data set. Now the Analyte column will always get filled.	8.5.10	12/12/17
6	All Users	Assign Transitions	X			The Assign Transitions ions always uses the first displayed ion set as the base data file to use for additional transitions. This is bad if there are more than one data files loaded (which is possible in a Sciex environment) or in a HT-A environment. The base data file is now the row that is chosen in the Assigned Transitions table.	8.5.10	12/12/17

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7	All Users	Config	X			Global – Configuration Templates – Template Name edit box does not align properly if column is wider than grid. This bug has been fixed.	8.5.10	12/12/17
8	All Users	GCV	X			If the Horizontal/Vertical windows are used, Normal may not be available if a new dataset is opened while in Horizontal or Vertical view. This bug has been fixed.	8.5.10	12/12/17
9	All Users	All Modules	X			HT Acquisition Tools – RapidFire – Offset Injection Times incorrectly did not show the window to allow offset injections. This bug has been fixed.	8.5.10	12/12/17
1	Thermo Users	GCV			X	Export Inclusion List feature tweaked	8.5.9	10/13/17
1	Thermo Users	GCV		X		Users may now export the Inclusion List for each sample of a sequence of full scan data	8.5.8	10/12/17
2	All Users	HC			X	The Hepatic Clearance report for LT-A data does not report the actual retention times (Analyte and IntStd) of the peaks of interest. It reports the expected retention times. The report has been changed such that the actual retention times are reported.	8.5.8	10/12/17
3	All Users	HC	X			The Percentage plot was not displaying data correctly. This bug has been fixed.	8.5.8	10/12/17
4	All Users	Exact Mass Library			X	Users are now given the choice to overwrite existing Drug Set Name if user attempts to add a Drug Set Name that already exists.	8.5.8	10/12/17
5	All Users	GCV	X			When saving the Sort Settings on the GCV, GMSU crashes. This bug has been fixed.	8.5.8	10/12/17
1	All Users	HC	X			If an LPR value triggers an Exception, the Intrinsic Clearance value is being reported incorrectly. This bug has been fixed.	8.5.7	08/04/17

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1	Sciex Users	Assign Transitions		X		For Sciex users, the Assign Transitions now has the following additional functions: • If Analyst 1.5 or greater is used and the .dam file used in the .wiff is available, the Analyte names (if they exist) will be extracted from the .dam file • Create All button to allow users to add all transitions at once. • Paste Cmpd Names button to allow users to paste cmpd names from an Excel list • Apply QMF'button to allow application of a saved QMF Set • Delete Rows button has been added.	8.5.6	5/20/17
1	All Users	Exact Mass Library	X			The Exact Mass Library – Set Editor was not allowing the addition of analytes to an existing set if the analyte did not have an assigned Int Std. This bug has been fixed.	8.5.5	4/28/17
1	All Users	HC			X	Added the ability to configure new chromatographic methods in this module. Previously users had to do this in the GCV.	8.5.4	4/24/17
2	All Users	HC	X			The RT Window was not functioning for HT-A data. This bug has been fixed.	8.5.4	4/24/17
1	Thermo Users	GCV	X			A full scan parsed sequence that uses a Drug Set was not having it's analyte exact mass recorded properly. This bug has been fixed.	8.5.3	4/19/17
1	Thermo Users	GCV			X	LAESI feature now supports UV channel	8.5.2	4/14/17
1	All Users	Calc Exact Mass	X			Masses saved to the Hi Res Library should be reported to only 4 decimals.	8.5.1	12/1/16
2	Thermo Users	GCV	X			The Matrix Chrom Review feature – Reset Axis button does not perform as expected. This bug has been fixed.	8.5.1	12/1/16
3	Thermo Users	GCV – Aria HT	X			For Aria HT data, a change in the Chromatography method code in 8.4.80 causes this data to not process correctly. This code has been fixed.	8.5.1	12/1/16

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