

#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU	Issue Date
				Major	Minor			
1	Sciex	Load Data	X			If Sciex data is HT-A, GMSU will not correctly assign chromatographic method data to HT-A peaks. This bug has been fixed	8.6.22	5/29/26
1	All Users	EM Calculator	X			If the last atom of a molecular formula is 2-character (e.g. Si), GMSU will not calculate the exact mass correctly. This bug has been fixed.	8.6.21	5/1/26
2	All Users	Archive	X			If any tables are too large, the Archive function will crash. This bug has been fixed.	8.6.21	5/1/26
1	All Users	GMSU Load	X			GMSU was not evaluating the .ini file correctly when GMSU database is SQL Server. This bug has been fixed.	8.6.20	2/10/26
1	Sciex	All Modules	X			The new Sciex OS software can produce Analyst-compatible .wiff and .wiff.scan files. Unfortunately, an additional .wiff2 file is also created. If users choose 'Open all data files in a directory', GMSU will initially process the .wiff files without error. However, if user closes GMSU and attempts to load the data again as 'Open all data files in a directory', GMSU will attempt to open the .wiff2 file and crash. This bug has been fixed.	8.6.19	2/6/26
2	All Users	Conf Util HC	X			The features added in 8.6.18 broke the Configuration Utility – Hepatic Clearance Constants – Existing Experiments – Copy Data From... dropdown box. This bug has been fixed.	8.16.19	2/6/26
1	All Users	All Modules		X		Added the ability of user to Deactivate Species Experiments, Chromatography Flags, and Results Flags.	8.6.18	1/18/26
2	Thermo	All Modules	X			If Parent/Parsed Full Scan Sequence Modifier workflow is used and one of the .raw files in the data set is corrupt, GMSU will crash and the entire Parsed data sets cannot be processed. This bug has been fixed.	8.6.18	1/18/26
1	All Users	HC	X			Hepatic Clearance Calculator crashes when opened on Windows 11. This bug has been fixed.	8.6.17	11/14/25

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1	Sciex	All Modules	X			When retrieving Calibr Std and QC Std nominal concentrations from the .wiff file, sometimes the value will be full precision (double). i.e. '0.001' is retrieved as '0.0099993487389283'. The value needs to be converted to non-full precision (single) i.e. '0.001' is retrieved as '0.001'. This bug has been fixed.	8.6.16	11/1/25
1	Sciex	All Modules	X			It was found that the boolDoAllTransitions function (8.5.63 and 8.6.14) was not recording database records correctly if user has opened all Sciex files in the data folder. The data could be processed without issue when initially opened, but would error out on the 3 rd or higher analyte if GMSU is closed, re-opened, and the same data opened again. This but has been fixed.	8.6.15	10/30/25
1	Sciex	All Modules		X		In GMSU 8.5.63, a Configuration Utility item (boolDoAllTransitions) was implemented that instructs GMSU to extract all transitions ions in the .wiff file experiment. This was implemented only for the Hepatic Clearance Calculator. It has now been implemented for Generic Chromatographic Viewer and Permeability Calculator.	8.6.14	10/22/25
1	Thermo	All Modules	X			GMSU would not retrieve the appropriate filter string for Int Std. This bug has been fixed.	8.6.13	1/1/25
1	Thermo	All Modules	X			The bug fix concerning Add Many compounds was still buggy. This bug has been fixed.	8.6.12	9/22/24
1	Thermo	All Modules	X			The ability to Add Many compounds to the Full Scan Exact Mass Library was broken in GMSU 8.5.72. This bug has been fixed.	8.6.11	9/20/24
2	Thermo	All Modules	X			GMSU was not configuring properly DrugSets with a mix of positive and negative polarity samples. GMSU was configuring incorrectly positive and negative chromatograms. This bug has been fixed.	8.6.11	9/20/24

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1	Thermo	All Modules	X			The ability to open DrugSets that have been configured in the Thermo sequence .sld was broken in GMSU 8.5.72. This bug has been fixed.	8.6.10	9/13/24
1	All Users	All Modules	X			The high-level variable GetUserNameA was not populating with the name of the user who has logged on to the computer. This bug has been fixed.	8.6.9	5/1/24
2	Sciex Users	DAM			X	Modified mixed cocktail .qmf and .dam file names from _P_N to PN.	8.6.9	5/1/24
1	Sciex Users	QMF			X	The .qmf created by importing data from an Excel file was listing the cmpds in the .qmf in reverse order to the Excel Input file. The .qmf cmpds now are listed in the same order as the Excel Input file.	8.6.8	4/3/24
2	Sciex Users	DAM			X	The DAM file directory path cell is overwritten if the Excel Input file calculated path does not exist. The DAM file directory path cell will now not be overwritten.	8.6.8	4/3/24
1	All Users	HC			X	User can now set a default Results Review value for the Results Review Dropdownbox in the Hep Cl Calculator. The default value is set in Configuration Utility – Flags window.	8.6.7	3/15/24
1	All Users	HC			X	The ‘Set New Species Default’ button was not working. The reason was that the code predates the newer Config Template functionality and the setting was not being applied to tblConfigTemplates. This bug has been fixed.	8.6.6	3/11/24
1	Sciex Users	DAM	X			If user attempts to create DAM files that are Pos/Neg and the Cocktail input file contains a mix of cocktails that have a mix of (Pos or Neg) and Pos/Neg transitions, GMSU will name all .dam files as if they are a mix of Pos/Neg. E.g. SN000_A_P_N.qmf. This bug has been fixed.	8.6.5	2/14/24
1	Sciex Users	DAM/QMF		X		Added functionality to allow users to create from a Cocktail input file a QMF that has both positive and negative transitions	8.6.4	1/26/24

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1	All Users	Generate Reports	X			In Generate Reports forms, the function GetColNumber was being called incorrectly. If form is called from Console and data has Calibr Plots, the Calibr Plot will not generate. This bug has been fixed.	8.6.3	9/28/23
2	All Users	HC			X	If pagesetup code encounters an error, user is prompted for each sheet. This is onerous if # of sheets to prepare is large. The prompt has been removed.	8.6.3	9/28/23
1	Thermo Users	All modules	X			If the last sample in sample list is manually integrated and user removes manual integration, GMSU crashes. This bug has been fixed.	8.6.2	8/7/23
1	Thermo Users	All modules	X			DoFullScanParent routine was not filling rsGSsets due to earlier logic change in how rsGSsets is filled. This bug has been fixed.	8.6.1	6/19/23
1	All Users	GVC		X		Enveda has purchased exclusivity of the GVC – Full Scan Trace Analysis Screening (FSTAS) function. FSTAS has been moved to a new GVC Menu item Enveda Tools, viewable only to Enveda customer	8.6.0	5/23/23
1	All Users	All Modules	X			For some reason, Access boolSavedChrom and boolDeactivate in modConserved.LoadData (used when populating Generated Reports Existing Data table) does not accept 1 and 0 for TRUE and FALSE, resulting in a blank Existing Data table. To resolve, changed 1 and 0 to TRUE and FALSE in query.	8.6.0	5/23/23
1	Thermo Users	Add Masses from Libr	X			GMSU crashes if user attempts to add a mass to the Exact Mass Database. This bug has been fixed.	8.5.92	4/5/23
1	Thermo Users	Add Masses from Libr	X			GMSU crashes if user attempts to add a mass from the Exact Mass Database. This bug has been fixed.	8.5.91	3/21/23
1	Sciex Users	DAM/QMF Creator	X			Tweaked the function of the new QMF viewer released in 8.5.86	8.5.90	3/10/23
1	Sciex Users	DAM/QMF Creator	X			Tweaked the function of the new QMF viewer released in 8.5.86	8.5.89	2/2/23

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1	Sciex Users	DAM/QMF Creator	X			Tweaked the function of the new QMF viewer released in 8.5.86	8.5.88	1/31/23
1	Sciex Users	DAM/QMF Creator			X	Tweaked the function of the new QMF viewer released in 8.5.86	8.5.87	1/28/23
1	Thermo Users	QMF Creator		X		A new QMF Creator module has been added that allows users to create .qmf files using input from an Excel file.	8.5.86	1/6/23
1	Thermo Users	EM Library			X	Database calls to tblHiResDataSets were optimized to allow for very large libraries	8.5.85	12/31/22
1	All Users	PK	X			Configuration default PK parameter units were not being applied to appropriate grid in PK Calculator module upon form load. This bug has been fixed.	8.5.84	12/11/22
1	All Users	All Modules			X	ADODB recordset connection can timeout if underlying table is large. This does not affect Access users, but can affect SQL Server users. To resolve, the connection commandtimeout was set to 0, which disables the timeout.	8.5.83	10/18/22
1	Thermo Users	All Modules	X			If data is full scan and varFilters has many entries and the Full Scan entry is the last entry, then it will not be recognized as the Full Scan filter. This bug has been fixed.	8.5.82	8/28/22
2	Thermo Users	All Modules	X			If data set is multi-analyte (Full Rooney) and a .raw file from the .sld doesn't exist in, the entire .sld will not be processed. This bug has been fixed.	8.5.22	8/28/22
3	All Users	GCV	X			If a report is created that includes a calibration curve, the calibration curve is placed in the middle of the report instead of the end of the report. This bug has been fixed.	8.5.22	8/28/22
1	All Users	Perm			X	User can now delete a DA0/60 or DB0/60 data point by Remove Peak at the chromatogram window	8.5.81	8/19/22

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1	Sciex Users	DAM Creator	X			Routine CreateCocktails incorrectly tried to load column numbers into rows of a grid. This bug has been fixed.	8.5.80	8/9/22
1	Thermo Users	HC	X			SigFig function decimal data type cannot handle extremely low numbers like $10^{(-30)}$, resulting in error in the function. This bug was fixed.	8.5.79	7/29/22
1	All Users	GCV	X			When user opens Configuration Utility from GCV, the current GCV Configuration Template should be loaded automatically in Configuration Utility. It is not – Default is initially displayed. This bug has been fixed.	8.5.78	7/13/22
2	All Users	GCV	X			8.5.77 Item 1 accidentally allows users to make changes in Retention Time even if underlying data is Saved and Locked. If data is Saved and Locked, user should not be able to make retention time changes. This bug has been fixed.	8.5.78	7/13/22
3	All Users	GCV Reports	X			Some user's report excessive crashing when attempting to generate Excel reports from GCV Generate Reports. The error refers to clipboard paste actions. The code uses clipboard to paste data into Excel. The code has been changed to not use the clipboard.	8.5.78	7/13/22
1	Thermo Users	GCV	X			For some reason, the buttons in frmSysSuitGroups (from Retention Time Utilities – Rooney) do not become visible when form is loaded. This bug has been fixed.	8.5.77	6/14/22
1	Sciex Users	DAM Creator	X			The function GetDuration was returning '1' instead of the actual .dam method duration. This bug has been fixed.	8.5.76	6/8/22
1	Thermo Users	GCV	X			Corrections in 8.5.74 that corrected GMSU's ability to distinguish between multiple analytes in fgGroups was not complete. This bug has been fixed.	8.5.75	5/26/22
1	Thermo Users	GCV	X			Corrections in 8.5.73 interfered with GMSU's ability to distinguish between multiple analytes in fgGroups. This bug has been fixed.	8.5.74	5/19/22

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1	Thermo Users	All Modules	X			GMSU 8.5.72 Item 6 conflicts with Exact Mass from SLD that has multiple cmpds. This bug has been fixed.	8.5.73	5/10/22
1	Thermo Users	All Modules	X			Exact Mass Library – Add a single cmpd was crashing. This bug has been fixed.	8.5.72	3/5/22
2	All Users	HC	X			New Scoring Configuration Utility entries are being duplicated. This bug has been fixed.	8.5.72	3/5/22
3	All Users	All Modules	X			If data has been loaded in a module that triggers the loading of Configuration Utility Template and the user opens Menu – Configuration Utilities, the current Configuration Utility Template is not loading as the current template in Configuration Utilities. This bug has been fixed.	8.5.72	3/5/22
4	All Users	HC			X	A new Scoring Configuration Utility item has been added: “Scoring: Activate Scoring Feature”. The Hepatic Clearance Scoring feature added in 8.5.63 forces users to apply the Scoring feature. Now users can deactivate the feature if desired.	8.5.72	3/5/22
5	Thermo Users	All Modules	X			If user enters a DrugSet name in the .sld User Colum 5, GMSU was not automatically processing that drugset name. This bug has been fixed.	8.5.72	3/5/22
6	Thermo Users	All Modules	X			If data is added to a record from the Exact Mass Library, the Analyte Exact Mass column was not being populated in the Sample List table. This bug has been fixed.	8.5.72	3/5/22
1	Thermo Users	GCV	X			In Full Scan Trace Analysis Screening module, if data set is large, Excel file report will crash. This bug has been fixed.	8.5.71	2/14/22
1	Thermo Users	All Modules	X			Fix in 8.5.68 broke Add Masses From Database. This bug has been fixed.	8.5.70	1/31/22
1	Sciex Users	DAM Creator	X			The DAM Creator was not entering provided parameters (DP, CE, CXP, EP). This bug has been fixed.	8.5.69	12/28/21
2	Thermo Users	GVC			X	Allow Configuration Utility setting ‘Force HT-A to integrate all signal’ (boolForceHTPeak) for LT data.	8.5.69	12/28/21

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3	All Users	HC	X			The new Scoring feature needed tweaks	8.5.69	12/28/21
1	Thermo Users	GCV	X			If .sld contains multiple cmpds, GMSU will not properly identify the different cmpds. This bug has been fixed.	8.5.68	12/10/21
1	Thermo Users	GCV	X			The Scoring feature needed tweaking for Thermo data.	8.5.67	11/22/21
1	Thermo Users	GCV	X			The Scoring feature needed tweaking for Thermo data.	8.5.66	10/21/21
1	All Users	HC	X			The Scoring feature was not automatically being applied when loading new data from Browse button when configured to do so in Configuration Utilities. This bug has been fixed.	8.5.65	9/24/21
1	All Users	GCV			X	Added System Suitability – Metrics Plot – Analyte – Peak Area Ratio Content.	8.5.64	9/22/21
1	All Users	EM Calculator	X			If 2-character atom is at end of mol formula, e.g. C27H38N2O4Si, calculation results in error. This bug has been fixed.	8.5.63	9/11/21
2	All Users	All Modules	X			When user clicks Calibration tab - ‘Apply to Chromatography’ button, calibr and QC std nominal concentrations are applied, but calculated concentrations are not calculated. This bug has been fixed.	8.5.63	9/11/21
3	All Users	HC		X		A scoring feature has been added to the Hepatic Clearance Calculator based on published IQC Validator (Drug Metab Dispos 44:1653–1661, October 2016)	8.5.63	9/11/21
4	Sciex Users	HC		X		A new Configuration Utility item ‘Extract all transition ions (Sciex only)’ has been added that, if set to ‘Yes’, instructs GMSU to extract all transitions ions in the .wiff file experiment.	8.5.63	9/11/21
5	Sciex Users	All Modules	X			If user opens a directory with many .wiff files, an incrementor is incremented incorrectly, resulting in the possibility that a .wiff file will not open. This bug has been fixed.	8.5.63	9/11/21

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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 Threshold 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 tweaked.	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 3 rd 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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#	Affected Users	Affected Modules *	Bug Fix	New Feature		Action Item	GMSU	Issue Date
				Major	Minor			
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 information, 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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