Peaks View Fields

The Peaks tab is only available when you use the Pro interface.

Field	Description
# of Results Stored	Number of results stored for the chromatogram.
% Amount	Peak amount as a percent of the amounts of all quantitated peaks (equal to the % Concentration) in the chromatogram.
% Area	Peak area as a percent of the area of all peaks integrated in the chromatogram.
% Deviation	Difference between the calculated and control amount or concentration values, expressed as a percentage of the control value.
% Height	Peak height as a percent of the height of all peaks integrated in the chromatogram.
% Time Corr. Area (CE/CIA Only)	Time corrected area of a peak expressed as a percentage of the total time corrected area in the electropherogram.
%Poly<MWM4 (GPCV Option)	Amount of polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM4.
%Poly<MWM5	Amount of polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM5.
%Poly<MWM6 (GPCV Option)	Amount of polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM6.
%Poly>MWM1 (GPCV Option)	Polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM1.
%Poly>MWM2 (GPCV Option)	Amount of polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM2.
%Poly>MWM3 (GPCV Option)	Amount of polymer, expressed as a percentage of the area of the entire distribution, that has a molecular weight less than the molecular weight entered in the GPC parameter MWM3.
2 Sigma (System Suitability Only)	Plate count based on the peak width at 60.7% of peak height.

Field	Description
2nd Derivative Apex	Retention time of the second derivative apex in minutes. This field is blank if Traditional integration is selected.
3 Sigma (System Suitability Only)	Plate count based on the peak width at 32.4% of peak height.
4 Sigma (System Suitability Only)	Plate count based on the peak width at 13.4% of peak height.
5 Sigma (System Suitability Only)	Plate count based on the peak width at 4.4% of peak height.
Acq Method Set	Method set used during data acquisition.
Acq. SW Version	Software version used to acquire the data.
Acquired By	User who starts data acquisition.
Acquisition Server	Acquisition server that controls the chromatographic system used for acquisition.
Adjusted RT (GPCV Option)	Retention time (in minutes) adjusted for variations in flow, as determined by a reference peak. If you do not specify a reference peak in the Calibration tab, this value equals retention time.
Alpha (GPCV Option)	Value that represents the slope of the theoretical viscosity law curve (Mark-Houwink constant).
Altered	Indicates if the sample has information that was changed in the Alter Sample window.
Amount	Amount of the peak.
Area	Peak area (in μV•sec).
Asym (System Suitability Only)	Asymmetry-based plate count.
Asym @ (10)^2 (System Suitability Only)	Peak asymmetry (tailing) at 10% of the peak height squared.
Asym @ (4.4)^2 (System Suitability Only)	Peak asymmetry (tailing) at 4.4% of the peak height squared.
Asym @ (10) (System Suitability Only)	Peak asymmetry (tailing) at 10% of the peak height.
Asym @ (4.4) (System Suitability Only)	Peak asymmetry (tailing) at 4.4% of the peak height.

Field	Description
Auto Additions	Auto addition sequence used with the 2690/2695 or 2790/2795 Module.
Average Detector Drift	Average segment drift in the detector signal over a specified time region in the chromatogram. Drift is the slope of the least squares line fitted to the data in the segment. This slope is calculated by subtracting the Y-value of the least-squares line at the last data point from the Y-value of the least-squares line at the first data point and dividing this difference by the time interval (in hours) between the first and last data points in the segment.
Average Detector Noise	Average segment RMS (root mean square) noise in the detector signal over a specified time region in the chromatogram.
Average Peak to Peak Noise	Average segment peak-to-peak noise in the detector signal over a specified time region in the chromatogram. Peak-to-peak noise is defined as the sum of the maximum and minimum differences (residuals) between each data point and the least-squares line.
Barcode/BCD	Barcode identification number of the vial (if acquired from a 2690/2695 or 2790/2795 Separations Module).
Baseline Drift (System Suitability Only)	Amount of drift observed for the region between the user-specified start and end times in the chromatogram (as you specified in the Suitability tab).
Baseline End (System Suitability Only)	End time for drift and noise calculations. For drift calculations, the system takes a millivolt reading at the Baseline End Time, then subtracts from this reading the Baseline Start Time reading to determine drift. For noise calculations, the system calculates noise in the region of the baseline specified by the % of Run Time Over Which To Average parameter and the Baseline Start Time and Baseline End Time.
Baseline Noise (System Suitability Only)	Amount of noise calculated for the region between the user-specified start and end times in the chromatogram (as specified by the user in the Suitability tab).
Baseline Start (System Suitability Only)	Start time for drift and noise calculations. For drift calculations, the system takes a millivolt reading at the Baseline End Time, then subtracts from this reading the Baseline Start Time reading to determine drift. For noise calculations, the system calculates noise in the region of the baseline specified by the Baseline Start and End Times and the % of Run Time to Average parameter.
Bath (Dissolution Option)	Bath (A or B) used to acquire the dissolution sample.
Build Version	Empower software version label and build date.
Calculated dn/dc	Calculated dn/dc for a broad standard peak (where dn/dc represents the change in refractive index over the change in

Field	Description
	concentration associated with the refractive index detector in use). The RI detector response for the broad standard peak and its dn/dc and exact concentration (entered during sample loading) are used to calibrate the RI concentration detector. Empower software displays a value in this peak field if the concentration detector is a calibrated refractive index detector (RI), concentration is entered in sample loading, and you did not enter a dn/dc value in the Slicing tab of the Processing Method window, you did enter a concentration during sample loading, and wanted to calculate an RI Calibration Constant.
Calibration ID	Calibration identifier generated by the database during data processing.
Channel	Name of the channel used to acquire data. The channel name originates from the associated instrument method used during data acquisition.
Channel Description	Text (as specified in the instrument method) used to describe the data channel.
Channel ID	Identifier generated by the database during data acquisition to identify each channel.
Channel Name	Name of the channel used to acquire data. The channel name originates from the associated instrument method used during data acquisition.
Channel Type	Type of data: 2D, 2D derived, or 3D. If identified as 2D derived, the 2D data is derived from an associated 2D or 3D channel.
Concentration	For *quantitated* peaks, the peak concentration calculated using peak response and the calibration curve when the X-value is set to Concentration. If the X-value is set to Amount, concentration equals concentration/injection volume. For *calibrated* peaks, the amount from the sample or default amount if the Sample Value Type parameter is set to Concentration. If the Sample Value Type is set to Amount, concentration equals amount/injection volume.
Control Value	Amount or concentration entered for the control (or quantitated standard used to calculate % Deviation).
Curve Id	Calibration curve identifier associated with the peak.
d (GPCV Processing Only)	Branching density, or the number of branches per dalton, weighted average of the individual slice values (assuming the Random or Star branching parameter has been specified in the Slicing tab of the Processing Method window).
Data End	Time data collection ended (in minutes), as measured from the

Field	Description
	injection time.
Data Start	Time data collection began (in minutes), as measured from the injection time.
Date Acquired	Start time and date of the acquisition run.
Date Processed	Date and time that the result was processed.
Deposition Time (CE/CIA Only)	Elapsed time after injection when and electrophoretic band exits from the capillary and is deposited on a Membrane Fraction Collector.
Det. Units	Detector units that appear on the y-axis of the chromatogram. The detector units originate from the associated instrument method used during data acquisition.
Detector Drift	Total drift in the detector signal over a specified time region in the baseline. Drift is the slope of the least squares line fitted to the data in the region. This slope is calculated by subtracting the y value of the least-squares line at the last data point from the y value of the least-squares line at the first data point and dividing this difference by the time interval (in hours) between the first and last data points of the region.
Detector Noise	Total RMS (Root Mean Square) noise in the detector signal over a specified time region in the chromatogram.
Dilution	Factor by which Empower software (during calibration) divides the calculated amount or concentration of each standard component. During quantitation, Empower software multiplies the amount (or concentration) read from the calibration curve (of the standard components) by the Dilution value to calculate amounts and concentrations for each unknown sample.
Dissolution Post Sample Wash Volume	The volume (in 2.5-mL increments) of post sample wash.
Dissolution Syringe Speed	Waters Transfer Module syringe speed.
Dissolved Amount (Dissolution Option)	Indicates (on the y-axis of the Dissolution plot) the amount of component that is dissolved at the time the sample was taken.
Dissolved Percent (Dissolution Option)	Indicates (on the y-axis of the Dissolution plot) the percent of the claimed amount of component that is dissolved at the time the sample was taken. The claimed amount is the amount the manufacturer claims is in the dosage form.
Dist Name (GPCV Option)	Name given when the peak's distribution was saved as a named distribution to be used with cumulative matching broad standard calibration.

Field	Description
dn/dc (GPCV Option)	Calculated dn/dc for a broad standard peak (where dn/dc represents the change in refractive index over the change in concentration associated with the refractive index detector in use). The RI detector response for the broad standard peak and its dn/dc and exact concentration (entered during sample loading) are used to calibrate the RI concentration detector. Empower software displays a value in this peak field if the concentration detector is a calibrated refractive index detector (RI), concentration is entered in sample loading, and you did not enter a dn/dc value in the Slicing tab of the Processing Method window, you did enter a concentration during sample loading, and wanted to calculate an RI Calibration Constant.
Elution Volume (GPCV Option)	Elution volume (mL) adjusted for variations in flow, as determined by a reference peak. If you do not specify a reference peak in the Calibration tab, this value equals flow rate multiplied by the retention time.
End Height	Height of peak integration at the end of a peak (in microvolts).
End Time	Peak end time (in minutes).
EP Plate Count (System Suitability Option)	Plate count based on peak width at 50.0% of peak height (using the constant 5.54) as specified by the European Pharmacopoeia.
Epsilon (GPCV Option)	Constant that determines the shape factor for Random intrinsic viscosity fit types.
f (GPCV Option)	Average number of arms of a star polymer, *f*, with a precision of 6.
f @ 5 (System Suitability Option)	Retention time minus the start point of the width at 5% peak height.
Faults	Indicates (when checked) a fault in the result (either a peak was faulted or noise/drift limits were exceeded). A fault can occur for these reasons: ▪ A peak in the chromatogram that was specified as a "must peak" in the Component table (Processing method window, Components tab) was not found during processing. ▪ A peak in the chromatogram had a defined System Suitability limit (for a specific field) that was exceeded during processing.
Fitted (A – F) (GPCV Option)	Coefficients of the polynomial curve fitted to the observed viscosity data within the intrinsic viscosity data region.
Fitted R and Fitted R^2 (GPCV Option)	Statistics calculated for the curve fitted to the observed viscosity data.
g (GPCV Option)	Stockmayer-Fixman branching weighted average of the

Field	Description
	individual slice values (assuming a Random intrinsic viscosity fit parameter has been specified in the Slicing tab of the Processing Method window).
g' (GPCV Option)	Average branching index for the peak.
g'LCB (GPCV Option)	Long chain branching index for the entire peak. If the Branching Model is Star, g' LCB (as well as g' SCB) is not calculated (blank) and enter a set of Linear K and alpha values for g' to be calculated.
g'SCB (GPCV Option)	Short chain branching index for the entire peak (GPCV processing only). Enter a set of Linear K and alpha values to calculate short chain branching.
Height	Height of the peak (in microvolts).
Id (GPCV Option)	Identifier of the distribution (if one is generated by the database).
Inflection Width	Width of the peak at the inflection point in seconds.
Injection	Number of the injection made from the vial.
Injection ID	Identifier generated by the database during data acquisition to identify each injection.
Injection Volume	Volume (in microliters) of the sample that was injected.
Injection Volume (Result)	Injection volume in microliters used to generate the data.
Instrument Method ID	Identifier generated by the database during data acquisition to identify the instrument method.
Int Type	Two-character label that describes the way a peak was integrated.
Integration Algorithm	Traditional or ApexTrack that Empower applies to integrate the data.
Integration System Policies	Displays the system policies that govern how the data was integrated. To view the system policies in Configuration Manager, select View > System Policies.
Intrinsic Viscosity (GPCV Option)	Viscosity of each standard as calculated from either: ▪ K, alpha, and molecular weight ▪ Viscosity channel data and molecular weight (universal calibration only)

Field	Description
IV Data Start and IV Data End (GPCV Option)	Start and end boundary time (in minutes) of the intrinsic viscosity data region, where peaks from the two channels overlap the calibration curve (GPCV processing only).
JP Plate Count (System Suitability Option)	Plate count based on peak width at 50.0% of peak height (using the constant 5.55 as specified in the Japanese Pharmacopeia).
JP15 Plate Count (System Suitability Option)	Plate count based on peak width at 50.0% of peak height (using the constant 5.54 as specified in the Japanese Pharmacopeia).
K (GPCV Option)	Mark-Houwink constant, K (Log K is the intercept of the Viscosity Law plot), calculated for the GPCV peak or entered for a GPCV peak.
K Prime (System Suitability Option)	Capacity factor, which is a measurement of the retention time of a sample molecule relative to column void volume (V0).
Label	User-defined markers specified during sample loading that instruct Empower software to perform bracketing.
Lambda (GPCV Option)	Displays the probability for long-chain branching factor, lambda, calculated during the Random fit of the intrinsic viscosity curve. Lambda is expressed as the number of branches per 1000 carbon atoms in the polymer.
Level	Indicates if a Level designation was used for a standard during sample loading. All vials identified with the same level label can be averaged when averaging by level is selected in the Processing Method window.
Linear alpha (GPCV Option)	User-entered alpha value in the sample (used to calculate the short-chain branching index).
Linear K (GPCV Option)	User-entered K value entered in the sample (used to calculate the short-chain branching index).
Manual	Indicates if the retention time, molecular weight, or viscosity fields have been manually entered.
Mass Injected (GPCV Option)	Total mass injected into the system. (GPCV Option)
Migration Time (CE/CIA Only)	Time required for a charged species to move a specified distance through a gel or other liquid matrix under the influence of an electrical field.
Mn (GPCV Option)	Number average molecular weight for the distribution. The source of the value may be either the value you entered in the Component Editor during sample loading or the value calculated by the software.
Mn visc (GPCV Option)	Number average molecular weight calculated from the viscosity

Field	Description
	data only.
Mobility (CE/CIA Only)	Rate at which an analyte migrates through the capillary matrix, calculated from capillary length, migration time, and applied voltage.
MP (GPCV Option)	Peak molecular weight at the peak apex for the detected peak. The value reported is one of these: ■ MP value entered during sample loading. ■ Molecular weights of the narrow standard peaks entered in the Component Editor during sample loading. ■ Each GPC peak between V0 and Vt for unknowns (broad and narrow). With GPCV unknowns, this is a single peak because you can enter only a single concentration during sample loading.
MS Match1-3 %Contamination	Mass peaks in the unknown spectrum that were not found in the matching library spectrum. This is usually indicates that the unknown compound is not pure.
MS Match1-3 CAS number	Chemical Abstracts Services (CAS) registration number of the spectrum which appears only if the matching spectrum comes from the Wiley library and has an assigned CAS number.
MS Match1-3 Formula	Chemical formula of the matching compound.
MS Match1-3 Lib. Name	Name of the library that contains the matching spectrum (user-defined or Wiley).
MS Match1-3 Mol. Wt	Molecular weight of the compound that produced the spectrum.
MS Match1-3 PBM Fit	Indicates the probability that the unknown spectrum was derived from the same compound as the reference spectrum, or from a stereoisomer.
MS Match1-3 Spect. Date	Date that the library spectrum was added to a user library (does not apply to Wiley spectra).
MS Match1-3 Spect. ID	For a user library, displays the spectrum identifier generated by the database during library matching. For the Wiley library, displays the Wiley Registry serial number.
MS Match1-3 Spect. Name	Name of the library that contains the matching spectrum (user-defined or Wiley).
MT Ratio (CE/CIA Only)	Migration time divided by the MT reference peak migration time.
Mv (GPCV Option)	Viscosity average molecular weight for the distribution. The value reported is blank for relative calibration. For universal calibration, the value is one of these:

Field	Description
	▪ Value calculated using the Mark-Houwink constants K and alpha that you entered during sample loading (GPC) ▪ Value calculated using the Mark-Houwink constraints calculated using data from the viscometer channel (GPCV) ▪ Mv value entered for a broad standard during sample loading
Mw (GPCV Option)	Weight average molecular weight for the distribution. The source of the value may be either the value you entered in the Component Editor during sample loading, or the value calculated by the software.
MW Marker 1-6 (GPCV Option)	Molecular weight marker entered in the Slicing property tab of the Processing Method window.
Mz (GPCV Option)	Z-average molecular weight for the distribution. The source of the value can be either the value you entered in the Component Editor during sample loading or the value calculated by the software. Ratio of the Z-average molecular weight to the weight-average molecular weight.
Mz+1 (GPCV Option)	Z+1-average molecular weight for the distribution. The source of the value can be either the value you entered in the Component Editor during sample loading or the value calculated by the software.
Mz+1/Mw (GPCV Option)	Ratio of the Z+1-average molecular weight to the weight-average molecular weight.
Name	Name of the processed peak.
Number of Sign Offs	Number of times a result was signed off.
Offset	The y-intercept (in plot units) if the baseline of the peak or peak clusters was extrapolated to time zero.
PDA Exposure Time	Set length of exposure time (in milliseconds) for the photodiodes in the 2996 Detector.
PDA Match1-3 Angle (PDA Option)	Difference in spectral shapes between an acquired spectrum and a library spectrum. Small values indicate that the spectra are similar; large values indicate greater degrees of spectral difference. A value of 0 indicates a perfect match.
PDA Match1-3 Error (PDA Option)	Indicates that an error condition occurred, preventing the calculation of PDA Match Angle and PDA Match Threshold.
PDA Match1-3 Flag (PDA Option)	Size of the PDA Match Angle relative to the PDA Match Threshold (Angle).

Field	Description
PDA Match1-3 Ideal (PDA Option)	Indicates that both spectra in the comparison have the same wavelength range and resolution.
PDA Match1-3 Lib. Name (PDA Option)	Name of the UV library containing the matching spectrum.
PDA Match1-3 Spect. Name (PDA Option)	Name of the library spectrum that was matched against the acquired spectrum during a library search.
PDA Match1-3 Threshold (PDA Option)	Displays the largest Match Angle that can be due to noise or solvent contribution, and not due to an actual difference in analyte.
PDA Match1-3 Wvln RMS (PDA Option)	Root-mean-squared (RMS) spectral difference between an acquired spectrum and a library spectrum at all wavelengths. The RMS value indicates how well the actual wavelengths of both spectra align. It is reported only for comparisons between spectra with the same ideal wavelength parameters. A value of 0 indicates that the wavelengths are well aligned.
Peak Codes	Informational and/or warning codes that Empower software encountered while processing this peak.
Peak Lambda Max	With PDA data, the lambda mass of the baseline-corrected peak apex spectrum. This is the wavelength where the maximum absorbance is found over the wavelength range specified by the spectral contrast parameter in the processing method.
Peak Level	Level designation used for a standard during sample loading.
Peak Sigma (GPCV Option)	Band broadening of the peak due to the polydispersity of the peak and the effects of the chromatographic system. This value is calculated only if you quantitate narrow standards with a relative calibration curve.
Peak to Peak Noise	Total peak-to-peak noise in the detector signal over a specified time region in the chromatogram (specified in the Noise and Drift tab of the Processing Method window). Peak-to-peak noise is defined as the sum of the maximum and minimum differences (residuals) between each data point and the least-squares line.
Peak Type	Displays the component as: ■ Found ■ Unknown ■ Missing ■ AIA peaks from imported results (peaks without baseline information, but with area, retention time, and height)
Peak Width	Default peak width used to detect the peaks in the chromatogram. The peak width value is copied from the

Field	Description
	processing method or calculated at the start of integration.
Percent Unknowns	Area percentage of unknown peaks.
Points Across Peak	Width of the peak in data points.
Polydispersity (GPCV Option)	Value calculated from the ratio Mw/Mn.
Processed As	Identifies how the result was processed (standard if calibrated, unknown if quantitated, or blank, if not calibrated or quantitated).
Processed By	Name of user who processed the data.
Processed Channel Descr.	Text entry (as specified in the instrument method) used to describe the data channel. If associated with a 2D derived channel, this column displays how the 2D channel was derived.
Processed Channel Type	Identifies the type of processed data, 2D or 2D derived. If identified as 2D derived, the 2D data is derived from an associated 2D or 3D channel.
Processing Locked	When checked, indicates that the chromatogram cannot be reprocessed. The associated data channel (or channel associated with the injection, sample, or sample set) was locked using the Lock Channel command from the Project window Edit menu.
Processing Method	Name of the method used to process the result.
Processing Method ID	Processing method identifier generated by the database when the processing method is stored.
Processing Node	Node name of the system used for processing.
Project Name	Project name for the row in the view table. This field is available only in Global view when in Multi-Project mode.
Purity Errors	Indicates (when checked) that an error occurred during Peak Purity testing.
Purity 1-4 Angle (PDA Option)	Relative spectral homogeneity across the peak (in degrees) for purity pass 1 to 4.
Purity 1-4 Flag (PDA Option)	Size of the Purity Angle relative to the Purity Threshold for each purity pass.
Purity 1-4 Threshold (PDA Option)	Peak threshold angle (in degrees) for purity pass 1 to 4.
Rel. Resol. (System Suitability)	Resolution difference (in minutes) of a peak relative to the reference peak (specified in the Rel Resol Reference column in

Field	Description
	the Component table). If you are using the EP or JP Pharmacopeia options, Relative Resol is calculated the same way as Resolution. If you are using the USP Pharmacopeia option, Rel Resol is calculated the same way as USP Resolution (HH). If you are using the All Pharmacopeia option, Rel Resol is calculated the same way as USP Resolution.
Relative MT (CE/CIA Only)	Migration time minus the RT Reference peak migration time.
Relative RT	Retention time minus the RT Reference peak retention time.
Resolution	Difference between the retention time of this peak minus the retention time of the preceding peak, divided by the sum of the peak width at 50%, and multiplied by a constant of 1.18.
Response (System Suitability Option)	Peak's Y-value, area, height, or a ratio, depending on the Y-Value flag and if an Internal Standard is being used.
Result #	Ordinal number for the result.
Result Codes	Informational and/or warning codes that Empower software encountered while processing the result.
Result Comments	Comments associated with the generation of the result.
Result ID	Result identifier generated by the database while processing a standard or unknown.
Result Type	Type of processing method used to process the chromatogram (LC, GC, IC, CE, CIA, GPC, PDA, or MS).
Retention Time	Peak retention time in minutes.
RF	Response factor calculated for the standard peaks. RF is defined as the detector response divided by either the amount or concentration, depending on the X value in the Component table for that peak's component.
RI Concentration Channel	Indicates that this result was collected from an RI detector (such as a Waters 2410). RI Concentration Channel was copied from the method set used to produce this GPC/V result.
RI Constant (GPCV Option)	Identifies the change in refractive index divided by the change in detector response in μV per unit gain. By this definition, the units of the constant are 1/μV. **Notes:** ■ For the calculation of RI Constant, the RI Sensitivity field must be filled for the standard in the Samples table of Run Samples. ■ The value of the RI Constant is blank by default if an RI

Field	Description
	calibration is not performed.
RI Sensitivity (GPCV Option)	Detector gain value (relative sensitivity) you entered for the sample during sample loading to scale the distribution area values. RI Sensitivity is required when the software is to calculate dn/dc or when you need to calibrate an RI detector (such as a Waters 2410).
RT Ratio	Retention time divided by the RT Reference peak retention time.
Run Time	Length of time (in minutes) used to collect data for the sample.
Sample Set Altered	Identifies whether or not the sample set was altered.
Sample Set Finish Date	Time and date that sample set acquisition finished.
Sample Set ID	Sample set identifier generated by the database during data acquisition.
Sample Set ID (Result)	Sample set identifier if the sample is part of a sample set.
Sample Set Method	Name of the sample set method used to run the sample set.
Sample Set Name	Name of the sample set.
Sample Set Start Date	Time and date that sample set acquisition started.
Sample Type	Type of sample (standard, unknown, or control) that was acquired from the specified vial.
Sample Values Used in Calculations	List of names and values of all of the alterable sample fields used to process the result, including the Sample Weight, Dilution, Injection Volume, and custom fields.
SampleName	Name of the acquired standard or unknown, as entered during sample loading.
SampleWeight	Factor by which Empower software (during calibration) multiplies the calculated amount of each standard component. During quantitation, Empower software divides the amount read from the calibration curve (of the standard components) by the Sample Weight value to calculate amounts for each unknown sample.
Sampling Rate	Sampling rate of the detector or busSAT/IN module used to collect data for the channel.
Scan Number	Number of the scan (instead of retention time) for the acquired spectrum. The scan number, which is proportional to the retention time, starts at 1 for the first scan and increases by 1 for each subsequent scan throughout the run. For example, a

Field	Description
	scan rate of 10 scans/sec and a 1-minute run time produces a total of 600 scans.
Selectivity	Ratio of retention time of the selected component to the retention time of the preceding peak minus the void volume.
Slope	The slope (in plot units/min) of the baseline drawn beneath the peak, or peak cluster, as determined during peak integration.
Software Version	Software version (Empower, v4.00 Millennium^{32}, Pre-v4.00 Millennium32, or imported from AIA) used to integrate the chromatogram.
Start Height	Height of peak integration at the start of a peak (in microvolts).
Start Time	Height of peak integration at the start of a peak (in minutes).
Structure 1-3 Description (Chemical Structures Option)	Description of the chemical structure.
Structure 1-3 Formula (Chemical Structures Option)	Formula calculated for the chemical structure.
Structure 1-3 Mol Wt (Chemical Structures Option)	Molecular weight calculated for the chemical structure.
Structure 1-3 Name (Chemical Structures Option)	User-defined name of the chemical structure.
Structure 1-3 Structure (Chemical Structures Option)	Chemical structure shown as a graphic.
Symmetry Factor	Peak tailing based on the EP and JP methods of determining peak asymmetry.
System Comments	Comments associated with the acquisition chromatographic system.
System Create Date	Date the acquisition chromatographic system was created.
System Name	Name of the chromatographic system used for acquisition.
System Sigma (GPCV Option)	Value for the axial dispersion correction width constant, sigma, for the system function. This value is calculated only if you quantitate narrow standards with a relative calibration curve.
Threshold	Default threshold (liftoff and touchdown) used to detect the peaks in the chromatogram. The threshold value is either copied from the processing method or calculated at the start of integration.

Field	Description
Time Corr. Area (CIA Option)	Area of a peak divided by its migration time. Time-corrected area (TCA) is calculated as follows: TCA = (Area)/(Migration Time) where: ■ Area = Integrated area of peak ■ Migration Time = Migration time of peak
Total Area	Sum of the peak areas for all integrated peaks.
Transfer Time (Dissolution Option)	Time at which the dissolution sample was transferred (or drawn).
Units	Units associated with the amount or concentration value entered for the components (for example, mg/mL).
USP Plate Count (System Suitability Option)	Plate count based on the USP tangent method of determining plate count.
USP Resolution (System Suitability Option)	Difference between the retention time of this peak minus the retention time of the preceding peak, divided by the sum of the peak width at a tangent peak width of 50%, and multiplied by a constant of 2.0.
USP Resolution (HH) (System Suitability Option)	Difference between the retention time of this peak minus the retention time of the preceding peak, divided by the sum of the peak width at a tangent peak width of 50%, and multiplied by a constant of 2.0/1.7.
USP Tailing (System Suitability Option)	Peak tailing based on the USP method of determining peak asymmetry.
Vessel (Dissolution Option)	Vessel number within the bath, from which the dissolution sample was acquired: ■ 1 to 8 with the 2690D/2695D Module ■ 1 to 99 without the 2690D/2695D Module
Vial	Vial number of the standard or sample in the autosampler, plate, or rack of samples. This number could also be the injection number if using a manual injector.
Vial ID	Identifier generated by the database during data acquisition for each vial.
Vial ID (Result)	Vial identifier generated by the Oracle database during data processing.
Width	Peak width in seconds defined as the difference between the start time (minutes) and the end time (minutes) multiplied by 60

Field	Description
	to convert to seconds.
Width @ 10% (System Suitability Option)	Peak width at 10.0% of peak height.
Width @ 13.4% (System Suitability Option)	Peak width at 13.4% of peak height.
Width @ 32.4% (System Suitability Option)	Peak width at 32.4% of peak height.
Width @ 4.4% (System Suitability Option)	Peak width at 4.4% of peak height.
Width @ 5% (System Suitability Option)	Peak width at 5.0% of peak height.
Width @ 50% (System Suitability Option)	Peak width at 50.0% of peak height.
Width @ 60.7% (System Suitability Option)	Peak width at 60.7% of peak height.
Width @ Baseline (System Suitability Option)	Peak width at the baseline as determined by the processing method.
Width @ Tangent (System Suitability Option)	Peak width at the baseline, calculated as the distance between the baseline intercepts of the tangent drawn at a percentage of the height on the front and back of the peak. If ApexTrack integration is used, a processing code S29 occurs indicating the Width at Tangent is calculated using lines tangent to the inflection points.
[n] P (GPCV Option)	Intrinsic viscosity of a peak at MP or the bulk intrinsic viscosity of a broad peak for which a GPCV distribution was calculated.
[n] w (GPCV Option)	Weight average intrinsic viscosity calculated for all GPCV peaks.