# Agilent 6530 Q-TOF LC/MS User Manual



Never work on the machine if you have not been trained to operate the machine.

# Step 1: Check the machine and login

Before starting your work, please do the following:

- a) Check solvents in the reservoir bottles (deionized water and acetonitrile). If the amount of solvents too low, please inform Michal Urban.
- b) Login to the operating system. You will receive the relevant data only after proper training.

# Step 2: Start Data Acquisition software

You see all of the Agilent MassHunter Workstation software icons on your desktop. To start the Data Acquisition program , double-click the

Data Acquisition icon.

Data Acquisition

#### Note:

When Data Acquisition opens, the software engines automatically start. If you need to restart them, right-click the Acq System Launcher icon in the system tray and click *Start Engines*.





### The windows where you do most of your work

Method Editor, Sample run and Worklist windows are tabbed here. These three windows are "sharing" this space. You click the tab to switch to different window

#### Show/hide the windows

You can show one window at a time on the screen or all seven windows. You can never hide all of the windows. To show or hide a window, you click the commands in the *View menu*. You can also hide a window by clicking the **X** icon in the upper right corner of the window.

When you click a window, the title of the active window changes to a different colour. Press **F1** to obtain help on the active window. You can also drag a window border to resize the window. If you double-click the title of the window, the window "floats" outside of the main window. You can double-click the title bar again to "dock" the window. You can also float and dock the window by right-clicking the title of the window and clicking *Floating* 

#### Instrument Status window



With this window you view the status of each device configured with the instrument–On, Off or Standby. You also set non-method control and configuration parameters for the LC devices and the MS instrument. You do not need to set up anything, everything is already configured. You can click the ? button in any device panel to get useful informations.

This window displays each device's current status both as text and by its color-coding: (Table 1).

Table 1: Color-coding of Instrument Status Window

Color	Status	
Red	Error	
Yellow	Not ready	
Purple	Pre run/Post run	
Blue	Running, Injecting	
Green	Idle	
Dark gray	Offline	
Light gray	Standby (for example, lamps off)	

# Actuals window

With this window you view the current value of selected instrument parameters.

Actuals					
Parameter	Value				
Q-TOF: TOF Vac	1.65E-07 Torr				
Q-TOF: Quad Vac	2.40E-05 Torr				
Q-TOF: Drying Gas	3.0 l/min				
Q-TOF: Error State	_				
Q-TOF: Ready State	False				
Q-TOF: Rough Vac	2.83E+00 Torr				
Q-TOF: Vaporizer/Sheath Gas Temp	125 °C				
Q-TOF: Gas Temp	300 °C				

# **Chromatogram Plot window**

With this window you monitor the chromatogram plots in real time. These plots can be user-defined signals and/or instrument parameters.



# **Spectrum Plot window**

With this window you monitor the spectral plots in real time.

Spectrum	n Plot									×
Centroi	id MS + MS1 L	ine Spectrur	n at 1.24 min.							
100K	m/z: 221.0588	221	.0588							
50K-	Height: 97771 81.9374	· · · · · · · · · · · · · · · · · · ·	311.0	801	513.0	051 596.	3153	769.4018		22.0051
0	100	200	300	400	500	600	700	800	900	
ママ	100	200	500	400	m/z (amu)	000	,	000	500	
Profile	MS + MS1 Prot	file at 1.24 m	in.							
8 100K−	Area: 362667	221	.0588							
	m/z: 221.0588							769.4018		
U	100	200	300	400	500	600	700	800	900	1000
					m/z (amu)					

#### **Method Editor window**

With this window you enter acquisition parameters for the method. There is no need to edit anything; everything is set for the general method!

Method Editor	x
🗄 🗋   🎷 🔲 💋   🎅   calibrant.m	🗸 🗸 Apply
Properties DA HiP Sampler HiP Sampler Pretreatment Bina	ry Pump Column Comp. DAD <mark>Q-TOF</mark>
Ion Source Ion Polarity Data Storage LC Stream	General Source Acquisition Ref Mass Chromatogram
Dual AJS ESI - Positive Centroid Waste	Ion Polarity (Seg)
Stop Time Time Segment and Experiment #	Positive Fast Polarity Switching     None      Centroid
C No Limit/As Pump	C Negative C Both C Profile
	LC Stream (Seg) Plot and Centroid Data Storage Threshold
	С мз МЗ МЗ/МЗ
	Waste Abs. threshold 200 Abs. threshold 5
	Apply Now Rel. threshold (%) 0.01 Rel. threshold (%) 0.01
Cycle Time 1 s	Do not wait for setpoints (e.g. temperature) to equilibrate
-	
Worklist Method Editor Sample Run	

#### Sample Run window

With this window you enter sample information to run individual samples interactively, and you can start a single sample run.

Sample Run					
Sample		Addition	al Information		
Name	Engela 1 Portion National -		Parameter Name	Parameter Value	•
Nume	peniper resources to allectors		Rack Position		
Injection Volume	As Method v µL		Plate Code	PlateOrVial	
			Plate Position		Ξ
Comment			Sample Type	Sample	
Data Ele			Method Type	Acquisition Only	
Data File			Balance Override	No Override	
Auto Incremen	t de la constante d		Equilib Time (min)	0	
News	Sample 0.01	Dut	Dilution	1	
rvame	Sampeurea View	v Data	Wt/Vol	0	
Path	C-\NassHurter\Data	*	ReadyTimeOut	2	

#### Worklist window

With this window you enter sample information for multiple samples. When you run the worklist, the samples are automatically run in the order listed in the worklist.

W	Worklist ×										
÷ E	🗅 📝 💾 💹 🕨 🔲 🔢 📴 SulfaWorklist.wkl										
		7	Sample Name	Sample Position	Method	Data File	Sample Type	Level Name	Comment	Sample Group	Info. 📤
	1	v	Sulfa1	P1-A1	AJSESI_default.m	sulfas001.d	Sample				
	2	v	Sulfa1	P1-A2	AJSESI_default.m	sulfas002.d	Sample				
	3	$\boldsymbol{\nu}$	Sulfa1	P1-A3	AJSESI_default.m	sulfas003.d	Sample				
•											•
	Worklist										
We	orklist	t N	Nethod Editor   Sample Run	1							

#### **Tune window**

With this window, you tune the mass spectrometer. You can us one of the automated tuning algorithms, or you can manually tune the instrument.



# Step 3: Tune TOF a Q-TOF

a) In the Context list, change the Acquisition mode to Tune mode in the main window at the top left.

File	View	Sample	Work	list
Conte	xt: Acq	uisition	-	La
For He	lp,F <mark>Acq</mark>	uisition e		
Instru	ment St	atus		'

The Tune window appears. Only the *Instrument Status window*, the *Actuals window*, and the *Tune window* are available in the *Tune context*. Note that you tune the TOF separately from the quadrupole.

#### **Tune window**

Tune File: TOFMassCalibration-3200mzRange.tun	Tune & Calibration Instrumer	it State			
Ion Polarity 🕟 Positive 🔿 Negative	_Q-TOF: Standard (3200 n	n/z) Extended Dynamic Range			
lon Source	Positive	🔿 Quadrupole	Mass Calibration / Check		
	Negative		C Transmission Tune		
Gas Temp 325 297 °C		C Both	C System Tune	🔲 Fragile Ions	
Drying Gas 5 5.0 1/min					
Nebulizer 20 psi			*		
VCap 4000 V 0.051 μA				Start TOF Mass	
Chamber 3.29 µA				Calibration	
Nozzle Voltage 2000 V					
Sheath Gas Temp 295 186 °C					
Sheath Gas Flow 12 12.0 1/min					
				Tune Report	
Calibrant Bottle 💿 None 🔿 A 🔿 B			-		
LC Flow to 🙃 Waste C MS					Apply

b) Turn on all machine components in the *Instrument Status window*.

Instrument Status						×
Sampler EMF⊙ 1.00µL	Binary Pump EMF⊙ 95.0 5.0 0.000 mL/min 0.00 bar	Column Comp. Not Ready EMF⊘ 23.03 °C 24.88 °C	VWD ENF ② ENF ③ 254 nm	Q-TOF Not Ready Dual AIS ESI Standard (3200) 2 GHz, Ext Dyn Range		Û
0.00 / 0.00					Instrument Not Ready 🗉	🕕 On 😑 Off

Turns on all components.

File View Tools Help Context: Tune   Layout: Default(sys).lyt   Layout: Def									
Instrument Status						×			
Sampler Idle EMF I I I I I I I	Binary Pump Idle EMF 95.0 5.0 0.400 mL/min 213.98 bar	Column Comp. Idle EMF⊘ ↓ 29.72 °C 25.33 °C	VWD EMF© 254 nm	Q-TOF Not Ready Dual AJS ESI Standard (3200) 2 GHz, Ext Dyn Range					
0.00 / 0.00					Instrument Not Ready	i 🕕 On 😑 Off			

- c) Then click on *Tune and Calibration*
- d) Select the polarity of TOF on the *Tune and Calibration* tab. If you are going to tune in Positive polarity, do the following: Click the **Positive** polarity button. If you are going to tune in Negative polarity, do the following: Click the **Negative** polarity button. Next, click *Mass Calibration / Check*.
- e) Then click Start TOF Mass Calibration and wait for the report. This may take about 5 minutes. If a report is displayed, the machine calibration has been successful.

Tune File: TOFMassCalibration-3200mzRange.tun	Tune & Calibration Instrument State	
Ion Polarity 💿 Positive 🔿 Negative	Q-TOF: Standard (3200 m/z) Extended Dynamic Range	
Ion Source	Positive     C Quadrupole	
Gas Temp 325 297 °C Drying Gas 5 5.0 1/min	Fragile Ions	
Nebulizer 20 psi		
VCap 4000 V 0.051 μΑ Chamber 3.29 μΑ	Start TOF Mass Calibration	
Nozzle Voltage 2000 V		
Sheath Gas Temp 295 186 °C		
Sheath Gas Flow 12 12.0 1/min	Tune Report	
Calibrant Bottle 💿 None 🔿 A 🔿 B		1
LC Flow to 💿 Waste C MS		Apply

f) The calibration is completed; you will switch back to *Acquisition* mode in the *Context list* of the main window.



# Step 4: Set up and run a method

Before measuring your sample, you must choose an appropriate method of measurement.

a) You select a method in the Method section of the main window.

Agilent MassHunter Workstation Data Acquisition											
File View Sample Worklist Method Tools Help											
Context: Acquisition 🔹 Layout: Deafault(sys).lyt 👻 🚼 🚽 🔒 🍈 🍈 💷 🔲 H Method: general_short_posi 👻 Vorklist:											
Instrument Status	Instrument Status X										
Sampler	Binary Pump	Column Comp.	VWD	Q-TOF	Parameter	Value					
Idle EMF	Standby EMF	Not Ready EMF⊘	Not Ready EMF⊘	Not Ready	Q-TOF: Quad Vac Q-TOF: Drying Gas	2.43E-05 Torr 3.0 l/min					
1.00μL	95.0 5.0 0.000 mL/min 0.18 bar	ری دور اور اور اور اور اور اور اور اور اور ا	254 nm	Dual AJS ESI Standard (3200) 2 GHz, Ext Dyn Range	Q-TOF: Error State Q-TOF: Ready State Q-TOF: Rough Vac Q-TOF: Vaporizer/Sheath Gas Temp Q-TOF: Gas Temp	- False 2.81E+00 Torr 125 °C 300 °C					
0.00 / 0.00		22.05 °C 23.38 °C	Instrumo	ent Not Ready							

We have created methods that you can use for routine measurements. Method of first choice is: general\_short\_positive(400ul).1ul.m

This method is suitable for most samples.

Note: If you need to develop a special method for measuring your substance, discuss it first with Michal Urban.

- b) Select a method from the tab: general\_short\_positive(400ul).1ul.m
- c) Turn on all machine components with the *On* button. All components of the machine will start work and will be in active mode, which will be shown in green colour in the *Instrument Status window*.

Instrument Status							
Sampler EMF©	Binary Pump Idle EMF 95.0 5.0 0.400 mL/min 213.98 bar	Column Comp. Idle EMF⊙ ↓ CD==CD 29.72 °C 25.33 °C	VWD	Idle EMF⊘ ↓	Q-TOF Not Ready Dual AIS ESI Standard (2000) 2 GHz, Ext Dyn Range		Û
0.00 / 0.00						Instrument Not Ready	] 🕕 On 🧲

# Step 5: Set up and run worklists

- a) Click Worklist
- b) Right-click the upper left corner of the worklist to display the following menu.

Worklist							
: 🗅   🎷 🛄 💹   🕨 🔳 🔢   🖻	SulfaWorklist.wkl		•				
1     Add Multiple Samples       2     Add Sample       3     Add Script	ample Position 41 42 43	Method AJSESI_default.m AJSESI_default.m AJSESI_default.m	Data File sulfas001.d sulfas002.d sulfas003.d	Sample Type Sample Sample Sample	Level Name	Comment	Sam
<u>C</u> opy Row(s) Add Copied Row <u>(</u> s)	-						
Delete Row(s)							
Add Col <u>u</u> mn(s) <u>S</u> how/Hide/Order Columns	-						
Text Size Add Wor <u>k</u> list	-						
Worklist <u>R</u> un Parameters Import Worklist							
Wrap           ✓           Track Worklist Run							
			Worklist				

- c) ClickAdd Multiple Samples.
- d) Paste the information into the worklist table, such as sample name, data file name, and path to save the file. The first line of the worklist is always the Blank sample measurement with vial position 1. The measurement of your sample or sample sequence follows. The last step is to wash with the injection of pure acetonitrile in the vial at position 1. Each acquisition (row) is measured for 13 minutes. To add a row to the worklist, right-click in the upper left corner of the worklist to display the menu and select Add Sample.

**Poznámka:** I recommend measuring Blank sample twice. The first blank measurement removes residue from the previous measurement and the second blank measurement equilibrates the machine.

e) Indicate the position of your sample in the Sample Position (2-99).

Workl	Worklist										
1											
		Sample Name	Sample Position	Method	Data File	Sample Type	Level Name	lnj Vol (μl)	Comment	Sample Group	Info.
1>	иb	lank20.1.20 <mark>2</mark> 0	Vial 1	general_short_positive(400u	D:\MassHunter\Data\Jindrich\Kasal	Sample		As Method			
2	νP	Ж1069 🤇	Vial 61	general_short_positive(400u	D:\MassHunter\Data\Jindrich\Kasal	Sample		As Method			
3	νw	/ashing	Vial 1	general_short_positi∨e(400u	D:\MassHunter\Data\Jindrich\Kasal	Sample		As Method			
4	νS	cript: SCP_PumpsAll	Off(){MH_Acq_Scripts.e:	xe}							
								Workliet			
								WUINIISU			

- f) In the last line, insert a request to stop the pumps after measuring the worklist. It is good to save solvents. Please right-click in the upper left corner of the worklist to display the menu and select *Add Script*. And select *SCP\_PumpsAllOff*.
- g) The sample must be completely dissolved in Agilent vials (<u>https://www.agilent.com/store/productDetail.jsp?catalogId=5190-4034</u>) with a cap having a septum (<u>https://www.agilent.com/store/productDetail.jsp?catalogId=5182-0717</u>). Never use different septum !!!



The concentration of your sample must be in the range of 10-40  $\mu$ g/ml. Sample preparation: Dissolve 1 mg of your substance in 1 ml of acetonitrile then take 0.01-0.04 ml of it and dissolve this amount in 1 ml of acetonitrile.

- a) Click the Start Worklist Run button () in the Worklist toolbar.
- b) The blank from vial 1 is then injected and measured. Violet colour with Sampler. Then the measurement of your samples continues according to the worklist. Blue colour on all machine components.

Agilent MassHunter Workstation Data Acquisition			
File View Sample Worklist Method Tools Help			
Context: Acquisition V Layout: Deafault(sys).lyt V	Method: general_short_posi      Worklist:	<b>(</b>	
Instrument Status	,	Actuals	×
Sampler Injecting EMFO I 100µL Vial 1 Some	VWD Prerun EMF©	Parameter         Value           Q-TOF: TOF Vac         1.65E-07 Torr           Q-TOF: Quad Vac         2.34E-05 Torr           Q-TOF: Drying Gas         8.01/min           Q-TOF: Error State	
0.00 / 0.00	Instrument Injecting 🔋 🕕 On 🥚 Off		
Chromatogram Plot	×	Spectrum Pane	×
TIC Binary Pump: Pressure	VWD: Signal A	UV UV	
3.857 3.657 3.657 3.657 3.657 3.657 3.657 3.657 3.577 3.5777 3.577 3.577 3.577 3.577 3.57777 3.5777 3.5777 3.57777 3.57777 3.57777 3.577777 3.577777 3.57777777777	4190 4190 min	x10 <sup>2</sup> 1 0.9 0.8 0.7 0.6 0.6 0.6 0.6 0.4 0.3 0.2 0.1 0 0.5 0 5 10 15 20 25 30 0 0 0 0 0 0 0 0 0 0 0 0 0	35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 nm
4100 4100 4170	4160 4160 11111	VWD Q-TOF	
Image: State of the state	Data File         Sample Type         Level Name         I           ssHunter/Data\Jindrich\Kasati Sample         As N           ssHunter/Data\Jindrich\Kasati Sample         As N	nj Vol (µl) Comment Sample Group Info. fethod effod effod	Errors and warnings 1. Skipping overlapped injection because High throughput Optimization is not en 2. Skipping overlapped injection because High throughput Optimization is not en
Method Editor Worklist Sample Run	Work	INST	Skipping overlapped injection because High     throughput Optimization is not en

🚟 Agilent MassHunter Workstat	ion Data Acquisition					
File View Sample Worl	klist Method Tools Help					
Context: Acquisition	∀     ∀     ∠ayout: Deafault(sys).lyt     √	] 🗄 -   🔒 🌘 🍈 🍈	Method: ger	neral_short_posi 👻 Worklist:		
Instrument Status				×		
Sampler	Binary Pump	Column Comp.	VWD	Q-TOF		
Run	Run	Run	Run	Run		
EMF	emf⊘	EMF⊘	EMF			
π	ā ā	L		Oual AJS ESI		
1.00 µL	90.8 9.2 0.400 mL/min		<b>4</b>	Standard (3200) 2 GHz, Ext Dyn Range		
<u> </u>	190.18 bar	29.99 °C 26.94 °C	254 nm			
Run 0.35 / 16.00 min Instrument Run 👔 🕕 On 😑 Off						

c) When all your samples have been measured and the final wash is complete, the pumps will automatically shut down.

# Step 6: Analysis of measured data

You can analyse your measured samples and look for the appropriate masses in Qualitative Analysis. You can find this program on your desktop



- Use the Qualitative Analysis program to do these steps and more:
- Review results for acquisition method development
- Find compounds
- Identify compounds
- Do molecular feature extraction
- Export results