

Comprehensive Test Mix for MassHunter Pesticide Triggered MRM Database and Library

Method Setup Guide

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NOTE

The Comprehensive Pesticide Test Mix is included with the G1733 Pesticide Triggered MRM Application Kit.

Agilent does not provide the actual acquisition methods to use with the Comprehensive Test Mix, due to the large number of instrument configurations that are possible.

Instead, Agilent provides this guide to explain how to create MRM methods that are used to create dMRM and tMRM methods for the test mix.

You will copy the values from the file **MRM_Methods_Pesticide.xlsx**, found on the *Support Disc*, to set up your MRM methods.

Before you begin, make sure that your system meets the installation requirements that are described in the *MassHunter Pesticide Triggered MRM Database and Library Quick Start Guide*.

For more detailed instructions, see the *Quick Start Guide* for this database, and the *MassHunter Data Acquisition for 6400 Series Triple Quadrupole LC/MS Familiarization Guide* and *online Help*.



Step 1. Set up the LC part of the method

Step 1. Set up the LC part of the method

1 Set up the solvent.

This step is identical for all LC configurations.

- Solvent A: 5 mM ammonium formate in 0.1% formic acid in water
- Solvent B: 5 mM ammonium formate in 0.1% formic acid in methanol

2 Set up the gradient.

The gradient setup is dependent upon the LC configuration. Some examples follow.

1290 Infinity LC system

1290 Infinity LC system with Agilent Eclipse Plus C18, 2.1 mm × 150 mm, 1.8 μm ZORBAX LC column (p/n 959759-902), included in the G1733BA Pesticide Triggered MRM Application Kit.

Time [min]	▲	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00		95.00	5.00	0.400	1200.00
0.50		95.00	5.00	0.400	1200.00
3.50		50.00	50.00	0.400	1200.00
17.00		0.00	100.00	0.400	1200.00
20.00		0.00	100.00	0.400	1200.00
20.10		95.00	5.00	0.400	1200.00

Stop time is 20:10.

1260 Infinity LC system

The 1260 Infinity LC system can have a lower backpressure (up to 600 bar) and a higher dead volume than the 1290 Infinity LC system.

Time [min]	▲	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00		95.00	5.00	0.400	600.00
▶ 3.50		50.00	50.00	0.400	600.00
17.00		0.00	100.00	0.400	600.00
20.00		0.00	100.00	0.400	600.00
20.10		95.00	5.00	0.400	600.00

Stop time is 20:10.

Step 2. Set up LC/MS ion source parameters

- Set up the ion source parameters in the MS part of the method.

For a multi-component method, the ion source parameters shown in the next figure are used to achieve the best overall sensitivity for all of the compounds in the Comprehensive Test Mix. You can make adjustments to optimize for individual compounds or submixes.

6460 LC/MS Ion source parameters for the 6460 LC/MS instrument:

Source parameters

Gas Temp:	<input type="text" value="120"/>	°C	<input type="text"/>	°C
Gas Flow:	<input type="text" value="5"/>	l/min	<input type="text"/>	
Nebulizer:	<input type="text" value="30"/>	psi	<input type="text"/>	psi
Sheath Gas Temp:	<input type="text" value="375"/>	°C		
Sheath Gas Flow:	<input type="text" value="12"/>	l/min		
	Positive		Negative	
Capillary:	<input type="text" value="3500"/>	V	<input type="text" value="3000"/>	V
			<input type="text"/>	V
Nozzle Voltage:	<input type="text" value="300"/>	V	<input type="text" value="500"/>	V

Step 3. Set up the MRM method

- 1 From the *Support Disc*, open the file **MRM_Methods_Pesticide.xlsx**.

This spreadsheet file contains eight tabs, **SubMix 1** through **SubMix 8**, one for each of the eight standard mixes in the Comprehensive Test Mix.

MRM	Compound Group	Compound	ISTD?	Precursor MS1 Res	Product Ion MS2 Res	Dwell	Fragment	Collision	Cell	Accel	Polarity
3	SubMix 1	Spirodiclo	FALSE	411.1 Unit	71.2 Unit	10	110	15	3	Positive	
4	SubMix 1	Diffufenic	FALSE	395 Unit	266 Unit	10	150	25	5	Positive	
5	SubMix 1	Diffufenic	FALSE	395 Unit	246 Unit	10	150	40	5	Positive	
6	SubMix 1	Fluopicol	FALSE	382.9 Unit	172.9 Unit	10	110	25	3	Positive	
7	SubMix 1	Fluopicol	FALSE	382.9 Unit	144.9 Unit	10	110	45	3	Positive	
8	SubMix 1	Prochlora	FALSE	376 Unit	308 Unit	10	70	5	3	Positive	
9	SubMix 1	Prochlora	FALSE	376 Unit	266 Unit	10	70	10	3	Positive	
10	SubMix 1	Proquinaz	FALSE	372.9 Unit	331 Unit	10	120	5	7	Positive	
11	SubMix 1	Proquinaz	FALSE	372.9 Unit	289 Unit	10	120	20	7	Positive	
12	SubMix 1	Flufenace	FALSE	364 Unit	194.2 Unit	10	90	5	3	Positive	
13	SubMix 1	Flufenace	FALSE	364 Unit	152.1 Unit	10	90	15	3	Positive	
14	SubMix 1	Azinphos	FALSE	346.05 Unit	132 Unit	10	70	8	3	Positive	
15	SubMix 1	Azinphos	FALSE	346.05 Unit	97 Unit	10	70	32	3	Positive	
16	SubMix 1	Isofenphc	FALSE	332 Unit	231 Unit	10	145	10	5	Positive	
17	SubMix 1	Isofenphc	FALSE	332 Unit	121 Unit	10	145	40	5	Positive	
18	SubMix 1	Dimoxyst	FALSE	327.1 Unit	205.1 Unit	10	115	5	3	Positive	
19	SubMix 1	Dimoxyst	FALSE	327.1 Unit	116 Unit	10	115	20	3	Positive	
20	SubMix 1	Azinphos	FALSE	318.02 Unit	261 Unit	10	60	0	3	Positive	
21	SubMix 1	Azinphos	FALSE	318.02 Unit	132.1 Unit	10	60	8	3	Positive	
22	SubMix 1	Buprofezi	FALSE	306.1 Unit	201.2 Unit	10	105	5	3	Positive	
23	SubMix 1	Buprofezi	FALSE	306.1 Unit	116.1 Unit	10	105	10	3	Positive	
24	SubMix 1	Fenamiph	FALSE	304.1 Unit	217.1 Unit	10	120	20	3	Positive	
25	SubMix 1	Fenamiph	FALSE	304.1 Unit	202 Unit	10	120	35	3	Positive	
26	SubMix 1	Azacoxat	FALSE	300 Unit	226.8 Unit	10	130	16	4	Positive	
27	SubMix 1	Azacoxat	FALSE	300 Unit	158.9 Unit	10	130	32	4	Positive	
28	SubMix 1	Spiroxami	FALSE	298.2 Unit	144.2 Unit	10	125	15	3	Positive	
29	SubMix 1	Spiroxami	FALSE	298.2 Unit	100.2 Unit	10	125	35	3	Positive	

- 2 Open the MassHunter Data Acquisition program.

Step 3. Set up the MRM method

3 In the Method Editor window, click **QQQ > Acquisition**.

The screenshot shows the Method Editor window with the Acquisition tab selected. The interface is divided into several sections:

- Tune file:** Shows the file path `shunes.TUNE.XML` and a `Browse...` button.
- Stop time:** Includes a radio button for `No limit/As Pump` and a time input field set to `1` min.
- Ion source:** A dropdown menu is set to `AJS ESI`.
- Time filtering:** A checkbox for `Peak width` is checked, with a value of `0.04` min.
- Time segments:** A table with the following data:

#	Start Time	Scan Type	Div Valve	Delta EMV (+)	Delta EMV (-)	Stored
1	0	MRM	To MS	200	0	<input checked="" type="checkbox"/>
- Acquisition Parameters Table:** A table with the following data:

Compound Group	Compound Name	ISID?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity
	Compound1	<input type="checkbox"/>	350	Unit	200	Unit	200	135	0	7	Positive
- Bottom Status:** Shows `4.91` cycles/s and `2035` ms/cycle.

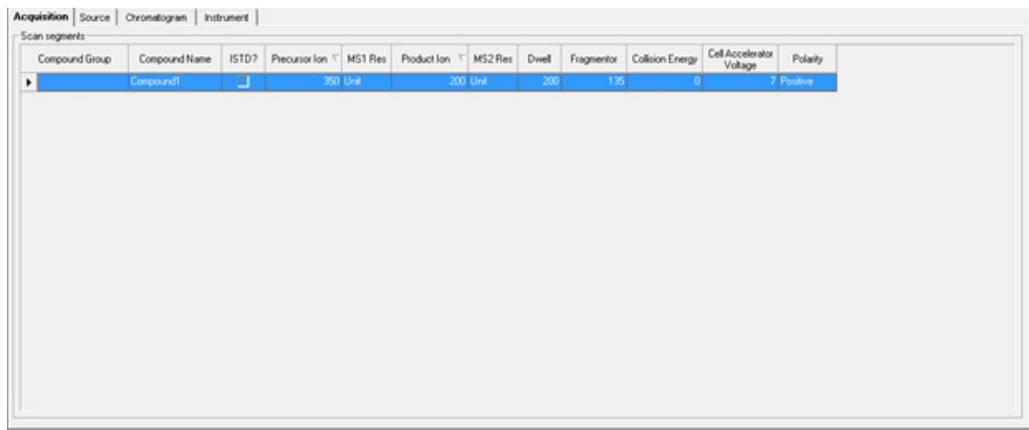
Step 3. Set up the MRM method

- 4 In the spreadsheet file, in the **SubMix 1** tab, select all of the cells that contain MRM information. Make sure that you select the two header rows. *Do not select the entire table!*

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	MRM												
2	Compound Group	Compound	ISTD?	Precursor MS1 Res	Product IC MS2 Res	Dwell	Fragment	Collision E	Cell Accel	Polarity			
3	SubMix 1	Spirodiclo	FALSE	411.1 Unit	71.2 Unit	10	110	15	3	Positive			
4	SubMix 1	Diflufenic	FALSE	395 Unit	266 Unit	10	150	25	5	Positive			
5	SubMix 1	Diflufenic	FALSE	395 Unit	246 Unit	10	150	40	5	Positive			
6	SubMix 1	Fluopicoli	FALSE	382.9 Unit	172.9 Unit	10	110	25	3	Positive			
7	SubMix 1	Fluopicoli	FALSE	382.9 Unit	144.9 Unit	10	110	45	3	Positive			
8	SubMix 1	Prochlora	FALSE	376 Unit	308 Unit	10	70	5	3	Positive			
9	SubMix 1	Prochlora	FALSE	376 Unit	266 Unit	10	70	10	3	Positive			
10	SubMix 1	Proquinaz	FALSE	372.9 Unit	331 Unit	10	120	5	7	Positive			
11	SubMix 1	Proquinaz	FALSE	372.9 Unit	289 Unit	10	120	20	7	Positive			
12	SubMix 1	Flufenace	FALSE	364 Unit	194.2 Unit	10	90	5	3	Positive			
13	SubMix 1	Flufenace	FALSE	364 Unit	152.1 Unit	10	90	15	3	Positive			
14	SubMix 1	Azinphos-	FALSE	346.05 Unit	132 Unit	10	70	8	3	Positive			
15	SubMix 1	Azinphos-	FALSE	346.05 Unit	97 Unit	10	70	32	3	Positive			
16	SubMix 1	Isofenphc	FALSE	332 Unit	231 Unit	10	145	10	5	Positive			
17	SubMix 1	Isofenphc	FALSE	332 Unit	121 Unit	10	145	40	5	Positive			
18	SubMix 1	Dimoxyst	FALSE	327.1 Unit	205.1 Unit	10	115	5	3	Positive			
19	SubMix 1	Dimoxyst	FALSE	327.1 Unit	116 Unit	10	115	20	3	Positive			
20	SubMix 1	Azinphos-	FALSE	318.02 Unit	261 Unit	10	60	0	3	Positive			
21	SubMix 1	Azinphos-	FALSE	318.02 Unit	132.1 Unit	10	60	8	3	Positive			
22	SubMix 1	Buprofezi	FALSE	306.1 Unit	201.2 Unit	10	105	5	3	Positive			
23	SubMix 1	Buprofezi	FALSE	306.1 Unit	116.1 Unit	10	105	10	3	Positive			
24	SubMix 1	Fenamiph	FALSE	304.1 Unit	217.1 Unit	10	120	20	3	Positive			
25	SubMix 1	Fenamiph	FALSE	304.1 Unit	202 Unit	10	120	35	3	Positive			
26	SubMix 1	Azaconaz	FALSE	300 Unit	230.8 Unit	10	130	16	4	Positive			
27	SubMix 1	Azaconaz	FALSE	300 Unit	158.9 Unit	10	130	32	4	Positive			
28	SubMix 1	Spiroxami	FALSE	298.2 Unit	144.2 Unit	10	125	15	3	Positive			
29	SubMix 1	Spiroxami	FALSE	298.2 Unit	100.2 Unit	10	125	35	3	Positive			
30	SubMix 1	Cyprocon	FALSE	292.1 Unit	125.1 Unit	10	100	35	3	Positive			
31	SubMix 1	Cyprocon	FALSE	292.1 Unit	70.1 Unit	10	100	15	7	Positive			
32	SubMix 1	Isoprothi	FALSE	291.1 Unit	231 Unit	10	80	8	4	Positive			
33	SubMix 1	Isoprothi	FALSE	291.1 Unit	188.8 Unit	10	80	20	4	Positive			
34	SubMix 1	Myclobut	FALSE	289.1 Unit	125 Unit	10	110	35	3	Positive			
35	SubMix 1	Myclobut	FALSE	289.1 Unit	70.1 Unit	10	110	15	7	Positive			
36	SubMix 1	Fosthiazat	FALSE	284 Unit	228.1 Unit	10	90	5	3	Positive			
37	SubMix 1	Fosthiazat	FALSE	284 Unit	104.1 Unit	10	90	20	3	Positive			
38	SubMix 1	Disulfator	FALSE	275 Unit	89 Unit	10	130	5	5	Positive			

Step 3. Set up the MRM method

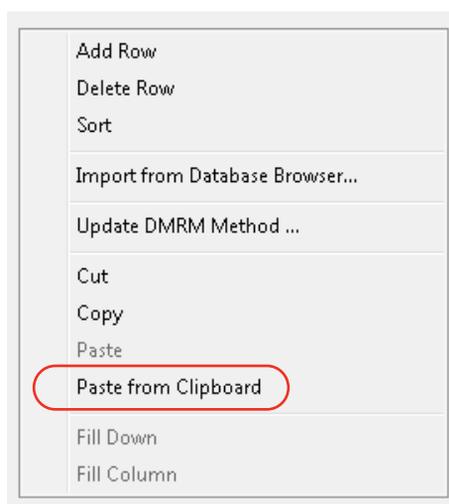
- 5 Copy the selected cells. (Press **Ctrl+C** or use the Copy command).
- 6 In the MassHunter Data Acquisition program, in the first line of the **Scan segments** table, click the leftmost column to select the first line.



The screenshot shows the MassHunter Data Acquisition software interface. At the top, there are tabs for 'Acquisition', 'Source', 'Chromatogram', and 'Instrument'. Below these tabs is a table titled 'Scan segments'. The table has the following columns: Compound Group, Compound Name, ISTD?, Precursor Ion, MS1 Res, Product Ion, MS2 Res, Dwell, Fragmentor, Collision Energy, Cell Accelerator Voltage, and Polarity. The first row of the table is highlighted in blue, indicating it is selected. The data in the first row is: Compound Group: (empty), Compound Name: Compound1, ISTD?: (empty), Precursor Ion: 350 Unit, MS1 Res: (empty), Product Ion: 200 Unit, MS2 Res: (empty), Dwell: 200, Fragmentor: 135, Collision Energy: 0, Cell Accelerator Voltage: 7, Polarity: Positive.

Compound Group	Compound Name	ISTD?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity
	Compound1		350 Unit		200 Unit		200	135	0	7	Positive

- 7 Right-click and click **Paste from Clipboard**.



The Scan segments table for instruments that are not equipped with iFunnel technology looks similar to the next figure.

Scan segments												
Compound Group	Compound Name	ISTD?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity	
	Compound1	<input type="checkbox"/>	350 Unit		200 Unit		200	135	0	7	Positive	
SubMix 1	Spirodiclofen	<input type="checkbox"/>	411.1 Unit		71.2 Unit		10	110	15	3	Positive	
SubMix 1	Diflufenican	<input type="checkbox"/>	395 Unit		266 Unit		10	150	25	5	Positive	
SubMix 1	Diflufenican	<input type="checkbox"/>	395 Unit		246 Unit		10	150	40	5	Positive	
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9 Unit		172.9 Unit		10	110	25	3	Positive	
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9 Unit		144.9 Unit		10	110	45	3	Positive	
SubMix 1	Prochloraz	<input type="checkbox"/>	376 Unit		308 Unit		10	70	5	3	Positive	
SubMix 1	Prochloraz	<input type="checkbox"/>	376 Unit		266 Unit		10	70	10	3	Positive	
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9 Unit		331 Unit		10	120	5	7	Positive	
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9 Unit		289 Unit		10	120	20	7	Positive	
SubMix 1	Flufenacet	<input type="checkbox"/>	364 Unit		194.2 Unit		10	90	5	3	Positive	
SubMix 1	Flufenacet	<input type="checkbox"/>	364 Unit		152.1 Unit		10	90	15	3	Positive	
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05 Unit		132 Unit		10	70	8	3	Positive	
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05 Unit		97 Unit		10	70	32	3	Positive	
SubMix 1	Isotfenphos-methyl	<input type="checkbox"/>	332 Unit		231 Unit		10	145	10	5	Positive	

The Scan segments table for instruments that are equipped with iFunnel technology, such as the 6490, looks similar to the next figure.

Scan segments												
Compound Group	Compound Name	ISTD?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity	
	Compound1	<input type="checkbox"/>	350 Unit		200 Unit		200	380	0	5	Positive	
SubMix 1	Spirodiclofen	<input type="checkbox"/>	411.1 Unit		71.2 Unit		10	380	15	3	Positive	
SubMix 1	Diflufenican	<input type="checkbox"/>	395 Unit		266 Unit		10	380	25	5	Positive	
SubMix 1	Diflufenican	<input type="checkbox"/>	395 Unit		246 Unit		10	380	40	5	Positive	
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9 Unit		172.9 Unit		10	380	25	3	Positive	
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9 Unit		144.9 Unit		10	380	45	3	Positive	
SubMix 1	Prochloraz	<input type="checkbox"/>	376 Unit		308 Unit		10	380	5	3	Positive	
SubMix 1	Prochloraz	<input type="checkbox"/>	376 Unit		266 Unit		10	380	10	3	Positive	
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9 Unit		331 Unit		10	380	5	7	Positive	
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9 Unit		289 Unit		10	380	20	7	Positive	
SubMix 1	Flufenacet	<input type="checkbox"/>	364 Unit		194.2 Unit		10	380	5	3	Positive	
SubMix 1	Flufenacet	<input type="checkbox"/>	364 Unit		152.1 Unit		10	380	15	3	Positive	
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05 Unit		132 Unit		10	380	8	3	Positive	
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05 Unit		97 Unit		10	380	32	3	Positive	

Note that polarity switching is supported for MRM, but the transitions within each compound need to have the same polarity. Polarity switching (positive and negative transitions within a compound) is not supported.

Step 3. Set up the MRM method

- 8 Remove the first compound from the Scan segments table:
 - a Select the first line. For the first method that you create, the line contains the compound **Compound1**. For the other methods, the line contains a compound from the previous submix.
 - b Right-click and click **Delete Row**. See the next figure.

Compound Group	Compound Name	ISTD?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity
SubMix 1	Compound1	<input type="checkbox"/>	350	Unit	200	Unit	200	135	0	7	Positive
			411.1	Unit	71.2	Unit	10	110	15	3	Positive
			395	Unit	266	Unit	10	150	25	5	Positive
			395	Unit	246	Unit	10	150	40	5	Positive
			382.9	Unit	172.9	Unit	10	110	25	3	Positive
			382.9	Unit	144.9	Unit	10	110	45	3	Positive
			376	Unit	308	Unit	10	70	5	3	Positive
			376	Unit	266	Unit	10	70	10	3	Positive
			372.9	Unit	331	Unit	10	120	5	7	Positive
			372.9	Unit	289	Unit	10	120	20	7	Positive
			364	Unit	194.2	Unit	10	90	5	3	Positive
			364	Unit	152.1	Unit	10	90	15	3	Positive
			346.05	Unit	132	Unit	10	70	8	3	Positive
			346.05	Unit	97	Unit	10	70	32	3	Positive
SubMix 1	Isoterphos-methyl	<input type="checkbox"/>	332	Unit	231	Unit	10	145	10	5	Positive

The final method now looks like the next figure.

Compound Group	Compound Name	ISTD?	Precursor Ion	MS1 Res	Product Ion	MS2 Res	Dwell	Fragmentor	Collision Energy	Cell Accelerator Voltage	Polarity
SubMix 1	Spirodiclofen	<input type="checkbox"/>	411.1	Unit	71.2	Unit	10	110	15	3	Positive
SubMix 1	Diflufenican	<input type="checkbox"/>	395	Unit	266	Unit	10	150	25	5	Positive
SubMix 1	Diflufenican	<input type="checkbox"/>	395	Unit	246	Unit	10	150	40	5	Positive
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9	Unit	172.9	Unit	10	110	25	3	Positive
SubMix 1	Fluopicolide	<input type="checkbox"/>	382.9	Unit	144.9	Unit	10	110	45	3	Positive
SubMix 1	Prochloraz	<input type="checkbox"/>	376	Unit	308	Unit	10	70	5	3	Positive
SubMix 1	Prochloraz	<input type="checkbox"/>	376	Unit	266	Unit	10	70	10	3	Positive
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9	Unit	331	Unit	10	120	5	7	Positive
SubMix 1	Proquinazid	<input type="checkbox"/>	372.9	Unit	289	Unit	10	120	20	7	Positive
SubMix 1	Flufenacet	<input type="checkbox"/>	364	Unit	194.2	Unit	10	90	5	3	Positive
SubMix 1	Flufenacet	<input type="checkbox"/>	364	Unit	152.1	Unit	10	90	15	3	Positive
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05	Unit	132	Unit	10	70	8	3	Positive
SubMix 1	Azinphos-ethyl	<input type="checkbox"/>	346.05	Unit	97	Unit	10	70	32	3	Positive
SubMix 1	Isoterphos-methyl	<input type="checkbox"/>	332	Unit	231	Unit	10	145	10	5	Positive

- 9 Click **Method > Save As** (or click  in the Method Editor toolbar) and save the method as **Pesticide_MRM_Mix1.m**.

Step 4. Set up a worklist to run the submixes

10 Delete all but one compound from the Scan segments table.

The Scan segments table cannot be empty. You need to leave one compound in the table.

11 Repeat step 4 through step 10 for each of the submixes.

When you save each method, use a name that reflects the submix name, such as **Pesticide_MRM_Mix2.m** for the values in the **SubMix 2** tab.

Step 4. Set up a worklist to run the submixes

- Set up the worklist as shown in the next figure. Inject the first standard twice to allow the system to come to equilibrium.

	<input checked="" type="checkbox"/>	Sample Name	Sample Position	Method	Data File	Sample Type	Level Name
1	<input checked="" type="checkbox"/>	SubMix_01	P1-A1	Pesticide_MRM_Mix1.m	todelete.d	Sample	
2	<input checked="" type="checkbox"/>	SubMix_01	P1-A1	Pesticide_MRM_Mix1.m	Submix_1.d	Calibration	1
3	<input checked="" type="checkbox"/>	SubMix_02	P1-A2	Pesticide_MRM_Mix2.m	Submix_2.d	Calibration	1
4	<input checked="" type="checkbox"/>	SubMix_03	P1-A3	Pesticide_MRM_Mix3.m	Submix_3.d	Calibration	1
5	<input checked="" type="checkbox"/>	SubMix_04	P1-A4	Pesticide_MRM_Mix4.m	Submix_4.d	Calibration	1
6	<input checked="" type="checkbox"/>	SubMix_05	P1-A5	Pesticide_MRM_Mix5.m	Submix_5.d	Calibration	1
7	<input checked="" type="checkbox"/>	SubMix_06	P1-A6	Pesticide_MRM_Mix6.m	Submix_6.d	Calibration	1
8	<input checked="" type="checkbox"/>	SubMix_07	P1-A7	Pesticide_MRM_Mix7.m	Submix_7.d	Calibration	1
9	<input checked="" type="checkbox"/>	SubMix_08	P1-A8	Pesticide_MRM_Mix8.m	Submix_8.d	Calibration	1

To create the dMRM and tMRM methods from the MRM methods that you just created, refer to the *Quick Start Guide* for this database, or the MassHunter Data Acquisition for 6400 Series Triple Quadrupole LC/MS *Familiarization Guide* or *online Help*.

Step 4. Set up a worklist to run the submixes

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In this Book

The *Method Setup Guide* describes how to create MRM methods for your specific LC/MS set up. The MRM methods are used to create Dynamic MRM (dMRM) and Triggered MRM (tMRM) methods for the Comprehensive Test Mix.

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