Waters[™]

Application Note

Bioanalytical Method Development with UNIFI: Compound Optimization for MRM Analysis

Waters Corporation

This is an Application Brief and does not contain a detailed Experimental section.

Abstract

The compound optimization functionality within the UNIFI Scientific Information System, part of the Regulated Bioanalysis System Solution, facilitates the fast, simple development of an MRM method for one or more compounds. The results generated can then be stored within the scientific library in the UNIFI System, allowing simple method generation and sharing of information between scientists.

Benefits

The compound optimization within the Waters UNIFI Scientific Information System delivers a fast, simple, consistent, and automated solution for the development of mass spectrometry multiple reaction monitoring (MRM) methodologies for bioanalytical studies.

Introduction

Successful bioanalysis relies on the development and validation of a reliable, robust, reproducible LC-MS methodology. A key component of this methodology is the mass spectrometry MRM method. Evaluating and developing this MRM method can be a long, exhaustive process requiring the evaluation of multiple parameters, such as: precursor and product ion combination, collision energy, temperatures and gas flows.

This process is not only time-consuming but often requires an experienced scientist to extract the optimal conditions. Additionally, the conditions once developed are typically confined to a study file and/or SOP and are not readily searchable by other scientists within the organization.

Results and Discussion

The UNIFI Scientific Information System has been designed to allow the scientist to manage, execute and store their analysis in a secure and compliant environment.



Figure 1 . UNIFI Scientific Information System

Once initiated, the laboratory data is contained and accessed within the UNIFI System via the "My Work" domain. Developing a new MRM method is performed via the "Compound Optimization" function (highlighted in red in Figure 2). The scientist is then able to input the ranges for each of the individual

parameters to be explored. This is controlled via an automated sequence of option boxes.

Waters UNIFI - Reg Bio 1 TQ System	Welcome to UNIT	Reg Bio 1 TQ System X		Search folders	IX ₽0
Reg Bio 1 TQ System	imization				ume Flow
Console Navigation System Reg Bio 1 TQ System Bioart Schern Manager	Compound List Import Create Modify Delete 1 Compound Name Mod	ettings ecular mastyformula Positive charge state Positive Adducts	lon modes: ESt+	Epperiment type: Formula	8
Sample Manager Xero TQ Monsu Summary: Setup Maintain Tools Setup Configure Detector Gain ScarWave Optimization Calibration Setup Calibration Calib	Optimize Results There are no results to show.	Create Compound			Start
Manual Tuning Sample Optimization Compound Optimization Pluidics Reset Instrument		Settings (formula)		0	0
Administrator, UNati (Administrat		Restore Defaults OK Cancel			

Figure 2. Developing an MRM method, top, and inputting parameters, bottom.

This functionality is illustrated in Figure 3 where capillary voltage, cone voltage range, collision energy range, and infusion sample location are selected. Undesired fragments such as the loss of water or CO_2 can be defined via a dropdown menu, ensuring a specific assay is developed free from interferences.

🔽 🔠 🗸 My Work 😂 Welcome to UNIFI] Reg Bio 1 TQ System 🛛 🗙		Search folders	P (
ng Bio 1 TQ System				
🖙 👻 Xevo TQ - Compound Optimization			O O C O R	sume Flo
Area Device - Compound Optimization rsuck Navigation System System Binary Solvent Manager Sample Manager Menu Summary Setup Optimize Results Configure Detector Gain Scativare Optimization Calibration Setup Calibration Setup Calibration Check Manual Tuning Sample Optimization Calibration Check Manual Tuning Sample Optimization Compound Optimization Compound Name Menual Tuning Sample Optimization Compound Optimization	ttings cular mass/formula Positive charge state Positive Adducts 1-1 ->++ Coptimization Capillary Voltage Optimization Auto Manual Set to: Cone Voltage Optimization Auto Range 5-40 Manual Set to: Collision Energy: 4-20 Sample Reservoir: Combined B OK Cancel	lon modes: ESI+	Experiment type: Formula	Start

Figure 3. Selecting the mass spectrometer's conditions.

Once the evaluation ranges for all of the MS parameters have been defined, the system automatically infuses the sample and acquires the necessary data. At the end of the acquisition, the data is saved and then displayed as a report to the scientist as shown in Figure 4.



Figure 4. Saving acquisition data.

The resulting MRM transitions, containing the optimized voltages and collision energies, are presented to the scientist in a tabular form. The scientist can then select the transitions best suited for the analysis at hand. These conditions are then exported to the "scientific library" within the UNIFI System for incorporation into the LC-MS method.

The UNIFI Scientific Information System is designed to operate in a workgroup or enterprise environment, with many users connected to and sharing a common central data server. Saving the optimized MS conditions in the scientific library allows them to be searched by any other scientist with access to the system. This functionality allows simple, fast searching of compounds or compound classes, promoting information sharing and productivity, while maintaining a streamlined operation.

Waters I	INIFE - F	Reg Bio 1 TQ Sys	tem	Reg Bio	1 TQ System ×				Search folders	۲ ۹
eg Bio :	Xevo	ystem TQ - Compoun	d Optimization					0	🖲 📴 😰 🕼 Stop Flow 🕼 Resu	ume Fl
Con	ipound kort C	d List reate Modify	Delete Settings					Ion modes: ESI+	Experiment type: Formula	1
	Comp	pound Name	Molecular mass/formula Positive charge state	Positive	Adducts					
1	Clope	edogrel	321.2	1-1 +H+						
									•	Start
Ор	timize I	Results		and the second second	Export Optimization Results					
Up	Dowr	n Export			Report Details					_
	Expor	rt? Precursor	Precursor Mass (m/z) Product	Product Mas	Name	Report1	Collis	sion Energy (eV) Intensity		
1	1	[M+H]+	322.14		Description		3.00	14.00 13968212.61		_
2	V	[M+H]+	322.14		Location	Company/Bioanalysis	3.00	20.00 10410097.78		
3		[M+H]+	322.14				3.00	20.00 1638708.18		
					Export to:	Default Custom Library •				
						OK Cancel				
Clo	pedogr	el Details								A.
dmi	istrate	Dr. UNIEDIAR								6

Figure 5. Exporting optimization results.

Conclusion

The compound optimization functionality within the UNIFI Scientific Information System, part of the Regulated Bioanalysis System Solution, facilitates the fast, simple development of an MRM method for one or more compounds. The results generated can then be stored within the scientific library in the UNIFI System, allowing simple method generation and sharing of information between scientists. This functionality:

- · Improves productivity
- · Ensures consistency of operation
- · Ensures the most selective and specific parameters are chosen
- · Promotes efficient sharing of data
- · Reduces the need for expert operation

Featured Products

UNIFI Scientific Information System <https://www.waters.com/134801648> Regulated Bioanalysis Platform Solution with UNIFI <https://www.waters.com/134613325>

720004289, March 2012

©2019 Waters Corporation. All Rights Reserved.