Waters® Alliance® LC/MS System

QuanLynx™ on Waters ZMD LC/MS System for Automated Methods Development
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Experiment Conditions

Calibration Curves

Results

Key Word:

QuanLynx

ZMD

Quantitation

Automation

1. Micromass Bruchure No. BR23.: QuanLynx…the software solution for automated LC-MS-MS method development and multi-compound quantification

QuanLynx is an integral function of the MassLynx™ software (version 3.3 or higher). It offers automated MS method development for quantitation using SIR or MRM. The automated process includes instrument optimization, data acquisition and quantification. QuanLynx can be implemented on tandem quadrupole instruments (Micromass® Quattro II™ , Quattro LC™ and Quattro Ultima™⁾ as well as single quadrupole instruments (Waters ZMD).

The application of QuanLynx on tandem quadrupole instruments has been shown elsewhere[1]. The purpose of this note is to demonstrate how QuanLynx can be utilized on a single quadrupole instrument such as the Waters ZMD. A mixture of Acetaminophen/Caffeine was used as the sample analyte. Manual quantitation of the mixture is also performed. The quantitation results by QuanLynx and by Manual quantitation are compared.

Experiment Conditions

HPLC:

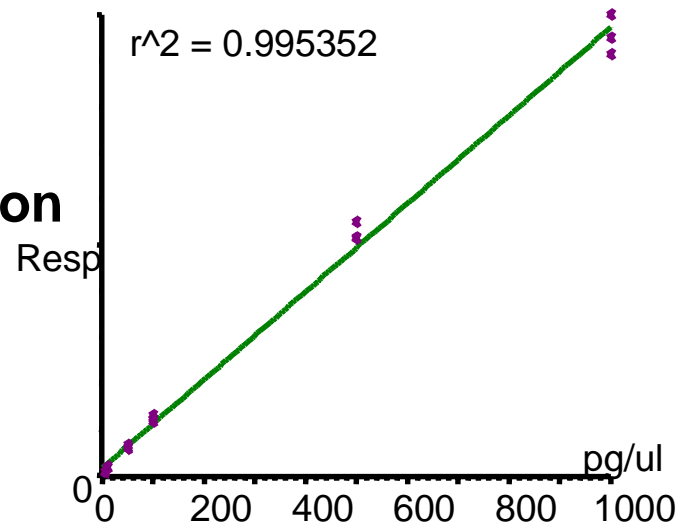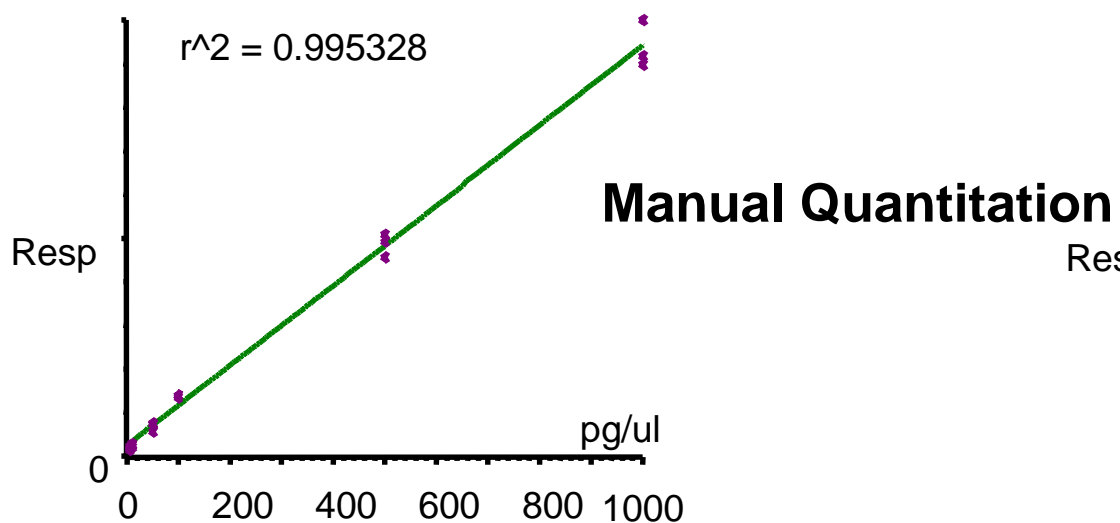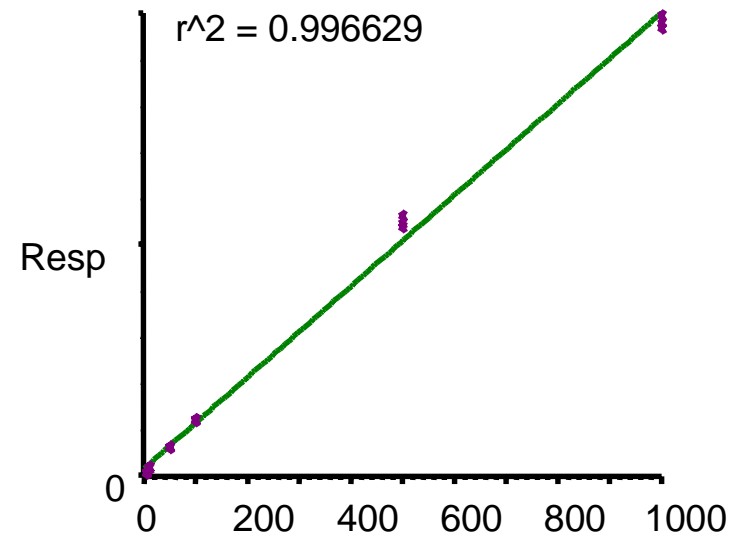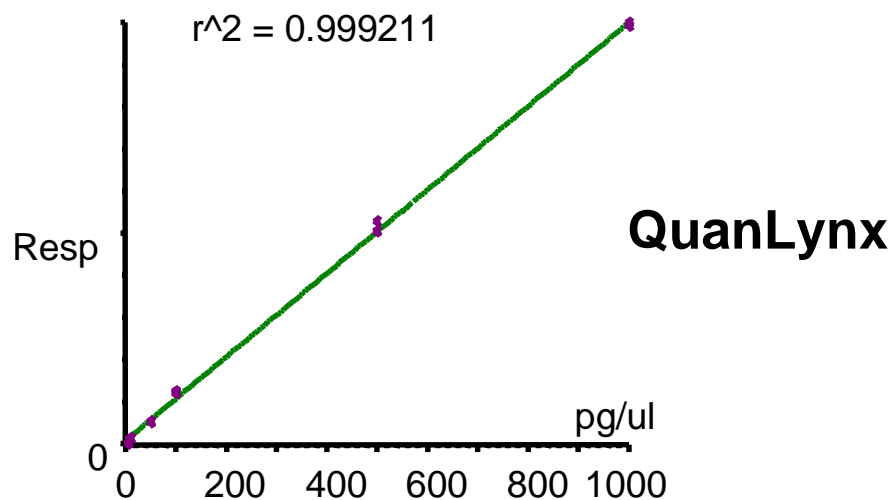|	
System:	Waters Alliance® 2690 with 996 PDA
Column:	Waters Symmetry® C_{18}, 3.5 µm, 2.1 x 50 mm
Mobile Phase:	MeOH/H_2O 30/70 Isocratic
Injection Volume:	10 µL
Flow Rate:	0.2 mL/min.

MS:

System:	Waters ZMD
Ionization Mode:	ESI+

Results on the next two pages show that in addition to saving in time, QuanLynx also offers better precision and accuracy, compared to manual quantitation.

Comparison of Calibration Curves

Acetominophen

Caffeine

r^2 = 0.999211

Resp

pg/ul

0

0   200   400   600   800   1000

QuanLynx

r^2 = 0.996629

Resp

0

0   200   400   600   800   1000

r^2 = 0.995328

Resp

pg/ul

0

0   200   400   600   800   1000

Manual Quantitation

r^2 = 0.995352

Resp

pg/ul

0

0   200   400   600   800   1000

Comparison of Results

		Acetaminophen		Caffeine	
		QuanLynx	Manual	QuanLynx	Manual
Mean	L1	219.1	220.7	227.7	229.7
(pg/μL)	L2	73.4	82.1	78.2	80.6
SD	L1	1.15	9.70	1.20	10.3
	L2	3.65	5.44	2.68	4.71
%CV	L1	0.53	4.40	0.53	4.48
	L2	4.97	6.63	3.42	5.85
% Error	L1	9.55	10.4	13.8	14.8
	L2	-2.13	9.47	4.26	7.46
LOD (pg/μL)		10.7	9.21	6.84	14.4
LOQ (pg/μL)		35.6	30.7	22.8	48.0
r^2		0.999	0.995	0.997	0.995