Appendix II  Calibration report DAD

Identification
Mass Range: 373.0 - 374.0
Filter: + c Full ms [ 350.00 - 475.00]
Expected RT (min): 3.75
Search window (sec): 60.00
View width (sec): 2.00
RT reference no
Identify by: Nearest RT
Min Peak Height(S/N): 3.00

Calibration
Component Type: Target Component
Number of Cal. Levels: 7
Number of QC Levels: 0
Internal Standard: VERAPAMIL
Response: Area
Curve: Linear
Origin: Include
Weighing: Equal
Calibration Units: NG/ML

Peak Integration
Smoothing points: 15
S/N Threshold: 0.50
Valley Detection: Disabled
Constrain Peak Width: Disabled

Advanced Component Options
Rise Percentage: 10.0
Valley S/N: 2.0
Peak S/N Cutoff: 200.0
Baseline Noise Tol.(%): 10.0
Min Num Scans in Basline: 16
Num Background Scans: 2

DAD

Equation: Y = 0.0124823 + 0.00400075*X RA^2 = 0.9990

<table>
<thead>
<tr>
<th>Cal. Level</th>
<th>Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.125 NG/ML</td>
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<tr>
<td>2</td>
<td>6.250 NG/ML</td>
</tr>
<tr>
<td>3</td>
<td>12.500 NG/ML</td>
</tr>
<tr>
<td>4</td>
<td>25.000 NG/ML</td>
</tr>
<tr>
<td>5</td>
<td>50.000 NG/ML</td>
</tr>
<tr>
<td>6</td>
<td>100.000 NG/ML</td>
</tr>
<tr>
<td>7</td>
<td>200.000 NG/ML</td>
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</tbody>
</table>

Standard Results

<table>
<thead>
<tr>
<th>Sample</th>
<th>Area Ratio</th>
<th>Area</th>
<th>Area Ratio</th>
<th>ISTD</th>
<th>Specified Amount</th>
<th>Calculated Amount</th>
<th>%Diff</th>
<th>%RSD</th>
<th>Excluded</th>
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<tbody>
<tr>
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<td>MAY26A15</td>
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<td>1563956</td>
<td></td>
<td>35057548</td>
<td>6.250 NG/ML</td>
<td>8.031 NG/ML</td>
<td>28.49</td>
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<td>33757349</td>
<td>12.590 NG/ML</td>
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<td>MAY26A17</td>
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<td>33365259</td>
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<td>33148481</td>
<td>50.000 NG/ML</td>
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<td>MAY26A20</td>
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<td>25606430</td>
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<td>-0.71</td>
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There are no QC results to report.
Calibration report Diltiazem HCl

Identification
Mass Range: 415.0 - 416.0
Filter: + c Full ms [350.00 - 475.00]
Expected RT (min): 5.26
Search window (sec): 60.00
View width (sec): 2.00
RT reference: no
Identify by: Nearest RT
Min Peak Height (S/N): 3.00

Calibration
Component Type: Target Component
Number of Cal. Levels: 7
Number of QC Levels: 0
Internal Standard: VERAPAMIL
Response: Area
Curve: Linear
Origin: Include
Weighing: Equal
Calibration Units: NG/ML

Peak Integration
Smoothing points: 15
S/N Threshold: 0.50
Valley Detection: Disabled
Constrain Peak Width: Disabled

Advanced Component Options
Rise Percentage: 10.0
Valley S/N: 2.0
Peak S/N Cutoff: 200.0
Baseline Noise Tol. (%): 10.0
Min Num Scans in Baseline: 16
Num Background Scans: 2

Cal. Level | Amount
---|---
1 | 3.125 NG/ML
2 | 6.250 NG/ML
3 | 12.500 NG/ML
4 | 25.000 NG/ML
5 | 50.000 NG/ML
6 | 100.000 NG/ML
7 | 200.000 NG/ML

Standard Results
<table>
<thead>
<tr>
<th>Sample</th>
<th>Area</th>
<th>Area Ratio</th>
<th>Area ISTD</th>
<th>Specified Amount</th>
<th>Calculated Amount</th>
<th>%Diff</th>
<th>%RSD</th>
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<tbody>
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<td>35055748</td>
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<tr>
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There are no QC results to report.
Calibration report Verapamil HCl

Identification
Mass Range: 455.0 - 456.0
Filler: + c Full m/z [350.00 - 475.00]
Expected RT (min): 6.49
Search window (sec): 60.00
View width (sec): 2.00
RT reference: yes
Identify by: Nearest RT
Min Peak Height (S/N): 3.00

Calibration
Component Type: Internal Standard
Number of Cal. Levels: i
Number of QC Levels: 0
Internal Standard:
Response: Area
Curve: Average RF
Origin: Ignore
Weighting: Equal
Calibration Units: NG/ML

Peak Integration
Smoothing points: 15
S/N Threshold: 0.50
Valley Detection: Disabled
Constrain Peak Width: Disabled

Advanced Component Options
Rise Percentage: 10.0
Valley S/N: 2.0
Peak S/N Cutoff: 200.0
Baseline Noise Tol. (%): 10.0
Min Num Scans in Basline: 16
Num Background Scans: 2

VERAPAMIL

Equation: Average Response Factor = 23471.6 %RSD = 5.3

Standard Results

<table>
<thead>
<tr>
<th>Sample</th>
<th>Area</th>
<th>Specified Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAY26A14</td>
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<td>MAY26A15</td>
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<td>1500.000 NG</td>
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<td>33365259</td>
<td>1500.000 NG</td>
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<tr>
<td>MAY26A20</td>
<td>31731356</td>
<td>1500.000 NG</td>
</tr>
</tbody>
</table>

There are no QC results to report.
Sample Name: SPiked PLSMA SAMPLE
Sample ID: 10
Acquisition Date: 27/05/99 03:42:20
Operator: C:\LCQ\data\DILTIAZEM
Data Path: 25NG/ML
Comments: Run Time (min): 7.24
Vial: 10
Samp Vol: 0.00
ISTD Amt: 0.000
Exp Method: C:\LCQ\Methods\DILTIAZEM
Proc Method:

Sample Type: Unknown
Cal. Level:
Software Revision: 1.2
Inj Vol (uL): 0.00
Samp Wt: 0.00
Dil. Factor: 1.00

<table>
<thead>
<tr>
<th>Name</th>
<th>Area</th>
<th>Area Ratio</th>
<th>Area Specified</th>
<th>Calculated Amount</th>
<th>%Diff</th>
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<tbody>
<tr>
<td>DAD</td>
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<td>N/A</td>
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<td>BB</td>
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