# Results – Detailed Report

# -

Report Name:

Generated by

# Data Files

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  | | --- | --- | | **MS Sample** | | | Data File: |  | | Folder: |  | | Injection: |  | | |  |  | | --- | --- | | **MS Control #1** | | | Data File: |  | | Folder: |  | | Injection: |  | |
| |  |  | | --- | --- | | **MS Control #2** | | | Data File: |  | | Folder: |  | | Injection: |  | | |  |  | | --- | --- | | **MS Control #3** | | | Data File: |  | | Folder: |  | | Injection: |  | |
| |  |  | | --- | --- | | **MS Control #4** | | | Data File: |  | | Folder: |  | | Injection: |  | | |  |  | | --- | --- | | **MS Control #5** | | | Data File: |  | | Folder: |  | | Injection: |  | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| |  |  | | --- | --- | | **Analog Sample** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | | |  |  | | --- | --- | | **Analog Control #1** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | |
| |  |  | | --- | --- | | **Analog Control #2** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | | |  |  | | --- | --- | | **Analog Control #3** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | |
| |  |  | | --- | --- | | **Analog Control #4** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | | |  |  | | --- | --- | | **Analog Control #5** | | | Data File: |  | | Folder: |  | | Injection: |  | | Channel: |  | |

Dedicated MS/MS Data

**Potential Metabolites**

None

| **Report** | **Peak ID** | **Name** | **Formula** | **Assigned** | **Neutral Mass** | **Average Mass** | ***m/z*** | **Charge** | **Peak Index** | **ppm** | **R.T. (min)** | **Peak Area** | **% Area** | **% Score** | **Peak Area – Analog** | **% Area – Analog** | **R.T. (min) - Analog** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

**Grouped Metabolites**

None

| **Group ID** | **Name** | **Formula** | **Neutral Mass** | **Charge** | **ppm** | **R.T. (min)** | **Peak Area** | **% Area** | **% Score** | **Count** | **Peak Area – Analog** | **% Area – Analog** | **R.T. (min) - Analog** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |

## Metabolite Chromatogram

## 

## Isotope Pattern Chromatogram



Analog Chromatogram



# Metabolite Details

None

|  |  |
| --- | --- |
| *-* | |
| Formula: |  |
| RT: | min |
| Neutral Mass: |  |
| Average Mass: |  |
| *m/z*: |  |
| ppm: |  |
| Score: | % |

## Metabolite XIC



## Product Ions Chromatogram



Fragment Isotope Pattern Chromatagram



## MS Spectrum MS/MS Spectrum



### Common Product Ions (m/z):

# Processing Parameters

## Compound Information

|  |  |
| --- | --- |
| Compound name: |  |
| Chemical formula: |  |
| Isotopic enrichment: |  |
| Ion Type: |  |
| Charge State: | From: To: |
| *m/z*: |  |

## Oligonucleotide Sequence

|  |  |
| --- | --- |
| Custom Amino Acids: |  |
| Custom Modifications: |  |

## Peak Finding Strategy

The following algorithms were used:

|  |  |
| --- | --- |
| TOF MS   * Predicted metabolites * Generic peak finding   + Mass Defect Filter   + Charge State Filter * Mass defect * Isotope pattern | TOF MSMS   * Characteristic product ions   + Find all specified ions   + Find at least ions * Characteristic neutral losses   + Find all specified losses   + Find at least losses * Internal Neutral Losses * Isotope Pattern (SWATH only) |

## Generic Parameters

### Biotransformations (Set used: )

| **Name** | **Mass Shift** | **Description** |
| --- | --- | --- |
|  |  |  |

### Chromatographic Data

*Chromatographic Peak*

Retention time window: to min

|  |  |  |
| --- | --- | --- |
|  | **MS Data** | **Analog Data** |
| XIC Width: Use mDaAutomatic | Wavelength (UV only): to nm  Time offset from MS: min |
| LC Peak Separation |  |  |
| Minimum peak width | sec. | sec. |
| Minimum peak intensity | |  |  | | --- | --- | | TOF MS: | cps | | TOF MSMS: | cps | |  |
| Use smoothing |  |  |
| Sample-control offset | min | min |
| Sample/control ratio | times greater than control signal |  |

### MS Parameters

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  | | --- | --- | | *m/z Tolerance* |  | | MS m/z Tolerance: |  | | Minimum MS peak intensity: |  | |  |  | | *Isotope Pattern Tolerances* |  | | Intensity tolerance: | % | | MS m/z tolerance: | mDa | | Minimum Score: | % | |  |  | | *Limits* |  | | Maximum number of unexpected metabolites: |  | | Mass range window (*m/z*): to | | | *Generic LC/MS Peak Finding*  Perform background subtraction:  *Chosen Adducts*   | **Ion Type** | **Charge** | **Radical** | | --- | --- | --- | |  |  |  | |

### MS/MS Parameters

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  | | --- | --- | | *MS/MS Finding* |  | | MS/MS m/z tolerance: | mDa | | Minimum MS/MS peak intensity: | cps | |  |  | | *MS/MS Isotope Finding* |  | | Intensity tolerance: | % | | MS/MS m/z tolerance: | mDa | |  |  | | *Source of Reference MS/MS Spectrum* |  | |  |  | | *MS/MS Spectrum* |  | | Use advanced MS/MS filter: |  | | Advanced MS/MS filter value: |  | | |  |  | | --- | --- | | *Similarity and Fragment Interpretation* |  | | MS/MS m/z tolerance: |  | | Minimum signal-to-noise ratio: |  | |  |  | |  |  | |  |  | |  |  | |  |  | |  |  | |

## Confirmation Scoring

| **Property** | **Maximum Score** |
| --- | --- |
| Mass defect |  |
| Isotope pattern |  |
| MS/MS |  |
| Mass accuracy |  |
| *Total confirmation score* |  |

## Compound-Specific Parameters

### Catabolites

Max. bonds to break:

Min. Nucleotides:

Include terminus n+1:

Include internal n-1:

The table of selected catabolites exceeds 200 rows. To view the table, please refer to the processing method via the software.

Catabolites Selected:

| **Residue Index** | **Name** | **Neutral Formula** | **Neutral Mass** |
| --- | --- | --- | --- |
|  |  |  |  |

### Isotope Pattern

****

Isotopes

| ***m/z*** | **Intensity (%)** | **Mass Offset** |
| --- | --- | --- |
|  |  |  |

|  |
| --- |
|  |
| Cutoff intensity for each isotope for metabolite XICs: % |

Isotope Enrichment

| **Element** | **Enrichment (%)** |
| --- | --- |
|  |  |

### Product Ions and Neutral Losses

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Reference MS/MS spectrum: | *Filters*   |  |  |  | | --- | --- | --- | |  | **From** | **To** | | **m/z** |  |  | | **Charge State** |  |  |   Show only product ions above: %  Mass accuracy within: mDa |
|  |
| Add product ions, neutral losses from Phase II metabolites: |

| **m/z** | **Z** | **Fragment Ion** | **Sequence** | **Error** | **PI** |
| --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |