Analysis Summary

SUBMISSION DETAILS

Analyzed By	LCMSDATA-1
Analysis Date	02/27/2023
Script Version	Script_v5.0
Acquired Date	2/23/2023
Project Code	SolidBio MicroDyst
Instrument	Q2
Project Leader	Shubha
Processed By	Marcy Matthews
Notebook Code	MDM000428

FILES

MIDA Database(s):

D:\MassHunter\Data\MIDA-f\DATA PROCESSING SCRIPT\SCRIPT 2\2023-02-24_LJZ230218_Insulin_Qv_DB.csv

Compound Reports:

D:\MassHunter\Data\MIDA-f\DATA PROCESSING SCRIPT\SCRIPT 2\0002H_LJZ230218_Insulin_D05ug_IP_MS_rep1Q2-27Pxxx_CompoundReportB06rev01.xls

D:\MassHunter\Data\MIDA-f\DATA PROCESSING SCRIPT\SCRIPT 2\0001H_LJZ230218_Insulin_D2ug_IP_MS_rep1Q2-27Pxxx_CompoundReportB06rev01.xls

ANALYSIS DETAILS

Sample	Body Water	Min. MIDA for EMx
05ug_IP-0002H	1.0%	0.025
2ug_IP-0001H	1.0%	0.025

PARAMETERS

Parameter	Value
Rt Difference Filter	1.7
Total Abundance Filter	30000
RMS Error Filter	0.015
DB Score Filter	1.0
Base Peak Abundance Filter	30000

% Theo EM0 Upper Limit	1.4
% Theo EM0 Lower Limit	-0.4
Peptide Std Dev Filter	2.0
Isotopomer Std Dev Filter	0.2
Use All Isotopomers for f	No
Combine peptides	Yes
Min. MIDA for EMx	human25
SILAC Masses	4
Sample:SILAC Ratio Upper Limit	20.0
Sample:SILAC Ratio Upper Limit	0.02
SILAC Std Dev Filter	2.0
Fractionated Samples	Yes
Saturation Limit	10000000.0
Offset Correction Slope	[1.0]
Offset Correction Intercept	[0.0]