

timstTOF Visualization App Tutorial

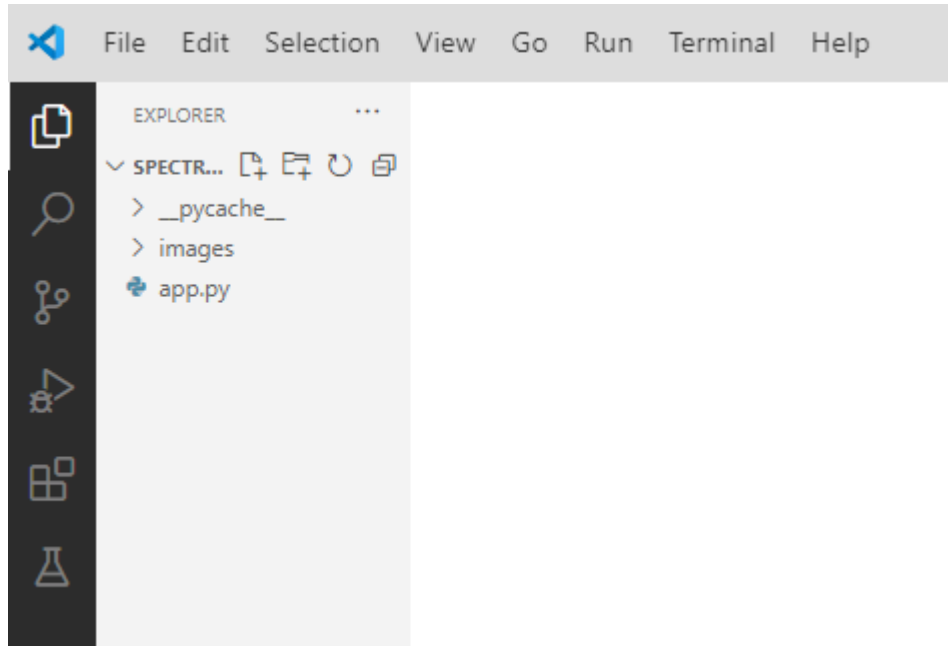
Software Installation

Necessary Software

- Install Python or Anaconda
 - <https://www.python.org/downloads/>
 - <https://www.anaconda.com/download>
- Install Visual Studio Code
 - <https://code.visualstudio.com/>

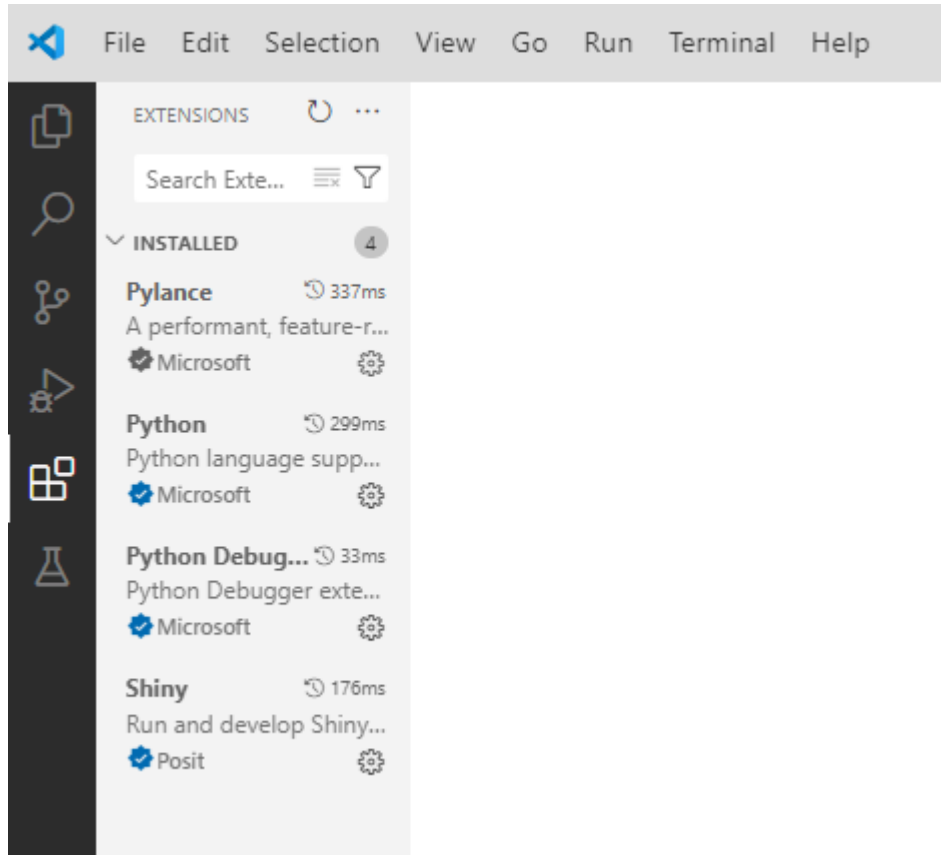
Getting Started

Getting started in Visual Studio Code



- Set the directory containing the `app.py` file as the working directory
- Open the `app.py` file by double-clicking on the file

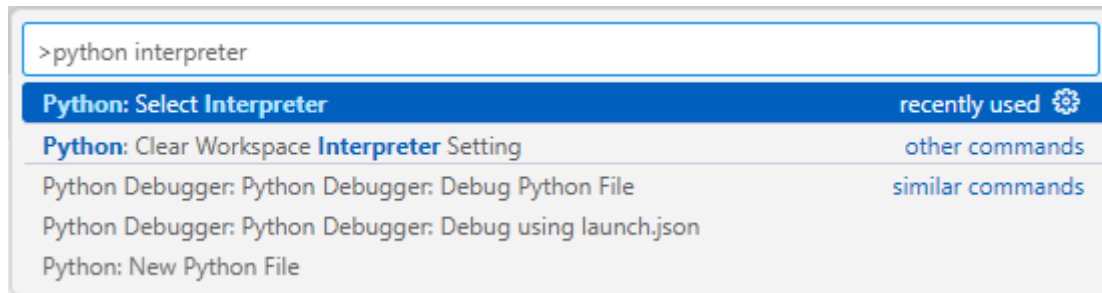
Install necessary extensions



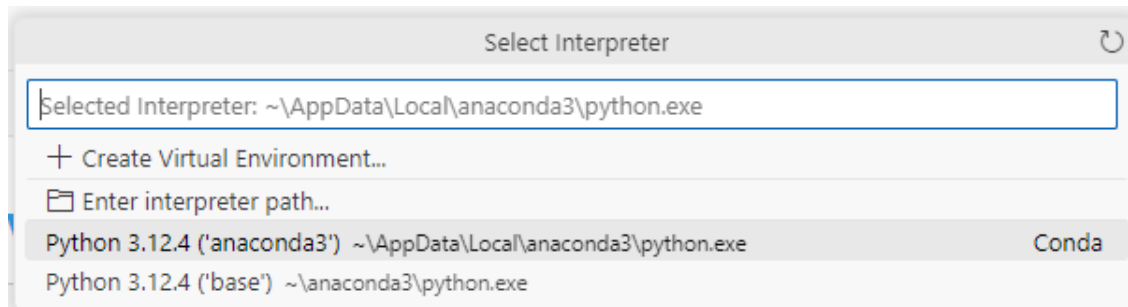
- Install Python and Shiny extensions using the Extensions:Marketplace tab

Set Python interpreter to current installation of Python/Anaconda

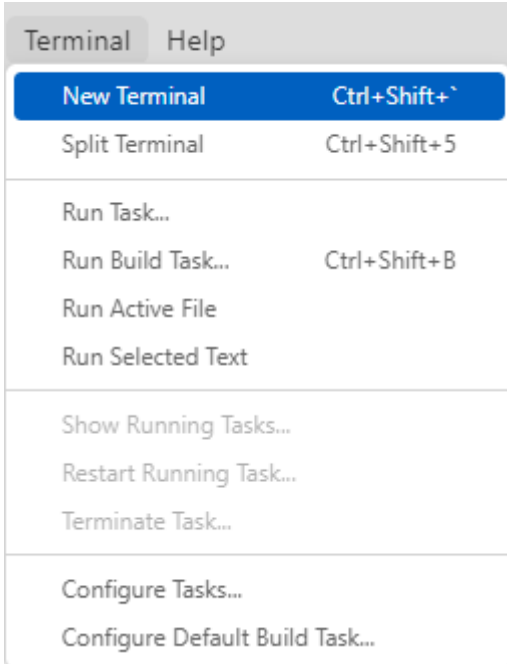
- Ctrl+Shift+P and search Python interpreter



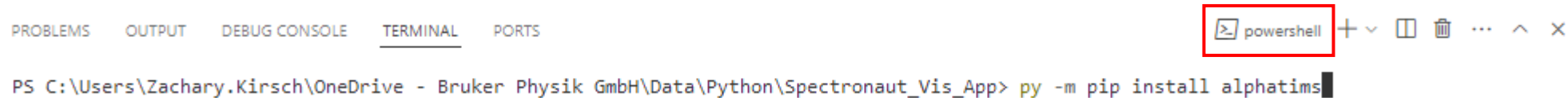
- Select current Python installation



Installing necessary Python libraries



- Open a new powershell terminal and use pip to install
 - alphasims, colorcet, faicons, hvplot, matplotlib-venn, scikit-learn, shiny, shinyswatch, and upsetplot



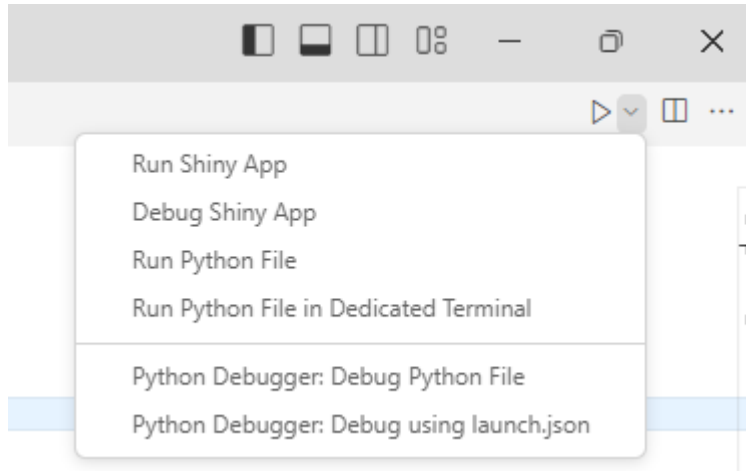
- Replace the part underlined in red with the library to install

Installing necessary Python libraries

```
# =====  
# Library Imports  
# =====  
#region  
from shiny import App, Inputs, Outputs, Session, reactive, render, ui, module  
from shinyswatch import theme  
#https://rstudio.github.io/shinythemes/  
from shiny.types import ImgData  
import alphasims.braker as atb  
import alphasims.plotting as atp  
from collections import OrderedDict  
from datetime import date  
from faicons import icon_svg  
#https://fontawesome.com/search?o=r&m=free  
import io  
import itertools  
from itertools import groupby  
import math  
import matplotlib  
import matplotlib.pyplot as plt  
from matplotlib.pyplot import cm  
import matplotlib.colors as mcolors  
from matplotlib.patches import Rectangle  
from matplotlib_venn import venn2, venn2_circles, venn3, venn3_circles  
import numpy as np  
import os  
import pandas as pd  
import pathlib  
import re  
from scipy.stats import norm  
import seaborn as sns  
from sklearn.decomposition import PCA  
from sklearn.pipeline import Pipeline  
from sklearn.preprocessing import StandardScaler  
from tkinter import *  
from upsetplot import *
```

- If any libraries are underlined in yellow, it means they aren't recognized by the IDE
- If you've already installed a library and it's not being recognized, either restart Visual Studio Code or make sure the correct Python interpreter is selected

Starting the Shiny app



- With the extensions and libraries installed, you should be able to run the app with Visual Studio Code recognizing it as a Shiny app

Using the App

File import

timsTOF Proteomics Data Visualization

File Import

Settings

ID Counts

Metrics

PTMs

PCA

Heatmaps

Mixed Proteome

PRM

Dilution Series

Raw Data

Export Tables

Upload Search Report

When uploading a new file after one has already been uploaded, click the apply changes button below

Upload search report:

Browse...

No file selected

Search software:

☒ Spectronaut

☐ DIA-NN

☐ FragPipe

☐ tims-DIANN (BPS)

☐ Spectronaut Library

Spectronaut: Make sure to use Shiny report format when exporting search results

Update from Metadata Table

☐ Update 'R.Condition' and 'R.Replicate' columns

☐ Update 'Concentration' column

☐ Remove/resort samples

Apply changes to search report /
reinitialize search report

Upload search
report (.tsv)

Select search
software

Updating result metadata

This is necessary when condition names are not native to the search report or if changes are needed for the order, presence, or names of samples

If changes are made to the metadata table, use these switches to specify the change and then click the “apply changes” button

Update from Metadata Table

- ☐ Update 'R.Condition' and 'R.Replicate' columns
- ☐ Update 'Concentration' column
- ☐ Remove/resort samples

Apply changes to search report /
reinitialize search report

Metadata Table

-Double click on any cell to update its contents

-To remove samples, add an 'x' to the 'remove' column. To reorder samples, number them in the order you want them to appear in the 'order' column

R.FileName	R.Condition	R.Replicate	order	remove	Concentration
20240613_1-1-3_K562-Yeast_EColi_10ng_OFF_1_Slot1-50_1_3848	1-1-3_10ng	1			
20240613_1-1-3_K562-Yeast_EColi_10ng_OFF_2_Slot1-50_1_3849	1-1-3_10ng	2			
20240613_1-1-3_K562-Yeast_EColi_10ng_OFF_3_Slot1-50_1_3850	1-1-3_10ng	3			
20240613_1-2-2_K562-Yeast_EColi_10ng_OFF_1_Slot1-48_1_3844	1-2-2_10ng	1			
20240613_1-2-2_K562-Yeast_EColi_10ng_OFF_2_Slot1-48_1_3845	1-2-2_10ng	2			
20240613_1-2-2_K562-Yeast_EColi_10ng_OFF_3_Slot1-48_1_3846	1-2-2_10ng	3			

R.FileName: (required, auto-filled)
Will be pre-filled from the report file.

R.Condition: (required)
Experimental condition names. If Condition was specified in Spectronaut, it will be added here. Otherwise, it needs to be filled out.

R.Replicate: (required)
Replicate numbers. Should be unique in each condition. . If Replicate was specified in Spectronaut, it will be added here. Otherwise, it needs to be filled out.

Order: (optional)
Specify the numerical order you want the runs shown in.

Remove: (optional)
Adding an 'x' means that you want to remove the run from the subsequent figures.

Concentration: (optional)
Should be the same value for each condition.

General Navigation

timsTOF Proteomics Data Visualization

Main navigation pane organized by the types of information to be plotted

- File Import
- Settings
- ID Counts**
- Metrics
- PTMs
- PCA
- Heatmaps
- Mixed Proteome
- PRM
- Dilution Series
- Raw Data
- Export Tables

Counts per Condition Average Counts CV Plots IDs with CV Cutoff UpSet Plot

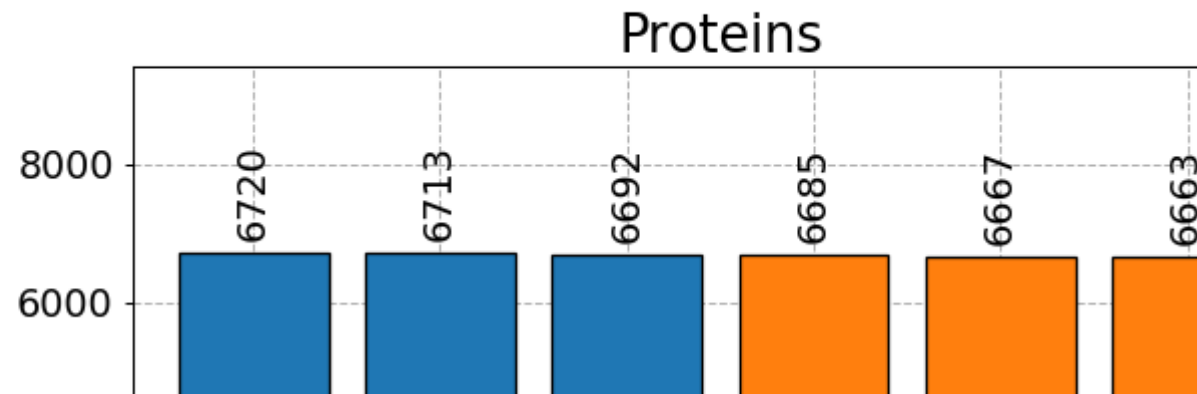
Plot width: 500 1,500 2,000

Plot height: 500 1,000 2,000

Choose what metric to plot:

all

Sub-menu navigation organized by the different available plots that can be generated



Coloring Options

File Import

Settings

ID Counts

Metrics

PTMs

PCA

Heatmaps

Mixed Proteome

PRM

Dilution Series

Raw Data

Export Tables

Color Settings

Column Check

Control Panel

Choose coloring option for output plots:
☐ Pick for me (rainbow)
☒ Pick for me (matplotlib tableau)
☐ Custom

Input color names from the tables to the right, one per line:

Note: replicates of the same condition will have the same color

Run

Color per run

Matplotlib Tableau Colors:

tab:blue

tab:orange

tab:green

tab:red

tab:purple

tab:brown

tab:pink

tab:gray

tab:olive

tab:cyan

CSS Colors:

black
dimgray
gray
darkgray
silver
lightgray
lightgrey
gainsboro
whitesmoke
white
snow
rosybrown
lightcoral
indianred
brown
firebrick
maroon
darkred
red
mistyrose
salmon
tomato
darksalmon
coral
orangered
lightsalmon
sienna
seashell
chocolate
saddlebrown
sandybrown
peachpuff
peru
linen

bisque
darkorange
burlywood
antiquewhite
tan
navajowhite
blanchedalmond
papayawhip
moccasin
orange
wheat
oldlace
floralwhite
darkgoldenrod
goldenrod
cornsilk
gold
lemonchiffon
khaki
palegoldenrod
darkkhaki
ivory
beige
lightyellow
lightgoldenrodyellow
olive
yellow
olivedrab
yellowgreen
darkolivegreen
greenyellow
chartreuse
lawngreen
honeydew
darkseagreen
palegreen
lightgreen

forestgreen
limegreen
darkgreen
green
lime
seagreen
mediumseagreen
springgreen
mintcream
mediumspringgreen
mediumaquamarine
aquamarine
turquoise
lightseagreen
mediumturquoise
azure
lightcyan
paleturquoise
darkslategray
darkslategrey
teal
darkcyan
aqua
cyan
darkturquoise
cadetblue
powderblue
lightblue
deepskyblue
skyblue
lightskyblue
steelblue
aliceblue
dodgerblue
lightslategray
lightslategrey
slategray

slategrey
lightsteelblue
cornflowerblue
royalblue
ghostwhite
lavender
midnightblue
navy
darkblue
mediumblue
blue
slateblue
darkslateblue
mediumslateblue
mediumpurple
rebeccapurple
blueviolet
indigo
darkorchid
darkviolet
mediumorchid
thistle
plum
violet
purple
darkmagenta
fuchsia
magenta
orchid
mediumvioletred
deeppink
hotpink
lavenderblush
palevioletred
crimson
pink
lightpink

- Multiple color setting options for colors to be used in plotting
- Can mix and match from those listed when using custom colors
- If there's only one sample condition, the "Pick for me" sections pick a color at random

Coloring Options

Color Settings Column Check Control Panel


Choose coloring option for output plots:

- ☐ Pick for me (rainbow)
- ☒ Pick for me (matplotlib tableau)
- ☐ Custom

Input color names from the tables to the right, one per line:

Note: replicates of the same condition will have the same color

Run	Color per run
1-1-3_10ng	
1-2-2_10ng	



Colors by condition according to the matplotlib tableau colors

Color Settings Column Check Control Panel


Choose coloring option for output plots:

- ☒ Pick for me (rainbow)
- ☐ Pick for me (matplotlib tableau)
- ☐ Custom

Input color names from the tables to the right, one per line:

Note: replicates of the same condition will have the same color

Run	Color per run
1-1-3_10ng	
1-2-2_10ng	



Colors by condition according to a rainbow color series split based on the number of conditions

Color Settings Column Check Control Panel

Choose coloring option for output plots:

- ☐ Pick for me (rainbow)
- ☐ Pick for me (matplotlib tableau)
- ☒ Custom

Input color names from the tables to the right, one per line:

Note: replicates of the same condition will have the same color

Run	Color per run
1-1-3_10ng	
1-2-2_10ng	



Colors by condition according to specified colors in the text area

File Import Formats

Uploading DIA windows to overlay

File Import

Settings

ID Counts

Metrics

PTMs

PCA

Heatmaps

RT, m/z, IM Heatmaps

Charge/PTM Precursor Heatmap

• CSV Format:

Upload DIA windows as a .csv:

Browse...

No file selected

Choose DIA windows to overlay:

☐ Imported DIA windows


☐ Lubeck DIA


☐ Phospho DIA


☒ None


	A	B	C	D	E	F	G
1	#MS Type	Cycle Id	Start IM [1/K0]	End IM [1/K0]	Start Mass [m/z]	End Mass [m/z]	CE [eV]
2	MS1	0	-	-	-	-	-
3	PASEF	1	0.965	1.12	725.13	736.24	-
4	PASEF	1	0.805	0.965	559.8	567.5	-
5	PASEF	1	0.6	0.805	350.68	382.04	-
6	PASEF	2	0.977	1.15	746.34	758.38	-
7	PASEF	2	0.87	0.977	574.21	582.01	-
8	PASEF	2	0.6	0.87	412.39	425.4	-
9	PASEF	3	0.986	1.19	769.41	782.64	-
10	PASEF	3	0.89	0.986	588.81	596.81	-
11	PASEF	3	0.6	0.89	437.42	447.23	-
12	PASEF	4	0.995	1.23	794.87	808.65	-
13	PASEF	4	0.9	0.995	603.8	612.07	-
14	PASEF	4	0.6	0.9	456.05	464.9	-


Uploading peptide list to track


 File Import


 Settings


 ID Counts


 Metrics


 PTMs

 PCA

 Heatmaps

 Mixed Proteome

 PRM

 Dilution Series

PRM List

PRM Table

PRM Peptide

Upload Peptide List:

Browse...

No file selected

• CSV Format:

	A	B
1	PG.ProteinGroups	EG.ModifiedPeptide
2	P00359	_TASGNIIPSSTGAAK_
3	P0A853	_KYDIPVVMDSAR_
4	P00330	_[Acetyl (Protein N-term)]SIPETQK_
5	P68104;Q5VTE0	_IGGIGTVPVGR_
6	P00924	_SIVPSGASTGVHEALEM[Oxidation (M)]R_
7	P00549	_GVFPFVFEK_
8	P00924	_IEEELGDNAVFAGENFHHGDK_

Referencing raw data files

- File Import
- Settings
- ID Counts
- Metrics
- PTMs
- PCA
- Heatmaps
- Mixed Proteome
- PRM
- Dilution Series
- Raw Data
- Export Tables

Multi-File Import

TIC Plot

BPC Plot

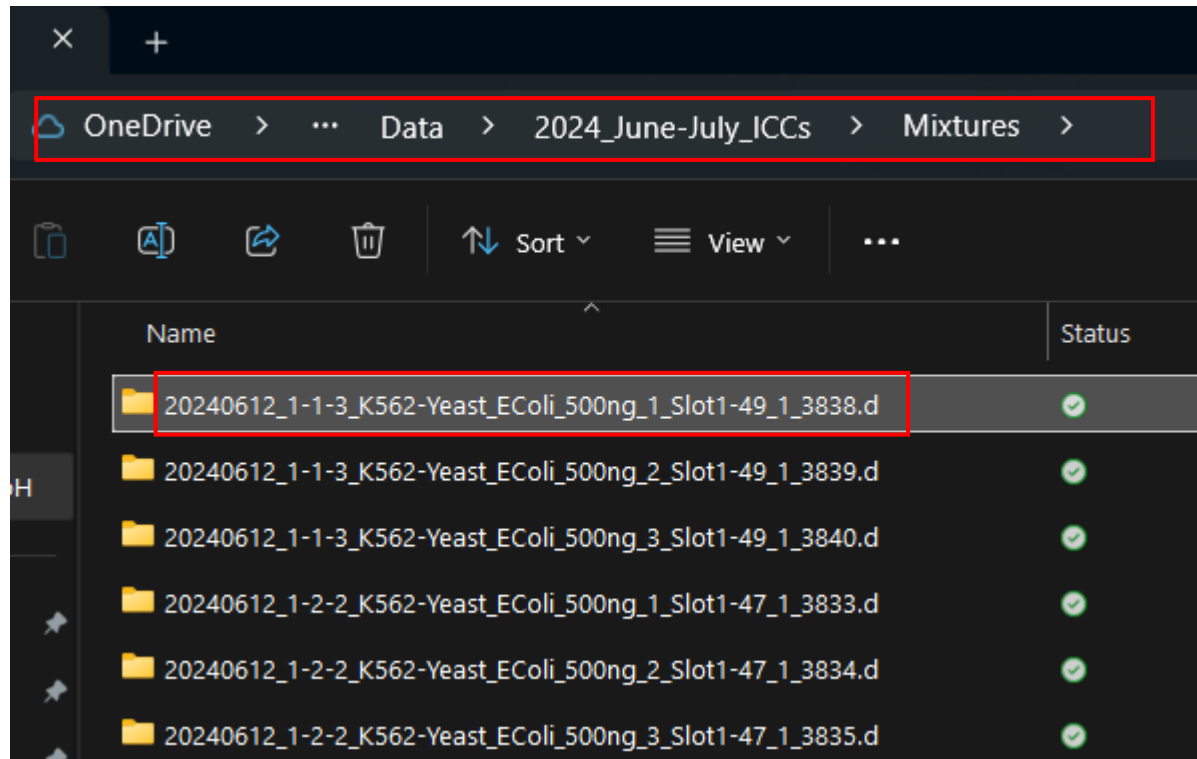
Accumulation Time

EIC Plot

EIM Plot

Paste the path for each .d file you want to upload (note: do not leave whitespace at the end):

ex - C:\Users\Data\K562_500ng_1_Slot1-49_1_3838.d



Name	Status
20240612_1-1-3_K562-Yeast_EColi_500ng_1_Slot1-49_1_3838.d	✓
20240612_1-1-3_K562-Yeast_EColi_500ng_2_Slot1-49_1_3839.d	✓
20240612_1-1-3_K562-Yeast_EColi_500ng_3_Slot1-49_1_3840.d	✓
20240612_1-2-2_K562-Yeast_EColi_500ng_1_Slot1-47_1_3833.d	✓
20240612_1-2-2_K562-Yeast_EColi_500ng_2_Slot1-47_1_3834.d	✓
20240612_1-2-2_K562-Yeast_EColi_500ng_3_Slot1-47_1_3835.d	✓

- Paste the full path of the .d folder for each file you want to plot into the text area
- Should look like the example text shown
- Avoid spaces, use a new line for each file