

Metabolomics Workbench NMDR study submission tutorial

Version 16 (Feb,2024)

Updates from version 15

New requirement for 'Sample source' column in study-design section

National Metabolomics Data Repository Online Data Submission Tutorial

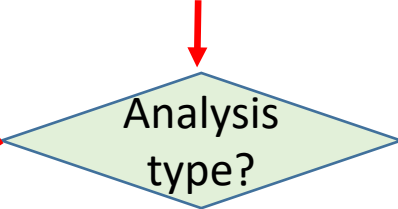
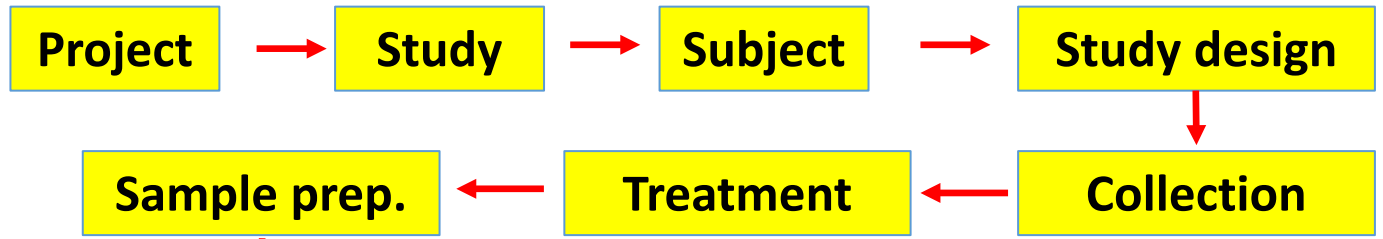
Before you start:

- ❖ Have a summary of the study ready (a paragraph describing the goal and design of the experiment for the benefit of the general research community- a publication abstract or equivalent would be ideal).
- ❖ Have a study design table ready with sample names and experimental variables in separate columns. Subject information and other measurements may also included.
- ❖ Make sure that **sample names** in submitted results tables exactly match those in the study design table. Otherwise you won't be able to proceed with the submission.
- ❖ Collect all relevant protocols and raw data for upload to the WorkBench. Protocol/methods files may be uploaded at appropriate points during the online metadata submission process whereas (large) raw data is uploaded during the final registration step (Step 7).

Online data/metadata submission flowchart

Project Information	Project ID	Project Name	Project Description
Study Information	Study ID	Study Name	Study Description
Subject Information	Subject ID	Subject Name	Subject Description
Study Design Information	Study Design ID	Study Design Name	Study Design Description
Collection Information	Collection ID	Collection Name	Collection Description
Treatment Information	Treatment ID	Treatment Name	Treatment Description
Sample Preparation Information	Sample Prep ID	Sample Prep Name	Sample Prep Description
Analysis Information	Analysis ID	Analysis Name	Analysis Description

Online GUI's

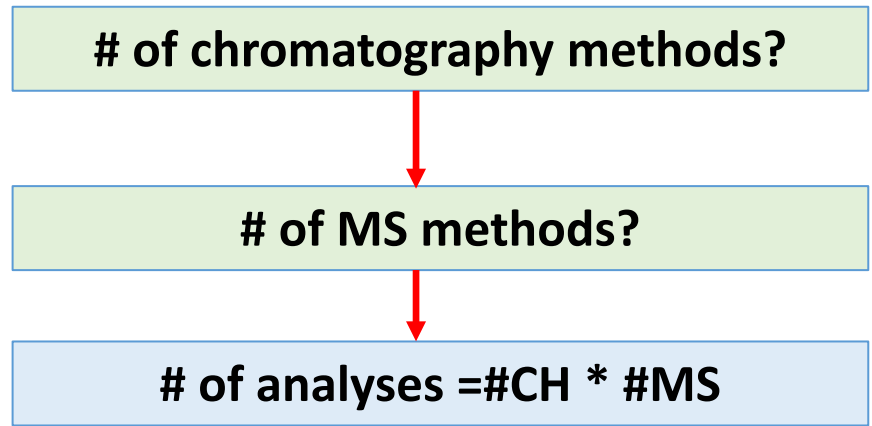


NMR

```

        mwTab file
        =====
        ANALYSIS_METADATA_TABLE
        =====
        ANALYSIS_ID      ANALYSIS_NAME      ANALYSIS_DESCRIPTION
        =====
        ANALYSIS_001    NMR_123            NMR Analysis 1
        ANALYSIS_002    NMR_456            NMR Analysis 2
        ANALYSIS_003    NMR_789            NMR Analysis 3
        ANALYSIS_004    NMR_012            NMR Analysis 4
        ANALYSIS_005    NMR_345            NMR Analysis 5
        ANALYSIS_006    NMR_678            NMR Analysis 6
        ANALYSIS_007    NMR_901            NMR Analysis 7
        ANALYSIS_008    NMR_234            NMR Analysis 8
        ANALYSIS_009    NMR_567            NMR Analysis 9
        ANALYSIS_010    NMR_890            NMR Analysis 10
        =====
        ANALYSIS_METADATA_TABLE
        =====
      
```

mwTab file



Chromatography

MS

Load binned NMR data table

Load results and metabolite metadata for each analysis

Online Data Submission

<https://www.metabolomicsworkbench.org/data/DRCCDataDeposit.php>

Register/login



Upload/manage studies

Upload and Manage Experimental Data and Metadata



Requirements for depositing data via the Metabolomics Workbench:

*****Please read the [NMDR study submission tutorial](#) first!*****

1. **Register** (you will then be authorized to submit studies)
2. **Log in**.
3. View the list of exemplary studies (below) for examples of best practices for study submissions.
4. The use of the common metabolite names in the [RefMet](#) database is *strongly encouraged* in order to be able to compare and contrast metabolite data across different experiments and studies. For your convenience an [online tool](#) is available to map your current metabolite identifications (where possible) to the corresponding RefMet names.
5. Use the **'New Data Upload'** tab to (a) register your study, (b) submit metadata and processed data and (c) upload raw data/supplementary material. Please indicate the date when the study may be made available to the public.
6. **E-mail us for additional assistance** (help@metabolomicsworkbench.org), if needed.

(a): Complete the registration form

Use separate submissions if your study contains both MS and NMR data

Specify the embargo date if applicable

Please tell us about the data you plan to upload. (* = required)

* mwTab file name	<input type="text" value="efahy_20210210_135208_mwtab.txt"/>	(Automatically assigned name)
* Name of archive file to be uploaded	<input type="text" value="EF-_45.zip"/>	(e.g. MyData.zip, MyData.7z or MyData.gz)
* Data type being submitted	<input type="text" value="MS"/>	(Use separate submissions for studies containing both MS and NMR data)
* Protocol methods filename(s)	<input type="text" value="PR_SP45.pdf"/> <input type="text" value="PR_TR45.pdf"/>	
* MS/NMR instrument manufacturer	<input type="text" value="ABI-SCIEX"/>	
* MS/NMR instrument model	<input type="text" value="4000-QTRAP"/>	
* Binary data format	<input type="text" value=".wiff"/>	(e.g. .WIFF (ABI/Sciex), .RAW (Thermo) or .d (Agilent))
* Multi-part study	<input type="text" value="No"/>	(For multi-part studies, add additional information such as "Study part m of n" in comments field)
* Embargo	<input type="text" value="Yes"/>	(e.g. If Yes, then please specify date below)
Embargo until	<input type="text" value="2021-06-12"/>	(e.g. 1 year, 6 months, or YYYY-MM-DD)
Open source text formats	<input type="text" value=".mzML"/>	

(b): Begin the online submission of metadata and results

Upload and Manage Experimental Data and Metadata

Overview

New Data Upload

List Data Uploads

Test Upload

Tutorials

Please click **New online study submission** button to start a new study submission and enter metadata and results for your study with DataTrack ID **561** and mwTab file name **efahy_20160407_093705**. You will be prompted to upload an archive file after successful completion of the online submission process.

New online study submission



(b): Begin the online submission of metadata and results

Start a new study from scratch (most common option, especially for new users)

or


use the Metabolon template if the new submission is composed of Metabolon analyses

(If your samples were analyzed by Metabolon, you MUST use this option)

or


use an existing study as a template for a new submission

[Start/Edit Data Submission](#) | [Examples of study design and data layouts](#) | [Online Study Submission Tutorial\(pdf\)](#)



OR

Important!!! If your samples were analyzed by Metabolon, you MUST use this option



OR


use an existing submission(s) as a template for a new submission (below)

List of stored mwTab files for user efahy and group members (most recent first)

Click on 'Edit mwtab' link to resume editing that file

[Sort by mwtab file \(date\)](#) [Sort by modified date](#) [Sort by username](#)

No study title (efahy_20210203_104154) DATATRACK_ID:2447	
<input type="button" value="Use as template"/>	efahy_20210203_104154_mwtab.txt <input type="button" value="View mwTab"/> <input type="button" value="Edit mwTab"/>
Eoin Test 13 analyses (efahy_20210125_999999) DATATRACK_ID:2390	



(b): Begin the online submission of metadata and results

Entering **Metabolon** data

The Metabolon template on the Metabolomics Workbench has 4 different combined LC/MS methods:

Low pH polar (LC/MS Pos early)

Low pH Lipophilic (LC/MS Pos late)

High pH (LC/MS Neg)

HILIC (LC/MS Polar Neg)

which correspond to 4 different sections (respectively) of the Metabolon results spreadsheet file:

Pos Early

Pos Late

Neg

Polar

Split your Metabolon results (1st column is metabolite names, subsequent columns are sample data) and metabolite metadata (1st column is metabolite names, subsequent columns are Pubchem id, KEGG, SMILES, etc) into these 4 sections based on the “PLATFORM” heading in the spreadsheet. Enter these data in the 4 “Data(Results)” sections of the submission form. Specify units of measurement for the data that you’re providing (Unnormalized data, normalized-Imputed Data, log-transformed data, etc.)

PLATFORM in Metabolon results spreadsheet	Workbench template results section	LC/MS method	MS Polarity
Pos Early	1	Low pH polar (LC/MS Pos early)	POS
Pos Late	2	Low pH Lipophilic (LC/MS Pos late)	POS
Neg	3	High pH (LC/MS Neg)	NEG
Polar	4	HILIC (LC/MS Polar)	NEG

Project information

Items in pink are required fields

Personal information such as name, address, email is autopopulated in the form based on your login credentials (but you may edit these fields if not correct or appropriate)

Start/Edit Data Submission | Examples of study design and data layouts | Online Study Submission Tutorial(pc

Jump to: Project Study Subject Study Design Collection Treatment Sampleprep Chrom. MS Data(Results) Finalize

project information	Add project metadata Reset
Project Title:	LIPID MAPS Lipidomics studies
Project Type:	MS quantitative analysis
Project Summary:	Multi-center quantitative lipidomics studies on samples from human and murine sources (LIPIDMAPS) The National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) in collaboration with the National Institute of Standards (NIST) recently produced a human plasma standard reference material (SRM 1950) for metabolite analysis. The SRM was prepared by
Institute:	University of California, San Diego
Department:	Bioengineering
Laboratory:	
Last Name:	Fahy
First Name:	Eoin
Address:	9500 Gilman ,La Jolla, CA 92093
Email:	efahy@ucsd.edu
Phone:	(111)-222-3333
Funding Source:	
Project Comments:	
Publications:	Quehenberger, O. et al Lipidomics reveals a remarkable diversity of lipids in human plasma. J Lipid Res. !
contributors:	
project information	Add project metadata Reset

Display all protocol/methods files uploaded in previous submissions

If the item you want is not available in a pull-down menu, choose "Add new item" from the list and type in your own value

Study information

Subject type is mandatory and creates context-specific metadata items in subsequent sections

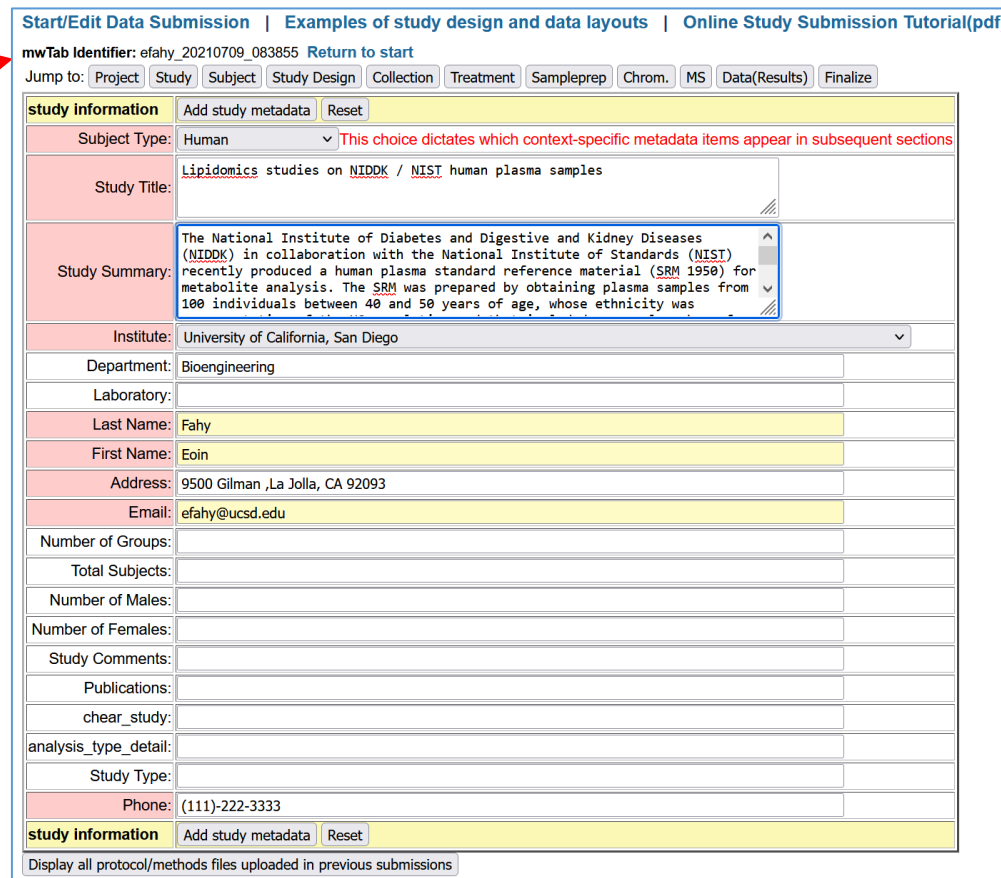
Study title should be unique (if you're submitting multiple studies)

Study summary is **very important** in order to describe the objectives of the experiment to the general public.

Ideally it should be a paragraph similar to an abstract in a publication

Personal information such as name, address, email is autopopulated in the form based on your login credentials (but you may edit these fields if not correct or appropriate)

This is your unique Submission identifier (contains your login name and date/time)



Start/Edit Data Submission | Examples of study design and data layouts | Online Study Submission Tutorial(pdf)

mwTab Identifier: efahy_20210709_083855 [Return to start](#)

Jump to: [Project](#) [Study](#) [Subject](#) [Study Design](#) [Collection](#) [Treatment](#) [Sampleprep](#) [Chrom.](#) [MS](#) [Data\(Results\)](#) [Finalize](#)

study information Add study metadata Reset

Subject Type: Human This choice dictates which context-specific metadata items appear in subsequent sections

Study Title: Lipidomics studies on NIDDK / NIST human plasma samples

Study Summary: The National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) in collaboration with the National Institute of Standards (NIST) recently produced a human plasma standard reference material (SRM 1950) for metabolite analysis. The SRM was prepared by obtaining plasma samples from 100 individuals between 40 and 50 years of age, whose ethnicity was

Institute: University of California, San Diego

Department: Bioengineering

Laboratory:

Last Name: Fahy

First Name: Eoin

Address: 9500 Gilman ,La Jolla, CA 92093

Email: efahy@ucsd.edu

Number of Groups:

Total Subjects:

Number of Males:

Number of Females:

Study Comments:

Publications:

chear_study:

analysis_type_detail:

Study Type:

Phone: (111)-222-3333

study information Add study metadata Reset

Display all protocol/methods files uploaded in previous submissions

Subject information

Choose subject species from pulldown menu or enter a new species (Latin name)

In cases where metabolites from multiple species are being assayed in the same experiment, separate the species names with a “/”

mwTab Identifier: msud_20180206_090350 [Return to start](#)

Jump to:

subject information	
	<input type="button" value="Add subject metadata"/> <input type="button" value="Reset"/>
Subject Type:	Cultured cells (entered in Study page)
Subject Species:	Mus musculus <input type="button" value="v"/> or (new): <input type="text"/>
Taxonomy ID:	10090
Genotype Strain:	<input type="text"/>
Age or Age Range:	<input type="text"/>
Weight or Weight Range:	<input type="text"/>
Height or Height Range:	<input type="text"/>
Gender:	Not applicable <input type="button" value="v"/>
Cell Biosource or Supplier:	<input type="text"/>
Cell Strain Details:	<input type="text"/>
Subject Comments:	<input type="text"/>
Cell Primary Immortalized:	<input type="text"/>
Cell Passage Number:	<input type="text"/>
Cell Counts:	<input type="text"/>

Study design information

This section contains essential study design information for the study which must include sample identifiers, sample source and at least one experimental variable(factor) in tabular format. An additional “subject_id” column relating the samples to a particular source (patient, animal, cell etc.) may also be included. Additional information unique to each sample (e.g. height, weight, BMI, age, assay measurement, etc.) may also be included but should NOT be designated as factors (Designate these as “Other” in the next step)

Include a column with raw data file names. Use multiple raw file columns if you have more than 1 raw file per sample (e.g. different LC methods, ion polarity)

Subject_ID	Sample_ID	Sample source	Genotype	Treatment	Batch	RAW_FILE_NAME
CA11	CA11W0	Liver	Wild-type	Control	B1a	SC_CA11W0.mzML
CA12	CA12W0	Liver	Wild-type	Control	B1a	SC_CA12W0.mzML
CA13	CA13W0	Liver	Wild-type	Control	B1a	SC_CA13W0.mzML
CA11	CA11W50	Liver	Wild-type	50uM	B1a	SC_CA11W50.mzML
CA12	CA12W50	Liver	Wild-type	50uM	B1a	SC_CA12W50.mzML
CA13	CA13W50	Liver	Wild-type	50uM	B1a	SC_CA13W50.mzML
CA14	CA14W0	Liver	Mutant	Control	B1a	SC_CA14W0.mzML
CA15	CA15W0	Liver	Mutant	Control	B1a	SC_CA15W0.mzML
CA16	CA16W0	Liver	Mutant	Control	B1a	SC_CA16W0.mzML
CA17	CA17W50	Liver	Mutant	50uM	B1a	SC_CA17W50.mzML
CA18	CA18W50	Liver	Mutant	50uM	B1a	SC_CA18W50.mzML
CA19	CA19W50	Liver	Mutant	50uM	B1a	SC_CA19W50.mzML

[Start/Edit Data Submission](#) | [Examples of study design and data layouts](#) | [Online Study Submission](#)

mwTab Identifier: efahy_20230814_171135 [Return to start](#)

IMPORTANT!!

Make sure that sample names in submitted results table(s) or file(s) exactly match those in the study design table.

Otherwise you won't be able to complete the submission.

(One needs to be able to relate experimental conditions in the study-design section via sample names in ALL submitted datasets)

Input **Study Design** information. Sample names, experimental factor(s), sample source and raw data file

Subject name and additional sample data are optional.

First row must contain headings. Data must be tab-delimited.

Subject_ID	Sample_ID	Sample source	Genotype	Treatment	Batch	RAW_FILE_NAME
CA11	CA11W0	Liver	Wild-type	Control	B1a	SC_CA11W0.mzML
CA12	CA12W0	Liver	Wild-type	Control	B1a	SC_CA12W0.mzML
CA13	CA13W0	Liver	Wild-type	Control	B1a	SC_CA13W0.mzML
CA11	CA11W50	Liver	Wild-type	50uM	B1a	SC_CA11W50.mzML
CA12	CA12W50	Liver	Wild-type	50uM	B1a	SC_CA12W50.mzML
CA13	CA13W50	Liver	Wild-type	50uM	B1a	SC_CA13W50.mzML
CA14	CA14W0	Liver	Mutant	Control	B1a	SC_CA14W0.mzML
CA15	CA15W0	Liver	Mutant	Control	B1a	SC_CA15W0.mzML
CA16	CA16W0	Liver	Mutant	Control	B1a	SC_CA16W0.mzML
CA17	CA17W50	Liver	Mutant	50uM	B1a	SC_CA17W50.mzML

Copy/paste as tab-delimited data from Excel or text file (View the “See examples..” link for more help)

[View/check study design](#)

[See examples of study design layout](#)

Then click on “View/check study design” to view in tabular format

Study design information

Instructions:

Sample names/identifiers in the **required 'Sample_ID'** column should be unique and should exactly match those names used in the processed results. The **required 'Sample source'** column (e.g. blood, urine, HEK cells, blank, buffer) must be completed. This may be the same or different for all samples. The **required 'Raw file name'** column must be completed when submitting raw data. The sample name to raw file name mapping is essential in order to enable re-analysis of raw data.

The optional **'Subject_ID'** column may be used to designate the submitter's source identifier for a given sample (e.g. subject/patient/animal identifier).

The **required 'Factor'** column(s) are used to assign experimental variables (factors) to sample groups (e.g. treatment condition, time, genotype, phenotype, etc.). Use an appropriate name for the factor heading (e.g. Genotype, Time, Drug treatment) - don't use 'Factor' which is too vague.

The optional **'Other'** column(s) may be used to include additional data such as BMI, age, glucose measurements, etc. that are unique to each sample.

These types of measurements should NOT be designated as factors.

Assign every column(below) as 'Subject ID'(optional), 'Sample ID'(required:1 and only 1), 'Sample source'(required:1 and only 1), 'Factor'(required:at least 1) or 'Other'(optional additional sample data). Columns assigned 'Ignore' will be ignored.

Process study design data Does submission contain raw data?:

<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Subject_ID	Sample_ID	Sample source	Genotype	Treatment	Batch	RAW_FILE_NAME
CA11	CA11W0	Liver	Wild-type	Control	B1a	SC_CA11W0.mzML
CA12	CA12W0	Liver	Wild-type	Control	B1a	
CA13	CA13W0	Liver	Wild-type	Control	B1a	
CA11	CA11W50	Liver	Wild-type	50uM	B1a	
CA12	CA12W50	Liver	Wild-type	50uM	B1a	
CA13	CA13W50	Liver	Wild-type	50uM	B1a	

Assign each column as "Subject_ID", "Sample_ID", "Factor", "Raw file name", "Other" or "Ignore"

After editing/assignment, proceed by clicking on "Process study design data"

Process study design data Does submission contain raw data?: Yes

<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Subject_ID	Sample_ID	Sample source	Genotype	Treatment	Batch	RAW_FILE_NAME	Raw file name
CA11	CA11W0	Liver	Wild-type	Control	B1a	SC_CA11W0.mzML	SC_CA11W0.mzML
CA12	CA12W0	Liver	Wild-type	Control	B1a	SC_CA12W0.mzML	SC_CA12W0.mzML
CA13	CA13W0	Liver	Wild-type	Control	B1a	SC_CA13W0.mzML	SC_CA13W0.mzML
CA11	CA11W50	Liver	Wild-type	50uM	B1a	SC_CA11W50.mzML	SC_CA11W50.mzML
CA12	CA12W50	Liver	Wild-type	50uM	B1a	SC_CA12W50.mzML	SC_CA12W50.mzML

Collection information

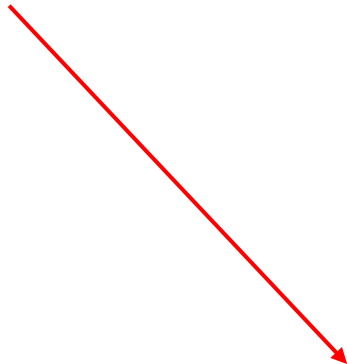
Metadata related to sample collection/ handling/storage

mwTab identifier: efahy_20151117_182353

collection information	Add collection metadata	Reset
Collection Summary:	Cells were counted, washed with cold PBS and then flash-frozen in liquid N2	
Collection Protocol ID:		
Collection Protocol Filename:	kdo_coll_428.txt	
Collection Protocol Comments:		
Sample Source/Type:	Tissues <input type="button" value="v"/>	
Collection Method:		
Collection Location:		

Tissue Cell Identification:	
Tissue Cell Quantity Taken:	
Upload Collection Protocol File(s)	<input type="button" value="Browse..."/> No file selected.

User may upload a methods/protocol file relating to sample collection



Treatment information

Metadata related to treatment protocols

mwTab identifier: efahy_20151117_182353

treatment information	Add treatment metadata <input type="button" value="Reset"/>
Treatment Summary:	RAW 264.7 cells were grown in individual core laboratories or centrally and treated for varying periods of time (0 to 24 hours) with Kdo2 lipid A (KLA) and/or compactin using protocols PP0000001004.pdf and PP00000002800.pdf available on the LIPID MAPS website. To account for
Treatment Protocol ID:	
Treatment Protocol Filename:	
Treatment Protocol Comments:	
Treatment:	
Treatment Compound:	Kdo2-Lipid A and Compactin

Sample prep. information

Metadata related to sample preparation protocols

mwTab identifier: efahy_20151117_182353	
sampleprep information	<input type="button" value="Add sampleprep metadata"/> <input type="button" value="Reset"/>
Sampleprep Summary:	Total lipids were extracted from the cell suspension (Bligh/Dyer). Ice-cold methanol (2.5 ml) was added to each 1 ml of DPBS containing the scraped cell suspension. A volume containing 600 pmol of each of the 18 d5-labeled DAG and TAG internal standards in toluene/methanol (1:1) was
Sampleprep Protocol ID:	
Sampleprep Protocol Filename:	
Sampleprep Protocol Comments:	
Processing Method:	
Processing Storage Conditions:	

Decision point: MS or NMR experiment?

Select analysis type: MS

If MS is chosen, the user is prompted to enter chromatography information



Choose number of chromatography methods for which you have data (default=1)

Number of chromatography methods used for which you have data: 1

Example: If only GCMS or RP-LCMS was used, select "1" (default)
If both HILIC and RP chromatography were used, select "2"

Chromatography information

Metadata related to chromatography (LC/GC) protocols

Number of chromatography methods used for which you have data:

Example: If only GCMS or RP-LCMS was used, select "1" (default)
If both HILIC and RP chromatography were used, select "2"

User may upload a methods/protocol file relating to chromatography

Chromatography Fields	Chromatography method 1
Chromatography Summary:	
Chromatography Type:	<input type="text" value="HILIC"/>
Instrument Name:	<input type="text" value="Thermo Scientific Transcend Duo LX-2 UHPLC"/>
Column Name:	<input type="text" value="Thermo Accucore 150 Amide (50 x 2.1mm, 2.6um)"/>
Solvent A (LC-MS):	<input type="text" value="95% acetonitrile/5% water; 0.1% acetic acid;"/>
Solvent B (LC-MS):	<input type="text" value="50% acetonitrile/50% water; 0.1% acetic acid"/>
Flow Gradient (LC-MS):	<input type="text" value="0.55 ml/min: 0-0.1 min: 0% B, 0.10-5.0 min:"/>
Flow Rate:	<input type="text" value="0.55 ml/min"/>
Column Temperature(°C):	<input type="text" value="45"/>
Methods Filename:	<input type="text"/>
Methods ID:	<input type="text"/>
Column Pressure:	<input type="text"/>

No file selected.

Number of MS conditions per chromatography method

In the case of LCMS this is typically 2 (Positive and negative ion mode)

mwTab identifier: efahy_20151117_182353

Number of MS conditions per chromatography method used for which you have data: 2 ▾

Add MS metadata

Example: If you have GCMS data in positive ion mode only, select "1" (default)
If you have both positive and negative ion mode LCMS data, select "2"

MS information

Metadata related to MS methods

The number of data columns will equal the number of chromatography conditions multiplied by the number of MS conditions. For example, if reversed-phase and HILIC chromatography were specified in conjunction with 2 MS modes (+ and – mode detection), then $2 \times 2 = 4$ columns are displayed

Hint: Fill out the parameters in the column on the left only, click the “Replicate..” button to copy the content to the other columns, then adjust any unique values as appropriate

mwTab identifier: efahy_20151117_182353

Number of MS conditions per chromatography method used for which you have data: 2 ▾

Add MS metadata

Example: If you have GCMS data in positive ion mode only, select "1" (default)
If you have both positive and negative ion mode LCMS data, select "2"

Replicate 1st column values to all other columns

Add MS metadata Reset

MS analysis fields	Ch.:HILIC (1)	Ch.:GC (2)
Instrument Name:	Agilent 6520 QTOF ▾	Agilent 5975C ▾
Instrument Type:	Q-TOF ▾	Linear quadrupole ▾
MS Type:	ESI ▾	EI ▾
Ion Mode:	NEGATIVE ▾	POSITIVE ▾
MS acquisition Comments:	-	-
Data processing Comments:		
Software/procedures used for feature assignments:		
Laboratory Name:	MRC2 (University of Michiga	MRC2 (University of Michiga
Operator Name:		
Detector Type:		

Enter processed data for each chromatography/MS combination that you have specified

Start/Edit Data Submission | Examples of study design and data layouts | Upload and Manage Data | Tutorial

mwTab identifier: efahy_20151117_182353

Dataset 1 of 2: Add Data for Reversed phase POSITIVE mode

Decision point: Targeted or untargeted data?

Option1: Measurements for **named** metabolites from **targeted** experiments, e.g. GC-MS analyses or LC-MS assays with known standards.

Option2: Measurements from **untargeted** experiments e.g. high-resolution LC-MS analyses. Detected features are typically m/z-retention time values

OPTION 1: Targeted assays containing identified (named) metabolites

Input Data in tab-delimited format in the text area below.
First column must contain metabolite names.
Subsequent columns must contain sample data with identical sample names as in Study Design submission.
First row must contain sample names.

Tabular results (typically tens or hundreds of named metabolites) are pasted into this textarea

Units of measurement (required):

[View/check metabolite data](#) [See examples of metabolite data layout](#) [Delete existing metabolite data \(this analysis only\)](#)

OPTION 2: Untargeted assays not containing identified (named) metabolites
(e.g. datasets with m/z, retention time features from LC-MS experiments, NMR binned data)

Add/replace results as a tab-delimited text file:
Ideally, feature names should be formatted as 'm/z underscore retention time', e.g. 645.5327_

IMPORTANT!: If unidentified features are listed by neutral mass rather than m/z ratio, this must be specified in the menu below
This will enable analysis of the dataset by a larger number of tools on the Metabolomics Workbench

Units of measurement (required): <input type="text"/>	Feature names contain m/z values*? (required): <input type="text"/>	Feature names contain retention time values? (required): <input type="text"/>	Time units: <input type="text"/>
---	---	---	----------------------------------

* By "m/z values" we are referring to mass-to-charge ratios and NOT neutral masses.

[Upload tab-delimited datafile](#) [Browse...](#) No file selected.

The first line in the submitted file should contain sample names exactly matching those that you submitted in the 'Study Design' section.

A file of tabular results (typically thousands of unidentified features) is uploaded here

Option1:
Targeted data

Enter processed data (metabolite identifications and measurements) for each chromatography/MS combination that you have specified

Start/Edit Data Submission | Examples of study design and data layouts | Upload and Manage Data | Tutorial

mwTab identifier: efahy_20151117_182353

Dataset 1 of 2: Add Data for Reversed phase POSITIVE mode

Metabolite	BCJ080212A01	BCJ080219A01	BCJ080226A01	BCJ080212A22	BCJ080219A22	BCJ080226A22
Margaric acid	3.5	25.6	85.5	43.9	47.9	29
Myristic acid	2.6	85.0	81.0	22.9	46.3	91
Oleic acid	20.2	28.5	1.0	11.1	95.4	69
Palmitic acid	16.0	7.2	10.6	70.1	28.0	62
Pentadecanoic acid	57.6	36.2	20.9	10.7	37.2	85
PGD2	8.3	66.1	4.7	75.6	51.3	55
PGE2	93.0	75.5	70.9	87.2	93.4	61
PGF2a	28.8	30.4	30.7	37.9	61.3	10
PGI2	32.3	76.8	48.5	70.5	1.9	29
stearic acid	29.3	57.1	16.3	78.8	67.5	14
Stearidonic acid	92.8	49.0	49.0	90.4	72.6	21
Tricosanoic acid	4.8	36.1	27.5	24.9	67.1	0

Units is a required field

mwTab identifier: efahy_20151117_182353

Input Data in tab-delimited format. First column must contain metabolite names. Subsequent columns must contain sample data with identical sample names as in Study Design submission. First row must contain sample names.

Copy/paste tabular data here
First row MUST contain sample names identical to those submitted in the "study design" step. First column must contain metabolite names or m/z-retention time identifiers in the case of unidentified ions (e.g. "231.4185_17.68")

Units of measurement:

View/check metabolite data | See examples of metabolite data layout

View the "See examples.." link for examples of datasets

Option1:
Targeted data

Processed data upload: Review in tabular form, then Upload data

Note: sample names must match those submitted in the “study design” section, otherwise a warning will be generated and this must be resolved before proceeding

PGF2a	28.8	30.4	30.7	37.9	61.3	10.2	70.3	78.2	23.6	81.7	57.3		
PGJ2	32.3	76.8	48.5	70.5	1.9	29.7	92.1	94.5	75.1	92.0	82.1		
stearic acid	29.3		57.1	16.3	78.8	67.5	14.6	85.3	94.4	63.9	16.3	12.5	
Stearidonic acid			92.8	49.0	49.0	90.4	72.6	21.9	54.1	6.3	26.6	97.9	77.4
Tricosanoic acid			4.8	36.1	27.5	24.9	67.1	0.4	50.8	23.0	13.3	82.4	85.3

Units of measurement:

[See examples of metabolite data layout](#)

metabolite_name	BCJ080212A01	BCJ080219A01	BCJ080226A01	BCJ080212A22	BCJ080219A22	BCJ080226A22	BCJ080212A22
Margaric acid	3.5	25.6	85.5	43.9	47.9	29.5	72.1
Myristic acid	2.6	85.0	81.0	22.9	46.3	91.9	26.1
Oleic acid	20.2	28.5	1.0	11.1	95.4	69.7	84.2
Palmitic acid	16.0	7.2	10.6	70.1	28.0	62.5	80.1
Pentadecanoic							

Option1:
Targeted data

Metabolite metadata upload

Copy/paste metabolite annotations in tabular format (PubChem CID, KEGG ID, InCHI Key, LC/GC retention time/index, etc.) Metabolite names MUST match those submitted in the previous data section. If you don't have any metabolite annotations, just submit the column of metabolite names.

mwTab identifier: efahy_20151117_182353

Metabolite metadata in tab-delimited format. First column must contain metabolite names. Subsequent columns should contain KEGG, PubChem identifiers, retention index, quantitated m/z, etc. First row must contain headings.

Metabolite Name	Pubchem Id	Kegg Id
Margaric acid	10465	-
Myristic acid	11005	C06424
Oleic acid	445639	C00712
Palmitic acid	985	C00249
Pentadecanoic acid	13849	C16537
PGD2	448457	C00696
PGE2	5283116	C00584
PGF2a	5280363	-
PGJ2	5311211	C05957
stearic acid	5281	C01530

[View/check metabolite metadata](#) [See examples of metabolite metadata layout](#)

Stearic acid	5281	C01530
Stearidonic acid	5282837	C16300
Tricosanoic acid	17085	-

[View/check metabolite data](#) [See examples of metabolite data layout](#)

[Upload metabolite metadata](#)

metabolite_name	Pubchem Id	Kegg Id
Margaric acid	10465	-
Myristic acid	11005	C06424
Oleic acid	445639	C00712
Palmitic acid	985	C00249
Pentadecanoic acid	13849	C16537
PGD2	448457	C00696
PGE2	5283116	C00584
PGF2a	5280363	-
PGJ2	5311211	C05957

After checking the table of metabolite annotations, click "Upload metabolite metadata"

Option1:
Targeted data

Repeat the data/metabolite metadata upload steps for each chromatography/MS analysis combination that you have specified

mwTab identifier: efahy_20151117_182353

Add DataSet 2 of 2 for Reversed phase NEGATIVE mode



mwTab identifier: efahy_20151117_182353

Finalize submission

When upload steps are complete click on "Finalize submission"

Users may view and analyze the study to review the data/metadata. This viewer simulates how the study will appear on the Metabolomics WorkBench after curation and database upload

Separate mwTab files are generated for each analysis combination

mwTab identifier: efahy_20151117_182353
[View consolidated mwtab file](#)

[View mwtab file for analysis 1:mwtab_analysis_1.txt](#) [View/analyze data](#) via WorkBench

[View mwtab file for analysis 2:mwtab_analysis_2.txt](#) [View/analyze data](#) via WorkBench

[Return to Raw Data Upload Page](#) to register your data set and upload your raw data and methods/protocol files.

Option2:
Untargeted data

Measurements from **untargeted** experiments e.g. high-resolution LC-MS analyses are uploaded as a tab-delimited text file containing a table of unidentified features (typically m/z-retention time values) and associated measurements.

OPTION 2: Untargeted assays not containing identified (named) metabolites

(e.g. datasets with m/z,retention time features from LC-MS experiments, NMR binned data)

Add/replace results as a tab-delimited text file:

Ideally, feature names should be formatted as 'm/z underscore retention time', e.g. 645.5327_24.91

IMPORTANT!:If unidentified features are listed by neutral mass rather than m/z ratio, this must be specified in the menu below

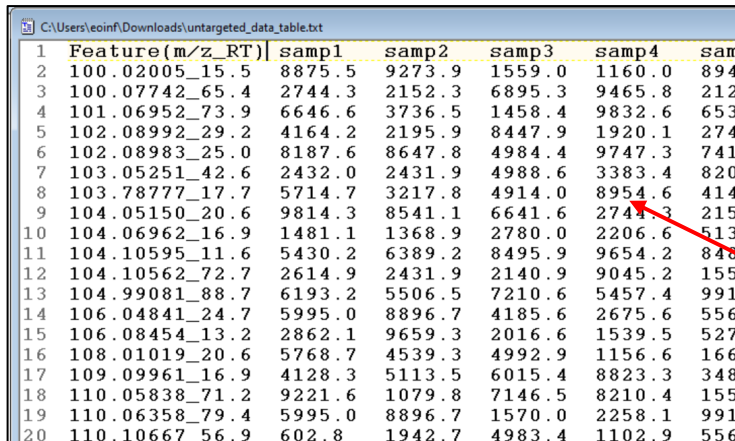
This will enable analysis of the dataset by a larger number of tools on the Metabolomics Workbench

Units of measurement (required): Peak area	Feature names contain m/z values*? (required): Yes	Feature names contain retention time values? (required): Yes Time units: Minutes
--	--	--

* By "m/z values" we are referring to mass-to-charge ratios and NOT neutral masses.

Upload tab-delimited datafile Browse... jwalejko_20181204_201054_mwtab.txt

The first line in the submitted file should contain sample names exactly matching those that you submitted in the 'Study Design' section.



Feature(m/z_RT)	samp1	samp2	samp3	samp4	samp
100.02005_15.5	8875.5	9273.9	1559.0	1160.0	894
100.07742_65.4	2744.3	2152.3	6895.3	9465.8	212
101.06952_73.9	6646.6	3736.5	1458.4	9832.6	653
102.08992_29.2	4164.2	2195.9	8447.9	1920.1	274
102.08983_25.0	8187.6	8647.8	4984.4	9747.3	741
103.05251_42.6	2432.0	2431.9	4988.6	3383.4	820
103.78777_17.7	5714.7	3217.8	4914.0	8954.6	414
104.05150_20.6	9814.3	8541.1	6641.6	2744.3	215
104.06962_16.9	1481.1	1368.9	2780.0	2206.6	513
104.10595_11.6	5430.2	6389.2	8495.9	9654.2	848
104.10562_72.7	2614.9	2431.9	2140.9	9045.2	155
104.99081_88.7	6193.2	5506.5	7210.6	5457.4	991
106.04841_24.7	5995.0	8896.7	4185.6	2675.6	556
106.08454_13.2	2862.1	9659.3	2016.6	1539.5	527
108.01019_20.6	5768.7	4539.3	4992.9	1156.6	166
109.09961_16.9	4128.3	5113.5	6015.4	8823.3	348
110.05838_71.2	9221.6	1079.8	7146.5	8210.4	155
110.06358_79.4	5995.0	8896.7	1570.0	2258.1	991
110.10667_56.9	602.8	1942.7	4983.4	1102.9	556

Select results file from your file system. **Sample names should exactly match those submitted in the "Study Design" section of the metadata submission**

Example of a file with untargeted MS data. Note the 1st column contains **m/z_retention time features**. Subsequent columns contain measurements for each sample.

Decision point: MS or NMR experiment?

NMR option

Select analysis type: NMR ▾
Select



mwTab identifier: efahy_20151112_141949

nmr information		Add nmr metadata	Reset
Instrument Name:	Bruker Avance III		
Instrument Type:	FT-NMR ▾		
NMR Experiment Type:	1D-1H ▾		
NMR Comments:			
Field Frequency Lock:	Deuterium		
Standard Concentration:	0.5 mM		
Spectrometer Frequency:	950 MHz		
NMR Probe:	cryo, inverse		
NMR Solvent:	D2O		
NMR Tube Size:	5mm x 7 in		
Shimming Method:	Topshim		

NMR experiment option

Add NMR results data

Decision point: Targeted or untargeted data?



Option1: Measurements for **named** metabolites from **targeted** NMR analyses.



OPTION 1: Targeted assays containing identified (named) metabolites

Input Data in tab-delimited format in the text area below.

First column must contain metabolite names.

Subsequent columns must contain sample data with identical sample names as in Study Design submission.

First row must contain sample names.

Units of measurement (required):

[View/check metabolite data](#)

[See examples of metabolite data layout](#)

[Delete existing metabolite data \(this analysis only\)](#)

Option2: Measurements from **untargeted** experiments e.g. binned NMR analyses. Detected features are typically binned chemical shift ranges.



OPTION 2: Untargeted assays not containing identified (named) metabolites

(e.g. datasets with m/z, retention time features from LC-MS experiments, NMR binned data)

Add/replace results as a tab-delimited text file:

Units of measurement (required):

The first 2 lines in the submitted file should contain sample names and corresponding experimental factors matching those that you submitted in the 'Study Design' section.

Start/Edit Data Submission link

All of a user's submissions are visible on this page

[Start/Edit Data Submission](#)

[Examples of study design and data layouts](#)

[Upload and Manage Data](#)

[Tutorial](#)

Start new study submission

List of stored mwTab files for user efahy (most recent first)

Click on a link to resume editing that file or use it as a template for a new submission

efahy_20151117_182353_mwtab_analysis_2.txt	View mwTab	View online
efahy_20151117_182353_mwtab_analysis_1.txt	View mwTab	View online
efahy_20151117_182353_mwtab.txt	View mwTab	Edit mwTab

View/download the completed mwTab files

These are saved in the user's login area

```
#METABOLOMICS WORKBENCH efahy_20151117_182353
VERSION 1
CREATED_ON November 17, 2015, 6:23 pm
#PROJECT
PR:PROJECT_TITLE LIPID MAPS Lipidomics studies
PR:PROJECT_TYPE MS quantitative analysis
PR:PROJECT_SUMMARY Multi-center quantitative lipidomics s
PR:PROJECT_SUMMARY sources (LIPIDMAPS)
PR:INSTITUTE University of California, San Diego
PR:DEPARTMENT Bioengineering
PR:LABORATORY Multiple centers
PR:LAST_NAME Fahy
PR:FIRST_NAME Eoin
PR:ADDRESS 9500 Gilman, La Jolla, CA, 92093, USA
PR:EMAIL efahy@ucsd.edu
PR:PHONE 858-534-4076
PR:FUNDING_SOURCE NIGMS
#STUDY
ST:STUDY_TITLE Timecourse on RAW 264.7 cells treated
ST:STUDY_TYPE Timecourse experiment
ST:STUDY_SUMMARY Lipidomics studies on macrophages - RA
ST:STUDY_SUMMARY and compactin. Experiments were conduc
ST:STUDY_SUMMARY serum. 8-timepoint study: Measurements
ST:STUDY_SUMMARY 24hrs for: (i) compactin, (ii) Kdo2-Li
ST:STUDY_SUMMARY (iv) control
ST:INSTITUTE University of California, San Diego
ST:DEPARTMENT Bioengineering
ST:LABORATORY Multiple centers
ST:LAST_NAME Fahy
ST:FIRST_NAME Eoin
```

The “View Online “ link allows users to view and analyze the study to review the data/metadata. This viewer simulates how the study will appear on the Metabolomics WorkBench after NMDR curation and database upload

The screenshot displays the Metabolomics Workbench interface. At the top, the logo and title 'METABOLOMICS WORKBENCH' are visible, along with a search bar and user login information ('You are logged in as efahy'). The navigation menu includes 'Home', 'Metabolomics Update', 'Data', 'Standards', 'Resources', 'NIH Metabolomics', 'Training', 'About', and 'Personnel'. The main content area is divided into several sections:

- User data from mwTab file:** Includes a link to 'Show named metabolites' and a set of tabs for 'All', 'Project', 'Study', 'Subject', and 'Sample'.
- Project Metadata:** A table listing project details:

Project Title	LIPID MAPS Lipidomics studies
Project Type	MS quantitative analysis
Project Summary	Multi-center quantitative lipidomics studies on
Institute	University of California, San Diego
Department	Bioengineering
Laboratory	Multiple centers
Last Name	Fahy
First Name	Eoin
- Chromatography:** A table providing technical details:

Chromatography Summary	High resolution separation was done using an Acquity UPLC system with a Waters column. Column flow was set to 400 l/min with a gradient. Buffer B is 100% acetonitrile. A column temp of 43 degrees Celsius.
Chromatography Type	Reversed phase
Instrument Name	Waters Acquity UPLC
Column Name	Acquity BEH HSS T3 (2.1x 100mm x 1.8 um)
Flow Gradient	100% acetonitrile
Flow Rate	400ul/min
Solvent A	1% acetonitrile in 0.1% formic acid
Solvent B	100% acetonitrile
- Analysis:** A table showing analysis parameters:

Analysis Type	MS
Instrument Name	ABI 4000 QTRAP
- Factors and experimental variables (factors):** A table with columns for Sample, Hours, Compactin (uM), KLA(ng/ml), and Sampledata. The data rows are:

Sample	Hours	Compactin (uM)	KLA(ng/ml)	Sampledata
BCJ080212A02	0.5	0	0	
BCJ080219A02	0.5	0	0	
BCJ080226A02	0.5	0	0	
BCJ080212A04	0.5	0	100	
BCJ080219A04	0.5	0	100	
BCJ080226A04	0.5	0	100	
BCJ080212A03	0.5	50	0	
BCJ080219A03	0.5	50	0	
BCJ080226A03	0.5	50	0	
BCJ080212A05	0.5	50	100	
BCJ080219A05	0.5	50	100	
BCJ080226A05	0.5	50	100	
BCJ080212A01	0	0	0	
BCJ080219A01	0	0	0	
BCJ080226A01	0	0	0	

The “View Online “ link allows users to perform analysis on their datasets via the mwTab format prior to NMDR registration and database upload

User data from mwTab file

[ANOVA analysis](#) | [Display t-test grid](#) | [Show z-scores](#) | [PCA analysis](#) | [LDA analysis](#)

Bar graph by sample | Boxplot | Boxplot | Bar graph by factor level | Select one factor

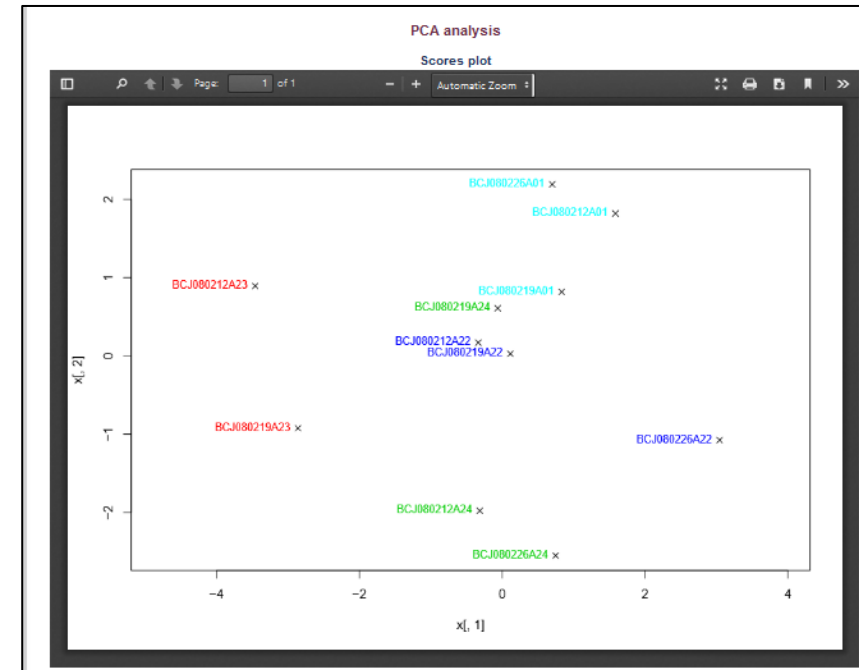
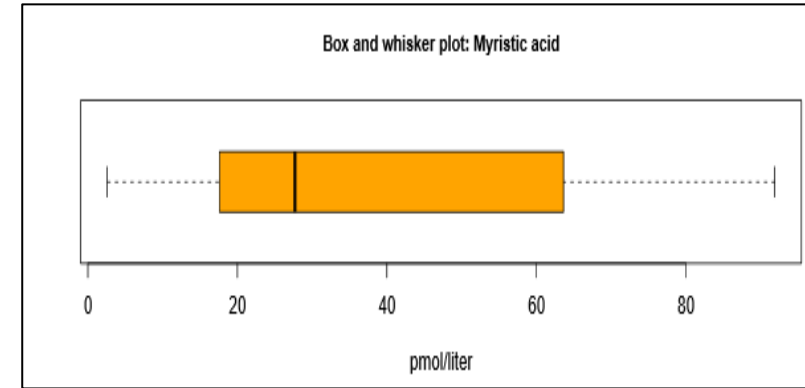
Bar graph (samples) | All samples | By factor | Bar graph by factor level | Display data for one factor

Sample	Myristic acid	Factors
BCJ080212A01	2.6	Hours:0 Compactin (uM):0 KLA(ng/ml):0
BCJ080212A02		
BCJ080212A03		
BCJ080212A04		
BCJ080212A05		
BCJ080212A06		
BCJ080212A07		
BCJ080212A08		
BCJ080212A09		
BCJ080212A10		
BCJ080212A11		
BCJ080212A12		
BCJ080212A13		
BCJ080212A14		
BCJ080212A15		
BCJ080212A16		
BCJ080212A17		
BCJ080212A18		
BCJ080212A19		
BCJ080212A20		
BCJ080212A21		
BCJ080212A22		
BCJ080212A23		
BCJ080212A24		
BCJ080212A25		
BCJ080212A26		
BCJ080212A27		
BCJ080212A28		
BCJ080212A29		
BCJ080212A30		
BCJ080212A31		
BCJ080212A32		
BCJ080212A33		
BCJ080212A34		
BCJ080212A35		
BCJ080212A36		
BCJ080212A37		
BCJ080212A38		
BCJ080212A39		
BCJ080212A40		
BCJ080212A41		
BCJ080212A42		
BCJ080212A43		
BCJ080212A44		
BCJ080212A45		
BCJ080212A46		
BCJ080212A47		
BCJ080212A48		
BCJ080212A49		
BCJ080212A50		

Box and whisker plot: Myristic acid

Factors

Factor level F1: Hours:0 | Compactin (uM):0 | KLA(ng/ml):0
Factor level F2: Hours:12 | Compactin (uM):0 | KLA(ng/ml):0
Factor level F3: Hours:12 | Compactin (uM):0 | KLA(ng/ml):100
Factor level F4: Hours:12 | Compactin (uM):50 | KLA(ng/ml):0



Edit your Data Submission (DataTrack_ID)

Resume submission or edit an existing submission from the “List Data Uploads” section at <https://www.metabolomicsworkbench.org/data/DRCCDataDeposit.php>

Upload and Manage Experimental Data and Metadata

Overview | **New Data Upload** | List Data Uploads | Test Upload | Tutorials

Summary of uploaded data sets

Please select an appropriate **DataTrack ID** from the table below to upload additional raw data files or select an appropriate **mwTab Filename** to edit metadata and results for already registered data.

DataTrack ID (upload raw data)	Study ID	Date Submitted	Data Type	mwTab FileName (edit study)	Archiv Filename	User Comments	Data Review Status	Data Review Comments	Uploaded Files
2880	-	2021-10-07	Target edMS	amat_20211007_101611_mwtab.txt	Tissue TCA	-	Incomplete - Needs further action	Hello, we have reviewed your study. Can you please update the metadata?	-
1559	ST001089	2018-11-05	Target edMS	amat_20181105_073530_mwtab.txt	Taurine data upload11052018	Not sure what the following refers to? CRC_25102018.7Z is	Complete - No further action required	Upload confirmed. Please ignore those comments.	MS.zip (7.9M) Book1.xlsx (16K)

Click on button to edit an existing submission

Upload raw data for a submission by clicking on the Upload button

Edit your Data Submission

Resume submission of a new study or edit an existing study from the online GUI at http://www.metabolomicsworkbench.org/data/ds_main.php

[Start/Edit Data Submission](#) | [Examples of study design and data layouts](#) | [Upload and Manage Data](#) | [Tutorial\(pdf\)](#)

To start new study submission return to the [New study registration](#) page

List of stored mwTab files for user efahy and group members (most recent first)

Click on 'Edit mwtab' link to resume editing that file

Sort by modified date Sort by user,filename

	efahy_20160407_091057_mwtab_analysis_1.txt	View mwTab	View online
Test study title EF...	efahy_20160407_091057_mwtab.txt	View mwTab	Edit mwTab
Test Study...	ivadivelu_20160404_160548_mwtab.txt	View mwTab	Edit mwTab

Use "Edit mwTab" link

Study editing interface: Jump to section of interest

Start/Edit Data Submission | [Examples of study design and data layouts](#) | [Upload and Manage Data](#) | [Tutorial](#)

Jump to: [Project](#) [Study](#) [Subject](#) [Study Design](#) [Collection](#) [Treatment](#) [Sampleprep](#) [Chrom.](#) [MS](#) [Data\(Results\)](#) [Finalize](#)

project information	Add project metadata Reset
Project Title:	LIPID MAPS Lipidomics studies
Project Type:	MS quantitative analysis
Project Summary:	Multi-center quantitative lipidomics studies on samples from human and murine sources (LIPIDMAPS)
Institute:	University of California, San Diego
Department:	Bioengineering
Laboratory:	Multiple centers
Last Name:	Fahy
First Name:	Eoin
Address:	9500 Gilman, La Jolla, CA, 92093, USA
Email:	efahy@ucsd.edu

After finalizing your online submission, upload your raw and supplementary data

[Start/Edit Data Submission](#)

[Examples of study design and data layouts](#)

[Upload and Manage Data](#)

[Tutorial\(pdf\)](#)

mwTab identifier: efahy_20160407_091057

[View consolidated mwtab file](#)

[View mwtab file for analysis 1:mwtab_analysis_1.txt](#) [View/analyze data via WorkBench](#)

[Upload raw data/supplementary data](#)

Upload your raw and supplementary data via a standalone FTP client
Your raw data should be submitted as a compressed file (.zip, .7Z, .gz, etc)

IMPORTANT! Please upload raw data in open-source format (e.g. mzML, mzXML, CDF)
if at all possible to enable re-use and re-analysis by other researchers

Please do not upload individual raw files- combine them in a single compressed archive (.zip,.7z)



Upload additional files for already registered data with data track ID

Please review the following information before you continue to upload data to remote directory :

- **Raw data upload:**

IMPORTANT! Please upload raw data in open-source format (mzML,mzXML,CDF) if at all possible to enable re-use and re-analysis.

Please do not upload individual raw files- combine them in a single compressed archive (.zip,.7z) first.

Compressed (zip, 7z) data files are selected and uploaded to the NMDR FTP server through a FTP client. A variety of free and commercial standalone file transfer clients exist to upload large data files directly to the FTP servers: [FileZilla](#)  , [WinSCP](#)  , etc. The usage of **FileZilla** is recommended for uploading data to the NMDR.

- Use the following credentials to upload data to the NMDR:

- **Server Name:** www.metabolomicsworkbench.org
- **User Name:** drccupload
- **Password:** #Vgy7ujmnbv\$

Password and directory location will be visible when you navigate to the appropriate datatrack_id in your data upload list

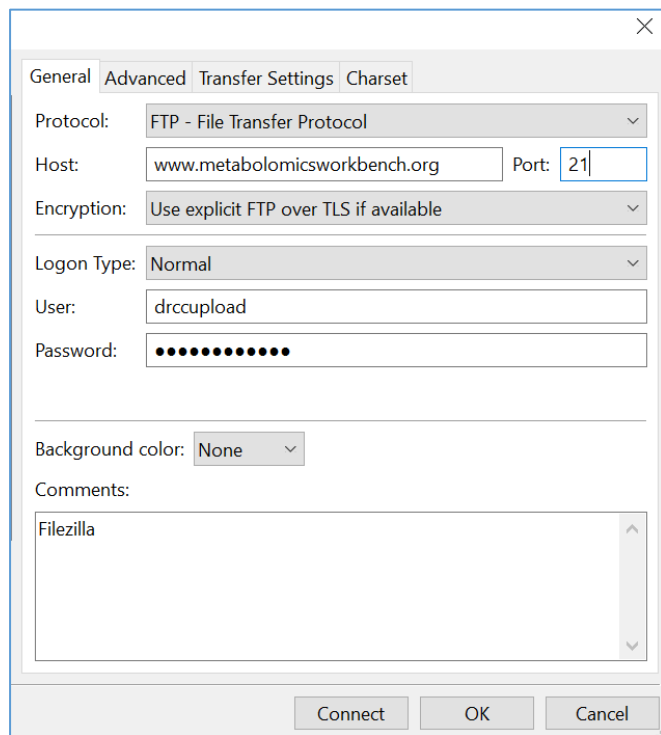
- After connecting to the NMDR FTP server, please change remote directory to before uploading the compressed (zip, 7z) data file.

Upon completion of registration, your dataset is entered in the NMDR processing queue where it will be curated and uploaded on the Metabolomics WorkBench public website (depending on embargo conditions)

Upload your raw and supplementary data via a standalone FTP client Filezilla is the recommended FTP client.

Download the free client at <https://filezilla-project.org>

(a)



General Advanced Transfer Settings Charset

Protocol: FTP - File Transfer Protocol

Host: www.metabolomicsworkbench.org Port: 21

Encryption: Use explicit FTP over TLS if available

Logon Type: Normal

User: drccupload

Password: ●●●●●●●●

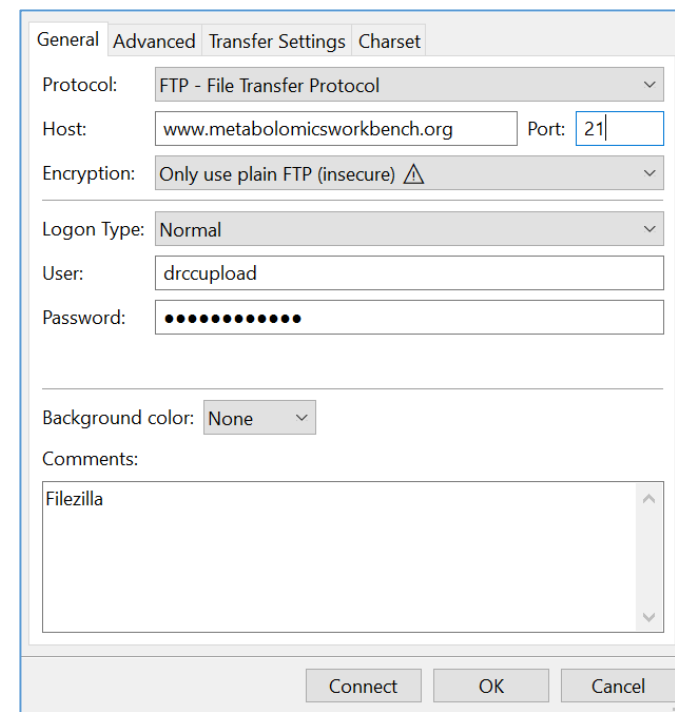
Background color: None

Comments: Filezilla

Connect OK Cancel

Filezilla settings

(b)



General Advanced Transfer Settings Charset

Protocol: FTP - File Transfer Protocol

Host: www.metabolomicsworkbench.org Port: 21

Encryption: Only use plain FTP (insecure)

Logon Type: Normal

User: drccupload

Password: ●●●●●●●●

Background color: None

Comments: Filezilla

Connect OK Cancel

**Note: If your upload fails using the default encryption settings (a), switch to the unencrypted setting (b)
The firewall rules at your institution may not allow FTP over TLS**

Then navigate to the remote directory given to you in the instructions before uploading files

Upon completion of registration, your dataset is entered in the NMDR processing queue where it will be curated and uploaded onto the Metabolomics WorkBench website (depending on user-specified embargo conditions)

It typically takes 5-10 working days for a submission to be reviewed and processed. **The submitter will then be notified and provided with a DOI and a private link to the study which may be shared with reviewers**

Things that slow down submission processing:

The submitter has not provided raw data files (or the files are incomplete/corrupt)

The submitter has not listed which raw files match each sample in the study-design section

The submitter has neglected to provide a required item in one of the metadata fields