

METABOLOMICS WORKBENCH DATA DEPOSITION
RILEY BROOK / KANAREK LAB
BOSTON CHILDREN'S HOSPITAL AND HARVARD MEDICAL SCHOOL

STAGE 1:
EXCEL FILES FOR DATA DEPOSITION

STUDY DESIGN

Template for study design: Sheet 1

<https://docs.google.com/spreadsheets/d/1SkFFhAYc1Ajp9OqGA8vEKKTXbl0-nClT3Ft5Hbf-tbU/edit?usp=sharing>

Steps

- 1) Fill out first column with *sample names* (you can use the same name as the raw file name). Include the pools.
- 2) Fill out second column with *sample source* (for example: mouse plasma).
- 3) Fill out the third column with a *factor* that identifies your groups. For the pool samples, you can put N/A. Example: this in this experiment we had plasma samples from mice with leptomenigeal metastasis (LM+) and without leptomenigeal metastasis (WT). I called the factor *disease* but you have some flexibility in terms of defining your samples (they will carefully review everything when you submit and they will communicate with you if something does not make sense and provide suggestions).
- 4) Fill out the fourth column with the *raw file names*. Be careful that these exactly match the raw file names that you plan to upload AND the Sample_ID name from the first column.
- 5) Copy and paste from your excel sheet into this box, and it should look something like what you see in the image below.
- 6) Choose *View/check study design*.

mwTab Identifier: jrileyb_20241104_105910 [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 names (if submitting raw data) are required.

Subject name and additional sample data are optional.

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

Sample_ID	Sample source	Disease	Raw file name
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT288_WTplasma_t	Mouse Plasma	WT	
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT288_WTplasma_t.raw			
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT289_WTplasma_t	Mouse Plasma	WT	
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT289_WTplasma_t.raw			
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT290_WTplasma_t	Mouse Plasma	WT	
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT290_WTplasma_t.raw			
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT291_LMplasma_t	Mouse Plasma	LM+	
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT291_LMplasma_t.raw			
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT292_LMplasma_t	Mouse Plasma	LM+	

[View/check study design](#) [See examples of study design layout](#)

- 7) After choosing *View/check study design*, it will load something similar to the following table.

- 8) You can read the instructions for what is required, but you will need the following columns: *Sample_ID*, *Sample Source*, *Factor*, and *Raw file name*. You will see in the instructions that you can add additional columns, but these are optional. **MAKE SURE YOU CHOOSE FROM THE DROP DOWN THE CORRECT IDENTIFICATION FOR THE COLUMN** (see arrows in image below).
- 9) Choose Yes from the drop down for *does this submission contain raw data?*
- 10) Choose *Process study design data*.

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?: Yes	
Sample_ID	Sample source	Factor	Raw file name
Sample_ID	Sample source	Disease	Raw file name
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT288_WTplasma_t	Mouse Plasma	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT289_WTplasma_t	Mouse Plasma	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT290_WTplasma_t	Mouse Plasma	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT291_LMplasma_t	Mouse Plasma	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT292_LMplasma_t	Mouse Plasma	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT293_LMplasma_t	Mouse Plasma	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT294_plasma_pool1xa	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT294_plasma_pool1xb	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT294_plasma_pool1xc	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT295_plasma_pool03xa	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT295_plasma_pool03xb	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT296_plasma_pool01xa	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT296_plasma_pool01xb	Mouse Plasma	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT297_WTserum_t	Mouse Serum	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT298_WTserum_t	Mouse Serum	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT299_WTserum_t	Mouse Serum	WT	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT300_LMserum_t	Mouse Serum	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT301_LMserum_t	Mouse Serum	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT302_LMserum_t	Mouse Serum	LM+	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT303_serum_pool1xa	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT303_serum_pool1xb	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT303_serum_pool1xc	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT304_serum_pool03xa	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT304_serum_pool03xb	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT305_serum_pool01xa	Mouse Serum	N/A	20240211_QEF1_HIL
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT305_serum_pool01xb	Mouse Serum	N/A	20240211_QEF1_HIL

ASSAYS

Template for Assay: Sheet 2

<https://docs.google.com/spreadsheets/d/1SkFFhAYc1Ajp9OqGA8vEKKTxb10-nClt3Ft5Hbf-tbU/edit?usp=sharing>

Steps

- 1) Transpose your normalized data file so the metabolite names are in the first column of the excel sheet and the sample names are in the first row at the top of the excel sheet, and beneath them are all the normalized peak areas. *To transpose, highlight the whole data set, copy, paste special > transpose*. Since these are the normalized peak area values, you won't have your pool samples here.
- 2) Copy and paste the contents of the excel file into the box.
- 3) For the *Units of measurement (required)*, you can put *a.u.*
- 4) Choose *View/check metabolite data*.

mwTab Identifier: jrileyb_20241104_105910 [Return to start](#)
Analysis: HILIC UNSPECIFIED (1)

OPTION 1: Assays containing identified (named) metabolite species

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.

```
metabolite_name 20240211_QEF1_HILIC_mouseplasma_serum_polars_XT288_WTplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT289_WTplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT290_WTplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT291_LMplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT292_LMplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT293_LMplasma_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT297_WTserum_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT298_WTserum_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT299_WTserum_t
20240211_QEF1_HILIC_mouseplasma_serum_polars_XT300_LMserum_t
```

Units of measurement (required):

[View/check metabolite data](#)

[See examples of metabolite data layout](#)

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

Note: I have not used OPTION 2, so I am not sure how this one works.

OPTION 2: Untargeted assays not containing identified (named) metabolite species

(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): Feature names contain m/z values*? (required): Feature names contain retention time values?(required): Time units:

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

[Upload tab-delimited datafile](#)

[Choose File](#)

No file chosen

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

[Finalize or edit "jrileyb_20241104_105910" study submission](#)

(In order to finalize the submission you must have added metabolite results for each analysis)

- 5) After choosing *View/check metabolite data* you should see something like the image below.
- 6) Choose *Upload data*.

Upload data		
metabolite_name	20240211_QEF1_HILIC_mouseplasma_serum_polars_XT288_WTplasma_t	20240211_QEF1_HILIC_mousep
alanine	235725948.3	208723099.2
Alpha.Ketoglutarate	29129995.71	69576112.63
arginine	1923905734	1374443148
aspartate	44808354.86	28409108.43
citrate	1674833676	2527047406
creatinine	341056641.4	462367059.8
cystine	42125031.86	22883320.21
fumarate	30021472.76	50827173.19
glutamate	96097293.02	82396918.5
glycine	5214659.573	5111026.954
histidine	4106165758	3028936571
hypoxanthine	17064054.25	17376022.62
INDOLE.3.ACETIC.ACID	1325694.213	1065704.168
isoleucine	300943560	149276881.2
leucine	413157676.6	188764696
lysine	441215843.7	338650789.4
methionine	378529274.7	235421082.2
niacinamide	193042967.8	106431050.8
palmitate	3134077401	4368421210
phenylalanine	256558103	150457583.2
proline	827388111.8	771124821.8
pyruvate	2086900.267	9118605.507
serine	29286969.01	21354739.01
threonine	130967079.2	109325846.2
THYMINE	10968914.76	20585018.04
tryptophan	625637596	643796719.6
tyrosine	362582912.4	293030312.5
valine	535648125.9	235415679.2
guanosine	N/A	N/A

Template for Metabolite metadata: Sheet 3

<https://docs.google.com/spreadsheets/d/1SkFFhAYc1Ajp9OqGA8vEKKTXbl0-nCl3Ft5Hbf-tbU/edit?usp=sharing>

Steps

- 1) If you have specific metabolites for your experiment, you will need to fill this out with those metabolites. If you are looking generally at polar metabolites from HILIC, you can copy and paste from the template sheet the metabolites that you report from your assay (*the sheet may not include all the polar metabolites, so you may need to add additional based on the metabolites you report*).
- 2) Copy and paste the contents of the excel sheet in the box.
- 3) Choose *View/check metabolite metadata*.

mwTab Identifier: jrileyb_20241104_105910 [Return to start](#)

Analysis: HILIC UNSPECIFIED(1)

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	retention time	quantified m/z	PubChem	KEGG	HMDB	Compound Formula
alanine	9.02	90.055	5950	C00041	HMDB0000161	C3H7NO2
Alpha.Ketoglutarate	10.57	145.0143				C5H6O5
arginine	14.23	175.119	6322 (ARGININE)	C00062 (ARGININE)	HMDB0000517 (ARGININE)	C6H14N4O2
aspartate	9.93	132.0302	5960	C00049	HMDB0000191	C4H7NO4
citrate	12.3	191.0197	311	C00158	HMDB0000094	C6H8O7
creatinine	4.86	114.0662	588	C00791	HMDB0000562	C4H7N3O
cystine	10.41	241.0311	67678	C00491	HMDB0000192	C6H12N2O4S2
fumarate	10.74	115.0037	444972	C00122	HMDB0000134	C4H4O4
glutamate	9.78	146.0459	33032	C00025	HMDB0000148	C5H9NO4

[View/check metabolite metadata](#)

[See examples of metabolite metadata layout](#)

4) After clicking *View/check metabolite metadata* you should see something like the image below.

5) Choose *Upload metabolite metadata*.

[Upload metabolite metadata](#)

metabolite_name	retention time	quantified m/z	PubChem	KEGG	HMDB	Compound Formula
alanine	9.02	90.055	5950	C00041	HMDB0000161	C3H7NO2
Alpha.Ketoglutarate	10.57	145.0143				C5H6O5
arginine	14.23	175.119	6322 (ARGININE)	C00062 (ARGININE)	HMDB0000517 (ARGININE)	C6H14N4O2
aspartate	9.93	132.0302	5960	C00049	HMDB0000191	C4H7NO4
citrate	12.3	191.0197	311	C00158	HMDB0000094	C6H8O7
creatinine	4.86	114.0662	588	C00791	HMDB0000562	C4H7N3O
cystine	10.41	241.0311	67678	C00491	HMDB0000192	C6H12N2O4S2
fumarate	10.74	115.0037	444972	C00122	HMDB0000134	C4H4O4
glutamate	9.78	146.0459	33032	C00025	HMDB0000148	C5H9NO4
glycine	9.84	76.0393	750	C00037	HMDB0000123	C2H5NO2
histidine	8.94	156.0768	6274	C00135	HMDB0000177	C6H9N3O2
hypoxanthine	5.5	137.0458	790	C00262	HMDB0000157	C5H4N4O
INDOLE.3.ACETIC.ACID	4.55	174.0561				C3H5O6P
isoleucine	6.18	132.1019	6306	C00407	HMDB0000172	C6H13NO2
leucine	5.58	132.1019	6106	C00123	HMDB0000687	C6H13NO2
lysine	13.89	147.1128	5962 (LYSINE)	C00047 (LYSINE)	HMDB0000182 (LYSINE)	C6H14N2O2
methionine	6.32	150.0583	6137	C00073	HMDB0000696	C5H11NO2S
niacinamide	3.03	123.0553				C6H6N2O
palmitate	1.85	255.233	985	C00249	HMDB0000220	C16H32O2
phenylalanine	4.9	164.0717	6140	C00079	HMDB0000159	C9H11NO2
proline	7.33	116.0706	145742	C00148	HMDB0000162	C5H9NO2
pyruvate	4.2	87.0088	1060	C00022	HMDB0000243	C3H4O3
serine	9.69	106.0499	5951	C00065	HMDB0000187	C3H7NO3
threonine	8.81	120.0655	6288	C00188	HMDB0000167	C4H9NO3
THYMINE	3.3	125.0357	1135	C00178	HMDB0000262	C5H6N2O2
tryptophan	6.36	205.0972	9060	C00525	HMDB0013609	C11H12N2O2
tyrosine	7.68	182.0812	6057	C00082	HMDB0000158	C9H11NO3
valine	7.2	118.0863	6287	C00183	HMDB0000883	C5H11NO2
guanosine	7.43	284.0989	6802	C00387	HMDB0000133	C10H13N5O5

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	Release date	Data Type	mwTab FileName (edit study)	Archive Filename	Data Review Status	Uploaded Files
5342 Upload	-	2024-11-04	-	Target edMS	jirleyb_20241104_105910_mwtab.txt Edit study	retinoids_mouse_plasma_serum_HILIC_XT4.zip	Response under review	HILIC_Plasma_Serum.zip (3.5G)
5326 Upload	-	2024-10-31	-	Target edMS	jirleyb_20241031_113710_mwtab.txt Edit study	retinoids_mouse_CSF_HILIC_XT3.zip	Response under review	CSF_HILIC.zip (2.1G)
5286 Upload	-	2024-10-11	-	Target edMS	jirleyb_20241011_095004_mwtab.txt Edit study	retinoids_mouse_plasma_serum_XT2.zip	Response under review	C18_Serum_Plasma_Retinoids.zip (4.1G)
5267 Upload	-	2024-10-07	2027-01-01	Target edMS	jirleyb_20241007_120309_mwtab.txt Edit study	retinoids_mouse_XT1.zip	Response under review	C18_CSF_retinoids.zip (3.2G)

Showing results 1 to 4 of 4

Results per page:

STAGE 2: ORGANIZING YOUR SUBMISSIONS

- You will create a new submission for every metabolomics experiment that you reference in your publication.
 - You can include two different columns as a part of one submission ([for example: if you ran mouse plasma on both C18 to detect folates and HILIC to detect polar metabolites, this can be part of one submission](#)).
 - Metabolomics Workbench prefers that you separate submissions based on tissue-type ([for example: if you ran mouse plasma and mouse CSF on both C18 to detect folates and HILIC to detect polar metabolites, the mouse plasma would be one submission and the mouse CSF would be a separate submission](#)).
- For multi-part studies (several experiments all belonging to the same project), you can indicate on the first page that it is a multi-part study. Despite what it says, you do not need to include in the comments “Study part m of n” unless you know.
 - Metabolomics Workbench reviewers will know something is a multi-part study if there are several submissions with identical Project Titles and Project Summaries.
- Submissions that are all a part of one project should have identical Project Titles and Project Summaries.
 - The Project Title and Project Summary are more generic and describe overarching goals and results, while the Study Title and Study Summary are more detailed. The Study Summary should clearly highlight the differences/how the study is unique and is included within the project.*

NEW SUBMISSION

Steps

- 1) Create account and login
- 2) Go to *New Submission* tab and fill out the information (see below)
 - a. **Name of raw data file(s) to be uploaded:** give your project a name (for example: `retinoids_mouse_CSF_HILIC.zip`)
 - b. **Data type being submitted:** choose among MS, Targeted MS, Untargeted MS, Targeted and untargeted MS (for Kanarek Lab projects, for the most part it will be Targeted MS)
 - c. **Protocol/methods filename(s):** protocol.docx
 - d. **MS/NMR instrument manufacturer:** Thermo
 - e. **MS/NMR instrument model:** Q Exactive Orbitrap
 - f. **Binary data format:** .RAW
 - g. **Open source text formats:** mzML
 - h. **MS level in raw data (if MS data):** choose MS2 only if applicable
 - i. **Multi-part study:** choose Yes or No
 - j. **Samples analyzed by Metabolon:** No
 - k. **Embargo:** choose Yes or No (generally yes if the paper has not been published yet)
 - l. **Embargo until:** provide date in the future
- 3) Submit

Overview

New Submission

List your submissions

Test FTP Upload

Tutorials

NOTE: Please do not use multiple tabs or browsers to do multiple simultaneous uploads.

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

* mwTab file name	jrileyb_20250102_102526_mwtab.txt	(Automatically assigned name)
* Name of raw data file(s) to be uploaded		(e.g. MyData.zip, MyData.7z)
* Data type being submitted		(Use separate submissions for studies containing both MS and NMR data)
* Protocol/methods filename(s)		
* MS/NMR instrument manufacturer		
* MS/NMR instrument model		
* Binary data format		(e.g. .WIFF (AB/Sciex), .RAW (Thermo) or .d (Agilent))
* Open source text formats		(e.g. mzML, mzXML, CDF)
MS level in raw data (if MS data)		(Specify the MS acquisition level in raw data files)
* Multi-part study		(For multi-part studies, add additional information such as "Study part m of n" in comments field)
* Samples analyzed by Metabolon		(For studies analyzed by Metabolon, you must use the Metabolon template during submission)
* Embargo		(If Yes, then please specify date below)
Embargo until		(e.g. 1 year, 6 months, or YYYY-MM-DD)
HHEAR/CHEAR study	☐	(For NIH's HHEAR/CHEAR program only. Add any additional information in comments field)
HHEAR/CHEAR project ID		(Required for HHEAR/CHEAR program only)
NIH funding source		(For NIH programs only)
NIH Common Fund component		(For NIH programs only)
Comments		

Submit

Reset

UPLOAD AND MANAGE EXPERIMENTAL DATA AND METADATA

Steps

- 1) Choose *New online study submission*.
- 2) You will see a page that asks whether you want to start a new online study submission or use another study as a template, choose *Start a new online study submission*.
 - a. After creating your first experiment submission, it will appear as an option to use as a template in future submissions, which may be helpful for creating additional submissions that are part of the same project. If it is the first submission for the project, choose *Start a new online study submission*.

Upload and Manage Experimental Data and Metadata



Please click **New online study submission** button to start a new study submission and enter metadata and results for your study with DataTrack ID **5504** and mwTab file name **jrileyb_20250103_135859**. You will be prompted to upload an archive file after successful completion of the online submission process.

[New online study submission](#)

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[UC San Diego](#)

PROJECT METADATA

Steps

- 1) Fill out all fields highlighted in red.
 - a. Project Title: may want to use your paper title ([this will be identical for all submissions for this project](#))
 - b. Project Summary: may want to use your paper abstract ([this will be identical for all submissions for this project](#))
- 2) **BCH Address:** 61 Binney St Boston, MA 02115
- 3) Choose *Add project metadata*.

mwTab identifier: jrileyb_20250103_135859

Jump to: [Study](#) [Subject](#) [Study Design](#) [Collection](#) [Treatment](#) [SamplePrep](#) [MS/NMR Data](#) [Finalize](#)

project information	Add project metadata Reset	
Project Title:		
Project Type:		
Project Summary:		
Institute:	Boston Children's Hospital	
Department:		
Laboratory:		
Last Name:	Brook	
First Name:	Jeannette	
Address:	61 Binney St, Boston, MA, 02115, USA	
Email:	jeannette.brook@childrens.harvard.edu	
Phone:		
Funding Source:		
Project Comments:		
Publications:		
contributors:		
project information	Add project metadata Reset	
Display all protocol/methods files uploaded in previous submissions		

STUDY METADATA

Steps

- 1) Fill out all fields highlighted in red.
 - a. Subject Type: choose an option from the drop-down menu
 - b. Study Title: should be more specific to the specific experiment/submission
 - c. Study Summary: should be more specific to the specific experiment/submission
- 2) **BCH Address:** 61 Binney St Boston, MA 02115
- 3) Choose *Add study metadata*.

mwTab Identifier: jrileyb_20250103_135859 [Return to start](#)

Jump to: [Project](#) [Study](#) [Subject](#) [Study Design](#) [Collection](#) [Treatment](#) [SamplePrep](#) [MS/NMR Data](#) [Finalize](#)

study information	Add study metadata	Reset
Subject Type:	Mammalian subjects This choice dictates which context-specific metadata items appear in subsequent sections	
Study Title:		
Study Type:		
Study Summary:		
Institute:	Boston Children's Hospital	
Department:		
Laboratory:		
Last Name:	Brook	
First Name:	Jeannette	
Address:	61 Binney St, Boston, MA 02115, USA	
Email:	jeannette.brook@childrens.harvard.edu	
Phone:	3035493341	
Number of Groups:		
Total Subjects:		
Number of Males:		
Number of Females:		
Study Comments:		
Publications:		
chear_study:		
analysis_type_detail:		
study information	Add study metadata	Reset
Display all protocol/methods files uploaded in previous submissions		

SUBJECT METADATA

Steps

- 1) Fill out all fields highlighted in red.
 - a. Subject Species: choose option from drop-down menu
- 2) Choose *Add subject metadata*.

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Jump to: [Project](#) [Study](#) [Subject](#) [Study Design](#) [Collection](#) [Treatment](#) [SamplePrep](#) [MS/NMR](#) [Data](#) [Finalize](#)

subject information	Add subject metadata Reset
Subject Type:	Mammal (entered in Study page)
Subject Species:	Mouse (Mus musculus)
Taxonomy ID:	10090
Genotype/Bacterial Strain:	
Age or Age Range:	
Weight or Weight Range:	
Height or Height Range:	
Gender:	
Animal Animal Supplier:	
Animal Housing:	
Animal Light Cycle:	
Animal Feed:	
Animal Water:	
Animal Inclusion Criteria:	
Species Group:	
subject information	Add subject metadata Reset
Display all protocol/methods files uploaded in previous submissions	

STUDY DESIGN

See *How To Create Metabolomics Workbench Excel Files* document.