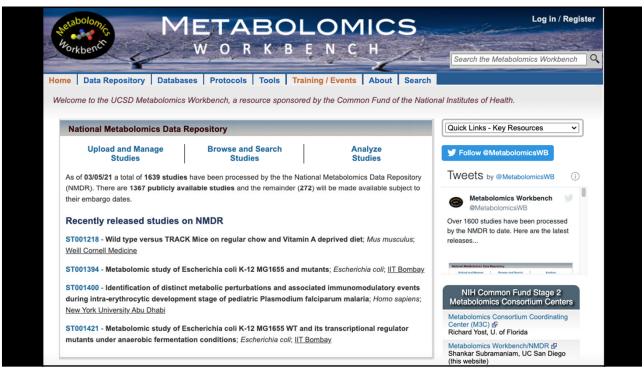
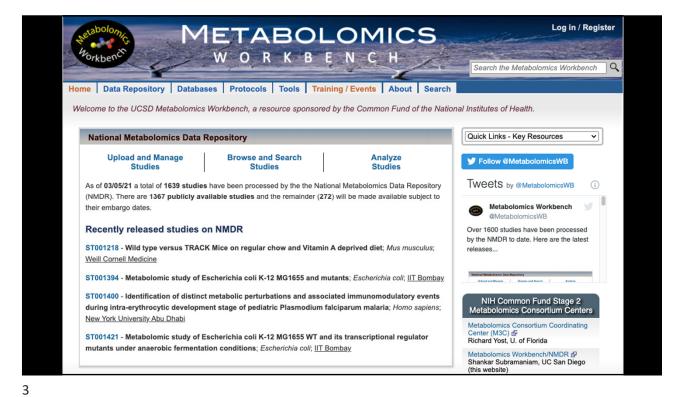
Metabolomics workbench

https://www.metabolomicsworkbench.org/

1

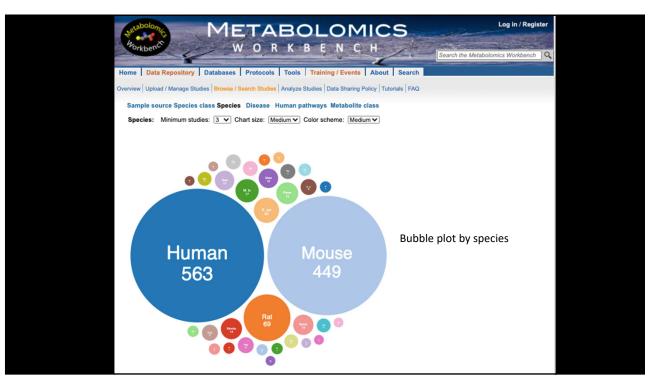




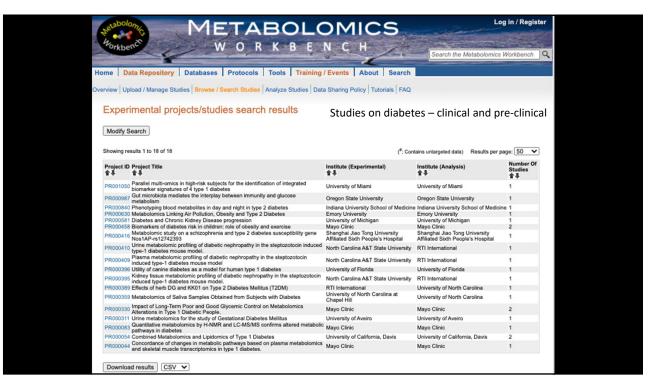
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Link to the first diabetes study

https://www.metabolomicsworkbench.org/data/DRCCMetadata.php?Mode=Project&ProjectID=PR001050

9

Summary of project PR001050

Data from proteomics, metabolomics, lipidomics and transcriptomics

This data is available at the NIH Common Fund's National Metabolomics Data Repository (NMDR) website, the Metabolomics Workbench, https://www.metabolomicsworkbench.org, where it has been assigned Project ID PR001050. The data can be accessed directly via it's Project DOI: 10.21228/M8ZX18
This work is supported by NIH grant, U2C- DK119886.

See: https://www.metabolomicsworkbench.org/about/howtocite.php $\mathcal Q$

Project ID:	PR001050
Project DOI:	doi: 10.21228/M8ZX18
Project Title:	Parallel multi-omics in high-risk subjects for the identification of integrated biomarker signatures of 4 type 1 diabetes
Summary:	Biomarkers are of paramount importance for early disease detection and are particularly valuable in type 1 diabetes (T1D) to prevent significant β cell loss before the onset of clinical symptoms. Thus far, single-omics studies have failed to identify such T1D biomarkers. Here, we present proof-of-concept studies to demonstrate the potential for identifying integrated biomarker signature(s) of T1D using parallel multi-omics. Blood from human subjects at high risk for T1D (and healthy controls; n=4 each) were subjected to parallel unlabeled proteomics, metabolomics, lipidomics, and transcriptomics. The integrated dataset was analyzed using Ingenuity Pathway Analysis (IPA) software for disturbances in the at-risk subjects compared to the controls.
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Phone:	305-482-4103

Perform statistical analysis | Show all samples | Show named metabolites | Download named metabolite data | Download all metabolite data | Download mwTab file (text) | Download mwTab file(JSON) | Download data (Contains raw data) Study ID ST001642 Lipidomics in high-risk subjects for the identification of integrated biomarker signatures of type 1 diabetes We present the lipidome of plasma collected from high-risk type 1 diabetes subjects. The methyl tert-butyl ether (MTBE) method was used for lipid extraction, followed by high performance liquid chromatography (HPLC) tandem mass spectrometry (LC-MS/MS) using a Q Exactive Orbitrap mass spectrometer and an Accela 600 HPLC. Lipid species were identified and quantified by analyzing the raw files in LipidSearch 4.2. Further analysis was conducted using Graphpad Prism and Ingenuity Pathway Analysis (IPA). University of Miami Bhattacharva Last Name First Name Address 1638 NW 10th Avenue, Room 706-A, Miami, FL 33136 Phone 305-482-4103 2021-01-06 Raw Data Yes Available Raw Data .raw File Type(s) Analysis LC-MS Type Detail Release 2021-01-25 Date Release

11

Statistics Toolbox for Study: ST001642

Title: Lipidomics in high-risk subjects for the identification of integrated biomarker signatures of type 1 diabetes

Select a dataset:

Reversed phase POSITIVE ION MODE ▼

Run analyses on data in Study ST001642 Dataset: Reversed phase POSITIVE ION MODE

Metabolite classes (all analyses combined)

- · Pie chart of metabolite super classes
- Pie chart of metabolite main classes
- · Pie chart of metabolite sub classes

Normalization and averaging

- · Show Metabolite averages per experimental factor
- · Perform normalization on data
- · Create Relative log abundance plots

Univariate analysis

- Perform multi-condition dot plot analysis New!
- Perform Volcano plot analysis
- Perform ANOVA analysis

MetENP: Metabolite enrichment and species-specific pathway annotation New!

- MetENPWeb analysis
- MetENP R package
- MetENP tutorial

Clustering and correlation

- · Perform hierarchial or heatmap cluster analysis
- · Perform Clustered correlation analysis
- · Perform Network analysis on correlated metabolites

Multivariate analysis

- · Perform Principal component analysis
- · Perform Linear discriminant analysis
- · Perform Partial least-squares discriminant analysis (PLS-DA)

Classification and feature analysis

- Perform OPLS-DA and VIP projection
- Random Forest and VIP projection

Mapping metabolites to human biochemical pathways

- · Map study metabolites to HMDB and KEGG pathways
- · Map study metabolites to pathways with ratio/t-test data