

Children's Health Exposure Analysis Resource (CHEAR)

CHEAR Data Submission and Review Portal (DSRP) - User Manual

Introduction

Welcome to the CHEAR Data Submission and Review Portal (DSRP)!

The URL for DSRP is: <https://cheardatacenter.mssm.edu/>

This User Manual outlines the Major Functions and Processes of DSRP and describes how to use them. This manual is for Primary Investigators (i.e., "PI"s) and their Co-Investigators. This manual is also available at the DSRP Q&A link:

[https://cheardatacenter.mssm.edu/CHEAR DSRP User Manual PI v2 0.pdf](https://cheardatacenter.mssm.edu/CHEAR_DSRP_User_Manual_PI_v2_0.pdf)

These users access the DSRP to upload their original study data and associated data dictionary, all project supporting documents, generate CHEAR participant IDs (PIDs), map CHEAR PIDs to original subject IDs and/or original sample IDs, map CHEAR SIDs (CHEAR Coordinating Center provides CHEAR SIDs to PI) to CHEAR PIDs, and retrieve lab result data.

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1.0 Getting Access to the Data Submission and Review Portal

All PIs and their Co-Investigators can access DSRP to view their CHEAR projects that have been initiated.

The Application and Review process is managed through a separate web site, “MyCHEAR” , at <https://mycheardatacenter.mssm.edu/>

- Once your project application has reached the appropriate status in MyCHEAR, you will receive an email from CHEAR Data Center (DC), informing you that your project is accessible via CHEAR DSRP. This email will provide login instruction and a temporary password, if you are a new CHEAR DSRP user.
- Upon logging in to the DSRP for the first time (see the “logging on” section below), you will be prompted to change your password.

1.1 System Requirements

The CHEAR Data Submission and Review Portal is an internet based system. To access it, you will need a computer that has internet connection and a web browser. Internet Explorer (v. 11 or higher) or Google Chrome (v. 50 or higher) is recommended. (Firefox is not recommended).

1.2 Logging on

Access the CHEAR Data Submission and Review Portal Home Page at the following URL.

<https://cheardatacenter.mssm.edu/>

The Home page displays Summary Info for Subjects and Samples already in the system, as well as a map of participating PI’s institutions. The map and Subject, Sample distributions will change when the underlying data change.

- Enter your Email Address and Password, and click the Log In button.
- If this is your first time logging on, please see the “Getting Access” Section above.

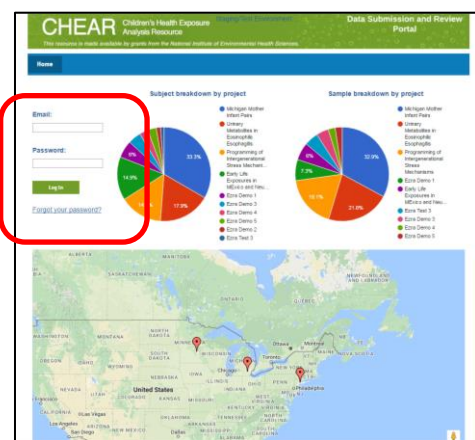
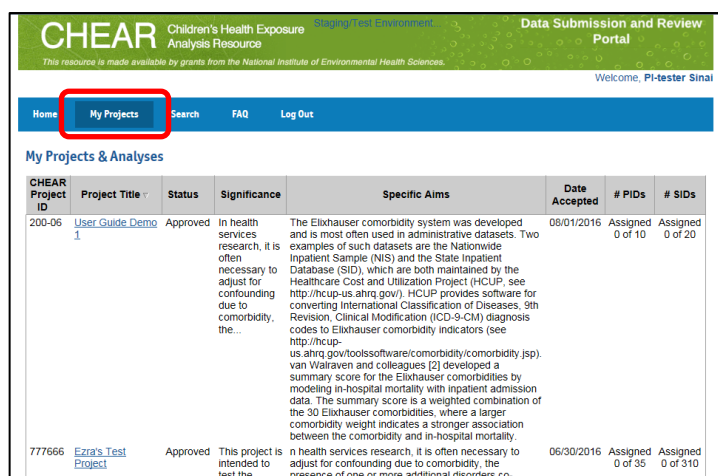


Figure 1 - Login screen

2.0 Retrieving CHEAR PIDs and Loading your Data Files

2.1 Accessing Your Projects

Once you have logged in, you can click on the “My Projects” link on the blue Navigation Bar at the top of the screen, which will show a list of the projects that you are assigned to as a PI or Co-Investigator (see Figure below).



CHEAR Project ID	Project Title	Status	Significance	Specific Aims	Date Accepted	# PIDs	# SIDs
200-06	User Guide Demo	Approved	In health services research, it is often necessary to adjust for confounding due to comorbidity, the...	The Elixhauser comorbidity system was developed and is most often used in administrative datasets. Two examples of such datasets are the Nationwide Inpatient Sample (NIS) and the State Inpatient Database (SID), which are both maintained by the Healthcare Cost and Utilization Project (HCUP, see http://hcup-us.ahrq.gov/). HCUP provides software for converting International Classification of Diseases, 9th Revision, Clinical Modification (ICD-9-CM) diagnosis codes to Elixhauser comorbidity indicators (see http://hcup-us.ahrq.gov/tools/software/comorbidity/comorbidity.jsp). van Walraven and colleagues [2] developed a summary score for the Elixhauser comorbidities by modeling in-hospital mortality with inpatient admission data. The summary score is a weighted combination of the 30 Elixhauser comorbidities, where a larger comorbidity weight indicates a stronger association between the comorbidity and in-hospital mortality.	08/01/2016	Assigned 0 of 10	Assigned 0 of 20
777666	Ezra's Test Project	Approved	This project is intended to test the	n health services research, it is often necessary to adjust for confounding due to comorbidity, the presence of one or more additional disorders co-	06/30/2016	Assigned 0 of 35	Assigned 0 of 310

Figure 2 – My Projects screen

- The list can be sorted by Project ID, Title, or Status, by clicking on the column headers.
- The information displayed within the columns has been gathered from your project application submitted via the “MyCHEAR” portal, and the total numbers of subjects and specimens were updated by the Lab Hub and the Data Center.
- Clicking on the Project Title will navigate you to the Project Detail screen.

2.2 Project Details

The “View Project” page lists the high-level project information that was provided on your project application in the “MyCHEAR portal” and the total numbers of subjects and specimens were updated by the Lab Hub and the Data Center.

At the bottom of the page, the set of Analysis for this project as specified within the “MyCHEAR portal” are listed.

CHEAR Children's Health Exposure Analysis Resource Paging/Test Environment Data Submission and Review Portal

This resource is made available by grants from the National Institute of Environmental Health Sciences. Welcome, PI-tester Sinai

[Home](#) [My Projects](#) [Search](#) [FAQ](#) [Log Out](#)

View Project

CHEAR Project ID: 200-06 CHEAR Project Status: Approved

Project Title: User Guide Demo 1

Significance: In health services research, it is often necessary to adjust for confounding due to comorbidity, the presence of one or more additional disorders co-occurring with a primary disorder. One popular method of comorbidity adjustment is the Elixhauser comorbidity system, [1] a set of 30 comorbidity indicators.

Specific Aims: The Elixhauser comorbidity system was developed and is most often used in administrative datasets. Two examples of such datasets are the Nationwide Inpatient Sample (NIS) and the State Inpatient Database (SID), which are both maintained by the Healthcare Cost and Utilization Project (HCUP, see <http://hcup-us.ahrq.gov>). HCUP provides software for converting International Classification of Diseases, 9th Revision, Clinical Modification (ICD-9-CM) diagnosis codes to Elixhauser comorbidity indicators (see <http://hcup-us.ahrq.gov/toolssoftware/comorbidity/comorbidity.jsp>). van Walraven and colleagues [2] developed a summary score for the Elixhauser comorbidities by modeling in-hospital mortality with inpatient admission data. The summary score is a weighted combination of the 30 Elixhauser comorbidities, where a larger comorbidity weight indicates a stronger association between the comorbidity and in-hospital mortality.

Subject Number: Assigned 0 of 10 **Sample Number:** Assigned 0 of 20

Date Accepted to CHEAR: 08/01/2016

Principal Investigator: PI-tester Sinai;

Contributing: Co-PI-Tester Sinai;

Step 1: Generate CHEAR Participant IDs (0 allocated already)

Step 3: Upload Data

Data Uploaded Active ▾

File Name	File Description	Date Uploaded	File	Uploaded By	Category
Generated IDs					
File Name	Date Uploaded	File	Uploaded By		

Analyses

Analysis Title	Analysis Method	Number of Subjects	Number of Samples
BM2 - Blood Metals Cs and Sb		5	10
BSMOKE - Tobacco Metabolites		5	10

Figure 3 – Project Detail screen

- The project level details will list the Number of Subjects and Specimens out of the total assigned to the project already allocated. If none have been generated yet, they will be listed as 0 (see circled section in Figure above).
- The Page contains several buttons, which will be described in detail below. Stepping through the actions available via the buttons will allow you to perform all the steps necessary for retrieving your CHEAR PIDs, mapping your original subject or specimen IDs, and uploading any project-related data and documents you may have.

2.3 Step 1: Generate CHEAR PIDs

The “View Project” page contains a button called “Generate CHEAR Participant IDs” (see figure below).

This button will allow you to generate and retrieve part or all the total number of CHEAR PIDs that have been assigned to this project. Each individual study subject should have a participant ID, regardless of sample availability.

us.ahrq.gov/toolsoftware/comorbidity/comorbidity.jsp). van Vliet and colleagues [2] developed a score for the Elixhauser comorbidities by modeling in-hospital mortality with inpatient admission summary score is a weighted combination of the 30 Elixhauser comorbidities, where a larger weight indicates a stronger association between the comorbidity and in-hospital mortality.

Subject Number: Assigned 0 of 10 **Sample Number:** Assigned 0 of 20

Date Accepted to CHEAR: 08/01/2016

Principal Investigator: PI-Tester Sinai;
Contributing: Co-PI-Tester Sinai;

Step 1: Generate CHEAR Participant IDs (0 allocated already)

Figure 4 – Generate CHEAR Participant IDs button

- Clicking the button navigates you to a separate “Generate PID page”

Home My Projects Search FAQ Log Out

Generate CHEAR Participant IDs

CHEAR Project ID: 200-06 CHEAR Project Status: Approved

Generate CHEAR Participant IDs for Project

Enter # of Participants:

Cancel Generate IDs

Figure 5 – Generate CHEAR Participant IDs screen

- Enter the Number of CHEAR PIDs that you would like to generate and retrieve, and click the “Generate IDs” button.

Note: you can enter part or all of the total number of PIDs you had specified for your project.

If you enter more than the total number, however, you will receive an alert message.

- The following page will appear with a downloadable set of CHEAR PIDs.

CHEAR Children's Health Exposure Analysis Resource Staging/Test Environment Data Submission and Review Portal

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Home My Projects Search FAQ Log Out

Generate CHEAR Participant IDs

CHEAR Project ID: 200-06 CHEAR Project Status: Approved

of Participant IDs Requested: 10

Download Participant IDs

Done

Figure 6 – Generated Participant IDs file

- The CHEAR PID file will open in Excel and will contain five columns as shown by the following figure, one containing the set of CHEAR PIDs and others containing CHEAR project ID, and time stamps. One column, Original Subject ID, is for you to map original subject IDs to CHEAR PIDs. You can save this file on your computer for reference, if desired.

A	B	C	D	E
CHEAR PID	Original Subject ID	CHEAR Project ID	Created Date Time	Modified Date Time
6561351	ori_sub_1	200-2017	5/1/2017 9:19	5/17/2017 11:05
8029779	ori_sub_2	200-2017	5/1/2017 9:19	5/17/2017 11:05
1356773	ori_sub_3	200-2017	5/2/2017 10:08	5/17/2017 11:05
3529823	ori_sub_4	200-2017	5/2/2017 10:08	5/17/2017 11:05
9369265	ori_sub_5	200-2017	5/3/2017 9:26	5/17/2017 11:05

Figure 7 – PIDs, once downloaded

- Note:** The CHEAR PIDs are also always available for download from the “View Project” page (see Figure below)

View Project

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Project Title: Production Placeholder

Significance: Placeholder Placeholder

Specific Aims: Placeholder Placeholder

Subject Number: Assigned 2 of 10 Sample Number: Assigned 0 of 20

Date Accepted to CHEAR: 02/01/2017

Principal Investigator: PI-tester Sinai; Xin Zheng;

Contributing:

Step 1: [Generate CHEAR Participant IDs \(2 allocated already\)](#)

Step 2 (optional): [Map Original Subject IDs](#) [Map Original Specimen IDs](#)

Step 3: [Upload Data](#)

Step 4, Update Status: [Ready for Stats Core Review](#)

Data Uploaded Active

File Name	File Description	Date Uploaded	File	Uploaded By Category
julia_canada.xlsx	aaa	02/13/2017		PI-tester SinaiData Dictionary / Codebook
Test Worksheet.xlsx	Production TEST file	02/13/2017		PI-tester SinaiData Dictionary / Codebook
CHEAR_DRMC_User_Manual_v3.docx	test for sizing	02/15/2017		PI-tester SinaiSupporting Documents for Project

Generated IDs

File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated

Analyses

Analysis Title	Sample Matrix	Lab Hub Assigned	Number of Samples	File Count
Analysis Placeholder			0	0

Figure 8 – Generated PIDs always available on the “View Project” Screen

2.4 Step 2a: (Optional) Map Original Subject ID's to CHEAR PIDs

The “View Project” page contains a button called “Map Original Subject IDs” (see figure below).

This button allows you to enter and map your original subject ID's (that you may have used to identify your subjects up to this point), to your CHEAR PIDs.

Based on the design of your study, you may have questions on how many or which study subjects require a CHEAR PID assignment. Please consult with your CHEAR Data Center analyst. You can email CHEARSupport@mssm.edu if you need to identify your analyst.

View Project

CHEAR Project ID:	200-2017	CHEAR Project Status:	Approved
Project Title:	Production Placeholder		
Significance:	Placeholder Placeholder		
Specific Aims:	Placeholder Placeholder		
Subject Number:	Assigned 2 of 10	Sample Number:	Assigned 0 of 20
Date Accepted to CHEAR:	02/01/2017		
Principal Investigator:	PI-tester Sinai; Xin Zheng;		
Contributing:			

Step 1: Generate CHEAR Participant IDs (2 allocated already)

Step 2 (optional): Map Original Subject IDs Map Original Specimen IDs

Step 3: Upload Data

Step 4, Update Status: Ready for Stats Core Review

Figure 9 – Map Original Subject IDs button – on the View Project page

- Clicking the “Map Original Subject IDs” button navigates you to a separate “Map Original Subject IDs” page (see figure below)

Map Original Subject IDs

CHEAR Project ID:	200-2017	CHEAR Project Status:	Approved
-------------------	----------	-----------------------	----------

Choose a CHEAR Participant ID	Original Subject ID
<input type="text"/>	<input type="text"/>

OR

Example:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

Assign

CHEAR Participant ID	Original Subject ID	Remove
----------------------	---------------------	--------

Done

Figure 10 – Map Original Subject IDs page

- There are two methods for mapping Original Subject IDs to CHEAR PIDs:
 - One by One, or
 - In Bulk (copy and paste all at once)
- To map “**One by One**”, begin entering the desired CHEAR PID in the Upper Left Hand field (the field will “auto-complete” by searching your CHEAR PIDs, as you type)

Map Original Subject IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Choose a CHEAR Participant ID

Original Subject ID

OR

Example: Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

CHEAR Participant ID	Original Subject ID	Remove
----------------------	---------------------	--------

Figure 11 – Map CHEAR PID to Original Subject ID (one by one) – enter PID

- Then enter the Original subject ID and click “Assign”

Map Original Subject IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Choose a CHEAR Participant ID

Original Subject ID

OR

Example: Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

CHEAR Participant ID	Original Subject ID	Remove
----------------------	---------------------	--------

Figure 12 – Map CHEAR PID to Original Subject ID (one by one) – enter Original Subject ID

- The resulting Mapping will appear at the bottom of the screen (and can be deleted if necessary via the “remove link”)

Map Original Subject IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Choose a CHEAR Participant ID Original Subject ID

OR

Example:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

[Assign](#)

CHEAR Participant ID	Original Subject ID	Remove
6561351	ori_sub_1	

[Done](#)

Figure 13 – Mapped CHEAR PIDs and Original Subject IDs

- To map by the “**In Bulk (copy and paste all at once)**” method, enter a Tab-Delimited set of CHEAR PID – Original Subject ID rows in the lower right Text Area.
NOTE: These values may be copied and pasted directly from an excel spreadsheet
 For example, copy the desired pairs from your local spreadsheet

A	B	C
CHEAR PID	Original Subject ID	
6561351		
8029779	ori_sub_2	

Figure 14 – Researcher’s CHEAR PID to Original Subject ID mapping file

- Paste them into the lower right text area, and click the “Assign” button.

Map Original Subject IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Choose a CHEAR Participant ID Original Subject ID

OR

Example:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

8029779 ori_sub_2

[Assign](#)

CHEAR Participant ID	Original Subject ID	Remove
6561351	ori_sub_1	

Figure 15 – Map CHEAR PID to Original Subject ID (in bulk)

- The resulting mapping of multiple pairs will now appear at the bottom of the screen, and can be deleted if necessary via the “remove link”.

Map Original Subject IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Choose a CHEAR Participant ID

Original Subject ID

OR

Example:

	A	B
1	CHEAR PID	Original PID
2	1475193	A231123
3	1155233	C123232

Copy and paste mapping of CHEAR PIDs / Original Subject IDs pairs:

Assign

CHEAR Participant ID	Original Subject ID	Remove
6561351	ori_sub_1	🗑
8029779	ori_sub_2	🗑

Done

Figure 16 – Mapped CHEAR PIDs and Original Subject IDs

- NOTE:** Once the PIDs have been mapped to original subject ID’s (by either method), the mapped values will always be accessible to download from the View Project screen, within the CHEAR Participant ID’s file (mentioned above).

File Name	File Description	Date Uploaded	File	Uploaded By	Category
Generated IDs					
CHEAR_Participant_IDs.xls			📎	System Generated	

Figure 17 – PIDs to Original Subject IDs mapping file is available on the “View Project” Screen

2.5 Step 2b: (Optional) Map Original Specimen IDs to Subjects

The “View Project” page contains a button called “Map Original Specimen IDs” (see figure below).

This button allows you to enter and map your original specimen ID’s (that you may have used to identify your specimens up to this point), to your subjects. You can map specimens to subjects either by linking to “CHEAR PID” or to “Original Subject ID” (if you have already provided Original Subject IDs, see previous section).

NOTE: While a subject can have more than one original specimen ID, the same specimen ID cannot be mapped to more than one subject.

View Project

CHEAR Project ID:	200-2017	CHEAR Project Status:	Approved
Project Title:	Production Placeholder		
Significance:	Placeholder Placeholder		
Specific Aims:	Placeholder Placeholder		
Subject Number:	Assigned 2 of 10	Sample Number:	Assigned 0 of 20
Date Accepted to CHEAR:	02/01/2017		
Principal Investigator:	PI-tester Sinai; Xin Zheng;		
Contributing:			

Step 1: [Generate CHEAR Participant IDs \(2 allocated already\)](#)

Step 2 (optional): [Map Original Subject IDs](#) [Map Original Specimen IDs](#)

Step 3: [Upload Data](#)

Step 4, Update Status: [Ready for Stats Core Review](#)

Figure 18 – Map Original Specimen IDs button – on the View Project page

- Clicking the “Map Original Specimen IDs” button navigates you to a separate “Map Original Specimen IDs” page (see figure below)
- The screen provides a Choice of which Subject Identifier to map Original Specimen IDs to:
 - Original Subject ID (if these had previously been entered)
 - CHEAR PID

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Data Submission and Review Portal
Welcome, Xin Zheng

[Home](#) [My Projects](#) [Search](#) [FAQ](#) [Admin](#) [Log Out](#)

Map Original Specimen IDs

CHEAR Project ID:	200-2017	CHEAR Project Status:	Approved
-------------------	----------	-----------------------	----------

Please select one of the following mapping options
Please select:

☐ Mapping of Original Subject ID's to Original Specimen ID's
☐ Mapping CHEAR PID to Original Specimen ID's

Original Specimen ID	Original Subject ID	CHEAR PID	Remove
<div>Done</div>			

Figure 19 – Map Original Specimen IDs page

- Once the CHOICE of subject identifier to be used for mapping is selected, the screen presents two methods for mapping Original Specimen ID's to subjects:
 - One by One, or
 - In Bulk (copy and paste all at once)
- To map “**One by One**”, begin entering the desired CHEAR PID / Original Subject ID (depending on your initial choice) in the Upper Left Hand field (the field will “auto-complete” as you type)

Map Original Specimen IDs

CHEAR Project ID: 200-2017

CHEAR Project Status: Approved

Please select one of the following mapping options

- ☐ Mapping of Original Subject ID's to Original Specimen ID's
☒ Mapping CHEAR PID to Original Specimen ID's

Type in a CHEAR PID

6561351

Type in a Original Specimen ID

OR

Assign

Figure 20 – Map Original Specimen IDs to PIDs page (one by one) – enter PID

- Then enter the original specimen ID and click “Assign”

Map Original Specimen IDs

CHEAR Project ID: 200-2017

CHEAR Project Status: Approved

Please select one of the following mapping options

- ☐ Mapping of Original Subject ID's to Original Specimen ID's
☒ Mapping CHEAR PID to Original Specimen ID's

Type in a CHEAR PID

6561351

Type in a Original Specimen ID

ori_spe_1

OR

Assign

Figure 21 – Map Original Specimen IDs to PIDs page (one by one) – enter Original Specimen ID

- The resulting Mapping will appear at the bottom of the screen (and can be deleted if necessary via the “remove link”)

[Home](#)
[My Projects](#)
[Search](#)
[FAQ](#)
[Admin >](#)
[Log Out](#)

Map Original Specimen IDs

CHEAR Project ID: 200-2017 CHEAR Project Status: Approved

Please select one of the following mapping options

☒ Mapping of Original Subject ID's to Original Specimen ID's
☐ Mapping CHEAR PID to Original Specimen ID's

Type in a Original Subject ID

Type in a Original Specimen ID

OR Assign

Example:

	A	B
1	PHJ67	ABC123
2	TV0X3	BCD456
3	UAEA8	CDE789

Copy and paste mapping of Original Subject IDs/ Original Specimen IDs pairs:

Original Specimen ID	Original Subject ID	CHEAR PID	Remove
ori_spe_1	ori_sub_1	6561351	

Figure 22 – Mapped Original Specimen IDs, Original Subject IDs and PIDs

To map by the “**Bulk (copy and paste all at once)**” method, enter a Tab-Delimited set of CHEAR-PID to Original Specimen ID pairs, or Original Subject ID to Original Specimen ID pairs in the Lower right Text Area. (corresponding to your initial mapping choice selection)

NOTE: These values may be copied and pasted directly from an excel spreadsheet

For example, copy the desired pairs from your local spreadsheet

A	B	C	D	E	F
CHEAR PID	Original Subject ID	Original Sample ID	CHEAR Project ID	Created Date Time	Modified Date Time
6457949	ori_sub_605	ori_spe_605	200-2017	6/5/2017 12:42	6/5/2017 12:49

Figure 23 – Researcher’s CHEAR PID – Original Subject ID – Original Specimen ID mapping file

and paste them into the lower right text area, and click the “Assign” button.

Map Original Specimen IDs

CHEAR Project ID: 200-2017

CHEAR Project Status:

Initial Data Reviewed by Stats Core

Please select one of the following mapping options

☒ Mapping of Original Subject ID's to Original Specimen ID's

☐ Mapping CHEAR PID to Original Specimen ID's

Type in a Original Subject ID

Type in a Original Specimen ID

OR

Assign

Example:

	A	B
1	PHJ67	ABC123
2	TV0X3	BCD456
3	UAE8	CDE789

Copy and paste mapping of Original Subject IDs/ Original Specimen IDs pairs:

ori_sub_605 ori_spe_605

Figure 24 – Map Original Specimen IDs to Original Subject IDs (in bulk)

- The resulting mapping of multiple pairs will now appear at the bottom of the screen, (and can be deleted if necessary via the “remove link”). Note that a single subject can be mapped to multiple Original Specimen IDs.

Original Specimen ID	Original Subject ID	CHEAR PID	Remove
ori_spe_2	ori_sub_2	8029779	
ori_spe_3	ori_sub_6	3598893	
ori_spe_4	ori_sub_6	3598893	
ori_spe_6	ori_sub_5	9369265	
ori_spe_605	ori_sub_605	6457949	

Done

Figure 25 – Mapped Original Specimen IDs, Original Subject IDs and PIDs

- NOTE:** Once the Original Specimen IDs have been mapped (by either method), the mapped values will always be accessible to download from the View Project screen, within the Original_Specimen_ID_mapping file.

Data Uploaded					Active
File Name	File Description	Date Uploaded	File	Uploaded By Category	
julia_canada.xlsx	aaa	02/13/2017		PI-tester SinaiData Dictionary / Codebook	
Test Worksheet.xlsx	Production TEST file	02/13/2017		PI-tester SinaiData Dictionary / Codebook	
CHEAR_DRMC_User_Manual_v3.docx	test for sizing	02/15/2017		PI-tester SinaiSupporting Documents for Project	
Generated IDs					
File Name	Date Uploaded	File	Uploaded By		
CHEAR_Participant_IDs.xls			System Generated		
Original_Specimen_ID_mapping.xls			System Generated		
Analyses					
Analysis Title	Sample Matrix	Lab Hub Assigned	Number of Samples	File Count	
Analysis Placeholder			0	0	

Figure 26 – Original Specimen IDs – Original Subject IDs – CHEAR PIDs mapping file is available on the “View Project” Screen

2.6 Step 3: Upload Study Results Data

The “View Project” page contains a button called “Upload Data” (see figure below). This button allows you to upload any project-related data that you have collected for your project (e.g., epidemiological data, questionnaire answers, demographics, etc.) You may also upload any additional supporting documents related to your project.

View Project

CHEAR Project ID:	200-2017	CHEAR Project Status:	Approved
Project Title:	Production Placeholder		
Significance:	Placeholder Placeholder		
Specific Aims:	Placeholder Placeholder		
Subject Number:	Assigned 2 of 10	Sample Number:	Assigned 0 of 20
Date Accepted to CHEAR:	02/01/2017		

Principal Investigator: PI-tester Sinai; Xin Zheng;
Contributing:

Step 1:

Generate CHEAR Participant IDs (2 allocated already)

Step 2 (optional):

Map Original Subject IDs

Map Original Specimen IDs

Step 3:

Upload Data

Step 4, Update Status:

Ready for Stats Core Review

Figure 27 – Upload Data button – on the View Project page

- Clicking the “Upload Data” button navigates you to a separate “Upload Project Data” page (see figure below)

CHEAR Children's Health Exposure Analysis Resource
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Staging Test Environment

Data Submission and Review Portal

Welcome, PI-tester Sinai

Home My Projects Search FAQ Log Out

Data Upload

CHEAR Project ID: 200-06 CHEAR Project Status: Approved

Upload a Project File

Category *:

Figure 28 – Upload Project Data Screen

- The Category menu contains 3 categories that you may select (see figure below)

Welcome, PI-tester Sinai

Home My Projects Search FAQ Log Out

Data Upload

CHEAR Project ID: 200-2017 CHEAR Project Status: Initial Data Reviewed by Stats Core

Category *:

Select Category

Data Dictionary / Codebook

Original Study Data

Supporting Documents for Project

Cancel

Upload a Project File

Upload

Figure 29 – Document Categories for upload.

- You can search your own local directory for a file to upload and attach a short description after selecting an upload file category.
- At least one “Data Dictionary / Codebook “ must be uploaded per project, since original study data files will need to be linked to it (see below).
- Uploading “Original Study Data” (epidemiological data, demographics data, etc.) requires some additional inputs:
 - You must indicate the associated Data Dictionary / Codebook (already uploaded).
 - You may select to indicate whether this data is de-identified.

Upload a Project File

Category *: Original Study Data

File *: Browse...

Short Description *:

Select Associated Codebook *:

Select Data Dictionary

De-identified? ☐

Cancel Upload

Figure 30 – Upload Data for “Original Study Data” category

- “Supporting Documents for Project” allows any type of file to be uploaded.

CHEAR Children's Health Exposure Staging/Test Environment Data Submission and Review Portal

This resource is made available by grants from the National Institute of Environmental Health Sciences.

Welcome, PI-tester Sinai

Home My Projects Search FAQ Log Out

Data Upload

CHEAR Project ID: 200-06 CHEAR Project Status: Approved

Upload a Project File

Category *: Supporting Documents for Project

File *: Choose File MSOW Pamphlet v3.pptx

Short Description *: test supporting document

Cancel Upload

Figure 31 – Data upload page for “Supporting Documents”

- Once the “Upload” button is clicked, the uploaded file will appear in the “Data Uploaded” section of the View Project page (see figure below).

NOTE: CHEAR Data Center personnel also have the ability to upload documents into your project space (this is especially relevant if you are collaborating with them on the content / structure of your data). You can tell who uploaded a file by looking at the “Uploaded By” column.

Step 1: Generate CHEAR Participant IDs (4 allocated already)

Step 2 (optional): Map Original Subject IDs Map Original Specimen IDs

Step 3: Upload Data

Step 4, Update Status: (Already updated) Current status: Initial Data Reviewed by Stats Core

Data Uploaded Active

File Name	File Description	Date Uploaded	File	Uploaded By Category
julia_canada.xlsx	aaa	02/13/2017		PI-tester SinaiData Dictionary / Codebook
Test Worksheet.xlsx	Production TEST file	02/13/2017		PI-tester SinaiData Dictionary / Codebook
CHEAR_DRMC_User_Manual_v3.docx	test for sizing	02/15/2017		PI-tester SinaiSupporting Documents for Project

Generated IDs

File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Original_Specimen_ID_mapping.xls			System Generated




Analyses



Analysis Title	Sample Matrix	Lab Hub Assigned	Number of Samples	File Count
Analysis Placeholder_1	Serum	T4 - Mt. Sinai	10	1

Figure 32 – Uploaded files displayed on View Project page

2.7 Archiving Uploaded Files

Files that you have uploaded may be “archived” (if they are incorrect or outdated, or have been replaced by a newer version).




Data Uploaded				
File Name	File Description	Date Uploaded	File	Uploaded By Category
CHEAR	project data dictionary	08/25/2016		PI-tester Sinai Data Dictionary / Codebook
Data_dictionary_template_v2.xlsx				
MSDW Pamphlet v3.pptx	test supporting document	08/25/2016		PI-tester Sinai Supporting Documents for Project
Specimen_Category.xlsx	Epi Data for Project	08/25/2016		PI-tester Sinai Project Results Data



Generated IDs			
File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Local_Specimen_ID_mapping.xls			System Generated

Analyses			
Analysis Title	Analysis Method	Number of Subjects	Number of Samples
BM2 - Blood Metals Cs and Sb		5	10
BSMOKE - Tobacco Metabolites		5	10

Figure 33 – Ability to Archive files

- To archive a file, click on the “archive” icon, next to the document (see figure above)
 - The system will prompt you for confirmation, and then archive your file.
- To see files that you have already archived, toggle the “File view selection box” to “Archived” (see figure below).
- To see your CURRENT set of files, toggle the selection back to “Active” (see figure below).

Data Uploaded				
File Name	File Description	Date Uploaded	File	Uploaded By Category
CHEAR	project data dictionary	08/25/2016		PI-tester Sinai Data Dictionary / Codebook
Data_dictionary_template_v2.xlsx				
MSDW Pamphlet v3.pptx	test supporting document	08/25/2016		PI-tester Sinai Supporting Documents for Project
Specimen_Category.xlsx	Epi Data for Project	08/25/2016		PI-tester Sinai Project Results Data

Generated IDs			
File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Local_Specimen_ID_mapping.xls			System Generated

Analyses			
Analysis Title	Analysis Method	Number of Subjects	Number of Samples

Figure 34 – File View selection box

2.8 Step 4: Submitting your Study Data for Review

Once you have uploaded ALL of your relevant study data, you should set the status of your Project to “Ready for Review by Stats Core”. This will automatically notify Data Center Statistical personnel that your data is ready for initial review.

Step 1: Reached the limit of CHEAR Participant IDs

Step 2: [Map Local Subject IDs](#) [Map Local Specimen IDs](#)

Step 3: [Upload Data](#)

Step 4, Update Status: [Ready for Stats Core Review](#)

Data Uploaded Active ▾

File Name	File Description	Date Uploaded	File	Uploaded By Category
-----------	------------------	---------------	------	----------------------

Figure 35 – Update Status

- Clicking the “Ready for Stats Core Review” will update the status of your project, and send a notification to Data Center Statistical-Core personnel.
 - Note:** You will still have full access to your project and files after this step.

View Project

CHEAR Project ID: 200-2017 **CHEAR Project Status:** Awaiting Review

Project Title: Production Placeholder

Significance: Placeholder Placeholder

Specific Aims: Placeholder Placeholder

Subject Number: Assigned 2 of 10 **Sample Number:** Assigned 0 of 20

Date Accepted to CHEAR: 02/01/2017

Principal Investigator: PI-tester Sinai; Xin Zheng;
Contributing:

Step 1: [Generate CHEAR Participant IDs \(2 allocated already\)](#)

Step 2 (optional): [Map Original Subject IDs](#) [Map Original Specimen IDs](#)

Step 3: [Upload Data](#)

Step 4, Update Status: (Already updated) Current status: Awaiting Review

Data Uploaded Active ▾

File Name	File Description	Date Uploaded	File	Uploaded By Category
julia_canada.xlsx	aaa	02/13/2017		PI-tester SinaiData Dictionary / Codebook
Test Worksheet.xlsx	Production TEST file	02/13/2017		PI-tester SinaiData Dictionary / Codebook
CHEAR_DRMC_User_Manual_v3.docx	test for sizing	02/15/2017		PI-tester SinaiSupporting Documents for Project

Generated IDs

File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Original_Specimen_ID_mapping.xls			System Generated

Figure 36 – Updated Project Status

- Once the “Ready for Stats Core Review” is clicked, the project Status appears as “Awaiting Review”
- The option to update the project status is no longer available.
- The project Status will change to “Initial Data Reviewed by Stats Core” when the DC Statistical Core finishes its review and release SIDs to the CHEAR Coordinating Center (CC).

3.0 Mapping CHEAR SIDs to PIDs, and Shipping your Samples

NOTE: This section assumes that you have already received the electronic set of SIDs and associated labels from CHEAR CC.

Once you have received your set of sample labels from CHEAR CC, which each have a barcoded Specimen ID (SID) encoded upon them, you can map each SID directly to a corresponding study participant via several methods available in the DSRP.

3.1 Navigate to the Map CHEAR Specimens to Participants page

- Log on and Navigate to your project.
- Click on the relevant project title that you want to map specimens for.
- Note: You can confirm that your project is ready for SID-to-PID mapping by seeing that the status reads “**Initial Data Reviewed by Stats Core**”

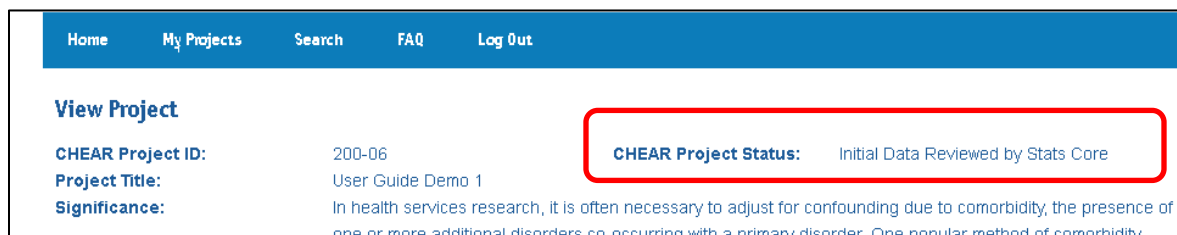


Figure 37 – Project Status on Project Review page

3.2 Map Specimens to Participants

- You can find two SID-PID mapping buttons on the Project Review page: “**Map CHEAR Specimens to Participants (one by one)**” or “**Map SIDs to PIDs in bulk**”. You can use either method to map your SIDs to PIDs.
 - **Note:** these buttons will only be available once the status of your project has been marked as “Initial Data Reviewed by Stats Core”

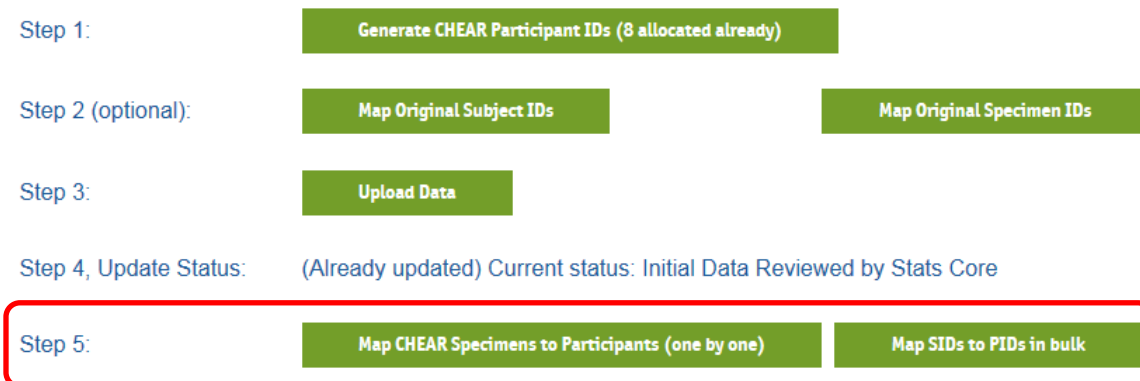


Figure 38 – Map CHEAR Specimens to Participants buttons on Project Review page

- Please click on the “Map CHEAR Specimens to Participants (one by one)” button to map SIDs to PIDs in one by one manner. The following mapping page will display.

Map CHEAR Specimen IDs

CHEAR Project ID: 999 CHEAR Project Status: Initial Data Reviewed by Stats Core

CHEAR PID

--All--

OR

Original Subject ID

--All--

OR

Original Specimen ID

--All--

Scan CHEAR SID *

Required Fields (*)

Select One or more Analyses that this Sample will be used for. (NOTE: More than one Analysis should only be selected for an SID if the receiving Lab will further aliquot the samples)

Analysis Name	Sample Matrix	Lab Hub Assigned
<input type="checkbox"/> Alex Test1		
<input type="checkbox"/> Alex Test2		
<input type="checkbox"/> Alex Test3		
<input type="checkbox"/> Metals Number 2		

Sample Quantity*: Sample Quantity (UOM)*: Concentration:
(required for DNA / RNA samples)

Optional Fields

Sample Collection Method:	<input type="text"/>	Sample Container Type:	<input type="text"/>	Sample Preservative:	<input type="text"/>
Sample Collection Date:	<input type="text"/>			Sample Aliquoting:	<input type="text"/>
Sample Storage Temp:	<input type="text"/>	Sample Freeze/Thaw Cycles:	<input type="text"/>	Sample Shipment Info:	<input type="text"/>
Comments by PI:	<input type="text"/>	Sample Group ID:	<input type="text"/>	Box-Position:	<input type="text"/>

☐ Keep Values in Fields for Next Assignment

Assign

Figure 39 – Map CHEAR Specimens to Participants (one by one) page

- This mapping approach provides several OPTIONS for how to map each CHEAR SID.
 - Map to CHEAR PID

- Map to Original Subject ID (if these were previously uploaded. See preceding sections)
 - Map to Original Specimen ID (if these were previously uploaded. See preceding sections)
 - **NOTE:** The system will only let you map a CHEAR SID to one of the above three options at a time. However, if you have selected to map to a CHEAR PID / Original Subject ID, and that Original Subject ID already has Original Specimen IDs mapped to it, the system will force you to further select a specific Original Specimen ID to map the CHEAR SID to.
- Select the PID / Original Subject ID / Original Specimen ID that you are mapping a particular CHEAR SID to.
 - You can then SCAN the full CHEAR SID directly from the Label into “CHEAR SID” text box (Red square in Figure 38)
 - Note: you can also type it in, if you prefer
 - Complete the “Required Fields” information (the system will alert if you do not fill out these fields)
 - Complete the “Optional Fields” information, if you prefer
 - Click the “Assign” Button
 - **Special Feature:** If there are multiple Samples that will require having the same / similar information entered in each of the Required / Optional fields, you can click on the “**Keep Values in Fields for Next Assignment**” checkbox (see screenshot below). This option will keep the values entered in the Required / Optional fields present for each CHEAR SID assignment.
 - When this option is not selected, the fields are cleared after each assignment).

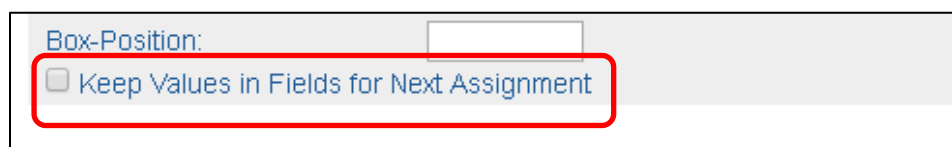


Figure 40 – Keep Values in Fields for Next Assignment flag

- The bottom of the screen displays the SID to PID mappings that you have completed. **Please Review.** If any of the mappings as entered are incorrect, they can be deleted by clicking on the associated “Remove” icon on the right-hand side.
- Once the mappings have been reviewed, clicking the “**Done**” button, which will navigate you back to the Project View.

Map CHEAR Specimen IDs

CHEAR Project ID: 200-04 CHEAR Project Status: Initial Data Reviewed by Stats Core

CHEAR PID OR Original Subject ID OR Original Specimen ID Scan CHEAR SID *

Required Fields (*)
Select One or more Analyses that this Sample will be used for. (NOTE: More than one Analysis should only be selected for an SID if the receiving Lab will further aliquot the samples)

Analysis Name	Sample Matrix	Lab Hub Assigned
<input type="checkbox"/> BM2 - Blood Metals Cs and Sb	Blood	Lab Test
<input type="checkbox"/> BSMOKE - Tobacco Metabolites	Urine	

Sample Quantity*: Sample Quantity (UOM)*: Concentration:
(required for DNA / RNA samples)

Optional Fields

Sample Collection Method:	<input type="text"/>	Sample Container Type:	<input type="text"/>	Sample Preservative:	<input type="text"/>
Sample Collection Date:	<input type="text"/>			Sample Aliquoting:	<input type="text"/>
Sample Storage Temp:	<input type="text"/>	Sample Freeze/Thaw Cycles:	<input type="text"/>	Sample Shipment Info:	<input type="text"/>
Comments by PI:	<input type="text"/>	Sample Group ID:	<input type="text"/>	Box-Position:	<input type="text"/>

☐ Keep Values in Fields for Next Assignment

Assign

Scan CHEAR SID	CHEAR PID	Original Subject ID	Original Specimen ID	Assigned Analyses	Sample Quantity	Sample Quantity (UOM)	Concentration	Sample Collection Method	Sample Container Type	Sample Preservative	Sample Collection Date	Sample Aliquoting	Sample Storage Temp	Sample Freezer/Thaw Cycles	Sample Shipment Info
2GL34	3087565	1281			500	ul					3/5/2009				
PI Comments:															
17KN1	3788007	1292			500	ul	1				6/15/2009				
PI Comments:															
41KX9	3788007	1292	999		500	ul	1				6/15/2009				
PI Comments:															
OY2S1	4826446	ori-sub_11			4.00	ml			undefined	undefined	1/1/2015		4	0	undefined
PI Comments:															
12C22	7098827				200.00	ul		needle	undefined	undefined	1/1/2015		-20	0	undefined
PI Comments:															

Figure 41 – Specimen ID – Participant ID mapping

- Please click on the “Map SIDs to PIDs in bulk” button to map many SIDs to PIDs at once. A mapping template, downloadable from DSRP, has to be used to conduct mapping in this manner. The following mapping page will display.

Welcome, PI-tester Sinai

Home My Projects Search FAQ Log Out

Data Upload

CHEAR Project ID: 200-2017 CHEAR Project Status: Initial Data Reviewed by Stats Core

Upload a Project File

Bulk Mapping: use SID-PID mapping template ([Download here](#)) to upload mapping file

Category *: SID-PID mapping

File *: Browse...

Short Description *: SID-PID mapping

Cancel Upload

Figure 42 – Map CHEAR Specimens to Participants (in bulk) page

- Please download the template and fill in all mandatory information. We encourage you to add all available optional information for each sample.

- Hint: file Original_Specimen_ID_mapping.xls, in the generated IDs section of the project review page, can be used to fill in the SID-PID mapping template.



Generated IDs			
File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Original_Specimen_ID_mapping.xls			System Generated



Figure 43 – Original_Specimen_ID_mapping.xls file in Generated IDs section of Project Review page

- Save you SID-PID mapping file on your local computer drive and name it meaningfully, such as SIDs-PIDs_mapping_CHEAR_Project_200-2017.xls where 200-2017 is the CHEAR project ID.
- Go to the bulk SID-PID mapping page, that is illustrated in Figure 42, browse to your mapping file (e.g. SIDs-PIDs_mapping_CHEAR_Project_200-2017.xls), and click the upload button.
- You should see your mapping file in the SID-PID mapping files section


Step 5:

Map CHEAR Specimens to Participants (one by one)
Map SIDs to PIDs in bulk

SID-PID mapping files Active

File Name	File Description	Date Uploaded	File	Uploaded By
SID-PID_mapping_template_2017_5_9.xlsx	SID-PID mapping	05/17/2017		Alex Zhitomirsky
test_SID-PID_mapping.xlsx	SID-PID mapping	05/18/2017		Alex Zhitomirsky

Data Uploaded

File Name	File Description	Date Uploaded	File	Uploaded By	Category
CRF Guide for MSDW_ezra_comments_v2.xlsx	test for encryption	03/02/2017		PI-tester Sinai	Original Study Data

Generated IDs



File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Original_Specimen_ID_mapping.xls			System Generated

Figure 44 – uploaded SID-PID mapping file

- The staffs at the Statistical Core of CHEAR DC will work with you closely to ensure the mapping is done correctly. Upon positive validation of your SID-PID mapping file, the staffs at Statistical Core will ingest SID-PID mapping data into DC database to update the Original_Specimen_ID_mapping.xls file.

3.3 Retrieve your Shipping Manifest

Once you have mapped PIDs to SIDs, a Shipping Manifest now appears in the Generated IDs section on the specific Analysis view (for which you had mapped the specimens). See circled portion on the screenshot above.




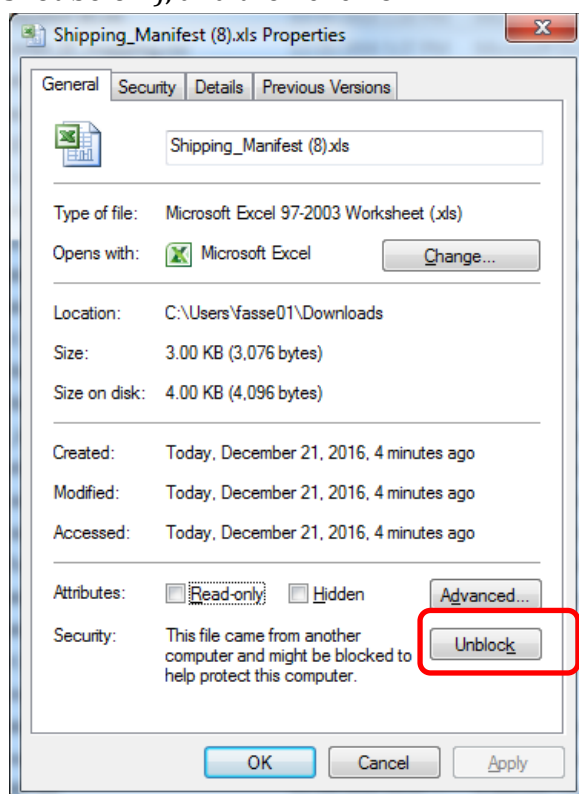
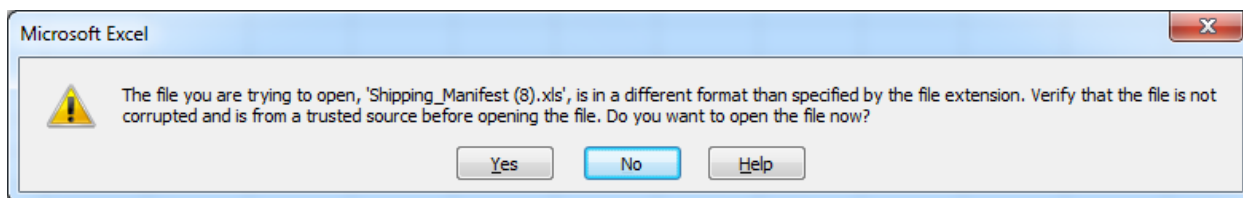
Generated IDs			
File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Original_Specimen_ID_mapping.xls			System Generated
Shipping Manifest - Lab Hub T1 - Emory			System Generated

Figure 45 Shipping Manifest file

- To download the Manifest, click on the “xls” icon.
- Important NOTE:** due to a very recent Microsoft release, there is an error opening the Excel file that may appear.
- We are working on fixing this. In the meantime the workaround is:
- The file may not open initially, or may look “blank” when opened
 - In windows, Right-click on the downloaded excel file, and click “Properties”
 - In the General tab of the properties window, click the “**Unblock**” button (see screenshot below), and then click OK.



- Now, try to re-open the excel file. You may be presented with the following alert. Click **Yes**

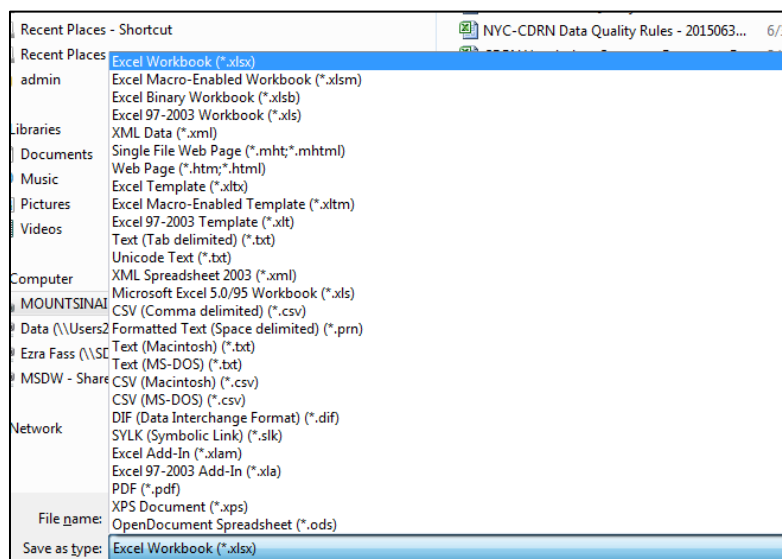


- The Shipping Manifest will open as a fully editable formatted excel document. Any data that had been entered on the screen shall be present on the Manifest.

Sample ID	Local SID	Lab Hub	Sample Group ID	Sample Collection Date	Sample Type	Sample Collection Method	Sample Container Type	Sample Preservative	Sample Quantity	Quantity UOM	Sample Aliquoting	Sample Storage Temp	Sample Freeze/Thaw Cycles	Sample Shipment Info
5X4P3	T2 - Michigan				WB				10/ml					
9NKH6	T2 - Michigan				WB				20/ml					
LSVU6	T2 - Michigan				WB				12/ml					

- Note:** Any changes made directly on the Excel file will not make their way back into the portal system unless directly entered onto the portal screen.

- **Note:** When saving the Shipping Manifest on your local computer, you should change the File Type to .xls / .xlsx to avoid re-encountering the formatting alerts mentioned above. (See screenshot below).



4.0 Retrieving Lab Analysis Data from the portal

NOTE: This section assumes that the Lab Hub has completed their sample analysis, and has uploaded their result data to the Data Submission and Review Portal.

4.1 Step One: Navigate to the Relevant “Analysis”

Step 1: Reached the limit of CHEAR Participant IDs

Step 2: [Map Local Subject IDs](#) [Map Local Specimen IDs](#)

Step 3: [Upload Data](#)

Data Uploaded Active

File Name	File Description	Date Uploaded	File	Uploaded By Category
CHEAR	project data dictionary	08/25/2016		PI-tester Sinai Data Dictionary / Codebook
Data_dictionary_template_v2.xlsx				
MSDW Pamphlet v3.pptx	test supporting document	08/25/2016		PI-tester Sinai Supporting Documents for Project
Specimen_Category.xlsx	Epi Data for Project	08/25/2016		PI-tester Sinai Project Results Data

Generated IDs

File Name	Date Uploaded	File	Uploaded By
CHEAR_Participant_IDs.xls			System Generated
Local_Specimen_ID_mapping.xls			System Generated

Analyses

Analysis Title	Analysis Method	Number of Subjects	Number of Sample
RM2 - Blood Metals Cs and Sb		5	10
BSMOKE - Tobacco Metabolites		5	10

Figure 46 Analyses list on Project View page

- Log on and Navigate to your project.
- Click on the Relevant Analysis Name that you want to retrieve Lab Data for. You will be navigated to the Analysis Level view.

4.2 Step Two: Retrieve Analysis Data

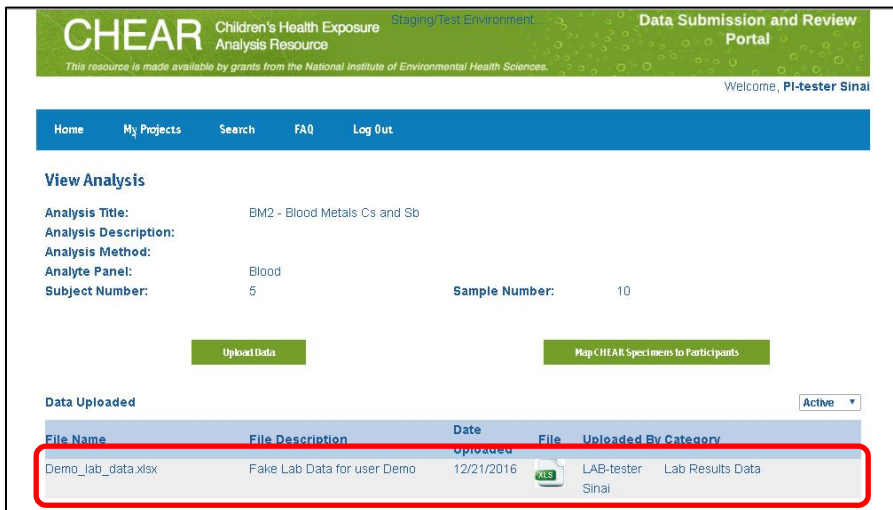


Figure 47 Analysis Result file (example)

- Any data uploaded at the Analysis Level will appear in the “Data Uploaded” section.
 - You will see the file Name, Description, date of upload and Who uploaded the file listed.
 - You can download each file listed by clicking on the “xls” icon.
- **NOTE:** for Metabolomics data (that has separately been posted to the Metabolomics Workbench) – a link ICON will appear, that when clicked will (in a separate browser tab) open the Metabolomics workbench directly for that project.

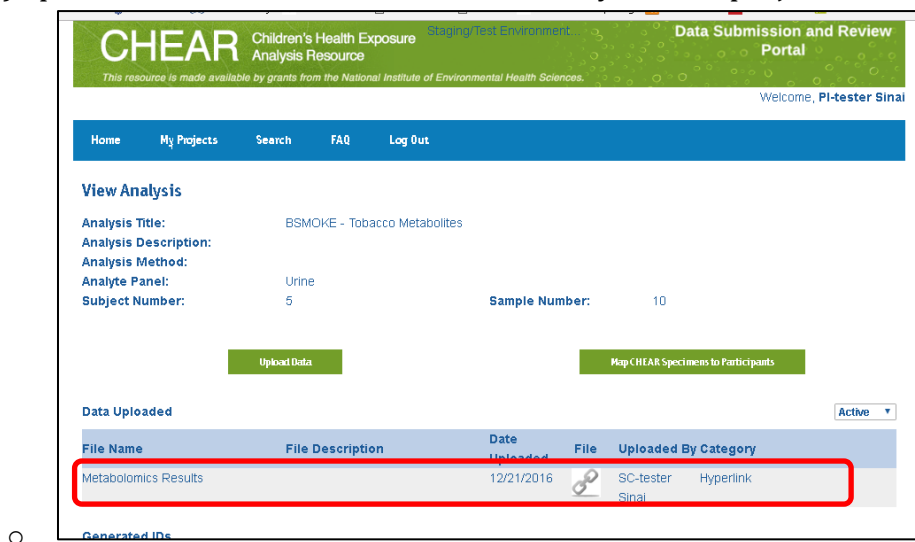


Figure 48– Metabolomics Result link