



Introduction

The ImmPort system supports the National Institute of Allergy and Infectious Diseases (NIAID) and Division of Allergy, Immunology, and Transplantation (DAIT) mandate to facilitate storage, sharing and analysis of research data.

This tutorial is intended as an introduction to the ImmPort data submission process. It is meant to supplement, but not replace interaction with the ImmPort staff. Contact the ImmPort staff for the preparation of the data for submission and using the analytical tools at BISC_Helpdesk@niaid.nih.gov.

Data Submission allows you to upload descriptive information about Studies, Subjects, Samples, Experiments, Protocols, Reagents, and Results. An ImmPort data submission package may include a complete data set or incremental data sets. The packages are transferred by secure ftp to the ImmPort system. The contents of the package are processed to store the results and make them available for the analysis, query and sharing tools of ImmPort.

A Research Project refers to a private workspace to be used by an individual or by a group researchers collaborating on a given project. The workspace provides access control to studies, experiments, results, and any accompanying data. If you need assistance in understanding what a Research Project is and whether you are associated with one, please contact the Help Desk.



Data Submission

The Data Submission main page is accessed by clicking on the "Submit Data" link from the menu bar either before or after signing in.

The screenshot shows the ImmPort website interface. At the top right, there are 'Log in' and 'Sign up FREE' buttons. The main navigation bar includes 'About ImmPort', 'Access Data', 'Tools', 'Resources', and 'News & Events'. The 'Access Data' menu is open, showing options: 'Submit Data', 'Submission History', 'Submission Resources', 'Research Data', 'Research Advanced Search', 'Reference Data', and 'Reference Advanced Search'. A callout box with an arrow pointing to 'Submit Data' contains the text: 'From the 'Access Data' menu, choose 'Submit Data'.'

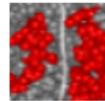
Flow Cytometry Analysis (FLOCK)

Flow cytometry analysis component includes:

- ▶ Automated cell population identification
- ▶ Result visualization in 2D and 3D
- ▶ Statistical analysis of population characteristics
- ▶ Automated mapping of populations across multiple samples



MHC Validation and Analysis



MHC Sequence Feature Variant Type (SFVT) Analysis enables genetic association analysis of classical HLA protein sub-regions defined with structural (e.g. helix) and functional (e.g. binding site) information.

MHC Alleles



Complete DNA and protein sequences, sequence features, and population frequencies of MHC, MIC and TAP alleles. Align MHC sequences horizontally to visualize extent of polymorphisms across all alleles in a locus.



Data Submission / Resource / Data Submission Templates

Help resources

[Submit Data](#) | [Submission History](#)

Resources ▾

- Tutorial
- User Guide**
- FAQs
- Templates to Download
- Template Change History
- XML Resources
- Example Data Packages
- Link to JRE

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→ [Download](#)

→ [Step 2:
Check Data in .zip file](#)

→ [Step 3:
Send Data in .zip file](#)

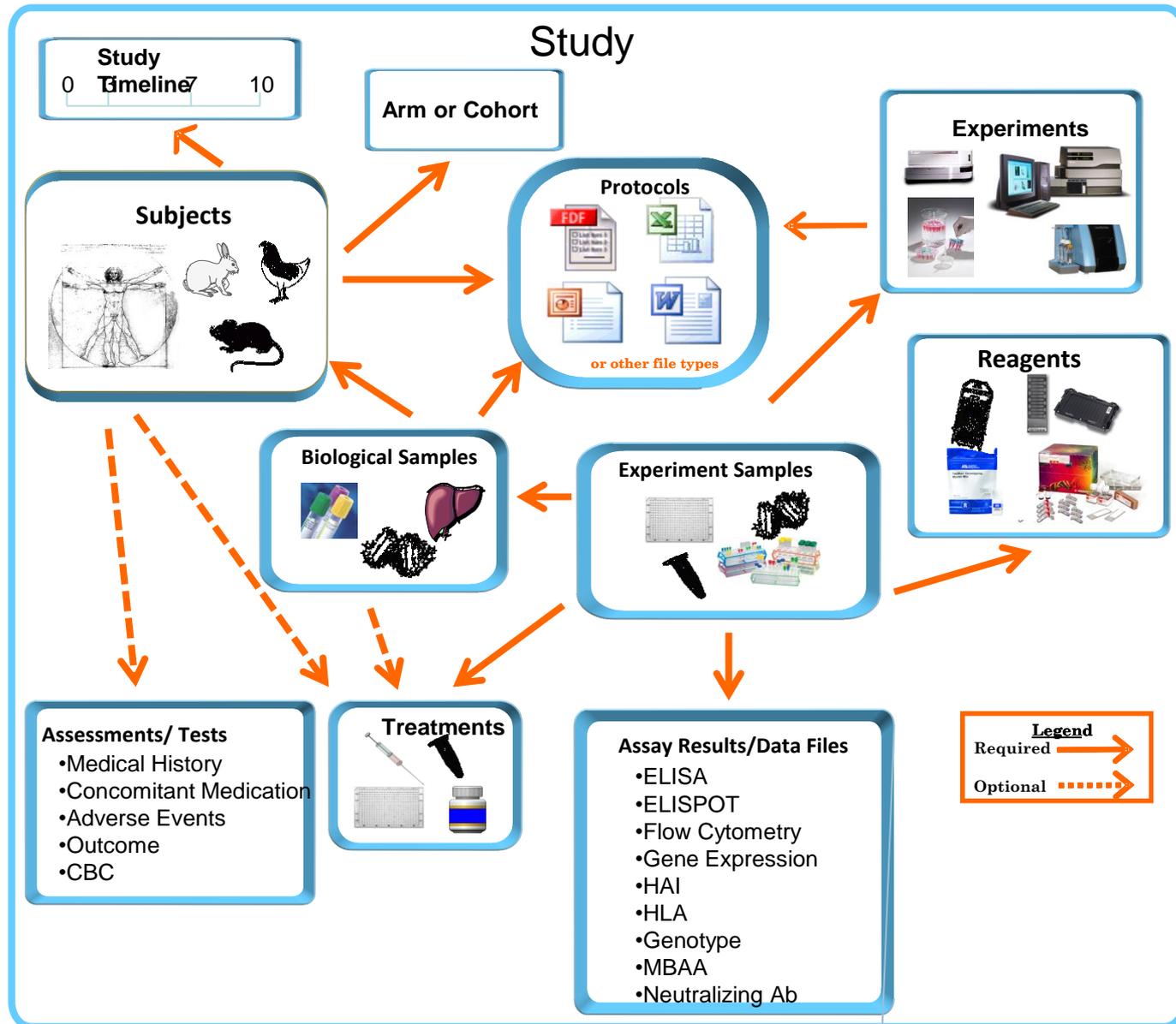
→ [Step 4:
Review Submission Status
& Results](#)

1. Which Data Submission Templates
Please contact us by email at [help](#).
The [User Guide](#) is a reference y
2. Complete the templates that are needed.
Note: Please save spreadsheet .xls templates as tab delimited .txt files.
3. Create a .zip file that contains the files you want to submit (e.g. results, protocols, bioSamples template, experimentSamples template, etc.).
4. Please check that you are using the [latest version](#) of the ImmPort data transfer templates.

ImmPort Research Data Class	Purpose	Spreadsheet Template	Required Data to Complete Metadata Form	XML Template	Latest Version/Date Available
Basic Study	Describes a study in terms of title, goals, endpoints, subject grouping (arms or cohorts), personel, planned visits or encounters and protocols using a single worksheet. A study design should be uploaded first.	basic_study_design.xls	<ul style="list-style-type: none"> ▶ Study User Defined ID ▶ Title, Description, Endpoints, Arms or Cohorst, Personnel, Period. Planned Visit. 		March 2012

The ImmPort Data Model

This diagram illustrates the relationships between research data components.





Summary of links to and from the metadata transfer files

This table summarizes how data elements can be linked together.

Link To: Link from:	Studies	Protocols	Subjects	Biological Samples	Experiments	Results	Reagents	Experiment Samples	Treatments	Control Samples	Standard Curve
Studies		One or many									
Subjects	One or many Study Arm or Cohort (one arm per study)	One or many									
Biological Samples	One	One or many	One						One or many		
Experiments		One or many									
Experiment Samples				One	One	One or many	One or many		One or many		
Results										One or many	One or many
Control Samples					One						
Standard Curve					One						



Metadata Transfer Templates

Step 1: Download and Complete Templates. The descriptive information about research data is captured in metadata transfer file templates. There are two formats provided on this site for the metadata templates: spreadsheet based and XML (eXtensible Markup Language) based. Both formats capture equivalent descriptive information.

There are 8 categories of metadata transfer templates
basic study design- Describe the purpose and goals of the research.

protocols – CRFs, sample preparation, assay procedures

reagents – Key components of assay (e.g. fluorochrome conjugated antibody)

subjectsHuman – Human subjects information including demographics and phenotype

subjectsAnimal. – Non-human research subjects descriptions including strain and phenotype

experiments– Describe experiments, including the hypothesis and experimental variables

bioSamples– Samples extracted and processed from subjects (e.g. blood, DNA) and applied treatments

experimentSamples– samples, reagents, and results form an assay. Note that there are templates tailored for assay types.

Treatments- define the amount, duration and temperature used to treat experiment and biological samples

There are additional templates to describe HLA and KIR typing systems

Derived or interpreted assay results are reported in a assay specific for ELISA, ELISPOT, Flow Cytometry, HAI, HLA, KIR, Neutralizing Ab results.

- Which Data Submission Templates do you need?
Please contact us by email at BISC_Helpdesk@niaid.nih.gov.
The [User Guide](#) is a reference you can use to determine which templates need to be completed.
- Complete the templates that are needed.
Note: Please save spreadsheet .xls templates as tab delimited .txt files.
- Create a .zip file that contains the files you want to submit (e.g. results, protocols, bioSamples template, experiment templates template, etc.).
- Please check that you are using the [latest version](#) of the ImmPort data transfer templates.

ImmPort Research Data Class	Purpose	Spreadsheet Template	Required Data to Complete Metadata Form	Latest Version/ Date Available
Basic Study	Describes a study in terms of title, goals, endpoints, criteria for study participation, subject grouping (arms or cohorts), personnel, planned visits or encounters and protocols using a single worksheet. A study design should be uploaded first.	basic_study_design.xls	<ul style="list-style-type: none"> Study User Defined ID Title Description Endpoints Inclusion and Exclusion Criteria 	February 2013



Data Submission Main Page.

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Work Flow Guide and Status Bar

Welcome to the ImmPort Experiment Data Submission Main Page!



The Experiment Data Submission module allows users to upload experiment data into the ImmPort DATABASE. Information about the experiment and its results are organized into several components including Subjects, Biological Samples, Experiment Samples, Protocols, Reagents, and Experiment Sample Results.

If this is your first time entering data, you will need the following:

- ▶ A set of protocol documents delineating your SOPs
- ▶ Reagent list
- ▶ A list of types of samples (blood vs lymphocytes vs serum, etc.)
- ▶ A system for uniquely defining each sample such that sample type, date of sample, type of analysis can be discerned

Please check that you are using the latest version of the ImmPort data transfer templates.

- ▶ [Data Submission Template Change History](#)
- ▶ [User Guide](#)
- ▶ [Tutorial](#)
- ▶ [Example Data Packages](#)
- ▶ [Data Package Validator](#)
 - ▶ This tool checks the format and content of the files in the data package and reports issues.
 - ▶ The tool is downloadable client side and executed from a graphical user interface.

Data Submission Frequently Asked Questions

BISC_Helpdesk@niaid.nih.gov

- **Which templates do I need?**

A complete data submission package will include all of the completed templates and result files. Incremental data submission packages will include some of the completed templates and perhaps results.
- **Why are there so many templates?**

ImmPort organizes descriptive information about research studies by commonly used domains or classes; studies, subjects, samples, protocols, experiments. The upload templates provide a means to capture relevant descriptive information about each data class and to link records from different data classes together.
- **Which templates should I complete first?**

The study and protocol templates are good candidates to complete first as the information to complete these templates are often available to the researcher at the beginning of a study. Protocols are referenced by other descriptive data types (e.g. subjects). Subjects and Biological Samples may be completed next when this data becomes available. Experiments, reagents and the samples associated with experiments are often the last descriptive data templates to be completed.
- **What sort of protocols should I describe?**

Among the types of protocols to consider including in your data submission package are subject recruitment and evaluation forms, CRFs (Clinical Report Forms), sample extraction and treatment protocols and assay procedures.
- **Which columns do I need to complete?**

There are a few required and several optional descriptive fields to complete in each template. To successfully load data into ImmPort, only the required fields in the templates need to be filled out. However, in order to fully use ImmPort's research data search capabilities, we encourage you to provide as much information as possible.
- **How do I know which columns are required?**

In the spreadsheet templates, the required columns have a white background and the column name has a red asterisk. The column names have comments that can be seen by hovering the cursor over the column name.
- **What is a user defined ID?**

The user defined ID is intended to be a short name for a metadata record (e.g. a subject or sample) and must be unique within the scope of a research project.
- **How do I link data elements together?**

The templates "talk" to each other via key linkages (for example, the Protocol IDs defined in protocols.xls will be referenced in bioSamples.xls when you indicate which protocol was used for a particular biological sample). It is important to make sure all of these key linkages match up when they are used.
- **How can I check that I've done things correctly?**

There is a Data Submission Validation tool that you can download and run on your computer.
- **What happened to XML templates?**

The XML formatted templates are phased out.



Spreadsheet Metadata Transfer File Features

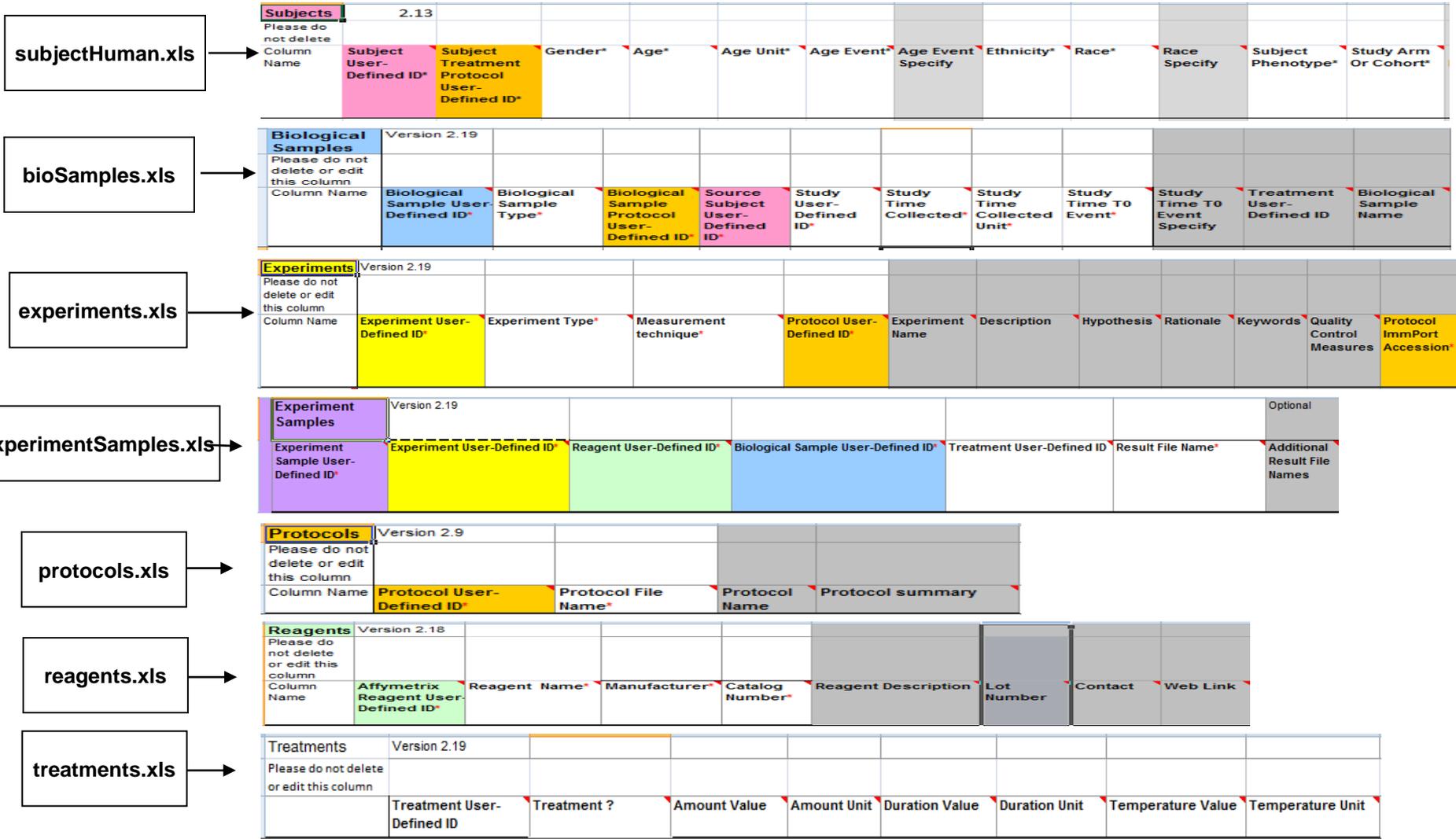
- **Do not edit or delete the column headers.** The column headers are used to ensure that the data the user enters is properly processed.
- Non-shaded columns are **required fields** to be completed but the shaded columns are optional fields.
- Explanatory **comments** which include the type of information and the size of text to enter into a cell are available by moving the cursor (mouse) over the column header name. Commented column headers have a small red triangle in the upper right corner of the cell.
- **Drop down lists** for some columns (e.g. measurement technique in experiments.xls) are activated by clicking on a cell in the column (i.e. controlled vocabulary).
- When working on the Excel templates, we recommend that you save these templates in Microsoft Excel format until you are ready to upload a submission package. At that point, you will save all templates as tab-delimited text file files.
- The following metadata categories use a **color code**:

Biological Samples:	blue
Experiments:	yellow
Experiment Samples:	purple
Protocols:	orange
Reagents:	light green
Subjects:	rose
Studies:	aqua
Treatments:	white

When linking entries in one metadata transfer file to another file, the color coding of column headers can be used as a guide to indicate how to make the link.

Comparison of Templates

If the metadata files completed were stacked on top of each other, a new perspective on how each is related can be observed. The color coding of the metadata categories and how they are represented in different files can be seen.





Protocols

The **protocols.xls** template captures information on how the Biological Sample was isolated, enriched, processed, treated or otherwise prepared for experimental use reagents to generate experiment results.

The columns in this template are Protocol User-Defined ID, Protocol File Name, and Protocol summary.

Protocols	Version 2.9			
Column Name	Protocol User-Defined ID*	Protocol File Name*	Protocol Name	Protocol summary
Please do not delete or edit this column				
	FlowCyt Splenic B cell isolation	Splenic_B_cell_isolation.pdf	Splenic Bcell Isolation	mouse splenectomy and B cell isolation
	FlowCyt Culture conditions	Culture_conditions.pdf	Culture conditions	Cell culture
	FlowCyt Protocol	FlowCytometry_Protocol.pdf	Flow protocol	Preparation of cells for flow analysis including fluorochrome-conjugated antibodies

This User-defined ID is similar to the one entered in subjects, bioSamples and experimentSample templates

File name MUST be **EXACTLY the same as protocol document** included in submission package including extension

Enter name of protocol

Enter protocol summary

Reagents

The **reagents.xls** template captures chemical compounds used to measure an Analyte(s). Different unique files of reagents worksheets can be selected for Array, ELISA, ELISPOT, FCM, HLA, Illumina and Other. The example given is a completed reagents version of ELISPOT. Please refer to the Data Submission user guide for detailed information.

Whenever there is a comma in a text in any cell, Microsoft Excel will add a double quote at the beginning of the text and a double quote at the end of the text.

	A	B	C	D	E	F	G	H	I	J	K
1	Reagents	Version 2.7									
	Please do not delete or edit this column										
2	Column Name	Flow Cytometry Reagent User-Defined ID*	Analyte Name*	Detector Name*	Reporter Name*	Is this a Reagent Set?*	Reagent Set Components- Reagent User-Defined IDs*	Reagent Set Components- ImmPort Reagent Accessions*	Manufacturer*	Catalog Number*	Reagent Name
3											
4		FlowCyt Annexin V FITC	Phosphatidy	Annexin V	FITC	N			BD Pharmingen	556419	Annexin V
5		FlowCyt anti CD24 PE	CD24	anti-CD24 ar	PE	N			BD Pharmingen	553262	anti-CD24 antibody
6		FlowCyt anti IgD bio SA PerCP	IgD	anti-IgD antik	PerCP	N			BD Pharmingen	553509, 554064	anti-IgD antibody
7		FlowCyt anti AA4.1 APC	AA4.1	anti-AA4.1 s	APC	N			e-bioscience	17-5892-81	anti-AA4.1 antibody
8		FlowCyt anti CD23 PE Cy7	CD23	anti-CD23 ar	PE-Cy7	N			e-bioscience	25-0232-82	anti-CD23 antibody
9		FlowCyt anti CD23 PE CP	CD19	anti-CD19 ar	PerCP	N			BD Pharmingen	557655	anti-CD19 antibody
10		FlowCyt anti CD21 Pac blue	CD21	anti-CD21 ar	Pacific blue	N			e-bioscience	57-0212-82	anti-CD21 antibody
11											

This User-defined ID is referenced in the experimentSample template defining samples used (templates are assay specific)

Indicate measured analyte

If reagent is a set, provide set components

Manufacturer

Catalog Number



Subjects

Two templates for human (**subjectsHuman.xls**) and non-human primate subjects(**subjectsAnimal.xls**) are available to collect Subjects information. These templates are available from **Step 1 of Data Submission**. Only one subjects.xml file is available for both of these templates.

Note: Subjects MUST link to a Protocol(s). This is a requirement on DAIT minimum information standards.

Subjects	2.13											
Please do not delete												
Column Name	Subject User-Defined ID*	Subject Treatment Protocol User-Defined ID*	Gender*	Age*	Age Unit*	Age Event*	Age Event Specify	Ethnicity*	Race*	Race Specify	Subject Phenotype*	Study Arm Or Cohort*

Reference the Subject User-ID in the bioSamples template

Enter Protocol ID

Gender can be male, female or unknown

Select age unit

Select the event used to calculate age

Preferred terms are in drop down list

Link the subject to a study's arm or cohort



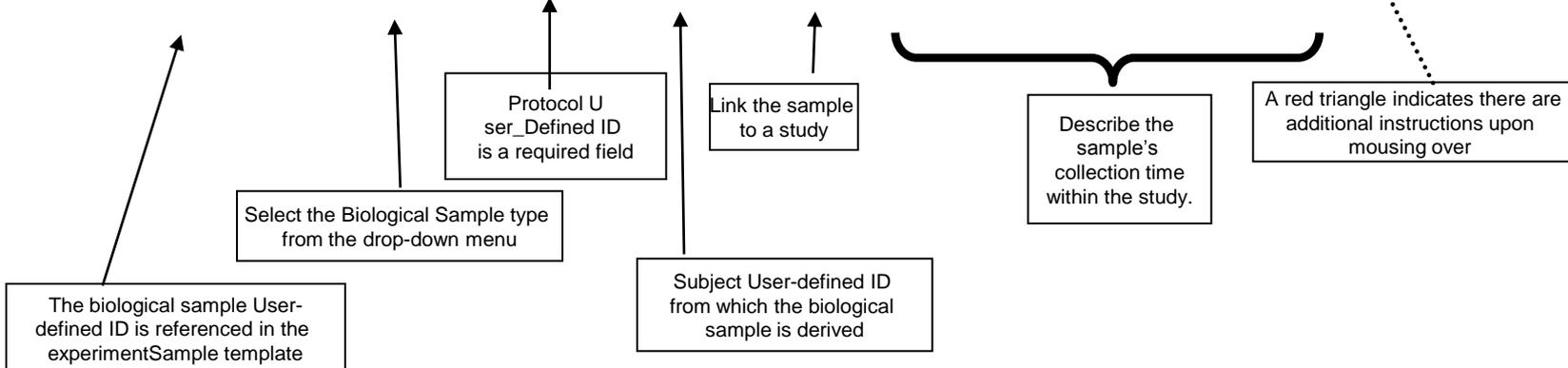
Biosamples

The **biosamples.xls** template captures biological material that has undergone isolation, processing and/or treatment prior to use in an experiment. The template is available from **Step 1: Submit Data**. Description on template may include links or references to a subject, protocols or a source biological sample.

bioSamples.xml is used to capture in a systematic way the metadata describing the biological samples used in an experiment. **Attention:** When an element uses a controlled vocabulary, the values are case sensitive and **MUST** be entered as specified.

Note: Biological Samples MUST link to a Protocol(s) and Subjects.

Biological Samples	Version 2.13							
Please do not delete or edit this column								
Column Name	Biological Sample User-Defined ID*	Biological Sample Type*	Biological Sample Protocol User-Defined ID*	Source Subject User-Defined ID*	Study User-Defined ID*	Study Time Collected*	Study Time Collected Unit*	Study Time T0 Event*





Experiments

The **experiments.xls** template captures the overall goal and methods of an experiment. The column "Experiment User-Defined ID" refers to the short name for the experiment. The "Experiment Name" column records a longer name. More detail can be provided about experiments, but that is the minimum data the user will need in filling out the template.

Note: Experiments MUST link to a Protocol(s). This is a requirement on DAIT minimum information standards.

	A	B	C	D	E	F	G	H	I	J	K
1	Experiments	Version 2.9.2									
2	Please do not delete or edit this column										
	Column Name	Experiment User-Defined ID*	Experiment Type*	Measurement technique*	Protocol User-Defined ID*	Experiment Name	Description	Hypothesis	Rationale	Keywords	Quality Control Measures
3		FlowCyt Expt									
4			Cellular_Phenotype	FCM	FlowCyt Splenic B cell isolation;FlowCyt Culture conditions;FlowCyt Protocol	Annexin+6 colo	Comparison of	BAFF has d	Based on :BAFF , spli		Normal flo
5											
6											

Title of the template: DO NOT EDIT it

DO NOT EDIT column A

Experiment Type is selected from the drop-down menu list

Links to protocols.xls

Enter a description of the experiment here

Enter a Name for the experiment

The measurement technique depends on type of experiment selected from drop-down list

Additional comments and user instructions for each column are described when you mouse over the column name

The Experiment User-defined ID will be referenced in the experimentSamples.xls template to link together all experiment samples for an experiment. Each unique experiment should be entered in its own row



Experiment Samples

The experiment samples templates are organized by assay type. If there are commonly used file formats for an assay type (e.g. Affymetrix gene expression arrays or Illumina genotyping arrays), there is often an experiment sample template for the assay type and file format. The experiment sample templates all capture the links between experiments, protocols, biological samples, and assay results.

When linking an experiment sample to more than one reagent, protocol or result file, please use a semi-colon (;) to separate the records.

Note: experiment samples link to a single biological sample.

Assay specific descriptive details.

experimentSamples.MBAA.xls [Compatibility Mode]												
A	B	C	D	E	F	G	H	I	J	K	L	
Experiment Samples		Version 2.19										
Experiment Sample User-Defined ID*	Experiment User-Defined ID*	Reagent User-Defined ID*	Biological Sample User-Defined ID*	Treatment User-Defined ID*	Assay ID*	Dilution Factor*	Result File Name*	Additional Result File Names	Assay Group ID	Plate Type		

experimentSamples.Flow_Cytometry.xls [Compatibility Mode]											
A	B	C	D	E	F	G	H	I	J		
Experiment Samples		Version 2.19								Optional	Optional
Experiment Sample User-Defined ID*	Experiment User-Defined ID*	Reagent User-Defined ID*	Biological Sample User-Defined ID*	Treatment User-Defined ID*	.FCS Result File*	Compensation or Control File Name(s)*	Marker Information File	Additional Result File Names			

experimentSamples.ELISA.xls [Compatibility Mode]												
A	B	C	D	E	F	G	H	I	J			
Experiment Samples		Version 2.19								Optional	Optional	Optional
1	Experiment Sample User-Defined ID*	Experiment User-Defined ID*	Reagent User-Defined ID*	Biological Sample User-Defined ID*	Treatment User-Defined ID*	Result File Name*	Additional Result File Names	Experiment Sample Name	Experiment Sample Description			

Enter the Experiment User-defined ID that the Experiment Sample is associated with

Enter the User-defined ID of the Reagent associated with the Experiment Sample

Enter the User-defined ID of the Biological Sample associated with the Experiment Sample

Enter the User-defined ID of the Treatment associated with the Experiment Sample

ImmPort derived data templates are recommended for some assay types (e.g. ELISA, HAI, etc.)

Enter supporting result files and description



Assay specific Experiment Samples templates and results formats are specified for commonly used immunological research methods.

Assay	Results Format	Controls	Compensation	Standard Curves
ELISA	ELISA_Results.txt			
ELISPOT	ELISPOT_Results.txt			
Flow Cytometry	.fcs format FCM_derived_data.txt	control samples .fcs format	compensation samples .fcs format	
Gene Expression	Affymetrix CEL Illumina GEO raw			
Genotyping	Affymetrix CEL Illumina Bead Studio			
Hemagglutination Inhibition	HAI_Results.txt			
HLA	HLA_Typing.txt			
Image Histology	Custom			
KIR	KIR_Typing_Results_Column.txt or KIR_Typing_Results_Column.txt			
Mass Spectrometry	Custom			
MBAA	MBAA_Results.txt	Control_Samples.txt		Standard_Curve.txt
qRT-PCR	PCR_Results.txt			
Virus Neutralization	Virus_Neutralization_Results.txt			



Treatments

Treatments are required for Experiment Samples and are optional for Biological Samples. The treatment template allows the user to define the amount, duration and temperature of treatments specific to individual Experiment Samples or Biological Samples.

The columns in this template are Treatment User-Defined ID, Treatment?, Amount Value, Amount Unit, Duration Value, Duration Unit, Temperature Value and Temperature Unit.

A	B	C	D	E	F	G	H	I
Treatments	Version 2.19							
Please do not delete or edit this column								
	Treatment User-Defined ID	Treatment ?	Amount Value	Amount Unit	Duration Value	Duration Unit	Temperature Value	Temperature Unit
		No No Yes						

Enter the Treatment User-defined ID that the Treatment is associated with

Use the drop down menu to define whether Experiment Samples or Biological Samples were treated

If Treatments are used at least one of the Treatment Value pairs is required

Treatment Value pairs are

- Amount Value/Unit,
- Duration Value/Unit
- Temperature Value/Unit



Example templates needed in Flow Cytometry data submission

Experiments.xls template (1 of 2)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Experiments	Version 2.3														
2	Please do not delete or edit this column															
	Column Name	Experiment User-Defined ID ¹	Experiment Type ¹	Measurement technique ¹	Protocol User-Defined ID ¹	Protocol ImmPort Accession ¹	Experiment Name	Description	Hypothesis	Rationale	Keywords	Quality Control Measures	Experimenters	Links to Publications	Constants	Condition Variables
3																
4		Experiment 10/1	Cellular_Phe	FCM	FlowCytometryProtocol		Annexin+6	Comparison	BAFF has d	Based on :BAFF, spleen, B cells			Eva Sadat		Cell type	Cultured

The Experiment User-defined ID will be referenced in the experimentSamples.xls template to link together all experiment samples for an experiment

Enter Experiment type used

Enter the Protocol User-Defined ID

Enter Measurement Technique

Enter a Name for the experiment

Enter a description of the experiment here

Enter a Hypothesis, Rationale, Keywords, Quality control measures, Links to publications, Constants, Conditional variables



Example templates needed in Flow Cytometry data submission Experiments.xls template (2 of 2)

	I	J	K	L	M	N	O	P
1								
2								
3	Hypothesis	Rationale	Keywords	Quality Control Measures	Experimenters	Links to Publications	Constants	Conditional Variables
4	T cell development is impaired in CPD knockout mice	Based on thymic atrophy and perturbations in other lymphoid cell populations, we expect that T cell development is also perturbed in CDP knockout mice	CPD, thymus, T cell		Jamie Lee	PMID: 11739170	Cell type	mouse genotype (WT versus CDP homozygous knockout)
5								

Enter experiment keywords here

Indicate who performed the experiment here

Indicate any links to publications here, such as a PMID number or a URL

Enter the experiment rationale here

Indicate what quality control measures were used here (e.g. duplicates, triplicates)

List the Constants and Conditional Variables in the experiment. In this example, thymocytes from a WT and mutant mouse are compared. Since only one cell type is used in the experiment, "Cell Type" is a Constant. The mouse genotype is the Conditional Variable in this experiment



Derived Data

1. Flow Cytometry Derived Data Report

The **FCM_derived_data.xls** template is available from **Step 1 of Data Submission**. Flow Cytometry Derived data refers to the measurement of the Experiment Sample to which the population cell number, population percentage or other statistics apply

	A	B	C	D	E	F	G	H	I	J	K
1	FCM analyzed results	Version 2.3									
2	Please do not delete or edit this column										
3	Column Name	Experiment Sample User-Defined ID*	Experiment Sample ImmPort Accession*	Population Description*	Population Definition (gating combination)*	Population Cell Number (please include unit)*	Base/Parent Population for Population Percentage*	Population Percentage (%)	Other Population Statistic(s)	Parameter Statistic(s)	Comments
4		101806_1		B-cells	Viable gate	911066 cells/sa	all events	72.80%			
5		101806_1		Annexin neg	Annexin negative	325251 cells/sa	B-cells	35.70%			
6		101806_1		AA4hi Imm	AA4hi	45210 cells/sa	B-cells and Annex	13.90%			

Enter the Population %

Enter the parameter statistics using the specified format

Enter the experiment Sample User-defined ID or Accession

Enter a description of the population defined by the gate(s)

Provide the gates used to define the population

Provide the number of cells/unit in the population

Specify the base or parent population, or indicate that it is "Total events"

Other population statistics and comments may be provided



Derived Data, continued

HLA Typing Summary Report

The **HLA_Typing.xls** template is available at **Step 1 of Data Submission**. Data is used to analyze HLA using controlled vocabulary unique to groups of populations using measurements of gene types like HLA-A, HLA-B, DPA1, DPB1, DQA1, DQB1, DRB1 etc. The loci names are available from the IMGT website (www.ebi.ac.uk/imgt/hla/) or the dbMHC (www.ncbi.nlm.nih.gov/mhc/) website. A horizontal format for collecting typing results is recommended.

Two columns must share a locus name with one column name ending in 'Allele 1' and the other column name ending in 'Allele 2'.

Note: Currently no validation of locus names is done.

	A	B	C	D	E	F	G	H	I	J	K	L	W	X	Y	Z
1	HLA Typing Results Please do not delete or edit this column	Version 2.7														
2	Column Name	Experiment Sample User-Defined ID*	HLA-A Allele 1	HLA-A Allele 2	HLA-B Allele 1	HLA-B Allele 2	HLA-C Allele 1	HLA-C Allele 2	HLA-DPA1 Allele 1	HLA-DPA1 Allele 2	HLA-DPB1 Allele 1	HLA-DPB1 Allele 2	HLA-DRB5 Allele 1	HLA-DRB5 Allele 2	Other	Other
3		HLA Typing Report 1	A*0101	A*0101	B*07021	B*07022										
4		HLA Typing Report 2	264	264	B*07022	B*07023										
5																
6																
7																
8																

Enter the Experiment Sample User-defined ID here

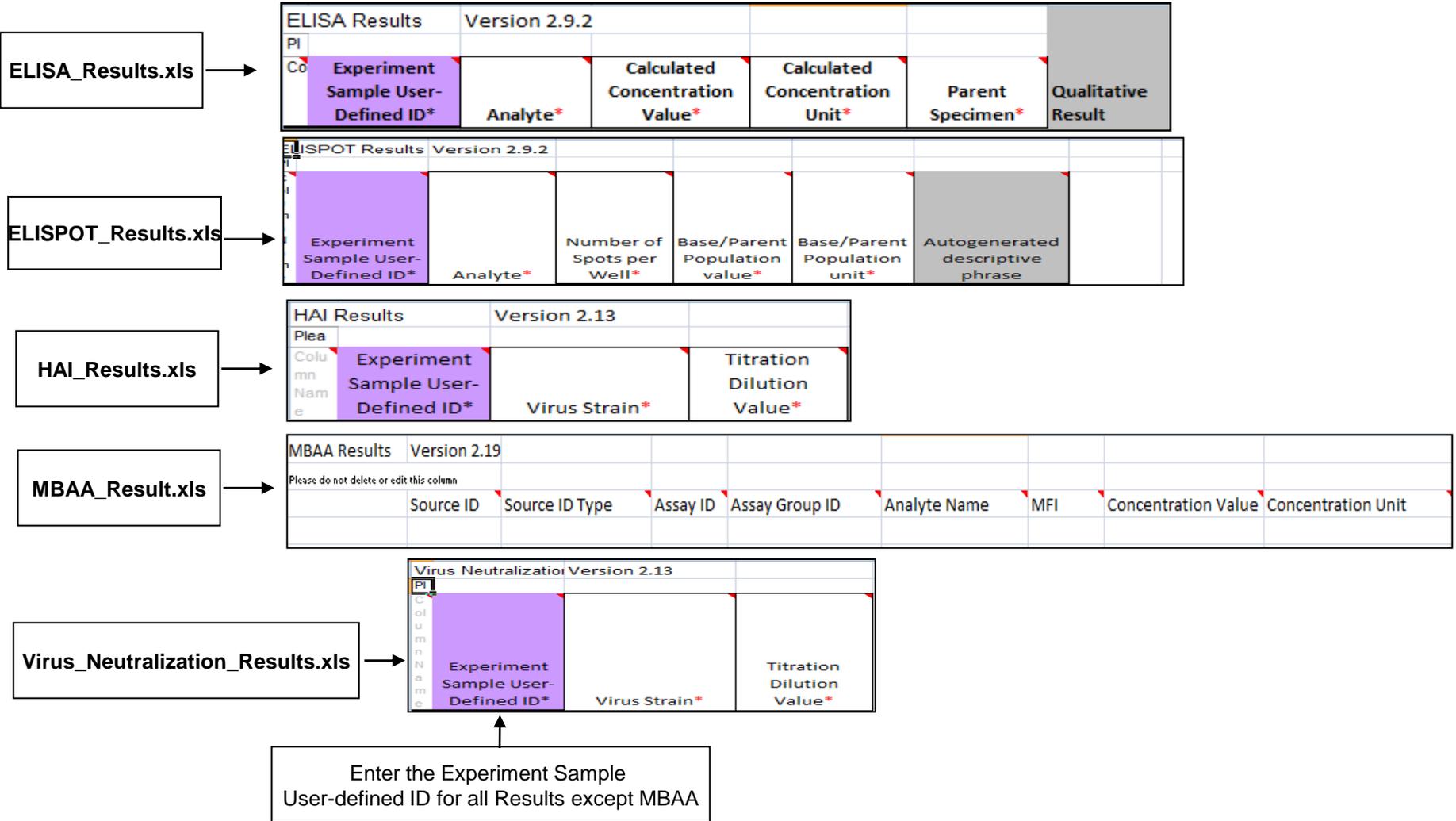
Any two columns must share the same locus name

Other loci from dbMHC are canonical and can be selected



Derived Data, continued

Additional derived data templates are available from **Step 1 of Data Submission**. Result types have unique templates to capture assay-specific descriptive information.





Save the spreadsheet file as tab-delimited text

Each template **must be saved in a tab-delimited text file (*.txt)** format in preparation for submission to ImmPort. Click on "File" in the Excel menu bar and choose "Save As". In the pop up window, click on the "Save as type" drop-down list, scroll down and choose "Text (tab-delimited) (*.txt)". When the pop window appears asking if the user wants to save the files as text, please select "Yes".

Note: The original names of the templates (e.g. protocols.txt) MUST be maintained.

Only one copy of each of the metadata files is included in a data submission package.

Choose "Save As"...

...which opens this "dialog box". From "Save as type, choose "Text (Tab Delimited)".

Clicking "Save" opens another dialog box.

Choose "Yes"

Microsoft Excel

experiments.txt may contain features that are not compatible with Text (Tab delimited). Do you want to keep the workbook in this format?

- To keep this format, which leaves out any incompatible features, click Yes.
- To preserve the features, click No. Then save a copy in the latest Excel format.
- To see what might be lost, click Help.

Yes No Help



Data Submission Package .zip file contents and structure

The ImmPort data submission package is a .zip file that includes all of the files the user wants to submit. There are many tools that can be used to create a ".zip" archive file. Select all of the files to be included and then create a .zip file (versus .zipping a folder with all of the files). Please do not select a folder or directory of files to ZIP- this confuses ImmPort's software.

Select all files to include in .zip

Review .zip file contents

Name	Type	Modified	Size	Ratio	Packed	Path
bioSamples.txt	Text Document	4/30/2007 4:50 PM	2,148	83%	361	
Custom2Marker.OPA	OPA File	4/30/2007 6:07 PM	1,279	54%	589	
Example_Illumina_Genotype_Result_File.txt	Text Document	4/30/2007 8:32 PM	351	40%	212	
experiments.txt	Text Document	4/30/2007 5:34 PM	1,196	76%	286	
experimentSamples.txt	Text Document	4/30/2007 7:55 PM	783	54%	360	
reagents.txt	Text Document	4/30/2007 5:05 PM	505	56%	223	
subjectsHuman.txt	Text Document	4/30/2007 4:47 PM	1,716	79%	354	



Data Submission / Data Submission Package Validator

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[Submit Data](#)
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[Step 1:](#)
[Download and Fill Templates](#)



[Step 2:](#)
[Check Data in .zip file](#)



[Step 3:](#)
[Send Data in .zip file](#)



[Step 4:](#)
[Review Submission Status
& Results](#)

Data Submission Package Validator

This tool checks the format and content of the files in a data package and reports issues. This tool is downloaded to your computer and run from a graphical user interface.

The Validator inspects completed templates (the metadata transfer files) for common formatting error and data integrity issues, checks for missing files, improperly formatted metadata files and references to other metadata within the data package, Integrity and structure of .zip files.

It is highly recommended to use the Validator before sending data into ImmPort as part of the data submission process.

When no issues are noted by the Validator, please submit the data submission .zip package to ImmPort.

The following requirements are important for the running the application:

- **Java configured to run from the Windows command prompt.**
- **JRE 1.5.X or later installed.**
- **Minimum size of memory required is 64 MB.**
- **Number of files to be unzipped is 76 files and 42 folders.**
- **Disc space needed is 8.33 MB.**
- **No file overwriting will occur by default.**



Uploading a file less than or equal to 1 Gigabyte -- Submit Online

Click on the send data file tab and if the page has timed out, log back into ImmPort and continue with the submission process. Select the **research project** to which the data will be submitted. If none has been created, the Principal Investigator or the Project Manager can create one. If there are multiple projects listed, the Principal Investigator or the Project Manager decides which project to select.



Research data will be stored in the private project workspace of your research project. Please select the Research Project and Grant/Contract number with which your data will be associated and enter any comments in the Notes text box. If you need assistance in understanding what a Research Project is and whether you are associated with one, please contact the Help Desk.

ImmPort accepts data submission packages in the "ZIP" format. (Please see the Data Submission User Guide for more information on how to create a .zip file.)

Please **DO NOT** include spaces in the .zip file name.

If your .zip file is less than or equal to 1 Gigabyte, please use the Submit on-line option.

- ▶ Check the "Upload Online" check box.
- ▶ Select the .zip file using the browse button.
- ▶ Click submit and

If your .zip file is great

- ▶ Uncheck the "Uplo
- ▶ Click submit and
- ▶ Contact the help

If this is your first time

- ▶ A set of protocol
- ▶ Reagent list
- ▶ A list of types of
- ▶ A system for unic

Please check that you are using the [latest version](#) of the ImmPort data transfer templates.

Research Project Title: TESTING: Bioinformatics Integration Support Project

Contract/Grant Number: HHSN2662004000765

Notes:

Upload Online

Browse...

Submit

Indicate any relevant notes pertinent to the uploaded data and ensure the Upload Online is checked

Browse for the file to upload from the local directory on your computer and then click 'Submit'



Uploading a file greater than 1 Gigabyte -- Submit Offline

To upload data files greater than 1 Gigabyte uncheck the upload button and click submit. The Upload ticket is used to track the package for

Data Submission / Experiment Data Submission

[Submit Data](#) | [Submission History](#) | [Resources](#) ▾



Research data will be stored in the private project workspace of your research project. Please select the Research Project and Grant/Contract number with which your data will be associated and enter any comments in the Notes text box. If you need assistance in understanding what a Research Project is and whether you are associated with one, please contact the Help Desk.

ImmPort accepts data submission packages in the "ZIP" format. (Please see the Data Submission User Guide for more information on how to create a .zip file.)

Please DO NOT include spaces in the .zip file name.

Please check that you are using the [latest version](#) of the ImmPort data transfer templates.

Research Project Title:

Notes:

Upload Online to be **unchecked**

Upload Online

TESTING: Bioinformatics Integration Support Project

Add relevant notes pertinent to the project or data being uploaded

Click to get the upload ticket number that can be used to 'track' the package uploaded into ImmPort.

Submit



Review Data Submissions History

When the .zip file has been sent to ImmPort, the web page will be redirected to the Data Submission History page that lists the data packages that have been sent.

An email confirmation is sent to the submitter that the data package has completed submission processing or that there have been some problems with the package.



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Data Submission / Data Submission History

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This page is a summary overview of the data submissions to a project. If you have access to more than one project, use the project filter to view the submission queue from other projects.

The data submitted to ImmPort can be queried and reviewed in [Research Data Search](#)

Filter By Project [Set Filter](#)

Click on a Ticket Number below to view a submission's details.

15 items found, displaying all items.

The status of the submitted data is indicated as either 'Pending' or 'Completed'. The nature of the error is indicated on the Ticket Number for debugging

Ticket Number	.ZIP File Name	Format	Status	Submitter	Submit Date
kilelbe_20091013_194	ELISA_example_Package.tab-delimited.zip	ELISA-MBAA_repo rt_file	Completed	kilelbe	10/13/2009 09:21:11
kilelbe_20091013_195	ELISPOT_example_Package.tab-delimited.zip	ELISPOT_report_file	Completed	kilelbe	10/13/2009 09:21:15
kilelbe_20091013_196	Flow_Cytometry_example_Package.tab-delimited.zip	FCM_report_file	Completed	kilelbe	10/13/2009 09:21:22
kilelbe_20091013_197	Gene_Expression_Example_Package.tab-delimited.zip	GEO_GSM_GCOS-MA S5_output	Started	kilelbe	10/13/2009 09:21:28



Review Data Submissions History

When the .zip file has been sent to ImmPort, the web page will be redirected to the Data Submission History page that lists the data packages that have been sent.

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Data Submission / Data Submission History

[Submit Data](#) | [Submission History](#) | [Resources](#) ▾



This page is a summary overview of the data submissions to a project. If you have access to more than one project, use the project filter to view the submission queue from other projects.

The data submitted to ImmPort can be queried and reviewed in [Research Data Search](#)

Filter By Project

Click on a Ticket Number below to view a submission's details.

5 items found, displaying all items.

Ticket Number	.ZIP File Name	Format	Status	Submitter	Submit Date
Bea1_20091021_222	ELISA_Example_Package.XML.zip	ELISA_report_file	Completed	Bea1	10/21/2009 14:24:42
Bea1_20091021_217	ELISA_example_Package.tab-delimited.zip	ELISA-MBAA_report_file	Completed	Bea1	10/21/2009 13:58:59
Bea1_20090902_143	extractXML#2.zip	Affy_GCOS-GDAS- GTYPE_Genotyping_output	Completed	Bea1	09/02/2009 16:09:00
Bea1_20090720_41	HLA_1reagentperlocus_Example_Package.tab-delimited.zip	HLA_typing_summary	Completed	Bea1	07/20/2009 15:03:56
Bea1_20090720_40	Gene_Expression_Example_Package.tab-delimited.zip	GEO_GSM_GCOS-MA S5_output	Completed	Bea1	07/20/2009 13:47:15

5 items found, displaying all items.

Legend:

- * Pending, The .zip file is in the data submission processing queue.
- * Started, The .zip file is being validated.
- * Completed, The .zip file is successfully processed and stored.
- * Rejected, One or more errors were encountered when processing the submitted files.

The status of the submitted data is indicated as either 'Pending' or 'Completed'. The nature of the error is indicated on the Ticket Number for debugging