# IMMPORT DATA SUBMISSION USER GUIDE


**Version 2.28**

**Bioinformatics Integration Support Contract (BISC), Phase III**

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## BISC Documentation Style Guide Version History

| Version | Date | Description |
|---|---|---|
| **2.28** | May, 2015 | - Combined templates for experiment samples, biosamples and experiment.<br>- Combined templates for lab test panel and lab tests.<br>- New template for assessments.<br>- |
| **2.27** | December, 2014 | - No changes to upload templates. |
| **2.26** | October, 2014 | -New templates available for Lab Test panel and Lab Test.<br>-Experiments must link to a study.<br>-Enhanced support for standardized cell population name and gating definitions in derived flow cytometry template. |
| **2.25** | July, 2014 | - New templates for Adverse Events and Substance Merging with Subject<br>-Human Subject Population column displays http://allelefrequency.net values. |
| **2.24** | June, 2014 | -Significant re-work of study, bioSample, experimentSample, reagent templates.<br>- New data dictionary is available with templates to describe templates, columns, rows, lists, data types, etc. |
| **2.19** | May, 2013 | - Changed TREATMENT to a required Experiment Sample attribute.<br>-Only one biological sample can be linked from an experiment sample.<br>- Added MBAA result support enhancements<br>- Discontinued support for XML template submission. |
| **2.18** | February 2013 | -Inclusion/exclusion criteria, publication references added to study design template<br>-Links from experiment samples to protocols removed |
| **2.17** | December 2012 | -Upgrade subject demographics<br>-Support HAI and Neutralizing antibody assay results |
| **2.13** | June 2012 | -References to arms from subjects and from bioSamples to studies required. Modified subject and sample templates. Created new assay specific experiment sample templates. |
| **2.8** | 04/28/2010 | - Study day as a required field in the Biosamples.xls<br>- On all edit pages, the delete button removed. |
| **2.7** | 02/02/2010 | - Changed 'gender' to a required SUBJECT attribute.<br>- Removed status from templates, changed affection_phenotype to subject_phenotype and made this a required field.<br>- Allowed multiple subject phenotypes to be entered into the metadata template using a standard separator to be defined.<br>- Require a SUBJECT link from a BIOSAMPLE (BS), Experiment Sample (ES) link to a Biosample (BS).<br>- Added upld_tct_num column in treatment_info table.<br>- Allow users to batch upload Flow text files for subsequent analysis |
| **2.3.2** | 09/30/2008 | - Added support for ELISA, ELISPOT, MBAA results per the DAIT Minimum Information Guidelines.<br>- Modified the experiment samples and reagent templates for ELISA, ELISPOT, MBAA results.<br>- Created new results templates for ELISA, ELISPOT and MBAA results.<br>- Modified the user guide and tutorials to support ELISA, ELISPOT and MBAA results. |

| Version | Date | Description |
|---|---|---|
| **2.3** | 07/23/2008 | Made revisions and incorporated DAIT Minimum Information Standards. |
| **2.2** | 03/19/2008 | Improvements made on the Data Submission process upload to allow greater than 100MB of data. Modified the ImmPort user interface. Implemented an off-line Data QC pipeline for HLA typing results. |
| **2.1.2** | December 2007 | No changes to Data Submission. |
| **2.1.1** | November 2007 | Data Submission Validator Beta to check for errors before submitting packages into ImmPort. |
| **2.1** | August 2007 | Added the ability to update research metadata for subjects, experiments, biological samples, experiment samples, reagents and protocols. |
| **2.0** | May 2007 | Implemented generation of Linkage Pedigree (pre MAKEPED) format (.ped and .info) files from uploaded genotype results. Enabled upload of derived flow cytometry results. |
| **1.4.1** | December 2006 | **No changes to Data Submission.** |
| **1.4** | October 2006 | Created tutorials for TagSNP, Data Submission. Enabled download of result file(s). |
| **1.3.1** | June 2006 | No changes to Data Submission. |
| **1.3** | June 2006 | Batch submission of genotyping data from Illumina panels in two formats. |
| **1.2.1** | May 2006 | XML based system for collecting descriptions of experiment results. |
| **1.2** | April 2006 | No changes to Data Submission. |
| **1.1** | January 2006 | **No changes to Data Submission.** |
| **1.0** | October 2005 | Initial release of the ImmPort website. |

# 1.0 HIGHLIGHTS OF IMMPORT VERSIONS

ImmPort releases updates on the data capture process to reflect changes in assay technology and improvements to support data sharing and re-use. These changes can include converting optional descriptive elements to required attributes, support new file formats, and adding new descriptive data concepts.

For more detailed information on each of the versions indicated, please refer to the ImmPort website templates history at https://immport.niaid.nih.gov/immportWeb/experimental/templateHistory.do

# 2.0 INTRODUCTION

## 2.1 DATA SUBMISSION GUIDE ORGANIZATION

Welcome to the ImmPort Data Submission User Guide. The ImmPort system supports the National Institute of Allergy and Infectious Diseases Division of Allergy, Immunology, and Transplantation mandate to facilitate storage, sharing and analysis of research data and metadata (descriptive information about data). This guide is intended as an introduction to ImmPort and specifically the data submission process. It is meant to supplement, but not replace interaction with the ImmPort staff. The user should contact the ImmPort staff for the preparation of the data for submission and using the analytical tools.

This guide is organized into the following sections

- A Quick Start Guide
- An Overview of the ImmPort Research Data Model and Data Submission process
- An Explanation of the Metadata upload File Templates
- Supplemental Information

## 2.2 WHAT ARE THE DATA SUBMISSION OPTIONS?

Contact the ImmPort staff for help (BISC_Helpdesk@niaid.nih.gov) with organizing, packaging, and loading of the data into ImmPort.
Read this guide then contact Helpdesk to ask questions and provide feedback and suggestions.
Submit data to ImmPort and contact the Helpdesk **(BISC_Helpdesk@niaid.nih.gov**) with any comments, questions, or recommendations.

## 2.3 QUICK START

Quick Start is intended for the experienced user who needs few hints or reminders on how to assemble and submit data to ImmPort.

If the user wants to take advantage of ImmPort's analysis, querying and sharing tools, please go to Step 1 of the data submission process in ImmPort and download the metadata upload templates that you need.

Complete the metadata upload templates required for your submission. In each template enter detailed information about one or more samples used in the experiment. Please complete all data entry categories that are not shaded gray.

When using .xls files for data entry save the files as tab delimited text files before zipping into an archive file.

Use a ZIP utility (e.g. 7-Zip, ZipIt or WinZIP) to put the files and completed metadata upload files into a .zip file.

If the user wants to store results or assay data only, use a utility to put the files into a .zip archive and proceed to Step 2 of the Data Submission Process.

Go to Step 2 of the Data Submission process in ImmPort (figure 2a) to install and run the Data Submission Validator.

**Figure 1a. Step 2 Check the Data Submission Package with the Validator tool.**

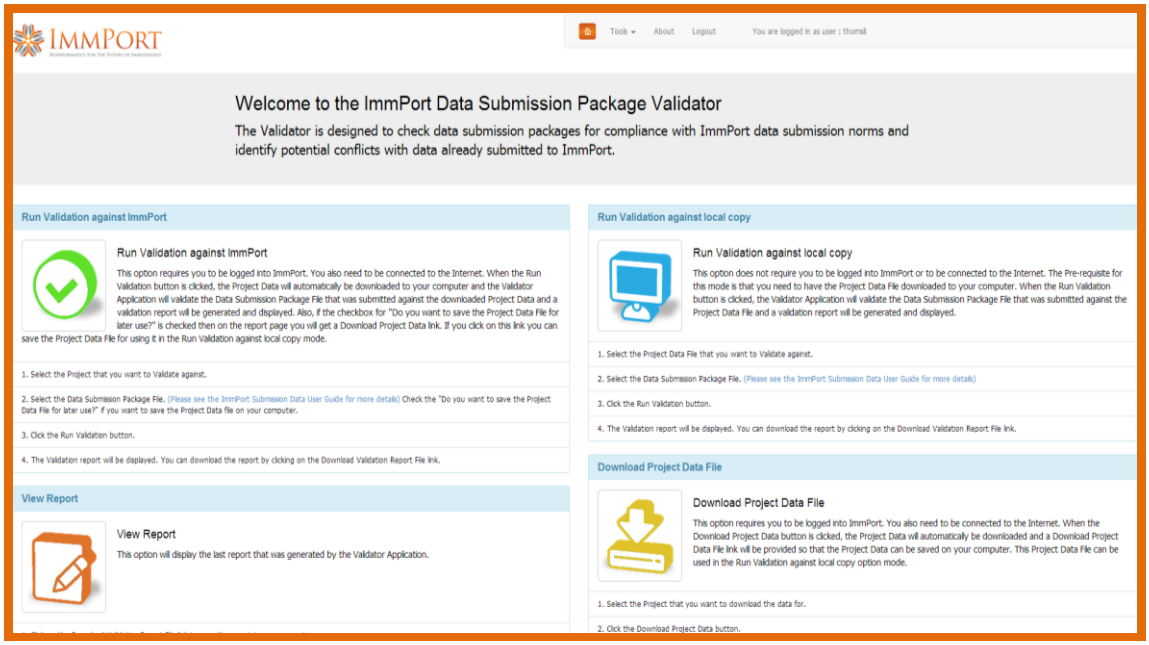
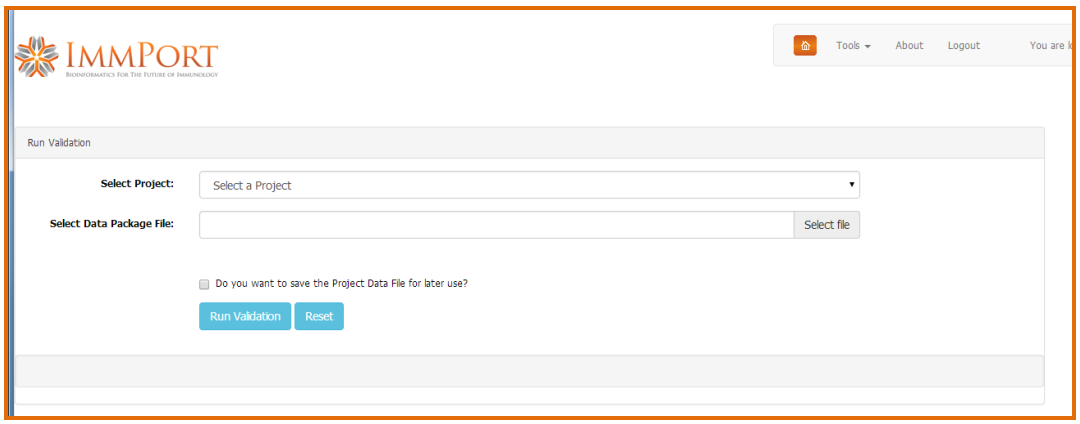


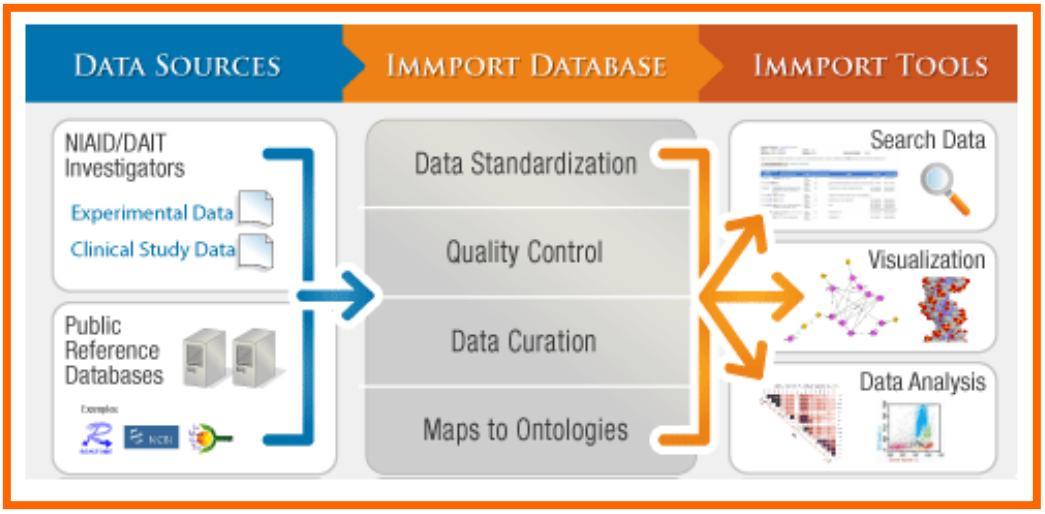

**Figure 1b. ImmPort Data Submission Validator online validation**



# 3.0 IMMPORT RESEARCH DATA MANAGEMENT AND SUBMISSION FOR NEW USERS

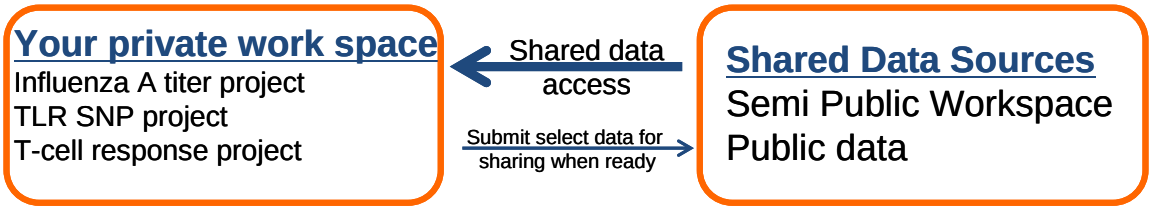
ImmPort is currently available to NIAID/DAIT funded researchers providing them with the ability to store, analyze, and share their research data. ImmPort also provides access to public reference data bases allowing researchers to utilize some of this information for their analyses (figure 2a).

**Figure 2a. ImmPort's capabilities**




While ImmPort offers this wide array of tools and data sharing capabilities, research data initially submitted by an investigator is placed into a private work space that is only available to that investigator and any other personal they choose. This work space can contain a number of different studies and allows an investigator and their staff to take full advantage of ImmPort's tools and shared data bases while their research data is not available to other registered users (figure 2b).

**Figure 2b. ImmPort's Management of Data Access**




The first step in the data submission process is to visit ImmPort's data submission page and down load metadata template files. The template files are available in .xls format. After downloading the template files, the ImmPort data submission process can be summarized as:

Enter your data into the metadata upload template(s)
Generate a .zip format archive file that includes the completed metadata upload files and any other files that are to be submitted (e.g. assay results files, protocol files, assay platform annotations, etc.)
Send the .zip file via a secure transmission method to the ImmPort system.

A more complete description of the steps involved in the data submission process follows.

## 3.1 IMMPORT RESEARCH DATA MODEL

The ability of ImmPort's tools to effectively annotate research data requires the capture of descriptive details at many levels in a study. To understand how this is achieved, the user should keep in mind the following definitions.

Metadata – collections of files containing detailed information and descriptions of the data
Templates – are .xls files for the structured listing of the detailed information and descriptions of the data
Transfer / Upload- submit, send or transmit data to ImmPort
Research Data / Assay Results – actual experiment data submitted by registered users
Reference data – data available from a number of public sources

ImmPort's model for handling research data is to partition information into seven metadata categories. Each category has its own .xls file or set of files for the entry of different types of information associated with an experiment. These categories are also called metadata classes in this guide.

The metadata categories and their functions are as follows:
**Study**: Studies provide the context and organization of a research effort. Studies organize subjects into groups (e.g. arms or cohorts) based on phenotype and/or treatment. The encounter schedule provides a guide as to the temporal relationship between samples and encounters (i.e is the sample taken before or after a treatment).

**Subjects**: Subjects may be patients or animals from which samples are taken for analysis. Two .xls templates (one for human and one for animal subjects) are available for recording subject information. In these files, treatment protocols used on the subjects can also be listed as well as many other details. Subjects are assigned to a single group (arms or cohorts) within a study and maybe linked to multiple studies.

**Biological Samples**: Describe the types of samples taken from subjects or cell culture and processed for the experiment (i.e. organs, tissue, blood, plasma, cell culture name, etc.), when the samples were taken in the course of a study and protocols used in the sample collection, processing, and/or treatment. Samples are linked to a single study.

**Experiments**: Describe the type of experiment, measurement technique and links to protocols used in the experiment.

**Experiment Samples**: The biological samples analyzed in an experiment are linked to the assay reagent, protocol and results via the experiment sample record. Since ImmPort offers the ability to submit data for a number of immunological, proteomic and genomic analysis methods, several different template files are available for listing sample details for different experiment approaches.

**Treatments**: Describe the experimental conditions for specific biosamples or experiment samples. Treatments link to experiment samples as well as biosamples if needed.

**Protocols**: Describe the methods and procedures in studies, subject recruitment/treatment, sample collection/preparation/treatment and experiments. Protocols may be PDF files, Word documents, excel or other file types.

**Reagents**: Provide detailed information about the reagents used in an experiment. Since different analysis platforms employ very different reagents, the reagents.xls file contains several tabs for entering platform specific details of the reagents that were used.

One of the important properties of these metadata categories is that the details listed in these files allow archived data to be linked by common information. For example, several different biological samples can be taken from a subject and used for different assays. If the experiments for these assays have been properly formatted and submitted to ImmPort, a user can search their private and/or shared databases for

what experiments and samples came from each subject to select data from a broader number of subjects or samples to perform a specific analysis. The linkage of archived data by the different metadata categories facilitating this capability is diagramed in figure 3.

**Lab Test Panels**: Provide a means to group clinical lab tests and links to study and protocols.

**Lab Tests**: Provide a means to describe and capture clinical lab test results.

### Figure 3a. ImmPort Research Data Model Classes

How the metadata classes are organized and linked in the ImmPort Research Data Model.

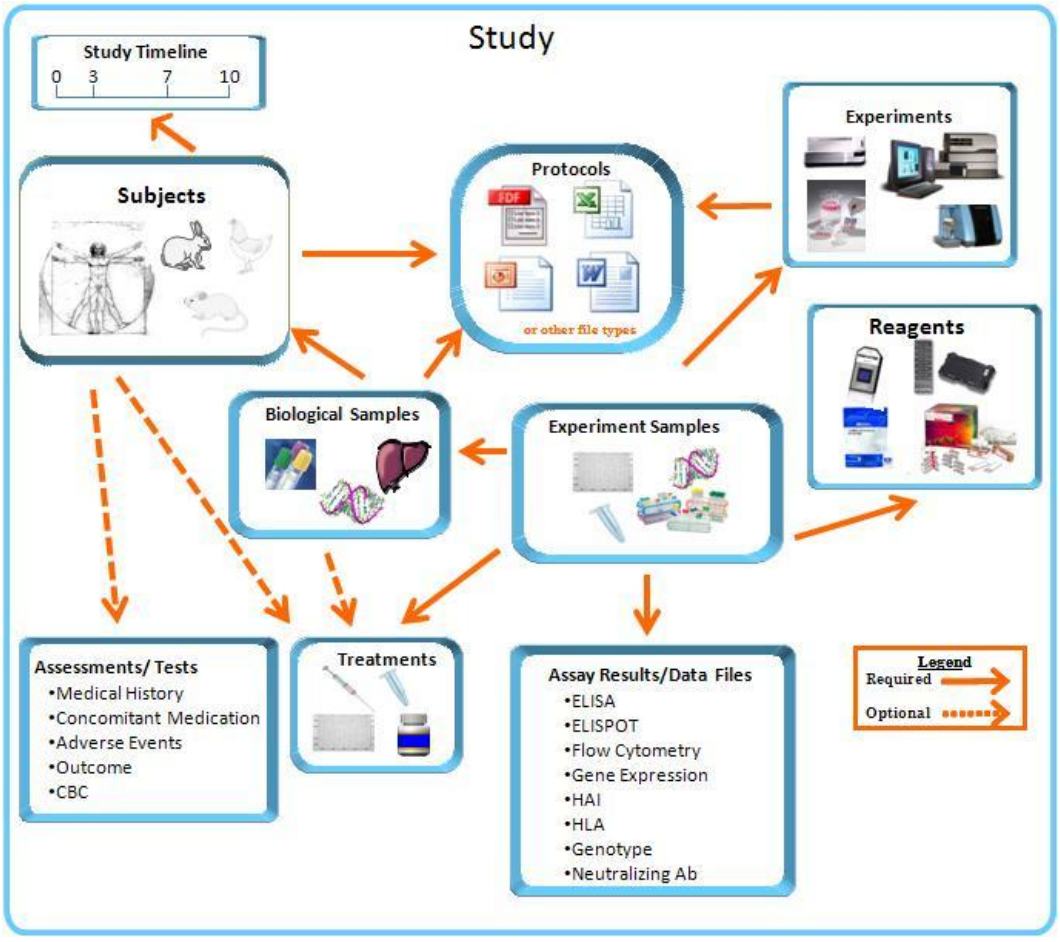
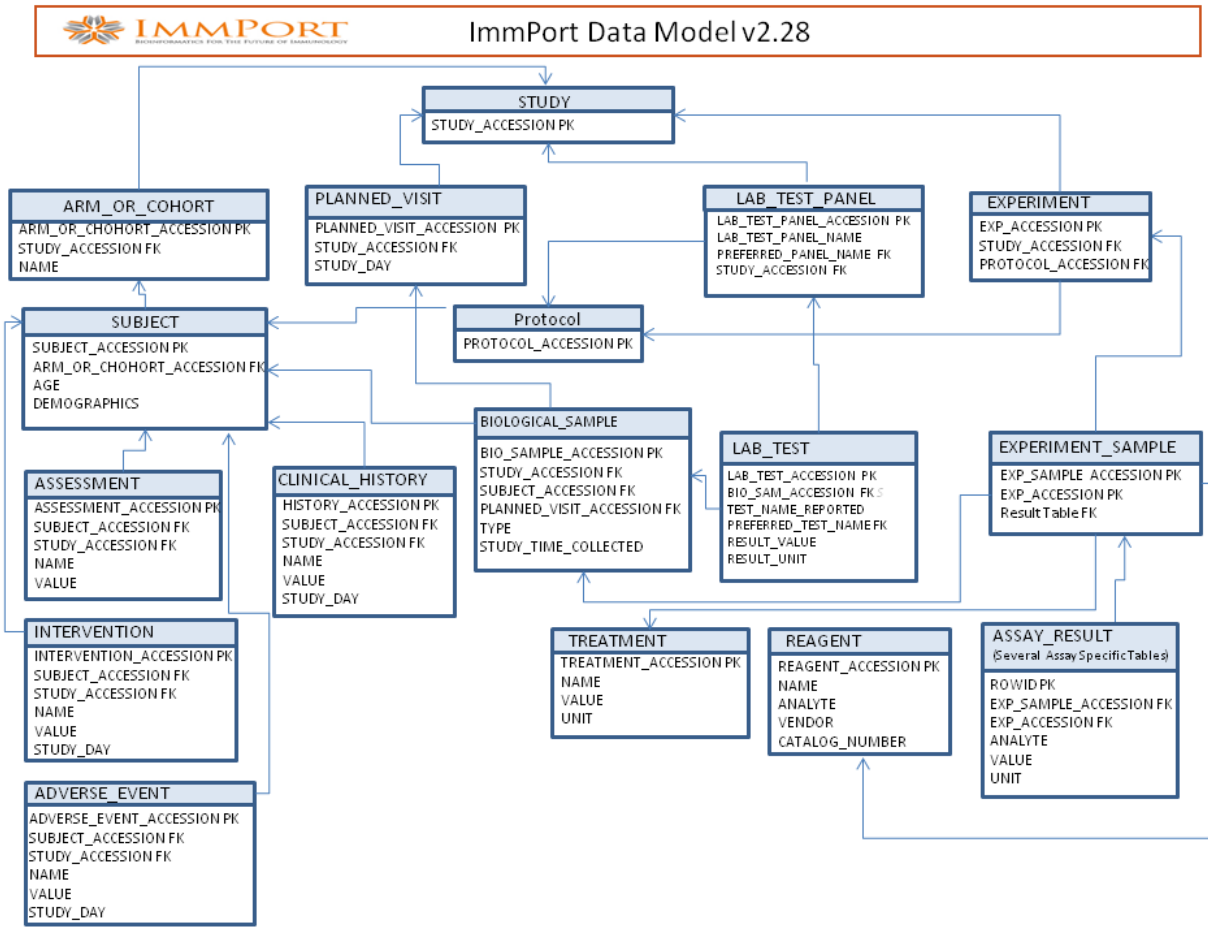


**Figure 3b. ImmPort Data Model Alternative View**

Illustration of the relationships between research data components




## 4.0 METADATA UPLOAD TEMPLATES OR DATA SUBMISSION TEMPLATES

Metadata upload templates enable the user to provide detailed information about how a study was conducted in a structured format for ImmPort to parse and store for subsequent queries or analysis.

Metadata templates for entering your data can be downloaded from the ImmPort Data Submission web page at "**Step 1: Download and Fill Templates**" (figure 4a). It is strongly recommended to download templates prior to submitting a data package to ensure use of the most current template file versions. The order in which metadata files are completed by the user depends on the data submission goals of the research team and what information they have already submitted to ImmPort.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

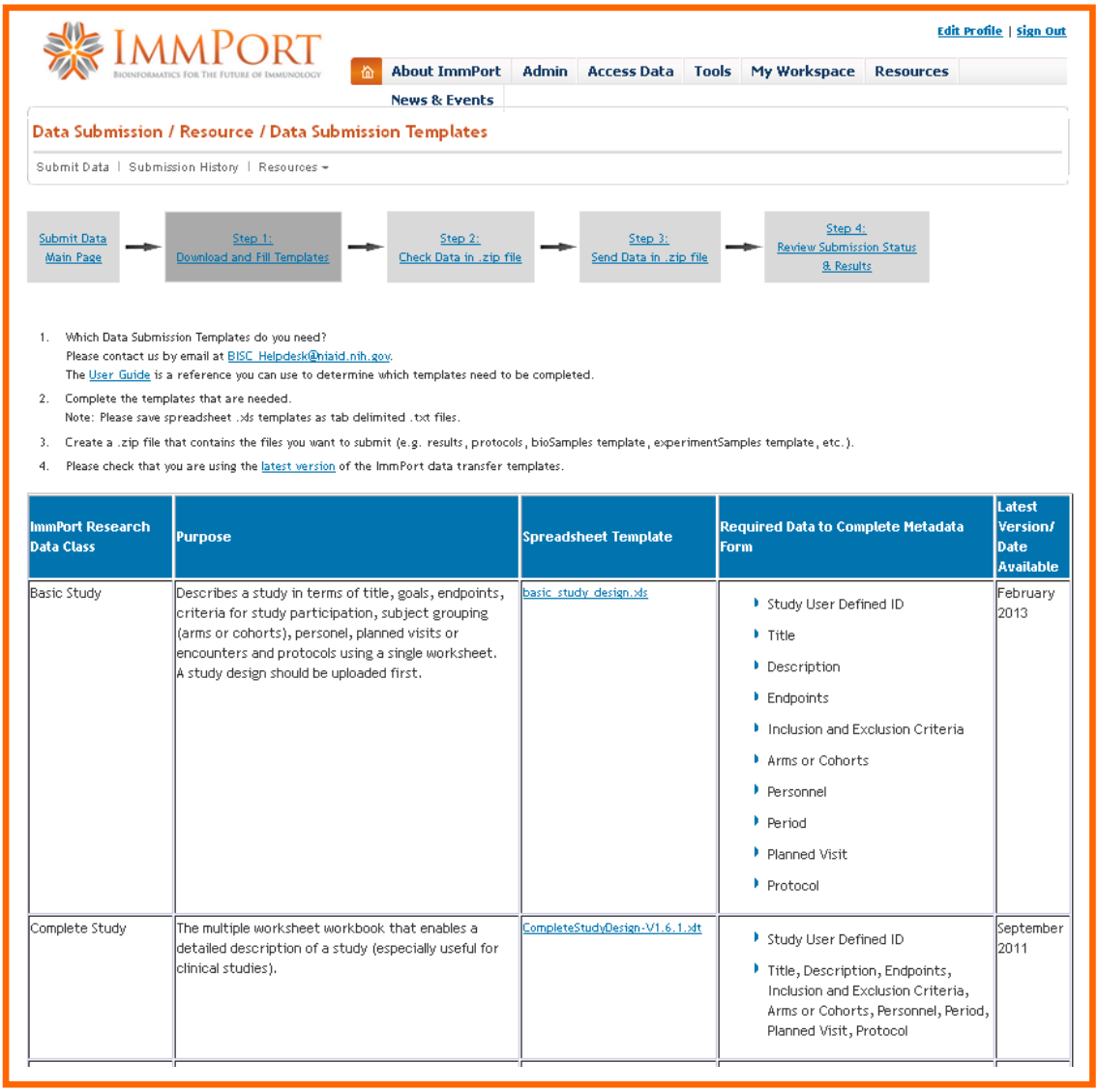
The templates are available in a spreadsheet-based .xls format or in a tab separated text format. **It should be noted that after entering your data into spreadsheet based .xls files, the files need to be saved as tab-delimited text files before they are zipped into a submission package and sent to ImmPort.**

Because metadata upload files are used to define and describe metadata items (e.g. samples, protocols, experiments, etc.) and define links or associations between metadata (e.g. linking a sample preparation protocol to a biological sample or experiment), the primary identifier used when defining and linking metadata is an item's User Defined ID. User Defined IDs are intended to be short names for each metadata item and are the primary means to link metadata in a specific project from different submitted experiments. As a result **the User Defined ID for a metadata item must be unique within the scope of a research project.** A Research Project generally refers to a private workspace created by the Principal Investigator (PI) to be used by an individual or by a group researchers collaborating on a given project. The Project created will be used to store study descriptions, experiments, results, and any accompanying data.

Some of the metadata upload files have several columns to list the User-Defined IDs for different items involved with linking data together (see figures 7a, 7b and 9a for examples). As a result, for subsequent data submissions with common samples, protocols or other details involved with data linkage**, the User Defined IDs (or ImmPort Accession number) and other identifiers must match exactly and are case sensitive.**

Examples and additional rules involved with User Defined IDs and data linkage will be presented in the following sections describing the metadata templates.

**Figure 4a Step 1: Download and Fill in templates with your data**




## 4.1 Spreadsheet Based Metadata upload File Features

The first three rows of the spreadsheet-based .xls metadata upload file contain file formatting structure and explanatory information for the user (e.g. comments). The column headers are used to ensure that data entered by the user is properly processed. **Do not edit or delete these column headers.**

There are drop lists with controlled vocabulary for some columns (e.g. Measurement technique in experiments.xls). These are activated by clicking on the data entry cell in the column.

**Note that whenever there is a comma with text in any cell, upon conversion to a .txt file Microsoft Excel will add a double quote at the beginning of the text and a double quote at the end of the text. This could result in a failed data submission and will not allow ImmPort to properly use this data.**

Upon completion of entering data into these templates, they must be saved as a tab-delimited text file with its ImmPort file name. As a result, for each data submission it is advisable to create a folder containing all the blank metadata templates you will need for a specific submission. The completed templates in this folder can then be zipped into one file for submission as described in sections 15 and 16.

### 4.1.1 Required and Optional Columns

Please see the ImmPort.Upload.Templates.Description.pdf document for a description of the template columns.

## 4.2 IMMPORT ACCESSIONS

ImmPort assigns accession numbers to key research metadata elements to ensure the global uniqueness of identifiers in ImmPort. The ImmPort accessions are an alternative means to identify User-Defined IDs to reference metadata items (e.g. reagents, protocols, or samples) already stored in ImmPort. When linking metadata information either the ImmPort accession OR the user-defined ID is used to make the link, but not both.

The naming convention for ImmPort accessions has a prefix based on the data category (Table 4a) and a numerical integer generated by ImmPort. For example, if you submit an experiment with one sample and a protocol, ImmPort accession numbers could look like; EXP3428 for the experiment, BS116067 for the biological sample and PTL2187 for the stored protocol document.

ImmPort accessions assigned to previously uploaded and stored data can be obtained from a data submission report, the experiment data management pages or from experiment data queries. More information on how to access this information can be found in the instructions on searching research data.

**Table 4a. ImmPort accession prefix abbreviations**

| ImmPort Accession | Description |
|---|---|
| BS | Biological Sample (BioSample) |
| EXP | Experiment |
| ES | Experiment Sample (ExpSample) |
| PTL | Protocol |
| REA | Reagent |
| SDY | Study |
| SUB | Subject |
| TRT | Treatment |
| LTP | Lab Test Panel |
| LT | Lab Test |
| AE | Adverse Event |
| AP | Assessment Panel |
| AC | Assessment Component |
| SM | Substance Merge |

## 4.3 Overview of ImmPort Data Submission Templates

The ImmPort templates used to capture descriptions of research data types/concepts are laid out together below (Figure 4d) to provide a means of understanding how they relate to each other and how they are organized.

**Figure 4d ImmPort Template Overview**

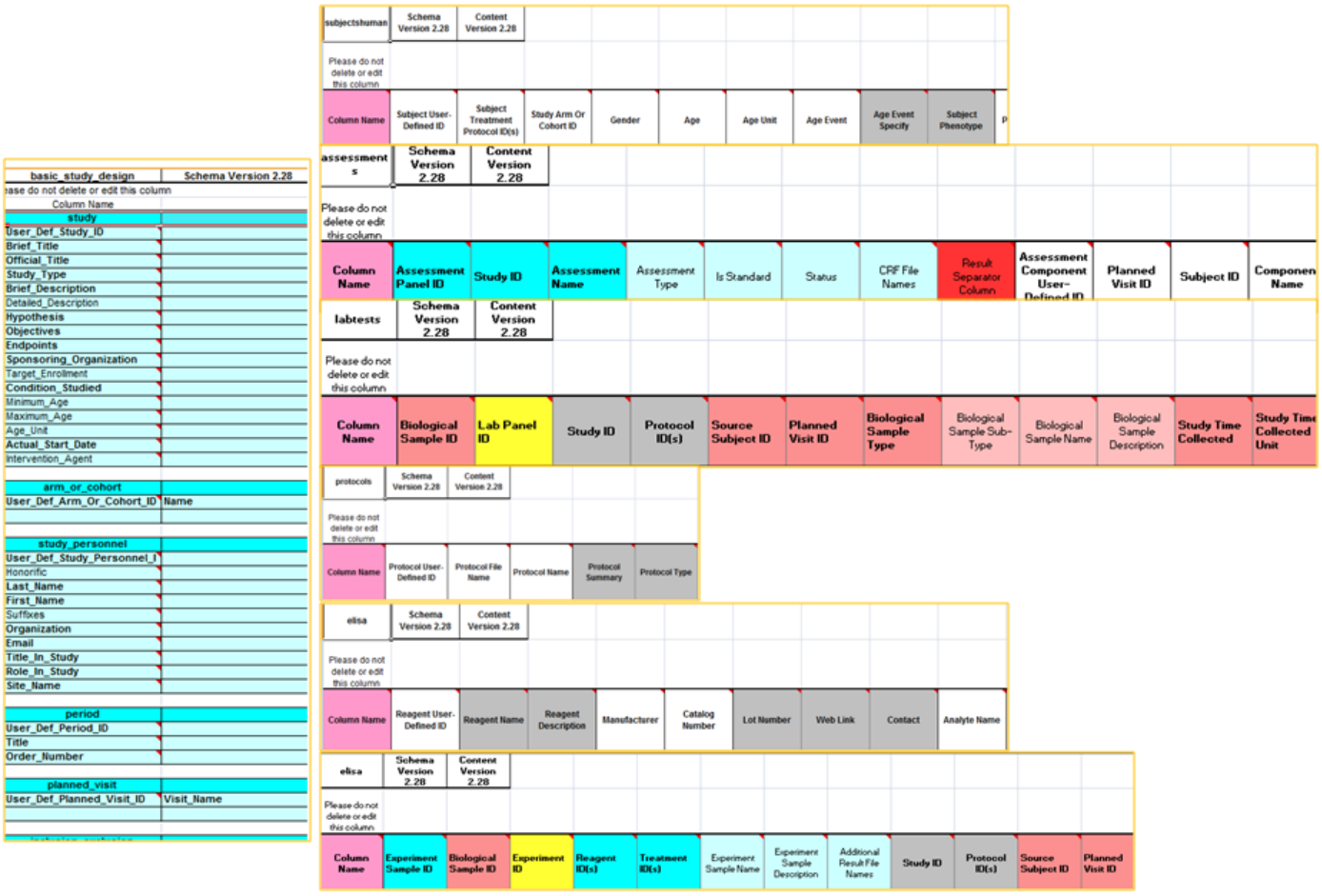



Table 4b is an overview of the data formats to be provided for assay results. Please contact ImmPort staff for questions and comments about assay result formats.

**Table 4b. Summary of the assay specific Experiment Samples templates and results formats 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<br>FCM_derived_data.txt | control samples<br>.fcs format | compensation samples<br>.fcs format | |
| Gene Expression | Affymetrix CEL<br>Illumina GEO raw<br>NCBI GEO accession | | | |
| Genotyping | Affymetrix CEL<br>Illumina Bead Studio<br>dbGAP accession | | | |
| Hemagglutination Inhibition | HAI_Results.txt | | | |
| HLA | HLA_Typing.txt | | | |
| Image Histology | Custom | | | |
| KIR | KIR_Typing_Results_Column.txt<br>or<br>KIR_Typing_Results_Column.txt | | | |
| Mass Spectrometry | Custom | | | |
| Multiplex Soluble Protein | MBAA_Results.txt | Control_Samples.txt | | Standard_Curve.txt |
| qRT-PCR | PCR_Results.txt | | | |
| Virus Neutralization | Virus_Neutralization_Results.txt | | | |

# 5.0 PROTOCOLS

Listing Protocols allows a user to provide detailed descriptions of methods related to subject treatment, sample collection, sample processing and other experimental methods. Protocol files may be in the form of PDFs, spreadsheets, word processor documents or other file formats.

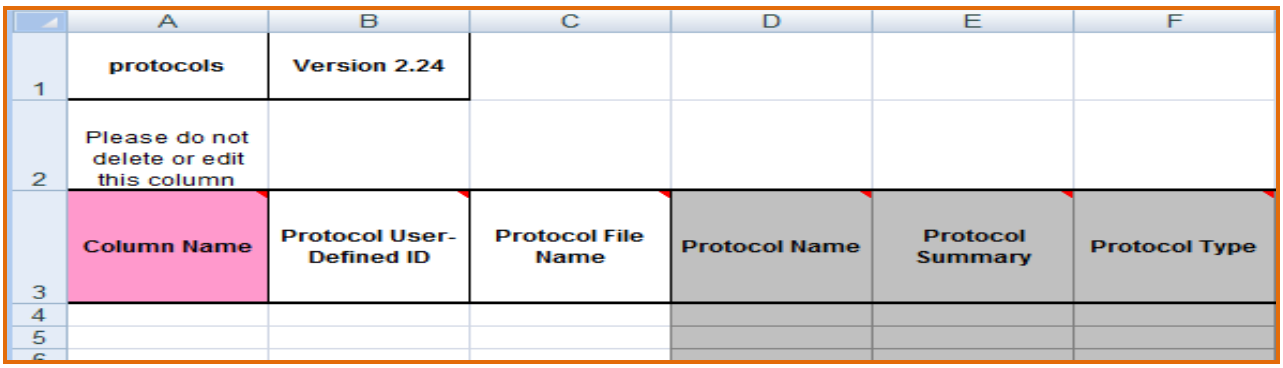
Protocols can be linked from:
Study
Subjects
Biological Samples
Experiments

Note: Protocols MUST be linked to Studies, Biological Samples, Experiments and Subject(s). This is a requirement on DAIT minimum information standards.

The protocols.xls template allows the user to define and describe protocols that can be referenced or linked by other metadata items (e.g. biological samples)

Upon completion of entering data into this template, it should be saved as a tab-delimited text file and must be saved with its ImmPort name of protocols.

**Figure 5a. protocols.xls template**



| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | protocols | Version 2.24 | | | | |
| 2 | Please do not delete or edit this column | | | | | |
| 3 | Column Name | Protocol User-Defined ID | Protocol File Name | Protocol Name | Protocol Summary | Protocol Type |
| 4 | | | | | | |
| 5 | | | | | | |

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 6.0 Study Design

There are two versions of the study design template: basic and complete. The basic study design template is recommended for the majority of ImmPort data upload efforts and differs from the other ImmPort templates in that is has a more vertical or "form" like organization. This is a consequence of placing several domains of study design on a single form. The row and column headers in **bold text** are required elements. There are comments for row and column headers that can be viewed by placing the mouse cursor over the column header name.

Figure 6. basic_study_design.xls template

| basic_study_design | Schema Version 2.28 |
|---|---|
| ase do not delete or edit this column | |
| Column Name | |
| **study** | |
| User_Def_Study_ID | |
| Brief_Title | |
| Official_Title | |
| Study_Type | |
| Brief_Description | |
| Detailed_Description | |
| Hypothesis | |
| Objectives | |
| Endpoints | |
| Sponsoring_Organization | |
| Target_Enrollment | |
| Condition_Studied | |
| Minimum_Age | |
| Maximum_Age | |
| Age_Unit | |
| Actual_Start_Date | |
| Intervention_Agent | |
| | |
| **arm_or_cohort** | |
| User_Def_Arm_Or_Cohort_ID | Name |
| | |
| | |
| **study_personnel** | |
| User_Def_Study_Personnel_I | |
| Honorific | |
| Last_Name | |
| First_Name | |
| Suffixes | |
| Organization | |
| Email | |
| Title_In_Study | |
| Role_In_Study | |
| Site_Name | |
| | |
| **period** | |
| User_Def_Period_ID | |
| Title | |
| Order_Number | |
| | |
| **planned_visit** | |
| User_Def_Planned_Visit_ID | Visit_Name |
| | |
| | |

Studies link to:
Protocols
and may link to:
Files
Publications

Studies are linked from:
Subjects
Biological Samples
Experiments
Lab Test Panel
Assessment Panel
Substance Merge

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 7.0 SUBJECTS

There are human and animal specific subject templates.

Subjects link to:
Protocols
Study Arms or Cohorts

Subjects are linked from:
Biological Samples
Assessment Components
Substance Merges

Note: When subjects are used they MUST link to a Protocol(s), and Study Arm or Cohort. This is a requirement of DAIT minimum information standards. If multiple protocols should be linked, a semi-colon (;) may be used to separate the user-defined of each protocol listed in a cell.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

### 7.1 SUBJECTSHUMAN.XLS

The subject information to be completed includes basic demographic and the arm or cohort to which the subject is linked in a study (figure 7). Completed files need to be saved as tab-delimited txt files before compressing into a zip archive.

Figure 7. subjectsHuman.xls template

| subjectshuman | Schema Version 2.28 | Content Version 2.28 | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Please do not delete or edit this column | | | | | | | | | | |
| Column Name | Subject User-Defined ID | Subject Treatment Protocol ID(s) | Study Arm Or Cohort ID | Gender | Age | Age Unit | Age Event | Age Event Specify | Subject Phenotype | P |

### 7.2 SUBJECTSANIMAL.XLS

This template is similar to the subjectHuman.xls but excludes human specific descriptive columns and includes laboratory animal specific columns including Strain Name and Strain Characteristics. For a detailed description of the column headers, please refer to the Glossary.

## 8.0 EXPERIMENT SAMPLES

An experiment sample is a biological sample that is treated in vitro in some way (including not treatment) and then assayed. The experiment sample template defines and annotates the assay results for a sample by linking samples, experiments, and results together. The template enables you to define a new experiment and/or a new biological sample. as well as a new experiment sample. The template supports multiple data annotation scenarios:

- Define a new experiment, a new biological sample and a new experiment sample
- Define a new experiment, link to a biological sample defined in ImmPort and a new experiment sample
- Link to an experiment defined in ImmPort, define a new biological sample and a new experiment sample

Whenever a new record is defined, all of the required attributes for defining a record must be completed.

Experiment Sample template files are used to name and describe the control and experimental samples used in an assay. To ensure accurate recording of information for a number of different platforms and assay methods, there are several different templates to choose from for specific applications.

For some assay methods, the assay results are also recorded in the experiment sample template by completing the set of columns for assay results (e.g. for HAI, complete Virus Strain and Titer). To enter multiple assay results for an experiment sample, simply copy and paste the set of columns needed to describe the results as many times for each assay results. For example, if an experiment sample was assayed for HAI for three viral strains, there would be three sets of HAI assay result columns. The experiment sample template for ELISA, ELISPOT, HAI, Virus Neutralization, and qRT-PCR enable capturing the assay results in the experiment samples template.

The experimentSamples assay-specific .xls templates are available for downloading on the data submission home page. The first three rows and column headers of these files are used to ensure that data entered by the user is properly processed. **Do not edit or delete these column headers.** See ImmPort.Upload.Templates.Description.pdf, for a complete description or definitions of the columns and elements.

The User-Defined IDs for the experiment sample, experiment, protocol, and reagent are meant to be simple names selected by the user for these items. As an alternative to the User Defined IDs, ImmPort accession numbers can be entered if available from previously stored data. If you are entering User defined IDs, you do not have to enter ImmPort accession numbers.

In addition to these required columns, the “Result File or Folder Name” (column K) must also be entered. This option allows ImmPort to find the necessary result file that is needed by some tools while other tools may require several files to be stored in a specific folder to be accessed by ImmPort.

Experiment Samples link to:
Biological Samples
Reagents
Experiments
Result file(s)
Treatments

Note: Experiment Samples MUST link to an Experiment, Reagent (one or more), Biological Sample (**only one**), and Result File (one or more).
Please note that only one biological sample can be linked to an experiment sample.

The experiment sample file names help enhance the accuracy of the assay annotation. Please choose the most appropriate template for your data upload.

**Figure 8. expSamples.ELISA.xls template**

| elisa | Schema Version 2.28 | Content Version 2.28 | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Please do not delete or edit this column | | | | | | | | | | | | |
| Column Name | Experiment Sample ID | Biological Sample ID | Experiment ID | Reagent ID(s) | Treatment ID(s) | Experiment Sample Name | Experiment Sample Description | Additional Result File Names | Study ID | Protocol ID(s) | Source Subject ID | Planned Visit ID |

Figure 12b highlights an example where the experiment sample template is tailored to capture assay specific information. Flow Cytometry assay runs include control results and compensation fcs result files. These should be linked to the fcs file from the sample(s) that were assayed in a run. All experiment

samples from the same flow cytometry run should be linked to the same set of compensation and control files.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 9.0 TREATMENTS

Treatments are required for Experiment Samples and are optional for Biological Samples. The treatment template (figure 9) allows the user to define the amount, duration and temperature of treatments specific to individual Experiment Samples or Biological Samples. Do not edit or delete these column headers.

Treatments are linked from:
Experiment Samples.

Figure 9. View of an empty Treatment template

| | A | B | C | D | E | F | G | H | I |
|---|---|---|---|---|---|---|---|---|---|
| 1 | treatments | Version 2.24 | | | | | | | |
| 2 | Please do not delete or edit this column | | | | | | | | |
| 3 | Column Name | Treatment User-Defined ID | Treatment Name | Treatment? | Amount Value | Amount Unit | Duration Value | Duration Unit | Temperatu Value |
| 4 | | | | | | | | | |
| 5 | | | | | | | | | |

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 10.0 REAGENTS

The reagents to be described to ImmPort are those used in an assay to find or characterize one or more analytes. Reagents can be microarray chips for gene expression or genotyping, fluorochome conjugated antibodies for flow cytometry, ELISA or ELISPOT antibodies, etc.

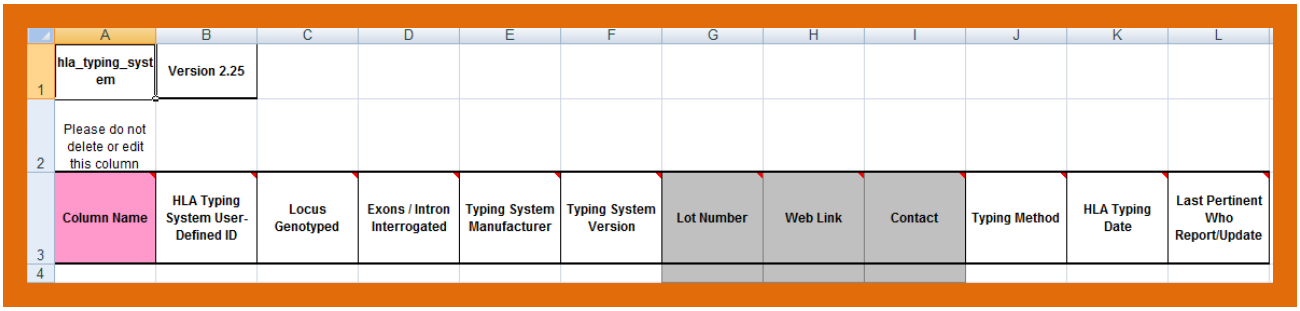
There is a reagents template for each assay type supported by ImmPort (e.g. Figure 11a). Each template is organized for entering information specific for each assay method. This organization facilitates the capture of assay specific reagent information that allows users to search for data in ImmPort.

**Figure 10a. View of an ELISA reagent template**

| | A | B | C | D | E | F | G | H | I | J | K | L |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | elisa | Version 2.25 | | | | | | | | | | |
| 2 | Please do not delete or edit this column | | | | | | | | | | | |
| 3 | Column Name | Reagent User-Defined ID | Reagent Name | Reagent Description | Manufacturer | Catalog Number | Lot Number | Web Link | Contact | Analyte Name | Analyte Description | Antibody Registry ID |
| 4 | | | | | | | | | | | | |

The format of the reagent templates is assay specific. As an example, the reagents-HLA worksheet (figure 11b) is used to describe reagents associated with HLA typing results and has a slightly different format than the ELISpot template. On the ImmPort web site, there are two additional files under example submission packages, the HLA_Typing_System_Allele_Ambiguity file and the HLA_Typing_System_Features file. These are intended to further annotate the HLA typing system that was employed

**Figure 10b. View of reagents-HLA template**



| | A | B | C | D | E | F | G | H | I | J | K | L |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | hla_typing_system | Version 2.25 | | | | | | | | | | |
| 2 | Please do not delete or edit this column | | | | | | | | | | | |
| 3 | Column Name | HLA Typing System User-Defined ID | Locus Genotyped | Exons / Intron Interrogated | Typing System Manufacturer | Typing System Version | Lot Number | Web Link | Contact | Typing Method | HLA Typing Date | Last Pertinent Who Report/Update |
| 4 | | | | | | | | | | | | |

## 11.0 Lab Tests

Lab Test template files are used to name and describe clinical lab tests and capture the test result. . Preferred values for lab test names from CDISC (cdisc.org) and SnoMED CT (***www.nlm.nih.gov/****snomed/* ) are provided to encourage use of standard terms.

Lab Tests link to:
Biological Sample
Lab Test Panel

Note: Lab tests MUST link to a biological sample and Lab Test Panel.

| labtests | Schema Version 2.28 | Content Version 2.28 | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Please do not delete or edit this column | | | | | | | | | | | | |
| Column Name | Biological Sample ID | Lab Panel ID | Study ID | Protocol ID(s) | Source Subject ID | Planned Visit ID | Biological Sample Type | Biological Sample Sub-Type | Biological Sample Name | Biological Sample Description | Study Time Collected | Study Time Collected Unit |

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 12.0 Assessments and Adverse Events

The Assessment template captures results from Case Report Forms and similar questionnaires in a standard format. This template is intended for human subjects.

The Adverse Event template records adverse events experienced by study subjects.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

# 13.0 EXPERIMENTS

This is a legacy template that will be supported for backward compatibility, but it's function is replaced by the Experiment Sample template. Experiment template files are used to provide detailed information about the type of analysis that was done and how it was done. This allows the entry of user defined definitions of names for the experiment, protocols and other information.

The experiments.xls template file is available on the data submission page and is standard for all submissions. The first three rows and column headers are used to ensure that data entered by the user is properly processed. Do not edit or delete these column headers.

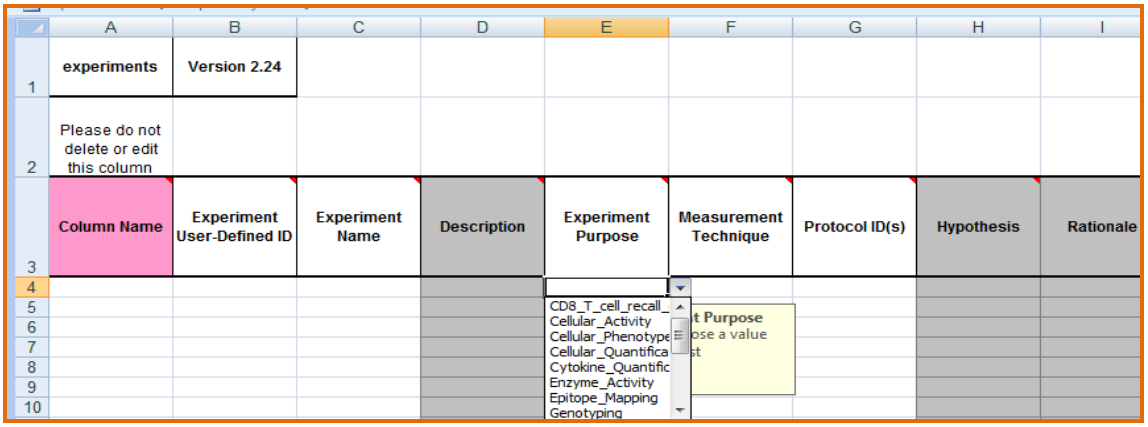
Experiments link to:
Protocols
Study

Experiments can be linked from:
Experiment Samples
Control Samples
Standard Curves

Note: Experiments MUST link to a single Study and one or more Protocols. This is a requirement of DAIT and ImmPort minimum information standards. If multiple protocols should be linked, a semi-colon (;) may be used to separate the user-defined of each protocol listed in a cell.

The Experiment Purpose and Measurement Technique can be selected from dropdown menus by selecting the data entry cells for this information.

Figure 8. experiments.xls template




**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

# 14.0 BIOSAMPLES

This is a legacy template that will be supported for backward compatibility, but it's function is replaced by the Experiment Sample template. ImmPort templates for biological samples allow the user to describe the characteristics of biological material (i.e. blood, sera, tissue, cell preparation, etc.) that has undergone isolation, processing and/or treatment prior to use in an experiment. In order to effectively describe a biological sample, as much information about the sources, conditions, and treatments should be captured in the template. Links to sample sources (e.g. subjects or other biological samples) and protocols can be defined.

The bioSamples.xls template file is available on the data submission page and is standard for all submissions. The first three rows and column headers are used to ensure that data entered by the user is properly processed. Do not edit or delete these column headers.

Biological Samples link to:
Study
Subjects
Other Biological Samples
Protocols.

Biological Samples are linked from:
Experiment Samples
Lab Tests

Note: Biological Samples MUST link to a Protocol(s) and Study. This is a requirement of DAIT and ImmPort's minimum information standards. If multiple protocols should be linked, a semi-colon (;) may be used to separate the user-defined of each protocol listed in a cell.

Fields required on this template are in white.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 15.0 Lab Test Panels

This is a legacy template that will be supported for backward compatibility, but it's function is replaced by the Lab Test template. Lab Test Panel template files are used to name and describe groups of clinical lab tests. Preferred values for Lab Test Panel names from CDISC (cdisc.org) and SnoMED CT (***www.nlm.nih.gov/****snomed/* ) are provided to encourage use of standard terms.

Lab Test Panels link to:
Study
Protocols

Lab Test Panels are linked from:
Lab Tests

Note: Lab test panels MUST link to a Study and one or more protocols.

**The file ImmPort.Upload.Templates.Description.pdf is a complete listing of all templates, their usage and content.**

## 16.0 Review of the ImmPort Metadata Files

In the preceding sections describing spreadsheet-based .xls metadata upload files, examples of completed templates were displayed.

Upon completion of entering data into these templates, they should be saved as tab-delimited text files and they must be saved with their ImmPort name (original ImmPort file names are listed in section 15.2.1). As a result, for each data submission package it is advisable to create a folder containing all the blank metadata templates you will need for a specific submission. The templates in this folder can be edited to contain the information and data needed for the submission before saving them as text files. The completed .txt versions of the templates in this folder can then be zipped into one .zip file for submission.

# 17.0 Derived Data Templates

NIAID DAIT strongly encourages the use of ImmPort derived data templates if there are applicable templates available. These templates facilitate the annotation and organization of assay results in a consistent fashion that allow the full set of descriptive data to be associated with the assay results. The derived results templates include:
FCM_derived_data.xls
HLA_Typing.xls
KIR_Typing
MBAA_ Results.xls

the following templates are legacy formats that can be used to add results to existing experiment samples.
ELISA_Results.xls
ELISPOT Results.xls
HAI_Results
PCR_Results
Virus_Neutralization_Results

## 17.1 Flow Cytometry Data Report

Flow Cytometry (FCM) derived data refers to the analysis results of .fcs file contents. As with the metadata upload files, the columns that must be completed are white and optional columns are shaded gray. The FCM_derived_data.xls template is available from Step 1 of Data Submission.

The required columns in the file are columns B, C, D, E, F, and G. The Experiment Sample User_Defined ID is used to link the derived data with the result file and the descriptions of how the data was generated and analyzed. The additional required columns capture details about analyzed FCM results that would be useful for queries such as population name and gating combination.

**Figure 17b. The ImmPort FCM analyzed results template**

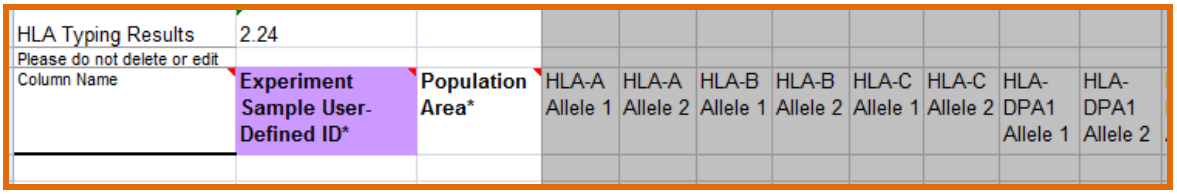
| fcm_derived_data | Version 2.24 | | | | | | |
|---|---|---|---|---|---|---|---|
| Please do not delete or edit this column | | | | | | | |
| Column Name | Experiment Sample ID | Population Name | Population Definition (gating combination) | Population Cell Number | Population Cell Number Unit | Workspace File | Comments |

## 17.2 HLA Typing Summary Report

The ImmPort HLA_Typing.xls template supports capturing the expert determined values for the HLA genes. The HLA_Typing.xls template format follows a commonly used structure where the HLA loci symbols are the column headers (figures 14b and 14c). The locus symbols are from the IMGT/HLA curated data repository (www.ebi.ac.uk/imgt/hla/). The commonly typed HLA loci are always displayed and the data provider can add additional loci symbols to the template by selecting from the drop down list in the “Other” column header. Note that two adjacent columns must have the same locus name. The typed values for each locus can be entered in any format as “free text”. An experiment sample ID is used in the template to link the HLA data with other results and metadata. This is the only required field. The

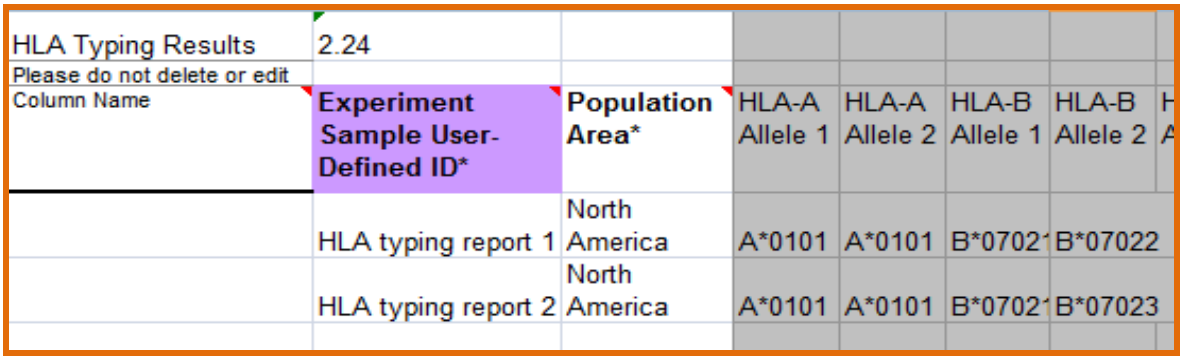
commonly typed HLA loci symbols are included as column headers. Additional HLA locus symbols are available from the dropdown list in the "Other" columns.

**Figure 17c. View of HLA_Typing.xls template**



| HLA Typing Results | 2.24 | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Please do not delete or edit | | | | | | | | | | |
| Column Name | **Experiment Sample User-Defined ID*** | **Population Area*** | 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 |
| | | | | | | | | | | |

**Figure 17d. Completed version of HLA_Typing.xls template**



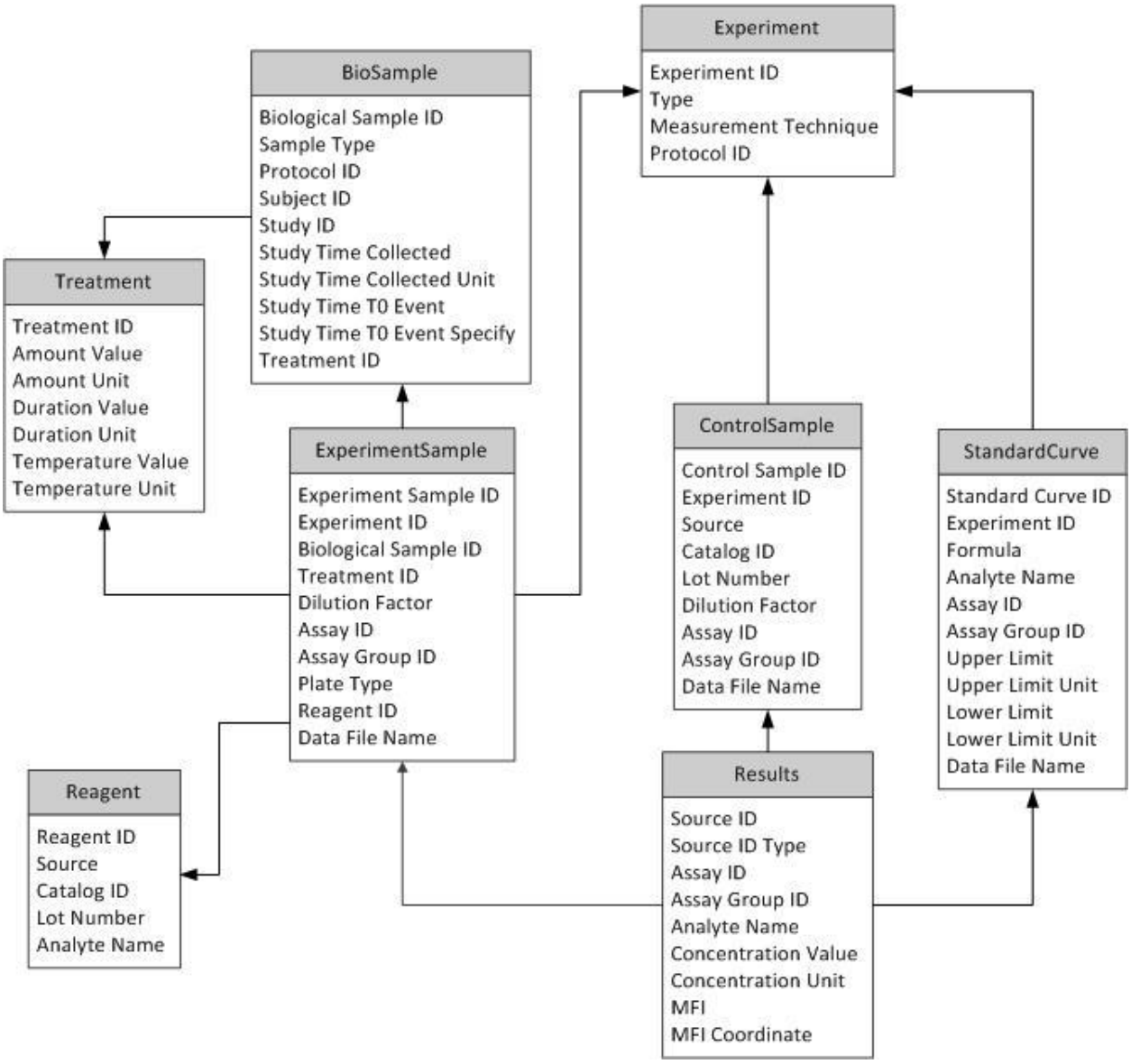
| HLA Typing Results | 2.24 | | | | | | |
|---|---|---|---|---|---|---|---|
| Please do not delete or edit | | | | | | | |
| Column Name | **Experiment Sample User-Defined ID*** | **Population Area*** | HLA-A Allele 1 | HLA-A Allele 2 | HLA-B Allele 1 | HLA-B Allele 2 | H A |
| | HLA typing report 1 | North America | A*0101 | A*0101 | B*0702 | B*07022 | |
| | HLA typing report 2 | North America | A*0101 | A*0101 | B*0702 | B*07023 | |
| | | | | | | | |

## 17.3 MBAA Results Report

The Multiplex Bead Array Assays (MBAA) data capture process was developed in coordination with the Human Immunology Project Consortium (***www.immuneprofiling.org)*** Data Standards Working Group. In addition to the experiment sample to results linkage that is common for all ImmPort results, there are two additional metadata or descriptive entities: Control Samples and Standard Curves.

**Figure 17e. MBAA Data Model**

This diagram highlights the relationship between experiments, samples, standard curves and MBAA results.




Figures 17f-i (below) highlight the structure of the templates used to capture MBAA results..

### 17.3.1 Control Sample

Control samples are often used for quality control and to allow comparison between assay runs or across labs. These control samples are distinct from biological samples since they are often purchased in bulk, and are not linked to particular study subjects. See Appendix 1.02 for more details.

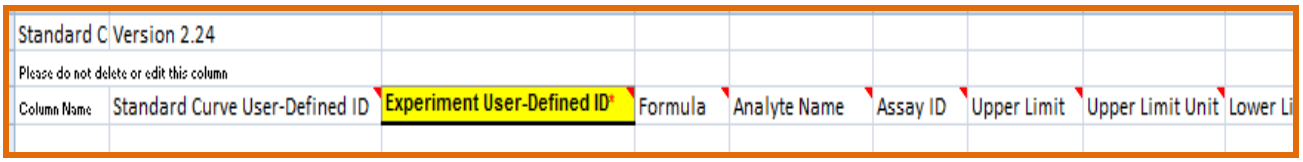
**Figure 17f. Control Samples**

| Control Samples | Version 2.24 | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Please do not delete or edit this column | | | | | | | | |
| Column Name | Control Sample User-Defined ID | Experiment User-Defined ID* | Source | Catalog ID | Dilution Factor | Assay ID | Result File Name | Assay Group ID |

### 17.3.2 Standard Curve

This is a new template for ImmPort. A standard curve is defined for each analyte in a batch (e.g., on a single plate). See Appendix 1.07 for more details.

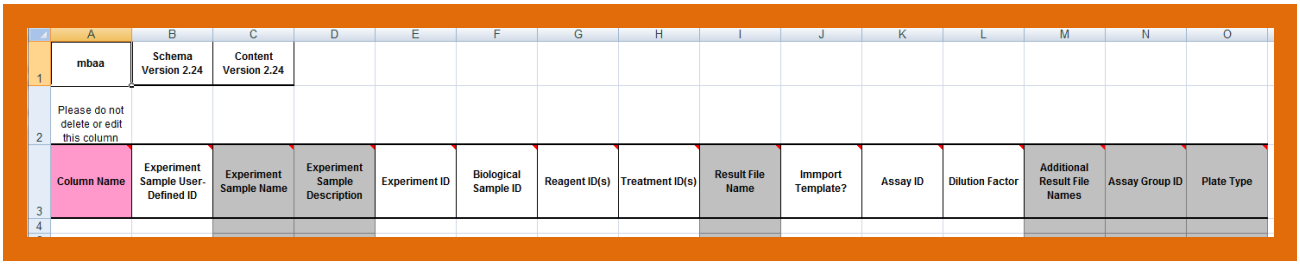
**Figure 17g. Standard Curves**




### 17.3.3 Experiment Sample MBAA

The expSamples.MBAA.txt template captures details such as Assay ID and Dilution Factor that are unique for this assay.

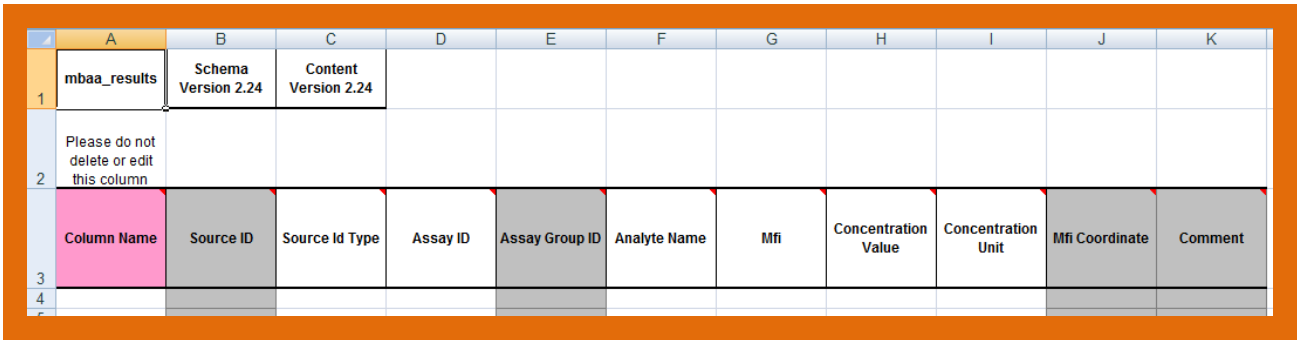
**Figure 17h. MBAA Experiment Sample**




### 17.3.4 MBAA Results Template

MBAA_Results.txt template captures the individual measurements of the analyte(s). There are three sources for results: experiment sample (assay run for a biological sample), control sample, and standard curve. The results file from Luminex or MSD is the primary output from the assay platform. It may consist of various formats (image, image interpreted to text, etc). One of the "commonly" seen formats is a tabular representation of the results where plate ID and plate location are critical identifying attributes. The type of material assayed (biological sample, control sample, standard curve) and the analyte assayed are provided by annotation mapping files. Since there are three sources for results, it is essential to indicate the source type when describing the source ID.

**Figure 17i. MBAA Derived or Interpreted Results**




In addition to the derived results, the bead level result files should also be included and linked to experiment sample, control sample and standard curve records as appropriate. See Appendix 4 for details about saving MBAA bead level result files.

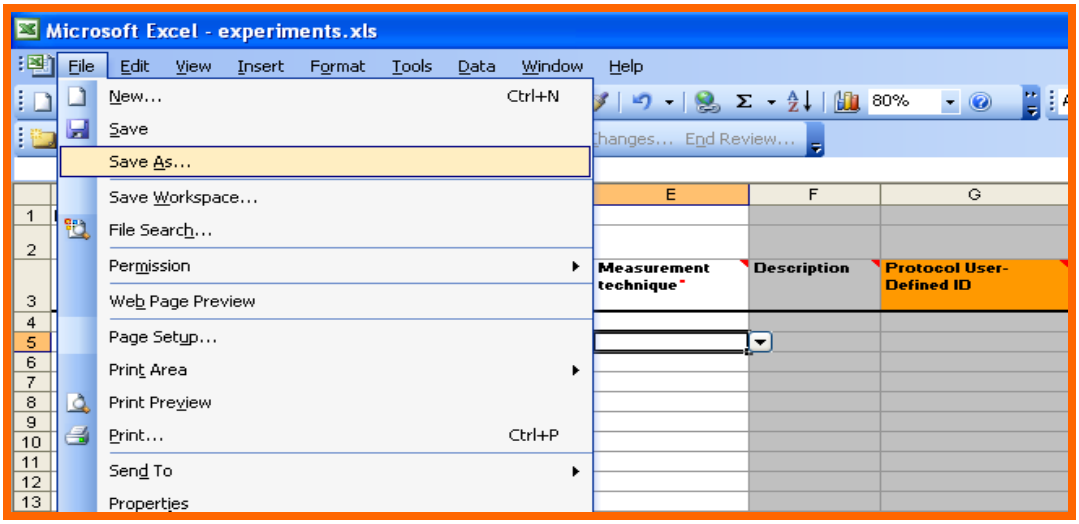
# 18.0 DATA SUBMISSION PACKAGE

An ImmPort data submission package may include completed metadata upload files, derived results templates and other files. The spreadsheet based templates must be saved as tab delimited text files before being compressed together into an ImmPort data submission package. For .xls file submission the files are packaged together into an archive .zip file format. When submitted to ImmPort, the contents of the package are processed to store the results and make them available for the analysis, query, or sharing of data in ImmPort. If the uploading and processing is successful or fails, the status of the upload can be viewed on the Submission History page.

## 18.1 SAVE THE SPREADSHEET-BASED FILE AS TAB-DELIMITED TEXT

The .xls based templates must be saved as tab-delimited text files by selecting the "Save As" option under the "File" Menu bar option (figure 15a).

**Figure 18a. Selecting 'Save As' from the' File' menu list**




In the pop up window opened by Save As, open the "Save as type" drop down list, scroll down the list and choose the "Text (Tab delimited) (*.txt)" document type (figure 15b)

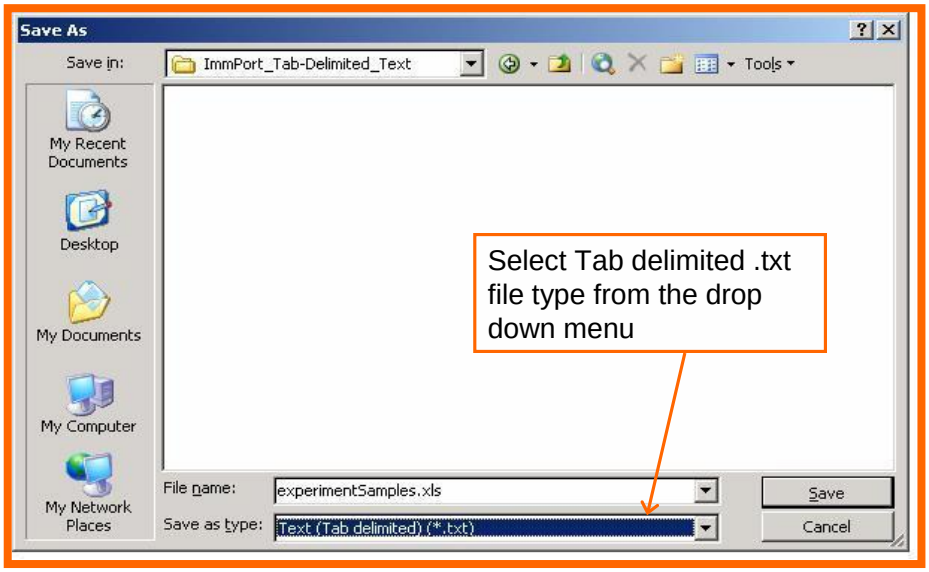


**Figure 18b. Selecting "Save as type" in a spreadsheet as tab delimited text**

After selecting the file type as .txt, press the save button. A dialog box will appear regarding the conversion of the file to a .txt format (figure 15c). Confirm that you wish to save the file in the text format by selecting "Yes" in the dialog box.

**Figure 18c. Saving a spreadsheet as text dialog box**


## 18.2 Creating an ImmPort Data Submission Package

An ImmPort data submission package is a .zip file that includes all of the files the data provider wishes to send (e.g. protocols, results, metadata, derived results, etc).

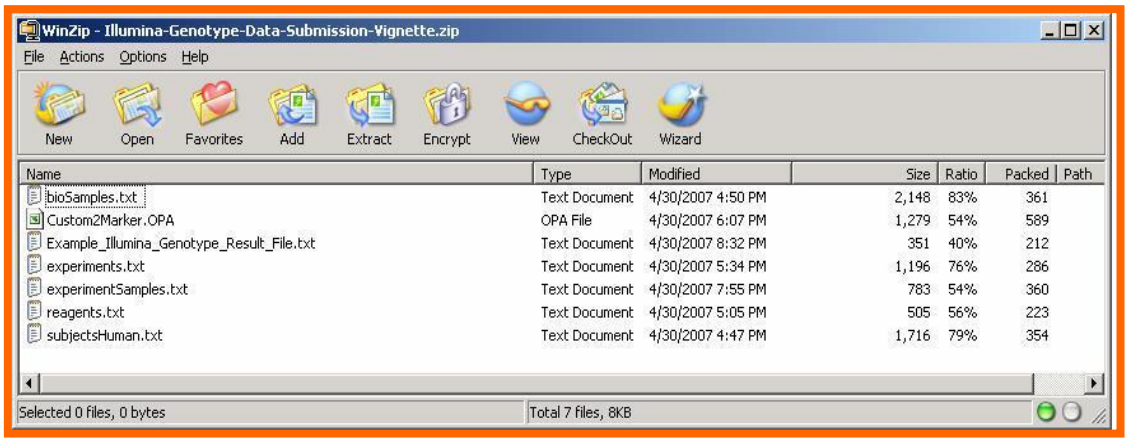
It is important that the completed metadata file names in the submission package are not modified from their original ImmPort assigned names. As a result, for each data submission package it is advisable to create a folder containing all the blank metadata templates you will need for a specific submission. The templates in this folder can be edited to contain the information and data needed for the submission before saving as .txt files. The completed .txt versions of the templates in this folder can then be compressed into one .zip file for submission.

### 18.2.1 ImmPort Metadata upload Tab-Delimited Format File Names (after conversion from .xls files when saving)

basic_study_design.txt
biologicalSamples.txt
experiments.txt
experimentSamples.[Assay Name].txt
protocols.txt
reagents.[Assay Name].txt
subjects.txt
treatments.txt

Only one copy of each of the completed metadata files should be included in the .zip file of the data submission package (figure 15d).

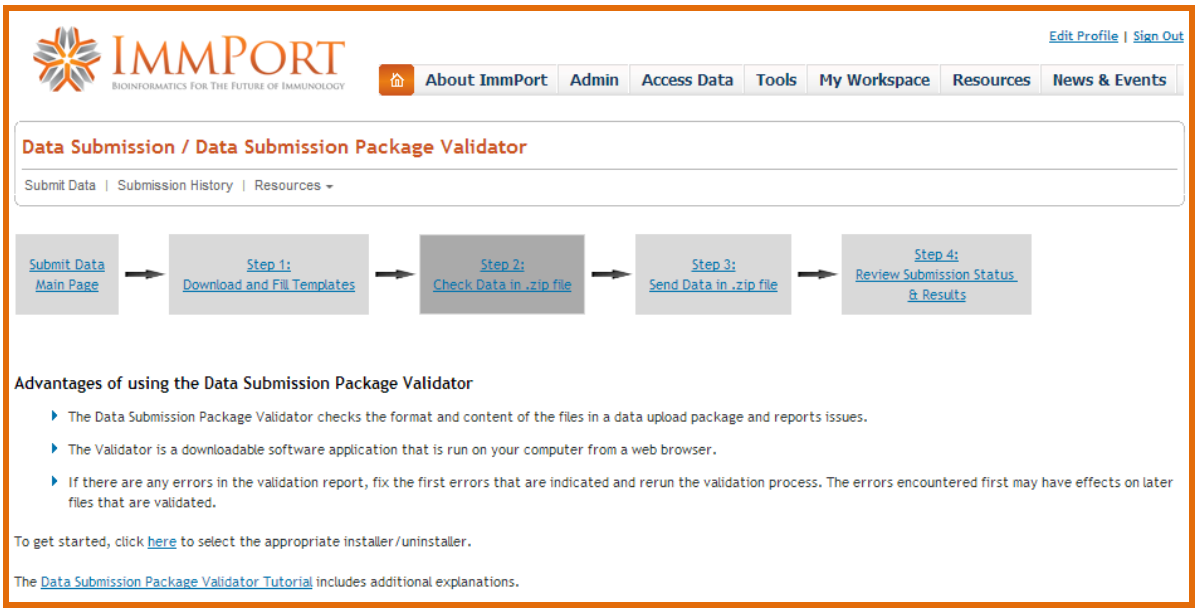
**Figure 18d. Example of an archive .zip file showing contents and structure**



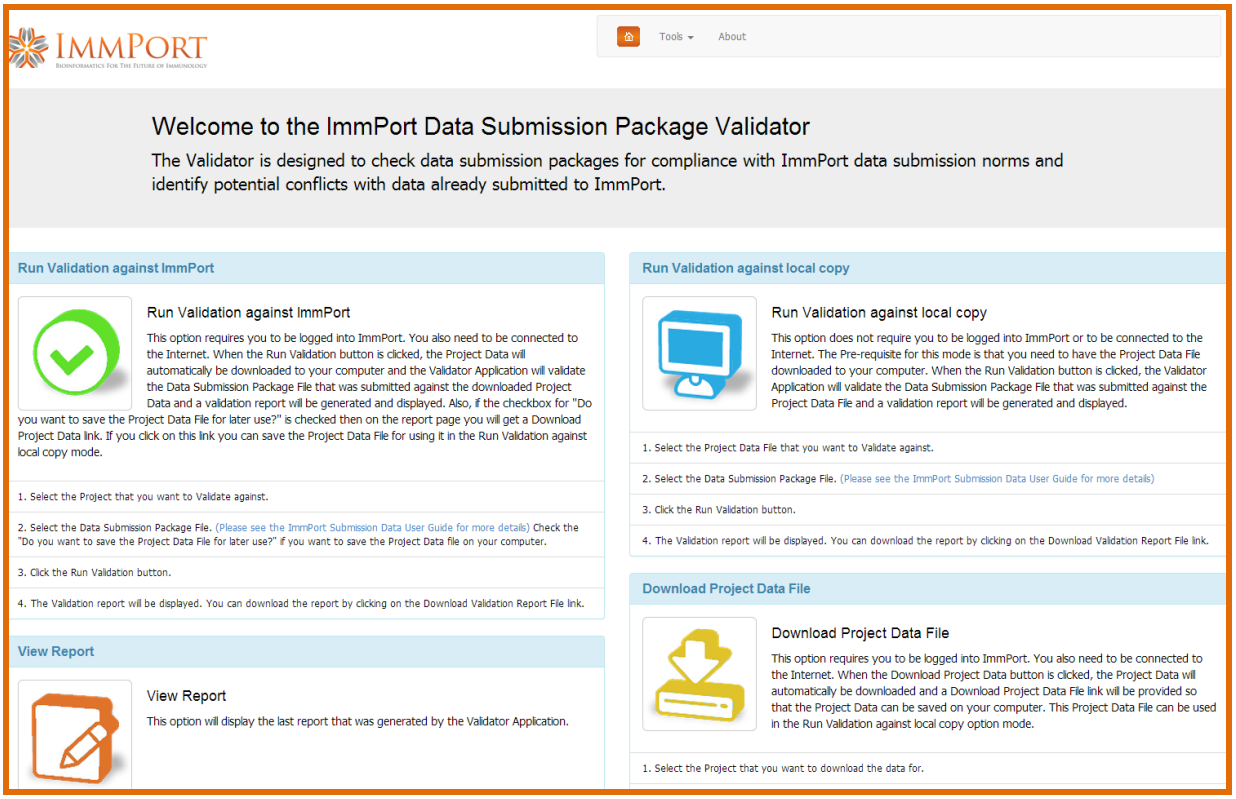

## 19.0 DATA SUBMISSION PACKAGE VALIDATOR

The ImmPort Data Submission Package Validator is available from Step 2 of ImmPort Data Submission and is used to check for compliance with ImmPort data submission norms and identify potential conflicts with data previously submitted to ImmPort.

## Figure 19a. ImmPort Data Submission Package Validator access




## Figure 19b. ImmPort Data Submission Package Validator




Running the Validator can be done in two modes: via internet connection against project data in ImmPort or run against a local copy of project data. The application checks for missing files, improperly formatted

metadata files, references to other metadata within the data package, verifies references to records in the ImmPort database, confirms the integrity and structure of .zip files, database column width checks, and guidance on metadata content utilizing ImmPort analysis tools. It is highly recommended to use the Validator before sending data into ImmPort as part of the data submission process.

Details on the installation and use of the Data Submission Package Validator are available in the user guide and tutorial that accompany the Validator.

## 20.0 SEND THE DATA SUBMISSION PACKAGE

Once files are compressed into a .zip archive file, proceed to Step 3 of the Data Submission process "Send Data in .zip file" by clicking on Step 3 in the Data Submission schematic (figure 17a). Selecting this option in the work flow diagram at the top of the page brings you to a page where the data provider must select a research project into which the data will be submitted (figure 17b). The user can also select if the data will be submitted electronically or if it is over 1 Gigabyte, it can be shipped to ImmPort for loading (table 17a).

**Figure 20a. Step 3: Choose the Research Project and select Upload option**


For electronic uploading of data less ≤ 1 Gigabyte, select the Research Project and Grant/Contract number with which your data will be associated and enter any comments in the Notes text box. The data provider must select a research project to which the data will be submitted. If there is no project to select, a research project must be created by the Principal Investigator or the project manager. ImmPort staff can also help with this task as requested. If there are multiple projects listed, please contact the Principal Investigator or the project manager to decide which project to select. The user can enter any extra information to be saved in the Notes text box.

After selecting the file to upload, click the submit button to start file transfer. Make sure you record the registration number you receive for the transfer. Depending on the size of the file being transferred it can take several minutes to several hours for the transfer to be completed.

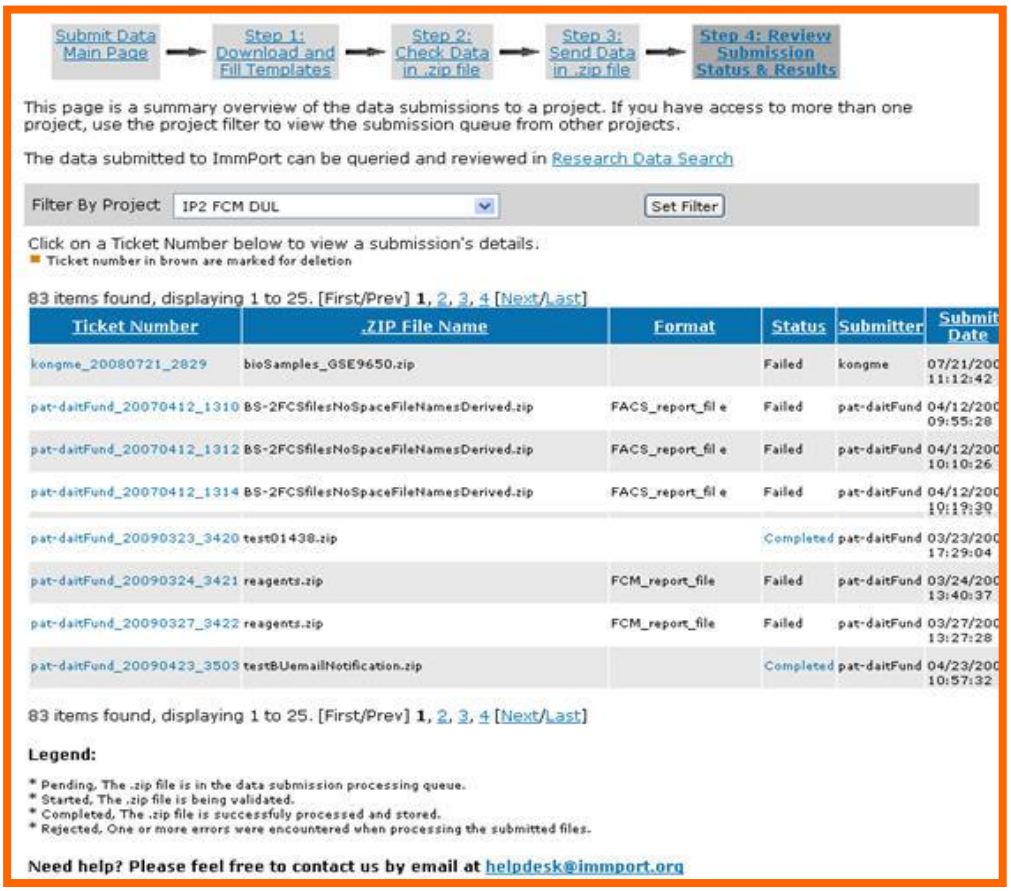
If uploading transfer packages larger than 1 Gigabyte, the data cannot be transferred by the standard uploading method. In this case uncheck the upload online box (figure 17b), select the file to transfer and hit the submit button to receive a registration number for the data transfer. The next step is to contact ImmPort staff at BISC_Helpdesk@niaid.nih.gov to arrange for your data to be uploaded.

| Table 17a. Summary of the data submission process (Online and Offline) | |
|---|---|
| **Files less than or equal to 1 Gigabyte Can be submitted online** | **Files greater than 1 Gigabyte Cannot be submitted online** |
| **Check upload online check box**<br>**Select the file using the browse button**<br>**Click submit**<br>**Record the registration number you receive** | **Uncheck upload online check box**<br>**Click submit**<br>**Record the registration number you receive**<br>**Contact the helpdesk (with registration number) to arrange for file delivery** |

## 21.0 DATA SUBMISSION HISTORY

When the data submission package .zip file has been sent to ImmPort, the web page will redirect the user to the Data Submission History page (figure 18a). The History page lists the data packages that have been sent to the research project and the status of the submission. Upon completion or termination of the transfer, the user will receive a confirmation email. The email, as well as the Data Submission History page, will indicate if the transfer was successful or not. If you have any problems or other questions about the submission process, ImmPort staff can be reached at BISC_Helpdesk@niaid.nih.gov to answer any questions or resolve any problems you encounter.

**Figure 21a. Step 4: Review Submission Status & Results - Data Submission History**



# APPENDIX 1 IMMPORT TEMPLATE DESCRIPTION FILE

The ImmPort Template Description file describes each template, the column and rows in the template, the data type for each field in the template, database column length, preferred vocabulary terms, etc. This file supsedes the appendices describing the templates.

# APPENDIX 2 SAVING MBAA PRIMARY BEAD LEVEL DATA

## Section 2.01 EXTRACTING BEAD LEVEL DATA FROM XPONENT

Extracting bead level data from xPONENT
Renan Sauteraud
March 14, 2013
Contents
1 General 1
2 Saving the raw bead events 1
2.1 Documentation . . . . . 1
2.2 HowTo . . . . . 1
2.3 xPONENT 1.x . . . . . 2
2.4 xPONENT 3.x . . . . . 2
3 References 2

1 General
Luminex's own software, xPONENT, outputs raw bead level data in csv (comma separated values) files.

2 Saving the raw bead events
2.1 Documentation
From xPONENT's documentation:
One can obtain the FI for each bead within each sample from a so-called rCSV file. To configure your instrument to automatically generate the rCSV files, simply go to the Admin page/CSV Options Tab and make sure the bottom-most checkbox is checked. If checked and a run is performed, the rCSV files will be located under:
C:/docs&settings/all users/application data/Luminex/xponent/batchXXX rcsv
2.2 HowTo
To save the individual bead fluorescence:
Admin section
rsautera@fhcrc.org
1
CSV Options Tab
Check `Automatically export results CSV file when batch is complete'
Check `Include Advanced Statistics'
Choose the destination folder in the `CSV File Export Folder' field.
Save
The files will be located in the destination folder, in a directory EXP NAME rcsv.
2.3 xPONENT 1.x
In the rst version of xPONENT, the filenames are Run[001-096].csv.
2.4 xPONENT 3.x
In the latest versions, the filenames use the following format: EXP NAME WELL ID.csv, with well id being A1-H12.

3 References

xPONENT 3.1 Software Manual:
http://www.luminexcorp.com/prod/groups/public/documents/lmnxcorp/89-00002-00-202.pdf
Obtaining FI of each bead within each sample:
http://www.luminexcorp.com/blog/its-all-about-the-stats/

## Section 2.02 EXTRACTING BEAD LEVEL DATA USING MASTERPLEX CT

Extracting bead level data using MasterPlex CT
Renan Sauteraud
March 7, 2013
Contents
1 General 1
2 Saving the raw bead events 1
3 Locating the files 2
4 Summary file 2
5 References 2

1 General
Classical statistical analysis of xMap, and notably MiraiBio's own analysis software, `MasterPlex QT', only uses the MFI. Therefore, saving the bead level information is set as an option in the acquisition software `MasterPlex CT' and needs to be enabled.

2 Saving the raw bead events
In order to save the bead level information, some options should be checked before starting the acquisition.
In the `Home' tab
Click the Setup `Modify' button to open the `Acquisition Setup' dialog box.
rsautera@fhcrc.org
1
`Setup' tab
v1.0 In the Output section, check `Save binary file also.'
v1.2.0.7 In the Output section, check `Save copy of output file in the output folder' and `Save copies of the individual well run files in the output folder'
Select a `Plate ID' and an `Output Folder'
OK

3 Locating the files
The files are located in the selected `Output Folder' and are based on the given `Plate ID'.
PLATE ID.lxd is the summary file used by the vendor's analysis software. It contains the calculated MFIs as well as information on the Setup of the acquisition and the analytes used. PLATE ID WELL.lxb are the binary files containing the raw bead events required to run LumiR.

4 Summary file
Unlike with other acquisition softwares, LumiR make use of the summary file produced by MasterPlex CT. If the .lxd file is provided, the package will extract the information regarding the matching of the bead ID with the analyte name. See the LumiR's User guide for more information.

5 References
MasterPlex CT 1.0 User's Manual:
http://www.miraibio.com/download-document/masterplex-ct-v1-user-s-manual.html
MasterPlex CT Tutorial:
http://www.miraibio.com/download-document/tutorial-for-masterplex-ct.html
2

## Section 2.03 EXTRACTING BEAD LEVEL DATA USING BIO-PLEX MANAGER

Extracting bead level data using Bio-Plex Manager
Renan Sauteraud
March 6, 2013
Contents
1 General 1
2 Saving the raw bead events 1
3 Exporting to XML 2
3.1 Export a single file . . . . . 2
3.2 Export as a routine . . . . . 2
4 References 2

1 General
This acquisition software from BioRad uses a proprietary file format thatcannot be read directly by LumiR. These files with a .rbx extension should be exported in XML in order to be read by read.experiment.

2 Saving the raw bead events
The first step is to make sure that the bead level information is saved by Bio-Plex. In the `Save As' dialog box, when saving protocols (extension .pbx) and results (.rbx), the compression mode must be disabled (default). Compression mode removes the raw bead event from the saved file in order to save space.
rsautera@fhcrc.org

3 Exporting to XML
For Bio-Plex data, LumiR requires a single .xml file per plate.
3.1 Export a single file
To export an existing file into XML:
Open a .rbx file
File Menu > Document Export
Choose `Bio-Plex XML'
Choose The destination File
Export
3.2 Export as a routine
To export automatically at the end of a run:
File Menu > Document Export Properties
Choose `Bio-Plex XML'
Check `Use Folder' in the Destination section and Choose the desired folder.
OK
Create or load a Protocol
Advanced Settings Button
Check `Auto save after run' and `Auto XML export after run'
OK

4 References
Bio-Plex Manager 6.1 User Guide:
http://www.bio-rad.com/webroot/web/pdf/lsr/literature/10022815.pdf


# APPENDIX 3 AFFYMETRIX GCOS/MAS 5 GENE EXPRESSION

MAS5.0 software generates six output files
- Chip File (.CHP)
- Expression Analysis File (.TXT)
- Report File (.RPT)
- Experiment Information File (.EXP)
- Cell Intensity File (.CEL)
- Data file (.DAT)

ImmPort requires a .CEL file for Affymetrix results. The other file types may be submitted as an additional result files.

A. Data File (.DAT)
This file contains raw image data of the chip.

B. Cell Intensity File (.CEL)
The .CEL file contains fluorescence intensities for each probe on the microarray. When the .CEL file is opened in either MAS 5.0 or dChip, these probe-specific intensity values are used to reconstruct the scanned image of the hybridized array. It is recommended that the investigator view the .CEL images for each sample to make sure there are no obvious chip defects. The probe-specific intensities in the .CEL file are also used in the Statistical Algorithm to calculate the probe-set-level Signals and Presence Calls recorded in the .CHP file.

C. Chip File (.CHP) and Expression Analysis File (.TXT)
The .CHP file contains Signal values and Presence Calls for each probe set on the microarray and is processed from the .CEL file. The .TXT file is a text version of the .CHP file with the same information in a tab-delimited format. The columns in the .TXT file are listed in the table below

D. Report File (.RPT)
The Report File summarizes background noise, housekeeping information, and spiked-in controls in the following format for the chip of interest. The file includes information such as:

- Filename
- Probe array type
- Algorithm
- Background
- Noise
- Total probesets and average signal
- Present probesets and average signal
- Absent probesets and average signal
- Marginal probesets and average signal
- Housekeeping controls
- Spike controls

E. Experiment Information File (.EXP)
The Experiment Information File is a text file containing sample information, fluidics settings and scanner settings. It includes information such as:

- Sample Info
1. Chip type
2. Sample type
3. Description
4. Project
- Fluidics
1. Protocol
2. Date of hybridization
- Scanner

1. Filter
2. Scan date
3. Scanner type
4. Number of Scans

# APPENDIX 4 ILLUMINA BEAD STUDIO FINAL REPORT

The Bead Studio report format is highly customizable in terms of content (i.e. which columns of data are included) and format (e.g. tab delimited or matrix). The required Final Report columns and their headers to be included in an Illumina Bead Studio Final Report are listed below. These columns may appear in any order within the file. Additional columns may be included in the Final Report.

Sample ID SNP Name Allele1 – Top Allele2 – Top GC Score

An extract from an Illumina Final Report in tab delimited form with the required columns is presented below.

[Header]
BSGT Version 2.3.15.14130
Processing Date 5/25/2006 13:33
Content GS000XXXX-OPA
Num SNPs 1152
Total SNPs 1152
Num Samples 96
Total Samples 96
[Data]
SNP Name Sample ID Allele1 – Top Allele2 – Top GC Score
rs977008 1445888_R001_C001 G G 0.8092

Sample Identifiers

The genotype results analytical support is envisioned to allow the investigator guided creation of linkage format files and marker information files that are acceptable to algorithms such as Haploview (http://www.broad.mit.edu/mpg/haploview) which are part of the ImmPort genetic analysis tool set. In order to generate linkage format files, it is necessary to associate the genotype results for a sample with the affectation status, gender and pedigree information for the individual or organism. To ease the task of generating these links, ImmPort supports designating whether the sample identifiers in the Sample ID column of the result file are subject identifiers or biological sample identifiers.

Annotation

The .opa manifest file describes an Illumina custom panel and serves as the annotation file. The .opa manifest file can be included in a data package and is declared in the reagents document.

An extract from an .opa manifest file is presented below for reference.

© Illumina, Inc. 2004
[Heading]
OPA, GS0006526-OPA
Test Version, 1227160
Test Version Name, 1227160
Test Name, Internal MHC OPAs
Bundle Index, 1 of 2
SNP Position, 1
Assay Format, Golden Gate
Date Manufactured, 2/1/2005
Loci Count, 1228 of 2521

Comment,
Ilmn ID, Name, oligo1, oligo2, oligo3, IllumiCode name, Illumicode Seq, Ilmn Strand, SNP, CHR, Ploidy, Species, MapInfo, TopGenomicSeq, CustomerStrand
rs1003878-121.1_T_F_1155586, rs1003878,
ACTTCGTCAGTAACGGACGACAGGCAGCTTACCAATAGGTCCTA,GAGTCGAGGTCATATCGTGACA
GGCAGCTTACCAATAGGTCCTG,
AGTTTGCACTAAAAAGAAATTCACTGCCAATCGAGCGCGATACATGTCTGCCTATAGTGAGTC,
0003, CTGCCAATCGAGCGCGATACAT, top,
[A/G],
6, diploid, Homo sapiens, 32407800,
TAACCCAGATACTTAAACAGTTGGAGCCAGTCTCCTTCAGACATAGTAAGAAGCCAGTAGAGATAAG
TTGATATATACAGGCAGCTTACCAATAGGTCCT
[A/G]
GAGTTTGCACTAAAAAGAAATTCAAATTGGCATATTAGTACAGTTATTTGGAGAGTGTATTTTTCACTA
ATTTTATCCTAGAAGTGAGGCTTTGAGAGGT,
BOT

# APPENDIX 5 GLOSSARY

D-1 Glossary Table

| Term | Definition | Examples |
|---|---|---|
| Biological Sample | Biological material that has undergone isolation, processing and/or treatment prior to use in an experiment. As much information about the sources, conditions, and treatments of the Biological Sample as possible should be captured and parsed into the database. Biological Sample attributes include all treatments and reagents used for sample processing and EXCLUDE reagents used to measure analytes; these would be captured in Experiment Sample description as Reagents. | Blood from patient X<br>Protein lysate from mouse brain<br>RNA isolated from T cells purified from the spleen of patient X with disease phenotype A and placed into cell culture and treated with IL-2 for 2 hrs at 37ºC<br>RNA labeled with Cy3 for microarray experiment |
| Biological Sample Protocol | A protocol file submitted by the user that describes how a Biological Sample was isolated, enriched, processed, treated, or otherwise prepared for experimental use. The Biological Sample Treatment Protocol serves to capture any information which does not need to be parsed into the database and will be stored as a blob. | Purification of mRNA from mouse lymphocytes.txt<br>Labeling RNA with Cy3 and Cy5.txt<br>B cell enrichment from bone marrow.txt |
| Reagent | Something used to measure an Analyte(s). In the case of a microarray, this would be the chip type and name. In many cases, this may include information about probes: name, type, description, manufacturer, software used to select probe, etc. | Affymetrix Gene Chip HGU95<br>Information in the .gpl and .cdf files for custom arrays<br>CD4-FITC, Pharmingen, clone 123<br>DNA oligo, sequence atgcctgatccgaat |
| Analyte | The target compound being measured in a single Biological Sample using Reagent(s) used to detect a single target compound. | IFNG mRNA<br>CD4 protein<br>SNP rs12345 "A" allele |

| D-1 Glossary Table | | |
|---|---|---|
| Term | Definition | Examples |
| Experiment Sample | Experiment Sample is distinguished from Biological Sample by the presence of Reagent(s). Reagent(s) captured for Experiment Sample are those specifically used to measure one or more analyte in the Biological Sample during the experiment. An Experiment Sample may also contain more than one Biological Sample. Thus, the combination of Biological Sample(s) + Reagent(s) used to measure an analyte(s) makes up an Experiment Sample. Replicates samples are stored as UNIQUE Experiment Samples that share the same Biological Sample, Experiment Sample attributes, and Experiment Sample Protocol, but were processed separately in the experiment. | RNA hybridized to Affy chip with 40,000 probes (one-color microarray)<br>Control RNA labeled with Cy3 plus patient RNA labeled with Cy 5 hybridized to cDNA array with 16,000 probes (2-color microarray)<br>T cells in one tube stained with CD4-FITC and CD8-PE (flow cytometry)<br>Protein lysate in one anti-CD3-coated well of a 96-well plate (ELISA)<br>1 patient sample hybridized to one well of an Affy SNP chip (genotyping) |
| Experiment Sample Result | Result includes all of the measured results for a single Experiment Sample. | In the case of a two-color microarray, this would correspond to the single results file that contains the results for multiple analytes measured in multiple Biological Samples.<br>This would also be the type of result captured in a single flow cytometry results file |
| Experiment Sample Results File | The file containing the minimally processed results generated from a single Experiment Sample. | Affymetrix .chp, .file ELISA experiment and contains data for all Experiment Samples |
| Protocol | A protocol file that describes how things are done. | Hybridization of labeled RNA to cDNA spotted array chip.txt (microarray)<br>Staining using CD4-FITC antibody (flow cytometry) |
| Experiment | One or more Experiment Sample(s) containing at least one biological sample from analytes are measured, evaluated, or collected for the purposes of testing hypotheses or theories, demonstrating known facts or theories or measuring/collecting data. | A series of Affy gene expression chips<br>A series of cDNA chips<br>5 tubes of T cells stained with CD4-FITC, CD8-PE, none, or both |
| Experiment | A label for the general type of experiment | Genotyping |

| D-1 Glossary Table | | |
|---|---|---|
| Term | Definition | Examples |
| Type | performed. | Molecular_Quantification<br>Cellular_Quantification |
| Experiment Measurement Technique | The experimental system upon which an experiment is based or performed. | Array<br>ELISPOT<br>ELISA<br>MBAA |
| Treatment | Captures descriptive information of experimental conditions for specific Experimental Samples and Biological Samples. | In cases where experiment samples may differ based on incubation temperature |

# APPENDIX 6 FAQS (FREQUENTLY ASKED QUESTIONS)

**Q. What can you send?**

**A. You can send just about any file or set of files to ImmPort. There are some size limitations when using the ImmPort web site interface, but if you have large files (1 Gigabyte or more) you can request a secure ftp account or make other arrangements to have data loaded.**

In addition, ImmPort can process descriptive information about your data which enables the use of analytical tools, advanced queries and sharing. ImmPort supports tab delimited files derived from spreadsheets (e.g. Excel).

**Q. What should you send?**

A. The question of what gets sent to ImmPort is a policy decision made by NIH staff, specifically NIAIAD DAIT program officers. The ImmPort staff is happy to help you organize and prepare your data submission packages.

**Q. What would you like to send to ImmPort?**

**A.** Although just about any file can be sent to ImmPort, what you or your team wish to do with the data once it is in ImmPort has a significant impact on how and what you send. In part that's because you can send just about any data and ImmPort will store it for you. To do more than just store it though, ImmPort has a higher threshold for how the data is described. For instance, if you want to use an ImmPort gene expression analysis tool, you'll need to tell ImmPort that you are sending gene expression data from well described samples that were assayed by a particular platform.

**Q. Why are there so many files to complete and what are they for?**

A. There is a metadata upload file for each metadata category. The metadata in one category can be linked to metadata in another category and to other files. By making the necessary associations between metadata and results, you can search for specific data to use with the ImmPort analysis tools. For example, a genotype assay result file from a custom panel can be submitted.

**Q. What is a data submission package?**

A. A data submission package is a .zip file containing a collection of metadata template and other files with many details about an experiment or study and the results.

**Q. What happens to a data submission package?**

A. Data submission packages are encrypted and transferred by secure ftp to the ImmPort system. The contents of the package will be processed to store the results and make them available for analysis, query or sharing in ImmPort.

**Q. Which metadata upload file is required to submit?**

A. Please refer to the Research Data Submission Instruction for complete details.

**Q. Where do I find if my data has submitted successfully?**

A. A Submission History page summarizes all the data that has been submitted within your project. You will also receive an email about the status of your submission.

**Q. How do I view my submitted data?**

A. By clicking on the Access Data link on the menu bar, you can see the options to search and display your data.

**Q. My submission failed because an invalid value was provided for a controlled vocabulary element.**

A. All controlled vocabulary values are case sensitive to ImmPort. The value specified in the completed ImmPort template file must exactly match one of the preferred vocabulary values found for that attribute.