

ImmPort Flow Cytometry: Data Management

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Flow Cytometry **B**

Data Management

- Upload Single File
- Upload Multiple Files
- View/Edit Uploaded Data
- Create Data Set
- View/Edit Data Sets

FLOCK

- Analyze Individual Files
- Analyze Data Sets

View/Edit Results

- FLOCK
- Centroid Files
- Cross Sample

Cross Sample

- Start Comparison

Help

Gene Expression (GDS)

- GDS Generation Results
- Single Module Results
- Pipeline Results
- User Guide

Genetic Analysis **B**

- User Guide (PED)
- Run .PED Generation
- Generation Results
- User Guide (IGAT)
- Run Genetic Analysis
- Analysis Results

MHC Analysis **B**

- Upload Data
- Create Data Set
- Analyze Data Set
- Analysis Results
- User Guide

tagSNP

- Run tagSNP
- Results

Access Data Management through the ImmPort Tools menu.

ImmPort Flow Cytometry: Data Management

Flow Cytometry Analysis (Beta) / Data Management / Overview

Flow Cytometry | **Data Management** | FLOCK | View/Edit Results | Cross Sample | Help

- Upload Single File
- Upload Multiple Files
- View/Edit Uploaded Data
- Create Data Set
- View/Edit Data Sets

The Data Management module allows the user to:

- ▶ Upload one or more flow cytometry data files for future analysis
- ▶ View and edit the uploaded .txt files, e.g., adding sample information, renaming markers.
- ▶ Put multiple .txt files into a data set that can be used either in batch FLOCK runs or Cross Sample Comparison
- ▶ View and edit the created dataset, e.g., adding/removing files, adding information for files in the dataset

The uploaded data file can be in either .fcs or .txt format. The filename can't contain the following characters: ' " \ and /. ImmPort automatically converts .fcs files to .txt files when the upload includes only .fcs files. The .txt files can be created using third party tools including Tree Star FlowJo™ on MacOS. For conversion details, please see the [help section](#).

Channels, such as forward scatter width (FSC-W), can distort FLOCK analysis result if included together with forward scatter height (FSC-H) in the .fcs data file. You can exclude these channels using Tree Star FlowJo™ on MacOS or you can modify and upload the .txt data file available after conversion on ImmPort. For details, please see the [help section](#).

The ImmPort FCS conversion component has been tested with a variety of BD (Becton, Dickinson and Company) flow cytometry instrument data files. The conversion results are highly consistent with those from Tree Star FlowJo™ channel output for FCS 2.0 and 3.0 files. Ongoing improvements will cover data files, both pre- and post-gated, from alternative flow cytometers. If you have data files from another vendor, please contact the [help desk](#) so that the ImmPort team can assist you with your data requirements.

Flow Cytometry Analysis Workflow



ImmPort Flow Cytometry: Uploading data

The screenshot shows the ImmPort web interface. At the top left is the ImmPort logo with the tagline 'BIOINFORMATICS FOR THE FUTURE OF IMMUNOLOGY'. To the right are navigation links for 'About ImmPort', 'Admin', and 'A'. Below the logo is a breadcrumb trail: 'Flow Cytometry Analysis (Beta) / Data Management / Overview'. A dropdown menu for 'Data Management' is open, with 'Upload Single File' circled in orange. Below this, the 'File Upload' form is visible, containing a project selection dropdown (set to 'Test research project for v2.8'), a note about file formats, input fields for 'Name' and 'Description', and three 'Browse...' buttons for 'Data File (.fcs)', 'Data File (.txt)', and 'Marker File (.info)'. A 'NOTE' section at the bottom states that clicking 'Upload' will upload files to the private project workspace and create a data set. The 'Upload' button is also circled in orange.

- Select project to store uploaded file
- Provide name and description
- Browse for files
- .info files are optional.
- Click 'Upload'

▪FLOCK requires FCS files to be converted to .txt format. FCS 2.0, 3.0 files will be automatically converted to .txt after uploading into ImmPort; conversion has been tested on a variety of Becton, Dickinson flow files. ImmPort also supports uploading of .txt converted files--Click 'Help' to view tutorials for converting FCS files to .txt prior to uploading.

ImmPort Flow Cytometry: Uploading data

Flow Cytometry Analysis (Beta) / Data Management / Package Upload

Flow Cytometry | Data Management | FLOCK | View/Edit Results | Cross Sample | Help

Upload Single File
Upload Multiple Files
View/Edit Uploaded Data

Complete Spreadsheet Data for Multiple Files
View/Edit Uploaded Data
Create Data Set
View/Edit Data Sets
Info File for Multiple Flow Cytometry Result Files
Assemble and Submit a .zip Folder with Result Files, Spreadsheet and .info File
Review Data Submission

The ImmPort Flow Cytometry multiple file upload process supports uploading of FCS files (.fcs) and tab delimited text files(.txt) converted from FCS files. Uploaded .fcs files are automatically converted to .txt via FCSTrans, the ImmPort flow cytometry data converter. All uploaded files will be stored in a private project workspace. For more information please see the [User Guide](#) or conversion tutorials found in the menu bar under [Help](#).

Batch Upload:

1. Complete the [flowTextFiles.xls](#) template.
 - ▶ This template provides the opportunity to rename data files, allows for the addition of descriptive information about each individual file being uploaded and enables marker name changes via the inclusion of a marker information file.
 - ▶ The .fcs or fcs .txt data file names may NOT contain the following characters:
 - ▶ The fcs data files should be compensated before sending to ImmPort.
2. Save the Excel flowTextFiles.xls template as a tab delimited text file (flowTextFiles.txt).
Please do not rename the flowTextFiles.txt file.
3. ZIP the completed template and the data files.
 - ▶ Create the ZIP file by selecting files from within a folder versus selecting the files individually.
 - ▶ Add marker (channel) information files at this time if they are to be included (optional). [example Marker File \(.info\)](#)
 - ▶ **Please do not include spaces in the .zip file name.**
 - ▶ You may find it helpful to review an [example multiple fcs files upload package](#).
4. Select the project to which the data will be saved
5. Use the Browse feature to select the .zip file and click Submit. Time to complete the processing of submitted data is dependent on the size of the submission queue.
6. To review the uploaded data go to [Data Management, View / Edit Uploaded Data](#)

Research Project Title: TESTING: Bioinformatics Integration Support Project

Notes:

Upload Online

For more information about Multiple File Upload please see the Multiple File Upload tutorial under the Flow Cytometry Help section

ImmPort Flow Cytometry: View/Edit Uploaded Data



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Flow Cytometry Analysis (Beta) / Data Management / Uploaded Files Search

Flow Cytometry | Data Management | **FLOCK** | View/Edit Results | Cross Sample | Help

Use the 'Uploaded Flow Files Search' section to find data files for FLOCK analysis, dataset creation or download of both .fcs files and .txt files. The number of items in a dataset is limited to 300.

Select project: Include Semi-Public files in the Search

Uploaded Flow Files Search

Search for Uploaded Files :

Results per page : 25

Submit

Cancel

- Advanced Search Attribute Tree
 - Flow
 - Subject
 - Biological Sample
 - Experiment
 - Experiment Sample
 - Reagent
 - Study

Flow: Name

Like

... Remove

Flow: Description

Use Advanced Search options to find files of interest. Use the buttons on the Uploaded Files table to view file detail, run FLOCK for all selected files, create datasets, delete and download .fcs files and .txt converted versions of the same files

... Remove

Page 3 of 15 | Details | Run FLOCK | Save To Set | Save All | Download | Delete | Displaying 51 - 75 of 351

Name	Description	Panel	Exp Sample Acc:	FCS Text File	Date Created	Created By
Arm4_Sub07213281_Vis	"Placebo immunotherapy	FSC-H SSC-H CD14 CD23		Arm4_Sub07213281_Vis	2010-05-13	Qian
Arm4_Sub07213191_Vis	"Placebo immunotherapy	FSC-H SSC-H CD14 CD23		Arm4_Sub07213191_Vis	2010-05-13	Qian
Arm4_Sub07183361_Vis	"Placebo immunotherapy	FSC-H SSC-H CD14 CD23		Arm4_Sub07183361_Vis	2010-05-13	Qian
Arm4_Sub07183251_Vis	"Placebo immunotherapy	FSC-H SSC-H CD14 CD23		Arm4_Sub07183251_Vis	2010-05-13	Qian
Arm4_Sub07143261_Vis	"Placebo immunotherapy	FSC-H SSC-H CD14 CD23		Arm4_Sub07143261_Vis	2010-05-13	Qian
Arm3_Sub07183181_Vis	"Immunotherapy with pla	FSC-H SSC-H CD14 CD23		Arm3_Sub07183181_Vis	2010-05-13	Qian
Arm3_Sub07183171_Vis	"Immunotherapy with pla	FSC-H SSC-H CD14 CD23		Arm3_Sub07183171_Vis	2010-05-13	Qian
Arm3_Sub07183151_Vis	"Immunotherapy with pla	FSC-H SSC-H CD14 CD23		Arm3_Sub07183151_Vis	2010-05-13	Qian
Arm3_Sub07183141_Vis	"Immunotherapy with pla	FSC-H SSC-H CD14 CD23		Arm3_Sub07183141_Vis	2010-05-13	Qian
Arm3_Sub07113201_Vis	"Immunotherapy with pla	FSC-H SSC-H CD14 CD23		Arm3_Sub07113201_Vis	2010-05-13	Qian

ImmPort Flow Cytometry: Uploaded File Detail

Tabbed display of File details

Flow Data Management | **File Detail**

Specimen_0 | Specimen_0 | Specimen_0
 01_Tube_00 5 | 01_Tube_00 4 | 01_Tube_00 3

Project: Liz's test project
 Name: Specimen_001_Tube_005
 Description:
 FCS Text File Name: Specimen_001_Tube_005.txt
 Exp Sample Accession:
 Panel: Forward Scatter|Side Scatter|anti-CD999 FITC-A|anti-IL888 PerCP-A|MCA Pacific Blue-A|TCR APC-A|BCR APC-Cy7-A|CDabc PE-A|IL-xyz PE-Cy7-A
 Number of Events: 10000
 Number of Markers: 10
 Minimum Intensity: 0.0
 Maximum Intensity: 1023.0
 Status: loaded
 Created By: Thomson
 Date Created: 2010-10-06
 Marker Information: *Click on user assigned name to edit*

FCS Name	User Assigned Name
FSC-A	Forward Scatter
SSC-A	Side Scatter
FITC-A	anti-CD999 FITC-A
PerCP-A	anti-IL888 PerCP-A
Pacific Blue-A	MCA Pacific Blue-A

Save Changes

- Edit Marker names here
- Click 'Save Changes'

ImmPort Flow Cytometry: Create Data Set for FLOCK or Cross Sample Analysis

Flow Cytometry Analysis (Beta) / Data Management / Create Analysis Set

Flow Cytometry | Data Management | FLOCK | View/Edit Results | Cross Sample | Help

Use the 'Uploaded Flow Files Search' section to find data files for dataset creation.
The number of items in a dataset is limited to 300.

Select project: TESTING: Bioinformatics Integration Support Project Include Semi-Public files in the Search

Uploaded Flow Files Search

Search for Uploaded Files : Results per page : 25

Advanced Search Attribute Tree

- Flow
 - Name
 - Text File Name
 - Description
 - Panel
 - Created By
 - Created By Last Name
 - Date Created

Flow: Name

Flow: Description

Use Advanced Search options to find files for datasets

*Use arrow button to move files in or out of analysis set.
Mouse-over column titles, click down arrow to hide or show columns.*

	Name	Description	FCS Text File	Date Created
<input checked="" type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2011-01-24
<input checked="" type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input checked="" type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input checked="" type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17
<input type="checkbox"/>	Specimen_001_Tuk	Specimen_001_Tuk	Specimen_001_Tuk	2010-11-17

**Create Set will provide a pop-up to name and save the set
Remove is used to remove files from the data set**

	Name	FCS Text File
<input checked="" type="checkbox"/>	Specimen_001_Tube_001	Specimen_001_Tube_001.txt
<input type="checkbox"/>	Specimen_001_Tube_009	Specimen_001_Tube_009.txt
<input type="checkbox"/>	Specimen_001_Tube_010	Specimen_001_Tube_010.txt
<input type="checkbox"/>	Specimen_001_Tube_011	Specimen_001_Tube_011.txt
<input type="checkbox"/>	Specimen_001_Tube_012	Specimen_001_Tube_012.txt

Use arrow button to select files for the dataset

