



# Sharing and Annotating Data in Compliance with MIFlowCyt: the Minimum Information about a Flow Cytometry Experiment

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# Why share your data?

- Carrots are tasty
  - Promote open scientific inquiry and progress in the field
  - Re-exploration of existing datasets
  - Reproducible research
  - Get credited for sharing good quality data
    - Thomson Reuters Data Citation Index
- Sticks hurt
  - Required by funding agencies and journals

# What to share?

- A dump of FCS files is not enough
  - Data without context are not understandable to others

[Cytometry A](#). Author manuscript; available in PMC 2009 Nov 5.

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doi: [10.1002/cyto.a.20623](#)

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NIHMSID: NIHMS76346

## MIFlowCyt: The Minimum Information about a Flow Cytometry Experiment

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[Author information](#) ► [Copyright and License information](#) ►

JAL and JS contributed equally to the work in this article

- Outlines the minimum information required to report about flow cytometry experiments
- Represents the community consensus
  - ISAC Recommendation
- Required/recommended by *Cytometry A* and *Nature*



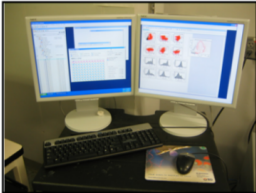
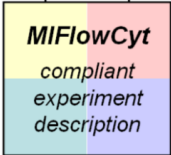
# MIFlowCyt components



Experiment overview



Sample description



Data analysis



Instrumentation

# MIFlowCyt components

## Experiment overview

- Purpose
- Keywords
- Experiment variables
- Date(s)
- Organization(s)
- Primary contact
- Quality control measures

## Sample description

- Description
- Sample material
- Treatment
- Fluorescent reagents
- Source
- Biological samples: Organism with taxonomy, phenotype, genotype, age, gender, ...
- Location for environmental samples

## Data analysis

- FCS data files
- Compensation and other transformations
- Gating details including gate description, statistics and boundaries or images or gate membership details

## Instrumentation details

- Make
- Model
- User-adjustable components (e.g., detector voltages)
- Customized configurations

## MIFlowCyt summary

- Formalizes what to describe so that others understand
- Does not prescribe how to share
- Does not prescribe how to do what you do

# How to share all these details?

You are doing most of it already

- Manuscript, e.g., the methods section
- Manuscript's supplemental information
- Data repository

The image is a promotional graphic for FlowRepository. It features a dark background with a grid of blue lines and a central light source. The logo 'FLOWRepository' is prominently displayed, with 'FLOW' in orange and 'Repository' in white. The 'O' in 'FLOW' is a stylized circle containing a flow cytometry plot. Below the logo, white text describes the repository's purpose: 'Use FlowRepository to access, review, download, deposit, annotate, share and analyze flow cytometry datasets.' At the bottom, an orange bar contains the website address 'www.flowrepository.org' in white text.

**FLOW**Repository

Use FlowRepository to access, review,  
download, deposit, annotate, share and  
analyze flow cytometry datasets.

[www.flowrepository.org](http://www.flowrepository.org)

## FlowRepository – What is it?

- A public online resource of annotated flow cytometry datasets
  - Primarily those associated with peer-reviewed publications
- Web-based application created by extending and adapting Cytobank
  - Mainly to incorporate MIFlowCyt and journal integration
- Open source
  - Affero General Public License
- Supported by ISAC, ICCS and ESCCA
- Hosted by Carnegie Mellon University



## FlowRepository – What do you need to start?

- A **computer** with **Internet connection**
  - Fast connection is good, especially when uploading large datasets
- Web browser
  - **Firefox** or **Chrome** recommended
  - Safari or Internet Explorer also work but may not look great
- Ability to run **Java** Applets in the Web browser
  - Required for online analysis and FCS de-identification

## Accessing FlowRepository

- Navigate your Web browser to <https://flowrepository.org>
- Demonstration (offline)
  - Access FlowRepository
  - Deposit, annotate and share a dataset

## Help

The following open access article describes how to upload and annotate flow cytometry data sets: Spidlen J, Breuer K and Brinkman R. Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) Compliant Manuscript Using the International Society for Advancement of Cytometry (ISAC) FCS File Repository (FlowRepository.org). [Current Protocols in Cytometry, UNIT 10.18, July 2012](#)

We also have a [Quick start guide](#) and a [FAQ](#) section.

You may download [slides](#) from our Workshop at CYTO 2012: Publishing MIFlowCyt Compliant Data to ISAC's FlowRepository.org for Cytometry A and Other Journals

Additional links and help options are listed in our [support](#) page.

You can contact us by filling out a [support ticket](#).

## Citing FlowRepository

Please reference us by citing:

Spidlen J, Breuer K, Rosenberg C, Kotecha N and Brinkman RR. FlowRepository - A Resource of Annotated Flow Cytometry Datasets Associated with Peer-reviewed Publications. [Cytometry A, 2012 Sep; 81\(9\):727-31.](#)

## Supporting Journal



## FlowRepository

**FlowRepository** is a database of flow cytometry experiments where you can query and download data collected and annotated according to the [MIFlowCyt standard](#).

## Query

Enter a term to search all publicly available experiments:

[Show query fields](#)

## Links

[Browse public datasets](#)

[Browse OMIP datasets](#)

[Referencing Flow Repository and Cytobank](#)

[Browse community datasets](#)

[Quick start guide](#)

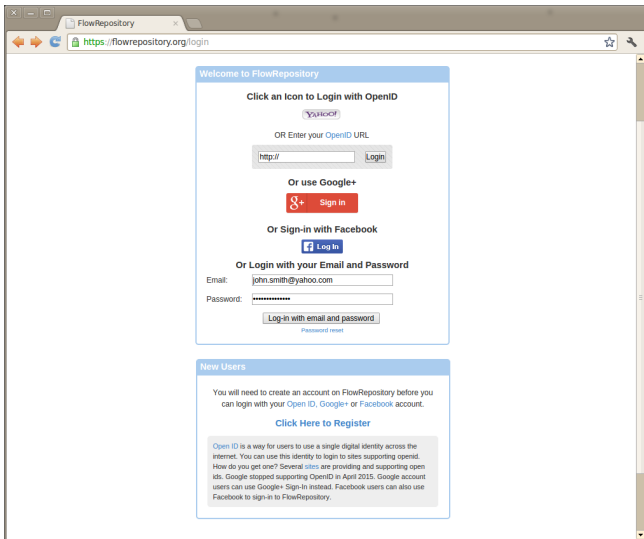
[FlowRepository Steering Committee & Advisory Board](#)

[Browse most popular datasets](#)

[Submit data](#)

[Funding](#)


# Register/login in order to be deposit data



The screenshot shows a web browser window with the address bar displaying "https://flowrepository.org/login". The page content is as follows:


**Welcome to FlowRepository**

**Click an Icon to Login with OpenID**




OR Enter your OpenID URL

**Or use Google+**



**Or Sign-in with Facebook**



**Or Login with your Email and Password**

Email:

Password:

[Password reset](#)

---

**New Users**

You will need to create an account on FlowRepository before you can login with your Open ID, Google+ or Facebook account.

[Click Here to Register](#)

Open ID is a way for users to use a single digital identity across the internet. You can use this identity to login to sites supporting openid. How do you get one? Several sites are providing and supporting open ids. Google stopped supporting OpenID in April 2015. Google account users can use Google+ Sign-In instead. Facebook users can also use Facebook to sign-in to FlowRepository.

# Registration

## Register for FlowRepository

Open ID is a way for users to use a single digital identity across the internet. You can use this identity to login to sites supporting openid. How do you get one? Several sites are providing and supporting open ids. Google stopped supporting OpenID in April 2015. Google account users can use Google+ Sign-In instead. Facebook users may use Facebook. Click [here](#) if you need help with this form.

First Name

Last Name

Sign-in with Google+ or Facebook, or select your Open ID provider



Open ID Provider

Contact Email

You can also opt-out and use an email/password login only (note that email / password login is always available even if you register using one of the above).



Contact Email

This shall match your Open ID, Facebook or Google+ registered email.

Privacy  Do not display my email address to other users

### Optional Information

Select Password

Confirm Password

Passwords can be used instead of OpenID, Google+ or Facebook login. Please use 8 or more characters and include a number, an upper-case character and a lower-case character.

ResearcherID   
(<http://www.researcherid.com>)

ORCID (<http://orcid.org>)

Location

Company/Organization

How did you find out about FlowRepository?

FlowRepository does not warrant or assume any legal liability or responsibility for the accuracy, completeness, or usefulness of any information displayed on this website.

I agree to the [FlowRepository Terms Of Service](#)

## Share your data - typical steps

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
  - Or prepare spreadsheets with annotations
- 4 Annotate the experiment
  - Describe samples and sample sources
  - Provide experimental variables
  - Describe instrumentation settings
- 5 Provide analysis details
  - Either analyze data online
  - Or upload third party analysis files (e.g., FlowJo workspaces, FCS Express projects, FACS Diva files, etc.)
- 6 Review (and improve) your MIFlowCyt compliance
- 7 Share with reviewers
- 8 Share with everyone

# Share your data - typical steps

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# Create a new experiment

## ▼ Bank New Experiment

\* Experiment Name

Project

\* Primary Researcher



Nima Aghaeepour

\* PI/Manager



Mario Roederer [invite a new user](#)

*Allow PI/Manager to have full access to experiment*

\* Starting Date   (yyyy-mm-dd)

End Date   (yyyy-mm-dd)

(optional)

\* Purpose



## Create a new experiment (continued)

**Conclusion**  
(optional)

Several immunophenotypes correlated with the survival times were identified. Details about this would typically be listed here but I am not at liberty to share this information during this talk.

**Comments**  
(optional)

For reagent and instrument details as well as the original manual gating strategy please see: Ganesan and Chattopadhyay et al., Immunologic and virologic events in early HIV infection predict subsequent rate of progression. Journal of Infectious Diseases, 2010;201:272-284.

**Quality Control Measures**  
(optional)

Per-channel empirical distribution comparison

**Quality Control Experiment**  
(optional)

-- None --

## Create a new experiment (continued)

**Keywords**  
(optional)

**Organizations**  
(optional)   
BC Cancer Agency, Terry Fox Laboratory  
University of British Columbia, Faculty of Medica

[Add new organization](#)

**Pubmed IDs**  
(optional)

**\* required field**

# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
  - Or prepare spreadsheets with annotations
- 4 Annotate the experiment
  - Describe samples and sample sources
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- 6 Review (and improve) your MIFlowCyt compliance
- 7 Share with reviewers
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# Data upload (Option 1, HTML5-based)

The screenshot shows a web browser window with the URL `flowrepository.org/experiments/754/upload_files.html`. The page header includes the FlowRepository logo and navigation links: [Inbox](#), [Profile](#), [Annotation Data](#), [Invite a User](#), [Support](#), and [Public View](#). A user is logged in as [Josef](#). The main content area is titled "Experiment: IDCRP's HIV Natural History Study" with ID `EB_FCM_ZZWW`. A green "Getting Started!" banner provides instructions on how to upload files, mentioning that the interface is experimental and based on HTML5. It also includes an "Important note" about the speed of the Drag & Drop feature. Below the banner is a section titled "Upload Experiment Files" with two buttons: "Add Files" and "Upload". A dashed box below these buttons contains the text: "Select files to upload to FlowRepository. Drag & drop files here or use the add files button above." The footer contains links for [Terms of Service](#), [Privacy Policy](#), [Support](#), [Feedback](#), and [Developers](#).

FlowRepository

Experiment: IDCRP's HIV Natural History Study ID: `EB_FCM_ZZWW` Labels: None Primary Researcher: [Nima Aghaesspour](#) Public: No MFlowCyt Score: 0.00%

[Back to Experiment](#)

**Getting Started!**

This data upload page is experimental. It is based on new HTML5 file interface and therefore, it requires recent versions of one of the major web browsers. If you have Java, or if you require FCS de-identification, then you may upload data using the regular [Java-based uploader](#) instead. In order to upload files from here, add individual files (not folders) to the upload list by dropping them in the upload box (preferable) or by selecting them using the [Add Files](#) button (less preferable), and hit the [Upload](#) button. Please be patient, you should be redirected back to the experiment page once all files are uploaded and processed on the server.

**Important note:** If you are adding many files, queuing those for upload using the Drag & Drop feature is much faster than the [Add files](#) button with most browsers. For example, in our testing with Google Chrome, adding 100 FCS files using the [Add Files](#) button took 23 seconds, while the Drag & Drop queued the 100 FCS files instantly.

**Actions**

[Delete Experiment!](#)  
[Remove partial in-progress uploads](#)

**Did you know?**

We have a [Quick start guide](#) and a [FAQ](#) section.

You can print/save your illustrations to PDF from the illustration view's left menu.

You can export your data to Excel from the Experiment Summary page.

Give other users full control to modify your experiments through the "Sharing Permissions" box.

Use the "Download Files" button to save copies of the original FCS Files to your computer.

**Upload Experiment Files**

[Add Files](#) [Upload](#)

Select files to upload to FlowRepository  
Drag & drop files here or use the add files button above

[Terms of Service](#) [Privacy Policy](#) [Support](#) [Feedback](#) [Developers](#)

# Data upload (Option 1, HTML5-based)

The screenshot shows a web browser window with the URL `flowrepository.org/experiments/754/upload_files_html5`. The page header includes the FlowRepository logo and navigation links: [Inbox](#), [Profile](#), [Annotation Data](#), [Invite a User](#), [Support](#), and [Public View](#). A user greeting "Welcome, Josef" and a [Logout](#) link are visible on the right.

The main content area features a blue header for the experiment: "Experiment: IDCRP's HIV Natural History Study" with ID `EB_FCM_ZZW`, labels "None", primary researcher `Nina Aghaepour`, and public status "No". An "MFlowCyt Score: 0.00%" is displayed on the right. Below this is an orange button for [Back to Experiment](#).

A green "Getting Started!" notification box contains the following text: "This data upload page is experimental. It is based on new HTML5 file interface and therefore, it requires recent versions of one of the major web browsers. If you have Java, or if you require FCS de-identification, then you may upload data using the regular [Java-based uploader](#) instead. In order to upload files from here, add individual files (not folders) to the upload list by dropping them in the upload box (preferable) or by selecting them using the [Add Files](#) button (less preferable), and hit the [Upload](#) button. Please be patient, you should be redirected back to the experiment page once all files are uploaded and processed on the server." An **Important note** states: "If you are adding many files, queuing those for upload using the Drag & Drop feature is much faster than the Add files button with most browsers. For example, in our testing with Google Chrome, adding 100 FCS files using the Add Files button took 23 seconds, while the Drag & Drop queued the 100 FCS files instantly."

On the left, a "Actions" sidebar includes links for [Delete Experiment!](#) and [Remove partial in-progress uploads](#). A "Did you know?" section provides instructions on printing, exporting to PDF, Excel, and sharing permissions.

The "Upload Experiment Files" section contains two buttons: "Add Files" and "Upload". Below them is a list of 10 files, each with a red 'X' icon and a filename: `167004.fcs`, `167005.fcs`, `167093.fcs`, `167106.fcs`, `167107.fcs`, `167195.fcs`, `167208.fcs`, `167209.fcs`, `167297.fcs`, `167310.fcs`, and `167311.fcs`. A dashed box indicates the area for drag-and-drop uploads, with a note: "You can still Drag and Drop files here. Hit the Upload button when you are ready."

# Data upload (Option 1, HTML5-based)

FlowRepository - IDCRP's HIV Natural History Study - Mozilla Firefox

flowrepository.org/experiments/754/upload\_files\_html5

FlowRepository

Inbox Profile Annotation Data Invite a User Support Public View

Welcome, Josef Logout

Experiment: IDCRP's HIV Natural History Study ID: EB\_FCM\_ZZW Labels: None Primary Researcher: Nina Aghaepour Public: No MFlowCyt Score: 0.00%

Back to Experiment

Getting Started!

This data upload page is experimental. It is based on new HTML5 file interface and therefore, it requires recent versions of one of the major web browsers. If you have Java, or if you require FCS de-identification, then you may upload data using the regular [Java-based uploader](#) instead. In order to upload files from here, add individual files (not folders) to the upload list by dropping them in the upload box (preferable) or by selecting them using the [Add Files](#) button (less preferable), and hit the [Upload](#) button. Please be patient, you should be redirected back to the experiment page once all files are uploaded and processed on the server.

**Important note:** If you are adding many files, queuing those for upload using the Drag & Drop feature is much faster than the Add files button with most browsers. For example, in our testing with Google Chrome, adding 100 FCS files using the Add Files button took 23 seconds, while the Drag & Drop queued the 100 FCS files instantly.

Upload Experiment Files

Add Files Upload Overall progress: 13%

X	167004.fcs	11%
X	167005.fcs	12%
X	167093.fcs	100%
X	167106.fcs	22%
X	167107.fcs	16%
X	167195.fcs	90%
X	167208.fcs	18%
X	167209.fcs	5%
X	167297.fcs	
X	167310.fcs	
X	167311.fcs	

Uploading...

Terms of Service Privacy Policy Support Feedback Developers

# Data upload (Option 2, Java-based)

Experiment: IDCRP's HIV Natural History Study ID: FR-FCM-ZZ2B Labels: None Primary Researcher: [Nima Azharpour](#) Public: No MIFlowCyt Score: 0.00%

[← Back to Experiment](#)

↓ Actions  
[Delete Experiment](#)

↓ Did you know?  
You can request a one-on-one session to get started with your data by filling out a [support ticket](#).  
A guide to Cytobank is available at [Current Protocols in Cytometry](#).  
We also have a [Quick start guide](#).  
You can print/save your illustrations to PDF from the Illustration view's left menu.  
You can export your data to Excel from the Experiment Summary page.  
Give other users full control to modify your experiments through the "Sharing Permissions" box.  
Use the "Download Files" button to save copies of the original FCS Files to your computer.

This experiment does not have any FCS files uploaded yet.

▶ Getting Started! ✕

### Upload Experiment Files

[Browse For Folder...](#) [Upload Selected Files](#)

[Select All](#) [Deselect All](#) [Select Flow Files](#) [Deselect Flw Files](#)

De-identify all FCS files before uploading

**No folder selected. Click on "Browse for Folder..." to select a folder.**

Filename	FCS Version	Upload?
----------	-------------	---------

Upload Progress:

# Data upload (Option 2, Java-based)

Experiment: IDCRC's HIV Natural History Study

ID: FR-FCM-ZZZB

Labels: None

Primary Researcher: Nima Agharepour

Public: No

MIFlowCyt Score: 0.00%

[← Back to Experiment](#)

▼ Actions

[Delete Experiment](#)

▼ Did you know?

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This experiment does not have any FCS files uploaded yet.

▶ Getting Started! ✕

Upload Experiment Files

De-identify all FCS files before uploading

Files:

Filename	FCS Version	Upload?
203037.fcs - 203037.fcs	FCS2.0	<input checked="" type="checkbox"/>
797946.fcs - 797946.fcs	FCS2.0	<input checked="" type="checkbox"/>
922911.fcs - 922911.fcs	FCS2.0	<input checked="" type="checkbox"/>
802565.fcs - 802565.fcs	FCS2.0	<input checked="" type="checkbox"/>
643079.fcs - 643079.fcs	FCS2.0	<input checked="" type="checkbox"/>
351452.fcs - 351452.fcs	FCS2.0	<input checked="" type="checkbox"/>
334791.fcs - 334791.fcs	FCS2.0	<input checked="" type="checkbox"/>
294897.fcs - 294897.fcs	FCS2.0	<input checked="" type="checkbox"/>
319267.fcs - 319267.fcs	FCS2.0	<input checked="" type="checkbox"/>
251284.fcs - 251284.fcs	FCS2.0	<input checked="" type="checkbox"/>
997430.fcs - 997430.fcs	FCS2.0	<input checked="" type="checkbox"/>
122405.fcs - 122405.fcs	FCS2.0	<input checked="" type="checkbox"/>
846228.fcs - 846228.fcs	FCS2.0	<input checked="" type="checkbox"/>
130119.fcs - 130119.fcs	FCS2.0	<input checked="" type="checkbox"/>
306870.fcs - 306870.fcs	FCS2.0	<input checked="" type="checkbox"/>
978630.fcs - 978630.fcs	FCS2.0	<input checked="" type="checkbox"/>

Upload Progress:

[Terms of Service](#)

[Privacy Policy](#)

[Support](#)

[Feedback](#)



# Data upload - de-identification (needs Java)

**De-identify all FCS files before uploading**

## De-identification

- Remove identifiers that could be used to identify an individual
- Generally, privacy rules do not apply on de-identified data
  - Allows for sharing
    - Check with your regulatory authority as applicable

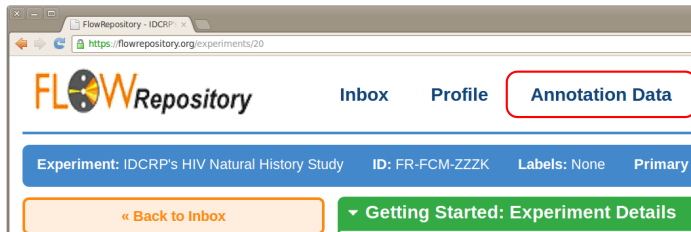
## Implementation in FlowRepository

- Automated removal of all keyword values unless in our *safe* list
  - Safe list: Over 220 keywords identified from hundreds of FCS data files produced by dozens of instruments from several vendors
  - Downside: Also removes everything unknown
- Integrated in the upload process
  - Performed locally → no sensitive information leaves your computer

# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
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  - Describe samples and sample sources
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- 6 Review (and improve) your MIFlowCyt compliance
- 7 Share with reviewers
- 8 Share with everyone

# Prepare annotation data



- Follow the Annotation Data link
  - Set of *concepts* applicable to samples even from different datasets

# Prepare annotation data – reagents

▼ Actions !

- [Add new keyword](#)
- [Add new organization](#)
- [Add new manufacturer](#)
- [Add new reagent](#)
- [Add new instrument](#)
- [Add organism](#)
- [Add new template for samples](#)
- [Add new template for sample sources](#)

▼ Did you know?

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Use the "Download Files" button to save copies of the original FCS Files to your computer.

Getting Started with MIFlowCyt Annotations! ×

Keywords Organizations Manufacturers **Reagents** Instruments Organisms Templates

New reagent

Search:

Analyte ▲	Analyte detector ⇅	Analyte reporter ⇅	Clone ⇅	Catalog nr ⇅	Manufacturer ⇅		
CD14	anti-CD14	Alexa 700	M5E2	BD#557923	<a href="#">BD Biosciences [website]</a>	Edit	Remove
CD14	anti-CD14	PE-Cy7	M5E2	eBio#25-0149	<a href="#">eBioscience [website]</a>	Edit	Remove
CD14	-	FITC	RMO52	IM0645	<a href="#">Beckman Coulter [website]</a>	Edit	Remove
CD14	-	PE-Cy7	M5E2	557742 1:50	<a href="#">BD Biosciences [website]</a>	Edit	Remove
CD3/CD14	Anti-CD3/CD14	PECy7		-	Unknown	Edit	Remove
VIVID/CD14	N/A	V450		N/A	Custom	Edit	Remove

Showing 1 to 6 of 6 entries (filtered from 110 total entries)

- Define reagents used in the dataset

## Prepare annotation data – add reagents

▼ New Reagent

Analyte \*

Analyte detector \*

Analyte reporter \*

Clone

Catalog nr \*

Manufacturer \*  [New](#)

- Provide details as required by MIFlowCyt

# Prepare annotation data – instruments

- Your instrument is most likely in the system already

Keywords Organizations Manufacturers Reagents **Instruments** Organisms Templates

New instrument

Search:

Model ▲	Manufacturer ▼	Other ▼	▼	▼
A10-Bryte	Apogee Flow Systems <a href="http://www.apogeeeflow.com">http://www.apogeeeflow.com</a>		Edit	Remove
A40-Military	Apogee Flow Systems <a href="http://www.apogeeeflow.com">http://www.apogeeeflow.com</a>		Edit	Remove
A50-Micro	Apogee Flow Systems <a href="http://www.apogeeeflow.com">http://www.apogeeeflow.com</a>		Edit	Remove
A50-Universal	Apogee Flow Systems <a href="http://www.apogeeeflow.com">http://www.apogeeeflow.com</a>		Edit	Remove
Accuri C6	Becton Dickinson (BD Biosciences) <a href="http://www.bdbiosciences.com">http://www.bdbiosciences.com</a>		Edit	Remove
Attune	Applied Biosystems <a href="http://www.appliedbiosystems.com">http://www.appliedbiosystems.com</a>		Edit	Remove
Auto-A40	Apogee Flow Systems <a href="http://www.apogeeeflow.com">http://www.apogeeeflow.com</a>		Edit	Remove

## Prepare annotation data – organisms

- The NCBI Taxonomy contains hundreds of thousands of organisms
- FlowRepository contains 20,000 of these
  - Selected based on either having a common English name or appearance in GeneBank
- But this is still a long list (for drop down selections)
  - We only show what has been used or explicitly requested

Keywords	Organizations	Manufacturers	Reagents	Instruments	Organisms	Templates
<a href="#">Add organism</a>						
Search: <input type="text"/>						
NCBI Taxonomy ID	Scientific name	Genbank common name				
2	Bacteria	eubacteria				
3055	Chlamydomonas reinhardtii	Chlamydomonas reinhardtii (green algae)				
4890	Ascomycota	ascomycetes				
4932	Saccharomyces cerevisiae	baker's yeast				
9541	Macaca fascicularis	crab-eating macaque				
9544	Macaca mulatta	Rhesus monkey				
9606	Homo sapiens	human				
9999	Spermophilus parryii	Arctic ground squirrel				
10090	Mus musculus	house mouse				
10116	Rattus norvegicus	Norway rat				

# Prepare annotation data – add organism

- Follow the Add organism link
- Start typing either the Latin or the English name
- Auto-complete will show suggestions after the first 3 characters

▼ Add organism from NCBI Taxonomy

Organism name or taxonomy ID:  
babo

Add this organism

Papio (9554) [ <b>baboons</b> ]
Papio anubis (9555) [Olive <b>baboon</b> ]
Papio cynocephalus (9556) [Yellow <b>baboon</b> ]
Papio hamadryas (9557) [hamadryas <b>baboon</b> ]
Theropithecus gelada (9565) [gelada <b>baboon</b> ]
Mandrillus (9567) [forest



# Prepare annotation data – templates

- Start with sample sources

Keywords Organizations Manufacturers Reagents Instruments **Organisms** Templates

[New annotation template for samples](#)  
[New annotation template for sample sources](#)

Search:

Annotation Type ▲	Template Name ▼	User ▼	Public ▼	▼	▼
Sample	Sample template Kollmann #1	Karin Breuer	yes	Show	Remove
Sample	JS Sample 1	Josef Spidlen	no	Show	Remove
Sample source	sample source template Kollmann #1	Karin Breuer	yes	Show	Remove
Sample source	12w MOLD/RkJ M mouse	Josef Spidlen	no	Show	Remove

Showing 1 to 4 of 4 entries

# Prepare annotation data – create sample source templates

- Different items required based on the sample source type
- Form changes accordingly
- Use ? for variable fields

Details for sample source template

Sample source type \* environmental ▾

Description \*

Location \*

Other

Cancel Save

# Prepare annotation data – create sample source templates

- Different items required based on the sample source type
- Form changes accordingly
- Use ? for variable fields

Details for sample source template

Sample source type \*

Description \*

Organism \*

Age \*   
Age unit \*

Gender \*   
Phenotype \*

Genotype \*

Treatment \*

# Prepare annotation data – create sample templates

**Details for sample template** ✕

Description \*  
PBMC from HIV+ Subject

Sample characteristic HIV+ New

Sample treatment  New

Staining -- None --  
B cells, MHCII, PerCPy5.5 (BD Biosciences BD#custom)  
T cells, CD40, FITC/OG (eBioscience eBio#11-0409)  
CD14 positive cells, CD14, Alexa 700 (BD Biosciences BD#557923)  
CD86, CD86, PE (eBioscience eBio#12-0869) New

Staining cocktail(s) -- None --  
Cocktail no. 1 New

Cancel Save

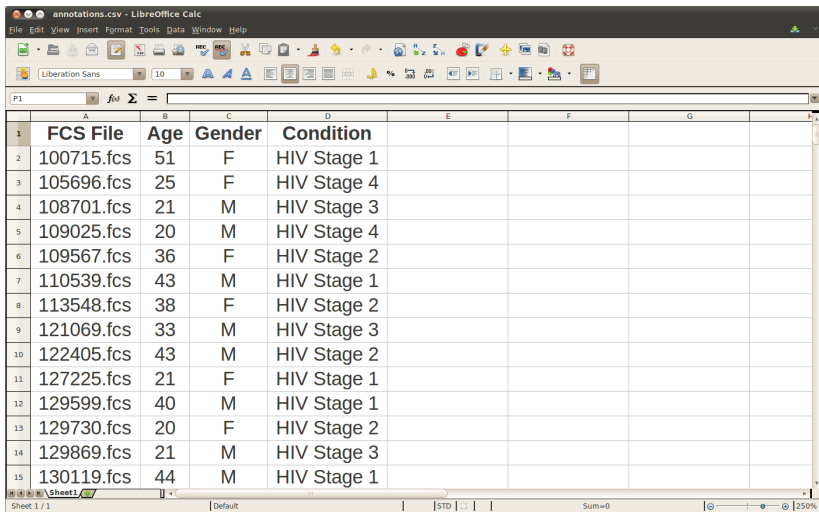
# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
  - Or prepare spreadsheets with annotations
- 4 Annotate the experiment
  - Describe samples and sample sources
  - Provide experimental variables
  - Describe instrumentation settings
- 5 Provide analysis details
  - Either analyze data online
  - Or upload third party analysis files (e.g., FlowJo workspaces, FCS Express projects, FACS Diva files, etc.)
- 6 Review (and improve) your MIFlowCyt compliance
- 7 Share with reviewers
- 8 Share with everyone

## Prepare spreadsheets with annotations

- Use your favorite spreadsheet editor
  - MS Excel, GoogleDoc Spreadsheet, OpenOffice Calc, etc.
- Name one column as **FCS File**; values should correspond to file names in your dataset
- Other “understandable” columns:
  - **Samples**: Sample Description, Sample Characteristic, Sample Treatment, Sample Source Description, Sample Source Treatment, Age, Age unit, Gender, Phenotype, Genotype, Location, Other Sample Source Information
  - **Experiment Variables**: Condition, Dose, Timepoint, Individual, Experimental variable sample type
  - **Instrumentation Details**: Instrument, Default Instrument Settings, Optical Filters Installation Dates, Other Flow Fluidics Information, Other Instrument Settings Information, Flow Cell Type

# Use your favorite spreadsheet editor



The screenshot shows the LibreOffice Calc application window titled "annotations.csv - LibreOffice Calc". The spreadsheet contains the following data:

	A	B	C	D	E	F	G
1	<b>FCS File</b>	<b>Age</b>	<b>Gender</b>	<b>Condition</b>			
2	100715.fcs	51	F	HIV Stage 1			
3	105696.fcs	25	F	HIV Stage 4			
4	108701.fcs	21	M	HIV Stage 3			
5	109025.fcs	20	M	HIV Stage 4			
6	109567.fcs	36	F	HIV Stage 2			
7	110539.fcs	43	M	HIV Stage 1			
8	113548.fcs	38	F	HIV Stage 2			
9	121069.fcs	33	M	HIV Stage 3			
10	122405.fcs	43	M	HIV Stage 2			
11	127225.fcs	21	F	HIV Stage 1			
12	129599.fcs	40	M	HIV Stage 1			
13	129730.fcs	20	F	HIV Stage 2			
14	129869.fcs	21	M	HIV Stage 3			
15	130119.fcs	44	M	HIV Stage 1			

Save as a CSV (Comma Separated Values) file

- Look in the File menu for Save As, Download, or Export

# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
  - Or prepare spreadsheets with annotations
- 4 **Annotate the experiment**
  - Describe samples and sample sources
  - Provide experimental variables
  - Describe instrumentation settings
- 5 Provide analysis details
  - Either analyze data online
  - Or upload third party analysis files (e.g., FlowJo workspaces, FCS Express projects, FACS Diva files, etc.)
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# Upload and annotation of your own dataset




- 1 Create a new experiment
- 2 Upload data (FCS files)
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  - Provide experimental variables
  - Describe instrumentation settings
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  - Or upload third party analysis files (e.g., FlowJo workspaces, FCS Express projects, FACS Diva files, etc.)
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- 7 Share with reviewers
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[« Back to Inbox](#)

[My Working Illustration »](#)

[MIFlowCyt Annotation »](#)

- ▼ Actions i
- Experiment**
- [Edit Experiment Details](#)
  - [Delete Experiment](#)
- FCS Files**
- [Download FCS Files](#)
  - [Upload More FCS Files](#)
  - [De-identify FCS Files](#)
  - [Review Keywords in FCS files](#)

- ▼ Sharing Permissions i
- Full Access Users
-  [Nima Aghaepour](#) [PR]
  -  [Josef Spidlen](#) [x]
  -  [Ryan Brinkman](#) [x]
- [Invite a new user](#)
- Share with a User (Full Access)
- 
- This experiment is currently **private**.
- 
- You can also **create a secret access code** to share with reviewers.
- 

▼ Did you know?

You can request a one-on-one session to get started with your data by filling out a

▼ Getting Started: Experiment Details x

This Experiment Details Page contains information about the experiment listed above.

- [Start describing samples](#)
- [Add flow cytometer information](#)
- [Review experiment variables](#)
- [Analyze your data on-line](#)
- [Review MIFlowCyt annotation](#)
- [Download FCS files](#)

For more tips and guides please see:

- [FlowRepository Quick start guide](#)
- [Documentation site for CytoBank and FlowRepository](#)

▶ Experiment Details i

▶ Illustrations i

▶ Attachments i

▼ FCS Files (466) i

[Download Files](#) [Upload More Files](#) [De-identify FCS Files](#) [Review Keywords in FCS files](#)

File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
100715.fcs <a href="#">details</a>	100715.fcs <a href="#">describe sample</a>	Tube_025		Panel 1	65016	4 MB
105696.fcs <a href="#">details</a>	105696.fcs <a href="#">describe sample</a>	Tube_009		Panel 1	455184	27.8 MB
108701.fcs <a href="#">details</a>	108701.fcs <a href="#">describe sample</a>	Tube_001		Panel 1	1000000	61 MB
109025.fcs <a href="#">details</a>	109025.fcs <a href="#">describe sample</a>	Tube_009		Panel 1	210186	12.8 MB
109567.fcs <a href="#">details</a>	109567.fcs <a href="#">describe sample</a>	Tube_017		Panel 1	160074	9.8 MB
110539.fcs <a href="#">details</a>	110539.fcs <a href="#">describe sample</a>	Tube_022		Panel 1	364212	22.2 MB
113548.fcs <a href="#">details</a>	113548.fcs <a href="#">describe sample</a>	Tube_003		Panel 1	177102	10.8 MB
121069.fcs <a href="#">details</a>	121069.fcs <a href="#">describe sample</a>	Tube_001		Panel 1	542538	33.1 MB
122405.fcs <a href="#">details</a>	122405.fcs <a href="#">describe sample</a>	Tube_010		Panel 1	476208	29.1 MB

# Describing samples

100715.fcs Sample Information

Apply template:  [Create templates](#)

Description \*

Sample source  [New](#)

Sample characteristic  [New](#)

Sample treatment  [New](#)

Staining  [New](#)

Staining cocktail(s)  [New](#)

[Save and proceed to next FCS file](#) [Apply to all undescribed FCS files](#) [Apply to undescribed FCS files in Panel 1](#)

# Describing samples – apply a template

100715.fcs Sample Information

Apply template: **PBMC from HIV+ Subject Template** [Create templates](#)

Description \*

Sample source  [New](#)

Sample characteristic **HIV+** [New](#)

Sample treatment **PBMCs were thawed in warm ..** [New](#)

Staining   
B cells, MHCII, PerCPCy5.5 (BD Biosciences BD#custo  
T cells, CD40, FITC/OG (eBioscience eBio#11-0409)  
CD14 positive cells, CD14, Alexa 700 (BD Biosciences I  
CD86, CD86, PE (eBioscience eBio#12-0869) [New](#)

Staining cocktail(s)   
Cocktail no [New](#)

[Save and proceed to next FCS file](#) [Apply to all undescribed FCS files](#) [Apply to undescribed FCS files in Panel 1](#)

# Describing samples – create a sample source

- Use templates again
- Adjust accordingly for each sample
- Or just leave it (we can fix it later using spreadsheets)

New sample source details

Create from template: HIV+ subject template

Sample source type \*

Description \*

HIV+ subject

Organism \*

Age \*

Age unit \*

Gender \*

Phenotype \*

Genotype \*

Treatment \*

None

# Describing samples – 3 options to save

100715.fcs Sample Information

Apply template:  [Create templates](#)

Description \*

Sample source  [New](#)

Sample characteristic  [New](#)

Sample treatment  [New](#)

Staining   
B cells, MHCII, PerCPy5.5 (BD Biosciences BD#custo  
T cells, CD40, FITC/OG (eBioscience eBio#11-0409)  
CD14 positive cells, CD14, Alexa 700 (BD Biosciences I  
CD86, CD86, PE (eBioscience eBio#12-0869) [New](#)

Staining cocktail(s)   
Cocktail no [New](#)

# Samples and sample sources are now described

Experiment: IDCRP's HIV Natural History Study ID: FR-FCM-ZZTB Labels: None Primary Researcher: Nima Aghaeepour Public: No MIFlowCyt Score: 61.50%

« Back to Inbox

My Working Illustration »

MIFlowCyt Annotation »

Actions

Experiment

- Edit Experiment Details
- Delete Experiment

FCS Files

- Download FCS Files
- Upload More FCS Files
- De-identify FCS Files
- Review Keywords in FCS files

Sharing Permissions

Full Access Users

- Nima Aghaeepour [PR]
- Josef Spidlen [X]
- Ryan Brinkman [X]

[Invite a new user](#)

Share with a User (Full Access)

This experiment is currently **private**.

Getting Started: Experiment Details

- Experiment Details
- Illustrations
- Attachments

FCS Files (466)

[Download Files](#) [Upload More Files](#) [De-identify FCS Files](#) [Review Keywords in FCS files](#)

File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
100715.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_025		Panel 1	65016	4 MB
105696.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_009		Panel 1	455184	27.8 MB
108701.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_001		Panel 1	1000000	61 MB
109025.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_009		Panel 1	210186	12.8 MB
109567.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_017		Panel 1	160074	9.8 MB
110539.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_022		Panel 1	364212	22.2 MB
113548.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_003		Panel 1	177102	10.8 MB
121069.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_001		Panel 1	542538	33.1 MB
122405.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_010		Panel 1	476208	29.1 MB
127225.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_021		Panel 1	257058	15.7 MB
129599.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_007		Panel 1	352314	21.5 MB
129730.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_017		Panel 1	390528	23.8 MB
129869.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_002		Panel 1	230852	14.1 MB

But not everything is correct!

- Our *Sample source organisms* vary in age and gender
- We left this out from our template
- Time to fix this
  - We can now use the spreadsheet created earlier



# Upload the spreadsheet as attachment

Experiment: IDCRP's HIV Natural History Study ID: FR-FCM-ZZB Labels: None Primary Researcher: Nima.Aghaeepour Public: No **MIFlowCyt Score: 61.50%**

« Back to Inbox

My Working Illustration »

MIFlowCyt Annotation »

Actions

- Experiment
- [Edit Experiment Details](#)
- [Delete Experiment](#)
- FCS Files
- [Download FCS Files](#)
- [Upload More FCS Files](#)
- [De-identify FCS Files](#)
- [Review Keywords in FCS files](#)

Sharing Permissions

Full Access Users

- [Nima Aghaeepour](#) [PR]
- [Josef Spidlen](#) [x]
- [Ryan Brinkman](#) [x]

[Invite a new user](#)

Share with a User (Full Access)

This experiment is currently **private**.

Getting Started: Experiment Details

Experiment Details

Illustrations

Attachments

File Name	Date	Uploaded By	Size	md5sum		
Attach a file						
<input type="button" value="Choose File"/> No file chosen						
<input type="button" value="Upload"/>						
FCS Files (466)						
<a href="#">Download Files</a> <a href="#">Upload More Files</a> <a href="#">De-identify FCS Files</a> <a href="#">Review Keywords in FCS files</a>						
File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
<a href="#">100715.fcs</a> details	<a href="#">show sample description</a>	Tube_025		Panel 1	65016	4 MB
<a href="#">105696.fcs</a> details	<a href="#">show sample description</a>	Tube_009		Panel 1	455184	27.8 MB
<a href="#">108701.fcs</a> details	<a href="#">show sample description</a>	Tube_001		Panel 1	1000000	61 MB
<a href="#">109025.fcs</a> details	<a href="#">show sample description</a>	Tube_009		Panel 1	210186	12.8 MB
<a href="#">109567.fcs</a> details	<a href="#">show sample description</a>	Tube_017		Panel 1	160074	9.8 MB
<a href="#">110539.fcs</a> details	<a href="#">show sample description</a>	Tube_022		Panel 1	364212	22.2 MB
<a href="#">113548.fcs</a> details	<a href="#">show sample description</a>	Tube_003		Panel 1	177102	10.8 MB
<a href="#">121069.fcs</a> details	<a href="#">show sample description</a>	Tube_001		Panel 1	542538	33.1 MB
<a href="#">122405.fcs</a> details	<a href="#">show sample description</a>	Tube_010		Panel 1	476208	29.1 MB

# Parse the attachment – click on (P)

Experiment: IDCRP's HIV Natural History Study ID: FR-FCM-ZZB Labels: None Primary Researcher: Nima Aghaeepour Public: No MIFlowCyt Score: 61.50%

« Back to Inbox




My Working Illustration »

MIFlowCyt Annotation »

Attachment was added to experiment.

### Getting Started: Experiment Details

- Experiment Details
- Illustrations
- Attachments

File Name	Date	Uploaded By	Size	md5sum
annotations.csv  	12:03 PM	 Josef Spidlen	15.5 KB	1de7e15...

Attach a file




No file chosen

### FCS Files (466)

[Download Files](#) [Upload More Files](#) [De-identify FCS Files](#) [Review Keywords in FCS files](#)

File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
100715.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_025		Panel 1	65016	4 MB
105696.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_009		Panel 1	455184	27.8 MB
108701.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_001		Panel 1	1000000	61 MB
109025.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_009		Panel 1	210186	12.8 MB
109567.fcs <a href="#">details</a>	<a href="#">show sample description</a>	Tube_017		Panel 1	160074	9.8 MB

Full Access Users

-  Nima Aghaeepour [PR]
-  Josef Spidlen [x]
-  Ryan Brinkman [x]

[Invite a new user](#)

Share with a User (Full Access)

This experiment is currently **private**.

localhost:8080/experiments/11/attachments/51/parse

## Information extracted from attachment

- Review the result

Note: We also provided one experimental variable (the condition)

The following information extracted from attachment annotations.csv

<b>FCS file</b>	<b>age</b>	<b>gender</b>	<b>condition</b>
100715.fcs	51	F	HIV Stage 1
105696.fcs	25	F	HIV Stage 4
108701.fcs	21	M	HIV Stage 3
109025.fcs	20	M	HIV Stage 4
109567.fcs	36	F	HIV Stage 2
110539.fcs	43	M	HIV Stage 1
113548.fcs	38	F	HIV Stage 2
121069.fcs	33	M	HIV Stage 3
122405.fcs	43	M	HIV Stage 2
127225.fcs	21	F	HIV Stage 1
129599.fcs	40	M	HIV Stage 1
129730.fcs	20	F	HIV Stage 2
129869.fcs	21	M	HIV Stage 3
130119.fcs	44	M	HIV Stage 1
132447.fcs	17	F	HIV Stage 1

# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
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- 7 Share with reviewers
- 8 Share with everyone

# Provide experimental variables

- Follow [Review experiment variables](#) in the Getting Started panel
- Or navigate to your [Working Illustration](#)

▼ Getting Started: Experiment Details ✕

This Experiment Details Page contains information about the experiment listed above.

- [Start describing samples](#)
- [Add flow cytometer information](#)
- [Review experiment variables](#)
- [Analyze your data on-line](#)
- [Review MIFlowCyt annotation](#)
- [Download FCS files](#)

For more tips and guides please see:

- [FlowRepository Quick start guide](#)
- [Documentation site for Cytobank and FlowRepository](#)

▼ Illustrations i

Name	Active Dimensions	Author	Created	Updated
<a href="#">Josef's Working Illustration</a>	Channels (0) x Populations (1) <a href="#">Print View</a>  PDF	 Josef Spidlen	May 2012	May 2012

[Reset Working Illustration](#)

# Provide experimental variables

▼ Figure Dimensions (Experimental Variables): Channels ⇄ Populations ⇄ Conditions ⓘ

**Available Dimensions** - Click to toggle on/off

Channels Populations Dosages Timepoints Conditions Individuals Sample Types Fcs Files Plate Column Plate Row Plate

**Arrange Dimensions** - Drag to prioritize dimensions, click Choose to change selections and ordering, click Setup/Gate to configure

**Channels** 32 channels Choose Setup

Unselected Channels:

- Panel 1
- Panel 2
- Panel 1
- Panel 2
- Panel 1
- Panel 2
- Ki67 - Panel 1
- Ki67 - Panel 2
- CD3 - Panel 1
- CD3 - Panel 2
- CD28 - Panel 1
- CD28 - Panel 2
- CD45RO - Panel 1
- CD45RO - Panel 2

Columns

**Populations** 1 of 1 selected Choose Gate

Ungated

Rows

**Conditions** 4 of 4 selected Choose Setup

- HIV Stage 1
- HIV Stage 4
- HIV Stage 3
- HIV Stage 2

Table 1

- Example: patients treated by various dosages of Lexiva™

# Provide experimental variables

▼ Figure Dimensions (Experimental Variables): Channels ↔ Populations ↔ Conditions ⓘ

Available Dimensions - Click to toggle on/off

Channels Populations Dosages Timepoints Conditions Individuals Sample Types Fcs Files Plate Column Plate Row Plate

Arrange Dimensions - Drag to prioritize dimensions, click Choose to change selections and ordering, click Setup/Gate to configure

**Channels** (32 channels) | Choose | Setup

Unselected Channels:

- Panel 1
- Panel 2
- Panel 1
- Panel 2
- Panel 1
- Panel 2
- KI67 - Panel 1
- KI67 - Panel 2
- CD3 - Panel 1
- CD3 - Panel 2
- CD28 - Panel 1
- CD28 - Panel 2
- CD45RO - Panel 1
- CD45RO - Panel 2

Columns

**Populations** (1 of 1 selected) | Choose | Gate

Ungated

Rows

**Conditions** (4 of 4 selected) | Choose | Setup

- HIV Stage 1
- HIV Stage 4
- HIV Stage 3
- HIV Stage 2

Table 1

**Dosages** | Choose | Setup

Click To Setup

Table 2

- Example: patients treated by various dosages of Lexiva™
- Click on Dosages, then Setup

## List doses

- Provide a comma-separated list of all doses

▼ Add Doses ⓘ

Enter a comma separated list of Doses to add:

Lexiva 1400 bid, Lexiva 1400 qd+Norvir 200 qd, Lexiva 700 bid+Norvir 100 bid



# Assign FCS files to the right doses

- Drag & Drop files into the appropriate boxes
- Or use the *Filter* with *Move to*

The screenshot shows a web-based interface for managing FCS files. At the top, there are four tabs: "All Doses", "Lexiva 1400 bid", "Lexiva 1400 qd+Norvir 200 qd", and "Lexiva 700 bid+Norvir 100 bid". The "All Doses" tab is selected, and the main heading is "All Doses". Below the heading is a instruction: "Drag files from 'Untagged' box to the 'Dose' boxes below to associate them with that tag. Use the 'Filter' and 'Move File' controls to move groups of files." The interface is divided into several panels. On the left is the "Untagged" panel, which contains a "Filter" input field, a "Move to..." dropdown menu, and a "Move file(s)" button. Below these are 14 file entries, each in a light blue box with a rounded rectangle on the right side, indicating it can be dragged. The files are: 134892.fcs (Tube\_021), 140801.fcs (Tube\_022), 145618.fcs (Tube\_011), 158322.fcs (Tube\_001), 158483.fcs (Tube\_012), 159665.fcs (Tube\_004), 162173.fcs (Tube\_005), 162520.fcs (Tube\_017), and 166139.fcs (Tube\_010). In the middle is the "Lexiva 1400 bid Tagged Files" panel, which contains 5 file entries: 100715.fcs (Tube\_025), 105696.fcs (Tube\_009), 108701.fcs (Tube\_001), 127225.fcs (Tube\_021), and 132447.fcs (Tube\_013). On the right is the "Lexiva 1400 qd+Norvir 200 qd Tagged Files" panel, which contains 4 file entries: 109025.fcs (Tube\_009), 110539.fcs (Tube\_022), 121069.fcs (Tube\_001), and 122405.fcs (Tube\_010). A mouse cursor is hovering over a file entry "132769.fcs (Tube\_002)" which is positioned between the middle and right panels, suggesting it is being moved from the "Untagged" panel to one of the "Dose" panels.

# Upload and annotation of your own dataset

- 1 Create a new experiment
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  - Describe samples and sample sources
  - Provide experimental variables
  - Describe instrumentation settings
- 5 Provide analysis details
  - Either analyze data online
  - Or upload third party analysis files (e.g., FlowJo workspaces, FCS Express projects, FACS Diva files, etc.)
- 6 Review (and improve) your MIFlowCyt compliance
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- 8 Share with everyone

# Instrumentation description

- Navigate to the details of an FCS file

The screenshot displays the FlowRepository web interface for an experiment titled "IDCRP's HIV Natural History Study". The URL is <https://flowrepository.org/experiments/11>. The experiment ID is FR-FCM-ZZB, and the primary researcher is Nima Aghaee pour. The MIFlowCyt score is 66.00%. The interface includes navigation buttons like "Back to Inbox", "My Working Illustration", and "MIFlowCyt Annotation". A sidebar on the left contains "Actions" (Experiment, Edit Experiment Details, Delete Experiment, FCS Files) and "Sharing Permissions" (Full Access Users: Nima Aghaee pour, Josef Spidlen, Ryan Brinkman). The main content area shows "Getting Started: Experiment Details" with sub-sections for Experiment Details, Illustrations, Attachments, and FCS Files (466). A table lists FCS files with columns for File Name, Sample, Tube Name, Experiment Variables, Panel, Events, and Size. The file 105696.fcs is highlighted with a red circle, and its "details" link is also circled.

File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
100715.fcs	<a href="#">show sample description</a>	Tube_025	HIV Stage 1, Lexiva 1400 bid	Panel 1	65016	4 MB
105696.fcs	<a href="#">show sample description</a>	Tube_009	HIV Stage 4, Lexiva 1400 bid	Panel 1	455184	27.8 MB
108701.fcs	<a href="#">show sample description</a>	Tube_001	HIV Stage 3, Lexiva 1400 bid	Panel 1	1000000	61 MB
109025.fcs	<a href="#">show sample description</a>	Tube_009	HIV Stage 4, Lexiva 1400 qd+Norvir 200 qd	Panel 1	210186	12.8 MB
109567.fcs	<a href="#">show sample description</a>	Tube_017	HIV Stage 2, Lexiva 700 bid+Norvir 100 bid	Panel 1	160074	9.8 MB
110539.fcs	<a href="#">show sample description</a>	Tube_022	HIV Stage 1, Lexiva 1400 qd+Norvir 200 qd	Panel 1	364212	22.2 MB
113548.fcs	<a href="#">show sample description</a>	Tube_003	HIV Stage 2, Lexiva 700 bid+Norvir 100 bid	Panel 1	177102	10.8 MB
121069.fcs	<a href="#">show sample description</a>	Tube_001	HIV Stage 3, Lexiva 1400 qd+Norvir 200 qd	Panel 1	542538	33.1 MB
122405.fcs	<a href="#">show sample description</a>	Tube_010	HIV Stage 2, Lexiva 1400 qd+Norvir 200 qd	Panel 1	476208	29.1 MB
127225.fcs	<a href="#">show sample description</a>	Tube_021	HIV Stage 1, Lexiva 1400 bid	Panel 1	257058	15.7 MB
129599.fcs	<a href="#">show sample description</a>	Tube_007	HIV Stage 1, Lexiva 700 bid+Norvir 100 bid	Panel 1	352314	21.5 MB
129730.fcs	<a href="#">show sample description</a>	Tube_017	HIV Stage 2, Lexiva 700 bid+Norvir 100 bid	Panel 1	390528	23.8 MB
129869.fcs	<a href="#">show sample description</a>	Tube_002	HIV Stage 3, Lexiva 700 bid+Norvir 100 bid	Panel 1	230852	14.1 MB

# Instrumentation description

- Press the *Describe instrument settings* button

The screenshot shows a web browser window with the URL [https://flowrepository.org/experiments/1/fcs\\_files/3043](https://flowrepository.org/experiments/1/fcs_files/3043). The page header includes: Experiment: IDCRP's HIV Natural History Study, ID: FR-FCM-ZZB, Labels: None, Primary Researcher: Nima Aghaepour, Public: No, and MIFlowCyt Score: 66.00%.

On the left sidebar, there is a 'Back to Experiment Summary' button and an 'Actions' section with links: [Download Tab-Separated Events File](#), [Show Sample Details](#), [De-identify the FCS file](#), and [Review Keywords in the FCS file](#). Below this is a 'Did you know?' section with several paragraphs of text and links.

The main content area has several sections:

- 100715.fcs - FCS File Information**
- 100715.fcs - FCS File Instrument Settings**: This section contains the text 'File-specific instrument settings have not been provided!' and a button labeled 'Describe instrument settings' which is circled in red.
- 100715.fcs - FCS File Laser Information**: This section contains a table with the following data:

ASF	Name	Delay
Blue	0.66	0.00
Red	0.55	-59.80
Violet	0.48	-24.40
Green	0.53	-82.60

Below the laser information is another section:

- 100715.fcs - FCS File Channel Information**: This section contains a table with the following data:

Channel Short Name	Channel Name	Gain	Bits	Amp	Range	Voltage	Amp Value
FSC-A		1	32		262207.0		0.0
FSC-H		1	32		262207.0		0.0
SSC-A		1	32		261588.0		0.0
B515-A	KI67	1	32		261588.0		0.0
R780-A	CD3	1	32		261588.0		0.0
B315-A	CD3	1	32		261588.0		0.0

# Instrumentation description

- Select the make and model of the instrument used

The screenshot shows the FlowRepository web interface for an experiment titled "IDCRP's HIV Natural History Study". The URL is [https://flowrepository.org/experiments/11/fcs\\_files/3043](https://flowrepository.org/experiments/11/fcs_files/3043). The interface includes a navigation bar with "Back to Experiment Summary", "100715.fcs - FCS File Information", "100715.fcs - FCS File Instrument Settings", and "100715.fcs - FCS File Laser Information". The "Describe instrument settings" dialog box is open, showing a dropdown menu for "Instrument \*". Below the dialog, a table displays channel information for the FCS file.

Channel Short Name	Channel Name	Gain	Bits	Amp	Range	Voltage	Amp Value
FSC-A		1	32		262207.0		0.0
FSC-H		1	32		262207.0		0.0
SSC-A		1	32		261588.0		0.0
B515-A	KI67	1	32		261588.0		0.0
R780-A	CD3	1	32		261588.0		0.0

# Instrumentation description

- New instruments may be added in the annotation data section

The screenshot shows the FlowRepository interface for an experiment titled "IDCRP's HIV Natural History Study". The URL is [https://flowrepository.org/experiments/11/fcs\\_files/0043](https://flowrepository.org/experiments/11/fcs_files/0043). The experiment ID is FR-FCM-ZZZB, and the primary researcher is Nima Aghaeeipour. The MIFlowCyt score is 66.00%. The page is divided into sections for "100715.fcs - FCS File Information", "100715.fcs - FCS File Instrument Settings", and "100715.fcs - FCS File Laser Information". A "Describe instrument settings" dialog box is open, showing a list of instrument models and a table of parameters.

**Describe instrument settings**

Instrument \*

- BactoCount IBC, Bentley Instruments
- BactoCount IBCm, Bentley Instruments
- BD FACSAria, Becton Dickinson (BD Biosciences)
- BD FACSAria II, Becton Dickinson (BD Biosciences)
- BD FACSAria III, Becton Dickinson (BD Biosciences)
- BD FACSAria, Becton Dickinson (BD Biosciences)
- BD FACSCalibur, Becton Dickinson (BD Biosciences)
- BD FACSCanto, Becton Dickinson (BD Biosciences)
- BD FACSCanto II, Becton Dickinson (BD Biosciences)
- BD FACSCount, Becton Dickinson (BD Biosciences)
- BD FACSScan, Becton Dickinson (BD Biosciences)
- BD Influx, Becton Dickinson (BD Biosciences)
- BD LSR, Becton Dickinson (BD Biosciences)
- BD LSR II, Becton Dickinson (BD Biosciences)
- BD LSRFortessa, Becton Dickinson (BD Biosciences)
- Bentley 150, Bentley Instruments
- Bentley Combi 150, Bentley Instruments
- Bentley FTS, Bentley Instruments
- Bentley FTS/FCM, Bentley Instruments
- Cell Lab Quanta MPL, Dako Cytomation

Parameter	Value
Age	0.0
Amp Value	0.0
R780-A	1
CD3	32
	261588.0
	0.0

# Instrumentation description

- **Simple case:** Same instrument with default settings for all FCS files

**Describe instrument settings** ✕

**Instrument \***

BD LSR II, Becton Dickinson (BD Biosciences) ▾

Use default instrument settings

**Installation dates for filters in optical paths**

The instrument has been purchased new on July 1, 2011; all optical filters are original and came with the instrument.

**Other**

PMT voltages specified within the FCS data files.

Use these settings for all FCS files in this experiment

Cancel Save

# Instrumentation description

- **Advanced case:** Describe all details
  - Required by MIFlowCyt for customized instruments only
  - See [http://flowrepository.org/quick\\_start\\_guide](http://flowrepository.org/quick_start_guide)

**Describe instrument settings** ✕

**Instrument \***

BD LSR II, Becton Dickinson (BD Biosciences) ▾

Use default instrument settings

**Flow cell type** Quartz cuvette ▾ [Add new flow cell type](#)

**Other flow fluidics**

**Optical paths** -- None -- ▾ [Add new optical path](#)



# Upload and annotation of your own dataset

- 1 Create a new experiment
- 2 Upload data (FCS files)
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# Analyze data online

- Navigate to your *Working illustration*
- Click on *Gate* in the Populations panel

▼ Figure Dimensions (Experimental Variables): Channels ◀ Populations ◀ Conditions ◀ Dosages ⓘ

**Available Dimensions** - Click to toggle on/off

Channels Populations Dosages Timepoints Conditions Individuals Sample Types Fcs Files

Plate Column Plate Row Plate

**Arrange Dimensions** - Drag to prioritize dimensions, click Choose to change selections and ordering, click Setup/Gate to configure

**Populations** 1 of 1 selected [Choose](#) [Gate](#)

Ungated

Columns

**Conditions** 4 of 4 selected [Choose](#) | [Setup](#)

HIV Stage 1

HIV Stage 4

HIV Stage 3

HIV Stage 2

Rows

**Dosages** 3 of 3 selected [Choose](#) | [Setup](#)

Lexiva 1400 bid

Lexiva 1400 qd+Norvir 200 qd

Lexiva 700 bid+Norvir 100 bid

Table 1

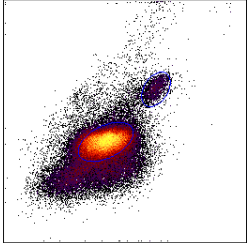
# Analyze data online

- Online data analysis is not our focus
- Only basic analysis supported

Draw Gates

Save & Return Select Rectangle Ellipse Polygon Quadrant Split Range Reset

File: 100715.fcs - Tube\_025



View

Active Population:  
Ungated

Up Down

Active Compensation:  
File Compensation

Plot Settings

Populations  
Manage View

Y: CD4 Arcsinh

X: CD28 Arcsinh

List of gates:  
Gate 1  
Gate 2  
Gate 3

Selected gate:

Name:

Global Gate  
 Tailored Gate

Apply Tailored Gate to Files...

Lock

Points Check Gate

# Analyze data online

More on analyzing data online in Cytobank or FlowRepository:

## **UNIT 10.17 Web-Based Analysis and Publication of Flow Cytometry Experiments**

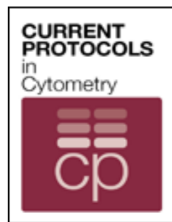
Nikesh Kotecha<sup>1,2,3</sup>, Peter O. Krutzik<sup>1,2</sup>,  
Jonathan M. Irish<sup>1</sup>

Published Online: 1 JUL 2010

DOI: 10.1002/0471142956.cy1017s53

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Lab Protocol Title



Current Protocols in  
Cytometry














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# Provide third party analysis files, figures, tables, etc.

- Upload these as attachments

Attachments i

File Name	Date	Uploaded By	Size	md5sum
<a href="#">annotations.csv</a>   File specific sample source details	Jun 07	 <a href="#">Josef Spidlen</a>	15.5 KB	1de7e15...
<a href="#">HIV_Analysis.jo</a>  Complete analysis in FlowJo	11:57 AM	 <a href="#">Josef Spidlen</a>	14.4 MB	d8a8ab5...
<a href="#">HIV_Analysis_Overview.png</a>  Overview figure	12:06 PM	 <a href="#">Josef Spidlen</a>	169.3 KB	4958a88...
<a href="#">HIV_Analysis_Class_Comparison.jpg</a>  HIV class comparison figure	12:06 PM	 <a href="#">Josef Spidlen</a>	201.9 KB	5795d5e...
<a href="#">All_Statistics.xlsx</a>  Tables and stats	12:07 PM	 <a href="#">Josef Spidlen</a>	253.6 KB	95641c1...
<a href="#">Extended_description.docx</a>  More details on experimental design	12:07 PM	 <a href="#">Josef Spidlen</a>	208.2 KB	76f301b...

Attach a file

No file chosen

# Upload and annotation of your own dataset

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[« Back to Inbox](#)

**Getting Started: Experiment Details**

[My Working Illustration »](#)

Experiment Details

[MIFlowCyt Annotation »](#)

Illustrations

**Actions**

Experiment

- [Edit Experiment Details](#)
- [Delete Experiment](#)

FCS Files

- [Download FCS Files](#)
- [Upload More FCS Files](#)
- [De-identify FCS Files](#)
- [Review Keywords in FCS files](#)

Name	Active Dimensions		Author	Created	Updated
<a href="#">Illustration 1</a>	Channels (3) x Fcs Files (2) x Populations (3)	<a href="#">Print View</a> <a href="#">PDF</a> <a href="#">Delete</a>	Josef Spidlen	11:37 AM	
<a href="#">Josef's Working Illustration</a>	Channels (3) x Fcs Files (2) x Populations (3)	<a href="#">Print View</a> <a href="#">PDF</a>	Josef Spidlen	May 2012	11:11 AM

[Delete My Saved Illustrations/Reset Working Illustration](#)

**Sharing Permissions**

Full Access Users

- [Nima Aghaepour](#) [PR]
- [Josef Spidlen](#) [x]
- [Ryan Brinkman](#) [x]

[Invite a new user](#)

Share with a User (Full Access)

This experiment is currently **private**.

[Share with Everyone](#)

You can also **create a secret access code** to share with reviewers.

[Share with Reviewers](#)

Attachments

File Name	Date	Uploaded By	Size	md5sum
<a href="#">annotations.csv</a> File specific sample source details	Jun 07	Josef Spidlen	15.5 KB	1de7e15...
<a href="#">HIV_Analysis.jo</a> Complete analysis in FlowJo	11:57 AM	Josef Spidlen	14.4 MB	d8a8ab5...
<a href="#">HIV_Analysis_Overview.png</a> Overview figure	12:08 PM	Josef Spidlen	169.3 KB	4958a88...
<a href="#">HIV_Analysis_Class_Comparison.jpg</a> HIV class comparison figure	12:08 PM	Josef Spidlen	201.9 KB	5795d5e...
<a href="#">All_Statistics.xlsx</a> Tables and stats	12:09 PM	Josef Spidlen	253.6 KB	95641c1...
<a href="#">Extended_description.docx</a> More details on experimental design	12:09 PM	Josef Spidlen	208.2 KB	76f301b...

**Attach a file**

No file chosen

**Did you know?**

You can request a one-on-one session to get started with your data by filling out a [support ticket](#).

A guide to Cytobank is available at [Current Protocols in Cytometry](#).

We also have a [Quick start guide](#).

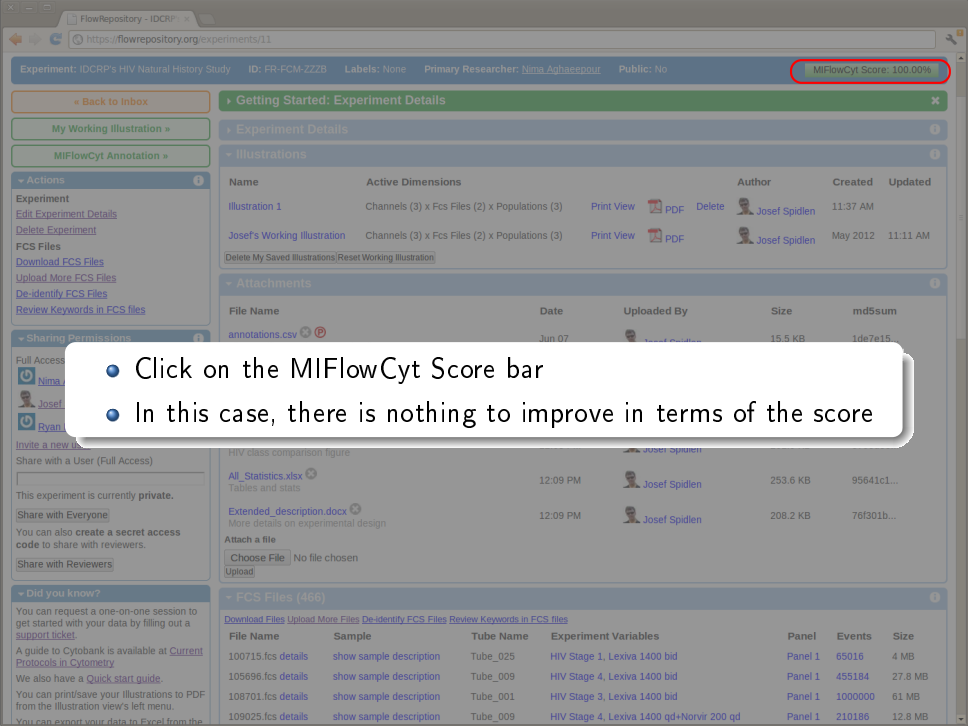
You can print/save your illustrations to PDF from the illustration view's left menu.

You can export your data to Excel from the

FCS Files (466)

[Download Files](#) [Upload More Files](#) [De-identify FCS Files](#) [Review Keywords in FCS files](#)

File Name	Sample	Tube Name	Experiment Variables	Panel	Events	Size
<a href="#">100715.fcs details</a>	<a href="#">show sample description</a>	Tube_025	HIV Stage 1, Lexiva 1400 bid	Panel 1	65016	4 MB
<a href="#">105696.fcs details</a>	<a href="#">show sample description</a>	Tube_009	HIV Stage 4, Lexiva 1400 bid	Panel 1	455184	27.8 MB
<a href="#">108701.fcs details</a>	<a href="#">show sample description</a>	Tube_001	HIV Stage 3, Lexiva 1400 bid	Panel 1	1000000	61 MB
<a href="#">109025.fcs details</a>	<a href="#">show sample description</a>	Tube_009	HIV Stage 4, Lexiva 1400 qd+Norvir 200 qd	Panel 1	210186	12.8 MB

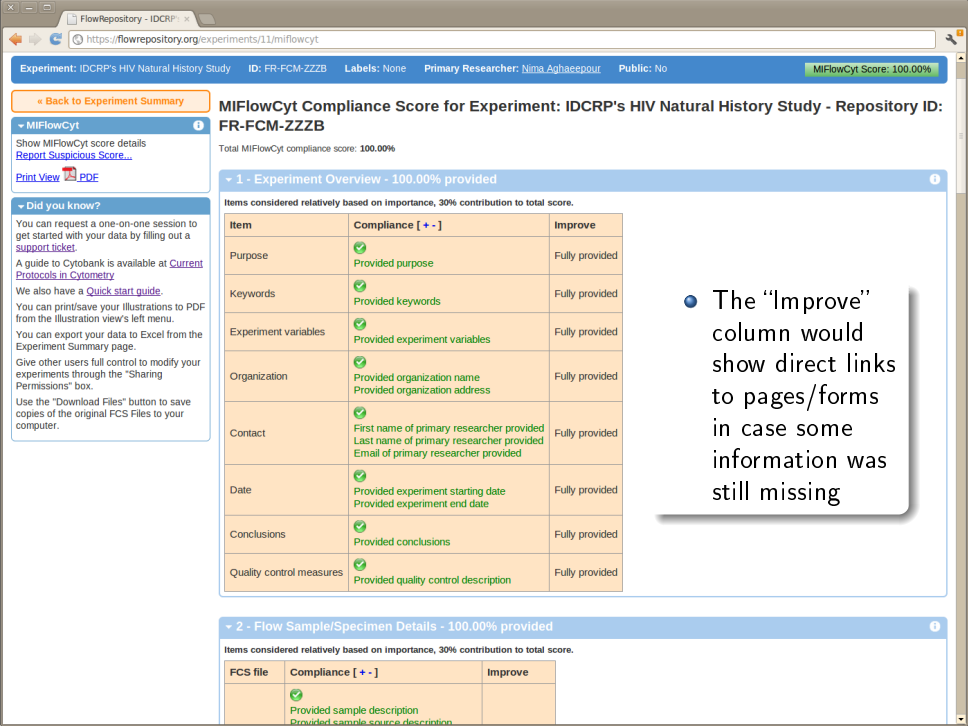


MIFlowCyt Score: 100.00%

- Click on the MIFlowCyt Score bar
- In this case, there is nothing to improve in terms of the score

File Name	Date	Uploaded By	Size	md5sum
annotations.csv	Jun 07	Josef Spidlen	15.5 KB	1de7e15
AI_Statistics.xlsx	12:09 PM	Josef Spidlen	253.6 KB	95641c1...
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109025.fcs details	show sample description	Tube_009	HIV Stage 4, Lexiva 1400 qd+Norvir 200 qd	Panel 1	210186	12.8 MB



« Back to Experiment Summary

MIFlowCyt

Show MIFlowCyt score details  
[Report Suspicious Score...](#)

[Print View](#) [PDF](#)

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A guide to Cytobank is available at [Current Protocols in Cytometry](#)

We also have a [Quick start guide](#).

You can print/save your illustrations to PDF from the illustration view's left menu.

You can export your data to Excel from the Experiment Summary page.

Give other users full control to modify your experiments through the "Sharing Permissions" box.

Use the "Download Files" button to save copies of the original FCS Files to your computer.

## MIFlowCyt Compliance Score for Experiment: IDCRC's HIV Natural History Study - Repository ID: FR-FCM-ZZZB

Total MIFlowCyt compliance score: 100.00%

### 1 - Experiment Overview - 100.00% provided

Items considered relatively based on importance, 30% contribution to total score.

Item	Compliance [ + - ]	Improve
Purpose	✓ Provided purpose	Fully provided
Keywords	✓ Provided keywords	Fully provided
Experiment variables	✓ Provided experiment variables	Fully provided
Organization	✓ Provided organization name Provided organization address	Fully provided
Contact	✓ First name of primary researcher provided Last name of primary researcher provided Email of primary researcher provided	Fully provided
Date	✓ Provided experiment starting date Provided experiment end date	Fully provided
Conclusions	✓ Provided conclusions	Fully provided
Quality control measures	✓ Provided quality control description	Fully provided

- The "Improve" column would show direct links to pages/forms in case some information was still missing

### 2 - Flow Sample/Specimen Details - 100.00% provided


Items considered relatively based on importance, 30% contribution to total score.

FCS file	Compliance [ + - ]	Improve
	✓ Provided sample description Provided sample source description	


# Upload and annotation of your own dataset


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- 8 Share with everyone


# Data sharing

Sharing Permissions 

Full Access Users

 [Nima Aghaeepour](#) [PR]

 [Josef Spidlen](#) [x]

 [Ryan Brinkman](#) [x]

[Invite a new user](#)

Share with a User (Full Access)

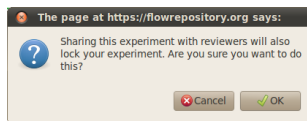
This experiment is currently **private**.

[Share with Everyone](#)

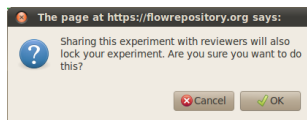
You can also **create a secret access code** to share with reviewers.

[Share with Reviewers](#)

## Share with reviewers




# Share with reviewers



Experiment was successfully updated. This experiment has been locked for reviewers' access and may be accessed via the following URL:

<https://flowrepository.org/id/RvFrFI5UsYaDgWZoVC6bxPrNUjMMcJlgxYxyXW5jXy62tFXyij1uHrxHvllL9nLL>

Please share this URL with your reviewers.

Sharing Permissions 

Full Access Users  
This experiment is currently **locked!** No users have full edit access.

This experiment is **shared with reviewers** via a [secret code](#). If your manuscript has been published already, please click [here](#) to publish this dataset and link it to the relevant journal and publication.

# What to do with the secret code?

- Share the “secret code” with the editor in your cover letter
- The editor will pass it to reviewers
- Reviewers will use it to obtain read-only access to your dataset
  - By navigating directly to <https://flowrepository.org/id/RvFrFI5UsYaDgWZ....>
  - Or entering RvFrFI5UsYaDgWZ.... in the “Query” field

Query i

Enter a term to search all publicly available experiments:

[Show query fields](#)



# What to do if editor/reviewer requires changes?

- Depending on the journal,
  - The editor may contact FlowRepository administrators and arrange for the dataset to be unlocked
  - Or, you may have to fill out a FlowRepository support ticket and ask for the dataset to be unlocked

---

[Terms of Service](#)

[Privacy Policy](#)

[Support](#)


[Feedback](#)

## Share your data - typical steps

- 1 Create a new experiment
- 2 Upload data (FCS files)
- 3 Prepare annotation templates
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  - Describe samples and sample sources
  - Provide experimental variables
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# Making the data public upon manuscript publication

- Depending on the journal,
  - The editor may contact FlowRepository administrators and arrange for the dataset to be published
  - Or, you may have to do this

▼ Sharing Permissions 

Full Access Users  
This experiment is currently **locked!** No users have full edit access.  
This experiment is **shared with reviewers** via a [secret code](#). If your manuscript has been published already, please click [here](#) to publish this dataset and link it to the relevant journal and publication.

# Making the data public upon manuscript publication

- Depending on the journal,
  - The editor may contact FlowRepository administrators and arrange for the dataset to be published
  - Or, you may have to do this

## ▾ Publish Your Experiment

Here, you can make your experiment public. Are you publishing your dataset because a related manuscript has been published? If so, please tell us which journal. Also, please tell us the manuscript identifier(s) (PubMed and/or PMC) if available already.

**PubMed ID(s):**  A comma-separated list of PubMed identifiers (optional).

**PMC ID(s):**  A comma-separated list of PMC identifiers (optional).

**Journal:**  Select a related journal if available in the list (optional).

**Other journal:**  Type in the name of a journal (optional, use only if journal isn't present in the list above).

Clicking on this button will publish the experiment and also link it to a journal or publication if specified.

### *Why two fields for journals?*

Journals that have been associated with FlowRepository experiments in the past are included in the provided list. If a journal hasn't been linked to any experiment before, please just write down the name and our administrative staff will do the rest. Specifically, we will lookup the journal, obtain its logo and URL, add it to the list, and link your experiment "properly".

### *My PubMed ID or PMC ID is not available yet, but it will be; what do I do?*

Sometimes, PubMed IDs or PMC IDs are not available right after the publication. For now, you may leave it blank and publish the experiment. Once the PubMed ID and/or PMC ID is available, you can come back and link the manuscript to your experiment.

# Summary

FlowRepository can be used to

- Access
- Review
- Download
- Deposit
- Annotate
- Share
- Analyze

flow cytometry datasets.

All you need is

- A computer with Internet connection and
- A web browser
  - With Java support if you want online analysis or de-identification

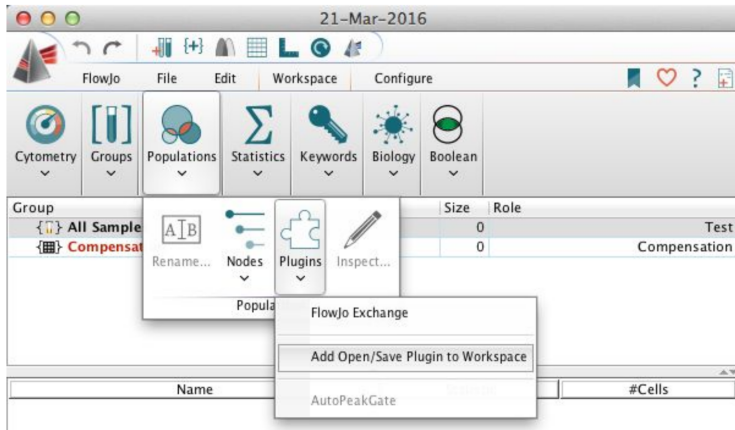
## How can other access the data you just shared?

- From their web browser by going <http://flowrepository.org>
- Directly from R
  - See <http://bioconductor.org/packages/FlowRepositoryR>

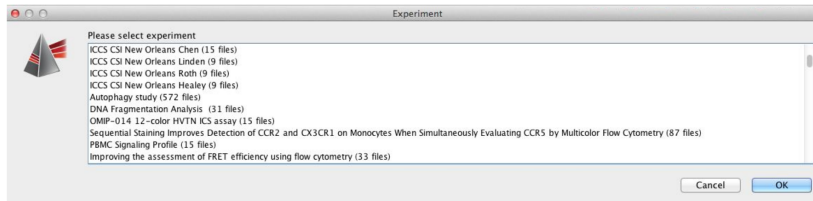
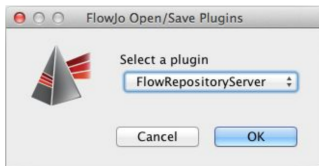
```
jspidlen@BIOINFO17L: ~
> library(FlowRepositoryR)
> flowRep.search('OMIP')
 [1] "FR-FCM-ZZ2L" "FR-FCM-ZZ2T" "FR-FCM-ZZ2V" "FR-FCM-ZZ3Z" "FR-FCM-ZZ3Y"
 [6] "FR-FCM-ZZ36" "FR-FCM-ZZ74" "FR-FCM-ZZ9H" "FR-FCM-ZZAZ" "FR-FCM-ZZEB"
[11] "FR-FCM-ZZEC" "FR-FCM-ZZWU" "FR-FCM-ZZK4" "FR-FCM-ZZNK" "FR-FCM-ZZX9"
[16] "FR-FCM-ZZQP" "FR-FCM-ZZSC"
> ds <- flowRep.get('FR-FCM-ZZAZ')
> summary(ds)
A flowRepData object (FlowRepository dataset) OMIP-022: Exemplary Data for comprehensive assessment of antigen-specific human t-cell functionality and memory
3 FCS files, 1 attachments, NOT downloaded
> ds <- download(ds)
Downloading to /home/jspidlen/FR-FCM-ZZAZ
File AFW002244_A6_A06.fcs downloaded.
File AFW002244_B6_B06.fcs downloaded.
File AFW002244_G6_G06.fcs downloaded.
File OMIPExampleData downloaded.
Download finished.
> library(flowCore)
> myFCS <- read.FCS(ds@fcs.files[[1]]@localpath)
> library(flowViz)
> plot(myFCS)
>
>
```

# How can other access the data you just shared?

- From their web browser by going <http://flowrepository.org>
- Directly from R
  - See <http://bioconductor.org/packages/FlowRepositoryR>
- From certain third-party software
  - Such as FlowJo :-)

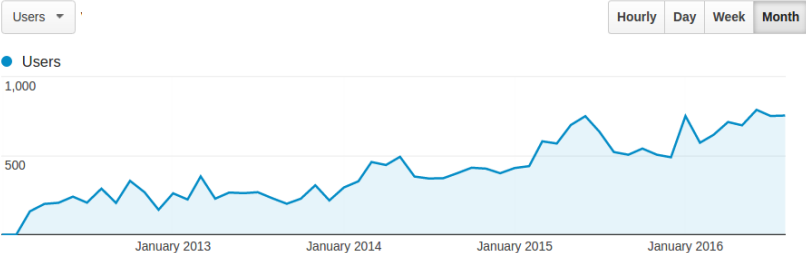


# Accessing FlowRepository data from FlowJo



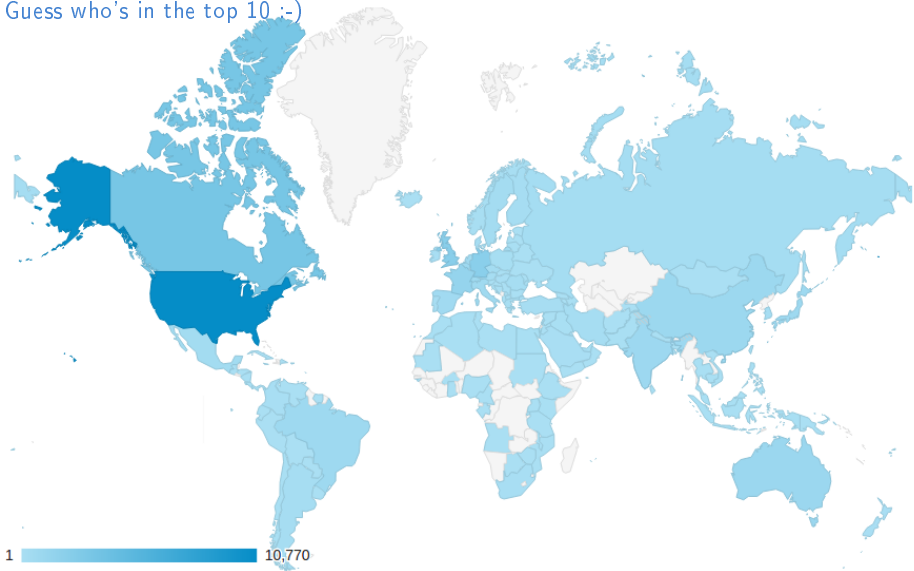


# Number of distinct users monthly



# FlowRepository Visits by Country (2012 – 2016)

Guess who's in the top 10 :-)



# FlowRepository Visits by Country (2012 – 2016)

Guess who's in the top 10 :-)

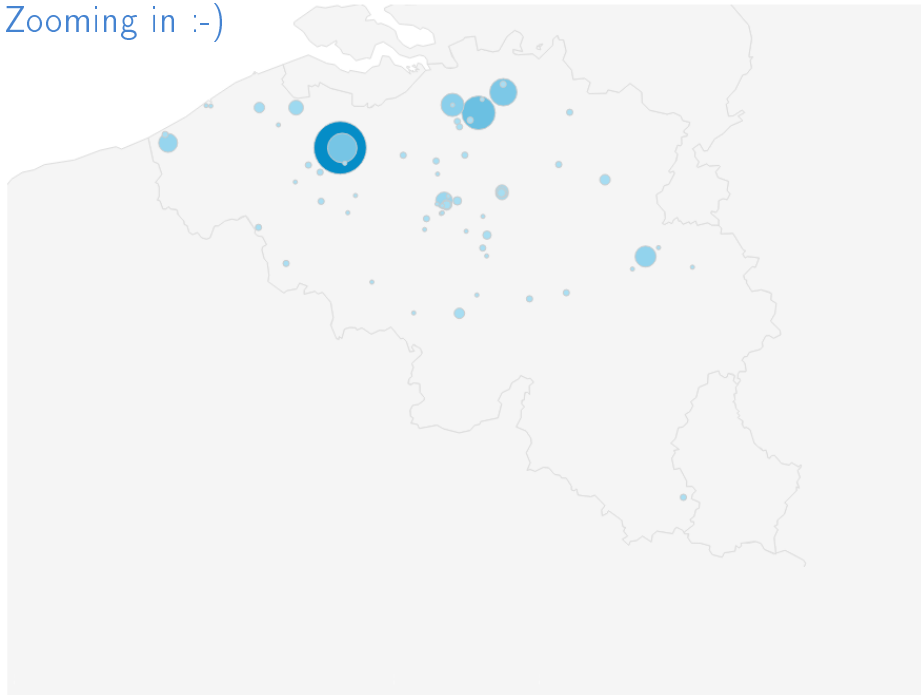
	Country	Visits
1.	United States	10,770
2.	Canada	3,316
3.	United Kingdom	2,176
4.	Germany	2,069
5.	France	1,382
6.	Australia	988
7.	China	927
8.	India	856
9.	Brazil	793
10.	<b>Belgium</b>	756

	Country	Visits
11.	Japan	756
12.	Switzerland	723
13.	Italy	664
14.	Spain	611
15.	Netherlands	539
16.	Mexico	443
17.	Czech Republic	414
18.	Sweden	409
19.	Russia	327
20.	Singapore	317

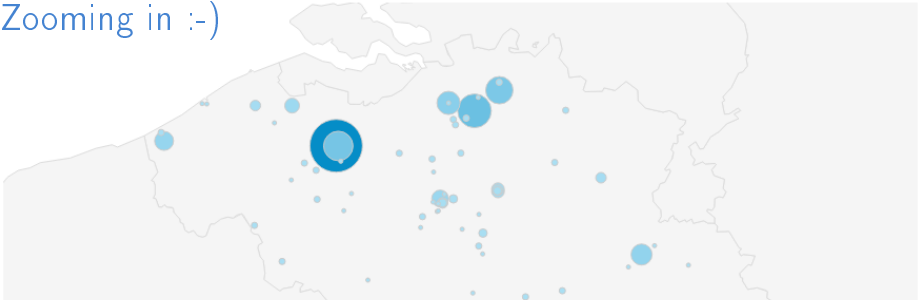
34,500 visits from 144 countries worldwide

1 10,770

Zooming in :-)



Zooming in :-)

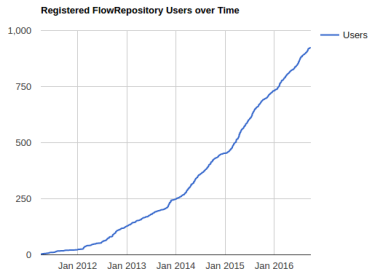


	<b>City</b>	<b>Visits</b>
1.	Ghent	296
2.	Ranst	87
3.	Zoersel	64
4.	Antwerp	45
5.	Leuven	36
6.	Liege	33
7.	Veurne	28
8.	Brussels	23
9.	Maldegem	18
10.	Ixelles	14

	<b>City</b>	<b>Visits</b>
11.	Hasselt	8
12.	Bruges	8
13.	Charleroi	7
14.	Woluwe-Saint-Lambert	4
15.	Wavre	4
16.	Boechout	3
17.	Malle	3
18.	Dendermonde	3
19.	Nazareth	3
20.	Oudenaarde	3

## Some more stats... (as of September 2016)

- 927 Registered users
- 709 Datasets
  - 349 of these public
- 84,853 FCS files (640 GB)
- 20,346 dataset downloads



Please share your data.

## Additional resources

- Spidlen J, Breuer K and Brinkman RR. Preparing a Minimum Information about a Flow Cytometry Experiment (MIFlowCyt) Compliant Manuscript Using the International Society for Advancement of Cytometry (ISAC) FCS File Repository (FlowRepository.org). *Curr Protoc Cytom.* 2012 Jul; Chapter 10: Unit 10.18.
- Spidlen J, Breuer K, Rosenberg C, Kotecha N and Brinkman RR. FlowRepository – A Resource of Annotated Flow Cytometry Datasets Associated with Peer-reviewed Publications. *Cytometry A.* 2012 Sep;81(9):727-31
- Spidlen J and Brinkman RR. Use FlowRepository to share your clinical data upon study publication. *Cytometry B Clin Cytom.* 2016 Jun; doi: 10.1002/cyto.b.21393. [Epub ahead of print]
- FlowRepository quick start guide:  
[https://flowrepository.org/quick\\_start\\_guide](https://flowrepository.org/quick_start_guide)

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**NIH NIAID VRC** Mario Roederer

**Cytometry A** Attila Tárnok

**Wiley** Larry Graup

**ISAC** Michelle Butler

**ISAC**

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**Terry Fox Research Institute**

**Wallace H. Coulter Foundation**

**Michael Smith Foundation for Health Research**