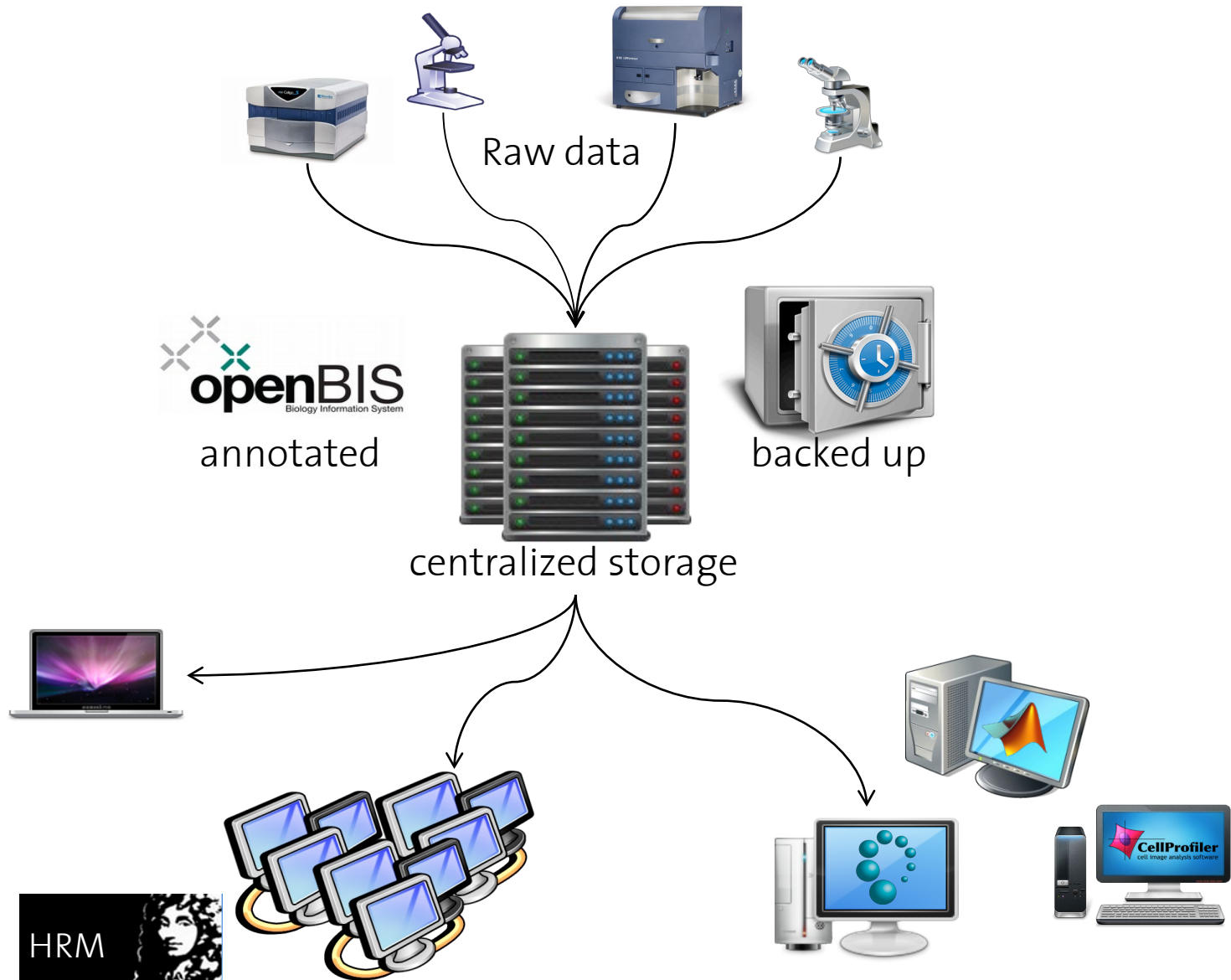


# Streamlined data management of shared laboratory resources with the openBIS Importer Toolset

<https://obit.ethz.ch/>

Aaron Ponti ([aaron.ponti@bsse.ethz.ch](mailto:aaron.ponti@bsse.ethz.ch)), Single Cell Facility, D-BSSE, ETH Zurich





# openBIS – open Biology Information System

openBIS is an **extensible, open source** software **framework** for **constructing** user-friendly, scalable and powerful **information systems** for **data** and **metadata** acquired in biological experiments.

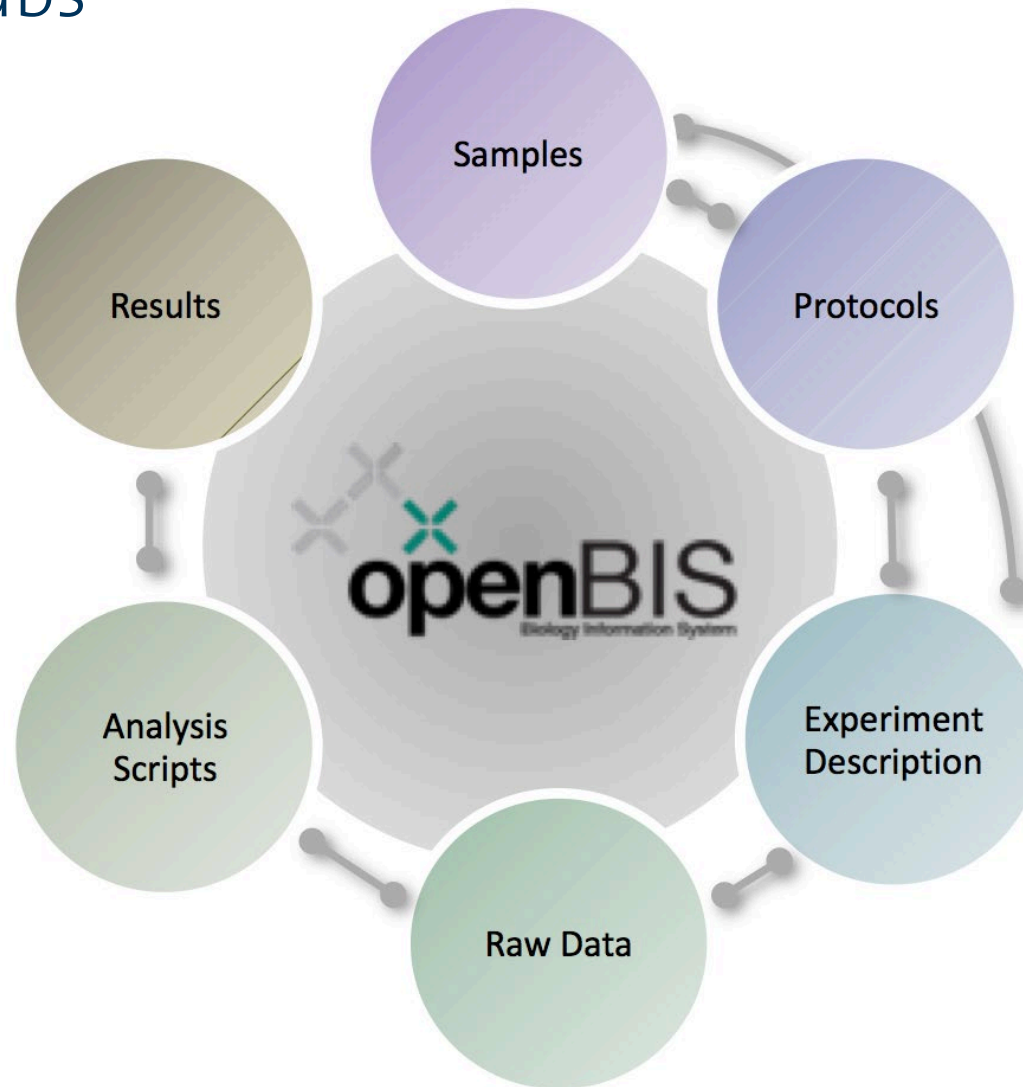
It enables users to **collect, integrate, share, publish data** and to **connect to data processing pipelines**.

<https://sis.id.ethz.ch/software/openbis.html>





# openBIS in labs



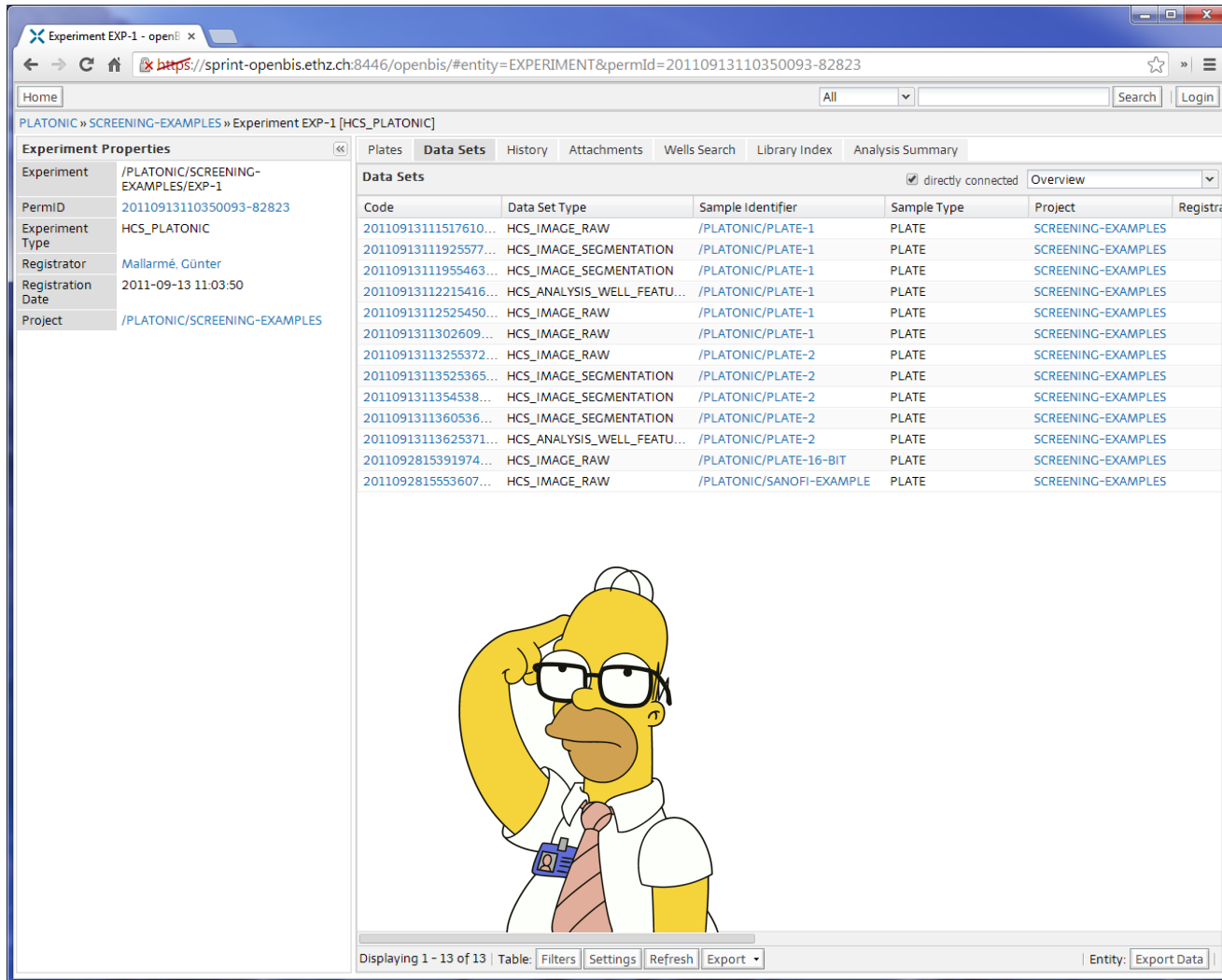
# openBIS core

- Separate metadata ([application server](#)) and data ([data store server](#))
- Clean and flexible hierarchical metadata structure:
  - [Space](#) > [Project](#) > [Experiment](#) > [Sample](#) > [Dataset](#) > [File](#)
  - Authorization at space level
  - Samples and datasets: entities have parent/child or container/contained relationships
  - Datasets belong to samples or experiments
  - All entities have user defined [types](#), [properties](#) and [vocabularies](#)
  - [Attachments](#) can be associated to most entities
- Information indexing and searching by metadata
- Rich set of [APIs](#) and [plug-in](#) interfaces
  - Java, Python, Jython, **JSON RPC services**

# openBIS extensions

- **Core plug-ins**
  - Dropboxes (dataset ingestion)
  - Master data (import/export/update)
  - Data sources (additional databases)
  - Aggregation (reporting) plug-ins (metadata collection)
  - Processing plug-ins (on datasets)
  - Ingestion plug-ins (create/update entities)
  - Maintenance tasks (update/fix)
  - Web applications / **JSON RPC services** (custom openBIS views)
- An organized set of core plug-ins can become a “**core technology**”
- Core plug-ins extend openBIS APIs to interface with custom client apps

# openBIS “vanilla”



The screenshot displays the openBIS web interface for an experiment. The browser address bar shows the URL: `https://sprint-openbis.ethz.ch:8446/openbis/#entity=EXPERIMENT&permId=20110913110350093-82823`. The page title is "Experiment EXP-1 [HCS\_PLATONIC]".

**Experiment Properties**

Experiment	/PLATONIC/SCREENING-EXAMPLES/EXP-1
PermID	20110913110350093-82823
Experiment Type	HCS_PLATONIC
Registrar	Mallarmé, Günter
Registration Date	2011-09-13 11:03:50
Project	/PLATONIC/SCREENING-EXAMPLES

**Data Sets**

Code	Data Set Type	Sample Identifier	Sample Type	Project	Registration Date
20110913111517610...	HCS_IMAGE_RAW	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
20110913111925577...	HCS_IMAGE_SEGMENTATION	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
20110913111955463...	HCS_IMAGE_SEGMENTATION	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
20110913112215416...	HCS_ANALYSIS_WELL_FEATU...	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
20110913112525450...	HCS_IMAGE_RAW	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
2011091311302609...	HCS_IMAGE_RAW	/PLATONIC/PLATE-1	PLATE	SCREENING-EXAMPLES	
20110913113255372...	HCS_IMAGE_RAW	/PLATONIC/PLATE-2	PLATE	SCREENING-EXAMPLES	
20110913113525365...	HCS_IMAGE_SEGMENTATION	/PLATONIC/PLATE-2	PLATE	SCREENING-EXAMPLES	
2011091311354538...	HCS_IMAGE_SEGMENTATION	/PLATONIC/PLATE-2	PLATE	SCREENING-EXAMPLES	
2011091311360536...	HCS_IMAGE_SEGMENTATION	/PLATONIC/PLATE-2	PLATE	SCREENING-EXAMPLES	
20110913113625371...	HCS_ANALYSIS_WELL_FEATU...	/PLATONIC/PLATE-2	PLATE	SCREENING-EXAMPLES	
2011092815391974...	HCS_IMAGE_RAW	/PLATONIC/PLATE-16-BIT	PLATE	SCREENING-EXAMPLES	
2011092815553607...	HCS_IMAGE_RAW	/PLATONIC/SANOFI-EXAMPLE	PLATE	SCREENING-EXAMPLES	

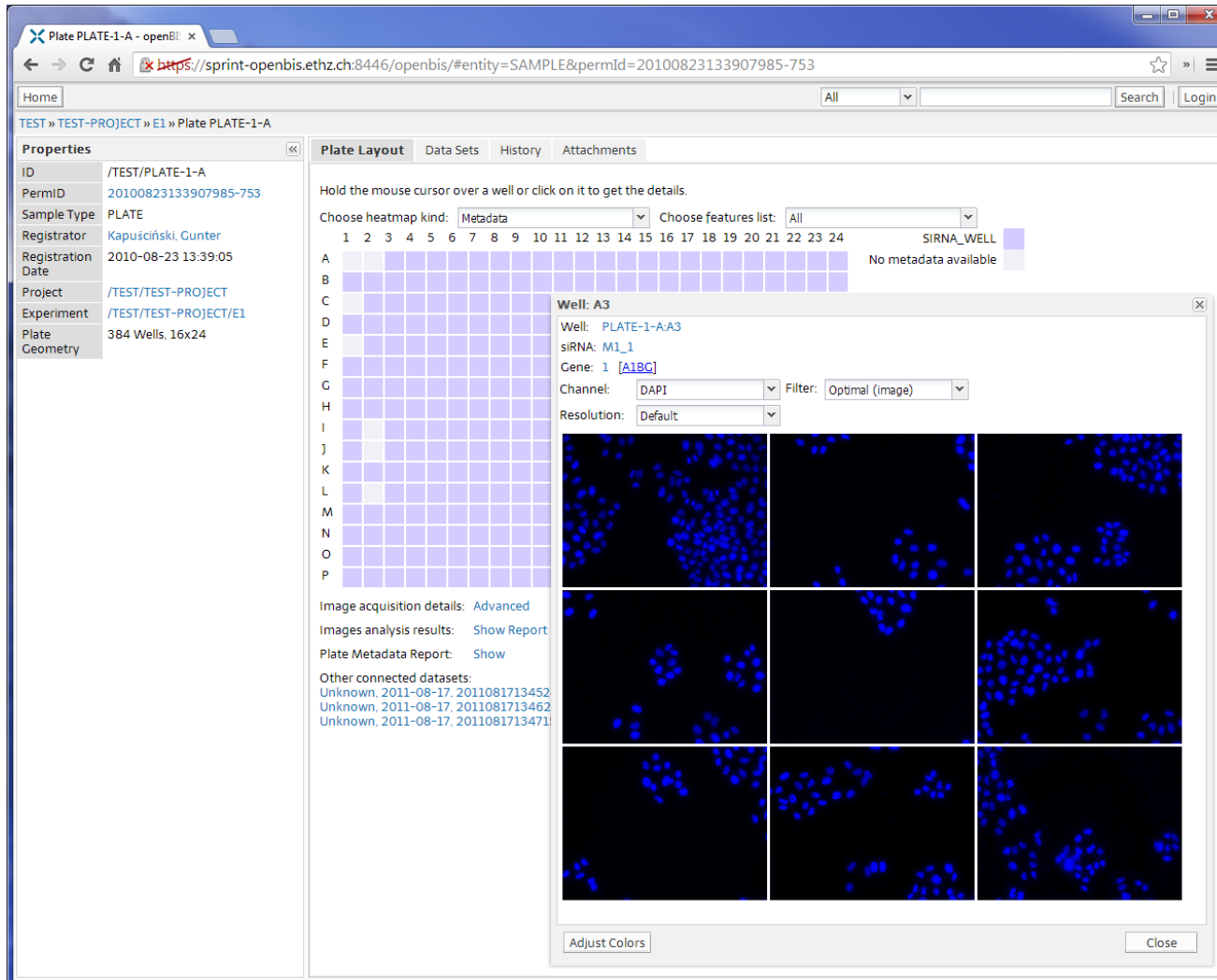
At the bottom of the interface, there is a cartoon image of Homer Simpson thinking, and a status bar indicating "Displaying 1 - 13 of 13" and "Export Data".

# Current technologies





# Screening core technology



The screenshot shows a web browser window displaying the OpenBIS interface for a plate named 'PLATE-1-A'. The browser address bar shows the URL: `https://sprint-openbis.ethz.ch:8446/openbis/#entity=SAMPLE&permId=20100823133907985-753`. The interface includes a navigation menu with 'Home', 'Search', and 'Login'. The main content area is divided into a 'Properties' sidebar and a 'Plate Layout' main panel.

**Properties sidebar:**

- ID: /TEST/PLATE-1-A
- PermID: 20100823133907985-753
- Sample Type: PLATE
- Registrar: Kapuściński, Gunter
- Registration Date: 2010-08-23 13:39:05
- Project: /TEST/TEST-PROJECT
- Experiment: /TEST/TEST-PROJECT/E1
- Plate Geometry: 384 Wells, 16x24

**Plate Layout:**

Hold the mouse cursor over a well or click on it to get the details.

Choose heatmap kind: Metadata | Choose features list: All

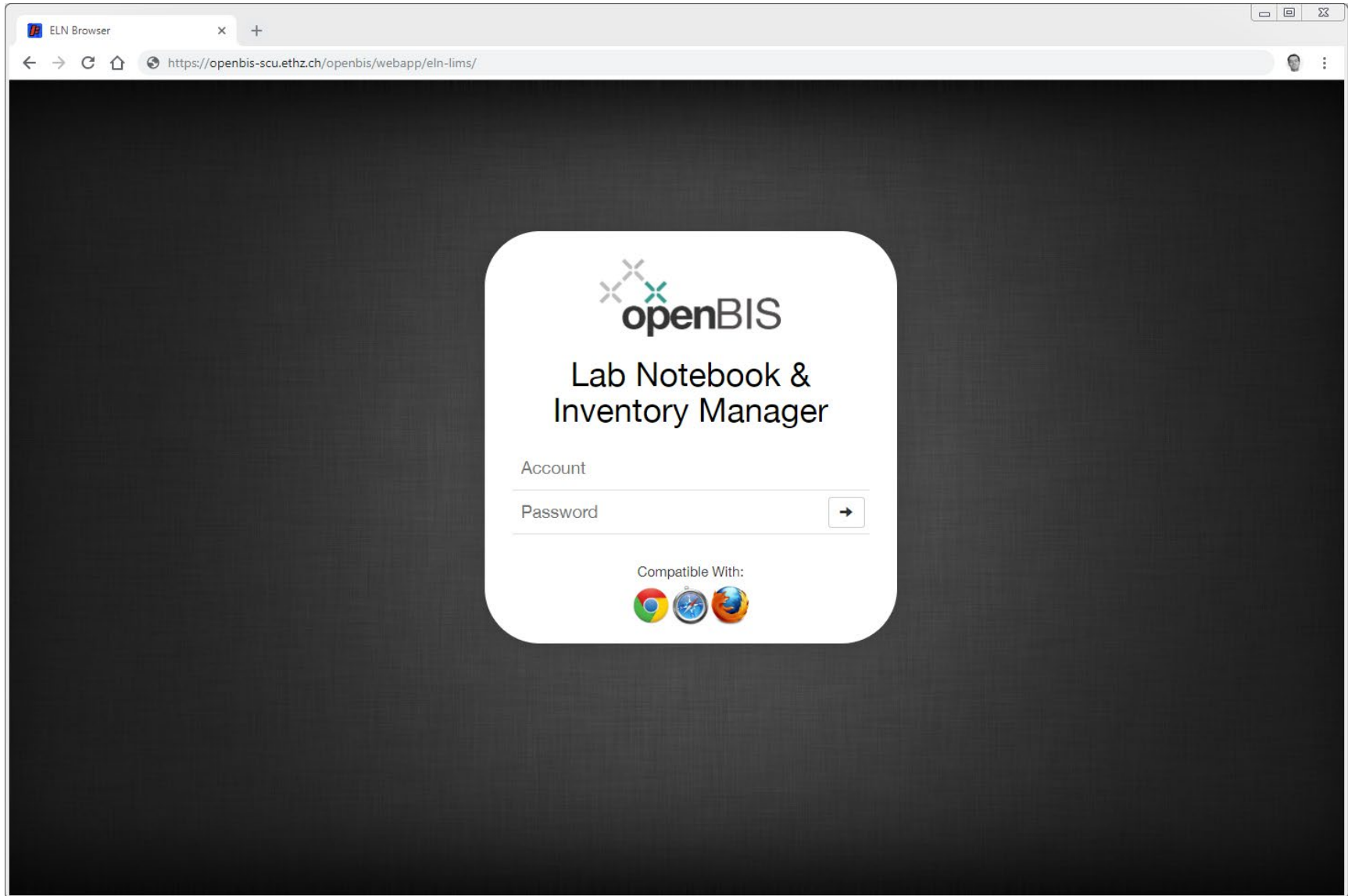
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 SIRNA\_WELL

A B C D E F G H I J K L M N O P

**Well: A3 details:**


- Well: PLATE-1-A.A3
- siRNA: M1\_1
- Gene: 1 [A|B|C]
- Channel: DAPI | Filter: Optimal (image)
- Resolution: Default

The well details panel displays a 3x3 grid of fluorescence microscopy images showing blue-stained cells. Below the images are buttons for 'Adjust Colors' and 'Close'. Additional links for 'Image acquisition details', 'Images analysis results', and 'Plate Metadata Report' are visible in the main panel.



ELN Browser x +

https://openbis-scu.ethz.ch/openbis/webapp/elc-lims/


  
**openBIS**

Lab Notebook &  
Inventory Manager

Account

Password

Compatible With:



# Custom web apps

Sample WB\_LEXA-ER-B112
Aaron

https://openbis-eln-lims.ethz.ch/openbis/webapp/eln-lims/?menuUniqueId=20150529105634255-266&viewName=showViewSamplePageFromPermlD&viewData=20150127162826183-170

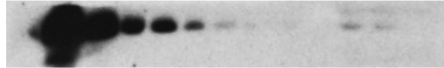
Search

- Lab Notebook
  - Diana Ottoz
    - Inducible Transcription Factor
      - Induction of the transcription factor in stan...
        - Detection of LexA-ER-B42 induction by
          - Detection of LexA-ER-B42 induction by
            - Detection of LexA-ER-B112 induction b**
              - 20150411133713019-242
              - 20150529105634255-266
            - Analysis of the abundance of the four varia...
              - Detection of LexA-ER-AD levels by west
                - 20150323152420797-202

- Inventory
- Utilities
- About


## Sample: Detection of LexA-ER-B112 induction by western blotting

/DIANA\_OTTOZ/INDUCIBLE\_TRANSCRIPTION\_FACTOR/INDUCTION\_OF\_TF/WB\_LEXA-ER-B112



- RAW\_DATA : 20150411133713019-242
  - original
  - WB\_LEXA-ER-B112-raw
- ELN\_PREVIEW : 20150529105634255-266
  - original
  - WB\_LEXA-ER-B112-citrine.png (398.3Kb)

**Files Uploader**



Auto upload on drop

**General**

**Name:** Detection of LexA-ER-B112 induction by western blotting

**Owner:** Diana Ottoz

**Experimental goals:** Analyze the full induction of LexA-ER-B112 on western blot by doing a dilution series.

**Experimental results:** LexA-ER-B112 full fold induction is between 200 and 400.

**Parents**

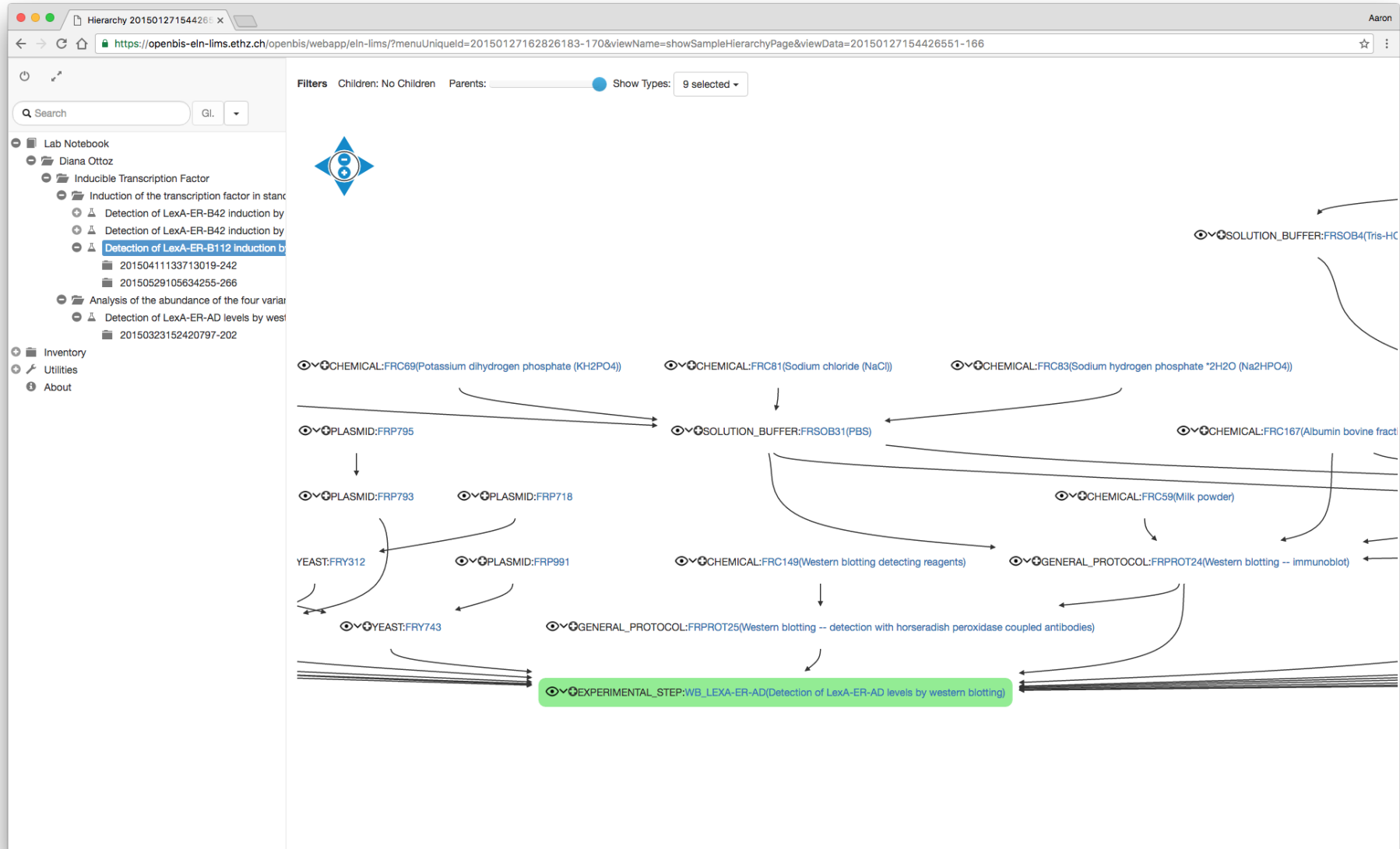
Annotation :: Comments	Experiment
SDC at 25°C	/MATERIALS/REAGENTS/MEDIA_COLLECTION
2000 nM for 24 hours	/MATERIALS/REAGENTS/SOLUTION_BUFFER_COLLECTION
empty	/MATERIALS/YEASTS/YEAST_COLLECTION_1
target	/MATERIALS/YEASTS/YEAST_COLLECTION_1
LexA-ER-B112 + target	/MATERIALS/YEASTS/YEAST_COLLECTION_1
OD normalized to 4.6; 20 µl of extract loaded on gel	/METHODS/PROTOCOLS/GENERAL_PROTOCOLS
10% gel, 1.5 mm thick	/METHODS/PROTOCOLS/GENERAL_PROTOCOLS
1 hour 20 minutes at 105 mA constant	/METHODS/PROTOCOLS/GENERAL_PROTOCOLS
blocked overnight at 4°C in PBS-T + 5% milk	/METHODS/PROTOCOLS/GENERAL_PROTOCOLS
anti-Citrine exposed for 1 hour	/METHODS/PROTOCOLS/GENERAL_PROTOCOLS
for 1 hour at room temperature	/METHODS/PROTOCOLS/WESTERN_BLOTTING_PROTOCOLS
for 1 hour at room temperature	/METHODS/PROTOCOLS/WESTERN_BLOTTING_PROTOCOLS

1 - 12 of 12 items    20 Per Page    Page 1 of 1

**Children**

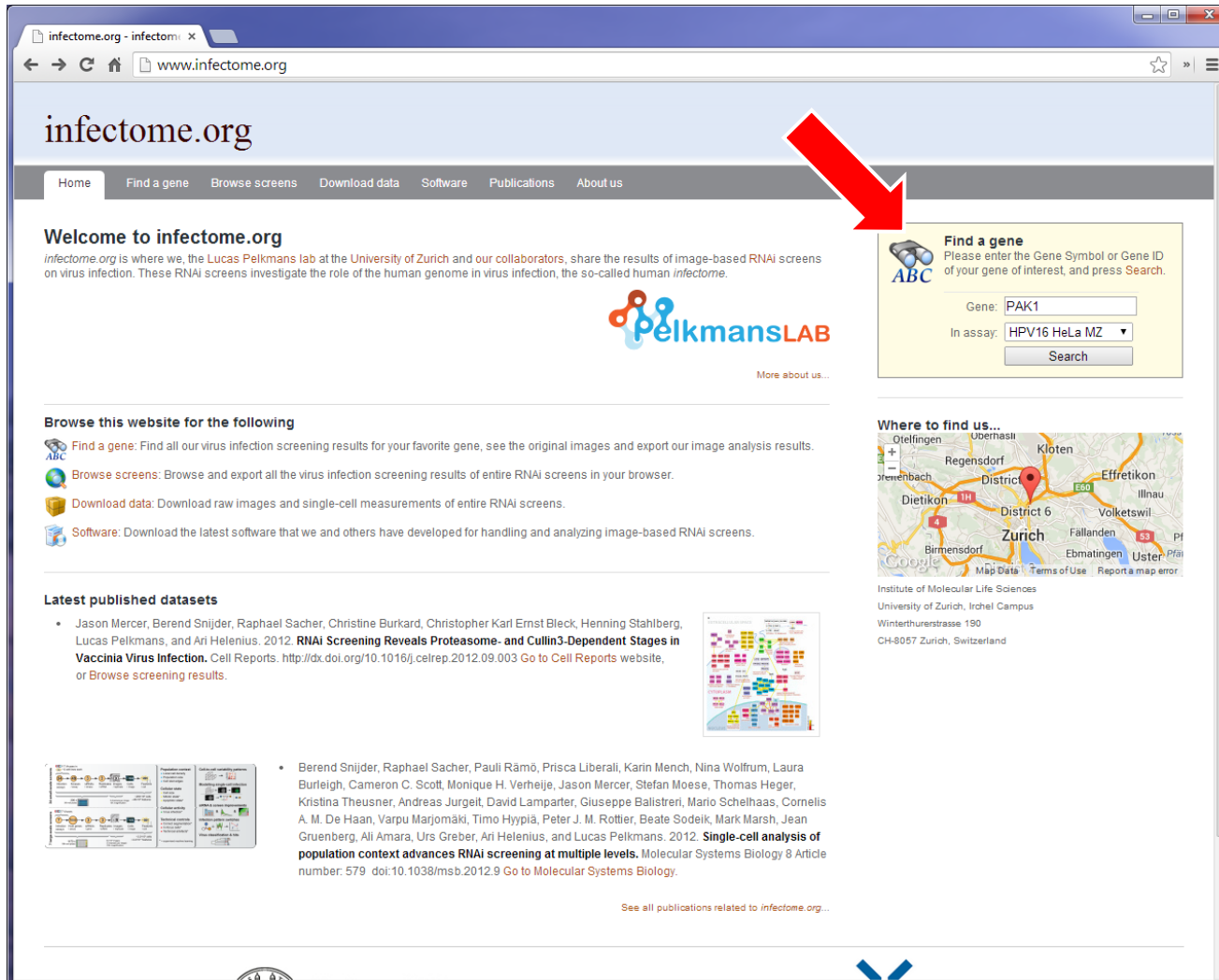
**Readout details**

# Custom web apps



The screenshot shows a web application interface with a sidebar on the left and a main content area on the right. The sidebar contains a 'Lab Notebook' section with a tree view of folders and files, including 'Inducible Transcription Factor' and 'Detection of LexA-ER-B112 induction by...'. Below the sidebar is an 'Inventory' section with 'Utilities' and 'About' links. The main content area features a search bar, filters, and a network diagram. The diagram consists of nodes representing various entities, such as 'CHEMICAL:FRC69(Potassium dihydrogen phosphate (KH2PO4))', 'PLASMID:FRP795', 'YEAST:FRY312', and 'EXPERIMENTAL\_STEP:WB\_LEXA-ER-AD(Detection of LexA-ER-AD levels by western blotting)'. The nodes are connected by arrows, indicating relationships or dependencies. The 'EXPERIMENTAL\_STEP' node is highlighted in green. The URL in the browser address bar is <https://openbis-eln-lims.ethz.ch/openbis/webapp/eln-lims/?menuUniqueId=20150127162826183-170&viewName=showSampleHierarchyPage&viewData=20150127154426551-166>.

# Embedded openBIS




infectome.org - infectome.org x

www.infectome.org

infectome.org

Home Find a gene Browse screens Download data Software Publications About us

**Welcome to infectome.org**  
infectome.org is where we, the **Lucas Pelkmans lab** at the University of Zurich and our collaborators, share the results of image-based RNAi screens on virus infection. These RNAi screens investigate the role of the human genome in virus infection, the so-called human *infectome*.




[More about us...](#)

**Find a gene**  
Please enter the Gene Symbol or Gene ID of your gene of interest, and press Search.

Gene:





In assay:

**Where to find us...**




Institute of Molecular Life Sciences  
University of Zurich, Irchel Campus  
Winterthurerstrasse 190  
CH-8057 Zurich, Switzerland

**Browse this website for the following**

-  **Find a gene:** Find all our virus infection screening results for your favorite gene, see the original images and export our image analysis results.
-  **Browse screens:** Browse and export all the virus infection screening results of entire RNAi screens in your browser.
-  **Download data:** Download raw images and single-cell measurements of entire RNAi screens.
-  **Software:** Download the latest software that we and others have developed for handling and analyzing image-based RNAi screens.

**Latest published datasets**

- Jason Mercer, Berend Snijder, Raphael Sacher, Christine Burkard, Christopher Karl Ernst Bleck, Henning Stahlberg, Lucas Pelkmans, and Ari Helenius. 2012. **RNAi Screening Reveals Proteasome- and Cullin3-Dependent Stages in Vaccinia Virus Infection.** Cell Reports. <http://dx.doi.org/10.1016/j.celrep.2012.09.003> Go to Cell Reports website, or [Browse screening results](#).
- 
- Berend Snijder, Raphael Sacher, Pauli Rämö, Prisca Liberali, Karin Mench, Nina Wolfrum, Laura Burteligh, Cameron C. Scott, Monique H. Verheije, Jason Mercer, Stefan Moese, Thomas Heger, Kristina Theusner, Andreas Jurgeit, David Lamparter, Giuseppe Balistreni, Mario Schelhaas, Cornelis A. M. De Haan, Varpu Marjomäki, Timo Hyypä, Peter J. M. Rottier, Beate Sodeik, Mark Marsh, Jean Gruenberg, Ali Amara, Urs Greber, Ari Helenius, and Lucas Pelkmans. 2012. **Single-cell analysis of population context advances RNAi screening at multiple levels.** Molecular Systems Biology 8 Article number: 579 doi:10.1038/msb.2012.9 Go to [Molecular Systems Biology](#).

[See all publications related to infectome.org...](#)



# Embedded openBIS

infectome.org - gene find x

www.infectome.org/find-a-gene.html?gene=PAK1&assay=20100702164638321-131297&go=now

infectome.org

Home Find a gene Browse screens Download data Software Publications About us

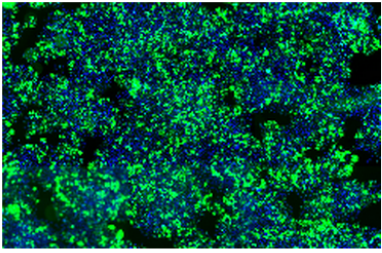
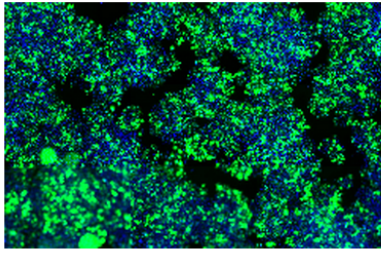
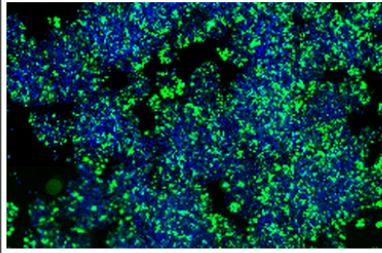
Gene PAK1 in experiment HPV16\_MZ\_2 [Find gene PAK1 in all experiments](#) [Show experiment HPV16\\_MZ\\_2](#)

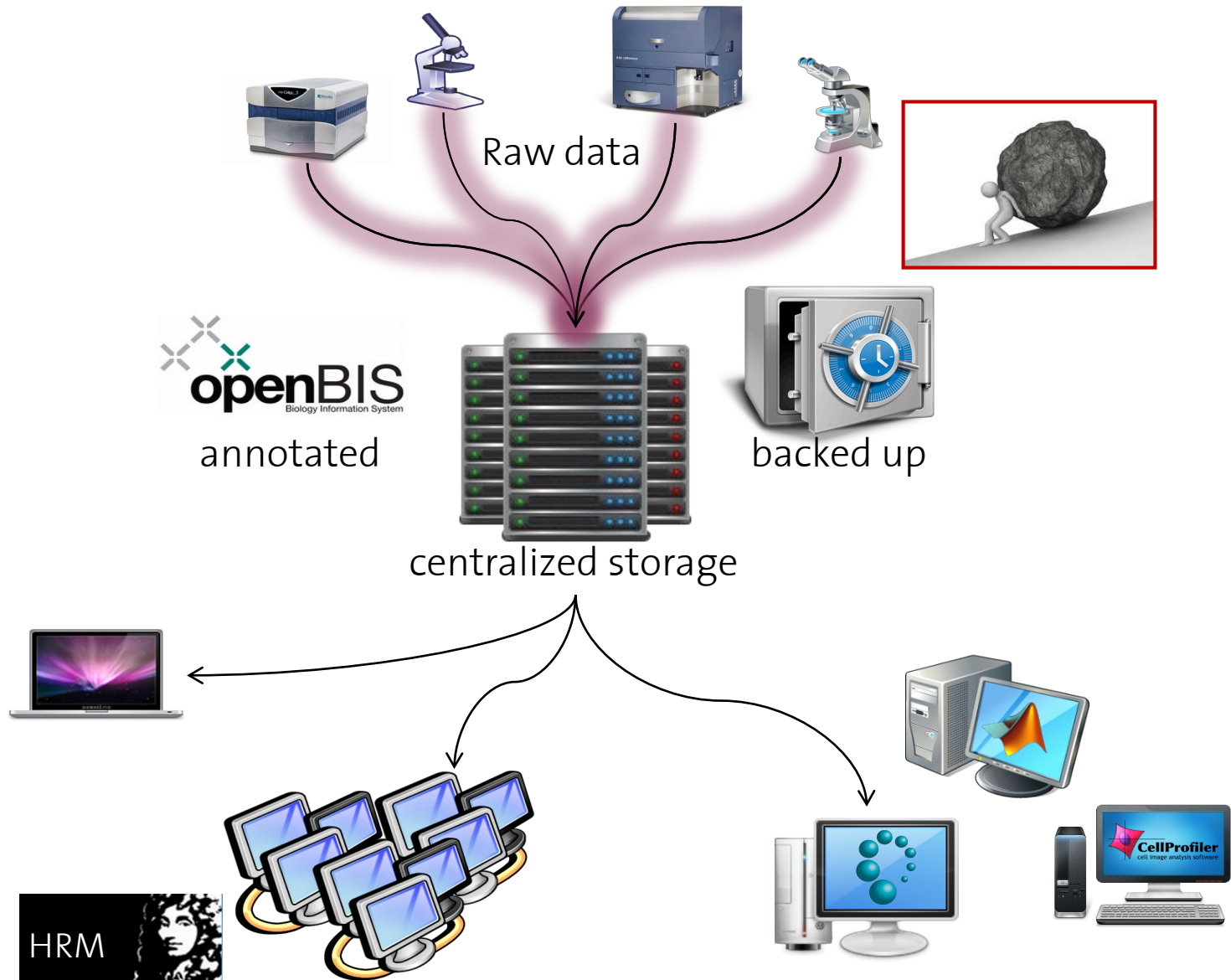
Description: -  
Gene Cards: [Show](#)  
Id: 5058

Feature	Median	Deviation	Rank (50)	siRNA 1 median	siRNA 1 repl. 1	siRNA 1 repl. 2	siRNA 1 repl. 3
Cell Number	10401.0000	1281.0000	44	11542.0000	11542.0000	9349.0000	11682.0000
InfectedCells	1934.0000	1470.0000	39	1934.0000	1409.0000	3688.0000	1934.0000
Infection Index (nor...	0.1656	0.1144	27	0.1656	0.1221	0.3945	0.1656
RelativeInfectionIndex	0.9113	0.4917	22	1.4169	1.4030	3.2163	1.4169
Log2RelativeInfectio...	-0.1340	0.6225	22	0.5027	0.4885	1.6854	0.5027
ZScore	-0.0488	0.5031	17	0.8806	NaN	1.3069	0.4544
MAD	-0.1467	0.6056	23	0.5460	0.5460	1.6724	0.4589
Mean_Cells_Intensit...	0.0467	0.0040	34	0.0893	0.0428	0.0893	0.0921
Mean_Cells_Intensit...	0.0248	0.0038	31	0.0258	0.0258	0.0381	0.0211
Mean_Image_Intens...	0.0198	0.0049	33	0.0233	0.0233	0.0344	0.0196
Mean_Nuclei_BinCor...	0.3268	0.0270	17	0.3302	0.4363	0.3302	0.3241
Mean_Nuclei_Intensi...	0.0800	0.0214	24	0.1425	0.0638	0.1425	0.1531
Mean_Nuclei_Intensi...	0.0269	0.0031	25	0.0286	0.0286	0.0454	0.0241
ModelRawII	0.2248	0.1421	17	0.4539	0.3669	0.5378	0.4539
ModelRawInfected	1833.0000	1637.0000	32	4422.0000	3747.0000	4422.0000	4767.0000

Displaying 1 - 48 of 48 | Table: [Filters](#) [Export](#)

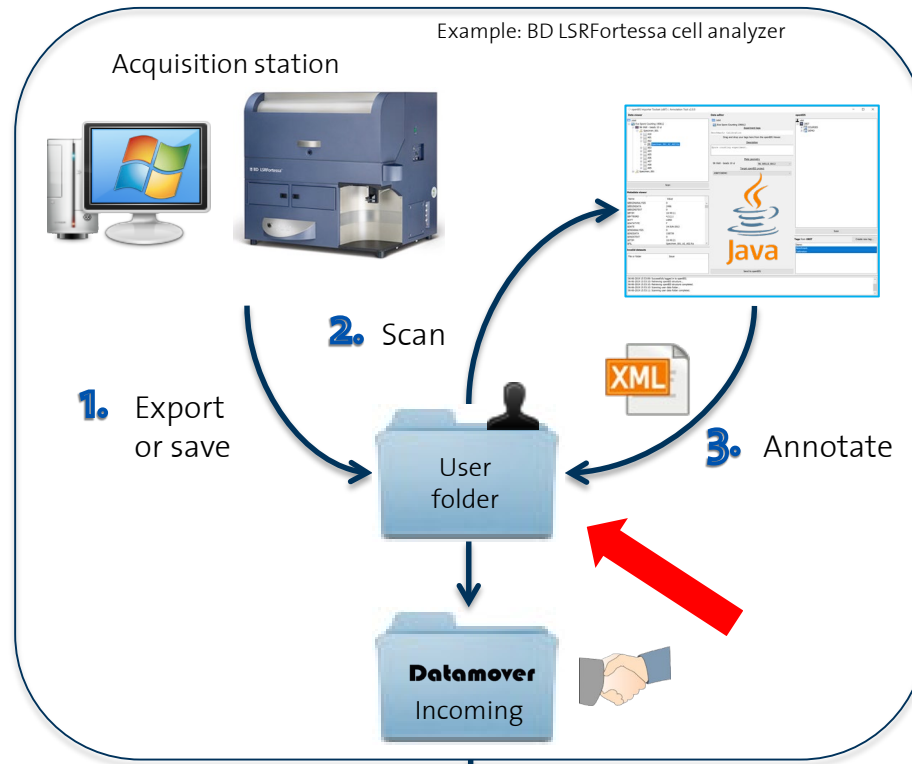
Merged Channels:  DAPI  VIRUS-INFECTION

	repl. 1	repl. 2	repl. 3
siRNA 1			

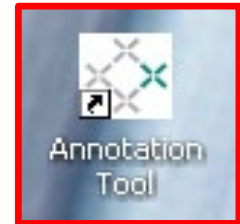


## oBIT – openBIS Importer Toolset

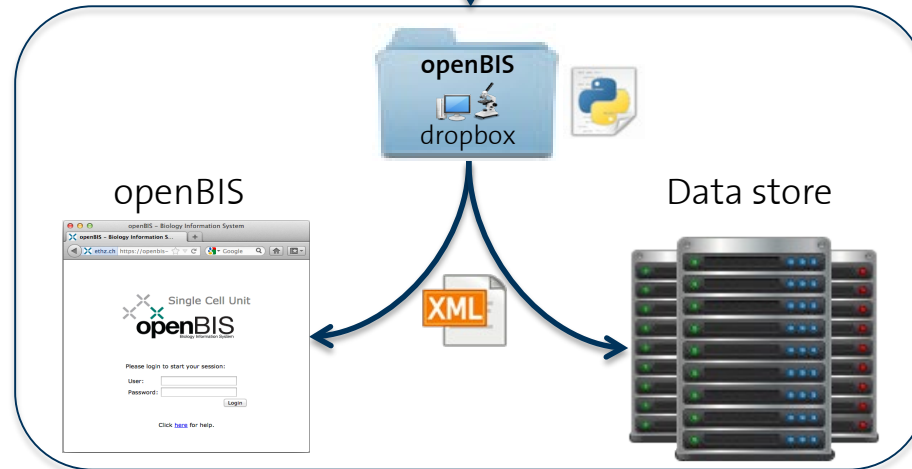
- The **openBIS Importer Toolset** is a tightly integrated collection of tools that allows for the semi-automated, semi-supervised registration of annotated datasets into openBIS directly from the acquisition stations.
- It also extends openBIS with custom data viewers and server-side core plug-ins packaged into two new core technologies (flow cytometry and microscopy).



Annotation Tool



**Datamover** as a Windows service



# Supported hardware

## ■ Flow cytometry

- BD LSR Fortessa
- BD FACS Aria III
- BD Influx
- Bio-Rad S3e Cell Sorter
- BC MOFLO XDP Sorter

Flow Cytometry Core Technology

## ■ Microscopy

- All microscopes with native formats (ND2, LIF, CZI, ...)
- **YouSCOPE** acquisitions
- Generic TIFF series



Microscopy Core Technology



# Supported software

- Flow cytometry
    - BD FACS DIVA 6.x, 7.x, 8.x
    - BD Software 1.x
    - ProSort 1.x
    - Summit 1.x
    - FCS 3.0, 3.1
  - Microscopy
    - bio-formats 5.9.2
    - custom readers
- Flow Cytometry Core Technology
- Microscopy Core Technology
- openBIS 16.05.x (oBIT < 1.0), 18.06.x (oBIT 1.1), 19.06.x (oBIT 2.0)
    - ELN-LIMS plug-in integration (oBIT 2.0)

# oBIT configuration

oBIT for the facility administrator.

# Annotation Tool :: Admin

openBIS Importer Toolset (oBIT) :: Annotation Tool Admin v2.0.0 ✕

Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

- Set the openBIS URL (this is current default)

▼ ... + - ▲ ▼

- Accept self-signed SSL certificates when logging in to openBIS

▼

- Select the acquisition station or type

▼

Light microscopes (Open Microscopy Environment Bio-Formats compatible)

- User-friendly machine name

For reference, the machine host name is DESKTOP-9G6EK7E.

- Set user data directory

- Set Datamover incoming directory

It is **highly recommended** to set both folders on the same file system.

# Annotation Tool :: Admin



openBIS Importer Toolset (oBIT) :: Annotation Tool Admin v2.0.0

Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

- Set the openBIS URL (this is current default)

https://openbis-scu.ethz.ch/openbis

https://openbis-scu.ethz.ch/openbis

https://bs-openbis05-dev.ethz.ch/openbis

no

- Select the acquisition station or type

Microscopy

Light microscopes (Open Microscopy Environment Bio-Formats compatible)

- User-friendly machine name

DEVEL

For reference, the machine host name is DESKTOP-9G6EK7E.

- Set user data directory

E:\toOpenBIS

- Set Datamover incoming directory

E:\Datamover\incoming

It is **highly recommended** to set both folders on the same file system.

Save Close

# Annotation Tool :: Admin

openBIS Importer Toolset (oBIT) :: Annotation Tool Admin v2.0.0

Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

- Set the openBIS URL (this is current default)

https://openbis-scu.ethz.ch/openbis

- Accept self-signed SSL certificates when logging in to openBIS

no

- Select the acquisition station or type

Microscopy

Flow cytometry

Microscopy

- User-friendly machine name

DEVEL

For reference, the machine host name is DESKTOP-9G6EK7E.

- Set user data directory

E:\toOpenBIS

- Set Datamover incoming directory

E:\Datamover\incoming

It is **highly recommended** to set both folders on the same file system.

Save Close





# Annotation Tool :: Admin

openBIS Importer Toolset (oBIT) :: Annotation Tool Admin v2.0.0

Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

- Set the openBIS URL (this is current default)

https://openbis-scu.ethz.ch/openbis

- Accept self-signed SSL certificates when logging in to openBIS

no

- Select the acquisition station or type

Microscopy

Light microscopes (Open Microscopy Environment Bio-Formats compatible)

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DEVEL

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Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

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Microscopy

Light microscopes (Open Microscopy Environment Bio-Formats compatible)

- User-friendly machine name

DEVEL

For reference, the machine host name is DESKTOP-9G6EK7E.

- Set user data directory

E:\toOpenBIS

- Set Datamover incoming directory

E:\Datamover\incoming

It is **highly recommended** to set both folders on the same file system.

Save Close



# oBIT workflows

oBIT from the user perspective.

# BD BioSciences Cell Analyzers and Sorters

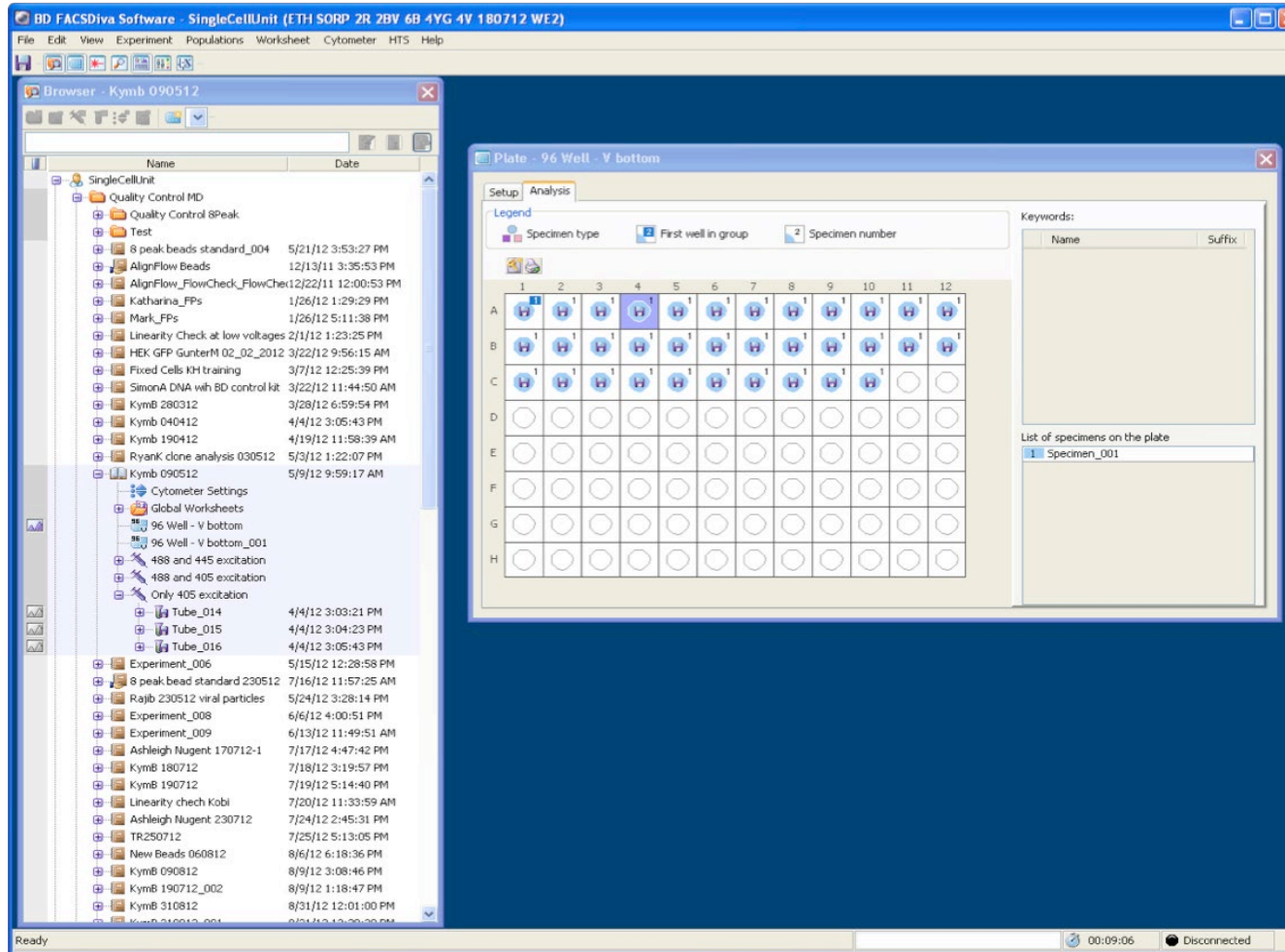
 **BD** LSRFortessa cell analyzer



<http://www.bdbiosciences.com/instruments/lsr/index.jsp>

# BD LSRFortessa cell analyzer


Export to  
user folder



The screenshot shows the BD FACSDiva software interface. On the left, a 'Browser' window displays a tree view of files and folders under 'SingleCellUnit'. The 'Kymb 090512' folder is selected. On the right, a 'Plate' window shows a 96-well plate layout. The 'Setup' tab is active, and the 'Analysis' section shows a legend with 'Specimen type', 'First well in group', and 'Specimen number'. The plate layout shows a grid of wells with icons representing specimens. The 'Keywords' section on the right lists 'Specimen\_001'.







**openBIS**  
Biology Information System


Version 2.0.0 (Java 11). Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

User name

Password

Login

×



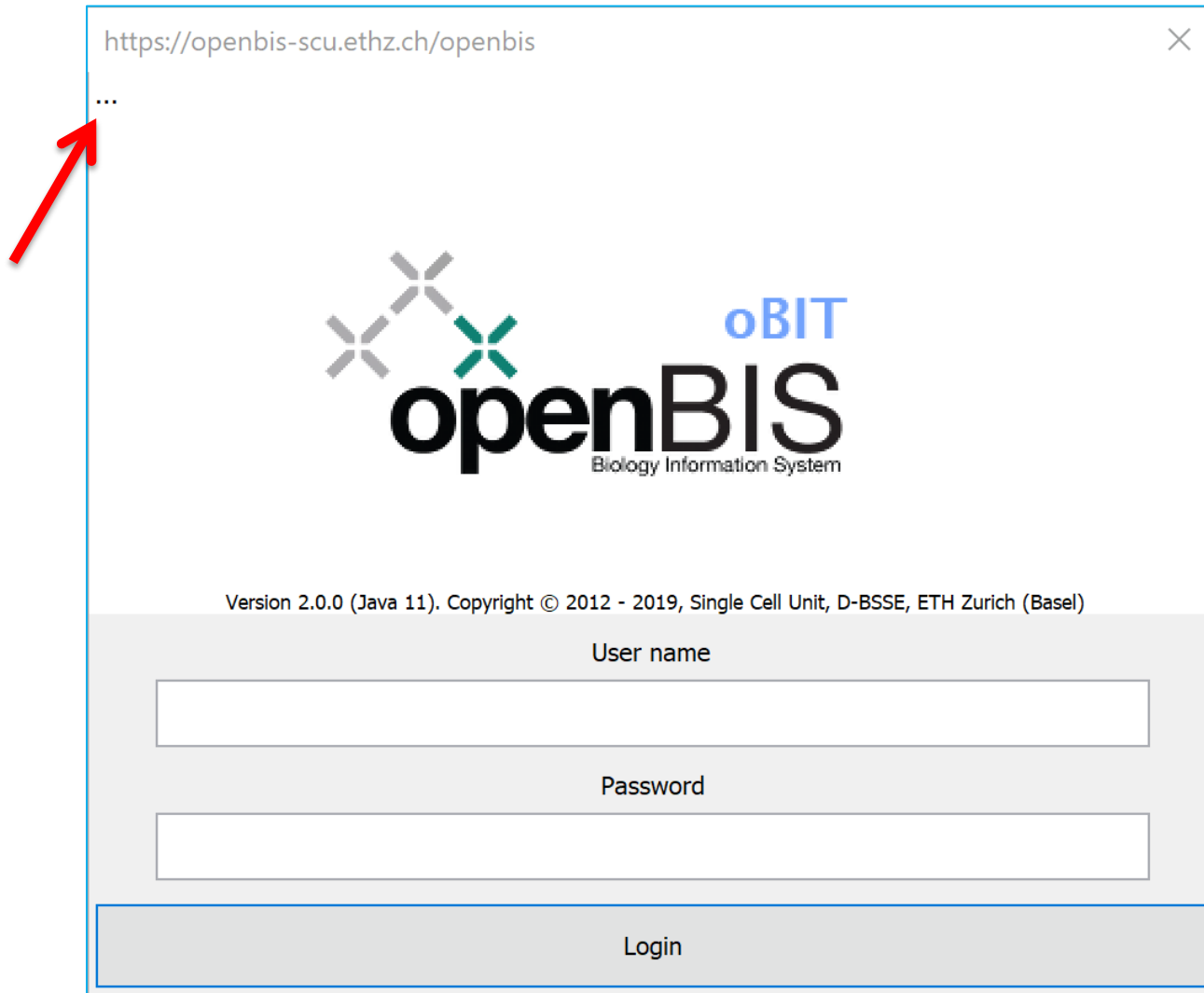
oBIT  
**openBIS**  
Biology Information System

Version 2.0.0 (Java 11). Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

User name


Password

Login



https://openbis-scu.ethz.ch/openbis

...



oBIT  
**openBIS**  
Biology Information System

Version 2.0.0 (Java 11). Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)


User name

Password

Login

https://openbis-scu.ethz.ch/openbis

...



Please choose the openBIS server you want to use:

- https://bs-openbis05-dev.ethz.ch/openbis
- https://openbis-scu.ethz.ch/openbis
- https://bs-openbis05-dev.ethz.ch/openbis

Select Cancel

Versi (Basel)

\_\_\_\_\_


Password

\_\_\_\_\_

Login

https://openbis-scu.ethz.ch/openbis

...



Please choose the openBIS server you want to use:

https://bs-openbis05-dev.ethz.ch/openbis

Set selected as default server

Select Cancel

Version

Basel)

\_\_\_\_\_


Password

\_\_\_\_\_

Login

https://openbis-scu.ethz.ch/openbis

...



Version 2.0.0 (Java 11). Copyright © 2012 - 2019, Single Cell Unit, D-BSSE, ETH Zurich (Basel)

User name

Password

Login



openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

### Data viewer

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - Specimen\_001

1

### Data editor

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Drag and drop your tags here from the openBIS Viewer.

Description

Spore counting experiment.

Plate geometry

96 Well - beads 10 ul 96\_WELLS\_8X12

Target openBIS project

/OBIT/DEMO

6

### openBIS

- obit
  - OBIT
    - COURSES
    - DEMO

4

Scan

### Metadata viewer

Name	Value
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	LSRII
\$DATATYPE	F
\$DATE	19-JUN-2012
\$ENDANALYSIS	0
\$ENDDATA	158739
\$ENDTEXT	0
\$ETIM	10:49:21
\$FIL	Specimen_001_A2_A02.fcs

2

### Invalid datasets

File or folder	Issue

3

### Tags from OBIT

Create new tag...

- Demo
- Benchmark
- Calibration

5

Send to openBIS

7

06-06-2019 15:53:09: Successfully logged in to openBIS.  
 06-06-2019 15:53:10: Retrieving openBIS structure...  
 06-06-2019 15:53:10: Retrieving openBIS structure completed.  
 06-06-2019 15:53:10: Scanning user data folder...  
 06-06-2019 15:53:11: Scanning user data folder completed.

openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

**Data viewer**

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - Specimen\_001

1

**Data editor**

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Drag and drop your tags here from the openBIS Viewer.

Description

Spore counting experiment.

Plate geometry

96 Well - beads 10 ul 96\_WELLS\_8X12

Target openBIS project

/OBIT/DEMO

6

**openBIS**

- obit
  - OBIT
    - COURSES
    - DEMO

4

**Metadata viewer**

Name	Value
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	
\$DAT	
\$END	
\$END	
\$ETIM	
\$FIL	

**Invalid datasets**

File or folder	Issue
obit\Experiment 2\protocol.zip	Invalid file type.

- Show in Windows Explorer
- Move to...
- Delete

14-08-2018 14:06:19: Retrieving c...

14-08-2018 14:06:22: Scanning user data folder...

14-08-2018 14:06:23: Error: Please fix the invalid datasets to continue!

14-08-2018 14:06:23: Scanning user data folder completed.

**Tags from OBIT** Create new tag...

- Demo
- Benchmark
- Calibration

7

5

openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

### Data viewer

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - Specimen\_001

1

### Data editor

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Drag and drop your tags here from the openBIS Viewer.

Description

Spore counting experiment.

Plate geometry

96 Well - beads 10 ul 96\_WELLS\_8X12

Target openBIS project

/OBIT/DEMO

6

### openBIS

obit

OBIT

Create new project

Create new tag

Scan

### Metadata viewer

Name	Value
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	LSRII
\$DATATYPE	F
\$DATE	19-JUN-2012
\$ENDANALYSIS	0
\$ENDDATA	158739
\$ENDTEXT	0
\$ETIM	10:49:21
\$FIL	Specimen_001_A2_A02.fcs

2

### Invalid datasets

File or folder	Issue

3

Send to openBIS

7

### Tags from OBIT

Create new tag...

- Demo
- Benchmark
- Calibration

5

06-06-2019 15:53:09: Successfully logged in to openBIS.  
 06-06-2019 15:53:10: Retrieving openBIS structure...  
 06-06-2019 15:53:10: Retrieving openBIS structure completed.  
 06-06-2019 15:53:10: Scanning user data folder...  
 06-06-2019 15:53:11: Scanning user data folder completed.

openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

**Data viewer**

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - Specimen\_001

1

**Data editor**

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Description

Spore counting experiment.

Plate geometry

96 Well - beads 10 ul 96\_WELLS\_8X12

Target openBIS project

/OBIT/DEMO

6

**openBIS**

- obit
  - OBIT
    - COURSES
    - DEMO

Set as default target project

5

Scan

**Metadata viewer**

Name	Value
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	LSRII
\$DATATYPE	F
\$DATE	19-JUN-2012
\$ENDANALYSIS	0
\$ENDDATA	158739
\$ENDTEXT	0
\$ETIM	10:49:21
\$FIL	Specimen_001_A2_A02.fcs

2

**Invalid datasets**

File or folder	Issue

3

Send to openBIS

7

**Tags from oBIT** Create new tag...

- Demo
- Benchmark
- Calibration

Scan

06-06-2019 15:53:09: Successfully logged in to openBIS.  
 06-06-2019 15:53:10: Retrieving openBIS structure...  
 06-06-2019 15:53:10: Retrieving openBIS structure completed.  
 06-06-2019 15:53:10: Scanning user data folder...  
 06-06-2019 15:53:11: Scanning user data folder completed.

openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

**Data viewer**

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - Specimen\_001

**Data editor**

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Drag and drop your tags here from the openBIS Viewer.

Description

Spore counting experiment.

Plate geometry

**openBIS**

oBIT

- OBIT
- COURSES
- DEMO

1

4

**Create new tag...**

Select space

OBIT

Tag name

Cell Migration

Tag description (optional)

Experiments associated with Cell Migration project (Grant #523).

Ok Cancel

2

**Metadata viewer**

Name	Value
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	LSRII
\$DATATYPE	F
\$DATE	19-JUN-2012
\$ENDANALYSIS	0
\$ENDDATA	158739
\$ENDTEXT	0
\$ETIM	10:49:21
\$FIL	Specimen_001_A2_A02.fcs

3

**Invalid datasets**

File or folder	Issue

7

**Tags from oBIT**

Demio

Benchmark

Calibration

5

06-06-2019 15:53:09: Successfully logged in to openBIS.

06-06-2019 15:53:10: Retrieving openBIS structure...

06-06-2019 15:53:10: Retrieving openBIS structure completed.

06-06-2019 15:53:10: Scanning user data folder...

06-06-2019 15:53:11: Scanning user data folder completed.

openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

**Data viewer**

- /obit
  - Eva Spore Counting 190612
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A10
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs**
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
      - Specimen\_001

**Data editor**

/obit

Eva Spore Counting 190612

Experiment tags

Benchmark; Calibration

Drag and drop your tags here from the openBIS Viewer.

Description

Spore counting experiment.

Plate geometry

**openBIS**

- obit
  - OBIT
    - COURSES
    - DEMO

Scan

**Metadata viewer**


Name	
\$BEGINANALYSIS	0
\$BEGINDATA	2496
\$BEGINTEXT	0
\$BTIM	10:49:11
\$BYTEORD	4,3,2,1
\$CYT	LSRII
\$DATATYPE	F
\$DATE	19-JUN-2012
\$ENDANALYSIS	0
\$ENDDATA	158739
\$ENDTEXT	0
\$ETIM	10:49:21
\$FIL	Specimen_001_A2_A02.fcs

**Invalid datasets**

File or folder	Issue
----------------	-------

06-06-2019 15:53:09: Successfully logged in to openBIS.  
06-06-2019 15:53:10: Retrieving openBIS structure...  
06-06-2019 15:53:10: Retrieving openBIS structure completed.  
06-06-2019 15:53:10: Scanning user data folder...  
06-06-2019 15:53:11: Scanning user data folder completed.

1



Attachments

4

2

3

7

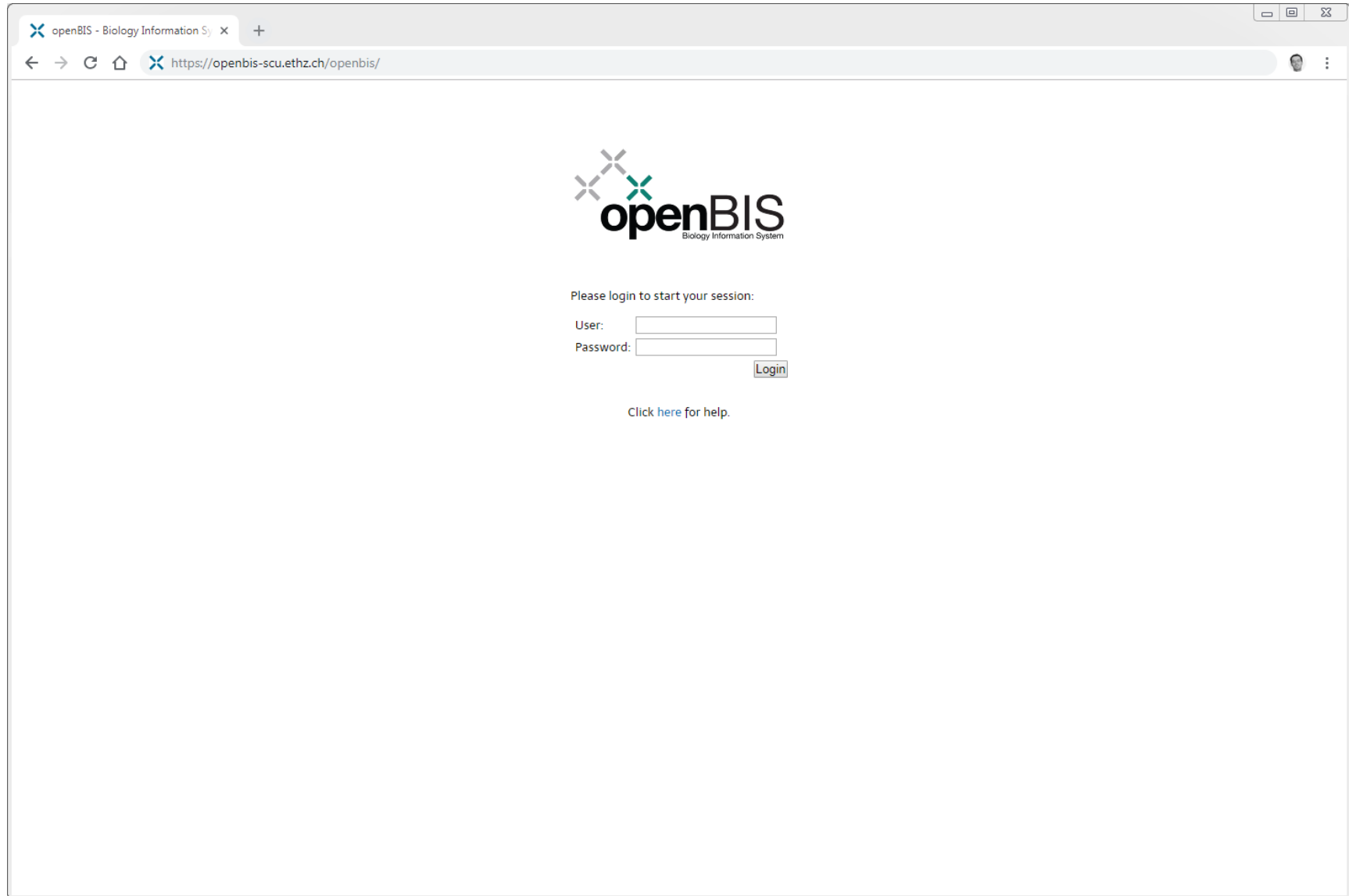
5

Send to openBIS

**Tags from OBIT** Create new tag...

- Demo
- Benchmark
- Calibration





The screenshot shows a web browser window with the following elements:

- Browser Tab:** openBIS - Biology Information System
- Address Bar:** <https://openbis-scu.ethz.ch/openbis/>
- Logo:** openBIS Biology Information System
- Text:** Please login to start your session:
- Form:** User:  Password:
- Button:** Login
- Text:** Click [here](#) for help.

Project viewer - openBIS - Biolog x +

https://openbis-scu.ethz.ch/openbis/

Browse ▾ New ▾ Import ▾ Utilities ▾ All ▾ Search Admin obit

## Project viewer

Filter by experiment name:

Sort experiments by:  Name  Name  Registration date  Registration date

### Spaces/Projects

- DEFAULT
- DEFAULT\_LAB\_NOTEBOOK
- METHODS
- OBIT
- COURSES
- DEMO
- STOCK\_CATALOG
- STOCK\_ORDERS

### Experiments for OBIT/DEMO

#### Microscopes

**Tags**  Cell Migration  Demo  No tags

**Machines**  Widefield 2  Widefield 1  Unknown

Experiment\_2  
[Cell Migration](#)  
Example microscopy acquisition.  
Acquired on [Widefield 2](#)

multiple\_datasets  
[Demo](#)  
Multiple dataset registration.  
Acquired on [Widefield 1](#)

#### Flow Cytometry Analyzers

**Tags**  Benchmark  Calibration  No tags

**Machines**  BD LSR FORTRESSA with HTS  Unknown

Eva Spore Counting 190612  
[Benchmark](#) [Calibration](#)  
Spore counting experiment.  
Acquired on [BD LSR FORTRESSA with HTS](#)

#### Flow Cytometry Sorters

**Tags**  No tags

**Machines**  BD FACS ARIA III  Unknown

150115KK YVI - Exp1  
*No tags assigned.*  
Quality control acquisitions.  
Acquired on [BD FACS ARIA III](#)



Object EVA\_SPORE\_COUNTING\_ x +

https://openbis-scu.ethz.ch/openbis/

Browse New Import Utilities All Search Admin obit

Project viewer Object EVA\_SPORE\_COUNTING\_190612\_190706141935771000

OBIT » DEMO » FLOW\_ANALYZERS\_EXPERIMENTS\_COLLECTION » Object EVA\_SPORE\_COUNTING\_190612\_190706141935771000 [LSR\_FORTESSA\_EXPERIMENT] Edit Delete Object

Contained Children Parents Data Sets History Attachments DataSet Uploader Experiment viewer

## Eva Spore Counting 190612

**Tags**  
Benchmark, Calibration

**Description**  
Sport counting experiment.

**Attachments**  
There are 8 attachments.

**Acquisition details**  
BD FACSDiva Software Version 6.1.3 on BD LSR FORTESSA with HTS. Acquired by SingleCellUnit and registered on Fri Jun 07 2019.

### Experiment

- Eva Spore Counting 190612
  - Plates
    - 96 Well - beads 10 ul
      - Specimen\_001
        - A01
        - A02
        - Specimen\_001\_A2\_A02.fcs**
        - A03
        - A04
        - A05
        - A06
        - A07
        - A08
        - A09
        - A10
- Tubes
  - Specimen\_001
    - Tube\_001
    - Tube\_002
    - Tube\_003

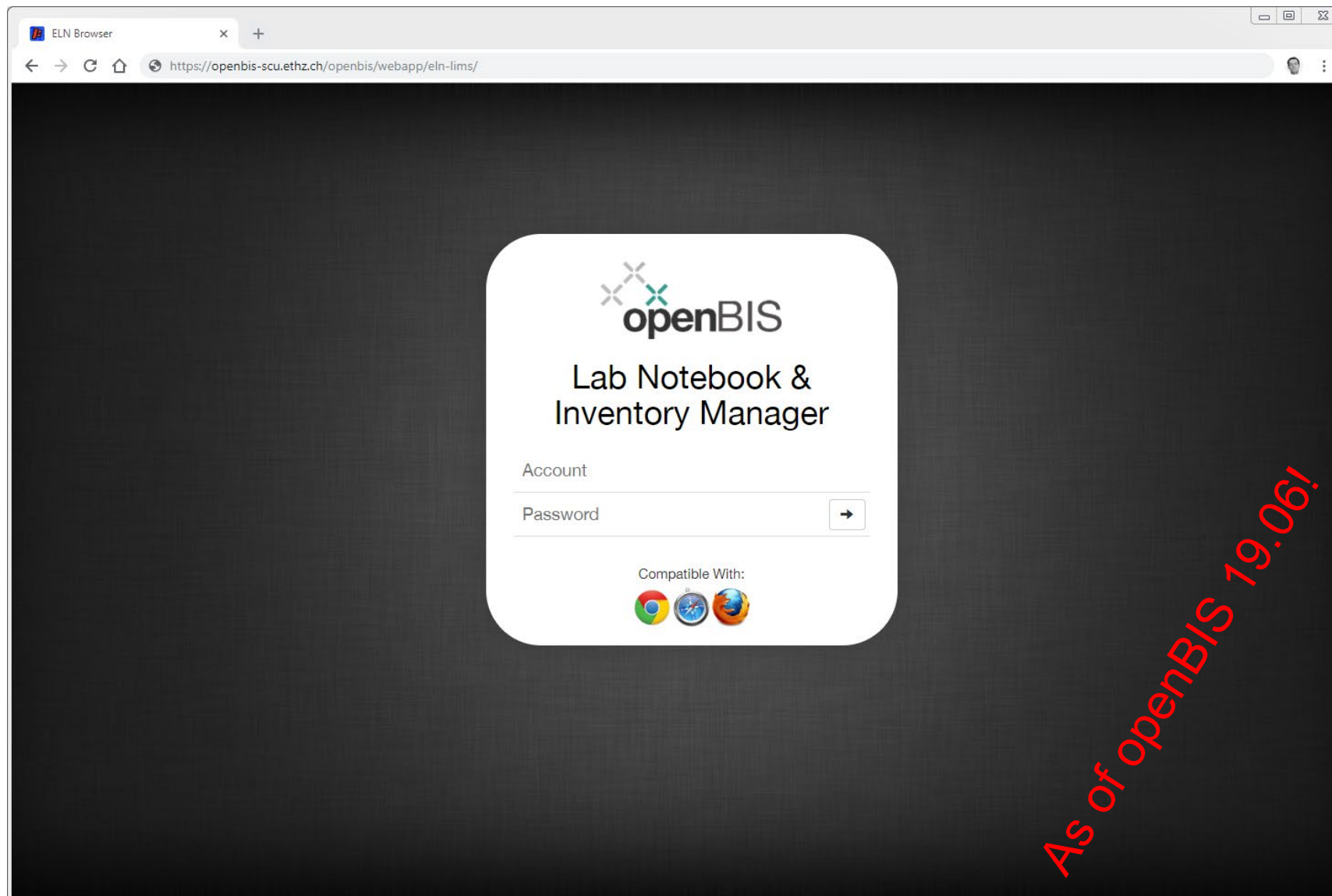
### Details

Specimen\_001\_A2\_A02.fcs

This file contains 11 parameters and 3551 events.


X axis: FSC-A Y axis: FSC-H Events to plot: 3551 Plot

Scale for X axis: Linear Scale for Y axis: Linear Sampling: Regular



ELN Browser x +

https://openbis-scu.ethz.ch/openbis/webapp/elc-lims/


  
**openBIS**

Lab Notebook &  
Inventory Manager

Account

Password

Compatible With:



*As of openBIS 19.06!*

Data Set 20190607141937008-48
+

<https://openbis-scu.ethz.ch/openbis/webapp/eln-liims/>

Global Search

- Lab Notebook
- My Space (Obit)
- Common Organization Units
- Courses
- Demo
  - Flow analyzers experiments collection
    - Eva Spore Counting 190612
      - 70um\_8peak\_20150115.pdf
      - 70um\_8peak\_20150119.pdf
    - 96 Well - beads 10 ul
      - 100um\_8peak\_20150116.pdf
      - 100um\_8peak\_20150119.pdf
    - A01
    - A02
      - 20190607141937008-48
    - A03
    - A04
    - A05
    - A06
    - A07
    - A08
    - A09
    - A10
    - LSR\_S17
      - Performance Tracking Report\_70um\_14012015.pdf
      - Performance Tracking Report\_70um\_19012015.pdf
      - Performance Tracking Report\_100um\_16012015.pdf
      - Performance Tracking Report\_100um\_19012015.pdf
    - Tube\_001
    - Tube\_002
    - Tube\_003
  - Flow sorters experiments collection
  - Microscopy experiments collection
  - Organization Unit Collection
- Others
- Others (disabled)
- Inventory
- Stock
- Utilities
- About

## Dataset: 20190607141937008-48

/OBIT/DEMO/FLOW\_ANALYZERS\_EXPERIMENTS\_COLLECTION/LSR\_W9/20190607141937008-48

☰
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M

### Data viewer

X axis: FSC-A
Y axis: FSC-H
Events to plot: 3551
Plot

Scale for X axis: Linear
Scale for Y axis: Linear
Sampling: Regular

### Identification Info

**Data Set Type:** LSR\_FORTESSA\_FCSFILE

**Code:** 20190607141937008-48

**Object:** /OBIT/DEMO/LSR\_W9

**Registrar:** etlserver

**Registration Date:** 2019-06-07 14:19:37

**Modifier:** etlserver

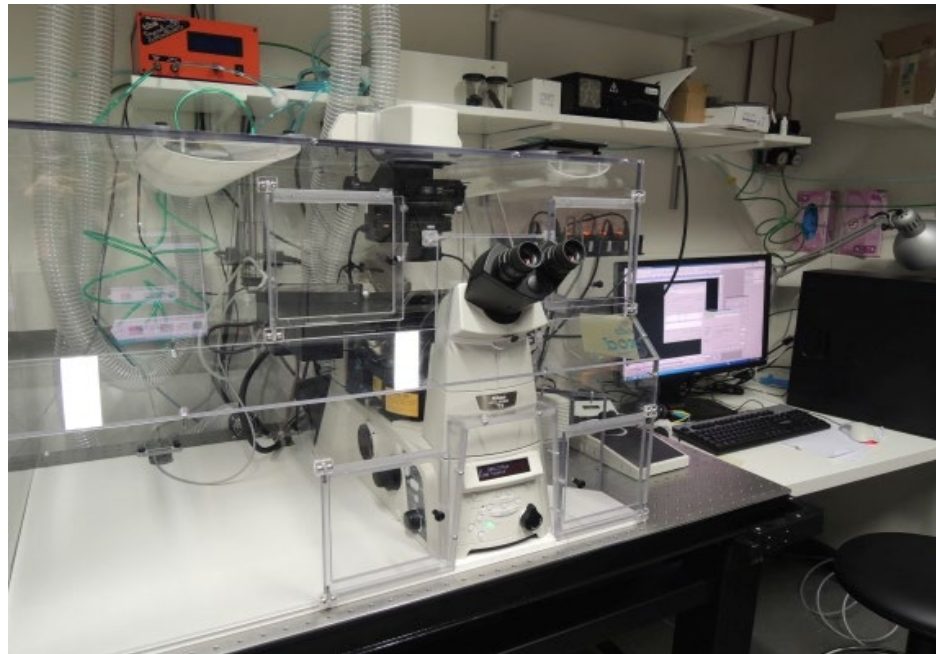
**Modification Date:** 2019-06-07 14:19:37

### Metadata Fields

**FCS parameters:**

- LSR\_FORTESSA\_FCSFILE : 20190607141937008-48
- Specimen\_001\_A2\_A02.fcs (155Kb)

# Light microscopes



bio-formats





openBIS Importer Toolset (oBIT) :: Annotation Tool v2.0.0

### Data viewer

- /obit
  - Experiment 1
  - Experiment 2
    - 2d10MDCK DAPI.nd2
      - 2d10MDCK DAPI.nd2 (series 1)**
      - 2d10MDCK DAPI.nd2 (series 2)
      - 2d10MDCK DAPI.nd2 (series 3)
      - 2d10MDCK DAPI.nd2 (series 4)
      - 2d10MDCK DAPI.nd2 (series 5)
    - Captured for 4.nd2
    - Test.nd2
    - Test001.nd2
    - Test13.2.13.nd2
  - Experiment 4
    - brainbow1corticalneurons.lif\_TileScan\_001

Scan

### Data editor

Experiment 2

Tags

Cell Migration

Drag and drop your tags here from the openBIS Viewer.

Description

Example microscopy acquisitions.

---

2d10MDCK DAPI.nd2

Description

First series in file.

Target openBIS project

/OBIT/DEMO

Send to openBIS

### openBIS

- obit
  - OBIT
    - COURSES
    - DEMO

Scan

---

**Tags from OBIT** Create new tag...

- Demo
- Benchmark
- Calibration
- Cell Migration**

### Metadata viewer

Name	Value
acquisitionDate	
channelColor0	0.0, 0.0, 255.0, 255.0
channelColor1	0.0, 0.0, 255.0, 255.0
channelColor2	255.0, 255.0, 255.0, 255.0
channelName0	DAPI
channelName1	DiR
channelName2	TD
datatype	uint16
emWavelength0	525.0
emWavelength1	700.0
emWavelength2	NaN
exWavelength0	NaN
exWavelength1	NaN

### Invalid datasets

File or folder	Issue

07-06-2019 13:06:08: Scanning user data folder...

07-06-2019 13:06:09: Successfully processed folder "obit".

07-06-2019 13:06:10: Scanning user data folder completed.

07-06-2019 13:06:16: Scanning metadata from 2d10MDCK DAPI.nd2

07-06-2019 13:06:17: Scanning metadata from 2d10MDCK DAPI.nd2 completed.



Object EXPERIMENT\_2\_19120614 x +

https://openbis-scu.ethz.ch/openbis/

Browse ▾ New ▾ Import ▾ Utilities ▾ All [?] Search [Admin] [obit]

Project viewer [Object EXPERIMENT\_2\_191206141334218000]

OBIT » DEMO » MICROSCOPY\_EXPERIMENTS\_COLLECTION » Object EXPERIMENT\_2\_191206141334218000 [MICROSCOPY\_EXPERIMENT] [Edit] [Delete Object]

Contained Children Parents Data Sets History Attachments DataSet Uploader Experiment viewer

## Experiment\_2

**Tags**  
Cell Migration

**Description**  
Example microscopy acquisitions.


**Attachments**  
There are 2 attachments.

**Acquisition details**  
This experiment was performed on **Widefield 2** and registered on Wed Jun 12 2019.

### Datasets (samples)

[Folder] [Eye] [ZIP]

Dataset Name	Size	Thumbnail Description
2d10MDCK DAPI.nd2	[316.16 MiB]	Microscopy image showing a grid of cells with blue DAPI staining.
aaron_3Ch.nd2	[6.20 MiB]	Microscopy image showing cells with green and red channels.
Captured for 4.nd2	[2.71 MiB]	Microscopy image showing cells with green channels.
Test.nd2	[113.28 MiB]	Microscopy image showing cells with red and green channels.
test001.nd2	[74.40 MiB]	Microscopy image showing cells with green and red channels.
test13.2.13.nd2	[168.50 MiB]	Microscopy image showing a single cell with green channel.



Object MICROSCOPY\_SAMPLE\_T x +

https://openbis-scu.ethz.ch/openbis/

Browse ▾ New ▾ Import ▾ Utilities ▾ All [?] Search Admin obit ▾

Project viewer [x] Object EXPERIMENT\_2\_191206141334218000 [x] Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [x]

OBIT » DEMO » MICROSCOPY\_EXPERIMENTS\_COLLECTION » Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [MICROSCOPY\_SAMPLE\_TYPE] [Edit] [Delete Object]

Contained Children Parents Data Sets History Attachments DataSet Uploader Dataset (sample) viewer

## 2d10MDCK DAPI.nd2

File/Series info

Experiment name	Experiment_2
Experiment description	Example microscopy acquisitions.
Dataset size	316.16 MiB
Dataset description	No description provided.
Current series	
Geometry [XYZ]	512x512x6, 3 channels, 7 timepoints
Voxel size [XYZ] (µm)	0.12x0.12x1.5

Dataset viewer

📄 🔍 📁 👁 📦

Data set  
2d10MDCK DAPI.nd2 (series 1) ▾

Channel  
Merged Channels ▾

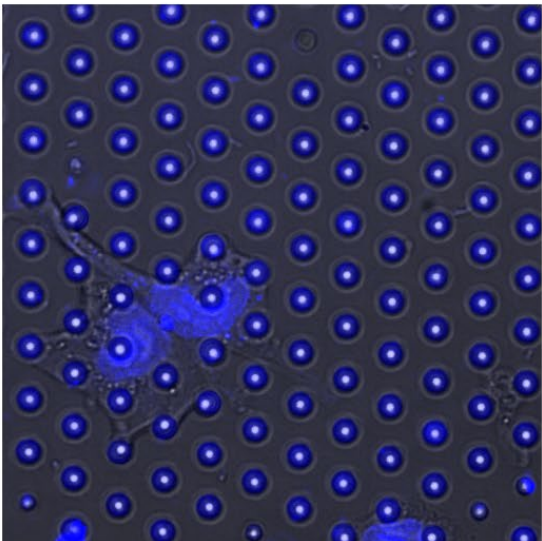
DAPI  DiR  TD

Filter  
Optimal image ▾

Resolution  
512x512 ▾

Time: 3 sec (4/7) Show Buttons

Depth: 4 (5/6) Show Buttons



Object MICROSCOPY\_SAMPLE\_T x +

https://openbis-scu.ethz.ch/openbis/

Browse ▾ New ▾ Import ▾ Utilities ▾ All [?] Search Admin obit ▾

Project viewer [x] Object EXPERIMENT\_2\_191206141334218000 [x] Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [x]

OBIT » DEMO » MICROSCOPY\_EXPERIMENTS\_COLLECTION » Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [MICROSCOPY\_SAMPLE\_TYPE] [Edit] [Delete Object]

Contained Children Parents Data Sets History Attachments DataSet Uploader Dataset (sample) viewer

## 2d10MDCK DAPI.nd2

File/Series info

Experiment name	Experiment_2
Experiment description	Example microscopy acquisitions.
Dataset size	316.16 MiB
Dataset description	No description provided.
Current series	
Geometry [XYZ]	512x512x6, 3 channels, 7 timepoints
Voxel size [XYZ] (µm)	0.12x0.12x1.5

series\_0 series\_1 series\_2 series\_3 series\_4

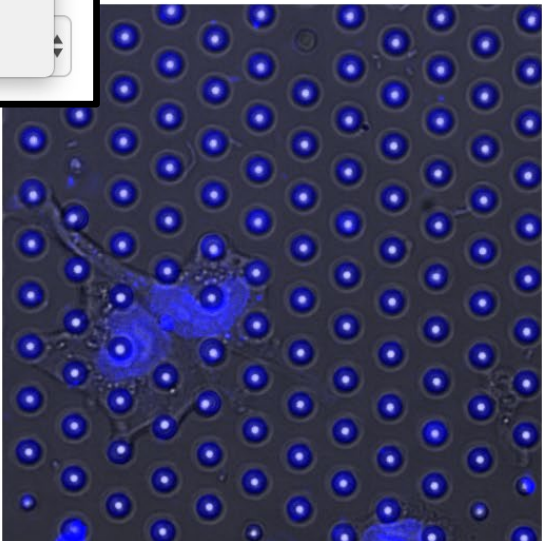
DAPI DIR TD

Filter: Optimal image

Resolution: 512x512

Time: 3 sec (4/7) Show Buttons

Depth: 4 (5/6) Show Buttons



Object MICROSCOPY\_SAMPLE\_T x +  
https://openbis-scu.ethz.ch/openbis/  
Browse ▾ New ▾ Import ▾ Utilities ▾ All [?] Search Admin ▾ obit ▾  
Project viewer [x] Object EXPERIMENT\_2\_191206141334218000 [x] Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [x]  
OBIT » DEMO » MICROSCOPY\_EXPERIMENTS\_COLLECTION » Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [MICROSCOPY\_SAMPLE\_TYPE] Edit Delete Object  
Contained Children Parents Data Sets History Attachments DataSet Uploader Dataset (sample) viewer

## 2d10MDCK DAPI.nd2

File/Series info

Experiment name	Experiment_2
Experiment description	Example microscopy acquisitions.
Dataset size	316.16 MiB
Dataset description	No description provided.
Current series	
Geometry [XYZ]	512x512x6, 3 channels, 7 timepoints
Voxel size [XYZ] (µm)	0.12x0.12x1.5

Dataset viewer

Data set  
2d10MDCK DAPI.nd2 (series 1)

### Filter

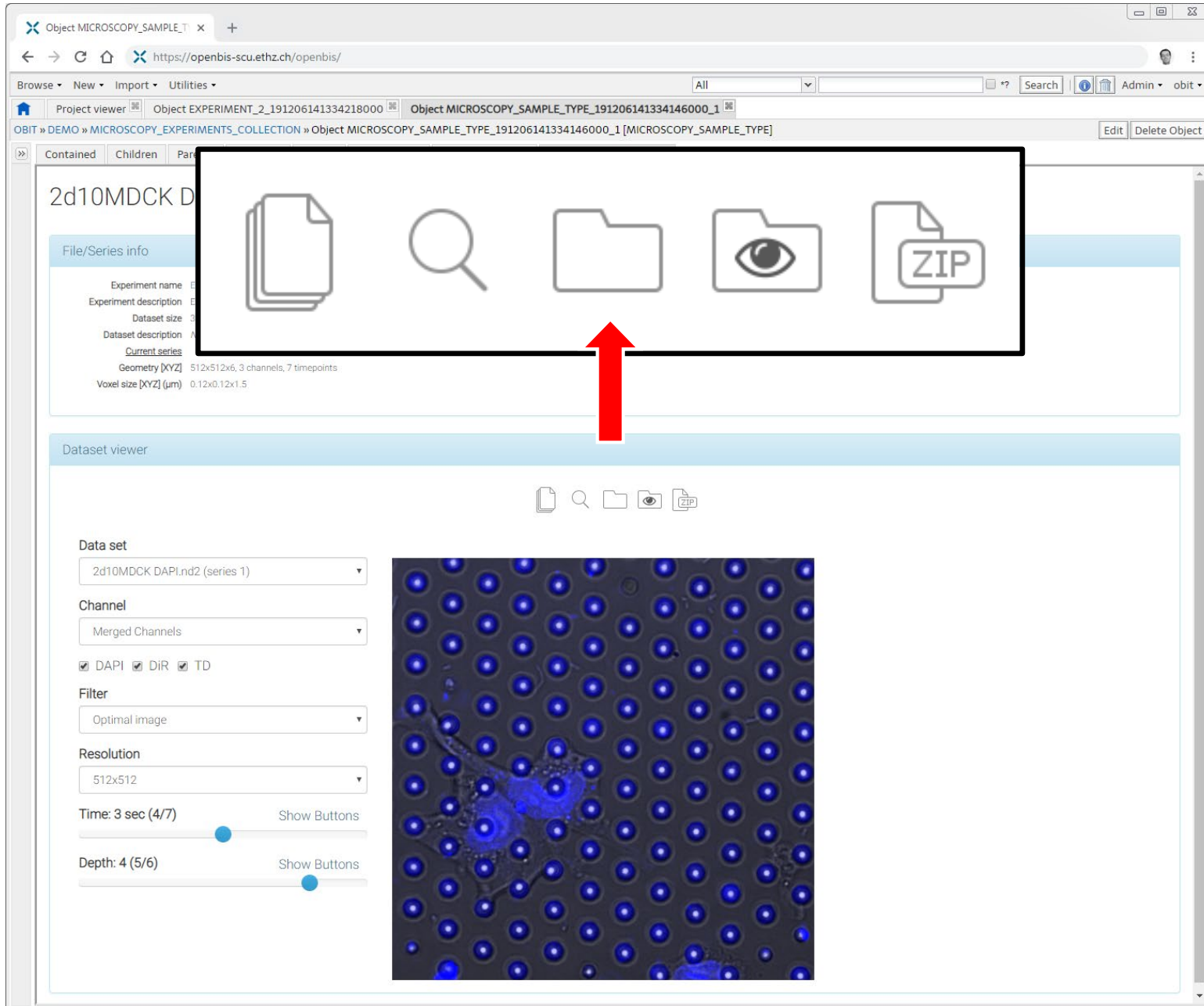
User defined ▾

DAPI (0, 142) Rescale Reset

DiR (34, 255) Rescale Reset

TD (0, 101) Rescale Reset





Object MICROSCOPY\_SAMPLE\_T x +

https://openbis-scu.ethz.ch/openbis/

Browse ▾ New ▾ Import ▾ Utilities ▾ All [?] Search [i] Admin ▾ obit ▾

Project viewer [x] Object EXPERIMENT\_2\_191206141334218000 [x] Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [x]

OBIT » DEMO » MICROSCOPY\_EXPERIMENTS\_COLLECTION » Object MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1 [MICROSCOPY\_SAMPLE\_TYPE] [Edit] [Delete Object]

Contained Children Par

### 2d10MDCK D

File/Series info

Experiment name: E  
Experiment description: E  
Dataset size: 3  
Dataset description: M  
Current series  
Geometry [XYZ]: 512x512x6, 3 channels, 7 timepoints  
Voxel size [XYZ] (µm): 0.12x0.12x1.5

Dataset viewer

File Search Folder Eye ZIP

Data set: 2d10MDCK DAPI.nd2 (series 1)

Channel: Merged Channels

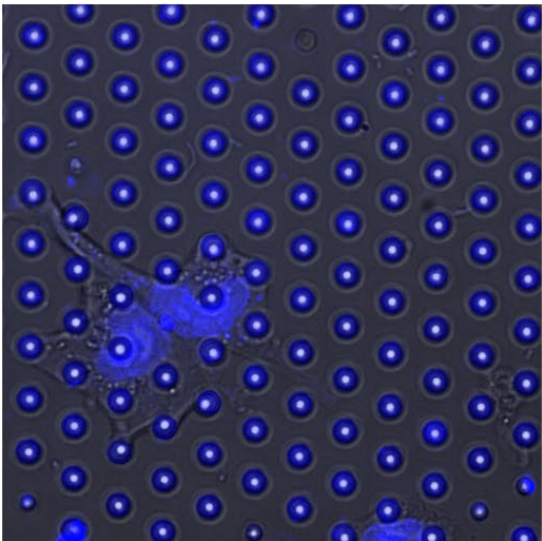
DAPI  DiR  TD

Filter: Optimal image

Resolution: 512x512

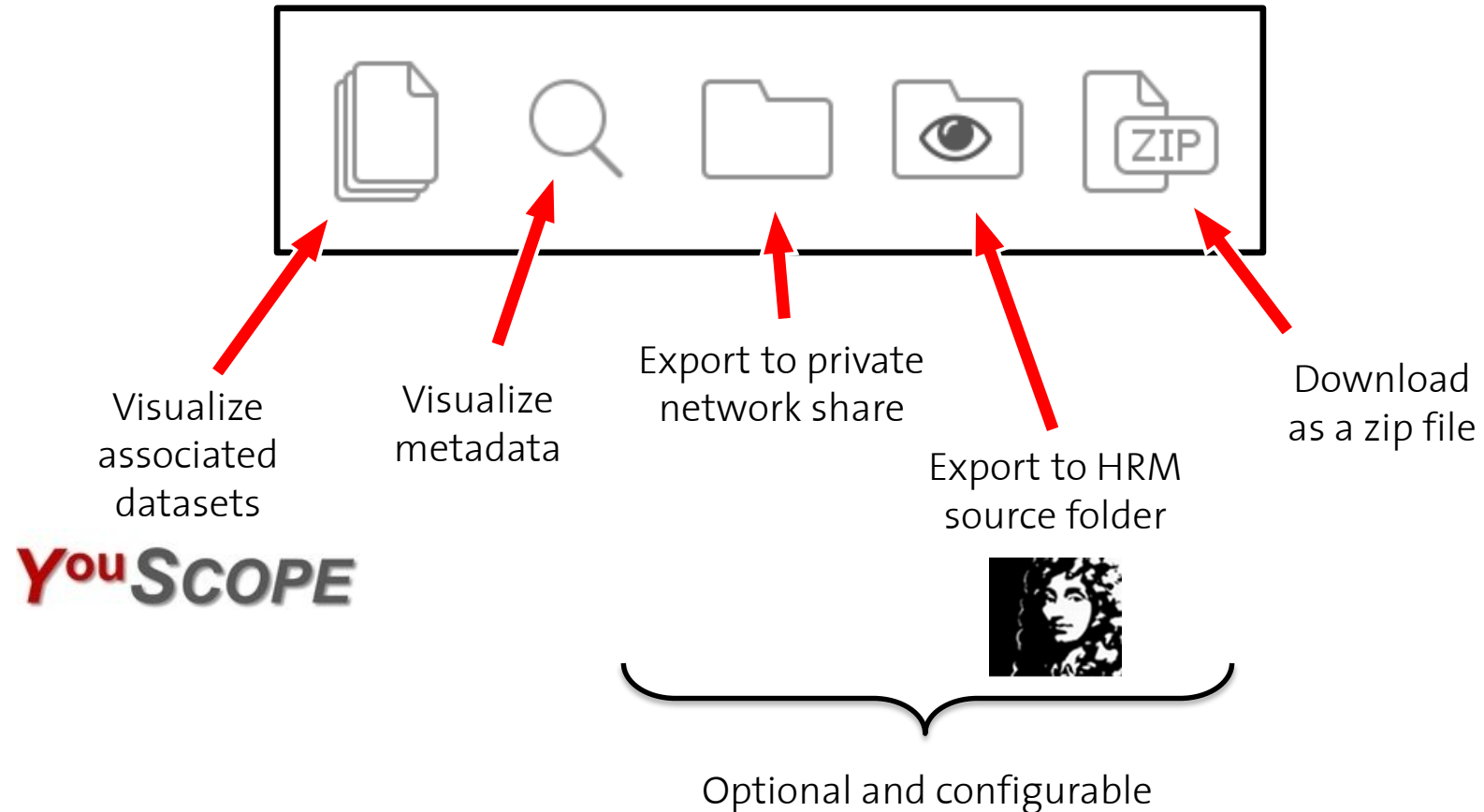
Time: 3 sec (4/7) Show Buttons

Depth: 4 (5/6) Show Buttons





# Experiment/dataset actions





# Huygens Remote Manager

[? Help](#)[Results](#) [pontia](#) [Home](#) Raw images

Preview

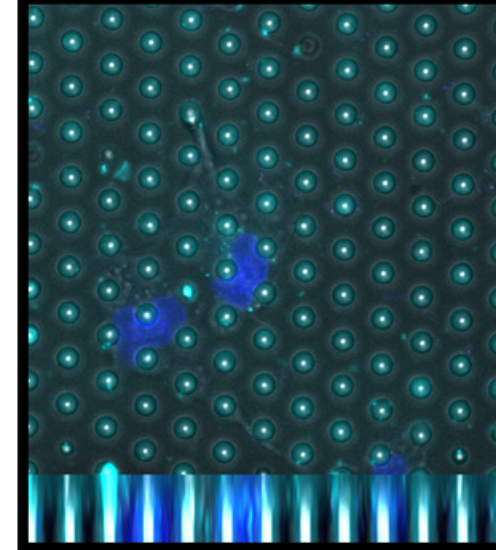
## Your raw files

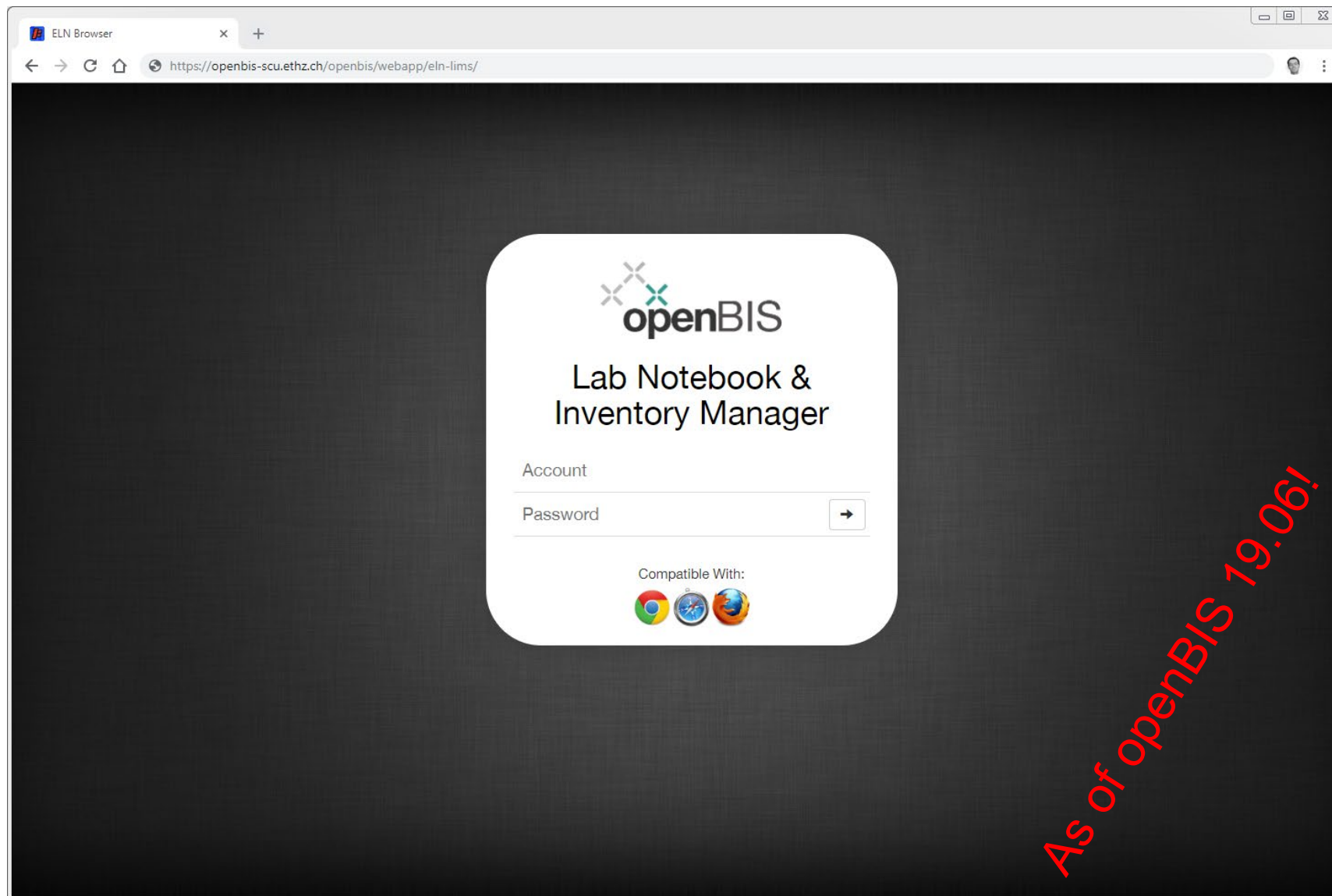
These are the original image files currently in your file area.

- Crop40-original\_crop.h5
- Embryo.ics
- Experiment 2/2d10MDCK DAPI.nd2
- HeLa\_2D\_tubulin.ics
- HeLa\_3D.ics
- HeLa\_coloc.ics
- OG488\_Dinoflagellate\_2\_raw\_confocal.h5
- OG488\_Dinoflagellate\_2\_raw\_joined.h5
- Pombe.ics
- U2OS\_dataset\_02\_R3D\_original.h5
- bad.lsm
- good.lsm
- test t1002.nd2
- widefieldTimeSeries.h5

[Re-create preview](#)


512 x 512 x 6 vx, 3 ch  
62.1 x 62.1 x 9  $\mu\text{m}^3$





ELN Browser x +

https://openbis-scu.ethz.ch/openbis/webapp/elc-lims/


  
openBIS

Lab Notebook &  
Inventory Manager

Account

Password

Compatible With:



*As of openBIS 19.06!*

Object EXPERIMENT\_2\_19120614 x +

https://openbis-scu.ethz.ch/openbis/webapp/elin-lims/

Global Search


Lab Notebook

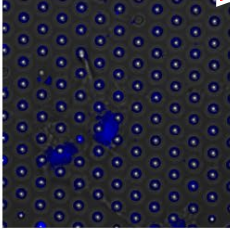
- My Space (Obit)
  - Common Organization Units
  - Courses
  - Demo
    - Flow analyzers experiments collection
    - Flow sorters experiments collection
    - Microscopy experiments collection
      - Experiment\_2**
        - 2d10MDCK DAPI.nd2
        - Captured for 4.nd2
        - Test001.nd2
        - Test13.2.13.nd2
        - Test.nd2
        - aaron\_3Ch.nd2
        - multiple\_datasets
      - Organization Unit Collection
    - Others
    - Others (disabled)
    - Inventory
    - Stock
    - Utilities
    - About

Object: Experiment\_2

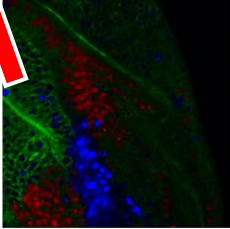
/OBIT/DEMO/MICROSCOPY\_EXPERIMENTS\_COLLECTION/EXPERIMENT\_2\_191206141334218000

File previews

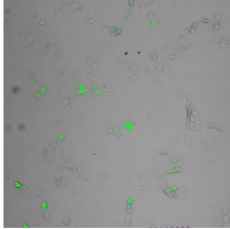




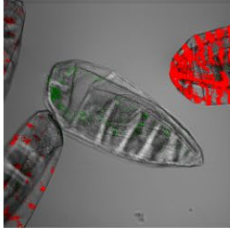
2d10MDCK DAPI.nd2  
316.16 MiB



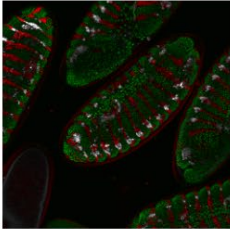
aaron\_3Ch.nd2  
6.20 MiB



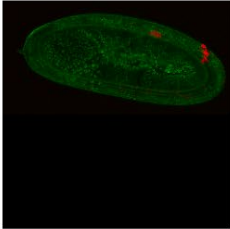
Captured for 4.nd2  
2.71 MiB



Test.nd2  
113.28 MiB



Test001.nd2  
74.40 MiB



Test13.2.13.nd2  
168.50 MiB

Parents


Type	Name	Modification Date
ORGANIZATION_UNIT	Cell Migration	2019-06-12 14:13:56

1 - 1 of 1 items 10 Per Page Page 1 of 1

Children

Select a dataset type

Files Uploader



Select files to upload

Create

Auto upload on drop

Object MICROSCOPY\_SAMPLE\_T
+

← → ↻ 🏠 <https://openbis-scu.ethz.ch/openbis/webapp/eln-lims/>

Global Search

- Lab Notebook
- My Space (Obit)
  - Common Organization Units
  - Courses
  - Demo
    - Flow analyzers experiments collection
    - Flow sorters experiments collection
    - Microscopy experiments collection
      - Experiment\_2
        - 2d10MDCK DAPI.nd2
        - Captured for 4.nd2
        - Test001.nd2
        - Test13.2.13.nd2
        - Test.nd2
        - aaron\_3Ch.nd2
      - multiple\_datasets
    - Organization Unit Collection
  - Others
  - Others (disabled)
  - Inventory
  - Stock
  - Utilities
  - About

## Object: 2d10MDCK DAPI.nd2

[/OBIT/DEMO/MICROSCOPY\\_EXPERIMENTS\\_COLLECTION/MICROSCOPY\\_SAMPLE\\_TYPE\\_191206141334146000\\_1](/OBIT/DEMO/MICROSCOPY_EXPERIMENTS_COLLECTION/MICROSCOPY_SAMPLE_TYPE_191206141334146000_1)

🔗 🖨️ 👤 📄 📁 📧

### Microscopy Viewer

**Data set**

2d10MDCK DAPI.nd2 (series 1)

**Channel**

Merged Channels

DAPI  DiR  TD

**Filter**

User defined

DAPI (0, 142) Rescale Reset

DiR (34, 255) Rescale Reset

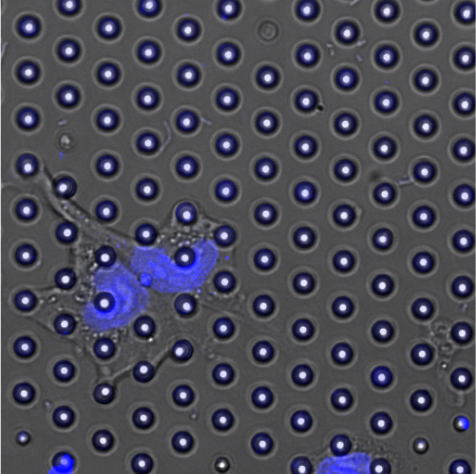
TD (0, 101) Rescale Reset

**Resolution**

512x512

**Time: 3 sec (4/7)** Show Buttons


**Depth: 4 (5/8)** Show Buttons



- MICROSCOPY\_IMG : 20190612141334737-312
- MICROSCOPY\_IMG\_THUMBNAIL : 2019061214
- MICROSCOPY\_IMG\_CONTAINER : 2d10MDCK
- MICROSCOPY\_IMG\_CONTAINER : 2d10MDCK
- MICROSCOPY\_IMG\_CONTAINER : 2d10MDCK
- MICROSCOPY\_IMG\_CONTAINER : 2d10MDCK
- MICROSCOPY\_IMG\_CONTAINER : 2d10MDCK

Select a dataset type

#### Files Uploader



Select files to upload

Create

Auto upload on drop

▼ **Metadata**

**Name:**  
2d10MDCK DAPI.nd2

**Size:**  
331522048

**Sample name:**  
2d10MDCK DAPI.nd2

▼ **Identification Info**

**Type:**  
MICROSCOPY\_SAMPLE\_TYPE

**Experiment:**  
/OBIT/DEMO/MICROSCOPY\_EXPERIMENTS\_COLLECTION

**Code:**  
MICROSCOPY\_SAMPLE\_TYPE\_191206141334146000\_1

**Registrar:**



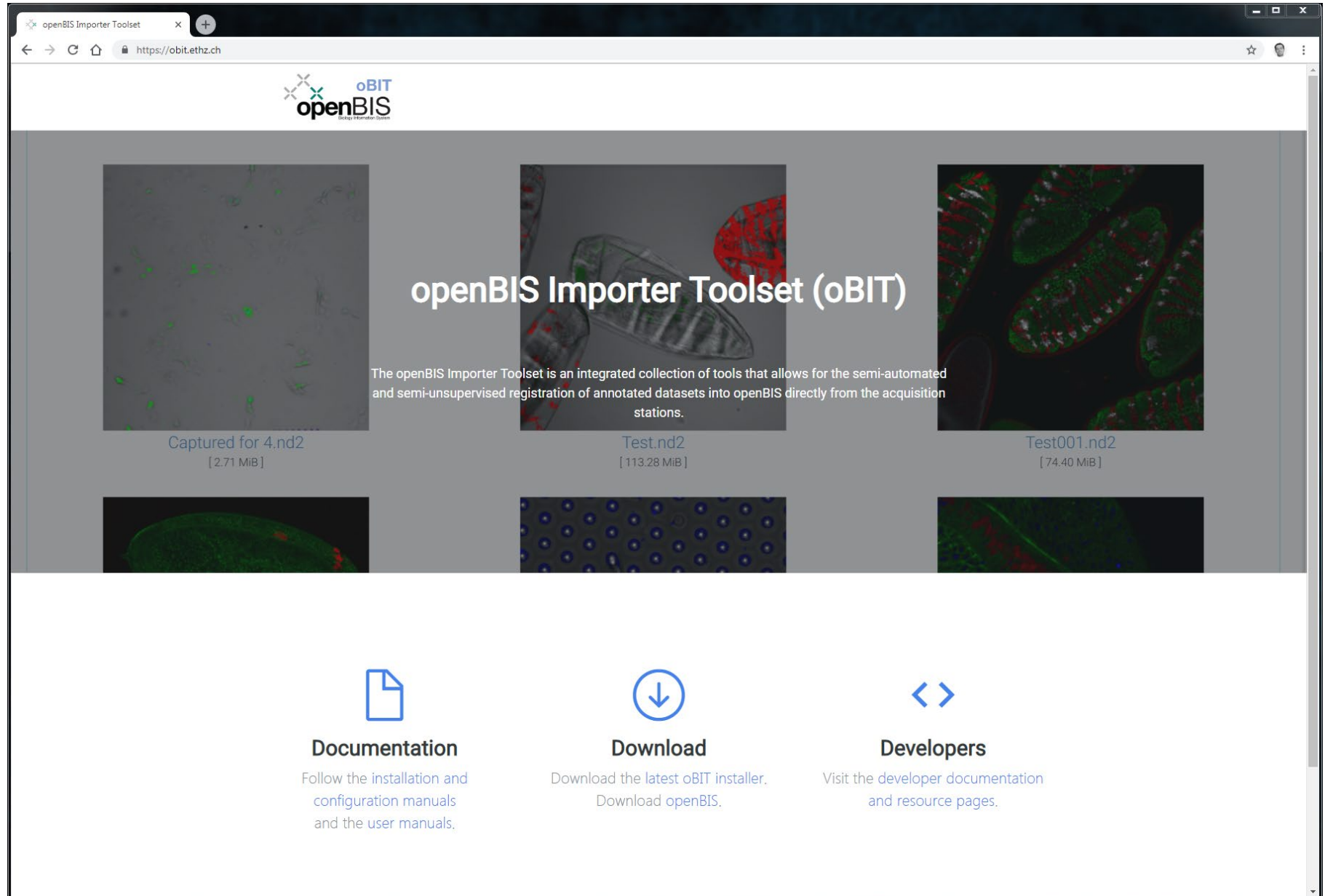
# oBIT documentation

The oBIT website has documentation for everyone.

New official project website (migration in process):

<https://obit.ethz.ch>





openBIS Importer Toolset

https://obit.ethz.ch

openBIS

## openBIS Importer Toolset (oBIT)

The openBIS Importer Toolset is an integrated collection of tools that allows for the semi-automated and semi-supervised registration of annotated datasets into openBIS directly from the acquisition stations.

Captured for 4.nd2  
[2.71 MiB]

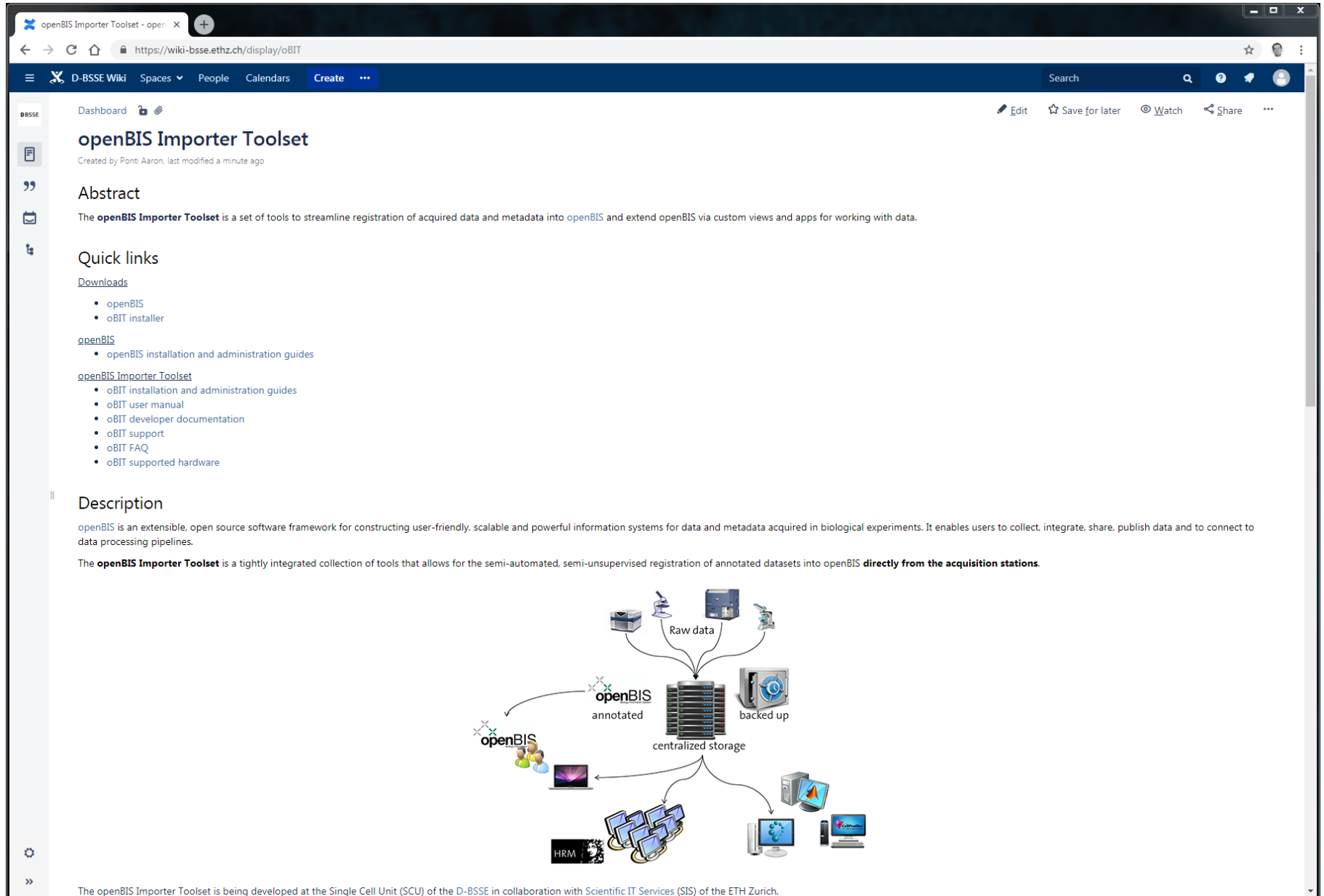
Test.nd2  
[113.28 MiB]

Test001.nd2  
[74.40 MiB]

**Documentation**  
Follow the installation and configuration manuals and the user manuals,

**Download**  
Download the latest oBIT installer.  
Download openBIS.

**Developers**  
Visit the developer documentation and resource pages.



The screenshot shows a web browser window displaying a wiki page titled "openBIS Importer Toolset". The browser's address bar shows the URL "https://wiki-bsse.ethz.ch/display/oBIT". The page content includes a dashboard, an abstract, quick links, and a description. The abstract states: "The **openBIS Importer Toolset** is a set of tools to streamline registration of acquired data and metadata into openBIS and extend openBIS via custom views and apps for working with data." The quick links section lists "Downloads" (openBIS, oBIT installer) and "openBIS" (openBIS installation and administration guides). The "openBIS Importer Toolset" section lists "oBIT installation and administration guides", "oBIT user manual", "oBIT developer documentation", "oBIT support", "oBIT FAQ", and "oBIT supported hardware". The description section states: "openBIS is an extensible, open source software framework for constructing user-friendly, scalable and powerful information systems for data and metadata acquired in biological experiments. It enables users to collect, integrate, share, publish data and to connect to data processing pipelines." and "The **openBIS Importer Toolset** is a tightly integrated collection of tools that allows for the semi-automated, semi-supervised registration of annotated datasets into openBIS **directly from the acquisition stations**." Below the text is a diagram showing "Raw data" from various sources (microscope, storage) being processed into "openBIS annotated" data, which is then stored in "centralized storage" (server rack) and backed up. The diagram also shows "openBIS" users and "HRM" (Human Resource Management) systems connected to the centralized storage.

Dashboard

## openBIS Importer Toolset

Created by Ponti Aaron, last modified a minute ago

### Abstract

The **openBIS Importer Toolset** is a set of tools to streamline registration of acquired data and metadata into openBIS and extend openBIS via custom views and apps for working with data.

### Quick links

#### Downloads

- openBIS
- oBIT installer

#### openBIS

- openBIS installation and administration guides

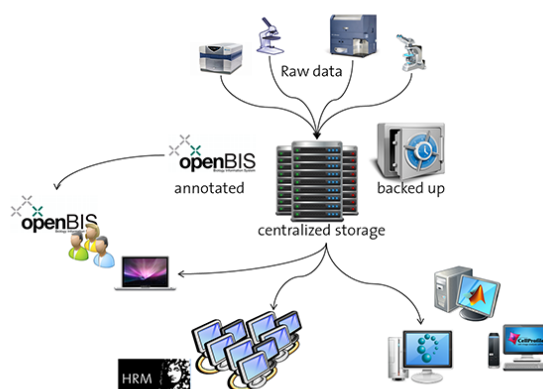
#### openBIS Importer Toolset

- oBIT installation and administration guides
- oBIT user manual
- oBIT developer documentation
- oBIT support
- oBIT FAQ
- oBIT supported hardware

### Description

openBIS is an extensible, open source software framework for constructing user-friendly, scalable and powerful information systems for data and metadata acquired in biological experiments. It enables users to collect, integrate, share, publish data and to connect to data processing pipelines.

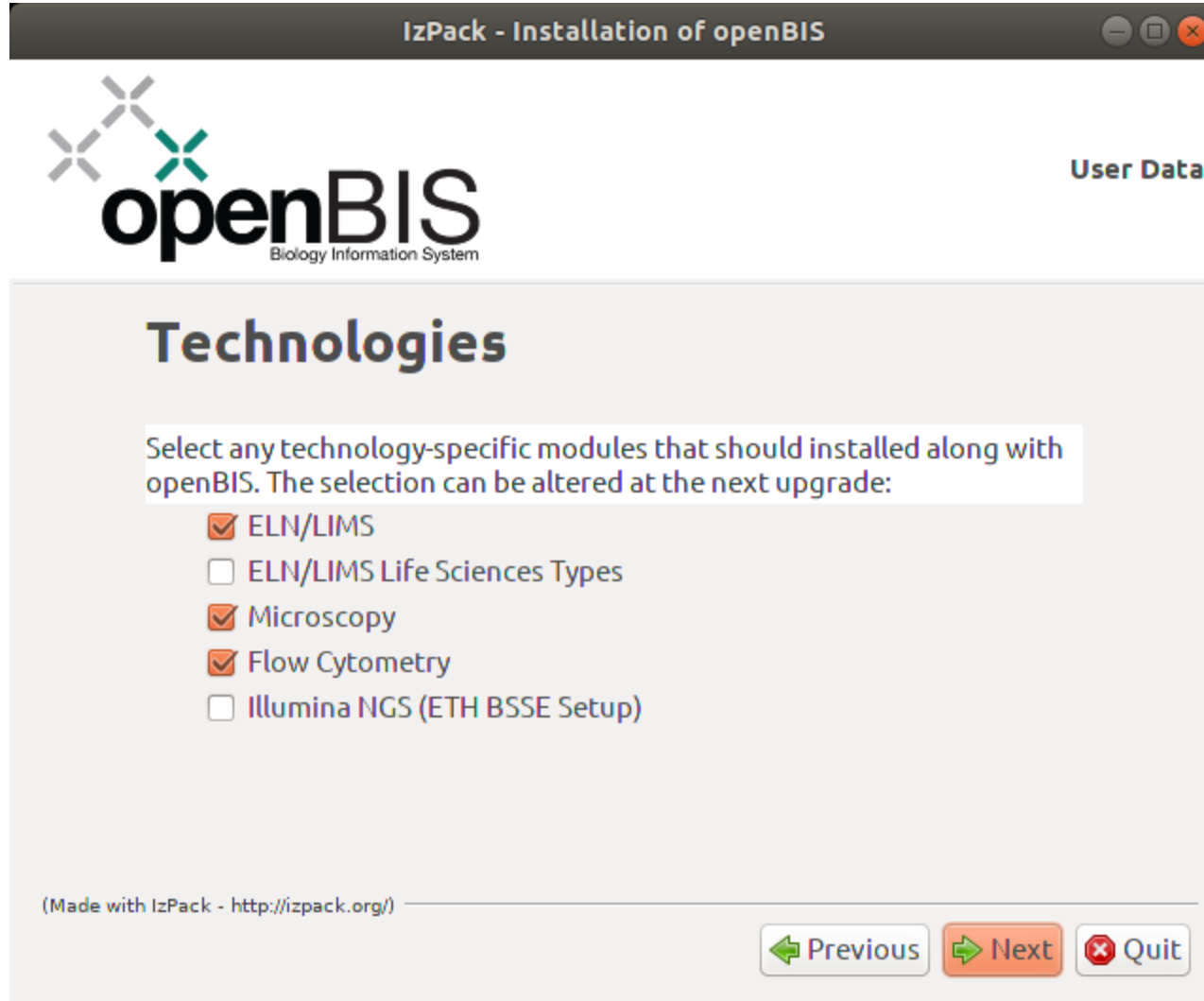
The **openBIS Importer Toolset** is a tightly integrated collection of tools that allows for the semi-automated, semi-supervised registration of annotated datasets into openBIS **directly from the acquisition stations**.




The diagram shows a central server rack labeled "centralized storage". Above it, "Raw data" from various sources (microscope, storage) is processed into "openBIS annotated" data. The annotated data is then stored in "centralized storage" and backed up. Below the storage, "openBIS" users and "HRM" (Human Resource Management) systems are shown connected to the centralized storage.

The openBIS Importer Toolset is being developed at the Single Cell Unit (SCU) of the D-BSSE in collaboration with Scientific IT Services (SIS) of the ETH Zurich.

# Installation :: openBIS and core technologies



IzPack - Installation of openBIS

 **openBIS**  
Biology Information System

User Data

## Technologies

Select any technology-specific modules that should installed along with openBIS. The selection can be altered at the next upgrade:

- ELN/LIMS
- ELN/LIMS Life Sciences Types
- Microscopy
- Flow Cytometry
- Illumina NGS (ETH BSSE Setup)

(Made with IzPack - <http://izpack.org/>)

← Previous   Next →   ✖ Quit

openBIS 19.06

# Installation :: openBIS Importer Toolset

```
Administrator: Windows PowerShell
openBIS Importer Toolset (oBIT) Installer v2.0.0
Copyright (c) 2015 - 2019, Aaron Ponti, D-BSSE ETHZ Basel

--- HOW TO GET HELP ---

For a detailed step-by-step guide, please refer to: https://wiki-bsse.ethz.ch/display/oBIT/Automated+oBIT+setup#StepByStep

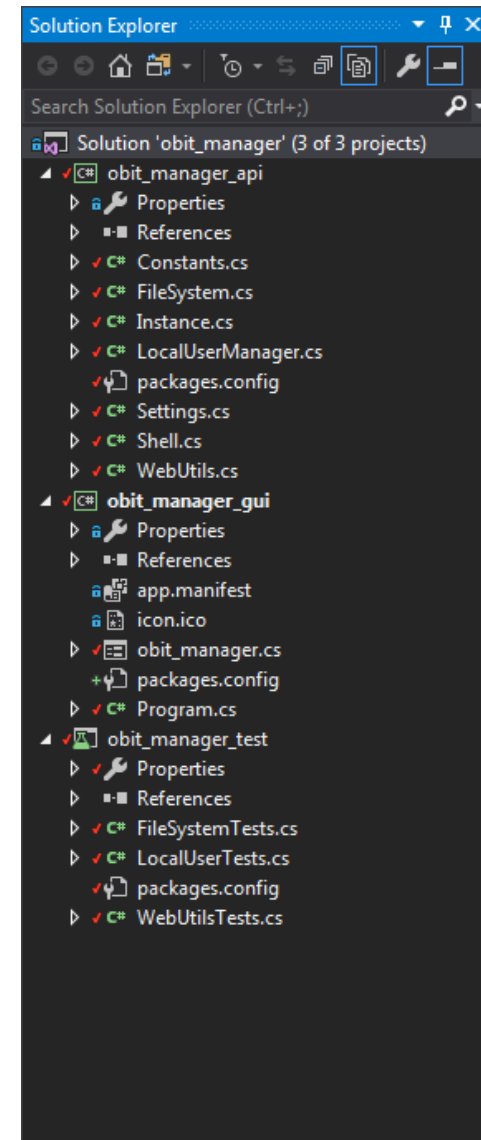
--- EXECUTION MODE ---

This script can be used to download, install and configure all components of the
openBIS Importer Toolset on this machine, or it can be used to prepare the setup
for a target machine that does not have internet connection. The target machine
can optionally be of different architecture (e.g. 32 instead of 64 bit).



Do you want to setup oBIT on this machine? (y/n) [Y]:
```

# Coming soon: oBIT Manager

- oBIT installation
- oBIT configuration
- oBIT upgrade
  
- oBIT components:
  - Annotation Tool
  - Datamover as a Windows Service
  - (OpenJDK) Java Runtime



# Development :: code repositories

-  Core technologies (server-side):
  - [https://github.com/aarpon/obit\\_microscopy\\_core\\_technology](https://github.com/aarpon/obit_microscopy_core_technology)
  - [https://github.com/aarpon/obit\\_flow\\_core\\_technology](https://github.com/aarpon/obit_flow_core_technology)
  - [https://github.com/aarpon/obit\\_shared\\_core\\_technology](https://github.com/aarpon/obit_shared_core_technology)
-  openBIS Importer Toolset (client-side)
  - [https://github.com/aarpon/obit\\_annotation\\_tool](https://github.com/aarpon/obit_annotation_tool)
  - [https://github.com/aarpon/obit\\_datamover\\_jsl](https://github.com/aarpon/obit_datamover_jsl)
  - [https://github.com/aarpon/obit\\_installer](https://github.com/aarpon/obit_installer)

## Summary

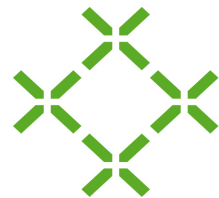
- The openBIS/openBIS Importer Toolset synergy aims to:
  - offer a powerful and scalable data and metadata management system
  - streamline data registration directly from shared acquisition machines
  - support multiple acquisition hardware classes
  - offer a reasonably simple way for third parties to add support for new hardware classes



# Acknowledgments

## SIS

Bernd Rinn  
Chandrasekhar Ramakrishnan  
Juan Fuentes Serna  
Franz-Josef Elmer  
Piotr Kupczyk  
Antti Luomi  
Jakub Straszewski  
Caterina Barillari  
Manuel Kohler



**D-BSSE**  
Department of Biosystems  
Science and Engineering

## ITSC

Vernon Bailey  
John Ryan  
Vincenzo Spanò  
Martin Fox



<https://obit.ethz.ch>