

# Data import using OMERO.insight

## 1. Start OMERO.insight & log in

- Open OMERO.insight.
- Enter server, username, and password.
- Click Login.

pm-omero.intranet.inp-greifswald.de [High]  

Username:  

Password:

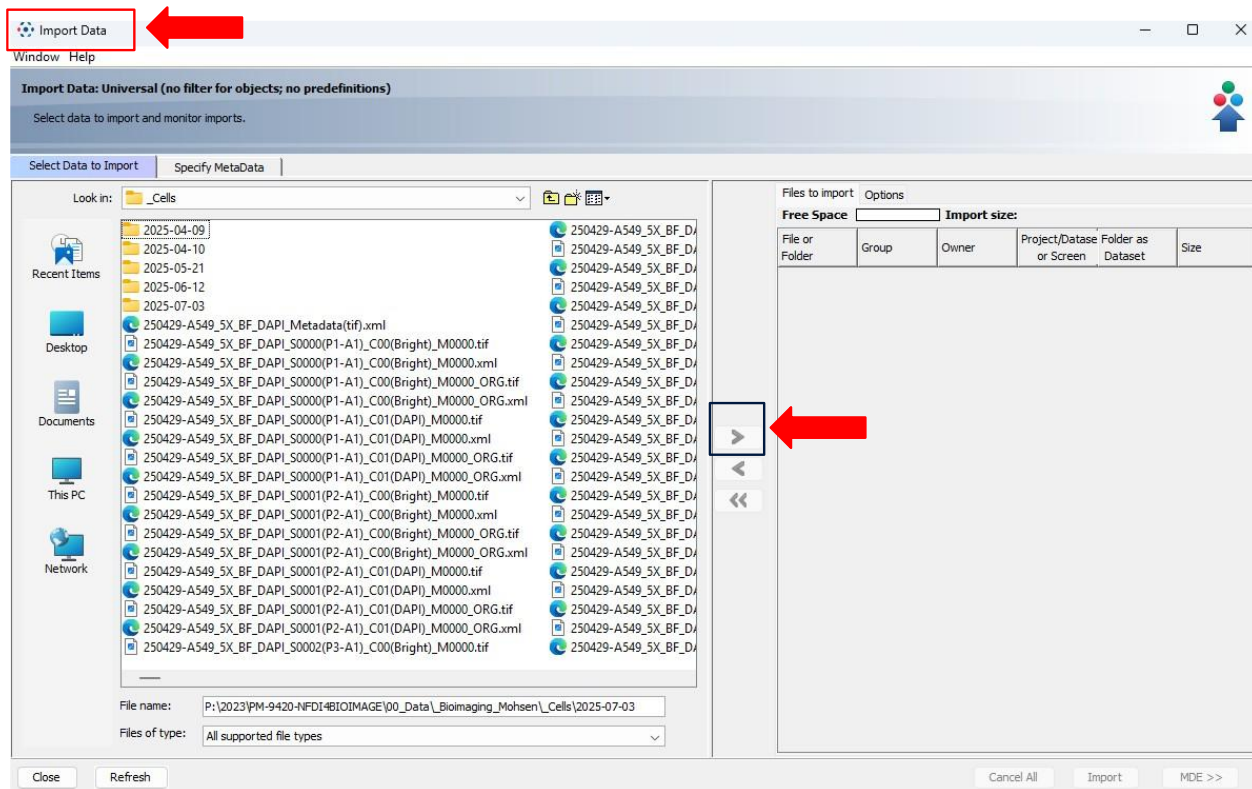
5.8.6

OMERO is distributed under the terms of the GNU GPL. For more information, visit [openmicroscopy.org](http://openmicroscopy.org)



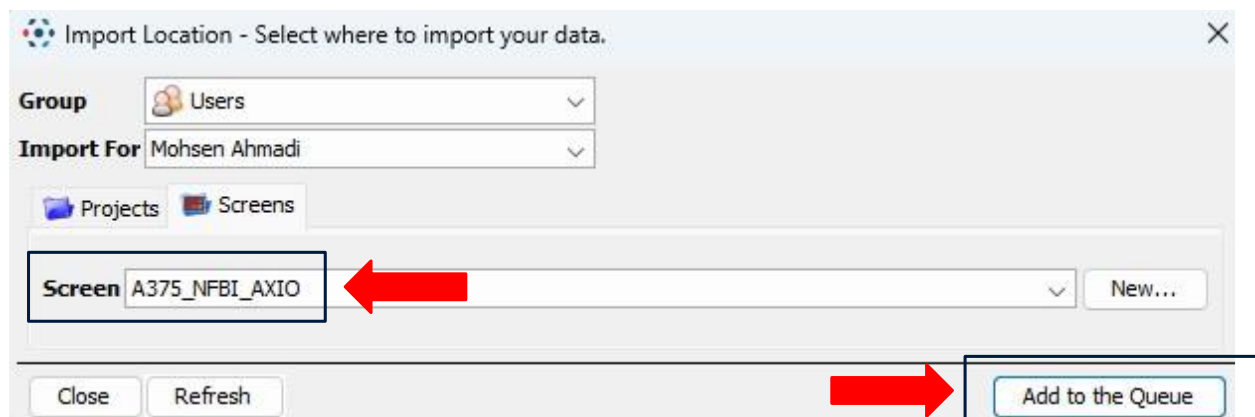
## 2. Open the “Import” dialog

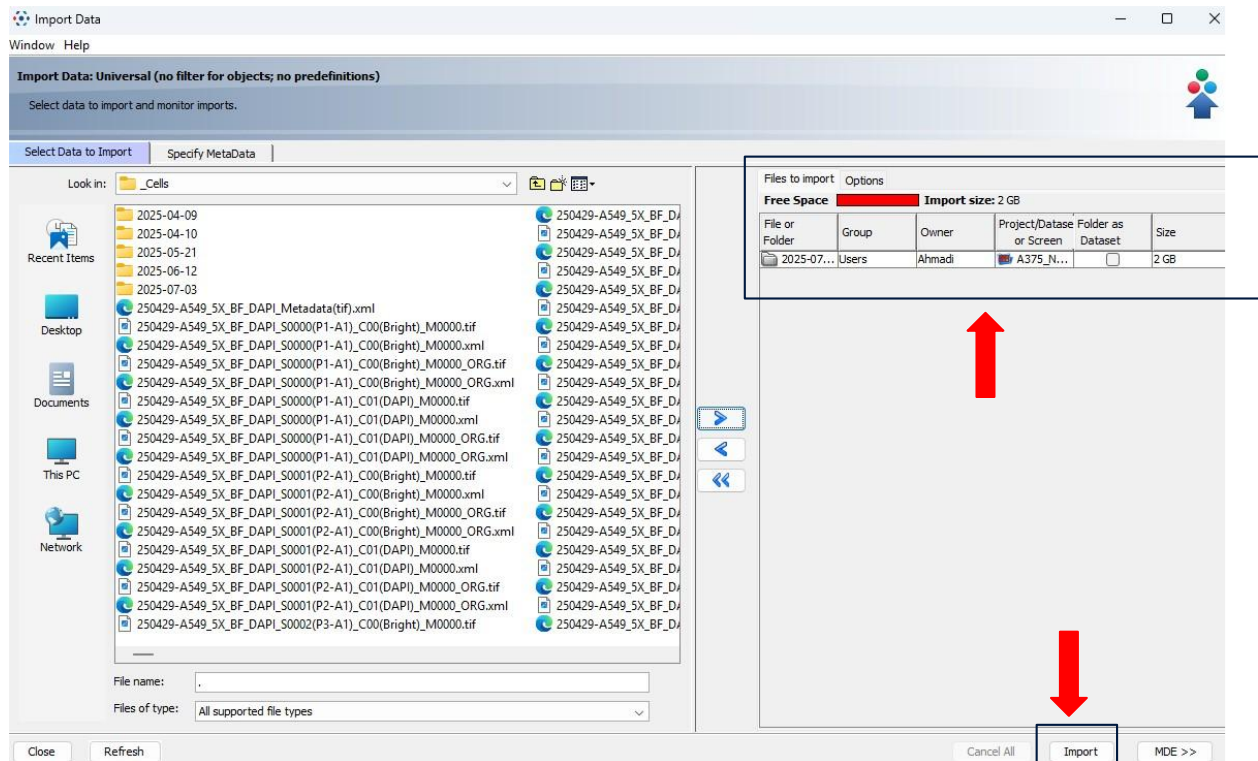
- In OMERO.insight, click the Import button (top toolbar).
- The *Import* window opens.
- In the left browser panel, navigate to the folder containing your .czi files.
- Select all relevant files (e.g. A375 images).
- Click the right arrow ( > ) to move them into the *Files to import* list.



### 3. Define the import destination (Screen)

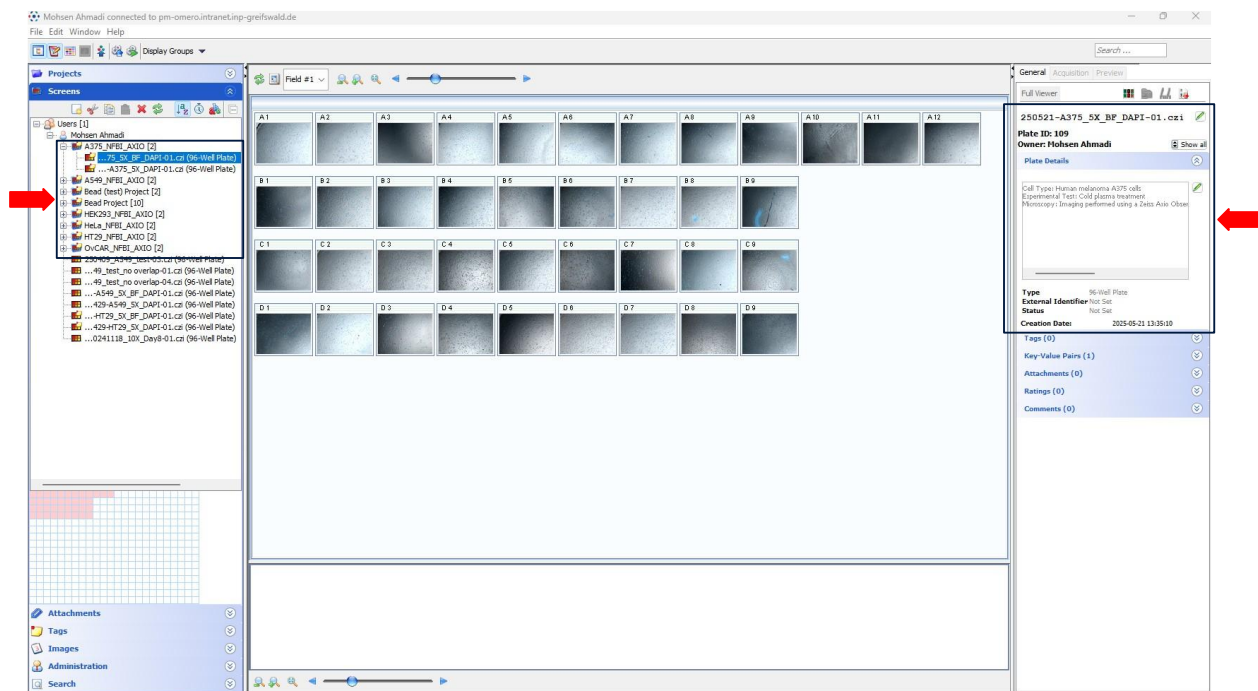
- In the *Import Location* section, choose:
  - Group: correct user/group.
  - Import to: select Screens.
- Either select an existing screen or click New... and create, e.g. Screen\_A375\_NFBI\_AXIO.
- Confirm the screen and click "Add to the Queue".
- Check that all files appear in the Import queue with the correct Screen and Well/Plate mapping.
- Click Import to start the upload and server-side conversion.





#### 4. Verify data in OMERO

- After completion, go back to the main OMERO.insight window.
- In the left tree, expand Screens → your Screen\_A375\_NFBI\_AXIO.
- Confirm that all images are listed and displayed as thumbnails.



# Stepwise data annotation in OMERO.web

## 1. Open OMERO.web & log in

- Navigate to your OMERO.web URL.
- Log in with your institutional credentials.

omero:4064 ▼

Username:

Password:

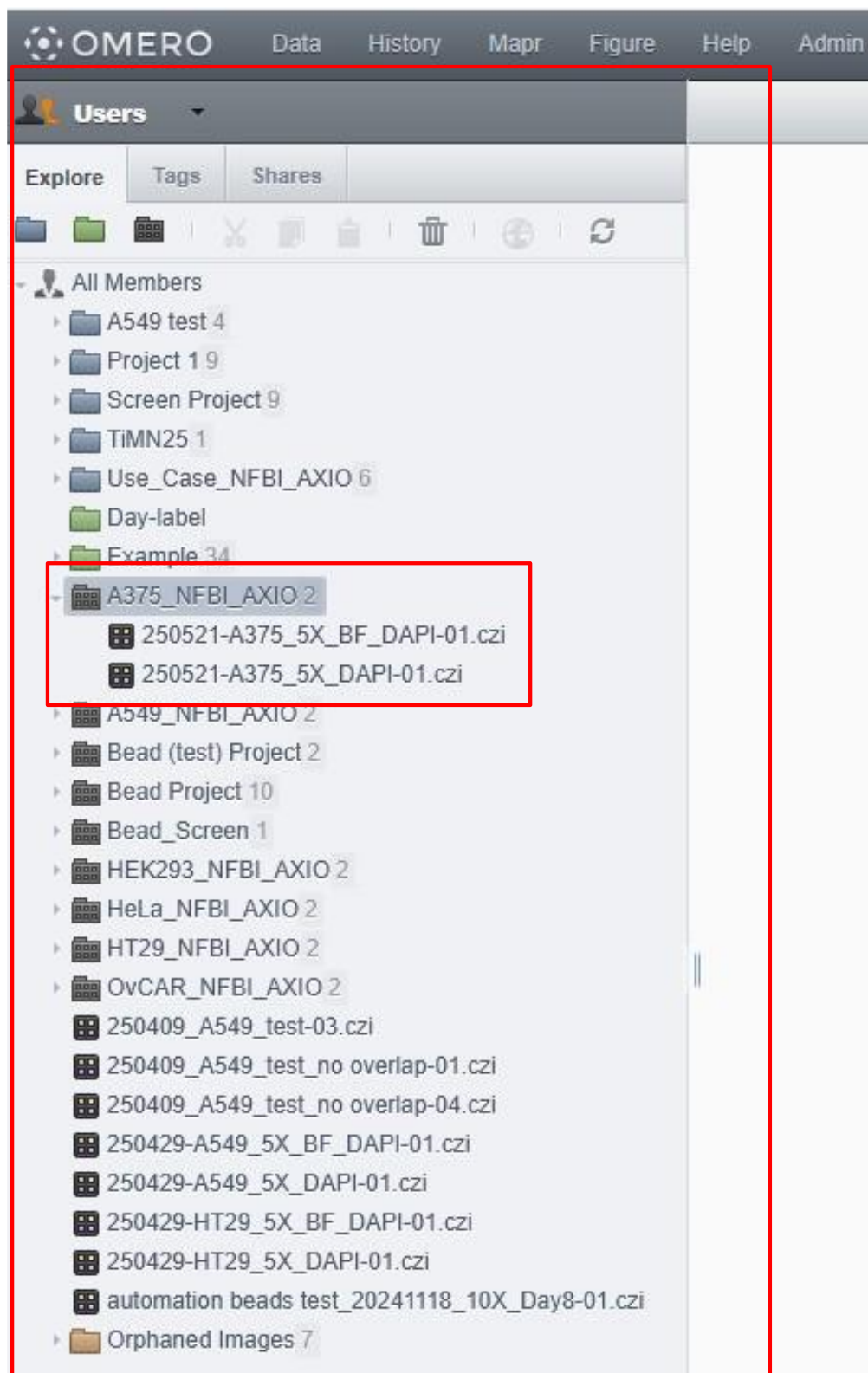
[Forgot your password?](#) [Login](#)

OMERO.web 5.20.0.  
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Download OMERO.insight for [Mac OS X](#), [Windows](#), [Linux](#)

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## 2. Navigate to the relevant Screen/Plate/Wells/Images

- Use the left panel (tree) to browse to the correct Screen → Plate → Well → Image.



### 3. Open the Metadata / Details panel of “Screen”

- On the right side, select the “General” tab.

- Screen metadata as Key–Value Pairs (KVPs) was added to the screen level using .JSON file created using Adamant and recorded on the eLabFTW.
- Tags can be created and add to the “Screen”.
- Attach supporting files (optional): In Attachments, upload relevant protocol PDFs, ELN exports, or README files, if needed.

General
Acquisition
Preview

A375\_NFBI\_AXIO

Screen ID: 101  
Owner: Mohsen Ahmadi
Show all

Screen Details

Cell Type: Human melanoma A375 cells  
Experimental Test: Cold plasma treatment  
Microscopy: Imaging performed using a Zeiss Axio Observer Z1 microscope equipped with brightfield and DAPI fluorescence channels

Creation Date: 2025-05-06 10:16:06  
Plate Count: 2 plates

Tags 0

Key-Value Pairs 1

Add Key Add Value

Screen metadata

Added by: Robert Wagner

screenID	INP_SBR
screenTitle	A375_NFBI_AXIO
screenAuthor	Steven Böttcher
screenDescription	Treated cells with Plasma under different height and time conditions
screenDate	2025-05-21

Attachments 0

Comments 0

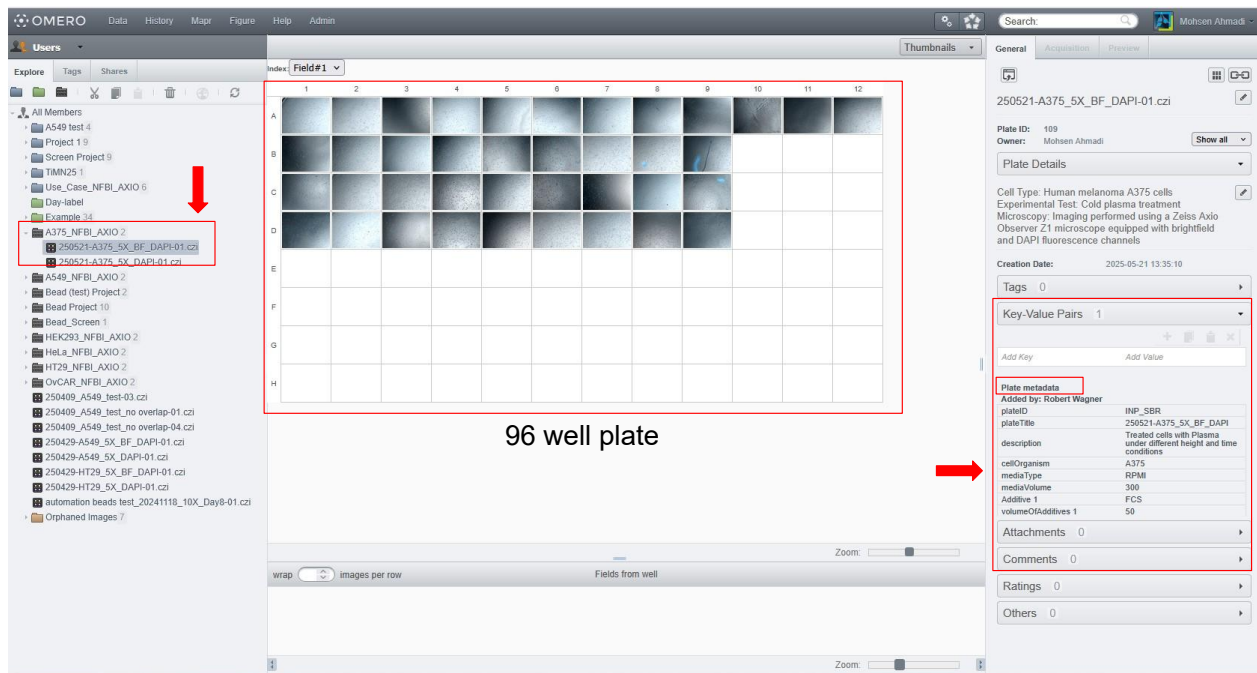
Ratings 0

Others 0

#### 4. View “Plate” overview

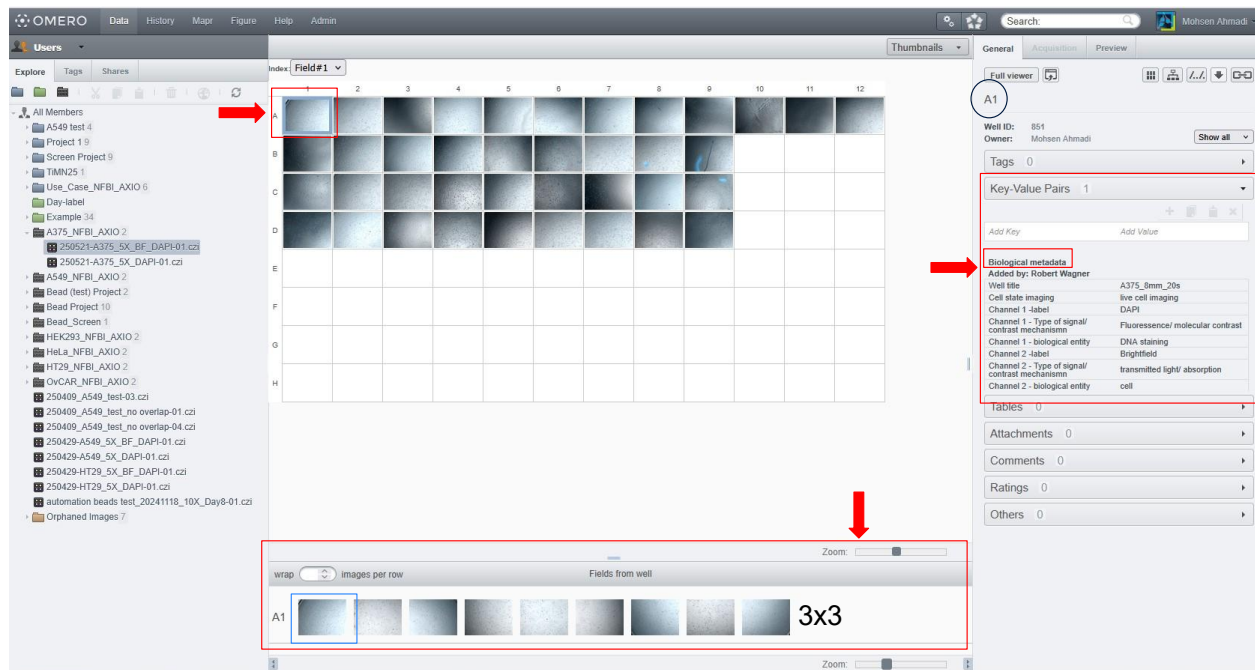


- The central panel displays the layout of the 96-well plate, showing thumbnails of all acquired image fields.
- Each well corresponds to 9 images (3x3 positions), allowing for structured visualization of datasets.
- On the right side, the “General” tab expands the KVPs section contain the plate metadata.
- Structured metadata was added using the .JSON file and the KVPs can be viewed for the selected plate.
- Attach supporting files (optional): In Attachments, upload relevant protocol PDFs, ELN exports, or README files, if needed.



## 5. View “Wells” overview

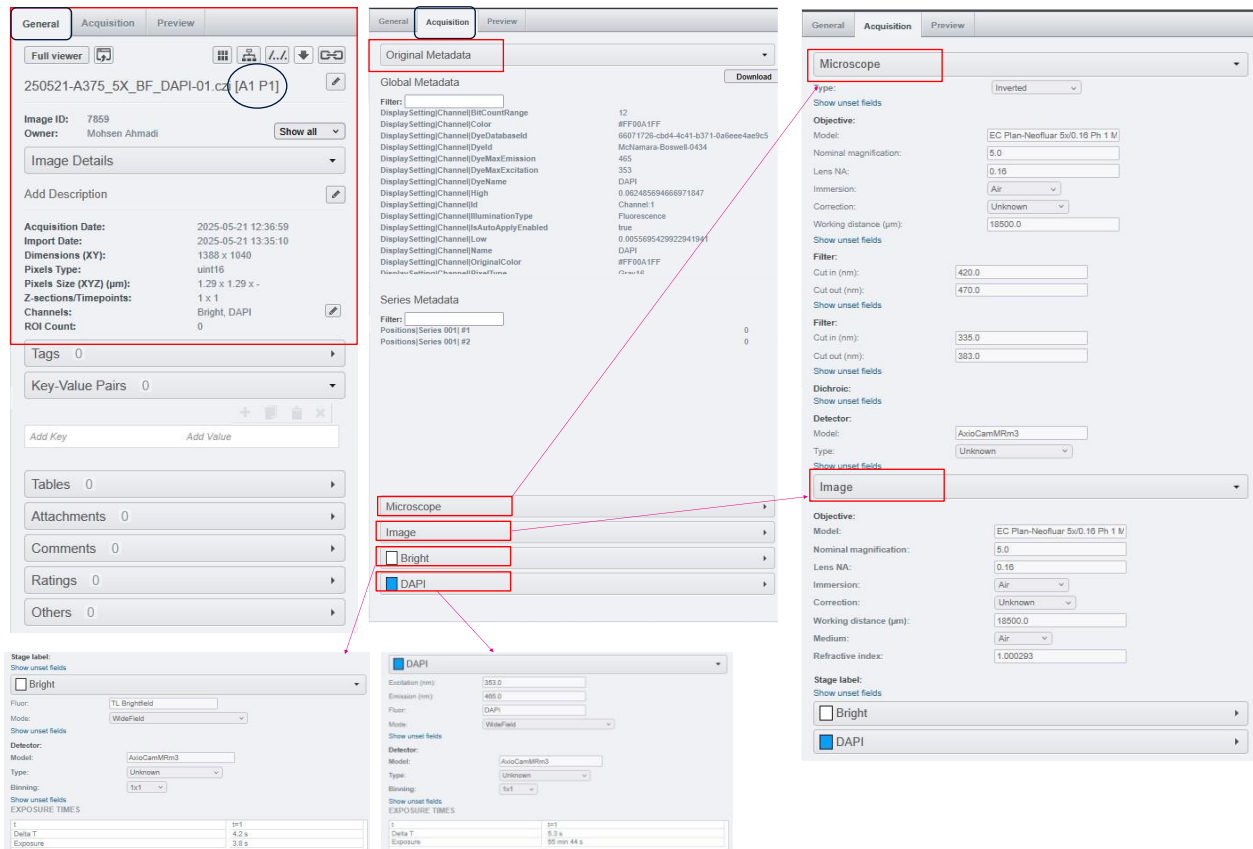
- Select the Well of interest.
- In the down navigation panel, expand the wells images (layout 3x3).
- In the right navigation panel, “General” tab expand the KVPs section contain the well metadata (biological metadata).
- Attach supporting files (optional): In Attachments, upload relevant protocol PDFs, ELN exports, or README files, if needed.



## 6. View “Images” overview

- Select the image of interest.
- On the right side, click on the “General” tab and expand the “General metadata” for well “A1” position “P1”.
- On the right side, click on the “Acquisition” tab to review embedded microscope information imported automatically with the image (*original metadata*, *microscope metadata*, and *image/channel* (e.g., Brightfield/DAPI metadata)).

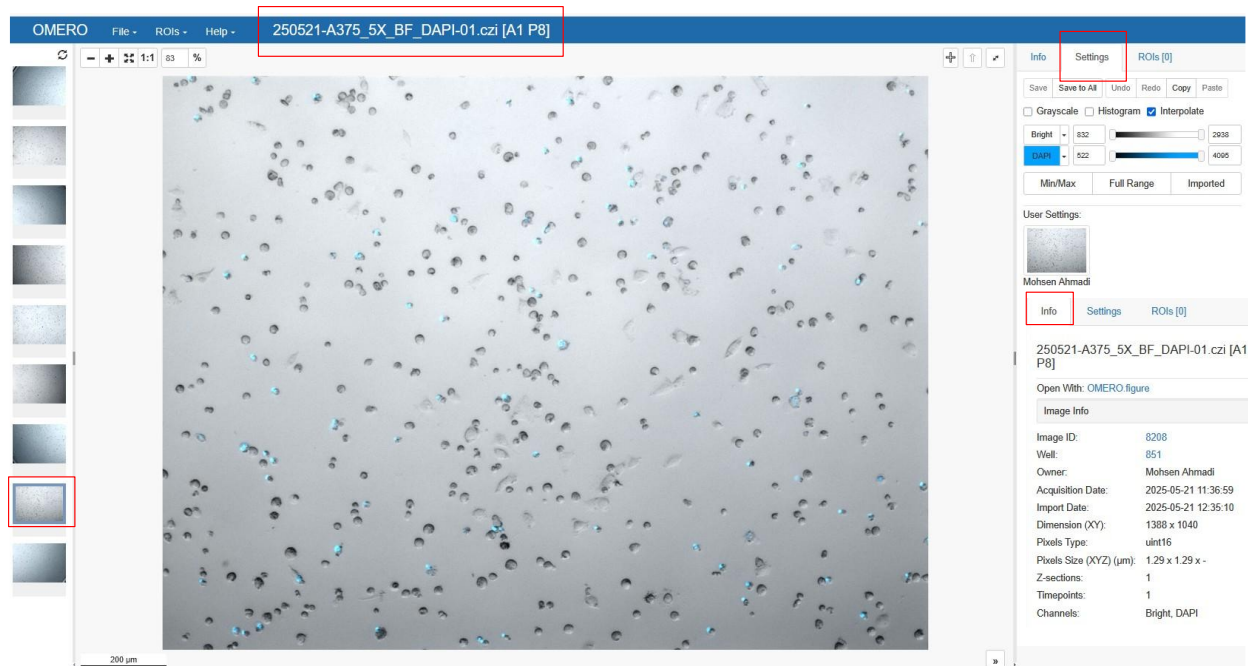




## Image visualization and channel adjustment in OMERO.web using OMERO.iviewer

### 1. Open the image by double click on it in OMERO.iviewer

- From the left-hand dataset panel, select the desired image file.
- The image opens in the central viewer window with thumbnails of all fields displayed along the left side.
- Each thumbnail represents a different image position captured during acquisition.
- Use the right-side “Settings” panel to toggle between available channels (e.g., *Brightfield* and *DAPI*).
- Adjust brightness, contrast, and color mapping to visualize overlaid nuclear staining (DAPI, shown in blue) on the brightfield background.
- Under “Histogram Settings”, refine intensity scaling using the *Min/Max* sliders.
- Apply *Full Range* to reset or imported to restore original settings from the acquisition metadata.
- Ensure cell nuclei and morphological features are clearly distinguishable.
- In the “Info” tab, verify acquisition parameters such as pixel dimensions (e.g.,  $1.29 \mu\text{m} \times 1.29 \mu\text{m}$ ), number of Z-sections, timepoints, and channels.
- Visually compare multiple fields (e.g., *A1 P8* vs. *A7 P5*) to assess cell density, staining intensity, or morphological differences resulting from plasma exposure or other treatments.



## 2. Save or export adjusted views (Optional)

- Use Save as .tiff or Open with OMERO.iviewer to generate publication-quality images.