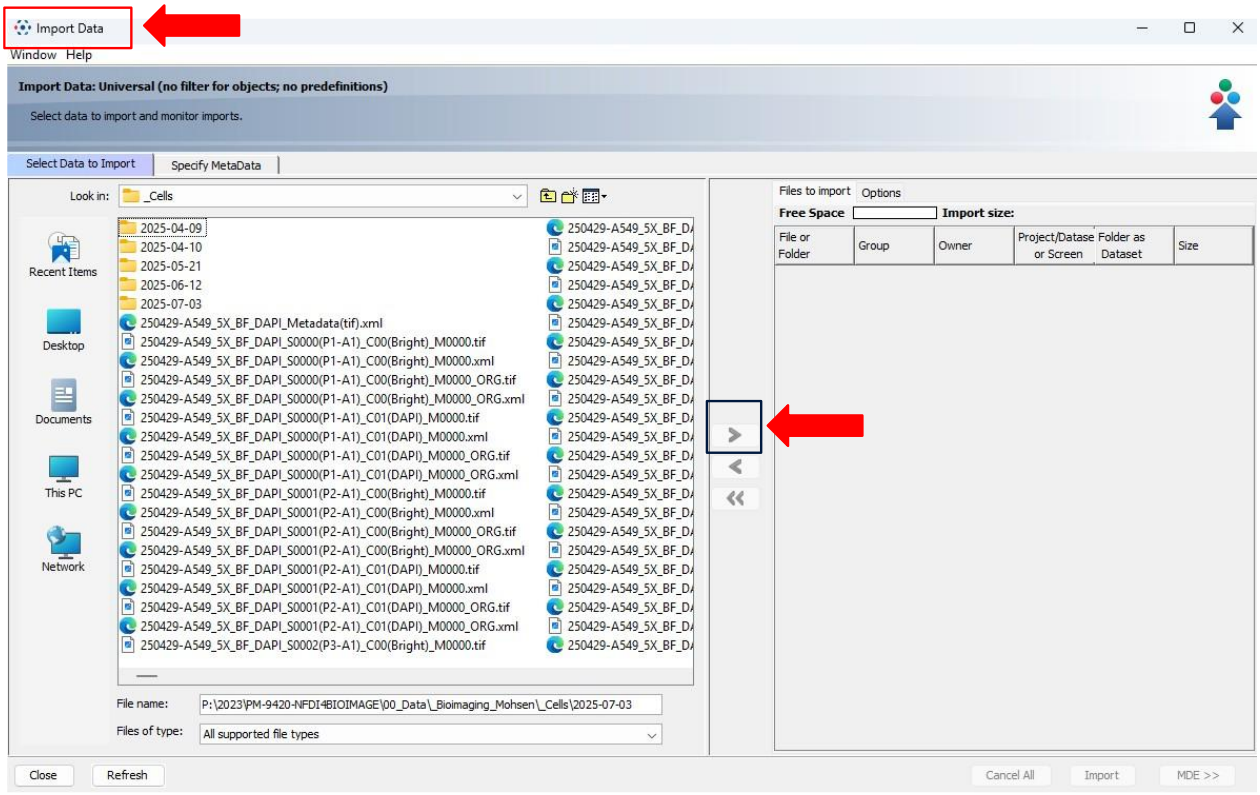
Data import using OMERO.insight

1. Start OMERO.insight & log in

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

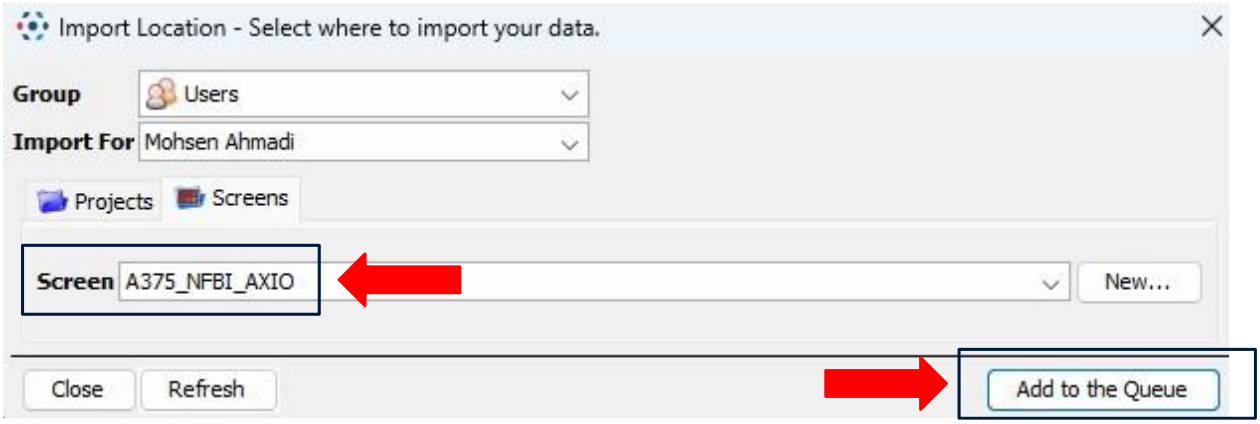
2. Open the “Import” dialog

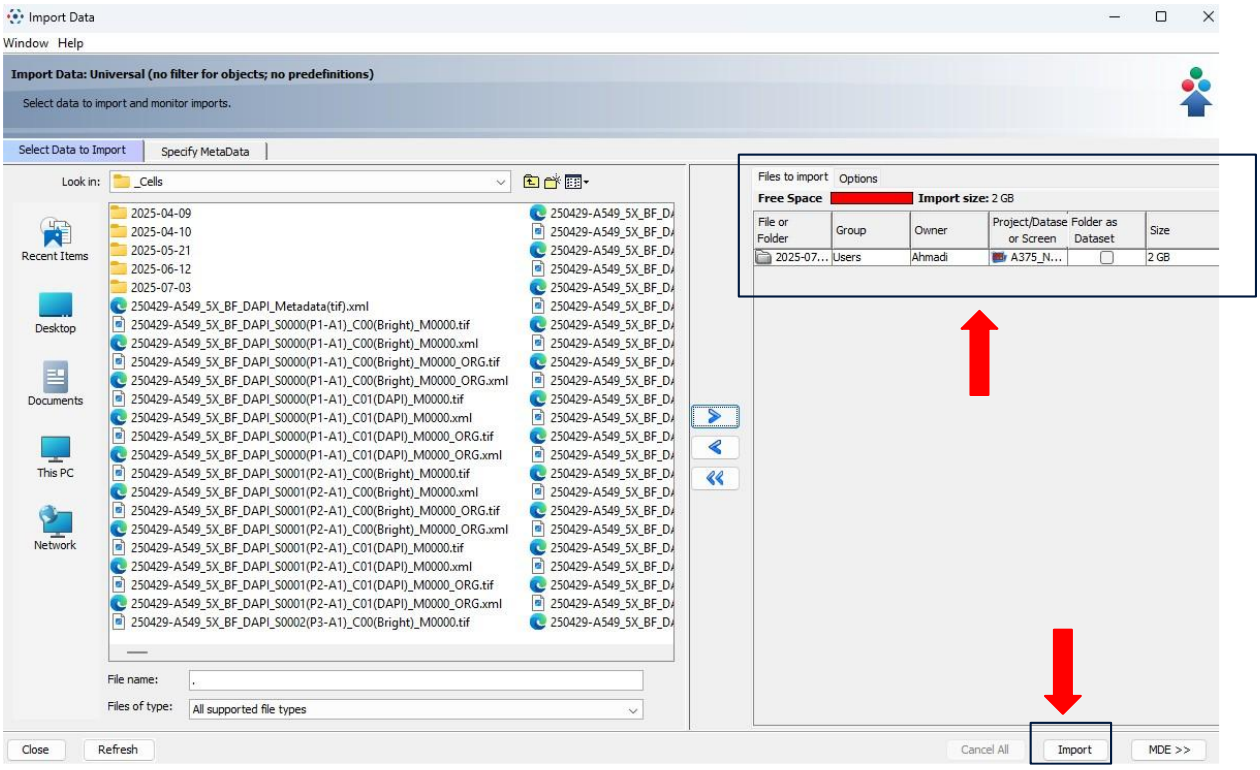
- In OMERO.insight, click the Import button (top toolbar).
- The *Import* window opens.
- In the left browser panel, navigate to the folder containing your .czi files.
- Select all relevant files (e.g. A375 images).
- Click the right arrow (>) to move them into the *Files to import* list.



3. Define the import destination (Screen)

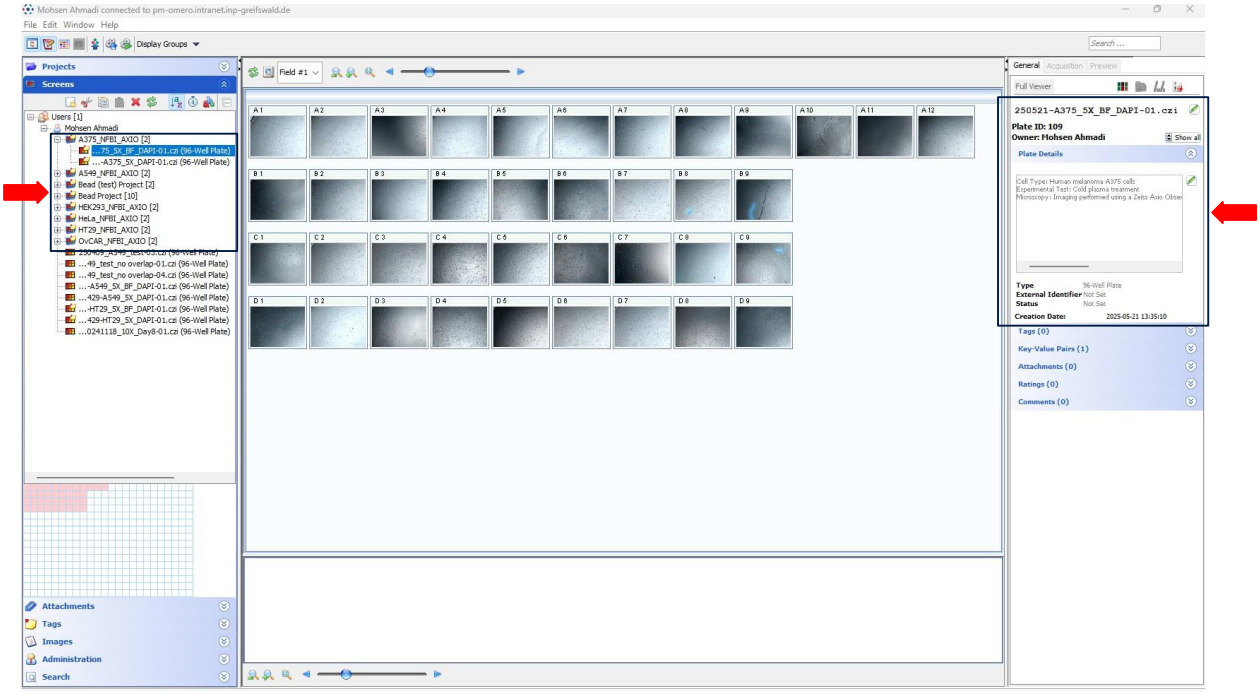
- In the *Import Location* section, choose:
  - Group**:** correct user/group.
  - Import to**:** select Screens**.**
- Either select an existing screen or click New… and create, e.g. Screen_A375_NFBI_AXIO.
- Confirm the screen and click “Add to the Queue”.
- Check that all files appear in the Import 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.



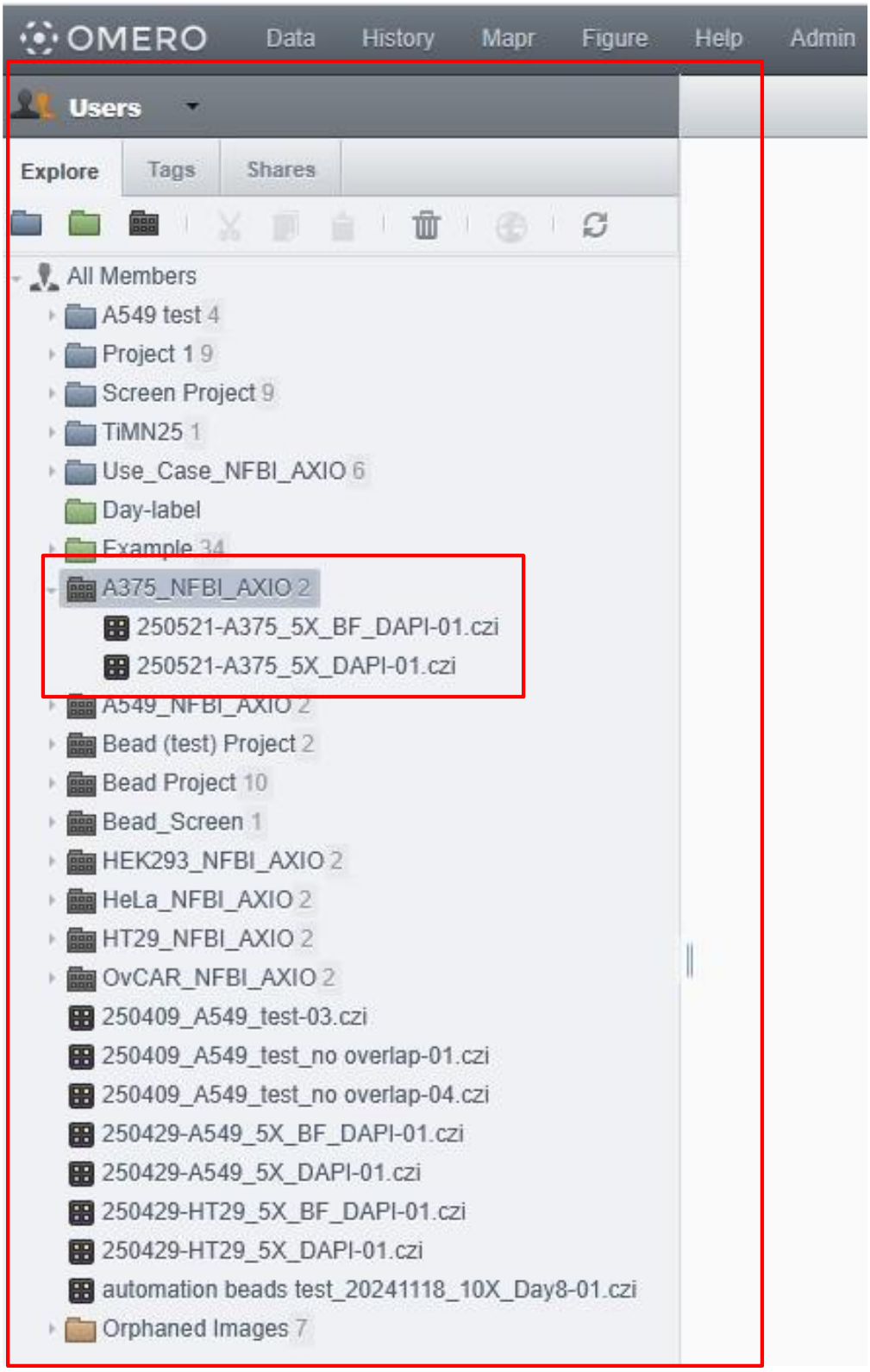
Stepwise data annotation in OMERO.web

1. Open OMERO.web & log in

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

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

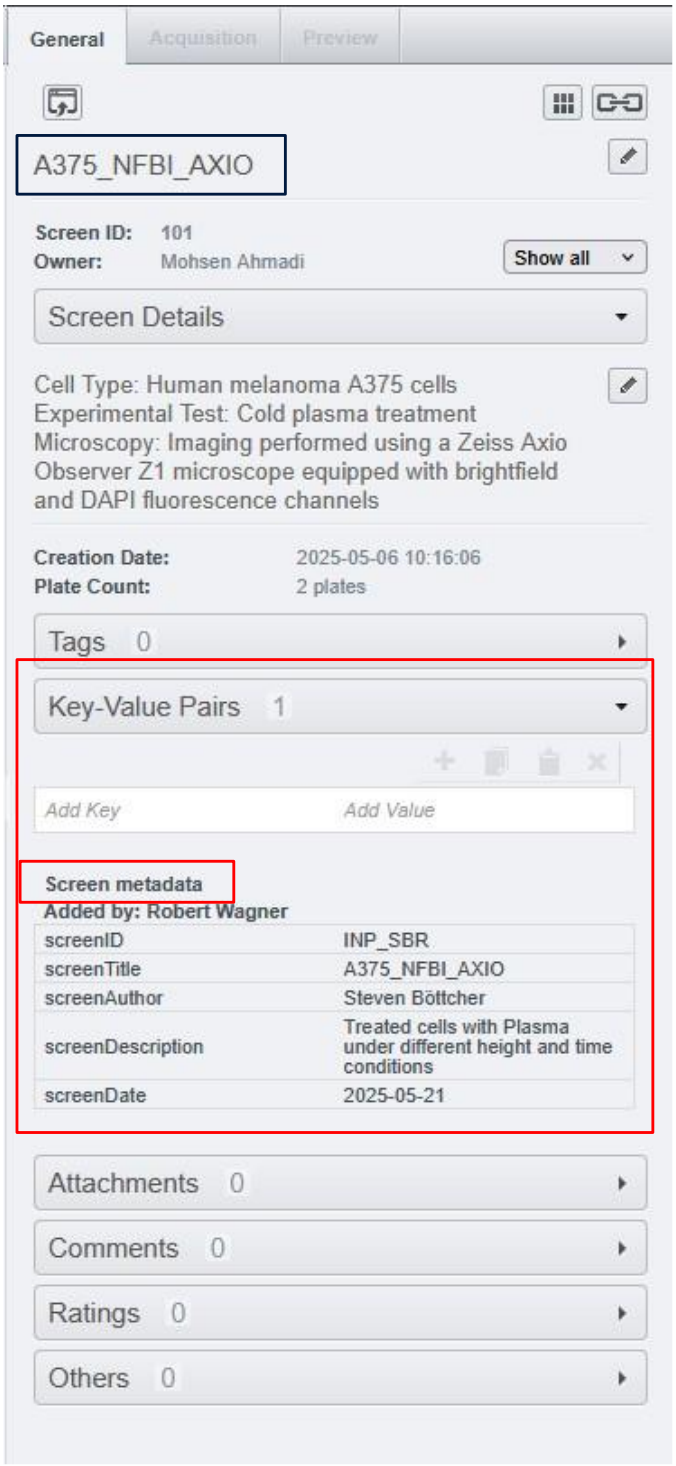
- Use the left panel (tree) to browse to the correct Screen → Plate → Well → Image.



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

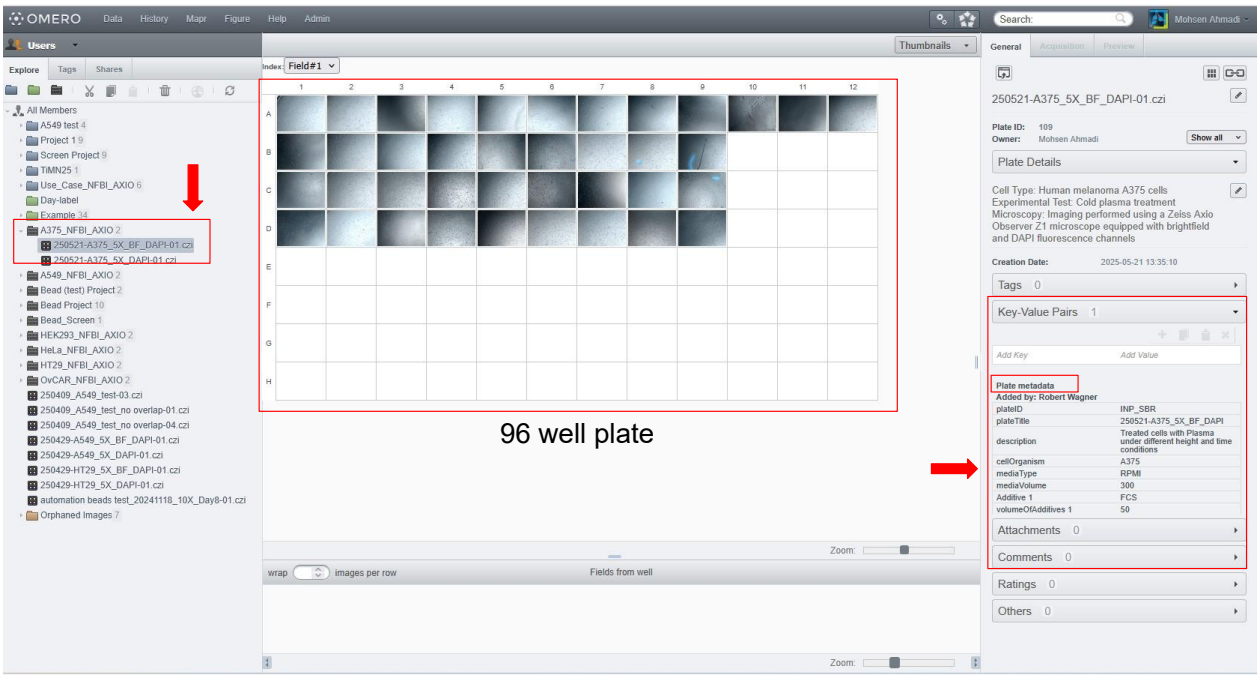
- On the right side, select the **“**General” tab.

- 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.



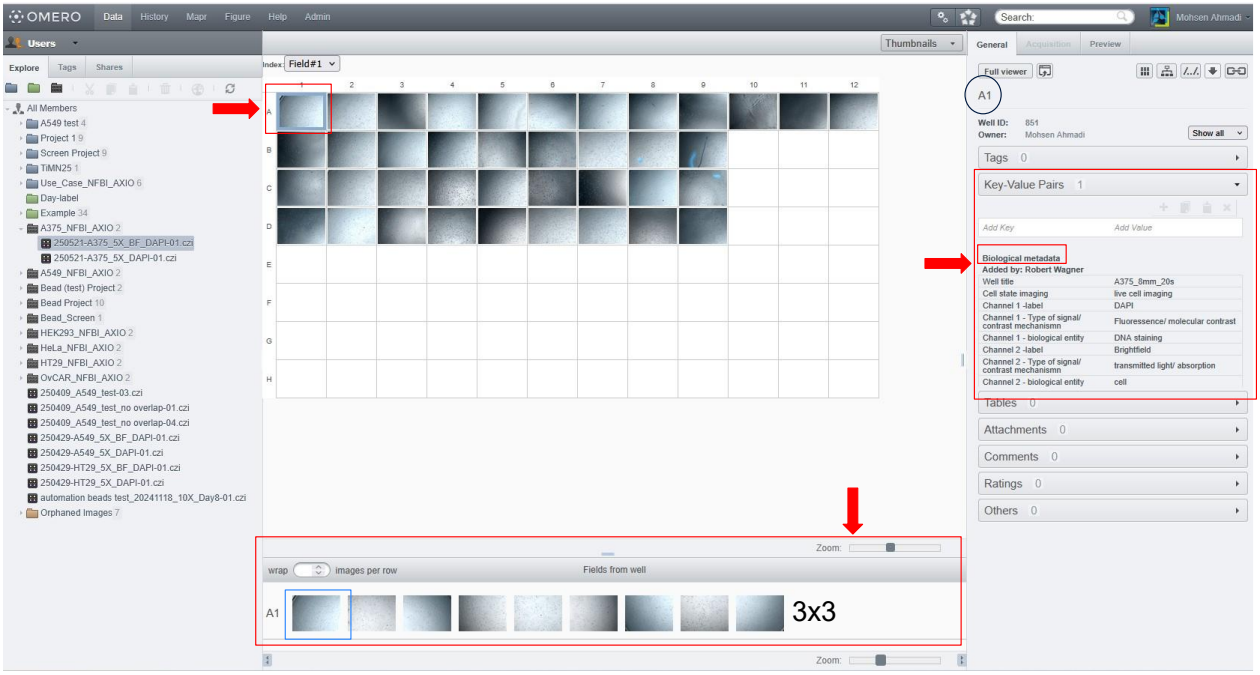
4. View “Plate” overview

- 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 3×3).
- 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).

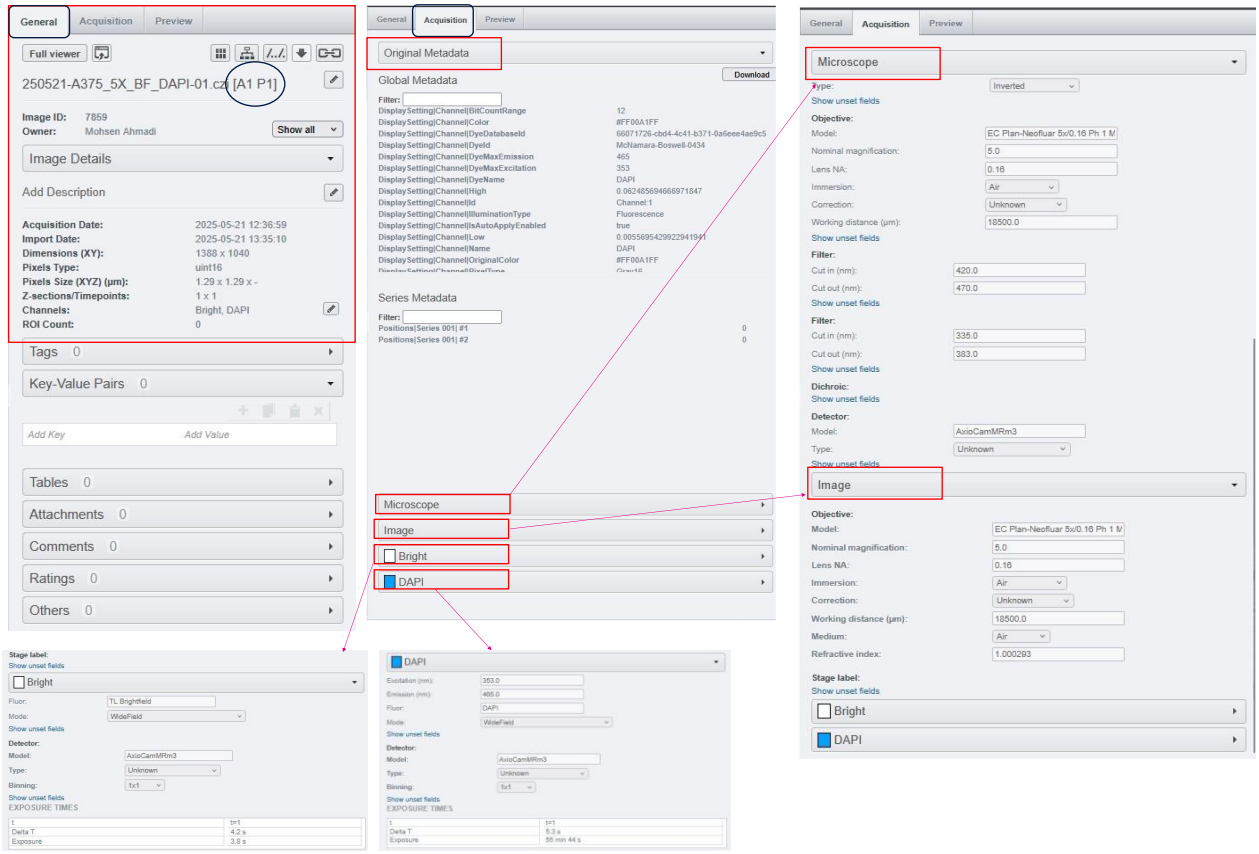
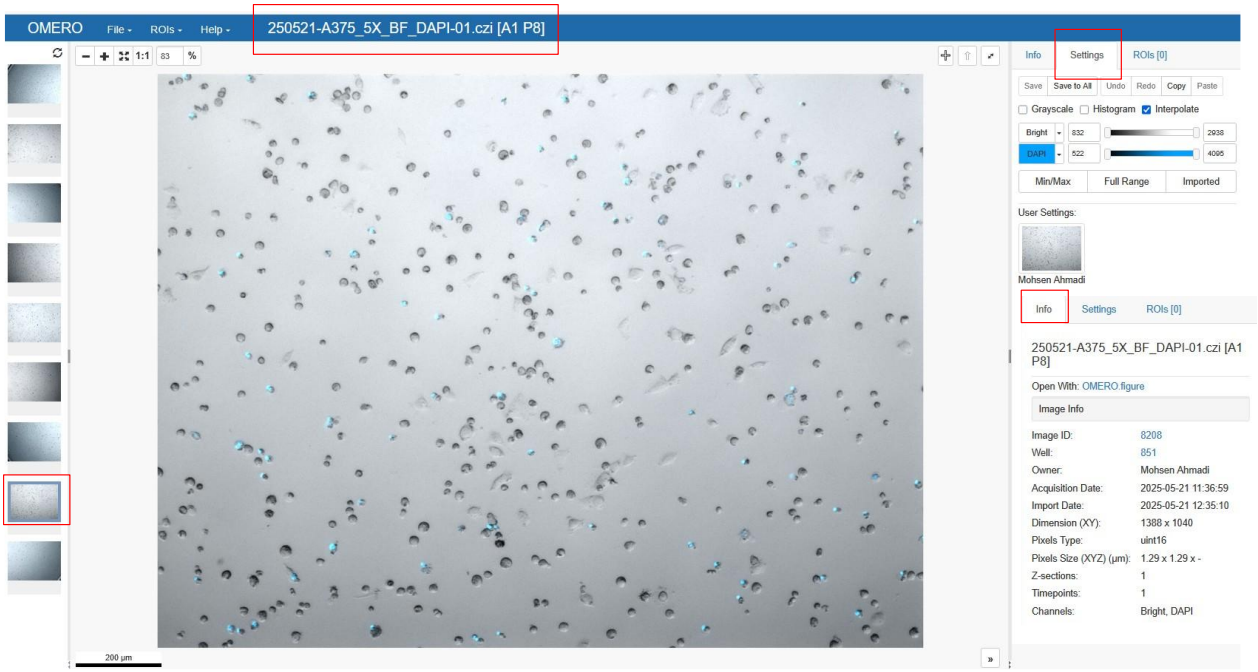


Image visualization and channel adjustment in OMERO.web using OMERO.iviewer

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 overlayed 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 µm × 1.29 µm), 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.