

Viewing Data

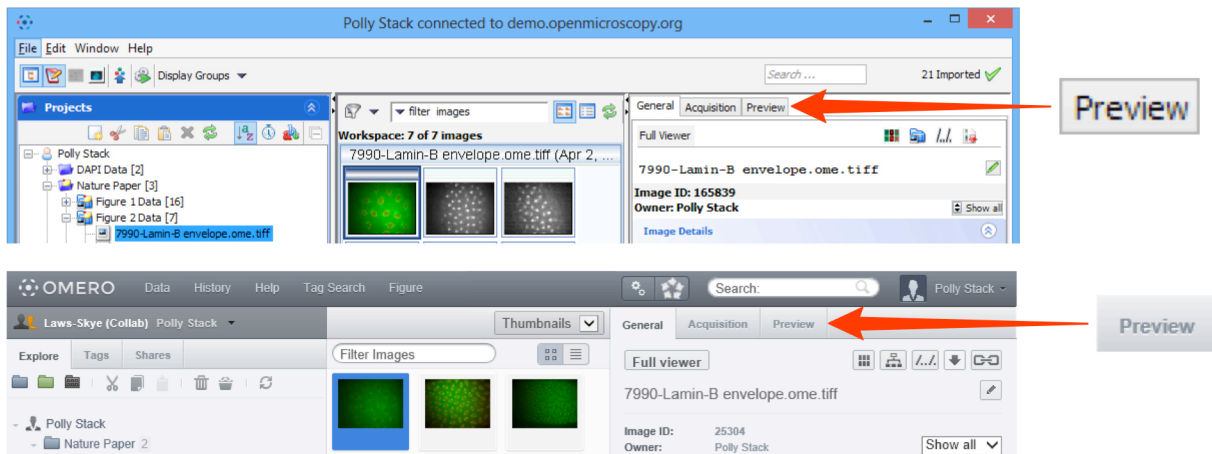
The workflows for using OMERO.insight and OMERO.web to view and work with image data are essentially the same in both clients.

- 1 Data can be viewed in two ways using:
 - the Preview pane on the right hand side panel
 or
 - the Full Viewer

The functionality of the controls in both viewers is the same.

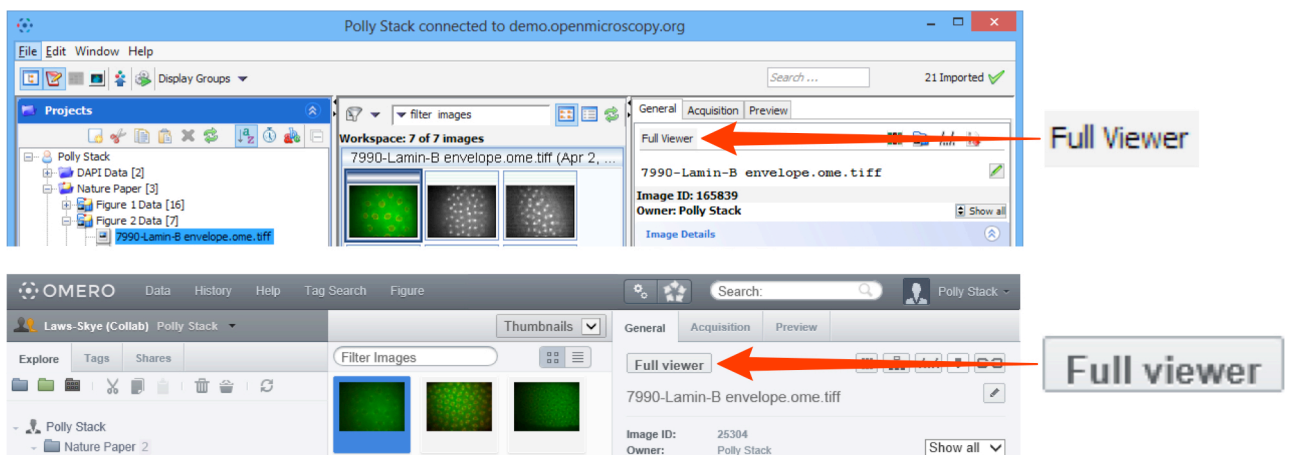
Select an image in the data tree or the central panel.

To view the image in the Preview pane click on the **Preview** tab in the right hand panel.



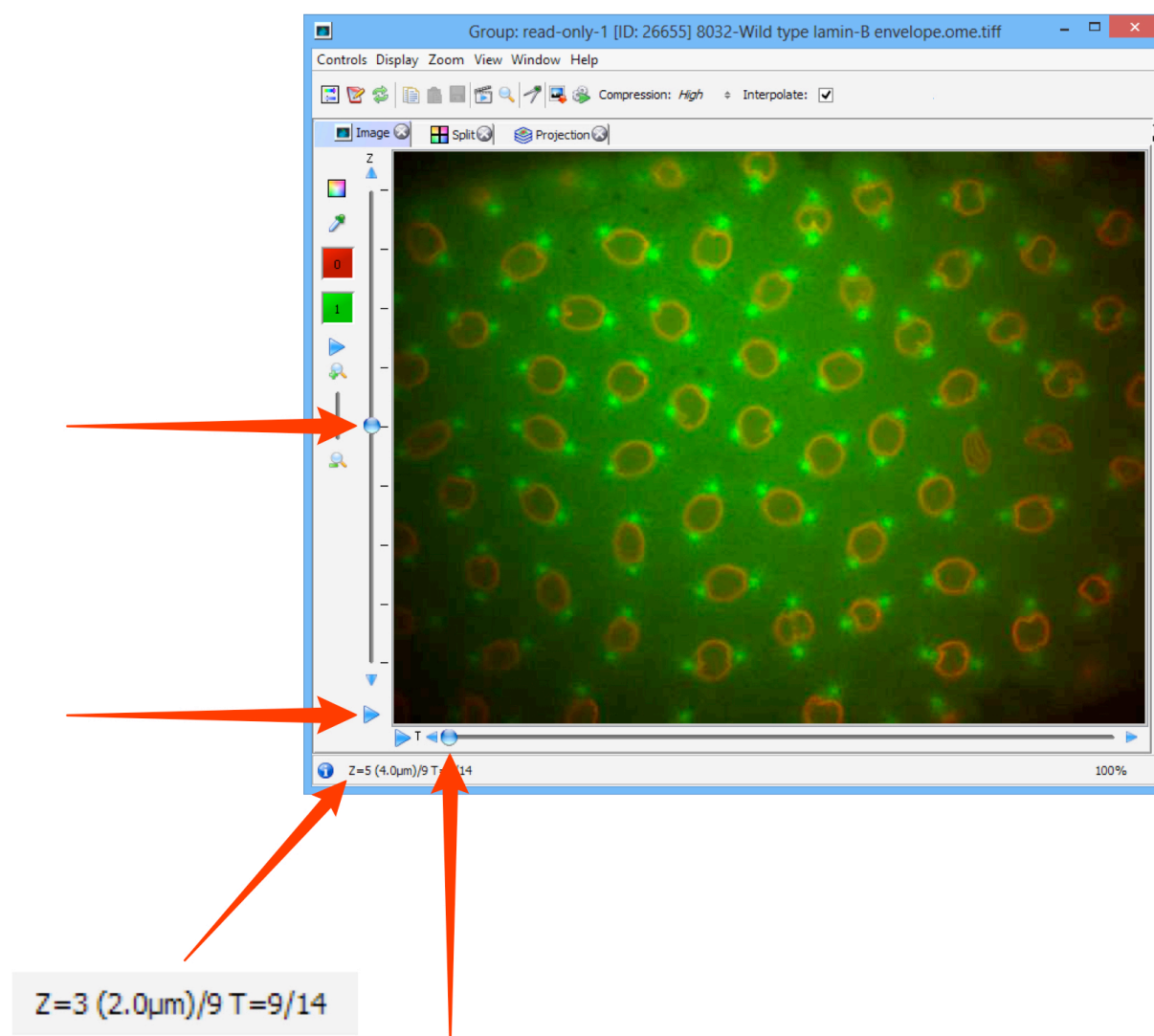
To view the image in the Full Viewer double-click on the image in the data tree or the thumbnail in the centre pane.

- or select the image and click on the **Full Viewer** button in the General or Preview panes in the right hand panel (also in the main toolbar in OMERO.insight).



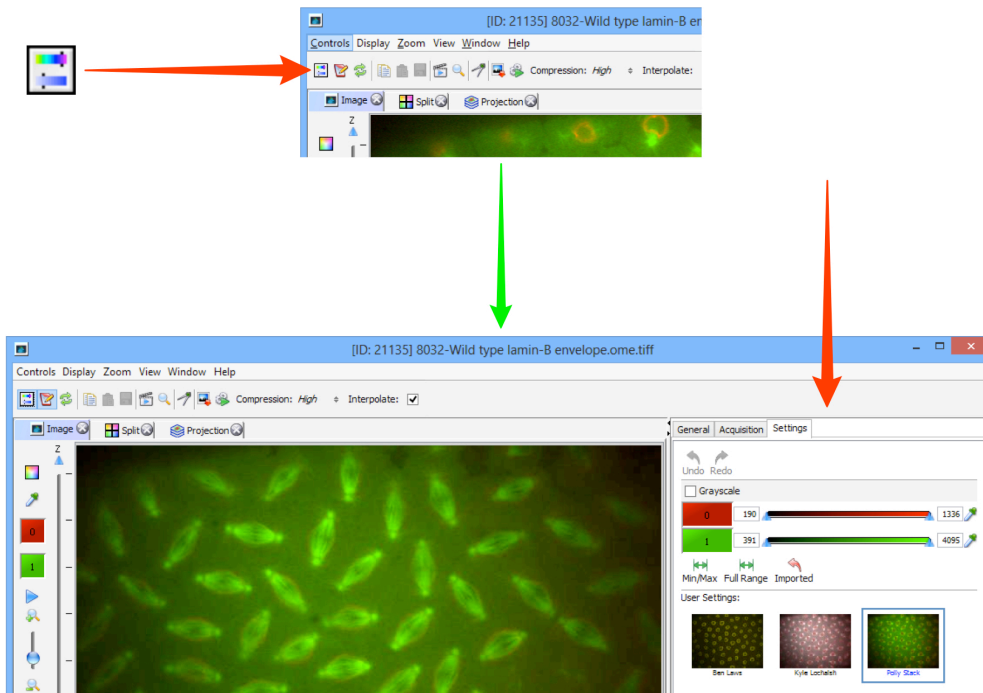
Note: The functionality and way the controls behave is essentially the same in the Full Viewer and Preview pane in both clients, and between OMERO.insight and OMERO.web.

- 2 Step through any Z stack using the slider on the left side or clicking on the up or down arrows at either end.
If the image data includes a time sequence, step or play through the time sequence (T) using the controls at the bottom of the viewer window.
Click the **Play** arrows at the the ends of the sliders to play through the Z stack or time points.
Z and T information is displayed in the bottom left corner.

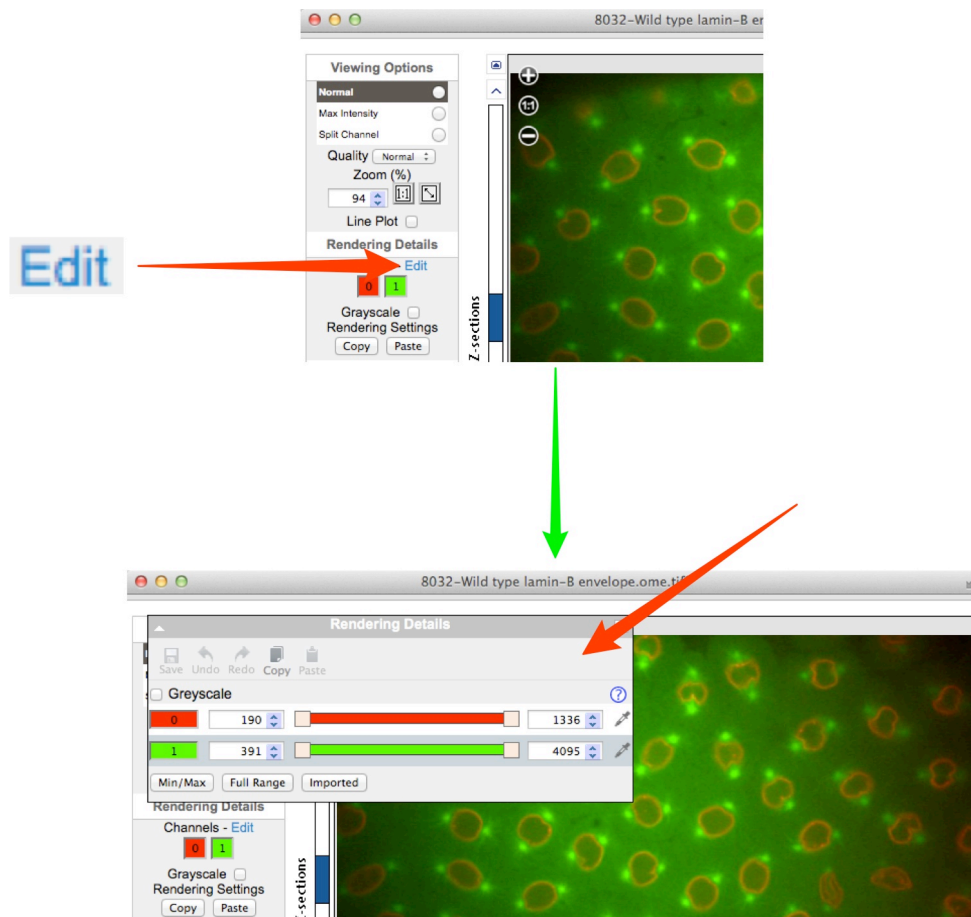


Data from JCB: Civelekoglu-Scholey et al., JCB, doi: 10.1083/jcb.200908150

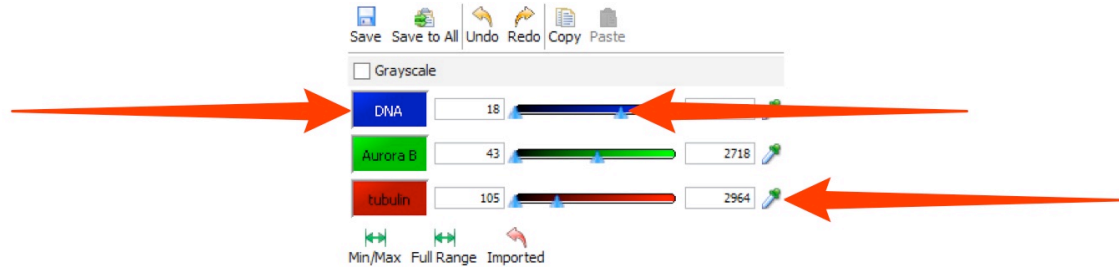
- 3 In the OMERO.insight Full Viewer, click on the icon to access the rendering settings controls.



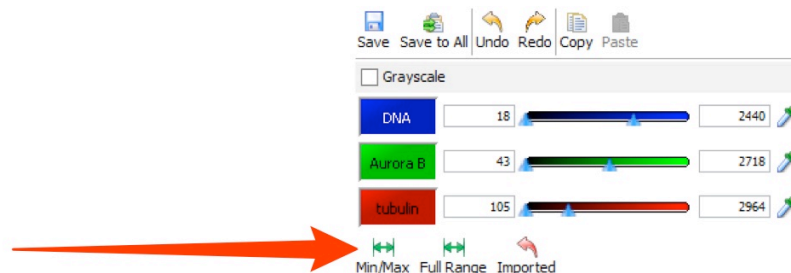
- 4 In the OMERO.web Full Viewer, click on the **Edit** link to open the rendering settings controls.



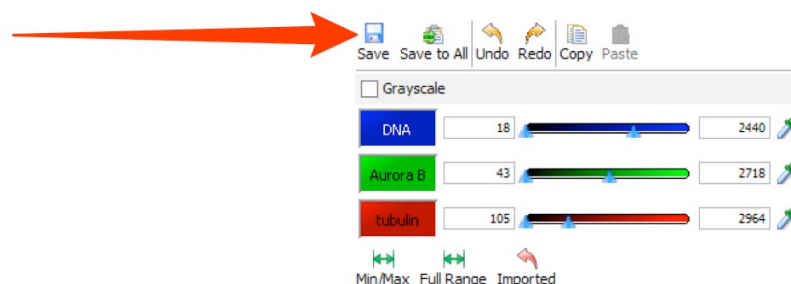
- 5 Click on the channel wells to toggle channels on or off.
Intensity values can be adjusted using the slider, or entered in the text boxes.
Click on the colour-picker to change the colour assigned to a channel.



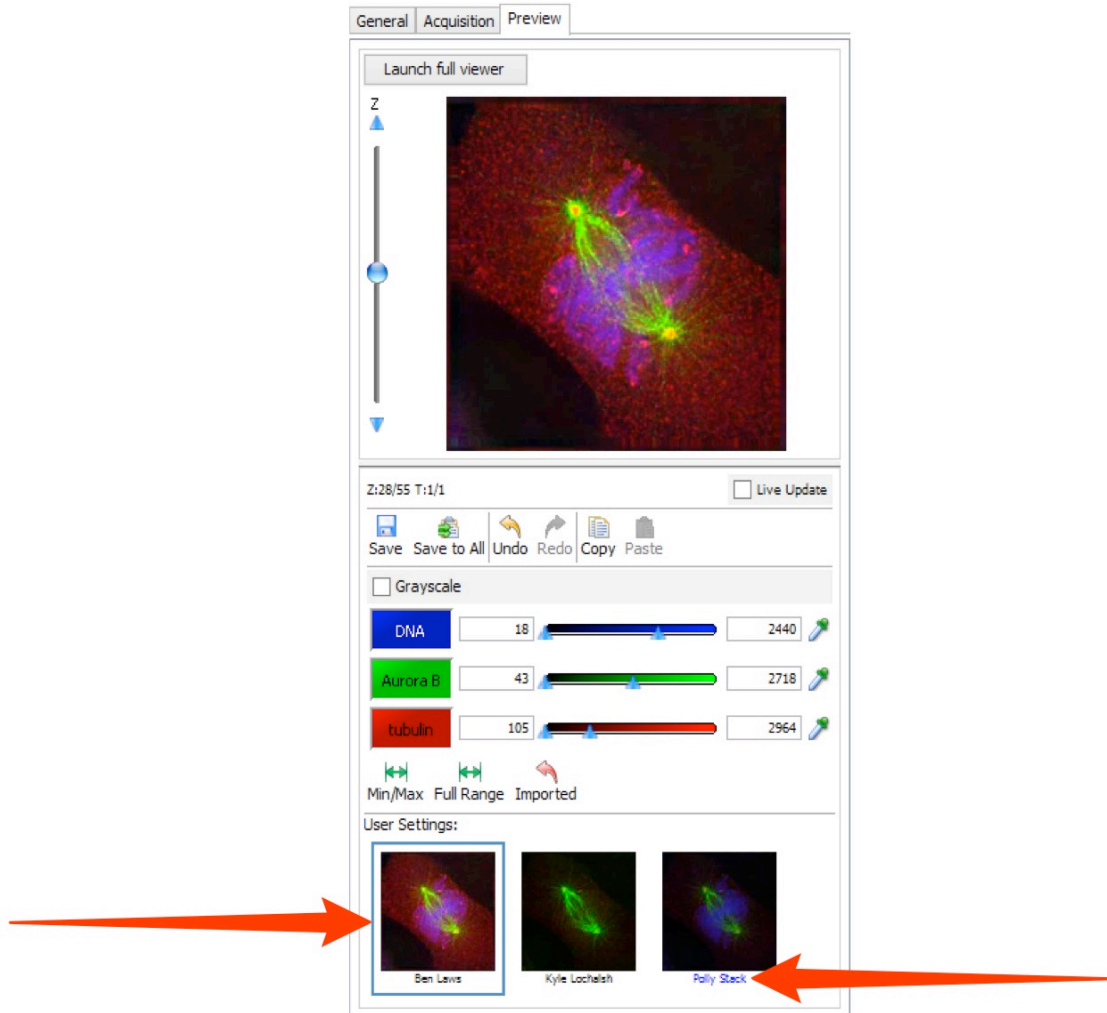
- 6 Click **Min/Max** to reset the slider values to the range for the image type.
Click **Full Range** to set the range of values to the minimum and maximum range of the pixel type of the image.
These values can be over-ridden by typing in the text box.
Click **Imported** to return all rendering to settings at import.



- 7 Click **Save** to save the rendering settings as yours and update the user settings thumbnail.
Selecting another user's settings, or another image, before saving your settings will lose any changes you have made.
Click **Save to All** to save the rendering settings to all images of the same type in the dataset.
Undo and **Redo**, and **Copy** and **Paste**, are available by keyboard shortcuts or the buttons at all times.



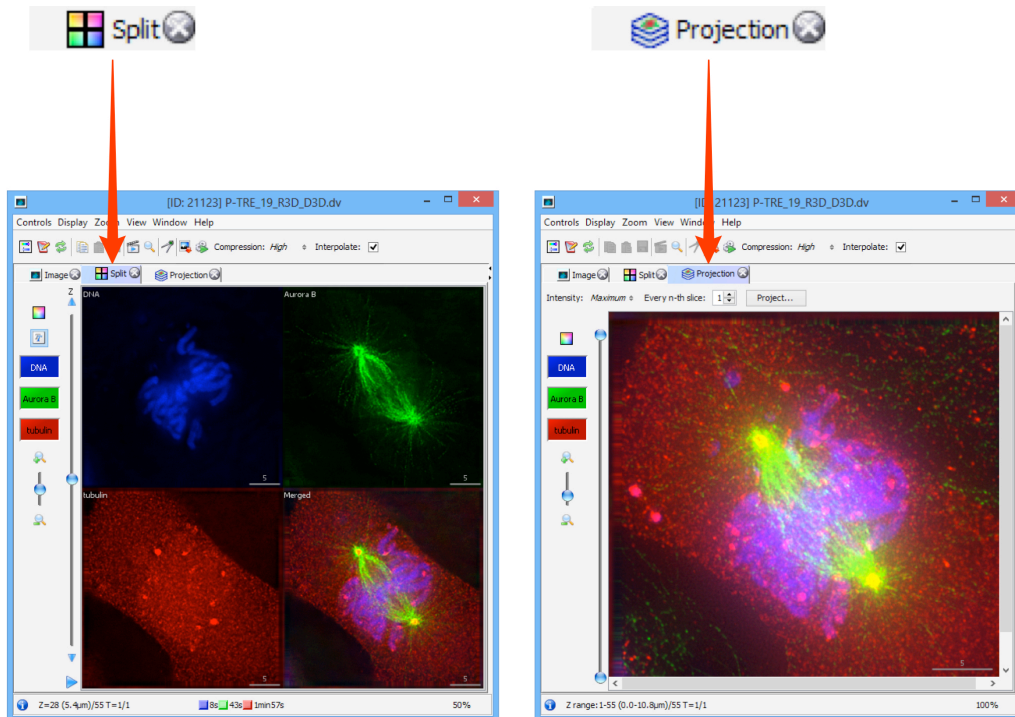
- 8 In appropriate groups other users can save their rendering settings for an image. Click on the thumbnail to select the settings saved by a user. The thumbnail for the currently selected settings is highlighted in blue. The settings belonging to the image's owner are distinguished by the blue text label.



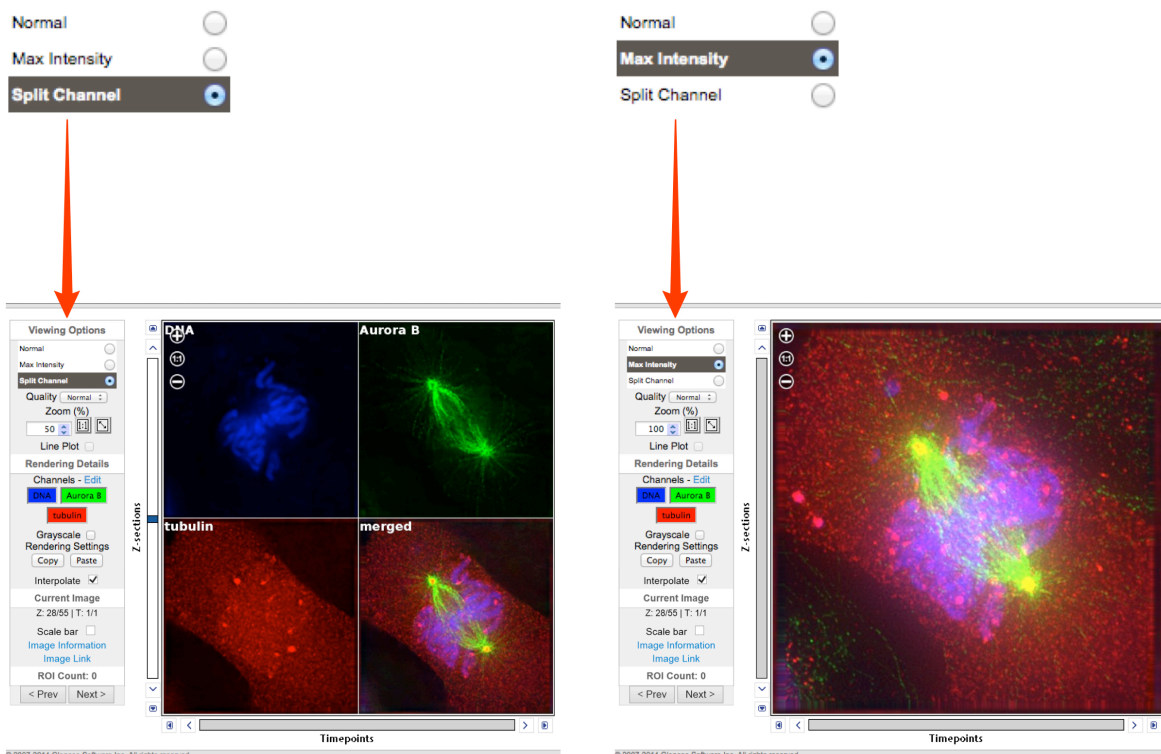
Full Viewer

- 9 Select the tabs above the image to show a **Split** channel and **Projection** views of the image data.
In the OMERO.web viewer select a **Split Channel** and **Max Intensity**.

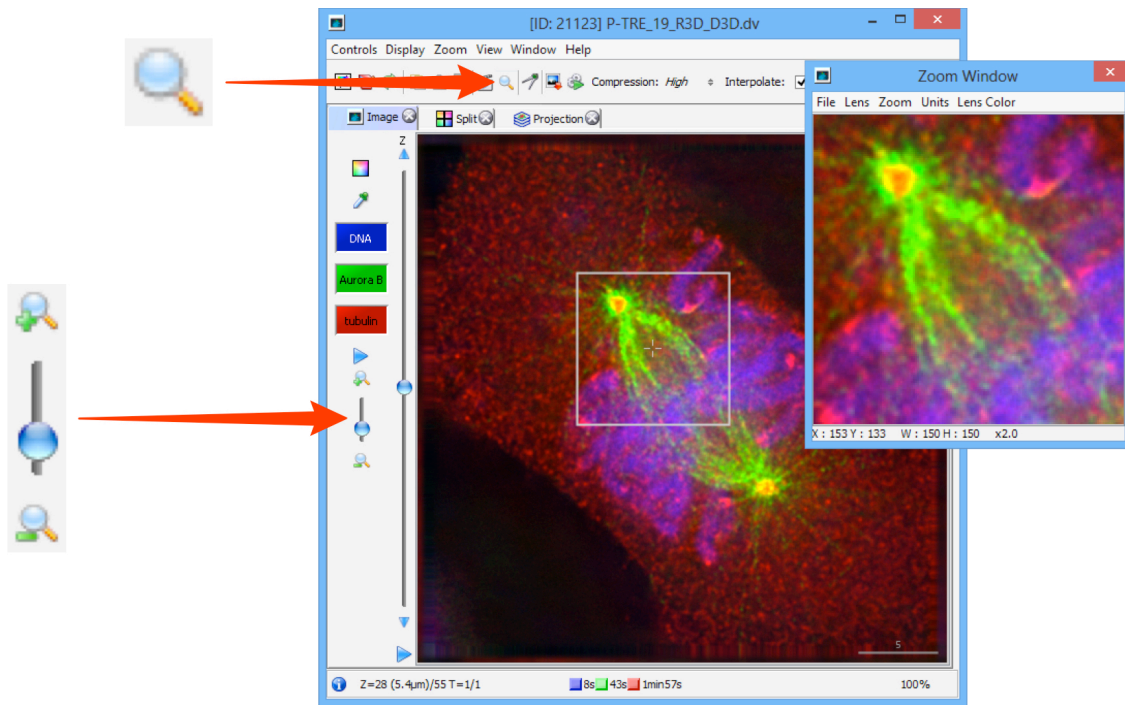
OMERO.insight:



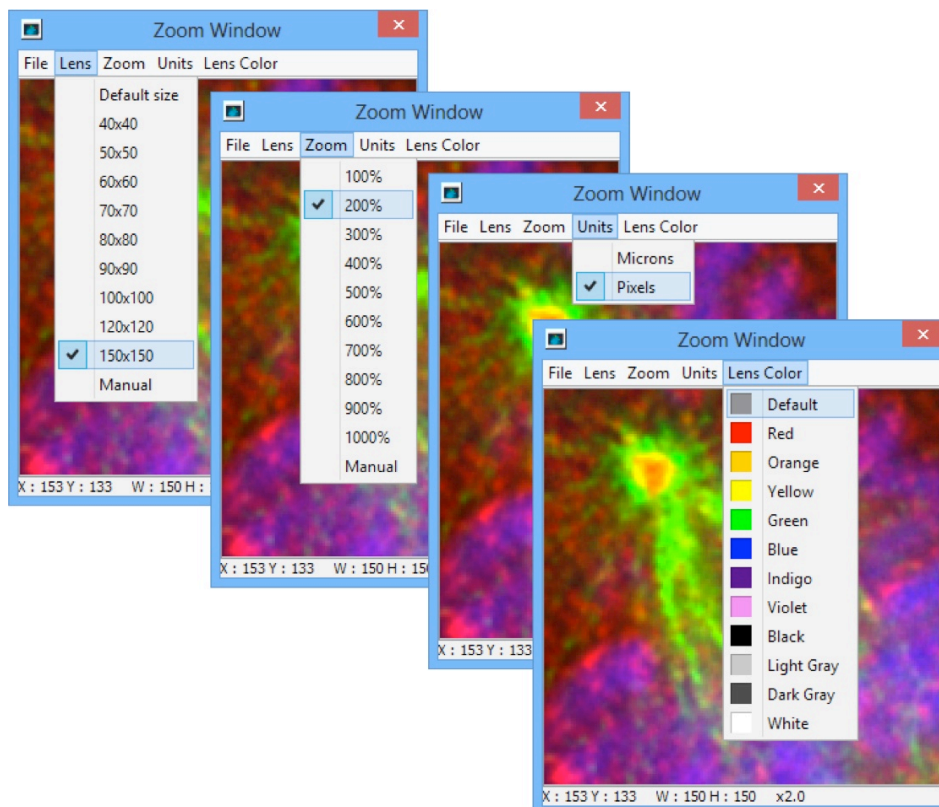
OMERO.web:



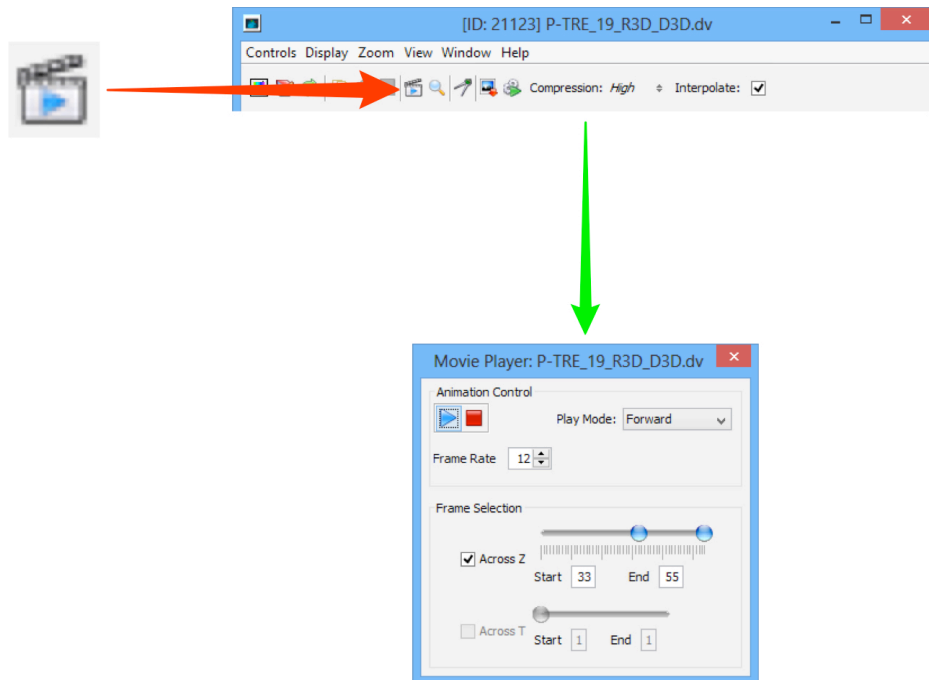
- 10** Zoom using the controls on the left side of the window.
Click on the **Magnifier** to view a selected area of the image in OMERO.insight.



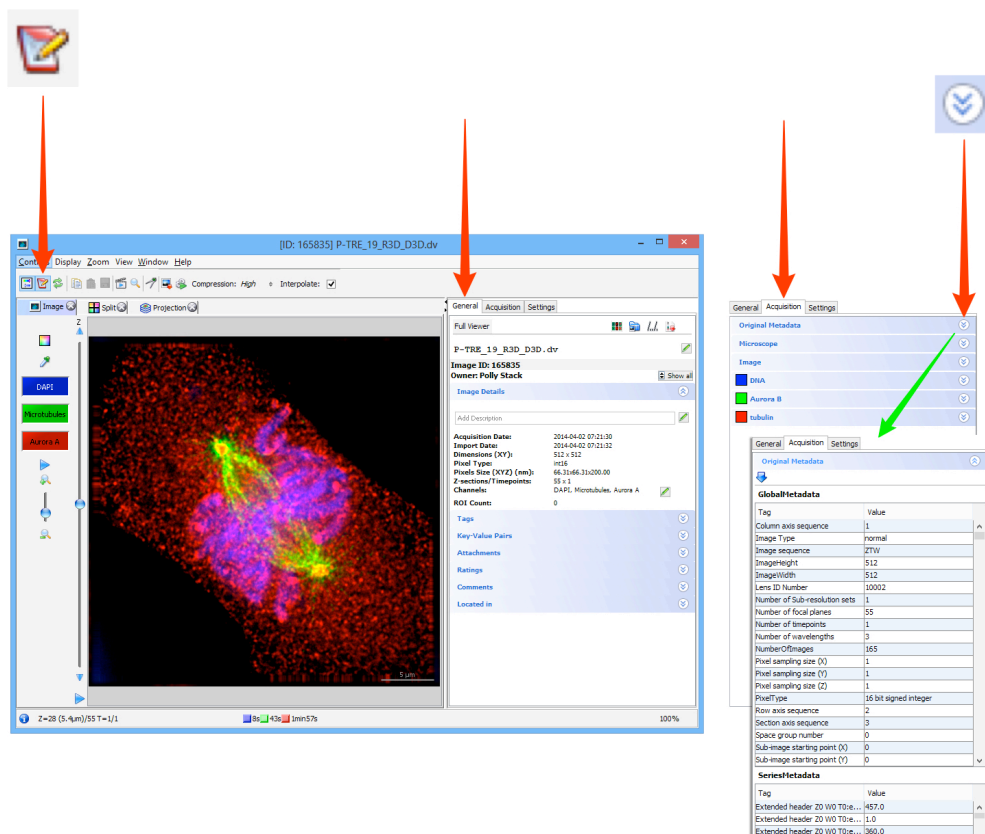
- 11** Click on the menu in the Zoom Window to configure size of lens, zoom percentage, units and the colour of the zoom box in the main image viewer.



- 12** Click on the movie player icon to play through Z-stacks and time sequences with more control in OMERO.insight.



- 13** Click on the **Metadata** button to open the metadata panel to the right of the image. The **General** tab shows the name and description, which are editable, summary data, rating, tags, attachments, comments and the location of the image data file in the OMERO.server managed repository. The **Acquisition** tab shows the original acquisition data imported with the image data.



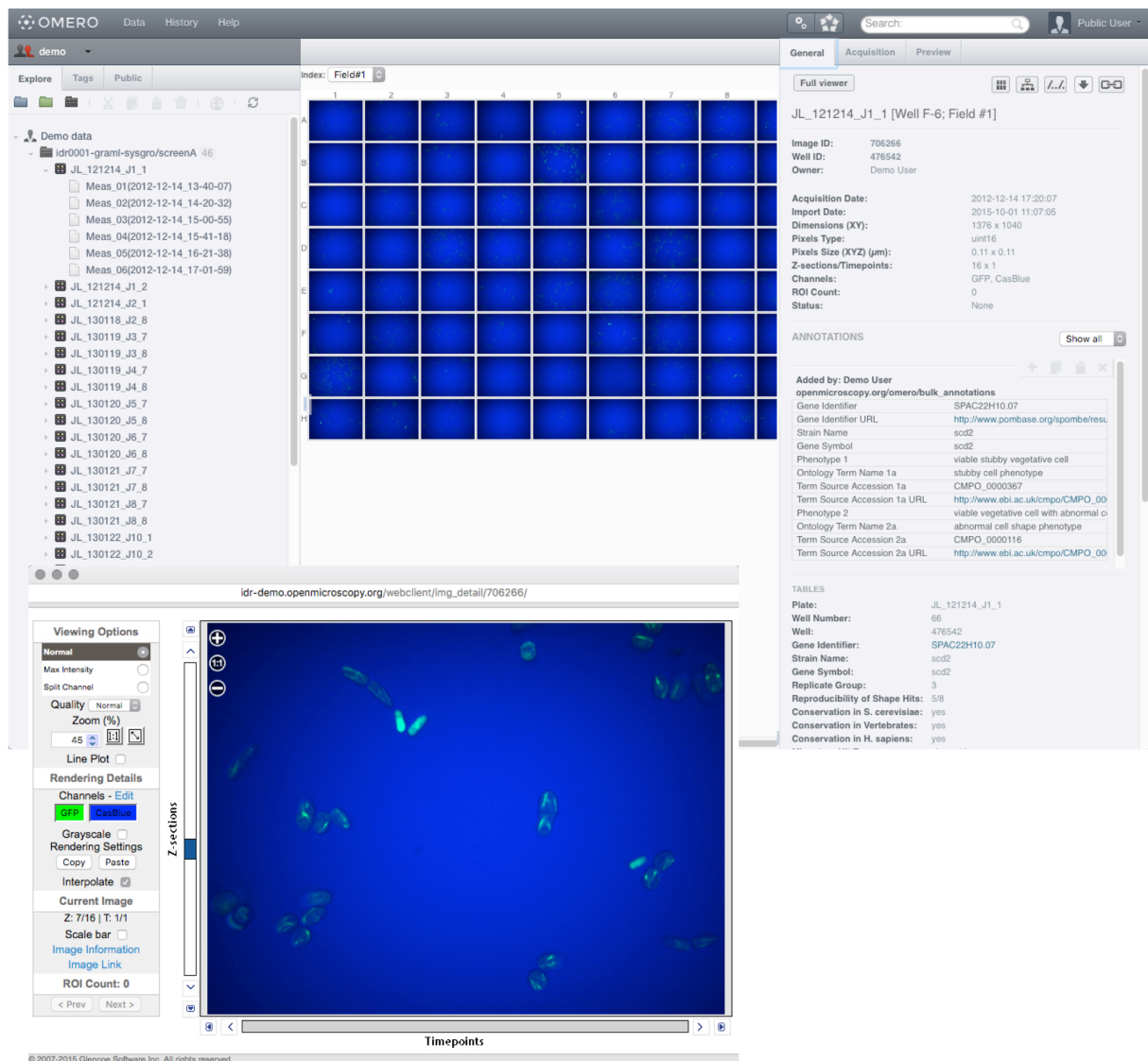
Viewing High Content Screening (HCS) Data

OMERO allows the importing, storing and viewing of screening data. Many common formats are supported as standard, although some screens benefit from custom handling of their metadata before or after import.

A demonstration server showing published screening and other high volume data is available for public viewing at:

<http://idr-demo.openmicroscopy.org>

- 1 In OMERO.web, screens are represented in the data tree by dark grey folders. Expand the **Screen** folder, expand the **Plate** container and select a **Run**. Click on a well in the plate shown on the centre pane to view the data in that well. Double-click on a well to open the image in the full viewer.



The screenshot displays the OMERO web interface with the following components:

- Data Tree (Left):** Shows a hierarchy of folders including 'Demo data', 'idr0001-graml-sysgro/screenA', and a list of measurement folders (Meas_01 to Meas_06) and image folders (JL_121214_J1_1 to JL_130122_J10_2).
- Central Plate View:** A grid of 8x8 wells (A-H, 1-8) showing fluorescence images. The selected well is JL_121214_J1_1 [Well F-6; Field #1].
- Metadata Panel (Right):**
 - General:** Image ID: 706266, Well ID: 476542, Owner: Demo User.
 - Acquisition:** Acquisition Date: 2012-12-14 17:20:07, Import Date: 2015-10-01 11:07:05, Dimensions (XY): 1376 x 1040, Pixels Type: uint16, Pixels Size (XYZ) (µm): 0.11 x 0.11, Z-sections/Timepoints: 16 x 1, Channels: GFP, CasBlue, ROI Count: 0, Status: None.
 - ANNOTATIONS:** Added by: Demo User, openmicroscopy.org/omero/bulk_annotations, Gene Identifier: SPAC22H10.07, Gene Identifier URL: http://www.pombase.org/spombe/res/, Strain Name: scd2, Gene Symbol: scd2, Phenotype 1: viable stubby vegetative cell, Ontology Term Name 1a: stubby cell phenotype, Term Source Accession 1a: CMPO_0000367, Term Source Accession 1a URL: http://www.ebi.ac.uk/ompa/CMPO_00, Phenotype 2: viable vegetative cell with abnormal o, Ontology Term Name 2a: abnormal cell shape phenotype, Term Source Accession 2a: CMPO_0000116, Term Source Accession 2a URL: http://www.ebi.ac.uk/ompa/CMPO_00.
 - TABLES:**
 - Plate: JL_121214_J1_1
 - Well Number: 66
 - Well: 476542
 - Gene Identifier: SPAC22H10.07
 - Strain Name: scd2
 - Gene Symbol: scd2
 - Replicate Group: 3
 - Reproducibility of Shape Hits: 5/8
 - Conservation in S. cerevisiae: yes
 - Conservation in Vertebrates: yes
 - Conservation in H. sapiens: yes
- Viewing Options (Bottom Left):** Includes controls for Normal/Max Intensity, Split Channel, Quality, Zoom (%), Line Plot, Rendering Details (Channels, Grayscale, Interpolate), Current Image (Z: 7/16, T: 1/1), Scale bar, Image Information, Image Link, and ROI Count: 0.

2

Metadata associated with any level from screens to wells can contain annotations such as gene or siRNA identifiers.

Annotations can be formatted as hyperlinks to online resources such as PomBase or Ensembl.

Click on the hyperlink to open a new page showing the appropriate online resource entry.

TABLES

Plate: JL_121214_J1_1

Well Number: 66

Well: 476542

Gene Identifier: **SPAC22H10.07**

Strain Name: scd2

Gene Symbol: scd2

Replicate Group: 3


Reproducibility of Shape Hits: 5/8

Conservation in *S. cerevisiae*: yes

Conservation in Vertebrates: yes

Conservation in *H. sapiens*: yes

SPAC22H10.07



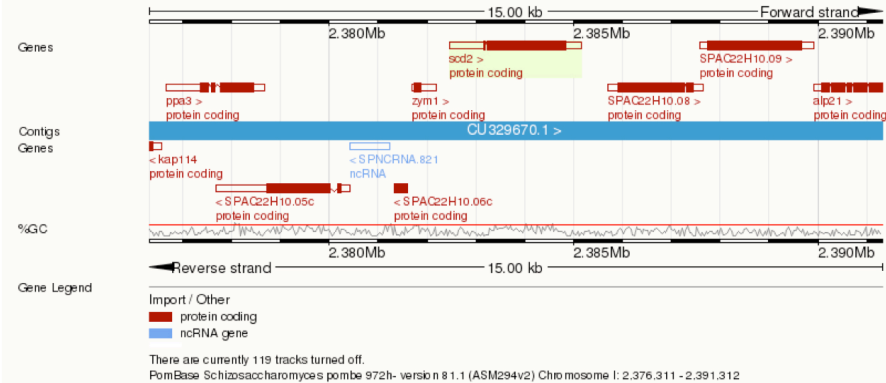
PomBase

e.g. cdc2*

The scientific resource for fission yeast
Home Find Tools Submit Downloads Genome Status Community About Help

scd2 (SPAC22H10.07)

Gene Standard Name	scd2	Characterisation Status	published
Systematic ID	SPAC22H10.07	Feature Type	protein coding
Synonyms	ral3	Name Description	Shape and Conjugation Deficiency, RAs Like
Product	scaffold protein Scd2	Product Size	536aa, 60.04 kDa
Genomic Location	Chromosome I, 2382470-2385153 (2684nt); CDS:2383172-2384835 (1664nt)		



kap114 ppa3 SPAC22H10.05c SPNCRNA.821 SPAC22H10.06c yzm1
scd2
SPAC22H10.08 SPAC22H10.09 alp21

[View in Genome Browser](#)

GO Molecular Function

Summary

Term Name	Count
phosphatidylinositol binding	35
protein binding	866
<ul style="list-style-type: none"> binds cdc42, shk1, scd1 	

Ontology Graph

Report an error | Help

Quick Links

- Gene Ontology:
 - Molecular Function
 - Biological Process
 - Cellular Component
- Phenotype:
 - Single-allele:
 - Population
 - Cell
 - Multi-allele:
 - Population
 - Cell
- Transcript
- Protein Features
- Sequence
- Gene Expression
- Pathway
- Taxonomic Conservation
- Orthologs
- Interactions:
 - Physical
 - Genetic
- External References
- Literature

Back to top

- 3 In OMERO.insight, click on the **Screen** accordion tab in the left hand panel. Images in any well can be opened in the full viewer for ROI viewing, addition or analysis.

