



<https://idr.openmicroscopy.org>

Image Data Resource (IDR)

Data Submission and Curation

Frances Wong

University of Dundee

OME

@openmicroscopy, @IDRNews



University of
BRISTOL



University
of Dundee

EMBL-EBI



IDR Homepage



The IDR logo, consisting of a stylized 'I' icon followed by the letters 'IDR'.

The Image Data Resource (IDR) is a public repository of image datasets from published scientific studies, where the community can submit, search and access high-quality bio-image data.

[Cell - IDR](#) [Tissue - IDR](#)

Name (IDR number)

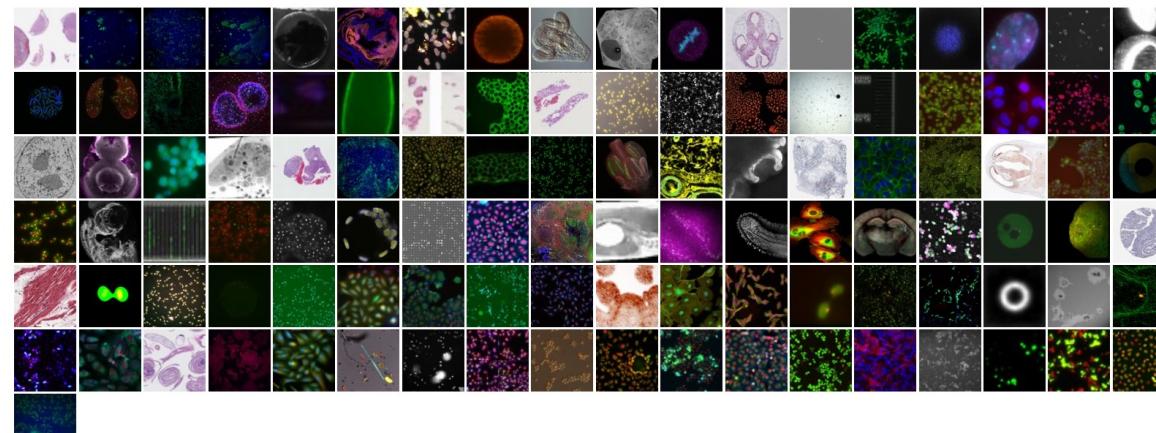
Type to filter values...

109 Studies

12,874,710 Images

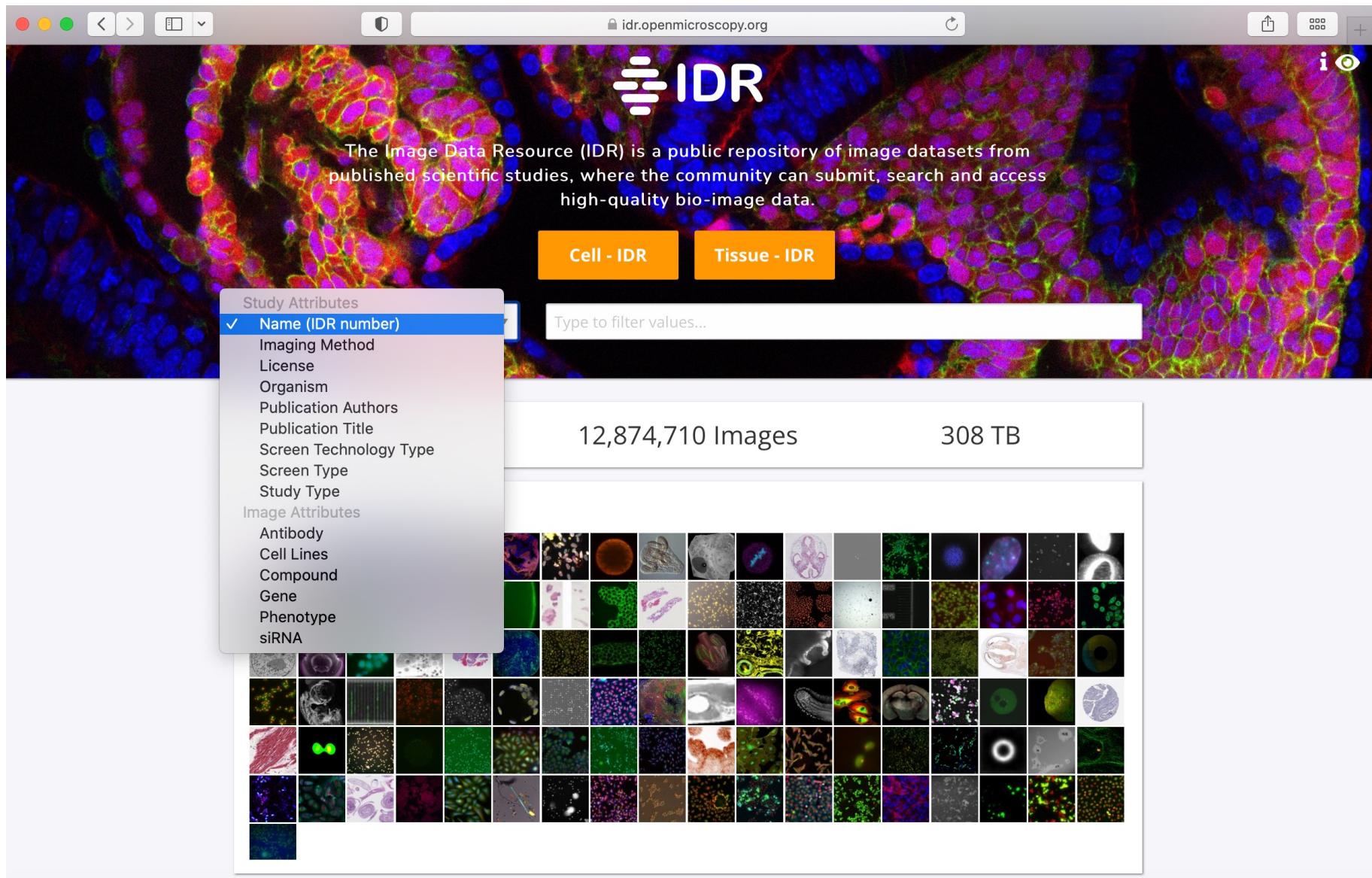
308 TB

Group Studies by type



<https://idr.openmicroscopy.org>

IDR Homepage



The IDR homepage features a large background image of a multi-colored fluorescence microscopy slide. At the top center is the IDR logo, which consists of five horizontal bars of increasing height followed by the letters "IDR". Below the logo is a text block: "The Image Data Resource (IDR) is a public repository of image datasets from published scientific studies, where the community can submit, search and access high-quality bio-image data." Two orange buttons below the text are labeled "Cell - IDR" and "Tissue - IDR". A search bar with the placeholder "Type to filter values..." is positioned to the right of the buttons. On the left side, a dropdown menu is open, showing a list of study attributes: Name (IDR number), Imaging Method, License, Organism, Publication Authors, Publication Title, Screen Technology Type, Screen Type, Study Type, and Image Attributes. The "Name (IDR number)" option is selected. Below the dropdown is a grid of small microscopy images, arranged in a 6x6 pattern, showing various cell types and staining patterns.

<https://idr.openmicroscopy.org>

IDR Homepage

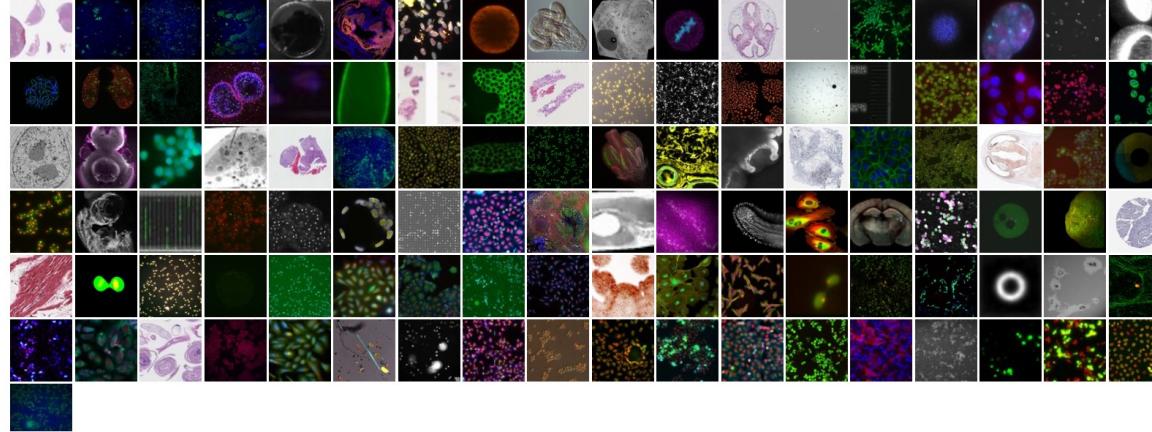


The IDR homepage features a large, vibrant fluorescence microscopy image of a tissue sample with multiple colored channels (red, green, blue) as the background. At the top center is the IDR logo, which consists of a stylized 'I' made of horizontal bars followed by the letters 'IDR'. Below the logo is a descriptive text block: "The Image Data Resource (IDR) is a public repository of image datasets from published scientific studies, where the community can submit, search and access high-quality bio-image data." Two orange buttons below the text are labeled "Cell - IDR" and "Tissue - IDR". Below these buttons are two input fields: "Name (IDR number)" with a dropdown arrow and "Type to filter values...". A red rectangular box highlights a summary section containing three statistics: "109 Studies", "12,874,710 Images", and "308 TB". Another red rectangular box highlights a grid of thumbnail images representing various microscopy studies. A toggle switch labeled "Group Studies by type" is located above the grid. The URL "https://idr.openmicroscopy.org" is displayed at the bottom of the page.

idr.openmicroscopy.org

109 Studies 12,874,710 Images 308 TB

Group Studies by type



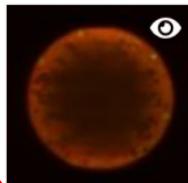
<https://idr.openmicroscopy.org>

Studies in IDR

109 Studies

Keenan SE et. al

idr0118

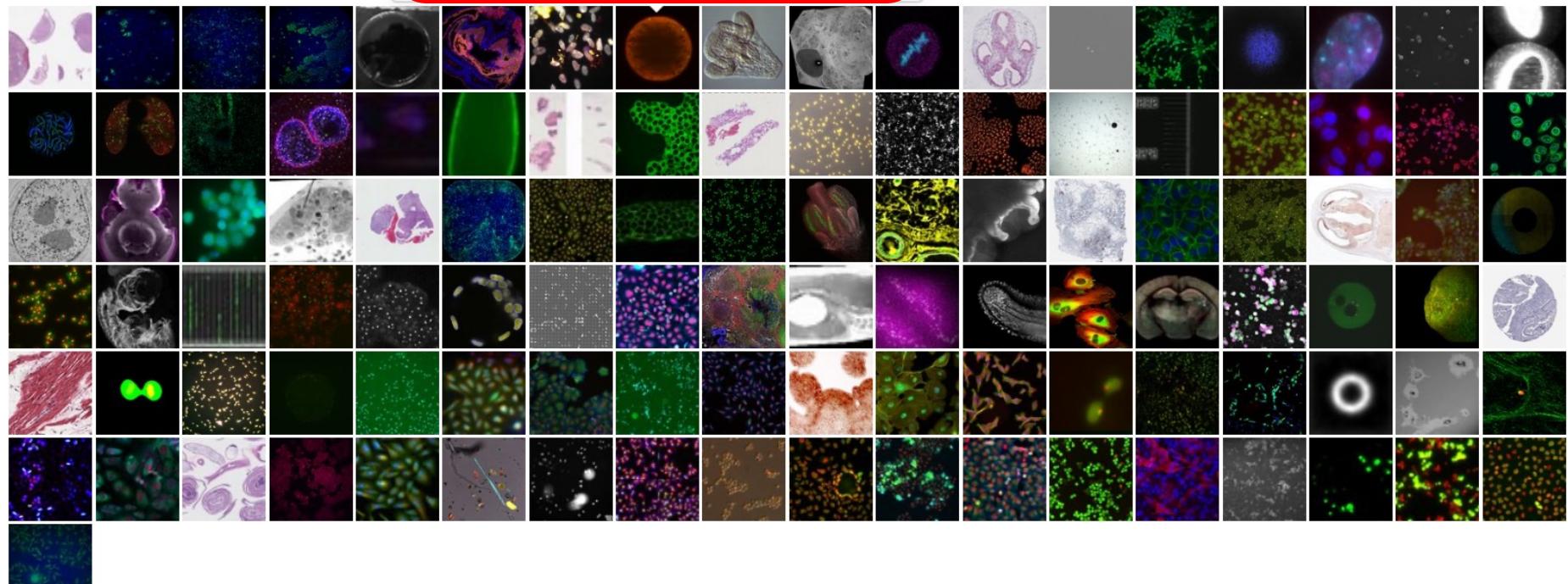


1 Experiment

Dynamics of Drosophila
endoderm specification

Group Studies by type

308 TB



Navigation from study thumbnail

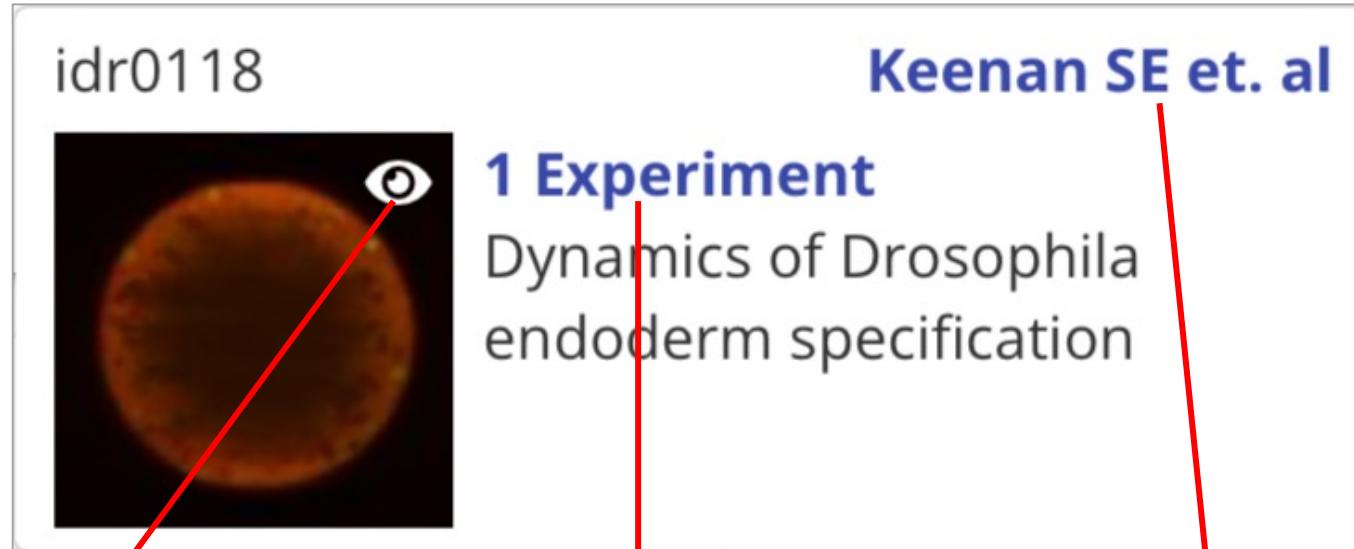


Image viewer

Study data

Publication (PubMed)

IDR Homepage



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[Cell - IDR](#) [Tissue - IDR](#)

Name (IDR number)

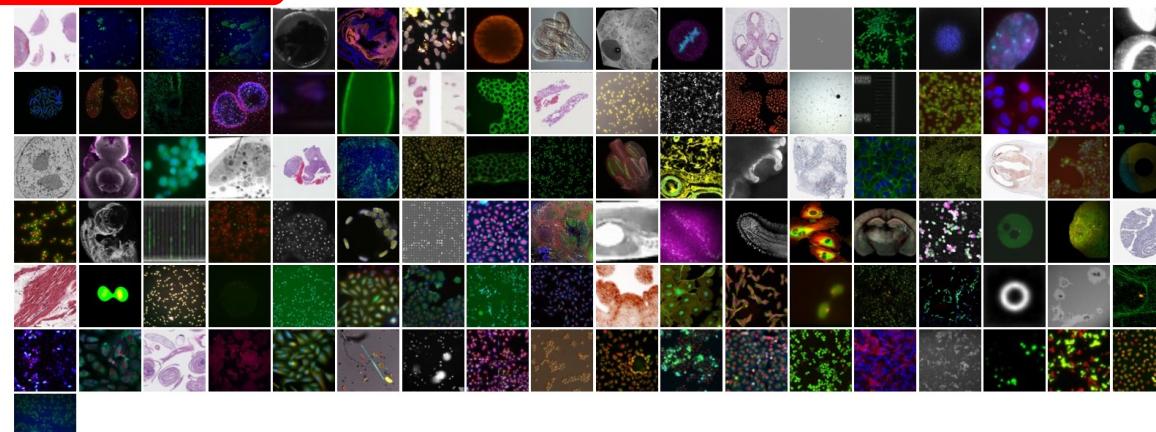
Type to filter values...

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<https://idr.openmicroscopy.org>

Examples of using IDR

Exploring IDR

Analyze Data



From publication to...

Find a specific IDR study from a publication. View images and Regions of Interest (ROIs) in IDR. Explore study metadata.

From gene to phenotypes

Query images by gene. Explore retrieved images and metadata, including associated phenotypes. View images in context of a plate.

From compound to analytics

Query images by compound. Find SARS-CoV-2 dataset. Explore images in relation to analytical data submitted by authors.



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Exploring IDR

Analyze Data

The IDR server is built with **OMERO**, allowing access to all image data and metadata via an open API in Python, R, Java, MATLAB and REST/JSON. See the [OMERO API guide](#) for more information.

For examples of analysis tools working with OMERO to access and analyze data, see the [analysis tools guide](#).



Analysis environment setup

Set-up local or on-the-cloud analysis environment. Access images and metadata using API. Run analysis examples. Add your own code.



Segment image and compare

Fetch image and labels from IDR. Segment nuclei using **StarDist**. Compare new labels with original. Validate software package. Save locally segmentation polygons as geojson.

Guidance for Data Depositors



- *What data can be submitted to the IDR?*
 - IDR accepts and publishes cell and tissue reference image datasets.
 - Non-reference cell or tissue image datasets are redirected to BioStudies or the BioImage Archive.
 - If dataset is EM data, it is redirected to EMPIAR.
 - IDR publishes fully anonymized data. Full de-identification from Private Health Identifiers (PHI) and Personal Identifying Information (PII) required by submitters before data transfer.

Guidance for Data Depositors



- *What is an IDR reference dataset?*
 - Datasets **associated** with an existing or upcoming publication.
 - **Complete** datasets – not just images supporting one figure in the publication.
 - Datasets whose metadata can be **integrated** with other datasets via identifiers from well-known biomolecular resources (Ensembl, NCBI Entrez Gene, RefSeq, PubChem, ChEBI etc).
 - Datasets generated using new imaging **methods** or new analysis methods.
 - Datasets that are likely to be **re-analysed or incorporated** into other studies or integrated with other imaging datasets.

Guidance for Data Depositors



- *Which license are datasets published under in IDR?*
 - To make IDR datasets as widely re-usable as possible, accepted datasets will be published under the Creative Commons Attribution 4.0 International license (CC BY 4.0, <https://creativecommons.org/licenses/by/4.0/>) or a more permissive license.

Guidance for Data Depositors



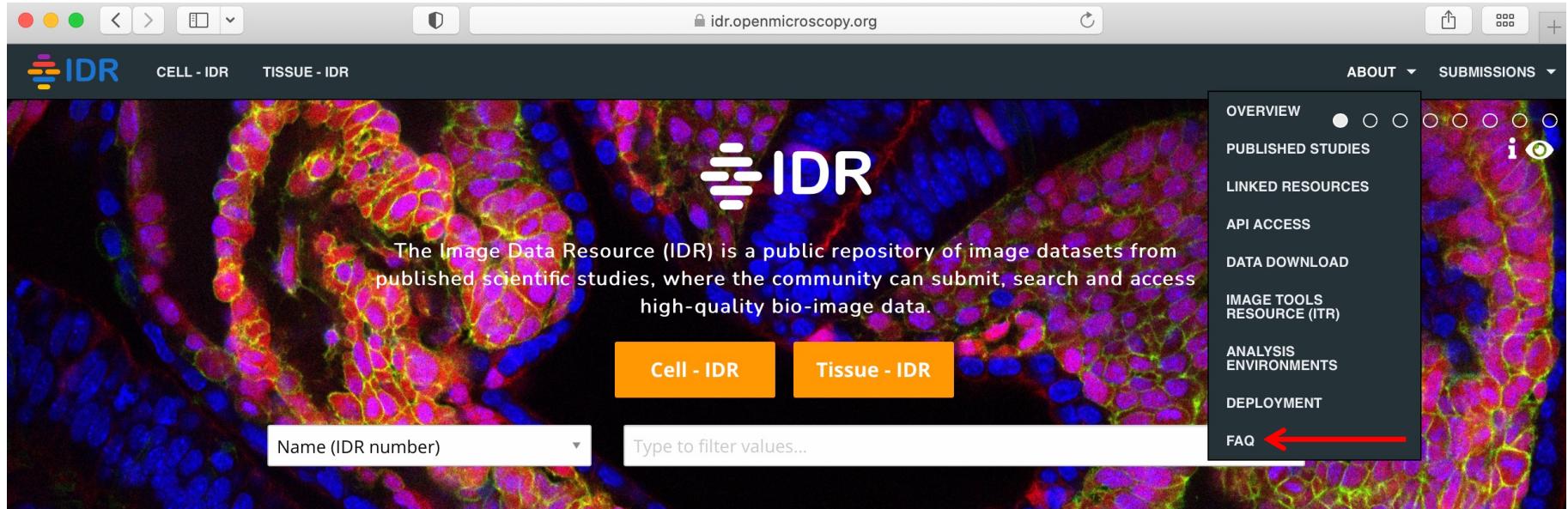
- *Is there a size limit for data deposition?*
 - There is no size limit to the data that can be published in IDR.
 - For very large depositions (>10TB), please contact IDR as early as possible as special arrangements may be needed for data transfer.

Guidance for Data Depositors

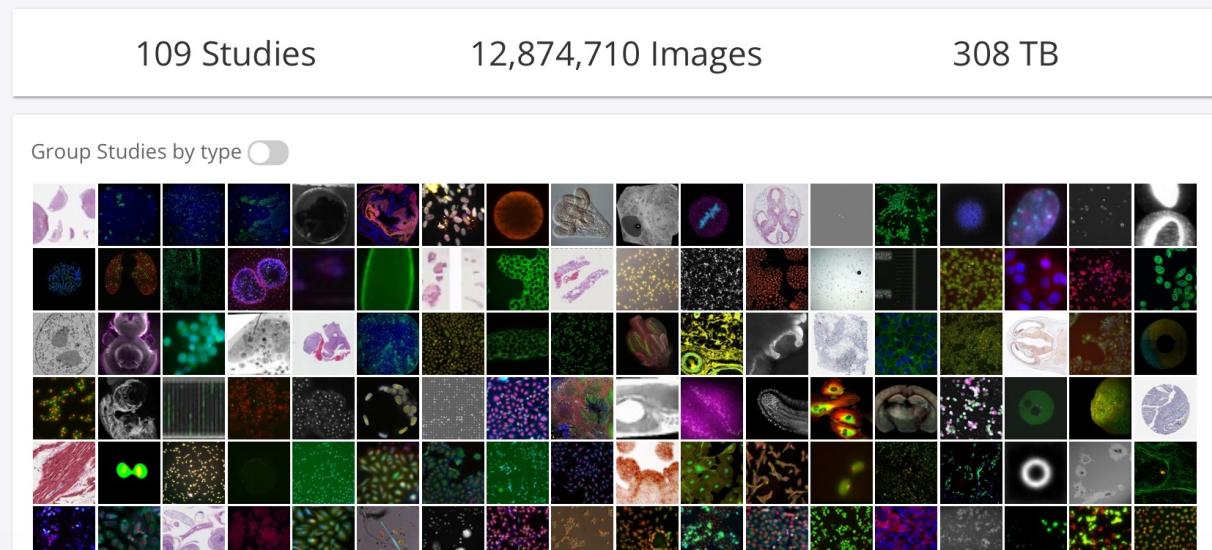


- *How much does it cost to publish data in IDR?*
 - Data deposition and publication is free-of-charge to the authors and is supported by grants from the BBSRC, Wellcome Trust and the European Commission.

FAQs

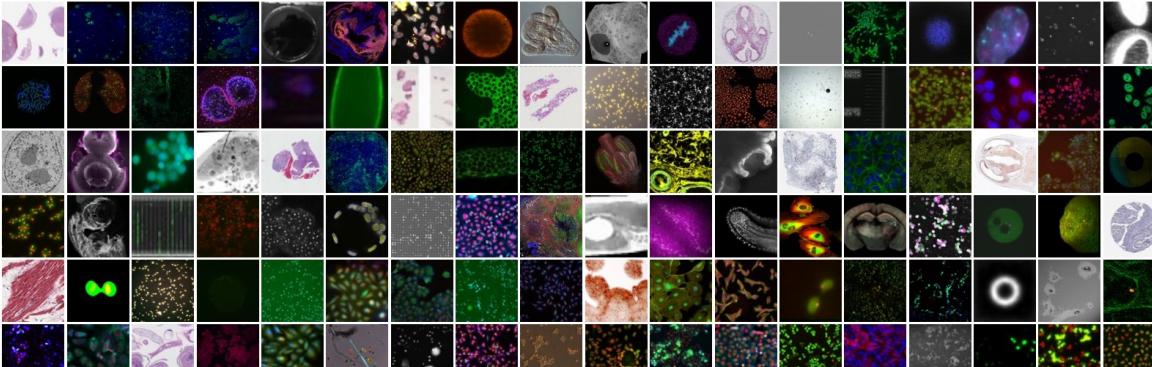


The IDR logo is displayed at the top left. The main heading reads: "The Image Data Resource (IDR) is a public repository of image datasets from published scientific studies, where the community can submit, search and access high-quality bio-image data." Below this are two orange buttons: "Cell - IDR" and "Tissue - IDR". A search bar has dropdown menus for "Name (IDR number)" and "Type to filter values...". To the right is a sidebar with links: OVERVIEW (radio buttons), PUBLISHED STUDIES, LINKED RESOURCES, API ACCESS, DATA DOWNLOAD, IMAGE TOOLS RESOURCE (ITR), ANALYSIS ENVIRONMENTS, DEPLOYMENT, and FAQ (which has a red arrow pointing to it).



109 Studies 12,874,710 Images 308 TB

Group Studies by type



<https://idr.openmicroscopy.org>



Overview

- IDR Submission Workflow
- IDR Submission Process
- IDR Metadata Templates
- Metadata Curation in IDR
- Value of Curation

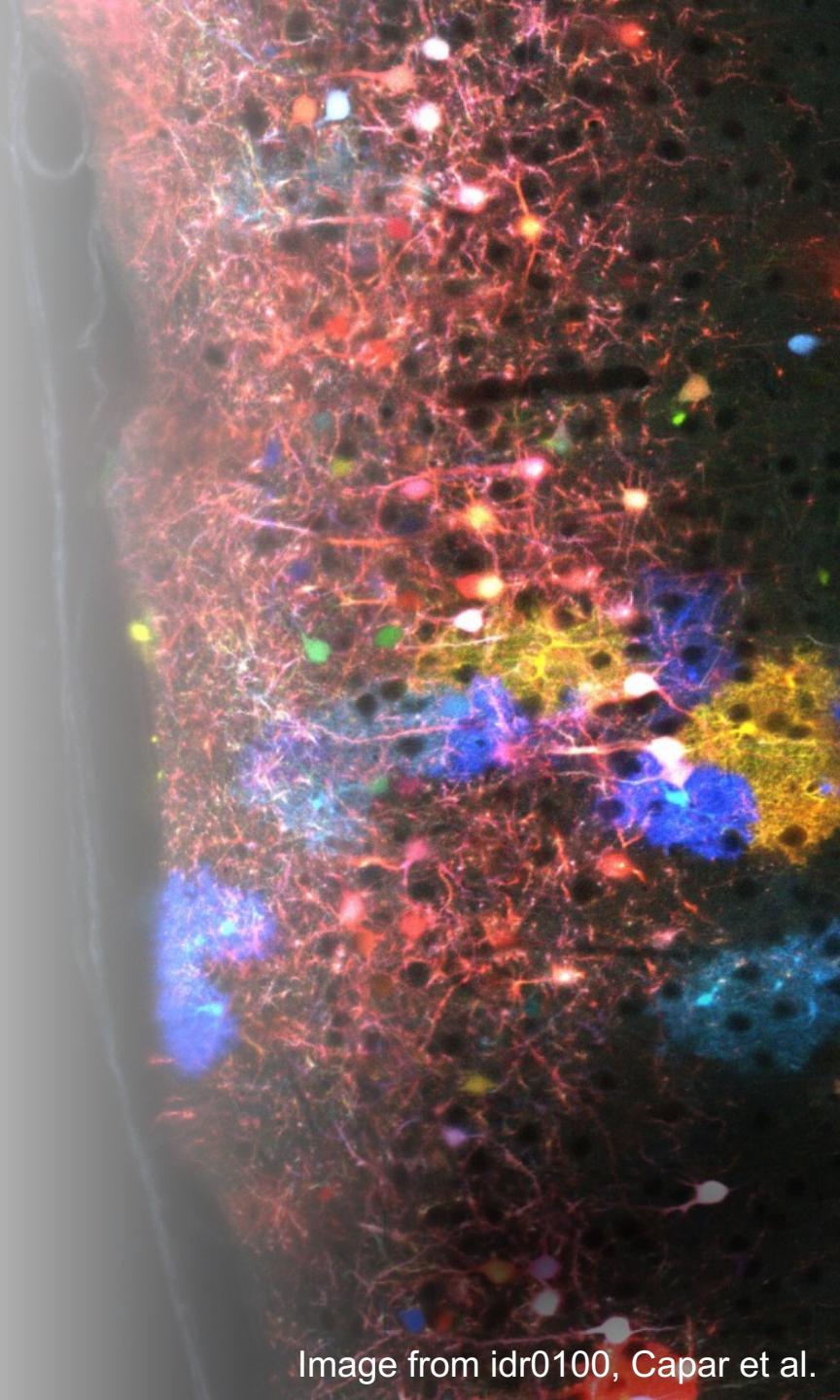


Image from idr0100, Capar et al.



<https://idr.openmicroscopy.org>

Submitting Data to IDR



To submit data to IDR, email
idr@openmicroscopy.org



Upload original, raw image files.



Fill in metadata templates.



Data published in IDR!

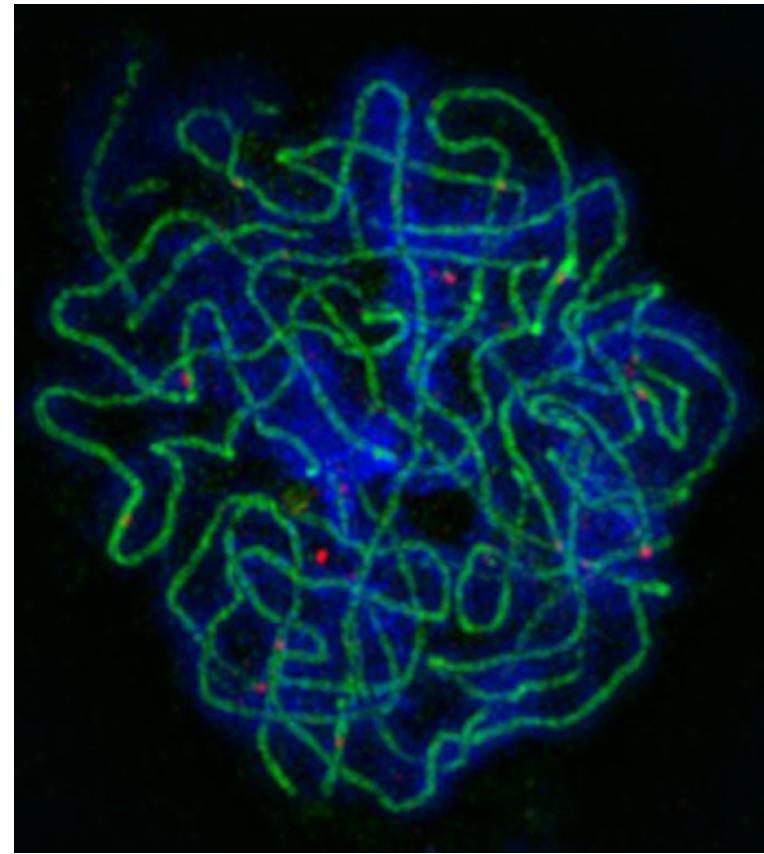
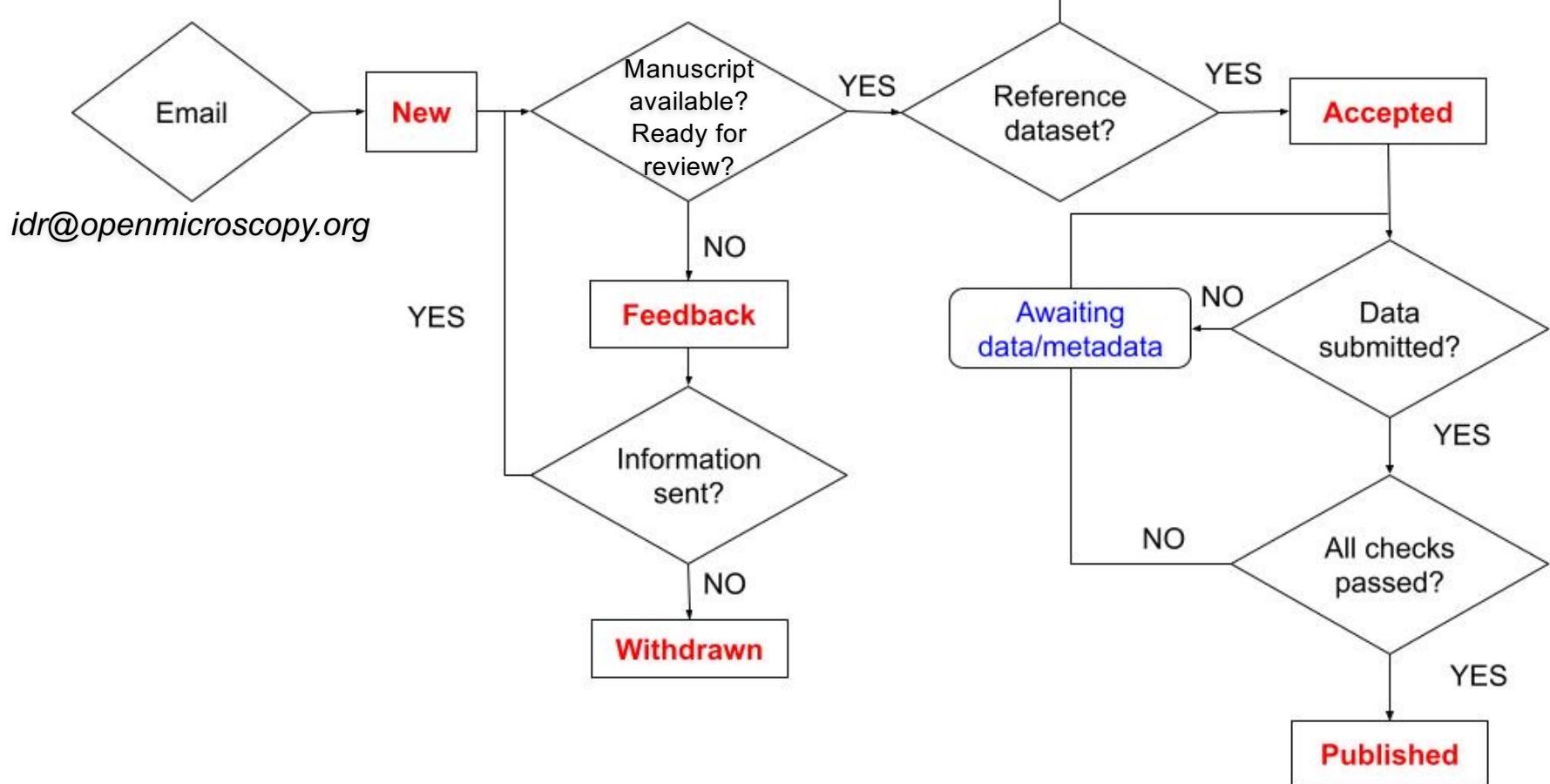
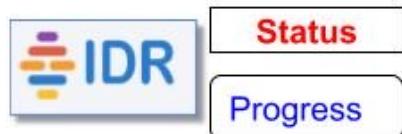


Image from idr0107, Morgan et al.

IDR Submission Workflow



BioImage Archive



IDR Submission Process



- Data
 - Images – upload original raw data, plus analyzed or processed data (if useful).
 - Metadata – fill in templates to provide information on study and images.

FAQ

Frequently asked questions

→ What are the file formats accepted?

The IDR uses the Bio-Formats library for reading imaging data. Bio-Formats supports over 150 proprietary and open file formats (see the [full list](#)). At a minimum, your data should be readable by an up-to-date version of Bio-Formats e.g. using the [showinf utility](#) or the Image/Fiji plugin.

What are the preferred formats for submission?

We strongly encourage imaging data deposition using open file formats such as OME-TIFF. Where possible the original raw data should be submitted, though you can also submit analyzed or processed data if you think it is more usable.

Supported Formats



Bio-Formats

[Downloads by version](#)
[Documentation by version](#)
[Licensing](#)

Previous topic

[Dataset Structure Table](#)

Next topic

[3i SlideBook](#)

Quick search

 Go

This Page

[Show Source](#)
[Show on GitHub](#)
[Edit on GitHub](#)

Supported Formats

Ratings legend and definitions

You can sort this table by clicking on any of the headings.

Format	Extensions	Pixels	Metadata	Openness	Presence	Utility	Export	BSD	Multiple Images	Pyramidal
3i SlideBook	.sld	▲	■	▼	▲	▼	×	✗	✓	✗
Andor Bio-Imaging Division (ABD) TIFF	.tif	▲	▲	■	▼	■	×	✗	✓	✗
AIM	.aim	■	▼	▼	▼	▼	×	✗	✗	✗
Alicona 3D	.al3d	▲	▲	▲	▼	■	×	✗	✗	✗
Amersham Biosciences Gel	.gel	▲	■	■	▼	▼	×	✗	✗	✗
Amira Mesh	.am, .amiramesh, .grey, .hx, .labels	▲	▼	▼	▼	▼	×	✗	✗	✗
Amnis FlowSight	.cif	■	■	■	▼	▼	×	✓	✓	✗
Analyze 7.5	.img, .hdr	▲	▲	▲	■	▼	×	✗	✗	✗
Andor SIF	.sif	■	▼	▼	▼	▼	×	✗	✗	✗
Animated PNG	.png	▲	▲	▲	■	▼	✓	✓	✗	✗
Aperio AFI	.afi, .svs	▲	▲	▲	■	■	×	✗	✓	✓
Aperio SVS TIFF	.svs	▲	▲	▲	■	■	×	✗	✓	✓
Applied Precision CellWorX	.htd, .pnl	▲	▲	■	▼	▼	×	✗	✓	✗
AVI (Audio Video Interleave)	.avi	■	▼	▼	▲	▼	✓	✓	✗	✗
Axon Raw Format	.arf	▲	▲	▲	▼	▼	×	✗	✗	✗
BD Pathway	.exp, .tif	▲	▲	■	▼	■	×	✗	✓	✗
Becker & Hickl SPC FIFO	.spc	▼	▼	■	▼	▼	×	✗	✓	✗
Becker & Hickl SPCImage	.sdt	▲	■	■	▼	▼	×	✗	✓	✗
Big Data Viewer	.xml, .h5	■	▲	▲	■	■	×	✗	✓	✓
Bio-Rad Gel	.1sc	■	▼	▼	▼	▼	×	✗	✗	✗
Bio-Rad PIC	.pic, .raw, .xml	▲	▲	▲	▲	▲	×	✗	✗	✗

Metadata Preparation for IDR



- Two study types



Screen – high content screens (HCS) or imaging studies performed in a plate format (e.g. 96 well plates).



Experiment – non-screen datasets or studies which group images into a number of distinct experiments.

- Empty templates can be downloaded at
<https://github.com/IDR/idr0000-lastname-example/archive/master.zip>
- Examples of completed templates of other studies can be found at <https://github.com/IDR/idr-metadata/>

IDR Metadata Templates



- **Study File**
 - Top level information about the study - title, description, protocols etc.
- **Assays File (experiments only)**
 - List of all images and description of imaged samples - treatments, channels (stain/label).
- **Library File (screens only)**
 - List plate layout and description of all imaged wells - treatments, channels (stain/label).
- **Processed File (if applicable)**
 - Analysis results relating to each image - phenotypes observed, quantification of label intensities.

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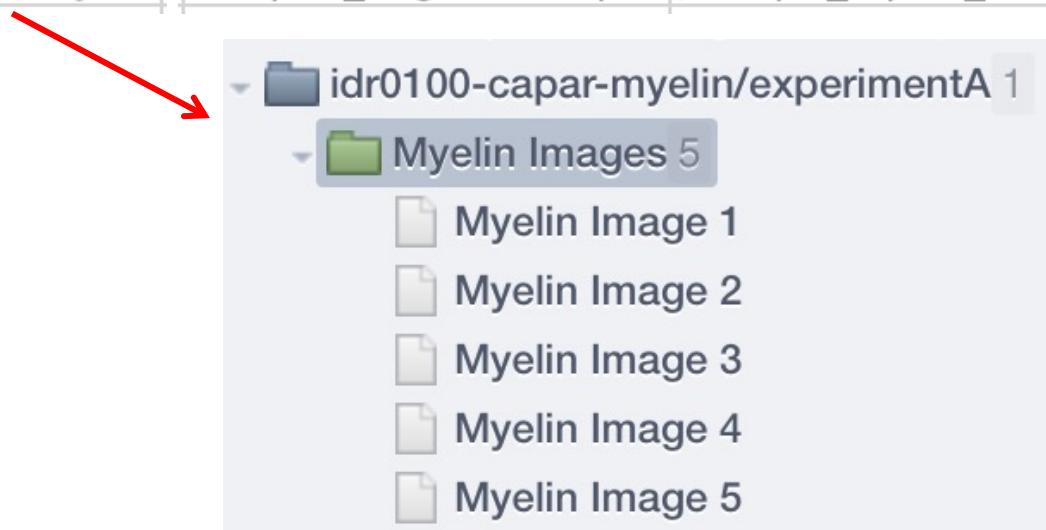
- Study File (Top level information about the study)
 - Title of the dataset
 - Contact details of the submitter
 - Information about the publication associated with your dataset
 - Description of the data
 - Keywords
 - Licence for your data
 - Copyright for your data

- **Study File**
 - Top level information about the study - title, description, protocols etc.
- **Assays File (experiments only)**
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IDR Metadata Templates

- Assays File (Experiments only)
 - List of all images and description of imaged samples - treatments, channels (stain/label).

B	Z	AA
Image Name	Image File	Comment [Image File Path]
Myelin Image 1	Sample1_Oligodendrocyte	/Sample_Myelin_Images1/Sample1_Oligodendrocyte.tif
Myelin Image 2	Sample2_Oligodendrocyte	/Sample_Myelin_Images2/Sample2_Oligodendrocyte.tif
Myelin Image 3	Sample3_Oligodendrocyte	/Sample_Myelin_Images3/Sample3_Oligodendrocyte.tif
Myelin Image 4	Sample4_Oligodendrocyte	/Sample_Myelin_Images4/Sample4_Oligodendrocyte.tif
Myelin Image 5	Sample5_Oligodendrocyte	/Sample_Myelin_Images5/Sample5_Oligodendrocyte.tif



IDR Metadata Templates



Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Public Public data

Explore Tags Shares

Add filter

Myelin Image 1

Image ID: 11576514
Owner: Public data

Show all

Image Details

Import Date: 2020-12-08 15:30:17
Dimensions (XY): 8346 x 2253
Pixels Type: uint8
Pixels Size (XYZ) (µm): 0.83 x 0.83 x 1.20
Z-sections/Timepoints: 47 x 1
Channels: Axon, Nucleus, Oligodendrocyte
ROI Count: 6

Attributes 8

Antibody

Added by: Public data

Antibody TUJ1
Antibody Identifier AB_2313773/AB_291637

Antibody

Added by: Public data

Antibody MBP
Antibody Identifier AB_325004

Antibody supplementary

Added by: Public data

Primary Antibody 1 MBP
Secondary Antibody & Dilution 4.00

Tables

Attachments 0

Comments 0

Zoom: [Slider]

The screenshot shows the IDR Metadata Templates interface. At the top, there's a navigation bar with links for Studies, Genes, Phenotypes, Cell Lines, siRNAs, Antibodies, Compounds, Organisms, and About. To the right of the navigation bar is a search bar with a magnifying glass icon. Below the navigation bar is a secondary header with tabs for General, Acquisition, and Preview, and icons for Full viewer, Print, and Download.

The main content area is divided into several sections. On the left, there's a sidebar titled "Explore" with options for Tags and Shares, and a "Public" section showing "Public data". The sidebar also contains a list of study entries, with one entry, "idr0100-capar-myelin/experimentA 1", and its sub-folders "Myelin Images 5" and "Myelin Image 1" through "Myelin Image 5", highlighted with a red rectangle.

In the center, there's a grid of six small thumbnail images. Below the thumbnails is a "Zoom" slider. To the right of the thumbnails, there's a detailed view of the first image, "Myelin Image 1". This view includes fields for "Image ID" (11576514), "Owner" (Public data), and a "Show all" button. Below this is a "Image Details" section with various metadata fields like Import Date, Dimensions, and Channels. Further down are sections for "Attributes", "Antibody", "Antibody", "Antibody supplementary", "Tables", "Attachments", and "Comments".

idr0100, Capar et al, DOI:10.12688/F1000RESEARCH.27139.1

IDR Metadata Templates

OMERO

File ▾

ROIs ▾

Help ▾

Myelin Image 1

47

- + × 1:1 7 %

+ ⬤ ↗

Info Settings

ROIs [6]

Save Save to All Undo Redo Copy Paste

 Grayscale Histogram Interpolate

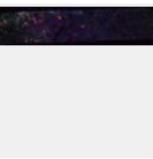
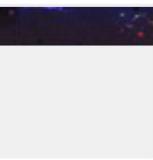
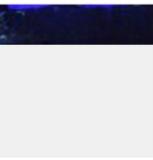
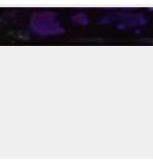
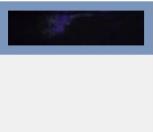
Axon	0	50
Nucleus	0	50
Oligodendrocyte	0	50

Min/Max Full Range Imported

User Settings:



Public data

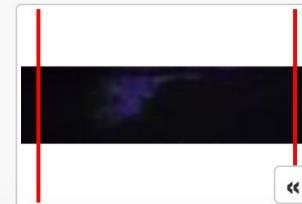


24



Z

2 mm

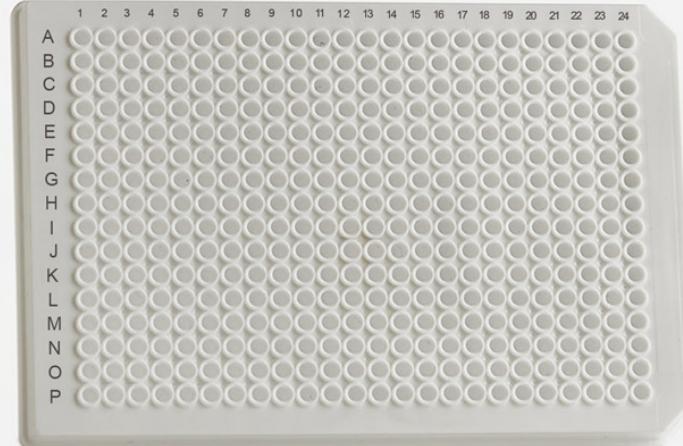


idr0100, Capar et al, DOI:10.12688/F1000RESEARCH.27139.1

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IDR Metadata Templates

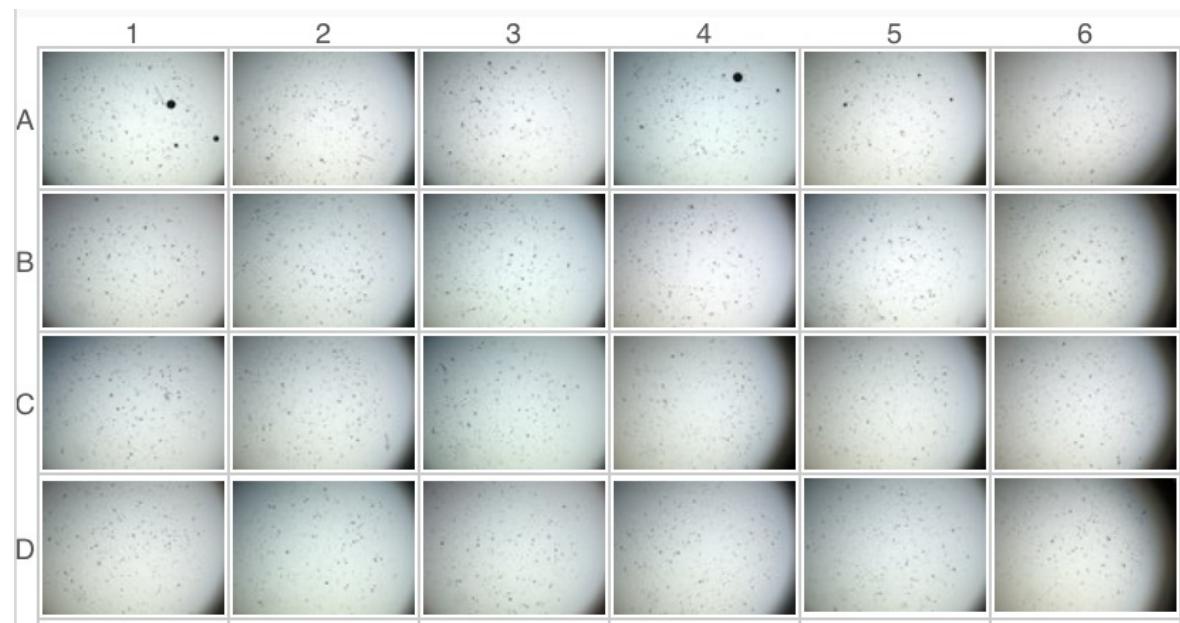
- Library File (Screens only)
 - List plate layout and description of all imaged wells - treatments, channels (stain/label).



IDR Metadata Templates

- **Library File (Screens only)**
 - List plate layout and description of all imaged wells - treatments, channels (stain/label).

	A	B
1	Plate	Well
2	Plate1	A01
3	Plate1	A02
4	Plate1	A03
5	Plate1	A04
6	Plate1	A05
7	Plate1	A06
8	Plate1	B01
9	Plate1	B02
10	Plate1	B03
11	Plate1	B04
12	Plate1	B05
13	Plate1	B06



IDR Metadata Templates

- Assays and Library Files
 - Description of each image

idr0100

A	B	C	D	E	F	G	H	I	
1	Dataset Name	Image Name	Characteristics [Organism]	Term Source 1 REF	Term Source 1 Accession	Characteristics [Cell Line]	Term Source 2 REF	Term Source 2 Accession	Comment [Cell Line]
2	Myelin Images	Myelin Image 1	Mus musculus	NCBITaxon	NCBITaxon_10090	mouse embryonic stem cell	EFO	EFO_0004038	Mouse D3 and E14 embryonic stem cells
3	Myelin Images	Myelin Image 2	Mus musculus	NCBITaxon	NCBITaxon_10090	mouse embryonic stem cell	EFO	EFO_0004038	Mouse D3 and E14 embryonic stem cells
4	Myelin Images	Myelin Image 3	Mus musculus	NCBITaxon	NCBITaxon_10090	mouse embryonic stem cell	EFO	EFO_0004038	Mouse D3 and E14 embryonic stem cells
5	Myelin Images	Myelin Image 4	Mus musculus	NCBITaxon	NCBITaxon_10090	mouse embryonic stem cell	EFO	EFO_0004038	Mouse D3 and E14 embryonic stem cells
6	Myelin Images	Myelin Image 5	Mus musculus	NCBITaxon	NCBITaxon_10090	mouse embryonic stem cell	EFO	EFO_0004038	Mouse D3 and E14 embryonic stem cells

idr0092

A	B	C	D	E	F	G	H	I	
1	Plate	Well	Characteristics [Organism]	Term Source 1 REF	Term Source 1 Accession	Characteristics [Strain]	Term Source 2 REF	Term Source 2 Accession	Characteristics [Tissue]
2	Plate1	A01	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
3	Plate1	A02	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
4	Plate1	A03	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
5	Plate1	A04	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
6	Plate1	A05	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
7	Plate1	A06	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
8	Plate1	B01	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
9	Plate1	B02	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
10	Plate1	B03	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
11	Plate1	B04	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine
12	Plate1	B05	Mus musculus	NCBITaxon	NCBITaxon_10090	C57BL/6JRj	EFO	EFO_0000606	small intestine

IDR Metadata Templates

- Assays and Library Files
 - Description of each image

idr0100

J	K	L	M	N	O
Comment [Gene Identifier 1]	Comment [Gene Symbol 1]	Comment [G	Comment [Gene Identifier 2]	Comment [Gene Symbol 2]	Comment [G
ENSMUSG00000041607	Mbp	Ensembl ver:	ENSMUSG00000062380	Tuj1	Ensembl ver:
ENSMUSG00000041607	Mbp	Ensembl ver:	ENSMUSG00000062380	Tuj1	Ensembl ver:
ENSMUSG00000041607	Mbp	Ensembl ver:	ENSMUSG00000062380	Tuj1	Ensembl ver:
ENSMUSG00000041607	Mbp	Ensembl ver:	ENSMUSG00000062380	Tuj1	Ensembl ver:
ENSMUSG00000041607	Mbp	Ensembl ver:	ENSMUSG00000062380	Tuj1	Ensembl ver:

Gene	
Added by: Public data	
Gene Identifier	ENSMUSG00000062380
Gene Symbol	Tuj1

Gene	
Added by: Public data	
Gene Identifier	ENSMUSG00000041607
Gene Symbol	Mbp

Mouse (GRCm39) ▾

Location: 18:82,493,271-82,603,762 Gene: Mbp

Gene: Mbp ENSMUSG00000041607

Description
Gene Synonyms
Location

About this gene
Transcripts

myelin basic protein [Source:MGD Symbol;Acc:MGD:96925] Hmbpr, goli-mbp, jve Chromosome 18: 82,493,271-82,603,762 forward strand. GRCm39:CM001011.3 This gene has 16 transcripts (splice variants), 284 orthologues and is associated with 45 phenotypes. Show transcript table

Summary ⓘ

Name Mbp (MGD Symbol)
CCDS This gene is similar to a CCDS gene on Mouse GRCm39: CCDS29373.1, CCDS29374.1, CCDS29376.1, CCDS29377.1, CCDS29378.1, CCDS29379.1, CCDS37875.1

UniProtKB This gene has proteins that correspond to the following UniProtKB identifiers: P04370

Ensembl version ENSMUSG00000041607.18

Gene type Protein coding

Annotation method Annotation for this gene includes both automatic annotation from Ensembl and Havana manual curation, see article.

Go to Region in Detail for more tracks and navigation options (e.g. zooming)

Ontologies

Organism	NCBI Taxonomy https://www.ncbi.nlm.nih.gov/taxonomy
Study Type Screen Type (HCS) Screen Technology Type (HCS) Library Type (HCS) Protocol	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Imaging Method	Biological Imaging Methods Ontology (FBbi) https://www.ebi.ac.uk/ols/ontologies/fbbi
Phenotype	Cellular Microscopy Phenotype Ontology (CMPO) https://www.ebi.ac.uk/cmpo/
Gene	Ensembl https://www.ensembl.org/ NCBI Gene https://www.ncbi.nlm.nih.gov/gene/
Protein	UniProt https://www.uniprot.org/
Clinical/Pathology	SNOMED CT https://bioportal.bioontology.org/ontologies/SNOMEDCT
Compound	PubChem https://pubchem.ncbi.nlm.nih.gov/

Compounds

Compound	
Added by: Public data	
Compound Name	olaparib 
Compound supplementary	
Added by: Public data	
Concentration (microMolar)	1
Based Treatment	23725625
PubChem CID	23725625
ChEMBL	CHEMBL521686
SMILES	<chem>C1CC1C(=O)N2CCN(CC2)C(=O)C3=C(C=CC(=C3)CC4=NNC(=O)C5=CC=CC=C54)F</chem>
InChI	<chem>InChI=1S/C24H23FN4O3/c25-20-8-5-15(14-21-17-3-1-2-4-18(17)22(30)27-26-21)13-19(20)24(32)29-11-9-28(10-12-29)23(31)16-6-7-16/h1-5,8,13,16H,6-7,9-12,14H2,(H,27,30)</chem>
InChIKey	FDLYAMZZIXQODN-UHFFFAOYSA-N
Secondary Name	AZD2281, KU0059436
Selectivity	PARP
Class	other

IDR Metadata Templates



- **Study File**
 - Top level information about the study - title, description, protocols etc.
- **Assays File (experiments only)**
 - List of all images and description of imaged samples - treatments, channels (stain/label).
- **Library File (screens only)**
 - List plate layout and description of all imaged wells - treatments, channels (stain/label).
- **Processed File (if applicable)**
 - Analysis results relating to each image - phenotypes observed, quantification of label intensities.

IDR Metadata Templates

- **Processed File (if applicable)**
 - Analysis results relating to each image - phenotypes observed, quantification of label intensities.

Others

Added by: Public data

Experimental Replicate Date	12/01/2021
Genetic Perturbation	kRas/PTEN-/-
Cell Number	23808
Cell Sheet Radius	3601.287644
Density	0.001656947



Cell Number	Cell Sheet Radius	Density
15719	3251.214766	0.001411485
16539	3061.27285	0.001640627
10015	2520.827441	0.001433786
10653	2590.744866	0.001408788
19016	3982.644759	0.001120787
22553	3948.528998	0.00137298
16505	2929.598927	0.001745582
13132	2837.417687	0.001488076
13571	2906.735666	0.001486384
34946	3990.590594	0.002050897
11674	2629.364668	0.001531984
17745	3037.163935	0.001729844
27716	4261.496778	0.00140595
33792	4751.251851	0.001404664
21752	3161.262274	0.001994126
23700	3598.53216	0.001667471
22920	3414.341064	0.001844919
24847	3377.257969	0.002032656
10759	2401.465031	0.001588429
13697	2780.553743	0.001590474
39823	4731.043657	0.00164657
31477	4370.913185	0.001528823
24349	3389.888748	0.001919733
23808	3601.287644	0.001656947

- **Study File**
 - Top level information about the study - title, description, protocols etc.
- **Assays File (experiments only)**
 - List of all images and description of imaged samples - treatments, channels (stain/label).
- **Library File (screens only)**
 - List plate layout and description of all imaged wells - treatments, channels (stain/label).
- **Processed File (if applicable)**
 - Analysis results relating to each image - phenotypes observed, quantification of label intensities.

Metadata Curation in IDR



OMERO Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Public Public data

Explore Tags Shares

Add filter

Exp1_rep1_0min_im1.tif

Exp1_rep1_0min_im2.tif

Exp1_rep1_0min_im3.tif

Exp1_rep1_0min_im4.tif

Exp1_rep1_10min_im1.tif

Exp1_rep1_10min_im2.tif

Exp1_rep1_10min_im3.tif

Exp1_rep1_10min_im4.tif

Exp1_rep1_15min_im1.tif

Exp1_rep1_15min_im2.tif

Exp1_rep1_15min_im3.tif

Exp1_rep1_15min_im4.tif

Exp1_rep1_1min_im1.tif

Exp1_rep1_1min_im2.tif

Exp1_rep1_1min_im3.tif

Exp1_rep1_1min_im4.tif

Exp1_rep1_20min_im1.tif

Exp1_rep1_20min_im2.tif

Exp1_rep1_20min_im3.tif

Exp1_rep1_20min_im4.tif

Exp1_rep1_25min_im1.tif

Exp1_rep1_25min_im2.tif

Exp1_rep1_25min_im3.tif

Exp1_rep1_25min_im4.tif

Exp1_rep1_2min_im1.tif

Exp1_rep1_2min_im2.tif

Exp1_rep1_2min_im3.tif

Exp1_rep1_2min_im4.tif

Exp1_rep1_30min_im1.tif

Exp1_rep1_30min_im2.tif

Exp1_rep1_30min_im3.tif

Exp1_rep1_30min_im4.tif

Exp1_rep1_35min_im1.tif

Exp1_rep1_35min_im2.tif

Exp1_rep1_35min_im3.tif

Full viewer

Exp1_rep1_0min_im1.tif

Image ID: 4496763
Owner: Public data

Image Details

Acquisition Date: 2013-11-15 16:02:
Import Date: 2019-01-11 16:41:
Dimensions (XY): 2048 x 2048
Pixels Type: uint16
Pixels Size (XYZ) (μ m): -x - y x 0.20
Z-sections/Timepoints: 25 x 1
Channels: 3-CY5, 5-TMR, 1-DAPI, 7-TRANS
ROI Count: 430

Attributes 5

Cell Lines

Gene

Biomolecular annotations

Analysis results

idr0047, Li et al, Scientific Data DOI:10.1038/s41597-019-0106-6

Attributes 1

Release Date	BIOSTUDIES / STUDIES / S-BIAD1
License	Release Date: 22 November 2018
Copyright	{JSON} {XML} {PageTab} {FTP}
Data Publisher	Gregor Neuert ¹
Data DOI	¹ Vanderbilt University
BioStudies Accession	Accession S-BIAD1
Annotation File	Description <p>We report a comprehensive single cell dataset of spatial distributions of nuclear and cytoplasmic mRNA as a function of time. We measure mRNA expression with single molecule RNA fluorescent in-situ hybridization microscopy in the yeast model organism <i>Saccharomyces cerevisiae</i> in tens of thousands of cells. The resulting dataset contains the discrete number of mRNA molecules in the nucleus and the cytoplasm for sixteen time points, two genes and two stress conditions each in biological duplicates or triplicates. We present these datasets as population means, fraction of cells above basal mRNA expression (ON-cells), the variance normalized by the expression mean (Fano factor), marginal probability of nuclear and cytoplasmic mRNA, and the joint probability of nuclear and cytoplasmic RNA expression. The reuse potential are in three areas: (1) development of discrete single cell modelling approaches, (2) building predictive models to study fundamental processes in transcription regulation, (3) development of single cell image processing approaches not possible with continuous, non-spatial datasets of low temporal resolution.</p>

BioStudies.

ebi.ac.uk
EMBL-EBI Services Research Training About us EMBL-EBI

Search BioStudies

Examples: hyperplasia, PMC516016

[Feedback](#) | [Login](#)

BIOSTUDIES / STUDIES / **S-BIAD1**

A microscopy data set of discrete spatial and temporal single molecule RNA expression in single cells

Gregor Neuert¹

¹ Vanderbilt University

Accession
S-BIAD1

Description

We report a comprehensive single cell dataset of spatial distributions of nuclear and cytoplasmic mRNA as a function of time. We measure mRNA expression with single molecule RNA fluorescent in-situ hybridization microscopy in the yeast model organism *Saccharomyces cerevisiae* in tens of thousands of cells. The resulting dataset contains the discrete number of mRNA molecules in the nucleus and the cytoplasm for sixteen time points, two genes and two stress conditions each in biological duplicates or triplicates. We present these datasets as population means, fraction of cells above basal mRNA expression (ON-cells), the variance normalized by the expression mean (Fano factor), marginal probability of nuclear and cytoplasmic mRNA, and the joint probability of nuclear and cytoplasmic RNA expression. The reuse potential are in three areas: (1) development of discrete single cell modelling approaches, (2) building predictive models to study fundamental processes in transcription regulation, (3) development of single cell image processing approaches not possible with continuous, non-spatial datasets of low temporal resolution.

Study type
FISH

Study Organism
Saccharomyces cerevisiae

Data files

Show 5 entries Search:

Name
20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1...

Showing 1 to 5 of 6,784 entries

Previous **1** 2 3 4 5 ... 1357 Next



The screenshot shows the BioImage Archive homepage. At the top, there's a navigation bar with links for Home, Browse, About us, Our roadmap, Case studies, FAQs, Help, Feedback, and Login. A search bar contains the text "Neuert" with a placeholder "Examples: brain, capsid". Below the navigation, there's a breadcrumb trail: BIOSTUDIES / BIOIMAGES / S-BIAD1. The release date is listed as 22 November 2018. On the right, there are download links for {JSON}, <XML>, -PageTab-, and FTP.

A microscopy data set of discrete spatial and temporal single molecule RNA expression in single cells

Gregor Neuert¹

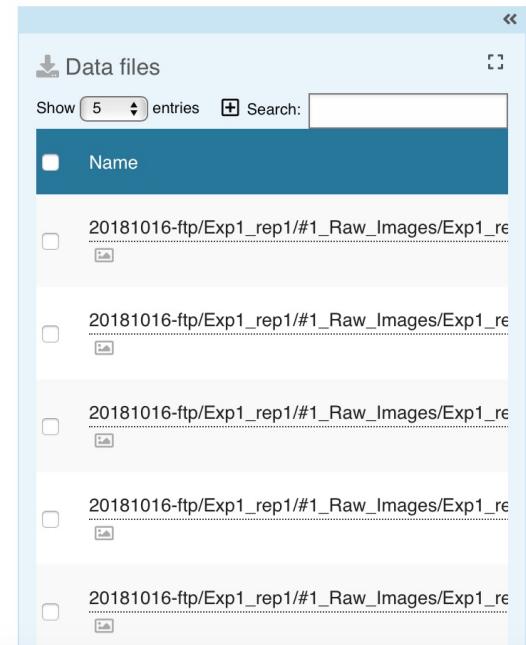
¹ Vanderbilt University

Accession

S-BIAD1

Description

We report a comprehensive single cell dataset of spatial distributions of nuclear and cytoplasmic mRNA as a function of time. We measure mRNA expression with single molecule RNA fluorescent in-situ hybridization microscopy in the yeast model organism *Saccharomyces cerevisiae* in tens of thousands of cells. The resulting dataset contains the discrete number of mRNA molecules in the nucleus and the cytoplasm for sixteen time points, two genes and two stress conditions each in biological duplicates or triplicates. We present these datasets as population means, fraction of cells above basal mRNA expression (ON-cells), the variance normalized by the expression mean (Fano factor), marginal probability of nuclear and cytoplasmic mRNA, and the joint probability of nuclear and cytoplasmic RNA expression. The reuse potential are in three areas: (1) development of discrete single cell modelling approaches, (2) building predictive models to study fundamental processes in transcription regulation, (3) development of single cell image processing approaches not possible with continuous, non-spatial datasets of low temporal resolution.



The screenshot shows a list of data files under the heading "Data files". There are five entries, each with a checkbox and a thumbnail preview. The entries are: 20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1_re, 20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1_re, 20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1_re, 20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1_re, and 20181016-ftp/Exp1_rep1/#1_Raw_Images/Exp1_re.

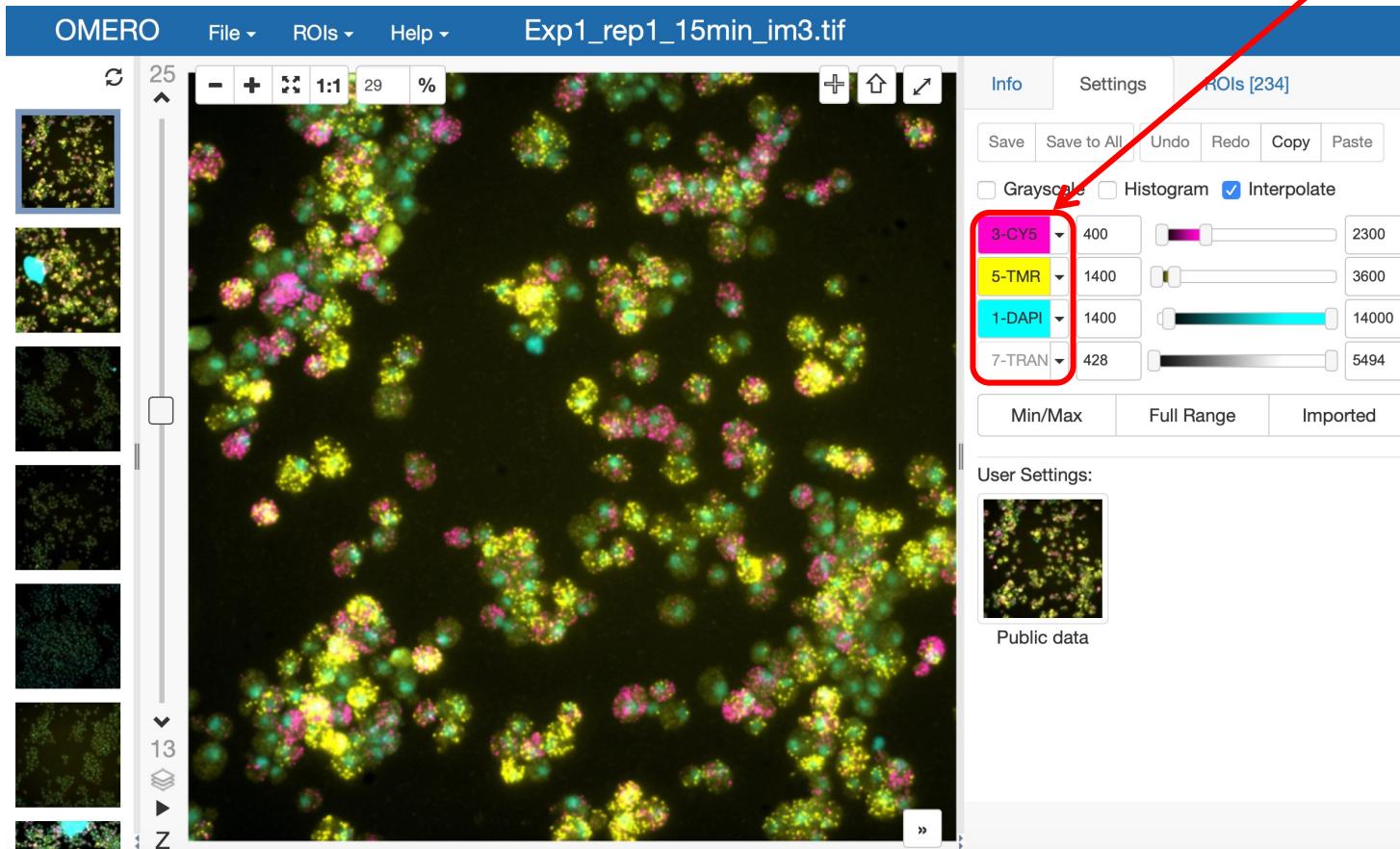
Metadata Curation in IDR

idr0047

Image Details

Acquisition Date:	2014-04-25 15:51:30
Import Date:	2019-01-11 16:40:50
Dimensions (XY):	2048 x 2048
Pixels Type:	uint16
Pixels Size (XYZ) (μm):	- x - x 0.20
Z-sections/Timepoints:	25 x 1
Channels:	3-CY5, 5-TMR, 1-DAPI, 7-TRANS
ROI Count:	234

Experimental metadata



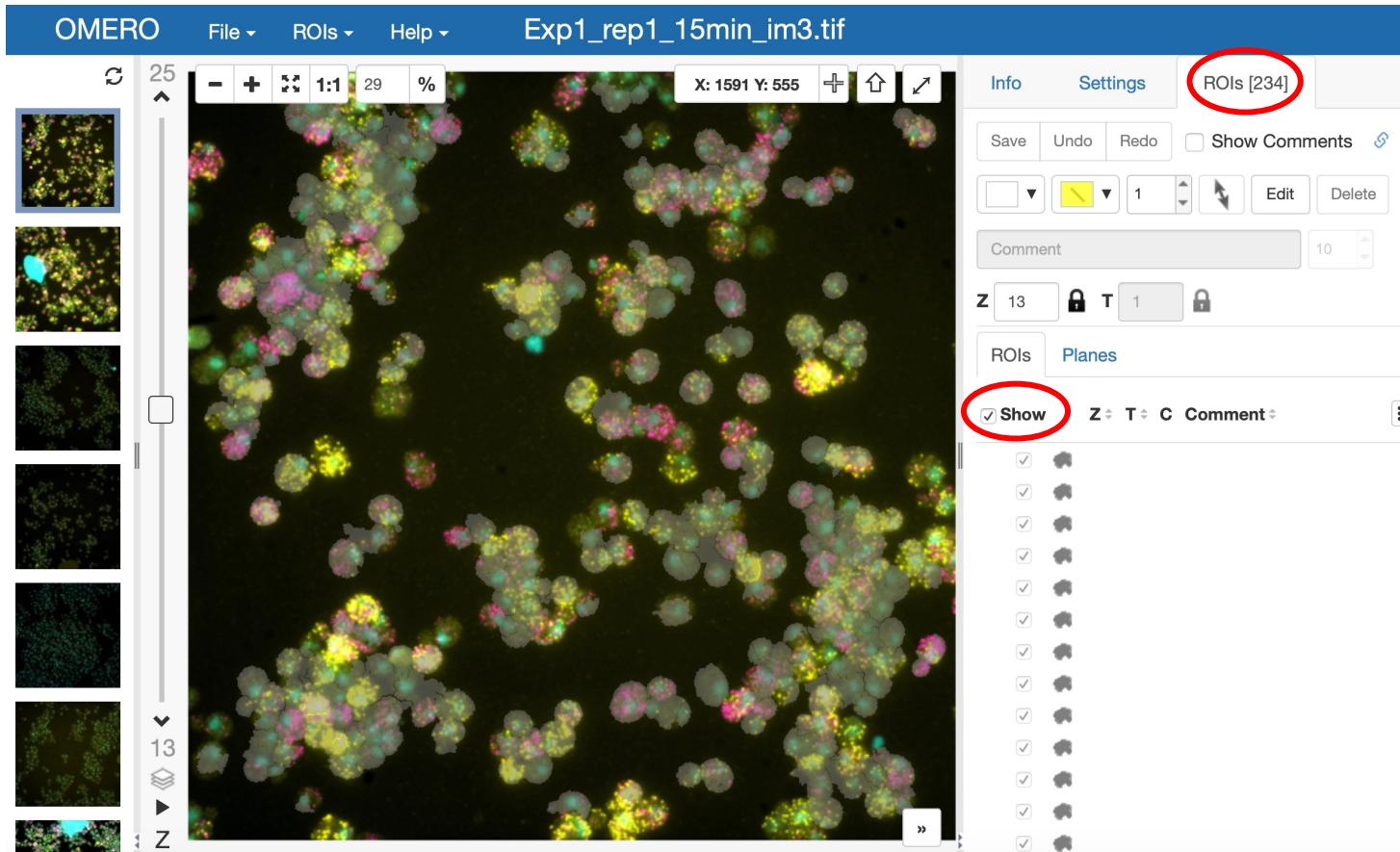
Metadata Curation in IDR

idr0047

Image Details

Acquisition Date:	2014-04-25 15:51:30
Import Date:	2019-01-11 16:40:50
Dimensions (XY):	2048 x 2048
Pixels Type:	uint16
Pixels Size (XYZ) (μm):	- x - x 0.20
Z-sections/Timepoints:	25 x 1
Channels:	3-CY5, 5-TMR, 1-DAPI, 7-TRANS
ROI Count:	234

Experimental metadata



Metadata Curation in IDR

Attributes 5 idr0047 Biomolecular annotations

Cell Lines

Added by: Public data

Cell Line	BY4741
-----------	--------

Gene

Added by: Public data

Gene Identifier	YDR536W
Gene Symbol	STL1

Gene Identifier YDR536W is circled in red.

Gene

Added by: Public data

Gene Identifier	YGR088W
Gene Symbol	CTT1

Organism

Added by: Public data

Organism	Saccharomyces cerevisiae
----------	--------------------------

Others

Added by: Public data

Protocol 1	Treatment - 0.2M NaCl, step
Protocol 2	Growth - CSM, 30C
Experimental Condition	0 minutes after osmotic stress
Comment	this is an image stack containing stacks of 4 different channels
Processed image 1	Exp1_rep1_0min_im1.companion.ome [3D]
Processed image 2	Exp1_rep1_0min_im1.companion.ome [Projection]

IDR Studies Genes Phenotypes Cell Lines

Public Public data

Type Gene Symbol... Match case ?

Gene 1

STL1 (1024) 3

- idr0047-neuert-yeastmrna/experimentA (1005) 10
 - > Exp1_rep1 63
 - > Exp1_rep1 processed 126
 - > Exp1_rep2 64
 - > Exp1_rep2 processed 128
 - > Exp2_rep1 72
 - > Exp2_rep1 processed 144
 - > Exp2_rep2 69
 - > Exp2_rep2 processed 138
 - > Exp2_rep3 67
 - > Exp2_rep3 processed 134
- idr0078-mattiazziusaj-endocyticcomp/screenA (18) 6
- idr0011-ledesmafernandez-dad4/screenA (1) 1

Biocuration: to easily find extensive and interlinked information at well-documented, stable resources.

IDR

- Image Visualisation
- Linked Metadata
- Querying Metadata
- Interactive Analysis

Value of Curation – Image Visualisation

IDR

The screenshot shows a web browser displaying the BioStudies website. The URL in the address bar is [ebi.ac.uk](https://www.ebi.ac.uk/biostudies/studies/S-BSST221). The page title is "BioStudies". The main content area displays a study titled "Imaging Mass Cytometry analysis of human non-pathological tonsils" with accession number S-BSST221. The study was released on 14 December 2018. The description section mentions the use of Fluidigm Hyperion for imaging mass cytometry, imaging human tonsil sections with 27 parameters, and having images for 3 different donors (one for donorA, and another one for donors 1 and 2). The right side of the screen shows a table titled "Data files" listing five files: d1 normalized_Bcl-6.png, d1 normalized_CD11b.png, d1 normalized_CD11c.png, d1 normalized_CD123.png, and d1 normalized_CD14.png. Each file includes its size (741 KB, 1.1 MB, 2.6 MB, 961 KB, 1.8 MB) and a brief description of the staining type and donor.

ebi.ac.uk

EMBL-EBI Services Research Training About us EMBL-EBI

BioStudies.

Search BioStudies Examples: hyperplasia, PMC516016

Home Browse Submit Help About BioStudies Feedback Login

BIOSTUDIES / STUDIES / S-BSST221

Release Date: 14 December 2018 {JSON} <XML> →PageTab ↗FTP

Imaging Mass Cytometry analysis of human non-pathological tonsils

Segura Elodie ¹

¹ Institut Curie

Accession

S-BSST221

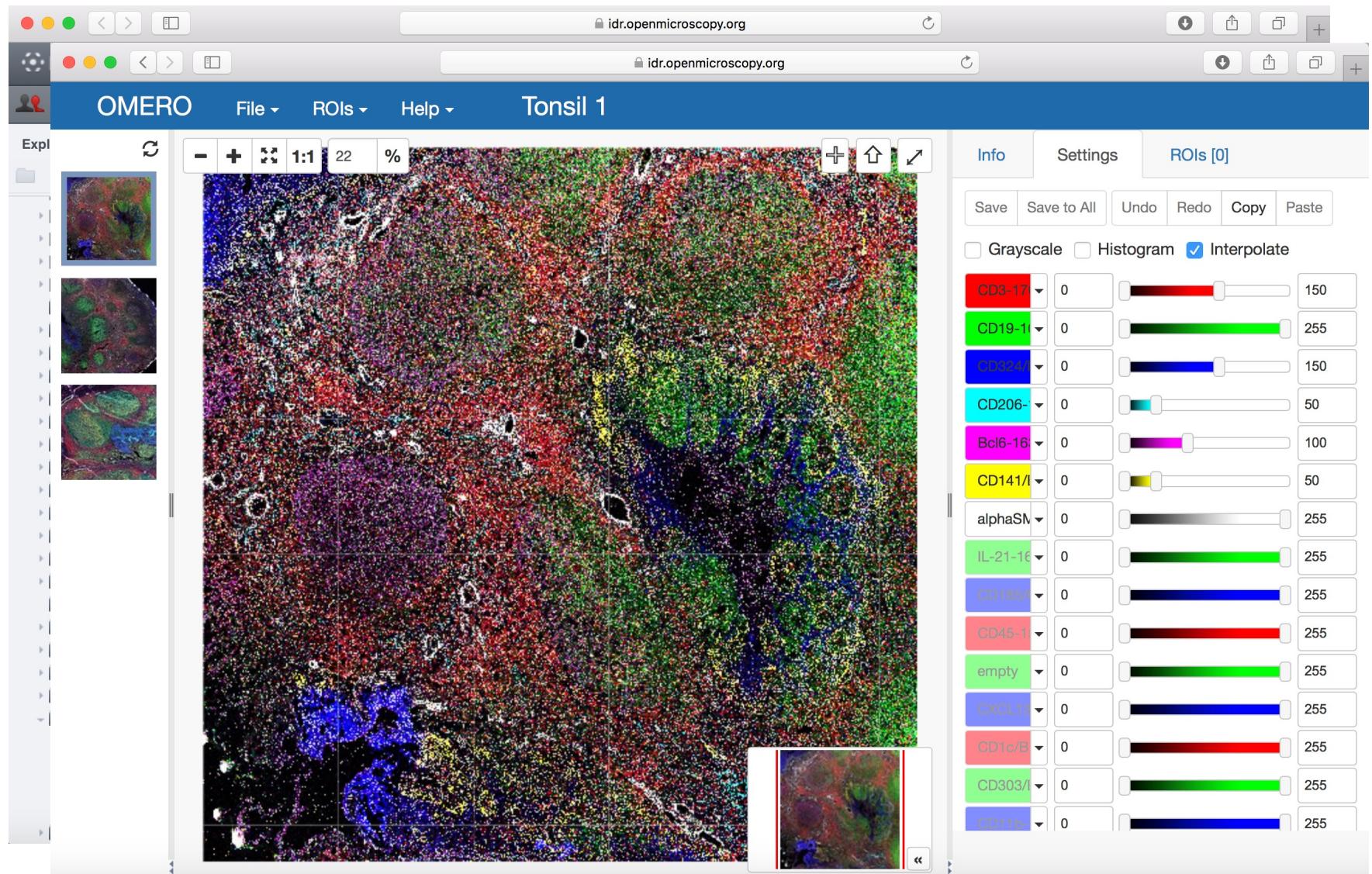
Description

We have used the Fluidigm Hyperion system for imaging mass cytometry. We have imaged human tonsil sections with 27 parameters, and have images for 3 different donors. We used 2 different panels (one for donorA, and another one for donors 1 and 2).

Data files

Name	Size	Description
d1 normalized_Bcl-6.png	741 KB	Bcl6 staining donor1
d1 normalized_CD11b.png	1.1 MB	CD11b staining donor1
d1 normalized_CD11c.png	2.6 MB	CD11c staining donor1
d1 normalized_CD123.png	961 KB	CD123 staining donor1
d1 normalized_CD14.png	1.8 MB	CD14 staining donor1

Value of Curation – Image Visualisation



idr0054, Durand et al, Scientific Data DOI:10.17867/10000122

Value of Curation – Image Visualisation

Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Public Public data

Explore Tags OMERO File ROIs Help hSIOs-1

50 µm

Info Settings ROIs [11]

Save Save to All Undo Redo Copy Paste

Grayscale Histogram Interpolate

0 3500 10000

Min/Max Full Range Imported

User Settings:

Public data

Intestinal Organoids 2

hSIOs-1

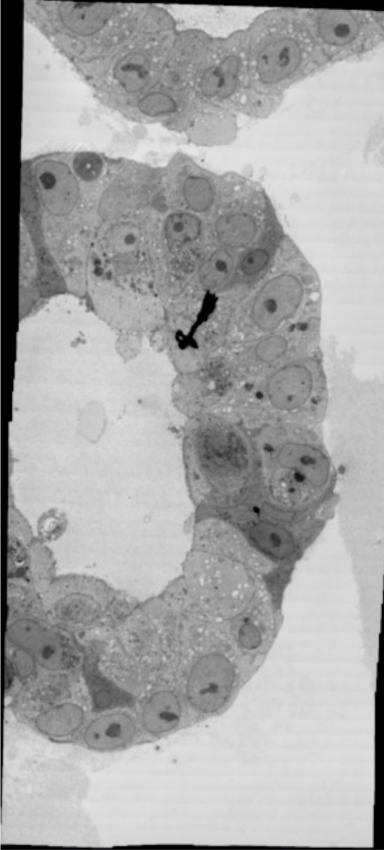
hSIOs-2

Attachments 0

Comments 0

Zoom: 100%

Search:



This screenshot shows the IDR (Integrating Data Resources) platform interface for visualizing electron microscopy images of intestinal organoids. The main window displays a grayscale electron micrograph of several intestinal organoids. A black arrow points to a specific feature within one of the cells. A red box highlights a cluster of three cells at the bottom left. A scale bar at the bottom left indicates 50 micrometers. The interface includes a navigation sidebar on the left with a tree view of data sets, a toolbar at the top with zoom and selection tools, and various settings and analysis tabs on the right. The title bar indicates the dataset is 'hSIOs-1'.

Value of Curation – Image Visualisation

Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Public Public data

Explore Tags OMERO File ROIs Help hSIOs-1

X: 33672 Y: 68035

500 nm

Zoom: 35% 1:1

Info Settings ROIs [11]

Save Save to All Undo Redo Copy Paste

Grayscale Histogram Interpolate

0 3500 10000

Min/Max Full Range Imported

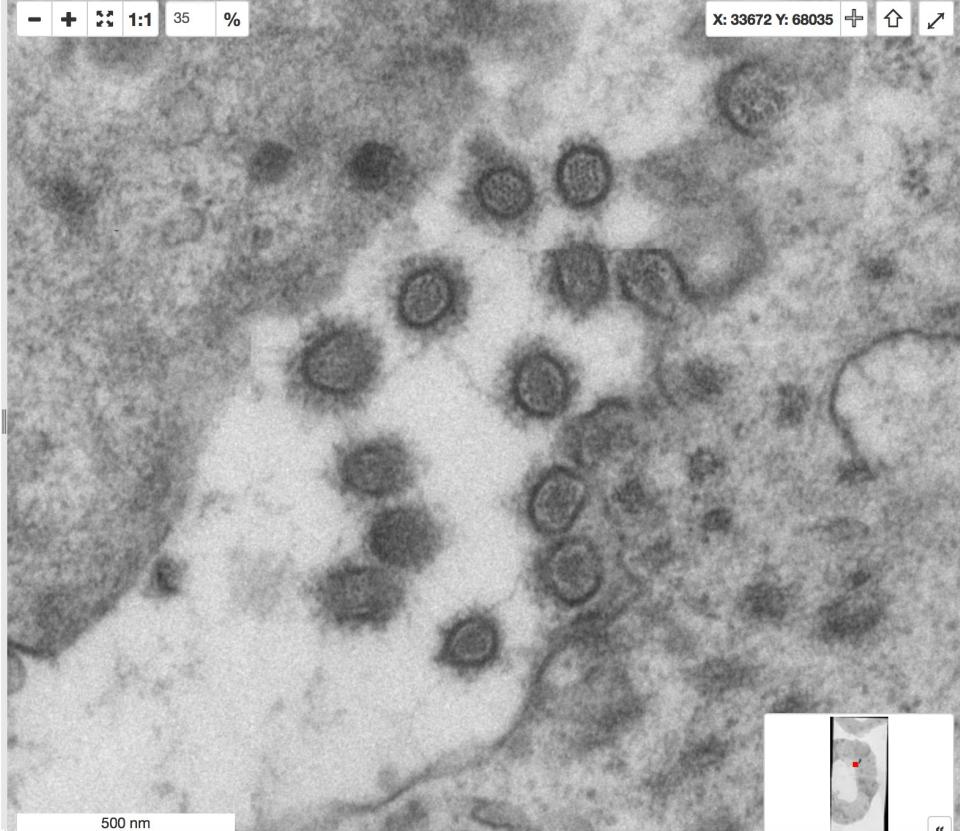
User Settings:

Public data

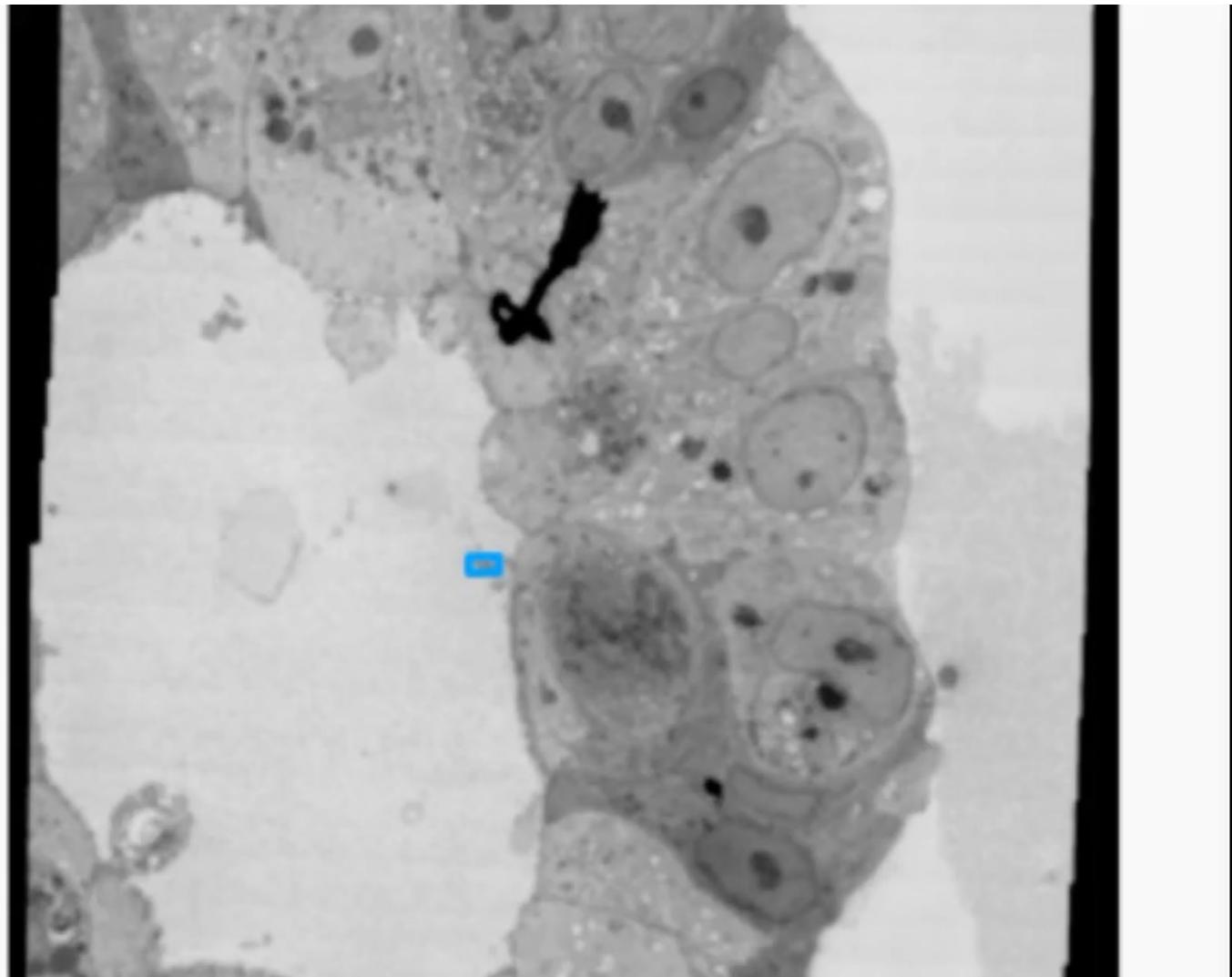
Intestinal Organoids

hSIOs-1 hSIOs-2

Attachments 0 Comments 0



Value of Curation – Image Visualisation





EMPIAR

Attributes 1

Publication DOI

Release Date

License

Copyright

Data Publisher

Data DOI

EMPIAR Accession

Annotation File

EMPIAR home | Deposition | REST API | FAQ | About EMPIAR | Policies | Feedback | Share

EMPIAR-10404

SARS-CoV-2 productively infects human gut enterocytes

Publication: SARS-CoV-2 productively infects human gut enterocytes
Lamers MM [id](#), Beumer J [id](#), van der Vaart J [id](#), Knoops K [id](#), Puschhof J, Breugem T, Ravelli RBG [id](#), van Schayck JP [id](#), Mykytyn AZ, Duimel HQ, van Donselaar E, Riesebosch S, Kuijpers HJH, Schipper D, van de Wetering WJ, de Graaf M, Koopmans M [id](#), Cuppen E [id](#), Peters PJ, Haagmans B [id](#), Clevers H [id](#)
Science
DOI: [10.1126/science.abc1669](https://doi.org/10.1126/science.abc1669)

Related IDR entry: [idr0083](#)

Deposited: 2020-04-30

Released: 2020-05-01

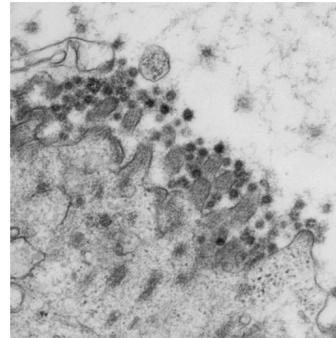
Last modified: 2020-05-01

Dataset size: 66.5 GB

Dataset DOI: [10.6019/EMPIAR-10404](https://doi.org/10.6019/EMPIAR-10404)

Experimental metadata: [Download xml](#)

Contains: stitched maps



Quick links

[EMDB](#)

[PDBe](#)

[BiolImage Archive](#)

[EMPIAR Quick tour](#)

[Statistics](#)

[Re-use case study](#)

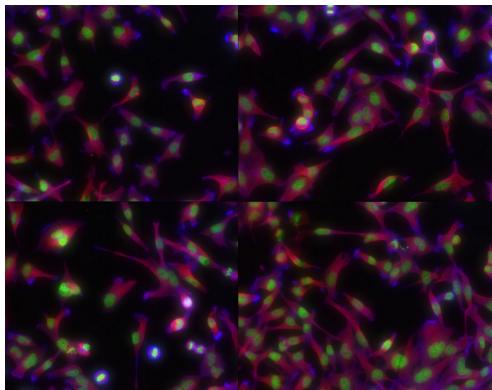
[EMPIAR@PDBj](#)

EMPIAR citations

Cryo-EM structure of the potassium-chloride cotransporter KCC4 in lipid nanodiscs.
Reid MS, Kern DM, Brohawn SG. (2020)

Development of basic building blocks

Value of Curation - Linked Metadata



idr0012

OMERO

Studies Genes Phenotypes Cell Lines siRNAs Antibodies

Public

Type Gene Symbol... Match case Add filter

Gene 1

- ASH2L (326) 6 
- ↳ idr0022-koedoot-cellmigration/screenA (288) 8
- ↳ idr0006-fong-nuclearbodies/screenA (16) 1
- ↳ idr0009-simpson-secretion/screenA (12) 6
- ↳ idr0013-neumann-mitocheck/screenA (6) 3
- ↳ idr0012-fuchs-cellmorph/screenA (2) 1
- ↳ HT28 2
 - HT28 [Well G13, Field 1]
 - HT28 [Well G13, Field 2]
- ↳ idr0010-doil-dnадamage/screenA (2) 1

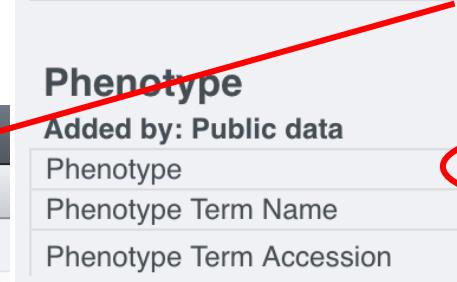


Attributes 8

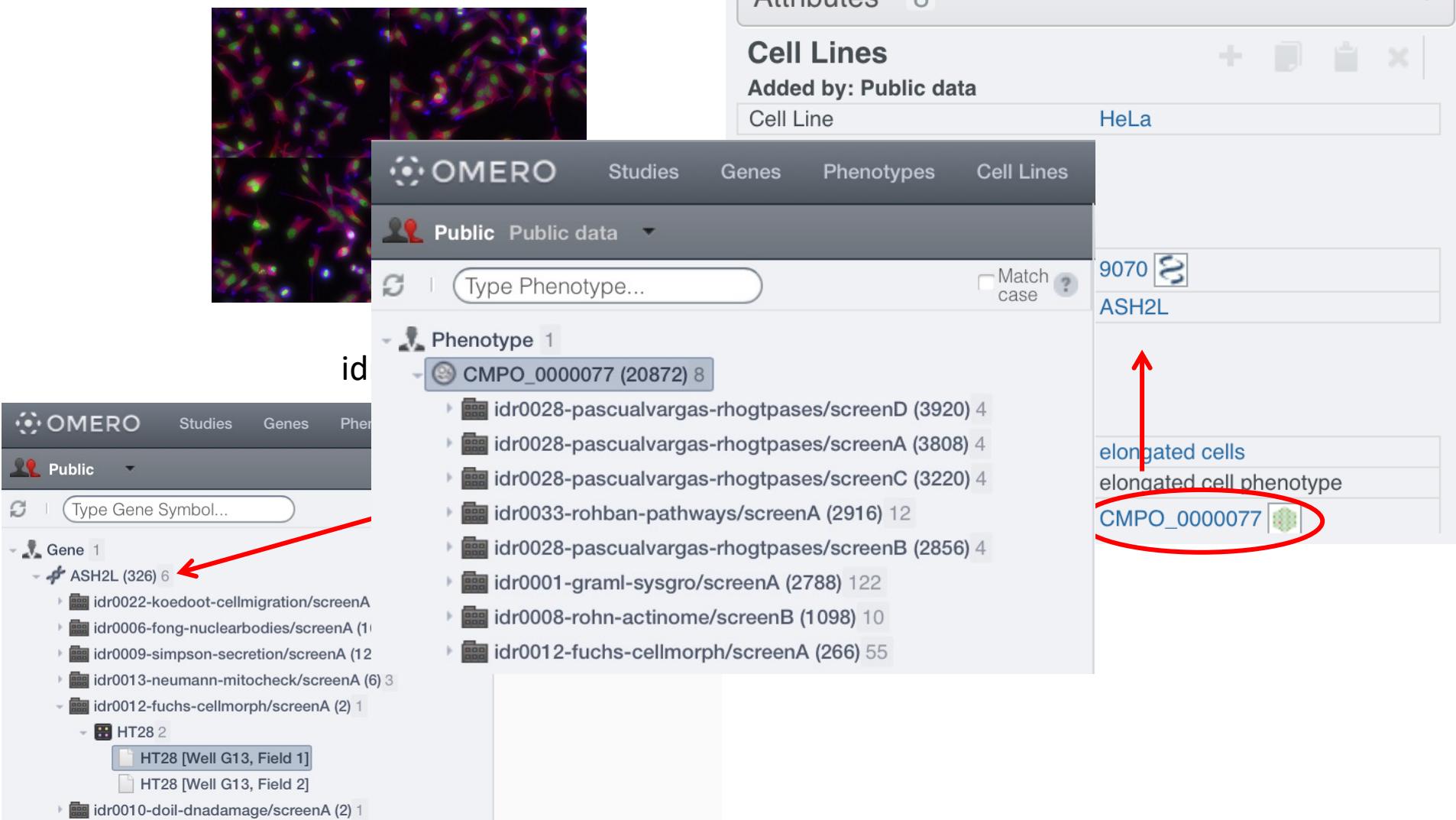
Cell Lines
Added by: Public data
Cell Line HeLa

Gene
Added by: Public data
Gene Identifier 9070 
Gene Symbol ASH2L

Phenotype
Added by: Public data
Phenotype elongated cells 
Phenotype Term Name elongated cell phenotype
Phenotype Term Accession CMPO_0000077 



Value of Curation - Linked Metadata



The screenshot illustrates the interconnected nature of biological data through linked metadata. On the left, the OMERO interface shows a search for the gene **ASH2L**. A red arrow points to the search result for **ASH2L (326)**, which is associated with six experiments. On the right, the **Cell Lines** section shows the **HeLa** cell line, which has an associated phenotype. A red circle highlights the entry **CMPO_0000077** under the **Phenotype 1** heading, which is linked to the **ASH2L** gene. A red arrow points from the **ASH2L** search result to this highlighted phenotype entry.

OMERO Studies Genes Phenotypes

Public Type Gene Symbol...

Gene 1

- **ASH2L (326)** 6
- ↳ idr0022-koedoot-cellmigration/screenA
- ↳ idr0006-fong-nuclearbodies/screenA (1)
- ↳ idr0009-simpson-secretion/screenA (12)
- ↳ idr0013-neumann-mitocheck/screenA (6) 3
- ↳ idr0012-fuchs-cellmorph/screenA (2) 1
- **HT28** 2
 - ↳ HT28 [Well G13, Field 1]
 - ↳ HT28 [Well G13, Field 2]
- ↳ idr0010-doil-dnадamage/screenA (2) 1

Attributes 8

Cell Lines
Added by: Public data
Cell Line HeLa

9070  **ASH2L**

elongated cells
elongated cell phenotype

CMPO_0000077 

Type Phenotype... Match case ?

Studies Genes Phenotypes Cell Lines

Public Public data

Phenotype 1

- **CMPO_0000077 (20872)** 8
 - ↳ idr0028-pascualvargas-rhogtpases/screenD (3920) 4
 - ↳ idr0028-pascualvargas-rhogtpases/screenA (3808) 4
 - ↳ idr0028-pascualvargas-rhogtpases/screenC (3220) 4
 - ↳ idr0033-rohban-pathways/screenA (2916) 12
 - ↳ idr0028-pascualvargas-rhogtpases/screenB (2856) 4
 - ↳ idr0001-graml-sysgro/screenA (2788) 122
 - ↳ idr0008-rohn-actinome/screenB (1098) 10
 - ↳ idr0012-fuchs-cellmorph/screenA (266) 55

Value of Curation – Querying Metadata



CELL - IDR TISSUE - IDR [ABOUT](#) ▾ [SUBMISSIONS](#) ▾

Search by: Compound ▾ Remdesivir

Found **216** images with **Compound: Remdesivir** in **1** study

Remdesivir

Study ID	Organism	Image count	Title	Sample Images	Link
idr0094B	Homo sapiens	216	Identification of inhibitors of SARS-CoV...	  	more...



SARS-CoV-2 and Remdesivir



Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Type Compound Name... Match case Add filter

Public Public data

Compound 1
Remdesivir (216) 1
idr0094-ellinger-sarscov2/screenB (216) 3
ESP0025721 72

20 μ M →

0.0064 μ M ←

Zoom: [Slider]

General Acquisition Preview

ESP0025721

Plate ID: 7824
Owner: Public data Show all

Plate Details

Creation Date: 2020-09-30 18:38:55

Attributes 0

Attachments 0

Comments 0

Tags 0

Ratings 0

Others 0

Value of Curation – Interactive Analysis



IDR Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About Search:

Public Public data ▾

Explore Tags Shares

idr0094-ellinger-sarscov2
idr0094-ellinger-sarscov2/screenA 64
idr0094-ellinger-sarscov2/screenB 102

ESP0025712
ESP0025713
ESP0025714
ESP0025715
ESP0025716
ESP0025717
ESP0025718
ESP0025719
ESP0025720
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ESP0025734
ESP0025735
ESP0025736
ESP0025737
ESP0025738
ESP0025739

General Acquisition Preview Show all

Owner: Public data

Screen Details

Publication Title
A SARS-CoV-2 cytopathicity dataset generated by high-content screening of a large drug repurposing collection

Screen Description
Dose response screen

Creation Date: 2020-09-30 15:09:06
Plate Count: 102 plates

Attributes 3

Data Publisher Universil +
10.1786/100001455
<https://doi.org/10.1786/10000148b>

Data DOI S-BIAD29
<https://www.ebi.ac.uk/biostudies/studies/S-BIAD29>

BioStudies Accession idr0094-screenB-annotation.csv
<https://github.com/IDR/idr0094-ellinger-sarscov2/blob/HEAD/screenB/idr0094-screenB-annotation.csv>

Annotation File

Analysis Notebook

Added by: Public data

Study Notebook idr0094-ic50.ipynb

Attachments 1

Comments 0

Tags 0

Ratings 0

idr0094, Ellinger et al Sci Data DOI:10.1038/s41597-021-00848-4

Open cloud and open analytics

IC50 exploration

This notebook demonstrates how to process plates associated to the paper [A SARS-CoV-2 cytopathicity dataset generated by high-content screening of a large drug repurposing collection](#). We explore the metadata linked to [idr0094-ellinger-sarscov2/screenB](#).

Calculate the half maximal inhibitory concentration IC50

The half maximal inhibitory concentration (IC50) is a measure of the potency of a substance in inhibiting a specific biological or biochemical function. IC50 is a quantitative measure that indicates how much of a particular inhibitory substance (e.g. drug) is needed to inhibit, *in vitro*, a given biological process or biological component by 50%.

```
In [11]: calculate_IC50 <- function(data){
  IC50 <- NA
  data.LL.4 <- NULL
  ctest <- filter(data, Inhibition != "NaN")
  data.LL.4 <- drm(Inhibition ~ Concentration, data = ctest, fct = LL.4(), control = drmc(errorm=FALSE))
  if (is.null(data.LL.4$convergence)) {
    IC50 <- ED(data.LL.4, 50, interval = "delta")[1]
  }
  returned_values <- list("ic50" = IC50, "data" = data.LL.4)
}
```

```
In [12]: values <- calculate_IC50(data)
IC50 <- values$ic50
IC50
```

Estimated effective doses

	Estimate	Std. Error	Lower	Upper
e:1:50	0.80772	0.12019	0.55701	1.05842
	0.807715887041243			

Plot the Dose Response curve

Discussion

The activity of the reference compound, remdesivir (IC50 = 0.76 μ M) was confirmed in this study.

Remdesivir targets the viral nsp12 RNA-dependent RNA polymerase⁽⁸⁾ and is currently under evaluation in an adaptive, randomized, double-blind, placebo-controlled phase III clinical trial⁽⁹⁾.

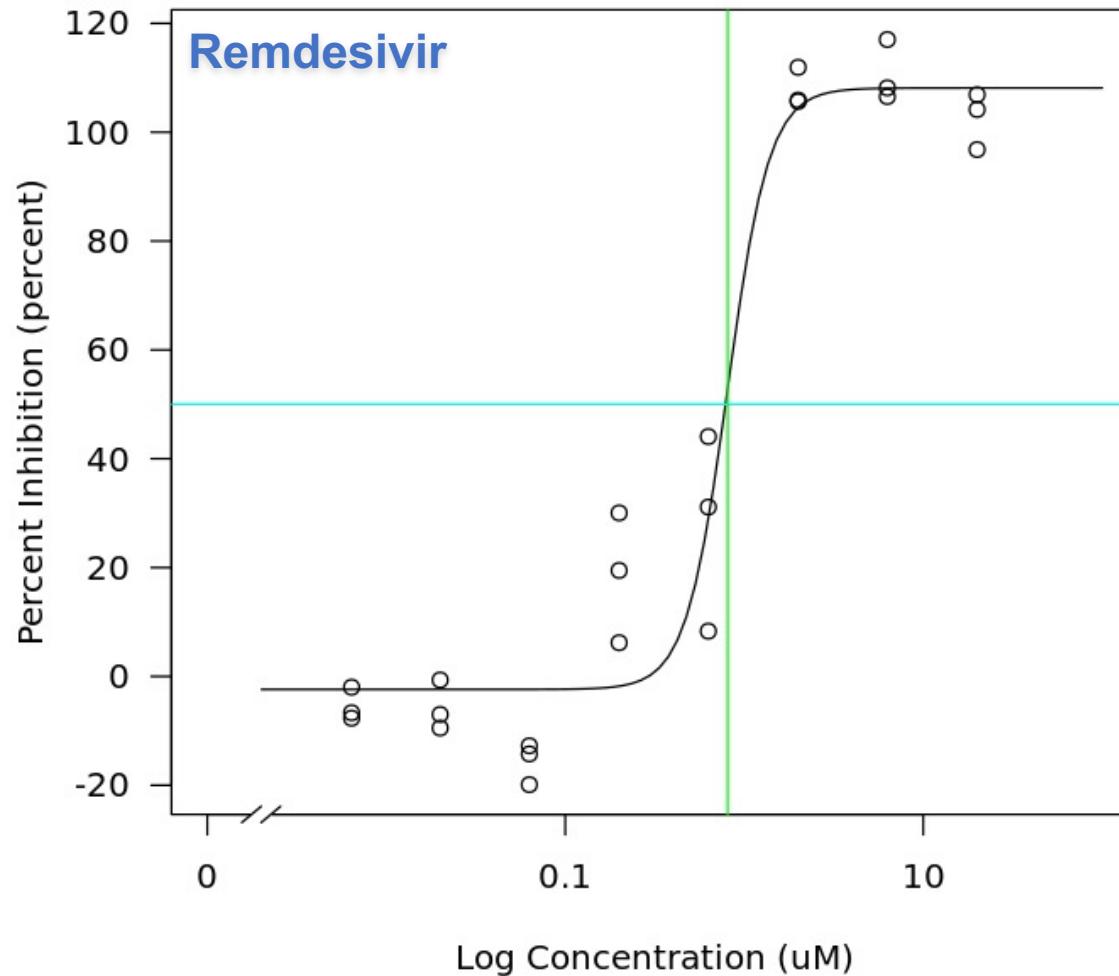
```
In [13]: options(repr.plot.width=6, repr.plot.height=5.8)
plot(values$data, broken = TRUE, type = "all",
  main = "Dose Response Curve (DRC)", xlim = c(0, 100),
  xlab = "Log Concentration ( $\mu$ M)",
  ylab = "Percent Inhibition (percent)")
abline(h = 50, col = "cyan")
abline(v = IC50, col = "green")
```

Dose Response Curve of Remdesivir

IDR



Dose Response Curve (DRC)



 WorkflowHub Search here.

 **Calculate the half maximal inhibitory concentration for each compound used in SARS-CoV-2 investigation** Version 2 (latest)

[Overview](#) [Files](#)

Workflow Type: Jupyter
[Stable](#)

 EOSC-Life

 EURO BIOIMAGING

<https://workflowhub.eu/>

Which diabetes related genes are expressed in the pancreas?

HumanMine

v12 February 2022

An integrated database of *Homo sapiens* genomic data

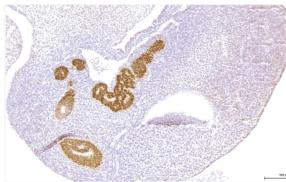
<https://www.humanmine.org/humanmine>



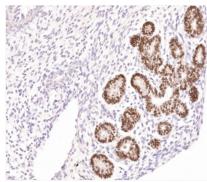
IDR MULTOMICS API



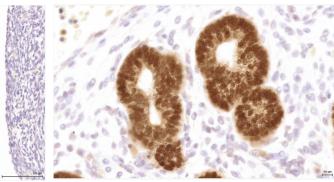
Images linked to gene PDX1



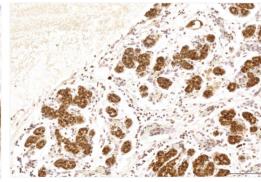
CS16



CS21



9PCW



15PCW

Developmental stage

TISSUE = "Pancreas"
DISEASE = "diabetes"

```
query.add_constraint("proteinAtlasExpression.tissue.name", "=", TISSUE)
query.add_constraint("proteinAtlasExpression.level", "IN", ["Low", "OF", "Medium", "High"])
query.add_constraint("organism.name", "=", "Homo sapiens")
query.add_constraint("diseases.name", "CONTAINS", DISEASE)

<BinaryConstraint: Gene.diseases.name CONTAINS diabetes>
```

Collect the genes

```
upin_tissue = list()
for row in query.rows():
    upin_tissue.append(row["symbol"])
unique = set(upin_tissue)
genes = sorted(genes, reverse=True)
```

Genes found

WFS1	VEGFA	TCP7L2	TBC1D4	SOD2	SLC30A8	PTPN22	PDX1
MIA3	KCNJ11	IR52	IRS1	INSR	INS	IGF2BP2	IER3IP1
HNF4A	HNF1B	HMGAI	HFE	GPD2	GCK	ENPP1	EIF2AK3
DNAJC3	CEL	CAPN10	APPL1	AKT2	ABCC8		

Search for images in IDR associated to the genes found in Humanmine

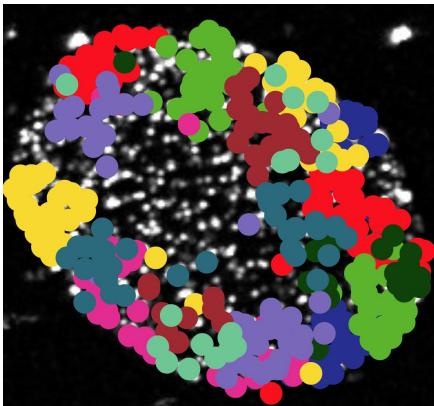
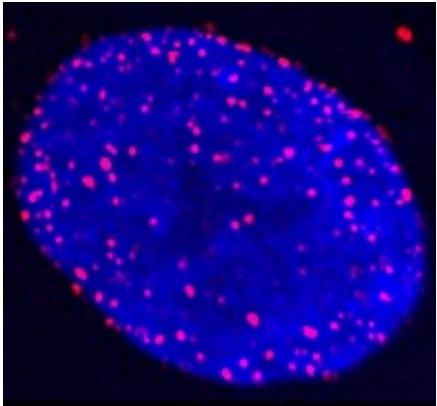
From the list of genes found using the intermine API, we are now looking in [Image Data Resource](#) for studies linked to those genes and with tissue as a Sample Type.

```
TYPE = "gene"
SAMPLE_TYPE = "tissue"
EXPRESSION_KEY = "Expression Pattern Description"
EXPRESSION = "Islets" # "Brain"
KEYS = ("phenotype":
        ("Phenotype Term Name",
         "Phenotype Term Accession",
         "Phenotype Term Accession URL",
         )
      )

projects = list()
for gene in genes:
    qs1 = {'key': TYPE, 'value': gene}
    url1 = URL.format(**qs1)
    json = session.get(url1).json()
    for m in json['maps']:
        qs2 = {'key': TYPE, 'value': gene}
        url2 = SCREENS_PROJECTS_URL.format(**qs2)
        json = session.get(url2).json()
        for p in json['projects']:
            value = find_type("project", p['id'])
            if value > -1:
                projects.append(value)
```

Integrating Multiomics Data

IDR

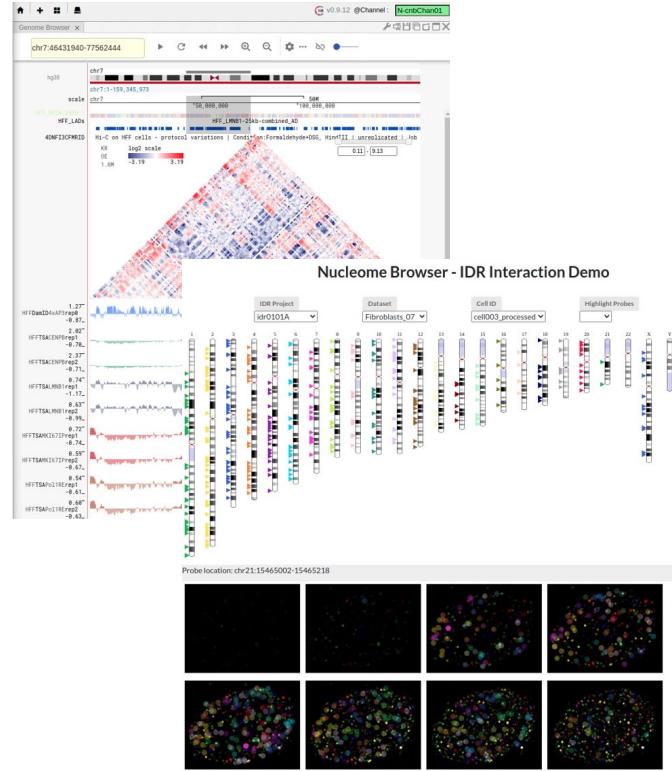


IDR MULTIOmICS API



Roi	shape	embryo_id	cell_id	cell_index	stage	amp_ind	x_um_abs	y_um_abs	z_um_abs	chr	chr_name	pos
2366788	6707352	8	1	8	zygote	27457	115.322565917969	98.31397705078129	52.2	4	chr4	14443209
2366788	6707353	8	1	8	zygote	27539	124.206032714844	106.547434082031	58.6	4	chr4	39484040
2366788	6707354	8	1	8	zygote	27587	114.997561035156	102.755710449219	57.0	4	chr4	78103929
2366788	6707355	8	1	8	zygote	27645	127.564416503906	109.472478027344	56.2	4	chr4	53199572
2366788	6707356	8	1	8	zygote	27796	136.989558105469	99.61399658203129	53.0	4	chr4	139525045
2366788	6707357	8	1	8	zygote	27872	123.447687988281	110.230822753906	41.8	4	chr4	153217076
2366788	6707358	8	1	8	zygote	27894	107.739118652344	99.72233154296879	49.8	4	chr4	78490414

idr0101, Payne et al *Science* DOI:10.1126/science.abc1669



Nucleome Browser
Xiaopeng Zhu, Yang Zhang, Jian Ma

Preprint: <https://doi.org/10.1101/2022.02.21.481225>



OMERO

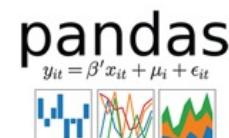


image.sc <https://forum.image.sc/>

List of available Notebooks

- [Java API](#)  
- [Python API](#)  
- [R API](#) 
- [CellProfiler & IDR](#) 
- [ilastik & IDR](#) 
- [Fiji & IDR](#) 
- [Orbit & IDR](#)  
- [QuPath & IDR](#)
- [IDR notebooks](#)  

Validate chosen tool against data in IDR



IDR Studies Genes Phenotypes Cell Lines siRNAs Antibodies Compounds Organisms About

Public Public data

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Add filter

grid icon

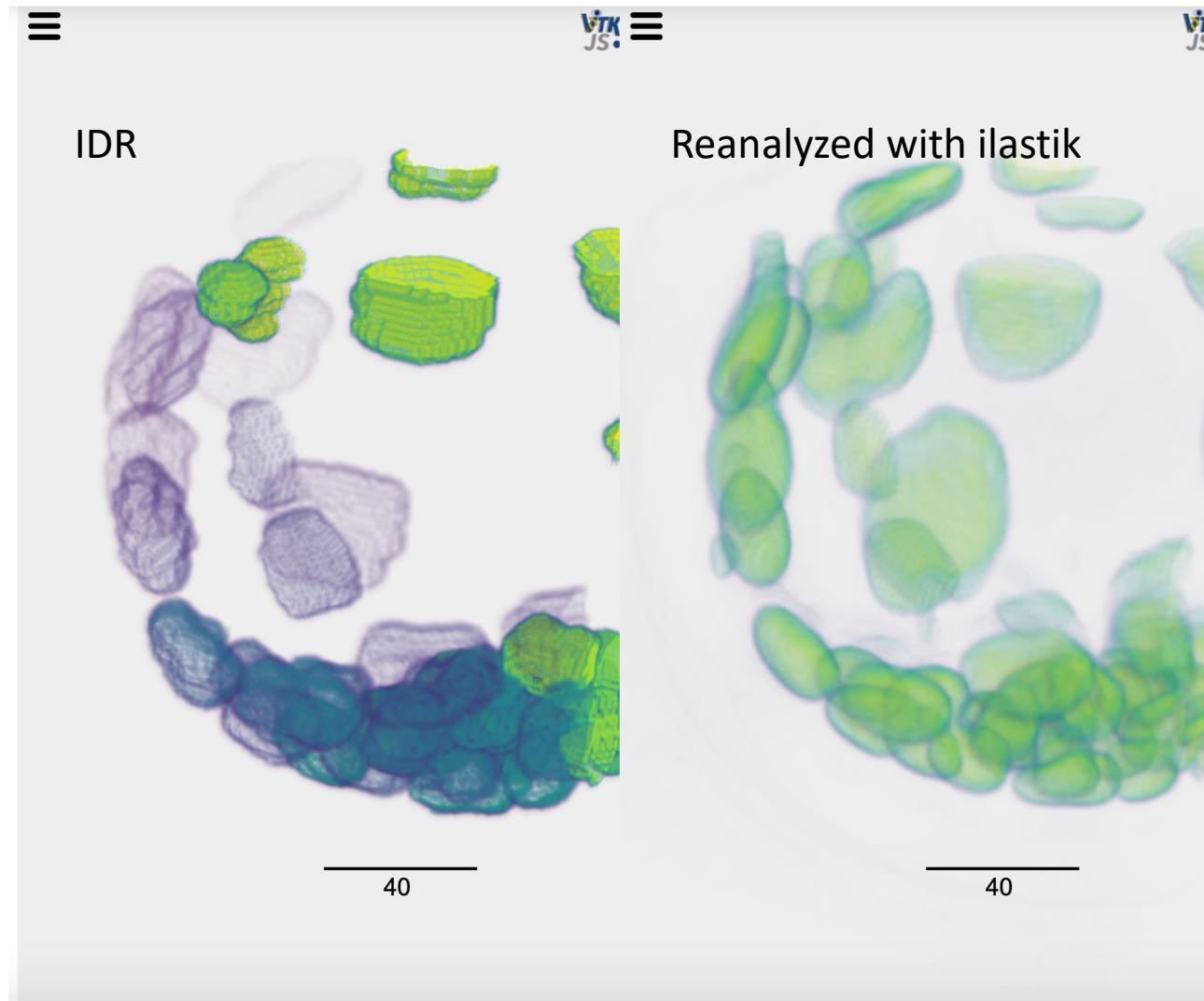
list icon

idr0062-blin-nuclearsegmentation/experimentA 5

- Acini 3
- Blastocysts 11
 - B1_C1.tif
 - B1_C2.tif
 - B2_C1.tif
 - B2_C2.tif
 - B3.tif
 - B4_C1.tif
 - B4_C2.tif
 - B4_C3.tif
 - B5_C1.tif
 - B5_C2.tif
 - B5_C3.tif
- E75 3
- E875 4
- Neural 1

idr0062 Blin et al, Plos Biology DOI:10.1371/journal.pbio.3000388

Compare ROIs in IDR to reanalysis output





<https://idr.openmicroscopy.org>

Submitting Data to IDR



To submit data to IDR, email
idr@openmicroscopy.org



Upload original, raw image files.



Fill in metadata templates.



Data published in IDR!

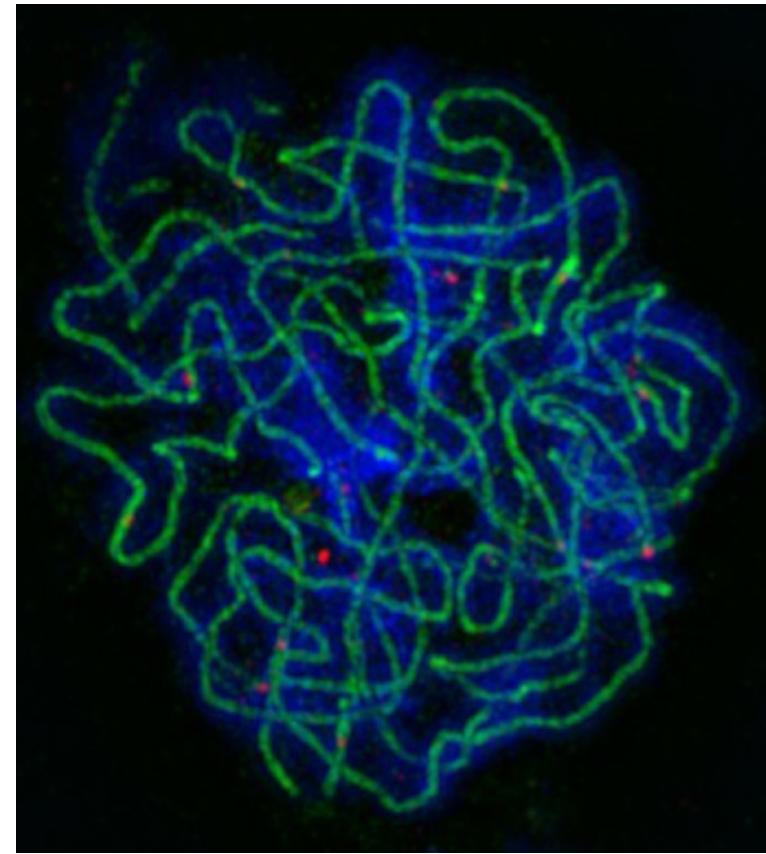
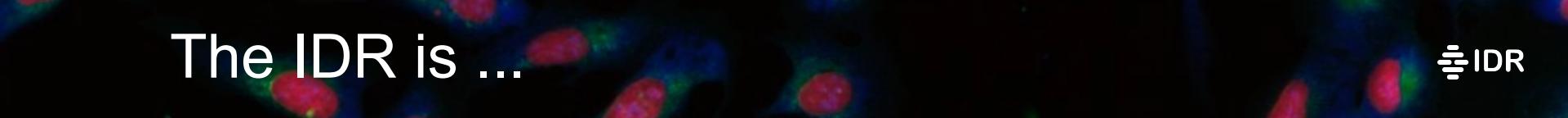


Image from idr0107, Morgan et al.



The IDR is ...



Publicly available, curated studies...

submitted by the community...

in a searchable, scalable platform...

that links metadata ...

and enables reanalysis ...

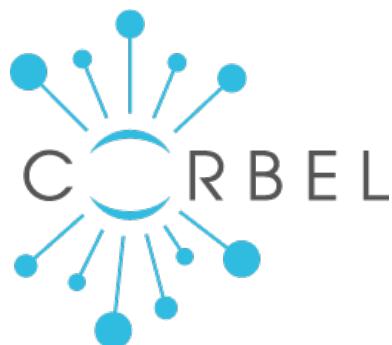
that can be deployed by others.

Thanks to the funders



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Chan
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Initiative 



GLOBAL
BIOIMAGING
growing collaboration



Thanks to the IDR Team



**Jason
Swedlow**



**Sebastien
Besson**



**Frances
Wong**



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