

JCB Data Viewer

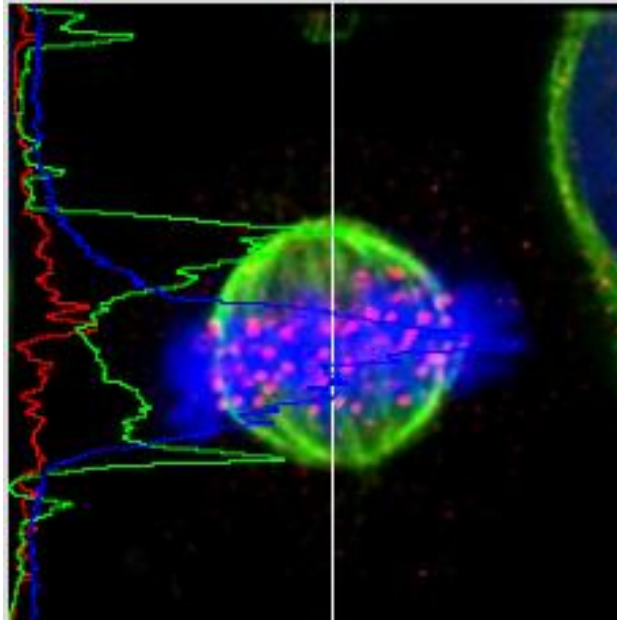
Bringing New Dimensions to Published Image Data

Liz Williams, PhD
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Why does a publisher care about OME/OMERO?

Our goal as a publisher:

- To ensure the integrity of the scientific record.
- To ensure that what our readers see is what the authors saw.



Why does a publisher care about OME/OMERO?

How do we ensure that what our readers see is what the authors saw?

- by promoting access to original image data
- by promoting sharing of original image data
- by promoting archiving of original image data

OME/OMERO and the **JCB** Data Viewer

- An OMERO-based, browser-based application for archiving, viewing, and sharing original, raw image files associated with *JCB* papers.
- Enables presentation and archiving of the original data as acquired by the user, pre-manipulation.
- Enables hosting and sharing of multidimensional, multichannel files from various types of imaging systems.
- Allows users (editors, reviewers, readers) to perform simple analyses of the data within the application and download the data in the open OME-TIFF format for more detailed analysis with their software of choice.
- Enables multidimensional publishing – far beyond what is possible with standard PDFs and html.

The screenshot shows a web browser window with the address bar containing <http://jcb-dataviewer.rupress.org/>. The page features the JCB Data Viewer logo on the left and the Glencoe Software and The Rockefeller University Press logos on the right. A navigation menu includes links for DATAVIEWER HOME, ARCHIVE, SUPPORTED FILE TYPES, INSTRUCTIONS FOR USE, FAQ, CONTACT, TERMS OF USE, and ABOUT. A 'log in' link is also present. The main content area is titled 'Welcome to the JCB DataViewer!' and contains a paragraph describing the application's purpose. Below this is a 'Featured Images' section with five entries, each including a thumbnail image, a title, authors, a DOI, and links for 'Full Viewer', 'Article', and 'Figure'. On the left side of the page, there is a 'Current Issue' section with a thumbnail and a search box.

JCB Data Viewer

THE ROCKEFELLER UNIVERSITY PRESS
QUALITY AND INTEGRITY

log in

DATAVIEWER HOME ARCHIVE SUPPORTED FILE TYPES INSTRUCTIONS FOR USE FAQ CONTACT TERMS OF USE ABOUT

Welcome to the JCB DataViewer!

The JCB DataViewer is a browser-based application designed to facilitate viewing, analysis, and sharing of multi-dimensional image data associated with articles published in **The Journal of Cell Biology**.

For more information about the JCB DataViewer click [here](#).

Featured Images

 **Defective nucleotide excision repair with normal centrosome structures and functions in the absence of all vertebrate centrin**
Tiago J. Dantas, Yifan Wang, Pierce Lalor, Peter Dockery, Ciaran G. Morrison
jcb, 2011. DOI: 10.1083/jcb.201012093
[Full Viewer](#) | [Article](#) | [Figure](#)

 **Integrins traffic rapidly via circular dorsal ruffles and macropinocytosis during stimulated cell migration**
Zhizhan Gu, Erika H. Noss, Victor W. Hsu, Michael B. Brenner
jcb, 2011. 193:61-70 DOI: 10.1083/jcb.201007003
[Full Viewer](#) | [Article](#) | [Figure](#)

 **A vertebrate N-end rule degron reveals that Orc6 is required in mitosis for daughter cell abscission**
Juan A. Bernal, Ashok R. Venkataraman
jcb, 2011. 192:969-978 DOI: 10.1083/jcb.201008125
[Full Viewer](#) | [Article](#) | [Figure](#)

 **Runx1 modulates adult hair follicle stem cell emergence and maintenance from distinct embryonic skin compartments**
Karen M. Osorio, Karin C. Lijja, Tudorita Tumbar
jcb, 2011. 193:235-250 DOI: 10.1083/jcb.201006088
[Full Viewer](#) | [Article](#) | [Figure](#)

 **HP1 α recruitment to DNA damage by p150CAF-1 promotes homologous recombination repair**
Céline Baldeyron, Gaston Soria, Danièle Roche, Adam J. L. Cook, Geneviève Almouzni
jcb, 2011. 193:61-65 DOI: 10.1083/jcb.201101030
[Full Viewer](#) | [Article](#) | [Figure](#)

Done

File Types Supported (using Bio-Formats)

Amira Mesh (.am, .hx, etc.)	Cellomics (.c01)	TillPhotonics TillVision (.vws)
Olympus Slidebook (.sld)	InCell 1000 (.xdce, .tif)	DICOM (.dcm, .dic, etc.)
DeltaVision (.dv, .r3d, etc.)	Zeiss AxioVision ZVI (.zvi)	Openlab LIFF (.liff)
Prairie Technologies TIFF (.tif, .xml, .cfg)	Bitplane Imaris (.ims)	Leica (.lei, .tif, .tiff)
PerkinElmer Opera Flex (.flex)	Maia Scientific (.tif)	Nikon NEF (.nef, .tif, .tiff)
MINC MRI (.mnc)	IVision (.ipm)	FITS (.fits)
Gatan digital micrograph (.dm3)	PerkinElmer (.ano, .cfg, .tim, etc.)	Li-Cor L2D (.l2d, .scn, .tif)
IPLab (.ipl)	Nikon ND2 (.nd2)	ImagePro Workspace (.ipw)
Alicona 3D (.al3d)	Visitech XYS (.xys, .html)	Olympus APL (.apl, .tnb, .mpb)
Metamorph STK (.stk, .nd)	Hamamatsu Aquacosmos NAF (.naf)	Aperio SVS TIFF (.svs)
Zeiss Laser-Scanning Micro. (.ism, .mdb)	Bio-Rad PIC (.pic, .xml, .raw)	Improvision TIFF (.tif)

And many more – more than 75 PFFs and growing.

1. Single Image Analysis

JCB Data Viewer

The Mini Viewer

The screenshot displays the JCB Data Viewer web interface in a Mozilla Firefox browser window. The page features the JCB Data Viewer logo and the Glencoe Software logo, which is associated with The Rockefeller University Press. A navigation menu includes links for 'DATAVIEWER HOME', 'ARCHIVE', 'SUPPORTED FILE TYPES', 'INSTRUCTIONS FOR USE', 'FAQ', 'CONTACT', 'TERMS OF USE', and 'ABOUT'. The main content area is titled 'Locus-specific and activity independent gene repositioning during early tumorigenesis' by K.J. Meaburn and T. Misteli, published in J Cell Biol. 2008, 180:39-50. The article is associated with a DOI of 10.1083/jcb.200708204. The interface shows 'Original Data' with a 'Download All Data as OME-TIFF' button (6 images) and links to 'Figure 1' and 'Figure 2'. A 'Manuscript Links' section and a 'Search' box are also present. The 'Legend' section explains that PTEN gene loci are shown in red and VEGF loci in green, with a note that the color of VEGF was changed to red in the main manuscript. The central focus is 'Figure 2', a 3D FISH image of control 3D cultures, with a 'Download Image as OME-TIFF' and 'Open Full Viewer' button. Below the main image are two smaller thumbnail images of the same data.

The Mini Viewer

Attribution & Maneuverability

Locus-specific and activity independent gene repositioning during early tumorigenesis

K.J. Meaburn, T. Misteli

J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)

Published Mon, 14 Jan 2008

(6 images)

- [Figure 1](#) [4]
- [Figure 2](#) [2]

Manuscript Links

Search

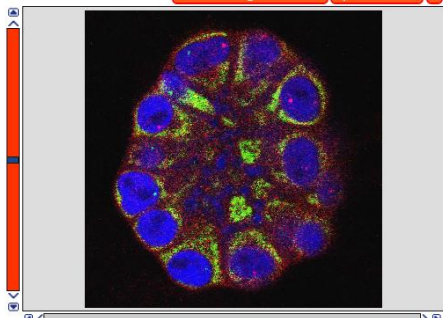
Search

Legend

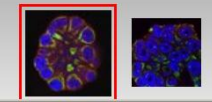
PTEN gene loci (red) and VEGF loci (green; the color of VEGF was changed to red in the main manuscript) were detected in paraformaldehyde fixed MCF10A/B2 cells grown for 20 days under 3D growth conditions. A representative acinus structure is shown. Whole acini were not imaged to reduce bleaching and to increase the number of acini analyzed. Instead the optical sections imaged totaled approximately 15-20µm in thickness.

Figure 2 [Select Images to Download](#)

[Download Image as OME-TIFF](#) [Open Full Viewer](#) X



FISH on control 3D cultures



Done

The Mini Viewer

Attribution & Maneuverability

Locus-specific and activity independent gene repositioning during early tumorigenesis

K.J. Meaburn, T. Misteli

J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)

Published Mon, 14 Jan 2008

Annotation

Legend

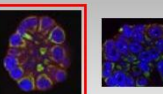
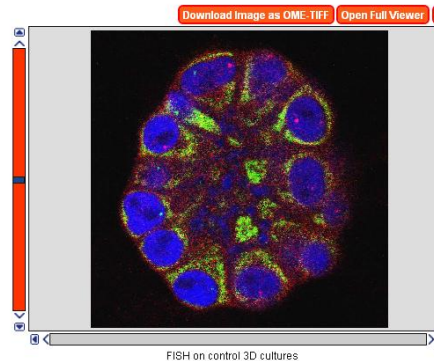
PTEN gene loci (red) and VEGF loci (green; the color of VEGF was changed to red in the main manuscript) were detected in paraformaldehyde fixed MCF10A.B2 cells grown for 20 days under 3D growth conditions. A representative acinus structure is shown. Whole acini were not imaged to reduce bleaching and to increase the number of acini analyzed. Instead the optical sections imaged totaled approximately 15-20µm in thickness.

F loci (green; d to red in the ed in A.B2 cells with inus structure t imaged to se the ad the optical kmetely

K.J. Meaburn, T. Misteli
J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)
Published Mon, 14 Jan 2008

Figure 2

Select Images to Download



The Mini Viewer

Attribution & Maneuverability

Locus-specific and activity independent gene repositioning during early tumorigenesis

K.J. Meaburn, T. Misteli

J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)

Published Mon, 14 Jan 2008

Annotation

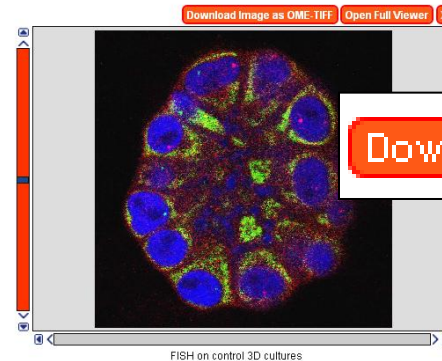
Legend

PTEN gene loci (red) and VEGF loci (green; the color of VEGF was changed to red in the main manuscript) were detected in paraformaldehyde fixed MCF10A.B2 cells grown for 20 days under 3D growth conditions. A representative acinus structure is shown. Whole acini were not imaged to reduce bleaching and to increase the number of acini analyzed. Instead the optical sections imaged totaled approximately 15-20µm in thickness.

F loci (green; d to red in the ed in BA B2 cells with inus structure t imaged to se the ad the optical kmetely

K.J. Meaburn, T. Misteli
J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)
Published Mon, 14 Jan 2008

Figure 2



Sharing & Re-analysis

Download Image as OME-TIFF

The Mini Viewer

Attribution & Maneuverability

Locus-specific and activity independent gene repositioning during early tumorigenesis

K.J. Meaburn, T. Misteli

J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [Article]

Published Mon, 14 Jan 2008

(6 images)

- Figure 1 [4]
- Figure 2 [2]

Manuscript Links

Annotation

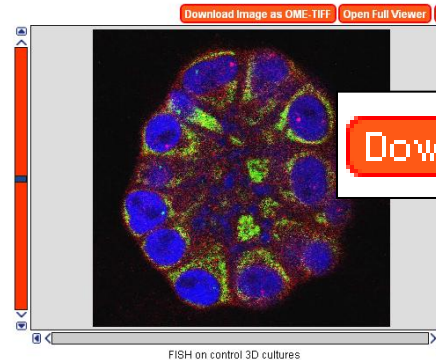
Legend

PTEN gene loci (red) and VEGF loci (green; the color of VEGF was changed to red in the main manuscript) were detected in paraformaldehyde fixed MCF10A.B2 cells grown for 20 days under 3D growth conditions. A representative acinus structure is shown. Whole acini were not imaged to reduce bleaching and to increase the number of acini analyzed. Instead the optical sections imaged totaled approximately 15-20µm in thickness.

F loci (green; d to red in the ed in BA B2 cells with inus structure t imaged to se the ad the optical imately

K.J. Meaburn, T. Misteli
J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [Article]
Published Mon, 14 Jan 2008

Figure 2



Sharing & Re-analysis

Download Image as OME-TIFF

Mining

Search

JCB Data Viewer

The Full Viewer

The screenshot displays the JCB Data Viewer web application in a Mozilla Firefox browser window. The browser's address bar shows the URL http://jcb-dataviewer.rupress.org/jcb_img_detail/205/2271. The page header features the JCB Data Viewer logo on the left, the Glencoe Software logo in the center, and The Rockefeller University Press logo on the right. A navigation menu below the header includes links for [DATAVIEWER HOME](#), [ARCHIVE](#), [SUPPORTED FILE TYPES](#), [INSTRUCTIONS FOR USE](#), [FAQ](#), [CONTACT](#), [TERMS OF USE](#), and [ABOUT](#). A [log in](#) link is also present.

The main content area displays the article title "Locus-specific and activity independent gene repositioning during early tumorigenesis" by K.J. Meaburn, T. Misteli, published in J Cell Biol. 2008. 180:39-50. The DOI is 10.1083/jcb.200708204. A link to the [Article](#) is provided.

On the left side, there is a "Viewing Options" panel with the following controls:

- Normal (selected) rendering mode
- Max Intensity (radio button)
- Split Channel (radio button)
- Quality: Normal (dropdown)
- Zoom: 50 (input field)
- Line Plot (checkbox)
- Rendering Details: Channels - Edit (button), Color (checkbox)
- Current Image: Z: 27/53 | T: 1/1
- Image Information: Image Link (button), Make Movie (button), Download OME-TIFF (button), Other Images (checkbox)

The central image is a microscopy image showing a cluster of cells with blue nuclei, green cytoplasm, and red puncta. To the left of the image is a vertical "Z-sections" slider, and below the image is a horizontal "Timepoints" slider.

At the bottom of the browser window, the footer text reads: ©2007-2011 Glencoe Software Inc. All rights reserved. Done

The Full Viewer

Annotation

The screenshot displays the JCB Data Viewer interface. On the left, an 'Image Information' panel is open, showing details for a FISH image. The main area shows a multi-color fluorescence image of a cell culture, with a 'Z-section' slider and 'Timepoints' controls at the bottom.

Image Information Panel:

- Basic Information**
 - Description: FISH on control 3D cultures
 - Authors: K.J. Meabum, T. Misteli
 - Title: Locus-specific and activity independent gene repositioning during early tumorigenesis
 - Citation: J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [\[Article\]](#)
 - Figure: Figure 2
 - Part:
- Dimensions**

Image Size	Pixel Size
X: 1024px	X: 0.0476µm
Y: 1024px	Y: 0.0476µm
Z: 53	Z: 0.3149µm
T: 1	
- Legend**
 - FISH on control 3D cultures

Main Image Area:

- Header: THE ROCKEFELLER UNIVERSITY PRESS, GLENCOE SOFTWARE, QUALITY AND INTEGRITY
- Navigation: TYPES, INSTRUCTIONS FOR USE, FAQ, CONTACT, TERMS OF USE, ABOUT
- Image: Fluorescence image showing cell nuclei (blue) and gene repositioning (green and red).
- Controls: Z-section slider, Timepoints slider.
- Footer: ©2007-2011 Glencoe Software Inc. All rights reserved.

The Full Viewer

Annotation

The screenshot displays the JCB Data Viewer interface. On the left, an 'Image Information' panel provides details about the image. The main area shows a 3D culture image with a 'Z-section' slider and a 'Timepoints' slider at the bottom. The interface includes a navigation menu and a search bar.

Image Information Panel:

Basic Information

Description: FISH on control 3D cultures
 Authors: K.J. Meabum, T. Misteli
 Title: Locus-specific and activity independent gene repositioning during early tumorigenesis
 Citation: J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [Article]
 Figure: Figure 2
 Part:

Dimensions

Image Size	Pixel Size
X: 1024px	X: 0.0476µm
Y: 1024px	Y: 0.0476µm
Z: 53	Z: 0.3149µm
T: 1	

Legend

FISH on control 3D cultures

Navigation Menu: TYPES | INSTRUCTIONS FOR USE | FAQ | CONTACT | TERMS OF USE | ABOUT

Search Bar: Positioning during early tumorigenesis

Image: A 3D culture image showing several cells with blue nuclei, green cytoplasm, and red spots. A 'Z-section' slider is visible on the left side of the image.

Timepoints: A slider at the bottom of the image area.

Footer: ©2007-2011 Glencoe Software Inc. All rights reserved. Done

Attribution & Maneuverability

Link to this page:
<http://jcb-dataviewer.rupress.org/jcb/img>

The Full Viewer

Annotation

Image Information

Basic Information

Description: FISH on control 3D cultures

Authors: K.J. Meabum, T. Misteli

Title: Locus-specific and activity independent gene repositioning during early tumorigenesis

Citation: J Cell Biol. 2008. 180:39-50 DOI: 10.1083/jcb.200708204. [Article]

Figure: Figure 2

Part:

Dimensions

Image Size	Pixel Size
X: 1024px	X: 0.0476µm
Y: 1024px	Y: 0.0476µm
Z: 53	Z: 0.3149µm
T: 1	

Legend

FISH on control 3D cultures

Data Presentation

Make Movie:

Axis: Z

Format: Quicktime .mov (Mac)

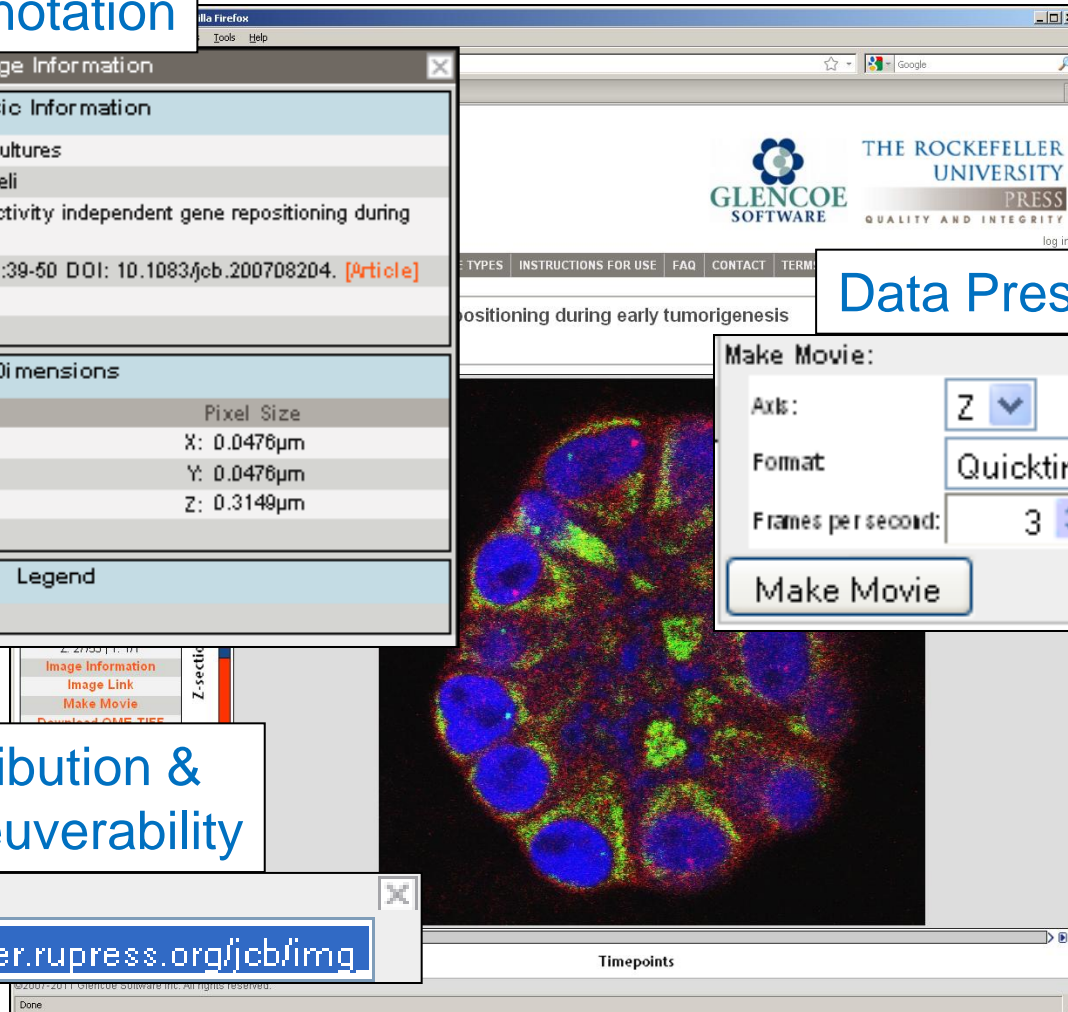
Frames per second: 3

Make Movie

Attribution & Maneuverability

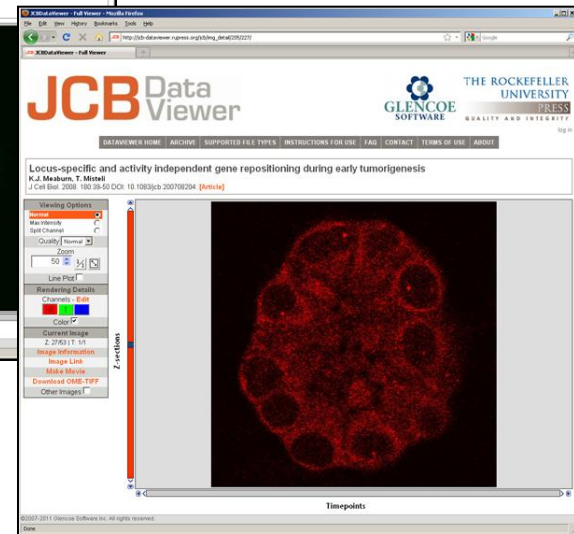
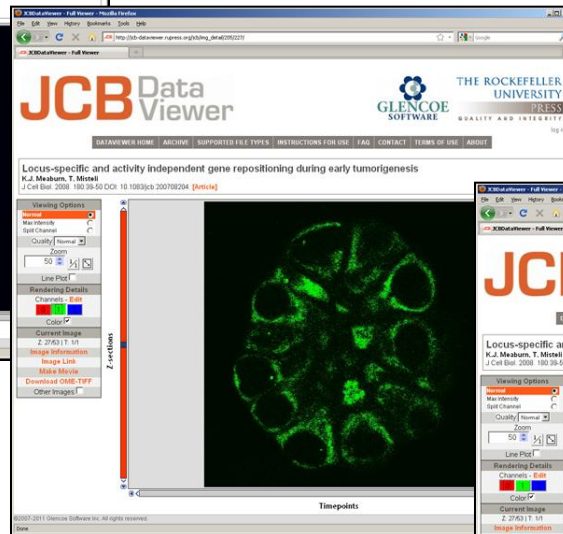
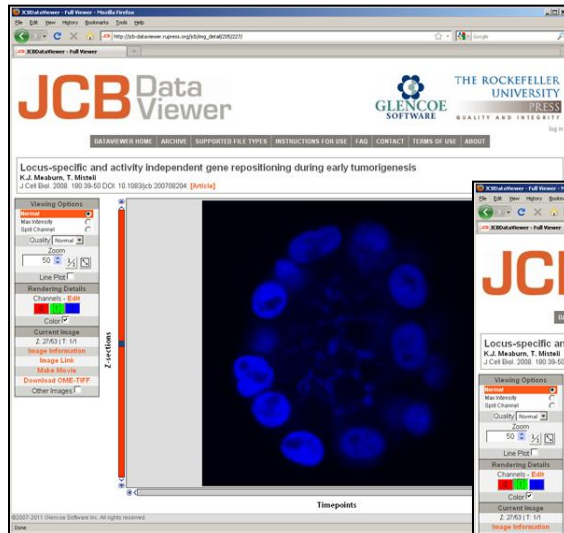
Link to this page:

<http://jcb-dataviewer.rupress.org/jcb/img>



JCB Data Viewer

Split-Channel View



JCB Data Viewer

Split-Channel View

The screenshot displays the JCB Data Viewer interface in a Mozilla Firefox browser window. The address bar shows the URL: http://jcb-dataviewer.rupress.org/jcb/img_detail/205/227/. The page header includes the JCB Data Viewer logo, the Glencoe Software logo, and The Rockefeller University Press logo with the tagline "QUALITY AND INTEGRITY". A navigation menu contains links for DATAVIEWER HOME, ARCHIVE, SUPPORTED FILE TYPES, INSTRUCTIONS FOR USE, FAQ, CONTACT, TERMS OF USE, and ABOUT. A "log in" link is also present.

The main content area features a title: "Locus-specific and activity independent gene repositioning during early tumorigenesis" by K.J. Meaburn, T. Misteli, published in J Cell Biol. 2008. 180:39-50. A DOI link is provided: [10.1083/jcb.200708204](https://doi.org/10.1083/jcb.200708204) with a link to the [Article].

The central visualization is a 2x2 grid of images showing a cell at different timepoints (w=0, w=1, w=2) and a combined view. The images show a cell with a red nucleus (w=0), a green nucleus (w=1), and a blue nucleus (w=2). The combined view shows the cell with all three channels overlaid. A vertical Z-sections slider is on the left, and a horizontal Timepoints slider is at the bottom.

On the left side, there is a "Viewing Options" panel with the following settings:

- Normal
- Max Intensity
- Split Channel (selected)
- Quality: Normal
- Zoom: 24
- Line Plot:
- Rendering Details: Channels - Edit (Red, Green, Blue), Color
- Current Image: Z: 27.53 | T: 1/1
- Image Information: [Image Link](#), [Make Movie](#), [Download OME-TIFF](#)
- Other Images:

At the bottom left, the copyright notice reads: ©2007-2011 Glencoe Software Inc. All rights reserved. Done

JCB Data Viewer

Line plots

The screenshot displays the JCB Data Viewer interface in a Mozilla Firefox browser window. The address bar shows the URL: http://jcb-dataviewer.rupress.org/jcb/img_detail/205/227/. The page header includes the JCB Data Viewer logo and the Glencoe Software logo, along with The Rockefeller University Press logo and the tagline "QUALITY AND INTEGRITY". A navigation menu contains links for DATAVIEWER HOME, ARCHIVE, SUPPORTED FILE TYPES, INSTRUCTIONS FOR USE, FAQ, CONTACT, TERMS OF USE, and ABOUT. A "log in" link is also present.

The main content area features the article title: "Locus-specific and activity independent gene repositioning during early tumorigenesis" by K.J. Meaburn, T. Misteli, published in J Cell Biol. 2008. 180:39-50. The DOI is 10.1083/jcb.200708204. A link to the article is provided.

The central visualization is a line plot showing gene expression data. The vertical axis is labeled "Z-sections" and the horizontal axis is labeled "Timepoints". The plot displays a green signal that fluctuates across both axes, with a prominent peak in the center. A vertical color bar on the left side of the plot indicates the intensity of the signal, ranging from red (high) to blue (low). The plot is overlaid on a grayscale image of a cell, which is also shown in a smaller view on the right side of the plot.

The left sidebar contains the "Viewing Options" panel, which includes controls for "Normal" (selected), "Max Intensity", "Split Channel", "Quality" (Normal), "Zoom" (48), "Line Plot" (checked), "Axis" (Horizontal), "Y" (497), and "showing Y" (497). The "Rendering Details" section includes "Channels" (Edit), "Color" (checked), "Current Image" (Z: 27/53 | T: 1/1), "Image Information", "Image Link", "Make Movie", "Download OME-TIFF", and "Other Images".

At the bottom of the browser window, the copyright notice reads: ©2007-2011 Glencoe Software Inc. All rights reserved. Done

2. High-Content Screen Analysis

High-Content Screen Data

The screenshot displays the JCBDataViewer interface within a Mozilla Firefox browser window. The address bar shows the URL: <http://envy.glencoesoftware.com:28000/jcb/browse/1252/53/>. The main content area is titled "JCBDataViewer - Browser" and features a "Download All Data as OME-TIFF" button (56 images) and a list of recent actions: Figure 1 [9], Figure 3 [0], Screen 1 [44], New Figure test [3], and Update Figure test [0].

The "Plates" section on the left lists plates P101 through P146, each with a "hide" dropdown menu. The main visualization area shows a large image of a well (Well B8, Field 1) containing green fluorescent cells. A color scale bar is visible on the left of the image. Above the image are buttons for "Download Image as OME-TIFF" and "Open Full Viewer". To the right of the image is a "metadata" panel with the following information:

- Plate #: 5
- Well: B8
- ORF: YNL338W
- Gene: -
- Alias: -
- Description: Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data, completely overlaps TEL14L-XC, which is Telomeric X element Core sequence on the left arm of Chromosome XV
- GO Biological: biological_process
- Process:
- GO Molecular: molecular_function
- Function:
- GO Cellular: cellular_component
- Component:
- go term: biological_process, cellular_component, molecular_function

Below the main image is a grid of 8 rows (A-H) and 12 columns (1-12) of smaller images. The cell in row B, column 8 is highlighted with a red box, indicating the current well being viewed.

High-Content Screen Data

Download All Data as OME-TIFF (56 Images)

- Figure 1 [9]
- Figure 3 [0]
- Screen 1 [44]
- New Figure test [3]
- Update Figure test [0]

Plates

P101 -hide- v

P102 -hide- v

P105 -hide- v

P106 -hide- v

P107 -hide- v

P108 -hide- v

P109 -hide- v

P110 -hide- v

P111 -hide- v

P112 -hide- v

P115 -hide- v

P117 -hide- v

P118 -hide- v

P119 -hide- v

P120 -hide- v

P121 -hide- v

P123 -hide- v

P124 -hide- v

P125 -hide- v

P126 -hide- v

P127 -hide- v

P128 -hide- v

P129 -hide- v

P130 -hide- v

P131 -hide- v

P132 -hide- v

P133 -hide- v

P134 -hide- v

P135 -hide- v

P136 -hide- v

P137 -hide- v

P138 -hide- v

P139 -hide- v

P140 -hide- v

P141 -hide- v

P142 -hide- v

P143 -hide- v

P144 -hide- v

P145 -hide- v

P146 -hide- v

P147 -hide- v

P148 -hide- v

P149 -hide- v

P150 -hide- v

P151 -hide- v

P152 -hide- v

P153 -hide- v

P154 -hide- v

P155 -hide- v

P156 -hide- v

P157 -hide- v

P158 -hide- v

P159 -hide- v

P160 -hide- v

P161 -hide- v

P162 -hide- v

P163 -hide- v

P164 -hide- v

P165 -hide- v

P166 -hide- v

P167 -hide- v

P168 -hide- v

P169 -hide- v

P170 -hide- v

P171 -hide- v

Done

Full Dataset Archiving & Sharing

- Plates
- P101 -hide- v
 - P102 -hide- v
 - P105 -hide- v
 - P106 -hide- v
 - P107 -hide- v
 - P108 -hide- v
 - P109 -hide- v
 - P110 -hide- v
 - P111 -hide- v
 - P112 -hide- v
 - P115 -hide- v
 - P117 -hide- v
 - P118 -hide- v
 - P119 -hide- v
 - P120 -hide- v
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 - P145 -hide- v
 - P146 -hide- v
 - P147 -hide- v
 - P148 -hide- v
 - P149 -hide- v
 - P150 -hide- v
 - P170 -hide- v
 - P171 -hide- v

High-Content Screen Data

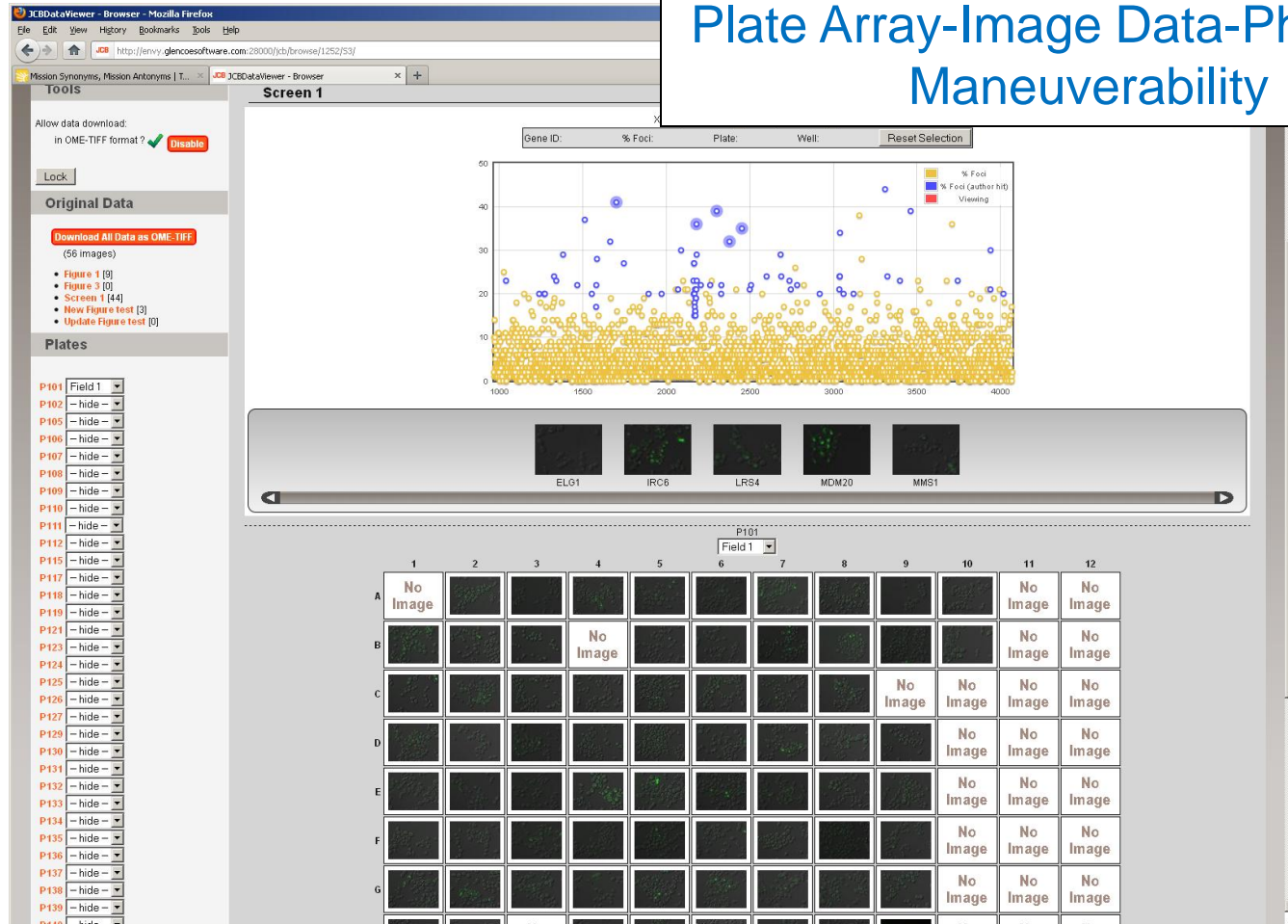
Plate Array-Image Data-Metadate Maneuverability

The screenshot displays the JCB Data Viewer interface in a Mozilla Firefox browser. The address bar shows the URL: <http://envy.glencoesoftware.com:28000/jcb/browse/1252/53/>. The interface is divided into several sections:

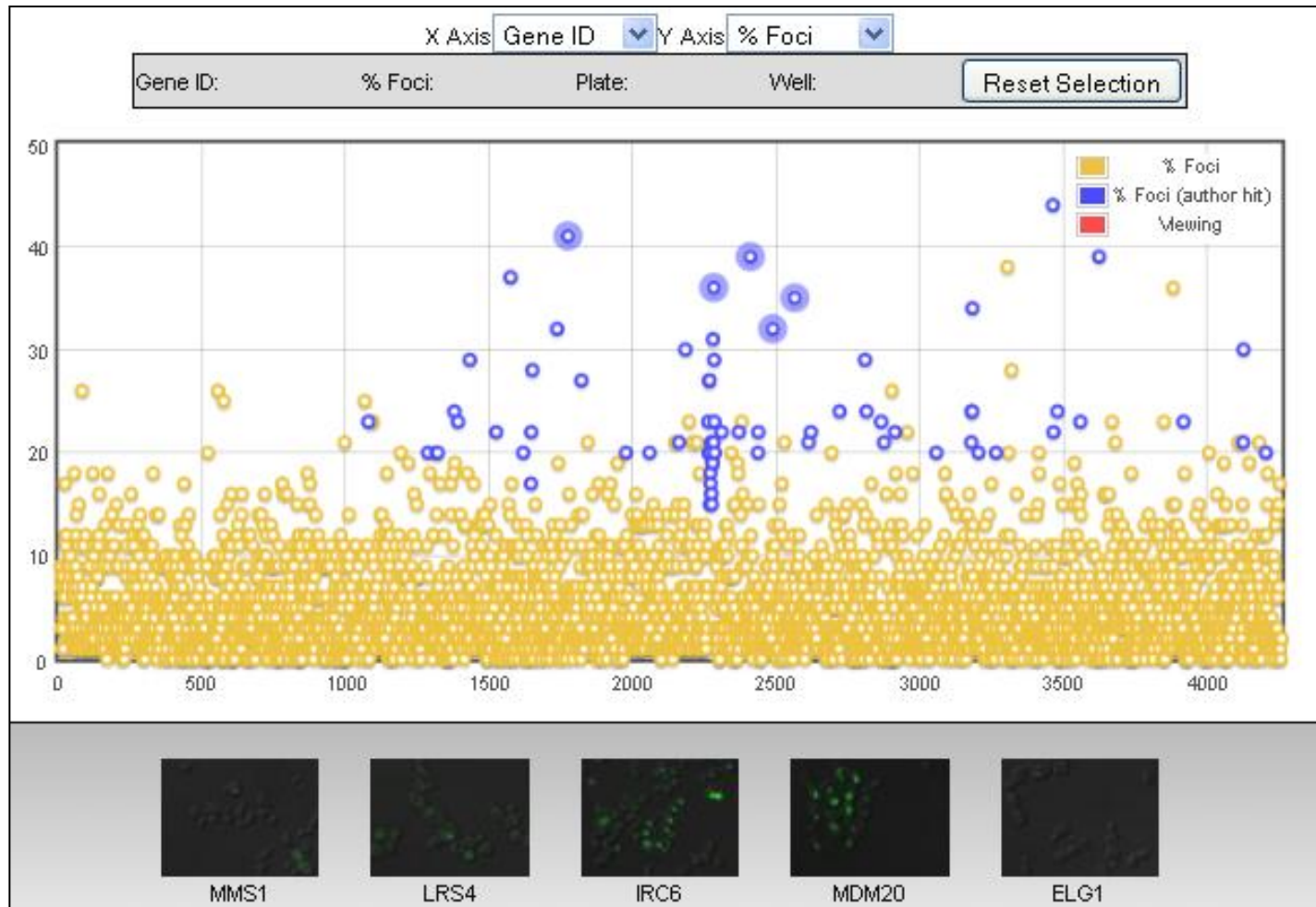
- Browser Window:** Shows the JCBDataViewer application running in Mozilla Firefox.
- Download Options:** A red button labeled "Download All Data as OME-TIFF" is visible, with a note "(56 Images)". Below it, a list of actions includes "Figure 1 [9]", "Figure 3 [0]", "Screen 1 [44]", "New Figure test [3]", and "Update Figure test [0]".
- Plates List:** A vertical list of plates from P101 to P146, each with a "hide" button.
- Image Viewer:** A central window showing a fluorescence image of cells. A color scale on the left indicates intensity. Above the image are buttons for "Download Image as OME-TIFF" and "Open Full Viewer". Below the image is the label "Well B8, Field 1".
- Metadata Panel:** A panel on the right titled "metadata" containing the following information:
 - Plate #: 5
 - Well: B8
 - ORF: YNL338W
 - Gene: -
 - Alias: -
 - Description: Dubious open reading frame unlikely to encode a protein, based on available experimental and comparative sequence data, completely overlaps TEL14L-XC, which is Telomeric X element Core sequence on the left arm of Chromosome XV
 - GO Biological: biological_process
 - Process:
 - GO Molecular: molecular_function
 - Function:
 - GO Cellular: cellular_component
 - Component:
 - go term: biological_process, cellular_component, molecular_function
- Plate Array Grid:** A grid of 96 wells (8 rows by 12 columns) labeled A-H and 1-12. The grid shows varying intensities of green fluorescence. The well at row B, column 8 is highlighted with a red box.

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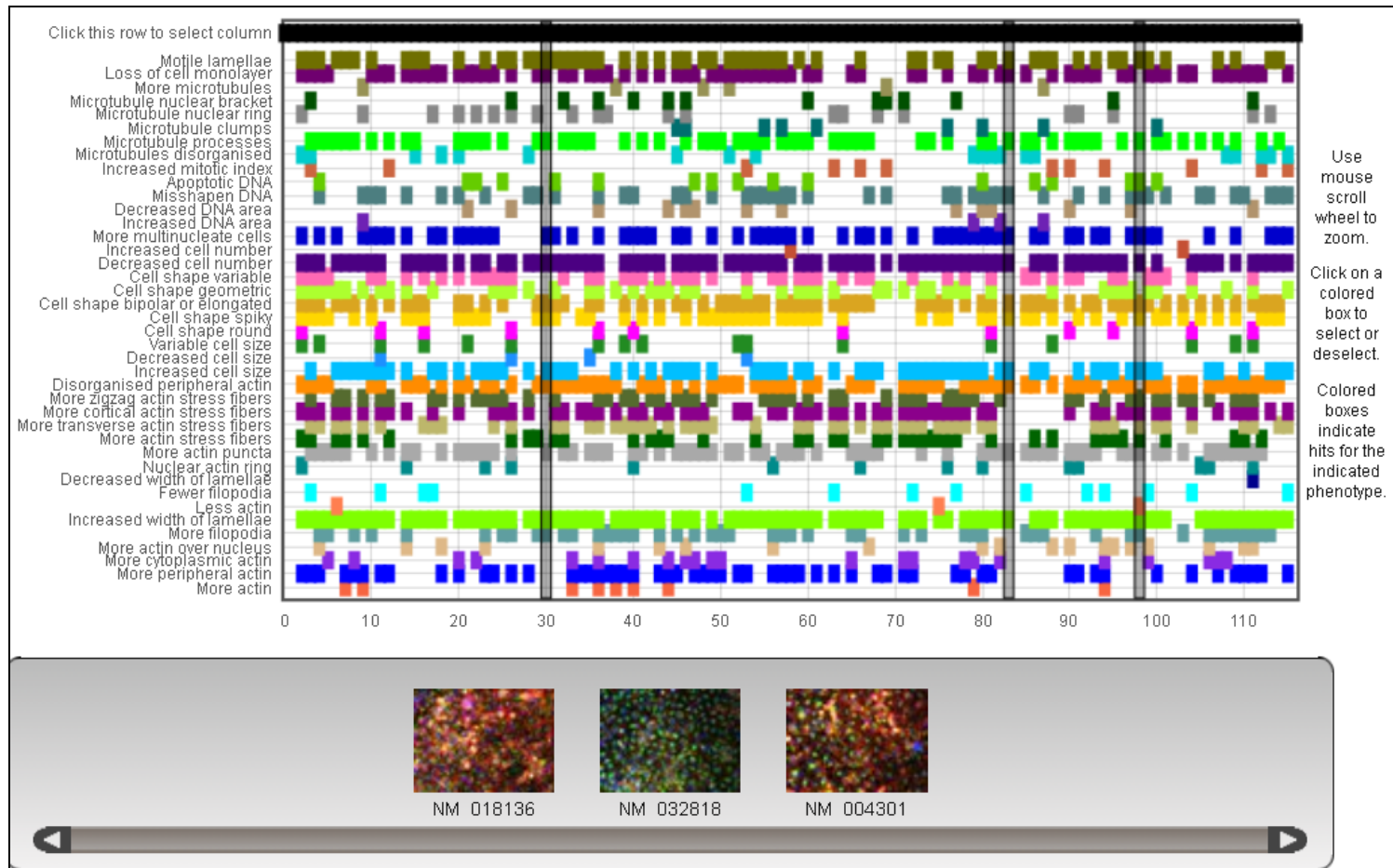
Plate Array-Image Data-Phenotype Maneuverability



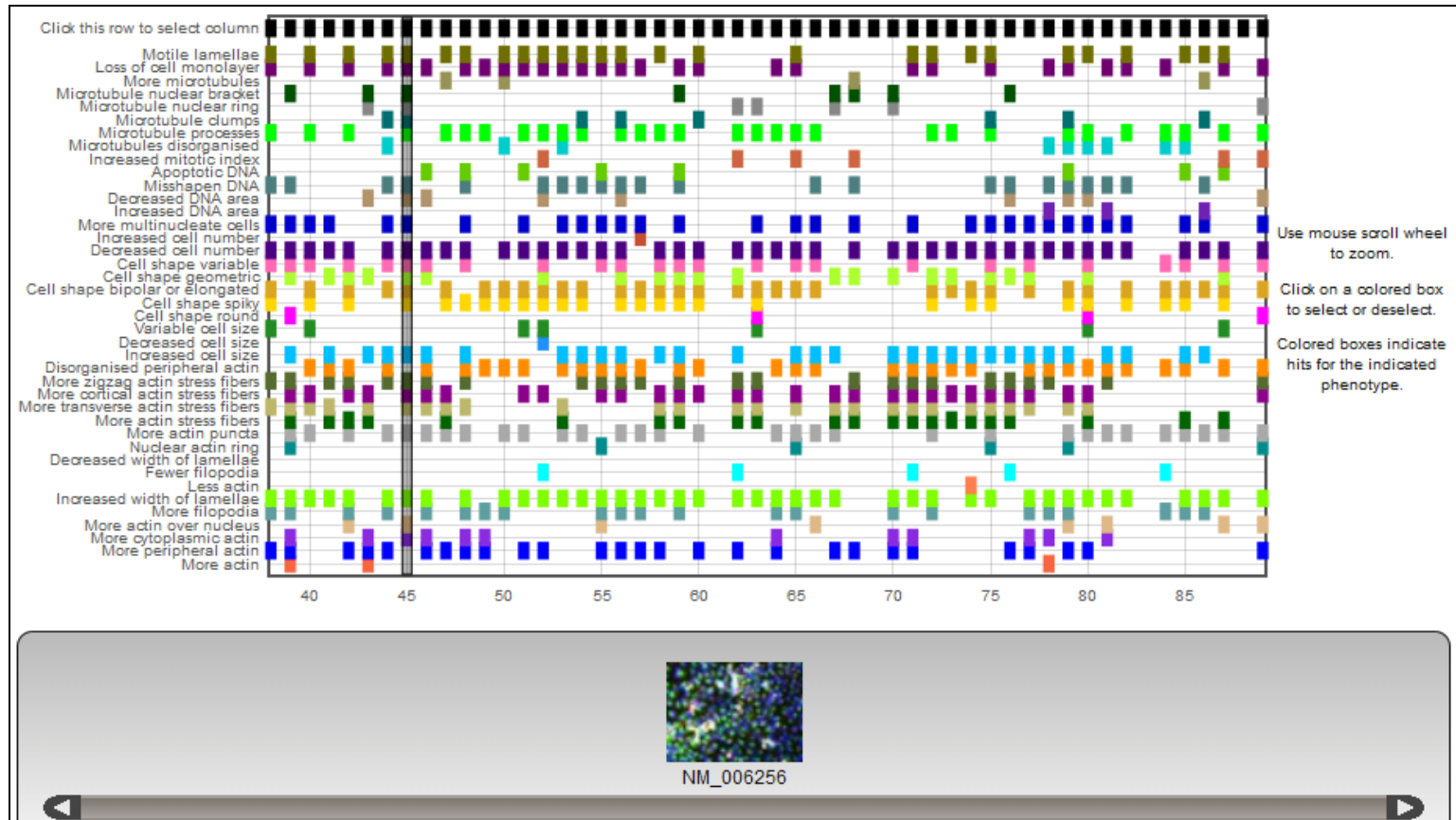
High-Content Screen Data



High-Content Screen Data



High-Content Screen Data



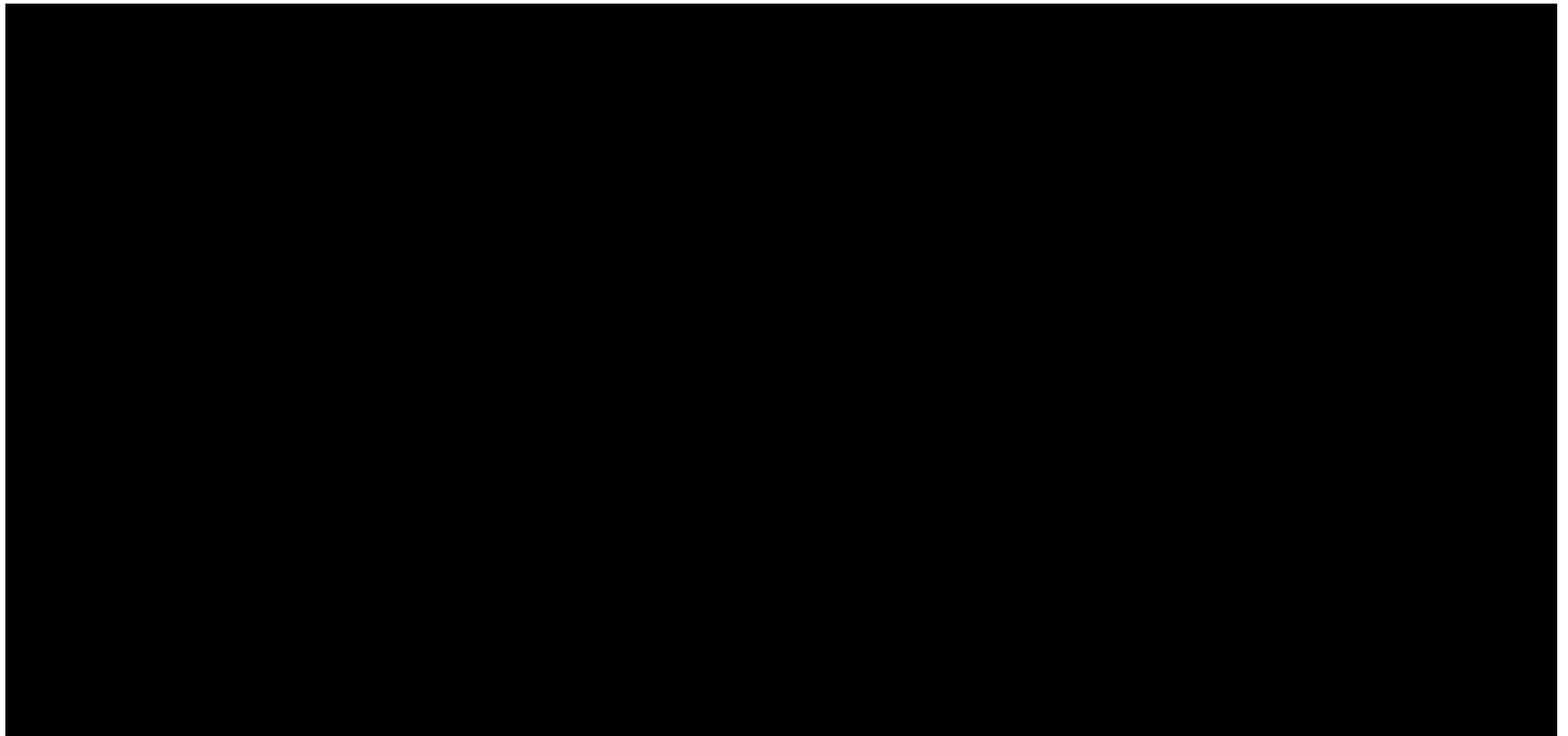
3. Tiled Image Analysis

Coming soon: BIG images

Ultra-large, high-resolution, tiled images:

- 921600 pixels x 380928 pixels
- 281 gigapixels total
- 16 GB
- 1.6 nm resolution component images

Ultra-large, high-resolution, tiled images



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difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (Fig. 5 A). We detected no change in chromosome staining with anti-phosphohistone H3 (Fig. 5 A) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the inner centromere (Fig. 5 B; Andrews et al., 2004). In Bod1^{siRNA} cells, we observed that although total MCAK present at unaligned centromeres was similar to control cells (Fig. 5 C), its precise localization was abnormal, forming multiple foci stretching out to one or both sister kinetochores.

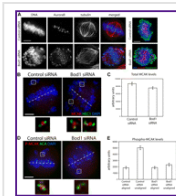


Figure 5. MCAK is not efficiently phosphorylated in Bod1^{siRNA} cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B–E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were treated with monastrol for 3 h and released into media containing MG132 for 1 h before fixing. (B and C) Cells were stained for total MCAK population, and levels at kinetochores were quantified. Boxed areas are magnified below the main images. (D and E) Cells were stained for phospho-Ser92-MCAK, and levels at aligned and unaligned kinetochores were quantified. Dashed lines indicate orientation of the metaphase plate. Error bars represent SD. Bars, 5 μm.

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Because MCAK localization to centromeres and kinetochores depends on the state of MCAK phosphorylation, we examined the levels of phosphorylated MCAK using an anti-phospho-Ser92 MCAK antibody (Andrews et al., 2004). Phosphorylation of MCAK was substantially reduced at the inner centromere of unaligned chromosomes in Bod1^{siRNA} cells compared with the control cells (Fig. 5, D and E). These results suggest that Bod1 depletion impairs the formation of bioriented attachments across sister kinetochores, possibly by impairing the correct localization of MCAK at centromeres and, thereby, preventing its phosphorylation and timely correction of syntelic attachments. We have not detected any effect of Bod1 on the in vitro phosphorylation of MCAK by Aurora B (unpublished data), so Bod1 may modulate MCAK phosphorylation by interacting with other proteins. Aurora B activity and kinetochore oscillations are necessary for syntelic correction (Lampson et al., 2004), and our data further suggest that syntelic correction may require MCAK phosphorylation. Whether there is any subtle perturbation in kinetochore oscillations in Bod1-depleted cells is not yet known and will require much higher resolution live cell imaging.

In summary, by using a cell cycle-dependent analysis of the *Xenopus* chromatin proteome, we have identified a novel protein required for proper chromosome biorientation called Bod1. Bod1 is a member of the FAM44 protein family and is highly conserved throughout metazoans. Depletion of Bod1 in human cells causes severe biorientation defects, although kinetochores appear to

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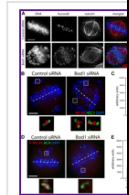
difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (Fig. 5 A). We detected no change in chromosome staining with anti-phosphohistone H3 (Fig. 5 A) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the

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Because MCAK localization to the inner centromere requires phosphorylation of MCAK at Ser92, we compared the correct localization of MCAK in control cells with that in Bod1-depleted cells. In vitro phosphorylation of MCAK at Ser92 and subsequent phosphorylation of MCAK at Ser92 are necessary for MCAK to oscillate between the inner centromere and kinetochores in response to perturbation in kinetochore tension.

In summary, by using a cell line that is a member of the FAM44

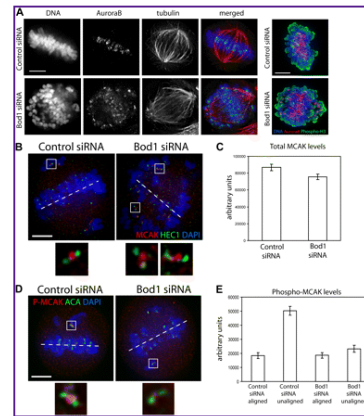


Figure 5. MCAK is not efficiently phosphorylated in Bod1^{siRNA} cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B–E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were treated with monastrol for 3 h and released into media containing MG132 for 1 h before fixing. (B and C) Cells were stained for total MCAK population, and levels at kinetochores were quantified. Boxed areas are magnified below the main images. (D and E) Cells were stained for phospho-Ser92-MCAK, and levels at aligned and unaligned kinetochores were quantified. Dashed lines indicate orientation of the metaphase plate. Error bars represent SD. Bars, 5 μ m.

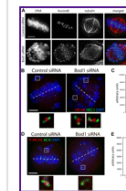
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difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (Fig. 5 A). We detected no change in chromosome staining with anti-phosphohistone H3 (Fig. 5 A) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the kinetochores (Fig. 5 C), its localization in control cells (Fig. 5 C), its

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Because MCAK localization is dependent on its phosphorylation state, we determined the localization of anti-phospho-Ser92 MCAK in control and Bod1 siRNA treated cells. The correct localization of MCAK in control cells is at the inner centromere. In Bod1 siRNA treated cells, MCAK is predominantly located at the kinetochores. These results suggest that MCAK phosphorylation and dephosphorylation are necessary for its function in chromosome biorientation.

In summary, by using a cell line that is a member of the FAM44

Figure 5. MCAK is not at the inner centromere in control and Bod1 siRNA treated cells. MCAK is released into the kinetochore region. Boxed areas are magnified and quantified. Dashed lines indicate

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- [Figure 5](#) [8]

Bod1, a Novel Kinetochores Protein Required for Chromosome Biorientation

I.M. Porter, S.E. McClelland, G.A. Khoudoli, C.J. Hunter, J.S. Andersen, A.D. Mcainsh, J.J. Blow, J.R. Swedlow
J Cell Biol. 2007. 179:187-197 DOI: 10.1083/jcb.200704098. [Article](#)

Figure 5

A

B

D

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difference in the amount of Aurora B in unaligned and apparently aligned chromosomes (Fig. 5 A). We detected no change in chromosome staining with anti-phosphohistone H3 (Fig. 5 A) or anti-phospho-CENP-A (not depicted) after Bod1 depletion. Because both are markers of Aurora B activity (Zeitlin et al., 2001), these results suggest that Aurora B kinase activity was not dramatically impaired by the loss of Bod1. To further assay the function of Aurora B, we determined the localization of MCAK, which localizes to the inner centromere in its phosphorylated form but concentrates at kinetochores in its dephosphorylated state (Andrews et al., 2004). At unaligned sister kinetochores or in kinetochore pairs not yet fully under tension, MCAK is predominantly located at the kinetochores. In control cells (Fig. 5 C), its

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Because MCAK localization is dependent on phosphorylation, we compared the localization of anti-phospho-Ser92 MCAK in control and Bod1 siRNA cells. In control cells, MCAK is correctly localized to the inner centromere. In Bod1 siRNA cells, MCAK is delocalized from the inner centromere. This delocalization is dependent on the correct localization of MCAK. In summary, by using a cell line that is a member of the FAM44C family, we have shown that MCAK is not efficiently phosphorylated in Bod1 siRNA cells.

Figure 5. MCAK is not efficiently phosphorylated in Bod1 siRNA cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B–E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were treated with monastrol for 3 h and released into media containing MG132 for 1 h before fixing. (B and C) Cells were stained for total MCAK population, and levels at kinetochores were quantified. Boxed areas are magnified in Figure 5 D and E.

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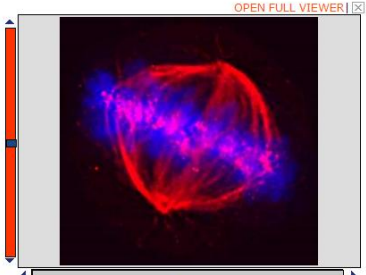
Figure 5. MCAK is not efficiently phosphorylated in Bod1 siRNA cells. (A) Aurora B is not delocalized in Bod1-depleted cells. Phospho-Ser10-histone H3 staining in control and Bod1 siRNA cells indicating Aurora B activity. (B–E) Cells were transfected with control or Bod1 siRNA. After 72 h, cells were treated with monastrol for 3 h and released into media containing MG132 for 1 h before fixing. (B and C) Cells were stained for total MCAK population, and levels at kinetochores were quantified. Boxed areas are magnified in Figure 5 D and E.

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J Cell Biol. 2007. 179:187-197 DOI: 10.1083/jcb.200704098. [\[article\]](#)

Figure 5

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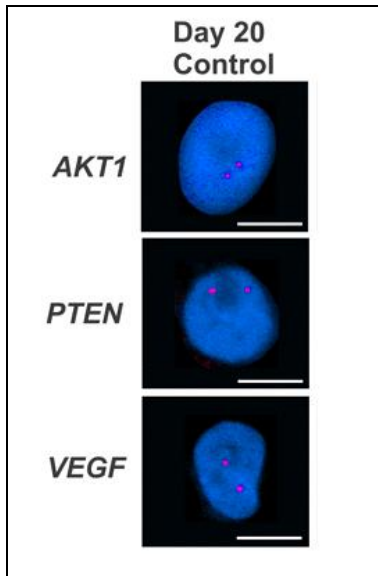


Control siRNA Aurora B

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Voluntary participation rate (as of January, 2012):

1.1 TB of image data (published and unpublished)

→ 221 published manuscripts

→ 780 published figures

→ 99,552 published images

→ 1,137,342 individual image frames

Where do we go from here?

- Continue to expand the range of data we can host.
- Continue to promote a new standard for sharing and archiving of published image data:
 - submission and publication of more than just 300 dpi, flat image data that editors, reviewers, and readers can only assume are fair representations of reality
 - public data archiving
 - greater openness in research
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<http://jcb-dataviewer.rupress.org>

with special thanks to Emma Hill, Mike Rossner, and:

