

New Tools for JCB

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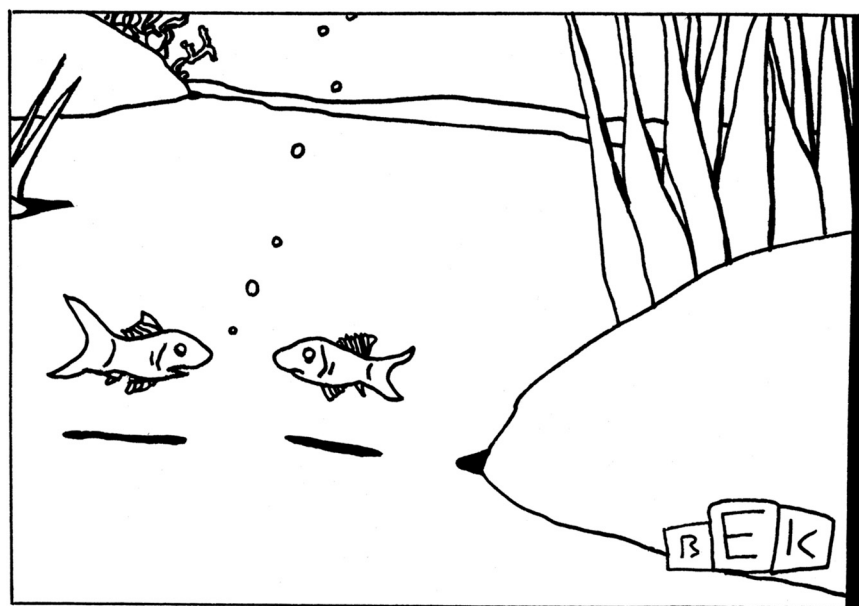
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New technologies and approaches in cell biology research necessitate new venues for information sharing and publication. *JCB* continues its support of innovation in publishing with the launch of Tools, a new article type for the description of methods and high-throughput datasets, and of a new interface for the JCB DataViewer for hosting high-content screening datasets in their entirety.

New research tools, new publishing tools

Progress in cell biology is driven by new technology. The use of the electron microscope in the 1950s revolutionized our thinking about cell structure and function and helped to launch the field of modern cell biology. In the decades since, countless other technological developments—such as confocal microscopy and the use of fluorescent proteins to investigate cellular dynamics in real time—have helped move cell biology forward. Currently, we are witnessing the expansive growth of another revolutionizing tool for the cell biology community: high-content screens (HCS). In such screens, any cellular feature that can be imaged and quantified can be used as the basis for a phenotypic assay, and cellular factors affecting specific phenotypes can be identified by screening mutant strains or RNAi libraries at the scale of whole genomes. Image-based screening transforms imaging from a largely descriptive method to one with which we can ask—for the first time—functional, quantitative, and mechanistic questions about cellular structures in an unbiased and



"I want the whole package—the little bowl, the colored pebbles, the plastic castle."

high-throughput fashion. HCS are complemented by other high-throughput screens—such as proteomic screens and protein interaction network screens—that also provide vast troves of information to mine.

As new tools for cell biology research emerge, the community requires venues to share the data derived from them. *JCB* proudly announces two new initiatives to this end: First, we announce the launch of *JCB Tools*, a new article type for describing important new methodologies or high-throughput datasets for the cell biology community. Second, we announce the expansion of the JCB DataViewer to accommodate HCS datasets in their entirety, providing the scientific community with an unprecedented resource for archiving and sharing primary HCS data.

JCB Tools

JCB Tools is a forum for the publication of fully peer-reviewed, novel HCS datasets, novel cell biological methods, and other community resources such as proteomic datasets or interaction network studies of immediate value and broad utility to the cell biology community. All image-based HCS data associated with Tools publications will be archived and made available to the public through the JCB DataViewer, and all other resources relevant to Tools publications, such as interaction network datasets and source code for computational methods, will be

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archived and made available as supplemental information through the *JCB* website. Importantly, all Tools publications, their associated supplemental information, and their associated HCS data in the JCB DataViewer will be freely available from the date of publication. For further details about this new article type, please see *JCB*'s Instructions for Authors at <http://jcb.rupress.org/site/misc/ifa.html>. We publish our first paper in the Tools format in this issue of *JCB* (Rohn et al., 2011), along with its associated HCS data in the JCB DataViewer.

HCS data and the JCB DataViewer

Existing publication tools for image data and—even more so—HCS data are extremely limited. To begin to address this, in 2008 *JCB* launched the JCB DataViewer, a browser-based application for viewing, analyzing, sharing, and archiving multidimensional image data and their associated metadata (Hill 2008). More than 79 different proprietary file formats currently can be viewed in the JCB DataViewer, allowing individual researchers to use their tool of choice for data acquisition while still making their data accessible to the general public. As of August 15, 2011, the JCB DataViewer contained 7,676 images (totaling 1,123,040 image frames) that represent original data for 195 papers published in *JCB* and that are viewed on average by more than 14,000 unique visitors per month.

JCB now announces the launch of a new, ground-breaking platform for publishing complete HCS datasets within the JCB DataViewer. This new platform can host datasets from high-content, multidimensional, image-based screens, including unbiased views of the original data as they were collected, metadata summaries describing the parameters of image data capture, summary plots of phenotypic data across all experimental samples, and more. Users can mine the data using built-in tools to select their own list of “hits” from 2D plots of gene IDs against scored parameters and to seamlessly move between these phenotypic summaries and the original data.

To develop this new technology, we used an HCS dataset for a genome-wide screen of 4,805 *Saccharomyces*

cerevisiae viable deletion strains for genes that affect the number of foci containing the Rad52 protein, which has been implicated in the homologous recombination pathway of DNA repair. These data were generously provided by Peter Thorpe, David Alvaro, Michael Lisby, and Rodney Rothstein. Published using conventional publishing technology, the original article describing this screen contained cropped images of fluorescence data for just two of the 4,805 strains analyzed (Alvaro et al., 2007); the rest of the data from the screen were inaccessible to readers. We now provide the complete dataset from this screen—consisting of 418,450 individual image frames, their associated metadata, and the complete results of the phenotypic analysis—as a proof of principle of the value of the new HCS interface of the JCB DataViewer to provide unprecedented access to entire, rich datasets for further data mining efforts. Please see the accompanying Comment by Thorpe et al. (2011) for a detailed account of the tools available and of the benefits to authors and to the scientific community of this new data presentation venue.

With the launch of *JCB* Tools and the expansion of the JCB DataViewer, *JCB* is pleased to usher in a new era for publishing and sharing of HCS and other high-throughput data, continuing a long tradition of innovation at *JCB*. As the needs of the cell biology community advance, *JCB* is proud to be a partner in the discovery process.

References

- Alvaro, D., M. Lisby, and R. Rothstein. 2007. Genome-wide analysis of Rad52 foci reveals diverse mechanisms impacting recombination. *PLoS Genet.* 3:e228. doi:10.1371/journal.pgen.0030228
- Hill, E. 2008. Announcing the *JCB DataViewer*, a browser-based application for viewing original image files. *J. Cell Biol.* 183:969–970. 10.1083/jcb.200811132. doi:10.1083/jcb.200811132
- Rohn, J.L., D. Sims, T. Liu, M. Fedorova, F. Schock, J. Dopie, M.K. Vartiainen, A.A. Kiger, N. Perrimon, and B. Baum. 2011. Comparative RNAi screening identifies a conserved core metazoan actinome by phenotype. *J. Cell Biol.* 194:789–805. 10.1083/jcb.201103168.
- Thorpe, P.H., D. Alvaro, M. Lisby, and R. Rothstein. 2011. Bringing Rad52 foci into focus. *J. Cell Biol.* 194:665–667. 10.1083/jcb.201108095.