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## Webinar 4: Group Comparison

May 21, 2020





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- April 30: Introduction to cBioPortal (recording on [cBioPortal.org](https://cBioPortal.org))
- May 7: Mutation Details & Patient View (recording on [cBioPortal.org](https://cBioPortal.org))
- May 14: Expression Data Analysis (recording on [cBioPortal.org](https://cBioPortal.org))
- May 21: Group Comparison
- May 28: API & R Client

All webinars are on Thursdays 11am-12pm EDT

# Questions?

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- Please ask questions using the Zoom Q&A feature
- We will try to answer some live, some directly, and some on future webinars
- Webinar recordings are posted on <https://cbioportal.org/tutorials/>
- If you still have questions after the webinar, please contact us at [cbioportal@googlegroups.com](mailto:cbioportal@googlegroups.com)



# Acknowledgements



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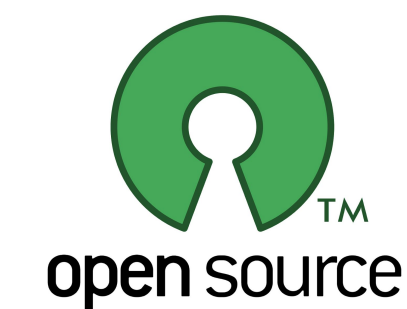


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## Funding: Present & past



Email: [cbioportal@googlegroups.com](mailto:cbioportal@googlegroups.com)

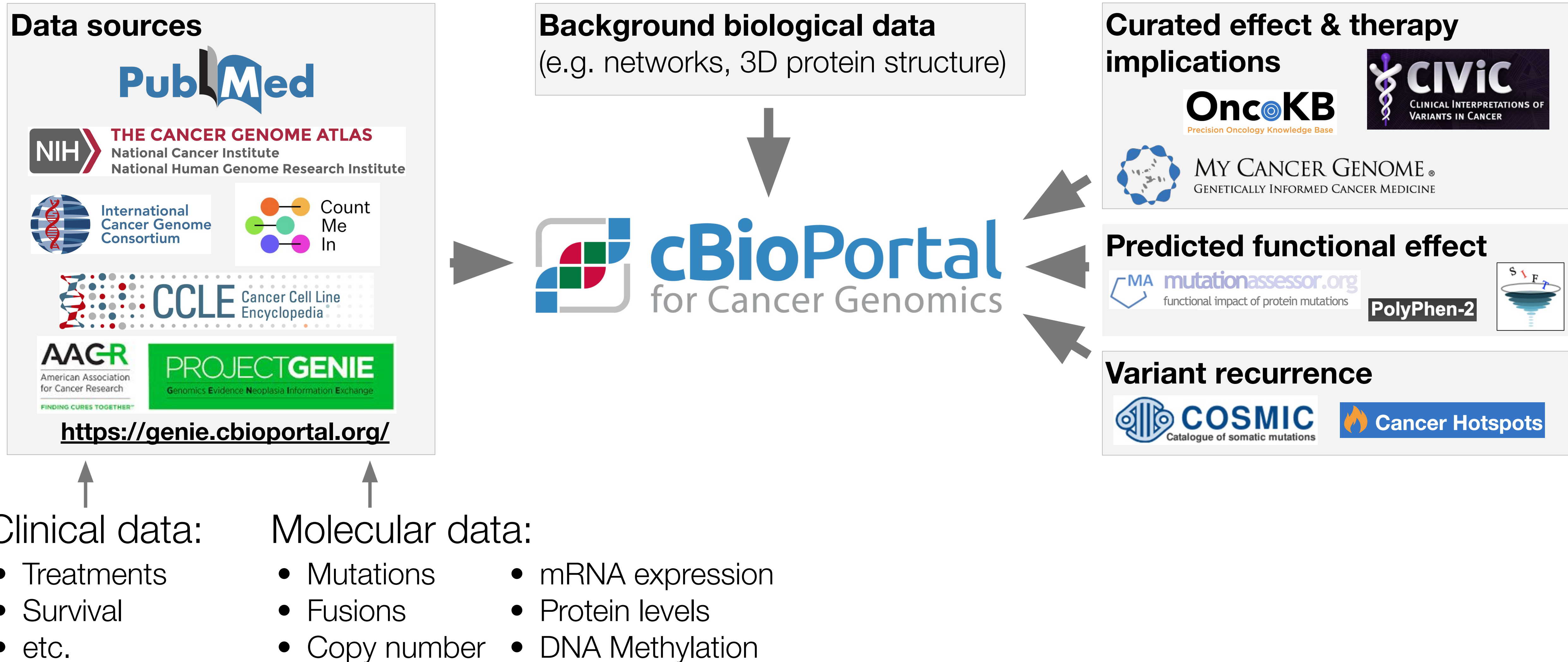
 [@cBioPortal](https://twitter.com/cBioPortal)

 [github.com/cBioPortal](https://github.com/cBioPortal)

- Platform for **exploratory and interactive visualization, analysis and download** of large-scale cancer genomics data sets
- **Open source** software jointly developed by Dana-Farber Cancer Institute, Memorial Sloan Kettering Cancer Center, Princess Margaret Cancer Centre, Children's Hospital of Philadelphia, and The Hyve
- **Public website** (cBioPortal.org) with public data (TCGA, ICGC, published sequencing studies)
- **Private instances** are installed at academic and commercial institutions world-wide



# Data in cBioPortal



- How can I compare samples with or without mutations in geneX?
- How can I compare samples with mutationY in gene X to other mutations in geneX?
- How can I compare samples with mutations in both geneX and geneY to samples with mutations in geneX or geneY?
- How can I compare outcomes in samples with high vs low expression in geneX?
- How can I compare samples with high expression in geneX and low expression in geneY to all other samples?




# Group Comparison

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- How to **define** groups?
- How to **refine** groups?
- What **analyses** does Group Comparison support?

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

# Getting help



[Data Sets](#) [Web API](#) [R/MATLAB](#) [Tutorials](#) [FAQ](#) [News](#)

## Tutorials

[Tutorial #1: Single Study Exploration](#)

### Tutorial Objectives

- Introduction
- Show the data
- Walk through the data
- Show how to use the data

[Tutorial #2: Single Study Query](#)

### Tutorial Objectives

- Show how to use the data
- Walk through the data

[Tutorial #3: Patient View](#)

### Tutorial Objectives

- Show how to use the data
- Walk through the data

[Tutorial #4: Virtual Studies](#)

### Tutorial Objectives

- Explain what the new group comparison functionality enables
- Delineate the different ways to define groups and enter the group comparison view
- Highlight potential use cases for group comparison functionality

[Tutorial #5: Onco Query Language \(OQL\)](#)


### Tutorial Objectives

- Explain what the new group comparison functionality enables
- Delineate the different ways to define groups and enter the group comparison view
- Highlight potential use cases for group comparison functionality

[Tutorial #6: Group Comparison](#)

### Tutorial Objectives

- Explain what the new group comparison functionality enables
- Delineate the different ways to define groups and enter the group comparison view
- Highlight potential use cases for group comparison functionality





[Data Sets](#) [Web API](#) [R/MATLAB](#) [Tutorials](#) [FAQ](#) [News](#)

## FAQs

- General Questions
  - What is the cBioPortal for Cancer Genomics?
  - How do I get started?
  - What data types are in the portal?
  - What is the process of data curation?
  - How do I get updates on new portal developments and new data sets?
  - Does the portal work on all browsers and operating systems?
  - How do I cite the cBioPortal?
  - Can I use figures from the cBioPortal in my publications or presentations?
  - Can I save or bookmark my results in cBioPortal?

### cBioPortal for Cancer Genomics Discussion Group

60 of 2034 topics (99+ unread) ★ 



PROTOCOL | CANCER

## Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal

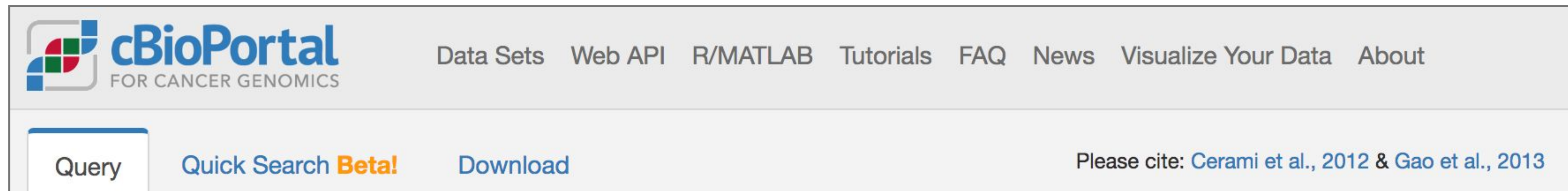
Jianjiong Gao<sup>1</sup>, Bülent Arman Aksoy<sup>1</sup>, Ugur Dogrusoz<sup>2</sup>, Gideon Dresdner<sup>1</sup>, Benjamin Gross<sup>1</sup>, S. Onur Sumer<sup>1</sup>, Yichao Sun<sup>1</sup>, Anders Jacobsen<sup>1</sup>, Rileen Sinha<sup>1</sup>, Erik Larsson<sup>3</sup>, Ethan Cerami<sup>1,4</sup>, Chris Sander<sup>1</sup>, and Nikolaus Schultz<sup>1</sup>

*Sci. Signal.* 02 Apr 2013:  
Vol. 6, Issue 269, pp. p11  
DOI: 10.1126/scisignal.2004088



# Using cBioPortal for publication

- **Please use cBioPortal in your publications!**
  - Figures are downloadable as PDF/SVG so you can customize them
- Cite the studies that generated the data you are using (if applicable)
- Cite cBioPortal



# Questions?

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- Join us for the remaining webinars
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- If you still have questions, please ask them via our Google Group or email directly [cbioportal@googlegroups.org](mailto:cbioportal@googlegroups.org)

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