



Webinar 4: Group Comparison

May 21, 2020





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Webinar Schedule



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

All webinars are on Thursdays 11am-12pm EDT

Questions?

- 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

Acknowledgements



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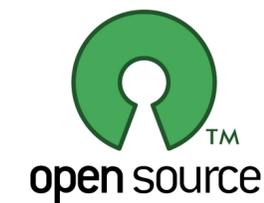


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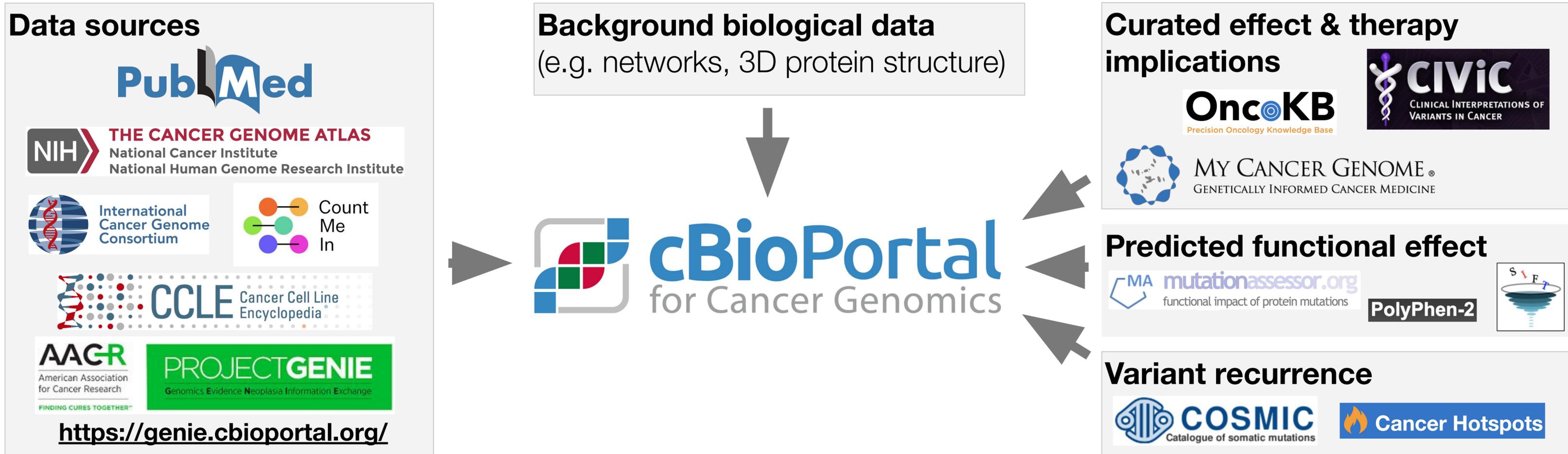
Email: cbioportal@googlegroups.com

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

 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



Clinical data:

- Treatments
- Survival
- etc.

Molecular data:

- Mutations
- Fusions
- Copy number
- mRNA expression
- Protein levels
- DNA Methylation

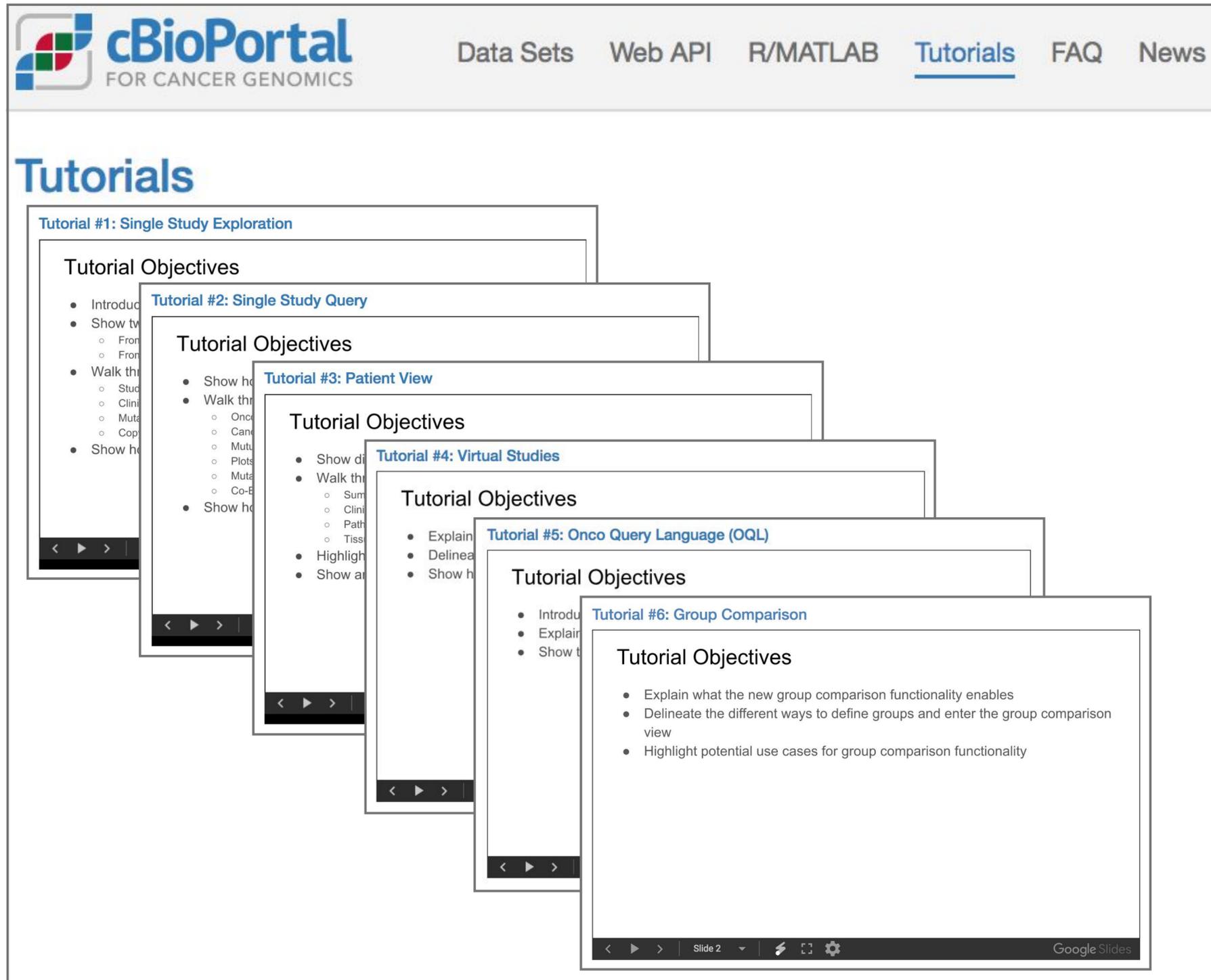
- How can I compare samples with or without mutations in geneX?
- How can I compare samples with mutationY in gene X to other mutations in geneX?
- How can I compare samples with mutations in both geneX and geneY to samples with mutations in geneX or geneY?
- How can I compare outcomes in samples with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

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

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

Getting help

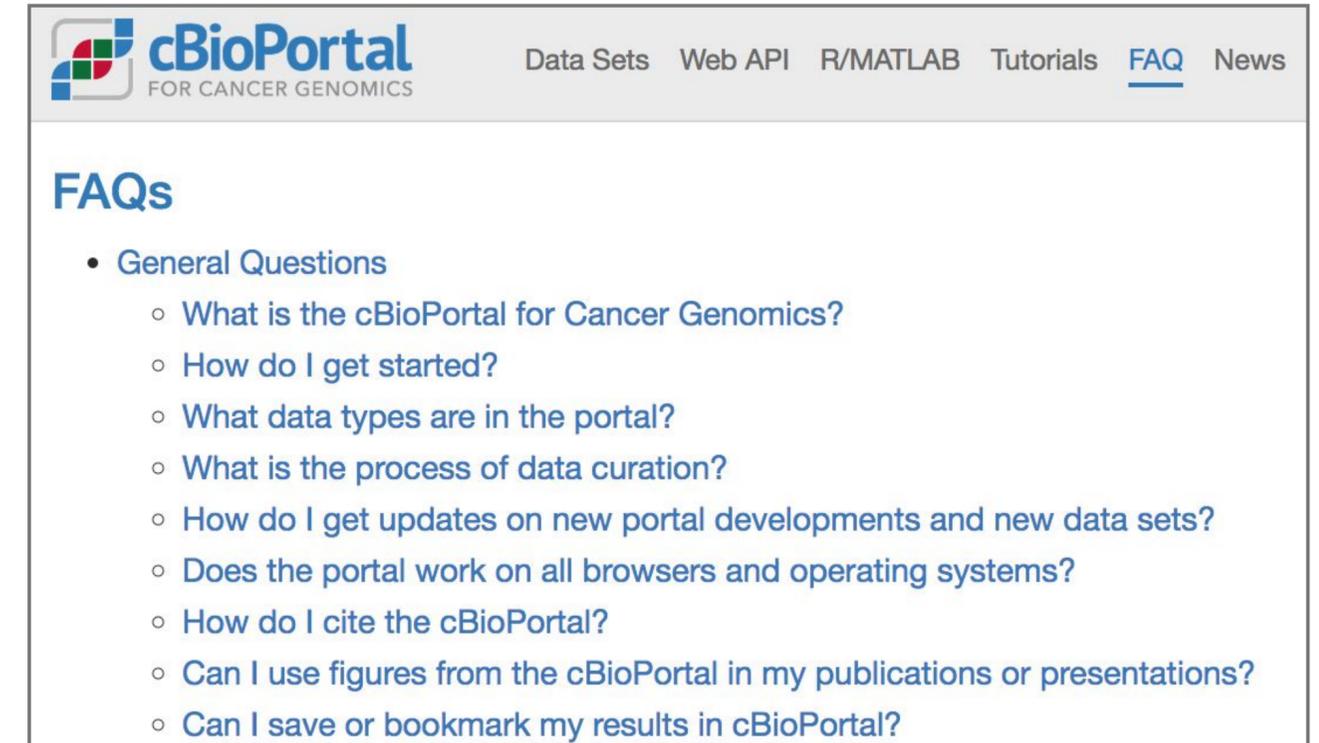


The screenshot shows the cBioPortal website's navigation bar with links for Data Sets, Web API, R/MATLAB, Tutorials, FAQ, and News. The main content area is titled "Tutorials" and displays a series of overlapping slides for various tutorials. The visible slides include:

- Tutorial #1: Single Study Exploration**
- Tutorial #2: Single Study Query**
- Tutorial #3: Patient View**
- Tutorial #4: Virtual Studies**
- Tutorial #5: Onco Query Language (OQL)**
- Tutorial #6: Group Comparison**

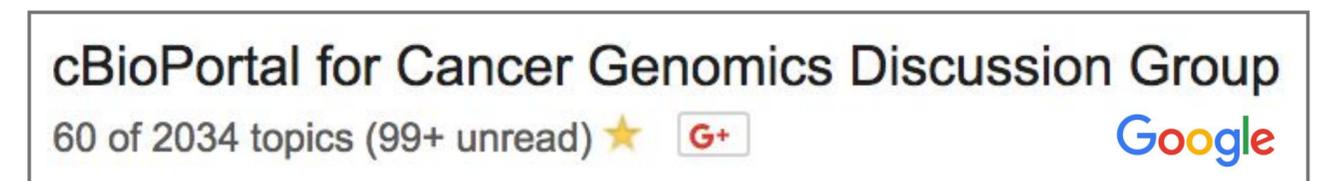
The "Group Comparison" slide is currently active and shows the following objectives:

- 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

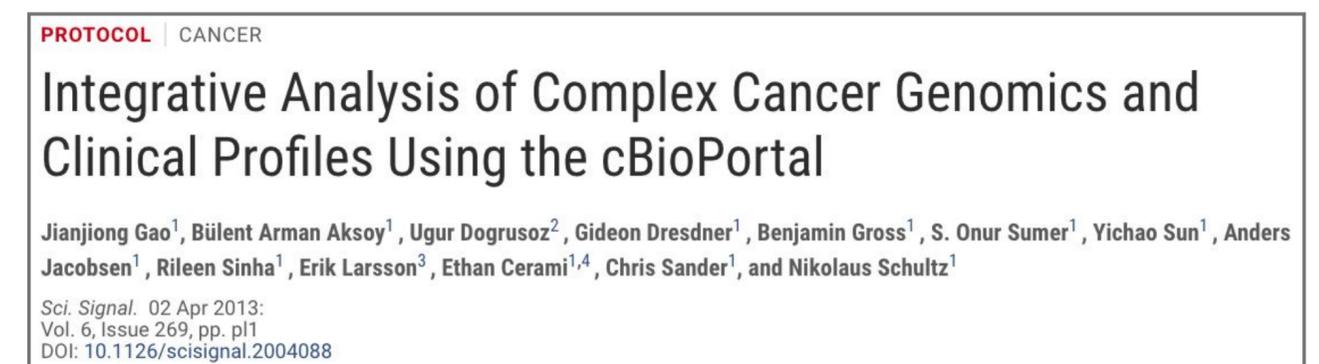


The screenshot shows the cBioPortal website's navigation bar and the "FAQs" section. The navigation bar includes links for Data Sets, Web API, R/MATLAB, Tutorials, FAQ, and News. The "FAQs" section is titled "FAQs" and contains a list of questions:

- 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?



The screenshot shows a Google Group titled "cBioPortal for Cancer Genomics Discussion Group". It indicates there are 60 of 2034 topics (99+ unread) and features a star icon and a Google+ icon. The Google logo is visible in the bottom right corner.



The screenshot shows the title and authors of a research paper:

PROTOCOL | CANCER

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

Jianjiog Gao¹, Bülent Arman Aksoy¹, Ugur Dogrusoz², Gideon Dresdner¹, Benjamin Gross¹, S. Onur Sumer¹, Yichao Sun¹, Anders Jacobsen¹, Rileen Sinha¹, Erik Larsson³, Ethan Cerami^{1,4}, Chris Sander¹, and Nikolaus Schultz¹

Sci. Signal. 02 Apr 2013:
Vol. 6, Issue 269, pp. p1
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



The screenshot shows the top navigation bar of the cBioPortal website. On the left is the cBioPortal logo with the text "FOR CANCER GENOMICS". To the right of the logo are several navigation links: "Data Sets", "Web API", "R/MATLAB", "Tutorials", "FAQ", "News", "Visualize Your Data", and "About". Below the navigation bar is a search area with a "Query" input field, a "Quick Search **Beta!**" button, and a "Download" button. On the far right of this section, there is a citation notice: "Please cite: [Cerami et al., 2012](#) & [Gao et al., 2013](#)".

Questions?

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