

## Access and Discover Biological Pathway Information from Pathway Commons

Augustin Luna<sup>1,2</sup>, Emek Demir<sup>3</sup>, Igor Rodchenkov<sup>4</sup>, Özgün Babur<sup>3</sup>, Jeffrey V Wong<sup>4</sup>, Chris Sander<sup>1,2</sup> and Gary Bader<sup>4</sup>

*Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston MA, USA<sup>1</sup> Cell Biology, Harvard Medical School, Boston MA, USA<sup>2</sup>, Oregon Health & Science University, Portland OR, USA<sup>3</sup>, University of Toronto, Toronto, Canada<sup>4</sup>*

Pathway Commons ([pathwaycommons.org](http://pathwaycommons.org)) serves researchers by integrating data from public pathway and interaction databases and disseminating this data in a uniform fashion. The knowledge base is comprised of metabolic pathways, genetic interactions, gene regulatory networks and physical interactions involving proteins, nucleic acids, small molecules and drugs. Alongside attempts to increase the scope and types of data, a major focus has been the creation of user-focused tools and resources that facilitate access, discovery and application of existing pathway information to aid day-to-day activities of biological researchers. Pathway Commons offers a number of tools for accessing and searching the integrated datasets. File downloads are available in Biological Pathway Exchange (BioPAX), Simple Interaction Format (SIF) and gene set (GMT) formats. Provided web services allow for integration with external tools and support full-text search of available data. Results from the web services is provided in the aforementioned formats, as well as, the Systems Biology Graphical Notation Markup Language (SBGNML) and Javascript Object Notation for Linked Data (JSON-LD) formats. Pathway Commons is also accessible via a number of web applications built on reusable Javascript components, including: 1) PCViz that allows the visualization of interaction data as simplified binary interaction networks from input gene names and 2) a web-based 'Search' application that enables users to query pathways by keyword and visualize returned pathways using SBGN with an automated layout. These web applications complement existing desktop software add-ons linking Pathway Commons to the Cytoscape (CyPath2) network analysis tool and the R (`paxtoolsr`) programming language. We additionally provide an online guide for those wishing to learn more about pathway resources and analysis with published case studies and guided workflows. Ongoing development of web applications will enhance the accessibility to pathways and integrate support for visualization and interpretation of experimental data.