

## Access and Discover Biological Pathway Information from Pathway Commons

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Pathway Commons ([www.pathwaycommons.org/](http://www.pathwaycommons.org/)) serves researchers by integrating data from public pathway and interaction databases and disseminating it 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 facilitate day-to-day activities of biological researchers. For those wishing to browse and discover pathways within the collection, we offer a web-based 'Search' application that enables users to query by keyword and visualize ranked search results. 'PCViz' is a web tool that accepts gene names and returns a customizable interaction network visualization based upon pathway data resources. These complement existing desktop software add-ons linking Pathway Commons to the Cytoscape (CyPath2) network analysis tool and the R (paxtoolsr) programming language. To facilitate analysis and interpretation of experimental data - for instance, enrichment studies that distill pathway alterations from underlying gene expression changes - pathway data file downloads can be directly used in software tools such as Gene Set Enrichment Analysis. For those wishing to learn more about pathway resources and analysis, an online 'Guide' includes case studies and guided workflows. Ongoing development of web apps will enhance the accessibility to pathways and integrate support for visualization and interpretation of experimental data.