

Access and Discover Pathways from Pathway Commons

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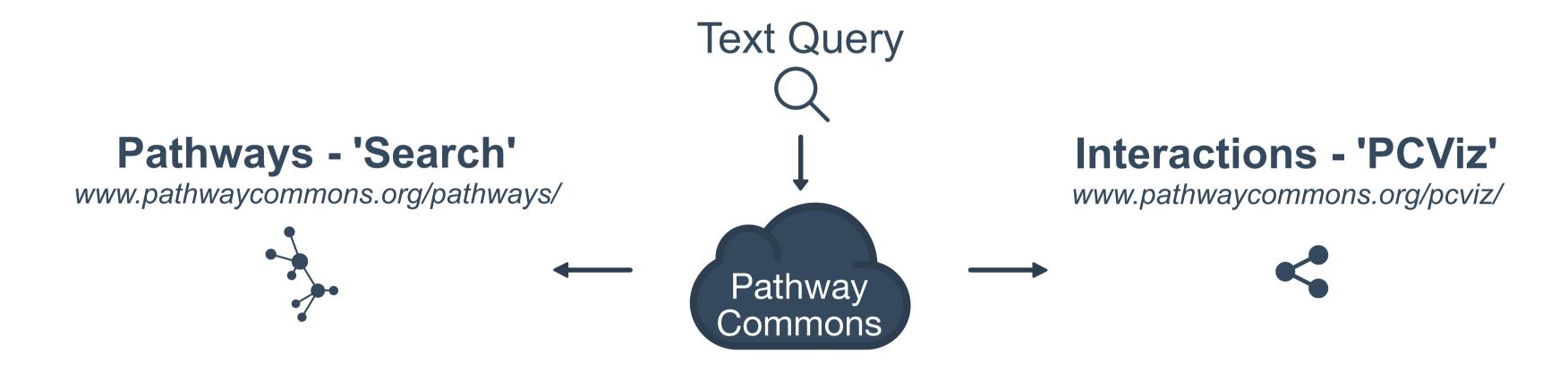
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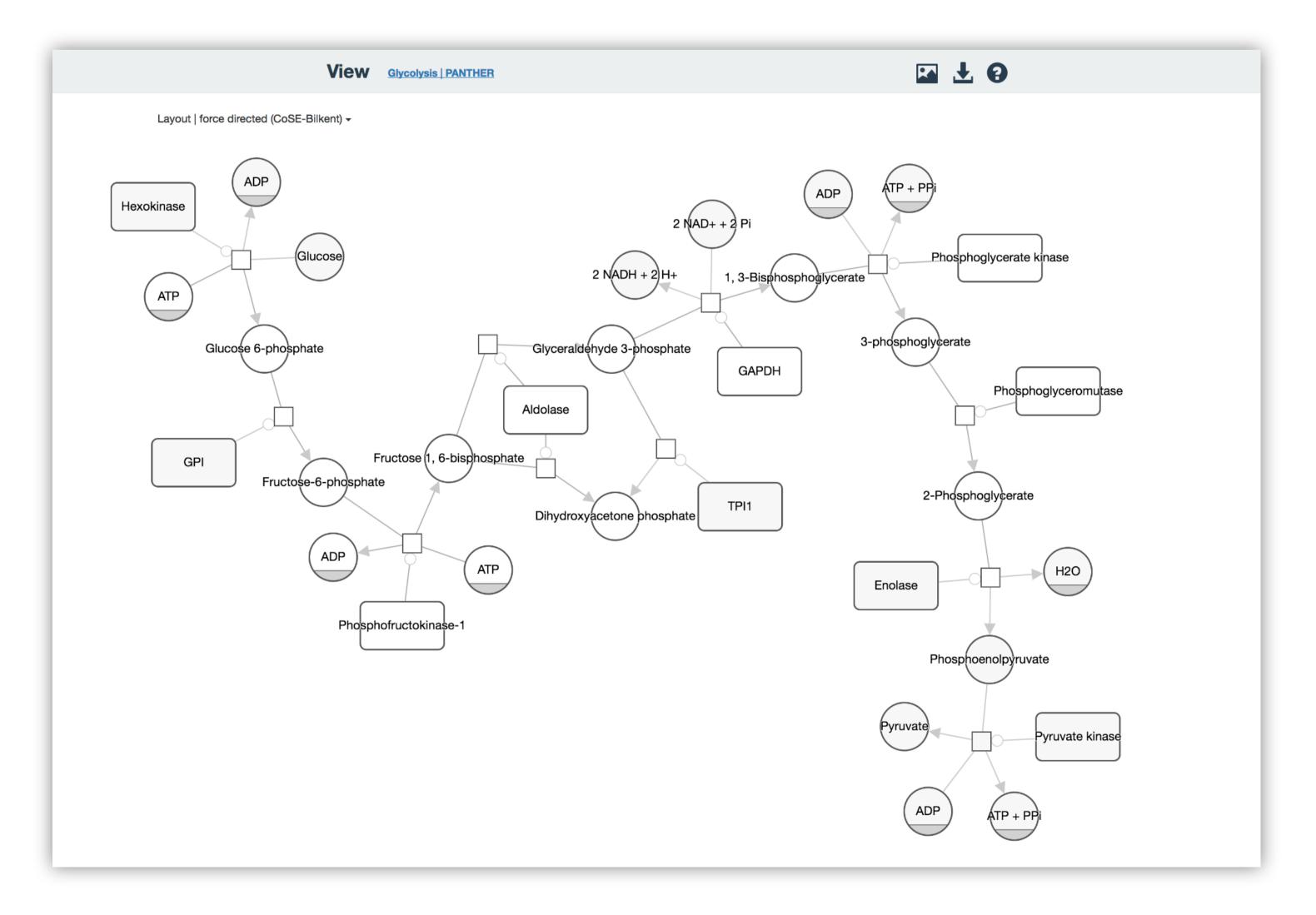
www.pathwaycommons.org

What is Pathway Commons?



Search pathways and interactions with apps





Get pathway and interaction data

Downloads

Perform enrichment analyses with **gene set database (GMT)** files which list genes in each pathway; View and analyze pathways using **Simple Interaction Format (SIF)** files which list interacting gene pairs; Get rich, machine-readable descriptions in the **Biological Pathway Exchange (BioPAX)** format.

Web services

Perform a full-text **Search** over the entire database; Use **Get** to retrieve a specific pathway or interaction in the database by URI in a variety of output formats (BioPAX, SIF, SBGN-ML, GMT); Use **Traverse** and **Graph** to access and navigate over pathways and interactions in the database.

Access software tools and components

Pathway Commons

Search and view pathways in **Cytoscape** with the **CyPath2 app**; Access the web services using the **cPath2-client** JavaScript library.

Biological Pathway Exchange (BioPAX)

Read, export and validate BioPAX using the Paxtools software library; Use R to interact with pathway data in BioPAX format using the **paxtoolsr package**; View and edit pathways using the **Chisio BioPAX Editor (ChiBE)**.

Systems Biology Graphical Notation (SBGN)

Use the **sbgnml-to-cytoscape** and **cytoscape-sbgn-stylesheet** JavaScript libraries to convert and render pathways encoded in SBGN-ML using cytoscape.js.



github.com/PathwayCommons

Access training materials for pathway analysis

Visit our **Guide** (www.pathwaycommons.org/guide/) to read case studies, primers and workflows for pathway analysis.

Pathway Commons, a web resource for biological pathway data. Cerami E. et al. Nucleic Acids Research, vol 39: D685-90, 2011.





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