

Tabela 1. The available analytical tools and web servers designed for mapping pathway data, including their functions, advantages, disadvantages, supported languages, types of identifiers, interactivity, sample representation, taxonomy considerations, differential expression analysis capabilities, and input/output formats.

Tools	What tools do	Advantages	Disadvantages	Languages	Type of Identifiers	Interac- tivity	Number of Samples	Ta- xonomy	Dif- fe- ren- tial Ex- pres- sion	Input	Output
Kegg Map- per	Provides a set of mapping tools (Reconstruct, Search, Color, and Join)	Effective inte- gration of di- verse biologi- cal data	Dependence on up-to-date	Python	Map number, K number	Yes	Not directly applicable	Yes	Yes	KEGG IDs	Interactive visualizati- ons
Reactome Knowledge- base	It provides mo- lecular details as an ordered net- work of transfor- mations	Enhanced High-Level Diagrams (EHLs)	Complexity of data for new us- ers	Python	UniProt IDs	Yes	Capable of dealing with large-scale data sets	<i>Homo sapiens</i>	Yes	Txt (Gene Ids, Pro- tein IDs)	PowerPoint
MetaCore™	Web-based com- putational plat- form	Provides visu- alization and network anal- ysis capabili- ties	Paid access	Perl, HTML/Ja- vaScript, Flash Player Plug-in	LocusLink, Swis- sProt, RefSeq, Uni- gene	Yes	Dependent on the specific data set used by the user	<i>Homo sapiens</i> , mamma- lian	Yes	Txt, Ex- cel, CSV, Af- fymetrix, Agilent	XML, JSON, CSV, TSV, PDF, PNG, JPEG, HTML, XLS, XLSX
MetaDrug™	Predicts major xenobiotic me- tabolites in hu- mans	Offers visual- ization of gene-signa- ture networks	Not specified	Not speci- fied	Not specified	Yes	Not specified	Human metabo- lism	Yes	Integra- tion with external software for broader data input	Visual network di- agrams

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Pathway Tools	Genome analysis and metabolic modeling	Expansive da- tabase schema	Certain features are available only in web mode	R, Com- monly Lisp, Java, Py- thon, Perl	BioCyc IDs	Yes	20,000+ orga- nisms databa- ses	<i>E. coli</i> , <i>B. subti- lis</i> and <i>P. diffi- cile</i>	Yes	GenBank, GFF	GenBank, GFF
MetPA	Analysis and visualization of metabolomic data	User-friendly, supports intu- itive and in- teractive data exploration	Not specified	R, Java	Compound names	Yes	Designed to handle large- scale metabo- lomic data	Covers 11 model orga- nisms	No	Not spe- cified	Visualized as a net- work on a web inter- face
Pathway Hunter Tool (PHT)	Analyses the shortest paths in metabolic path- ways	Uses chemi- cal structure information for path anal- ysis	Dependence on the chemical structure of the metabolites	Java	KEGG, BRENDA, and PROSITE IDs	Yes	Adaptable to various se- quenced ge- nomes	Yes	No	Txt (Me- tabolites IDs, enzyme IDs)	GML
Pathway Tools Cellu- lar Overview Diagram	Visual represen- tation of the bio- chemical net- work of an or- ganism	Automated layout, sup- ports large- scale data analysis	Learning curve for new users	Commonly Lisp	Gene IDs, protein IDs, metabolite names, reaction IDs	Yes	Can represent whole-organ- ism datasets	Yes	Yes	User-sup- plied tab- delimited files	Interactive web and desktop vis- ualizations

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Omics Viewer	Provides visual analysis of high-throughput experimental data	Allows intuitive visualization of omics data and customizable color schemes	Requires a comprehensive Pathway/Genome Database (PGDB) for the organism of interest	Commonly Lisp	Gene IDs, protein IDs, metabolite names, reaction IDs	Yes	The number of samples is variable	Yes	Yes	User-supplied tab-delimited files	Interactive web and desktop visualizations
Pathview	Tool set for pathway-based data integration and visualization	Easy to automate and integrate with pathway analysis tools	Requires user proficiency in R for effective use	R	12 types of gene/protein IDs, 21 types of compound/metabolite IDs	Yes	Capable of handling datasets from individual to large-scale studies	2000 species	Yes	Accepts data in matrix or vector format	KGML
PathVisio	Visualize, edit and analyze biological pathways	Cross-platform compatibility due to Java implementation	Requires users to manually input pathway data	Java	Not specified	Yes	Not specified	Yes	Yes	GPML, XML	SVG
iPath	Offers an interactive exploration of metabolism	Redesigned fast and lightweight interface	Requirement for internet access	Javascript, Perl	KEGG IDs, KOs, EC numbers	Yes	62 new KEGG pathway modules, 1700 new reactions, 1500 new KEGG Orthology entries, and close to 3000 new species	Yes	Yes	Txt	SVG, PNG, EPS, PDF

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DAVID	Integrates func- tional genomic annotations with intuitive graph- ical	Provides ex- ploratory vis- ualization tools for func- tional classifi- cation	Requirement for internet access	Perl and Java	Gene IDs, protein IDs	Yes	Not specified	Yes	Yes	Txt	HTML
Reactome	It provides an in- tuitive web- based user inter- face	Integration with various data analysis tools for ID mapping	Limited by the breadth of its cu- rated data	JavaScript, Perl	UniProt IDs, Gen- Bank/EMBL/DDBJ IDs, RefSeq IDs, EntrezGene IDs	Yes	Not specified	Human and 20 other species	Yes	Txt	SVG, PNG, EPS, PDF, MySQL, BioPAX, SBML, PSI-MI- TAB
CellDesigner	Modeling tool that allows users to visualize, model, and sim- ulate biochemi- cal networks	Offers a com- prehensive graphical rep- resentation of networks	Requires unders- tanding of SBML	Java	Not specified	Yes	Not applicable	No	Yes	SBML	SBML, PNG,SVG
GenMAPP	Allows users to visualize and an- alyze genome- scale data	Offers new visualization modes for complex data analysis	Limited primar- ily to the species and gene ids within its data- base	Visual Ba- sic 6.0	Ensembl gene IDs, UniProt IDs, En- trez Gene IDs, Af- fymetrix probe set IDs	Yes	Not specified	Yes	Yes	Microsoft Jet format for (.gex), (.gdb), (.mapp)	HTML, PNG, SVG

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KEGGChar- ter	Represents om- ics results and shows the taxo- nomic assign- ment of enzymes	Visual repre- sentation of functional an- notations in metabolic maps	Requires input data in specific formats	Python	KEGG IDs, KOs, EC numbers	No	Dependent on input data	Yes	Yes	TSV, Ex- cel	PNG
KGML-ED	Enables dynamic visualization, in- teractive naviga- tion, and editing of KEGG path- way diagrams	Supports dy- namic and in- teractive ex- ploration of pathways	Requires more computer resour- ces	Java	KEGG IDs	Yes	Not specified	No	Yes	KGML (KEGG Markup Lan- guage)	KGML