

# Peter D Karp

## List of Publications by Year in descending order

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140  
papers

24,747  
citations

20817

60  
h-index

12597

132  
g-index

145  
all docs

145  
docs citations

145  
times ranked

23707  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolic Modeling with MetaFlux. <i>Methods in Molecular Biology</i> , 2022, 2349, 259-289.	0.9	3
2	Pathway Tools Management of Pathway/Genome Data for Microbial Communities. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	4
3	Pathway Tools version 23.0 update: software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2021, 22, 109-126.	6.5	117
4	Pathway Tools Visualization of Organism-Scale Metabolic Networks. <i>Metabolites</i> , 2021, 11, 64.	2.9	9
5	Leveraging Curation Among Escherichia coli Pathway/Genome Databases Using Ortholog-Based Annotation Propagation. <i>Frontiers in Microbiology</i> , 2021, 12, 614355.	3.5	3
6	Pathway size matters: the influence of pathway granularity on over-representation (enrichment) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 5	2.8	158
7	The BioCyc Metabolic Network Explorer. <i>BMC Bioinformatics</i> , 2021, 22, 208.	2.6	9
8	The EcoCyc Database in 2021. <i>Frontiers in Microbiology</i> , 2021, 12, 711077.	3.5	122
9	Plant Metabolic Network 15: A resource of genome-wide metabolism databases for 126 plants and algae. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1888-1905.	8.5	114
10	The MetaCyc database of metabolic pathways and enzymes - a 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D445-D453.	14.5	606
11	Taxonomic weighting improves the accuracy of a gap-filling algorithm for metabolic models. <i>Bioinformatics</i> , 2020, 36, 1823-1830.	4.1	3
12	Simultaneous cross-evaluation of heterogeneous <i>E. coli</i> datasets via mechanistic simulation. <i>Science</i> , 2020, 369, .	12.6	105
13	Gene Dispensability in Escherichia coli Grown in Thirty Different Carbon Environments. <i>MBio</i> , 2020, 11, .	4.1	21
14	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
15	The MultiOmics Explainer: explaining omics results in the context of a pathway/genome database. <i>BMC Bioinformatics</i> , 2019, 20, 399.	2.6	5
16	Metabolic route computation in organism communities. <i>Microbiome</i> , 2019, 7, 89.	11.1	4
17	Using Pathway Covering to Explore Connections among Metabolites. <i>Metabolites</i> , 2019, 9, 88.	2.9	3
18	A Comparison of Microbial Genome Web Portals. <i>Frontiers in Microbiology</i> , 2019, 10, 208.	3.5	22

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19	The BioCyc collection of microbial genomes and metabolic pathways. Briefings in Bioinformatics, 2019, 20, 1085-1093.	6.5	582
20	The EcoCyc Database. EcoSal Plus, 2018, 8, .	5.4	75
21	The MetaCyc database of metabolic pathways and enzymes. Nucleic Acids Research, 2018, 46, D633-D639.	14.5	658
22	How accurate is automated gap filling of metabolic models?. BMC Systems Biology, 2018, 12, 73.	3.0	33
23	Evaluation of reaction gap-filling accuracy by randomization. BMC Bioinformatics, 2018, 19, 53.	2.6	14
24	Computing Metabolic Routes in the Human Microbiome. FASEB Journal, 2018, 32, .	0.5	0
25	Computing Metabolic Routes in the Human Microbiome. FASEB Journal, 2018, 32, lb121.	0.5	0
26	The Omics Dashboard for interactive exploration of gene-expression data. Nucleic Acids Research, 2017, 45, 12113-12124.	14.5	57
27	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. Nucleic Acids Research, 2017, 45, D543-D550.	14.5	541
28	Update notifications for the BioCyc collection of databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	11
29	The Time Is Right to Focus on Model Organism Metabolomes. Metabolites, 2016, 6, 8.	2.9	63
30	How the strengths of Lisp-family languages facilitate building complex and flexible bioinformatics applications. Briefings in Bioinformatics, 2016, 19, bbw130.	6.5	3
31	Pathway collages: personalized multi-pathway diagrams. BMC Bioinformatics, 2016, 17, 529.	2.6	19
32	How much does curation cost?. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw110.	3.0	43
33	Representation and inference of cellular architecture for metabolic reconstruction and modeling. Bioinformatics, 2016, 32, 1074-1079.	4.1	0
34	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Research, 2016, 44, D471-D480.	14.5	1,788
35	Pathway Tools version 19.0 update: software for pathway/genome informatics and systems biology. Briefings in Bioinformatics, 2016, 17, 877-890.	6.5	250
36	Crowd-sourcing and author submission as alternatives to professional curation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw149.	3.0	14

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37	Can we replace curation with information extraction software?. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw150.	3.0	23
38	Computational Metabolomics Operations at BioCyc.org. Metabolites, 2015, 5, 291-310.	2.9	26
39	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. Bioinformatics, 2015, 31, 616-617.	4.1	3
40	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. PLoS Computational Biology, 2015, 11, e1004087.	3.2	2
41	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. F1000Research, 2015, 4, 12.	1.6	1
42	Curation accuracy of model organism databases. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau058-bau058.	3.0	27
43	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. Nucleic Acids Research, 2014, 42, D459-D471.	14.5	1,023
44	A genome-scale metabolic flux model of Escherichia coli K12 derived from the EcoCyc database. BMC Systems Biology, 2014, 8, 79.	3.0	42
45	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. Nucleic Acids Research, 2014, 42, D677-D684.	14.5	25
46	Optimal metabolic route search based on atom mappings. Bioinformatics, 2014, 30, 2043-2050.	4.1	47
47	Addition of Escherichia coli K-12 Growth Observation and Gene Essentiality Data to the EcoCyc Database. Journal of Bacteriology, 2014, 196, 982-988.	2.2	9
48	Metabolic pathways for the whole community. BMC Genomics, 2014, 15, 619.	2.8	50
49	A framework for application of metabolic modeling in yeast to predict the effects of nsSNV in human orthologs. Biology Direct, 2014, 9, 9.	4.6	1
50	The EcoCyc Database. EcoSal Plus, 2014, 6, .	5.4	101
51	Computing minimal nutrient sets from metabolic networks via linear constraint solving. BMC Bioinformatics, 2013, 14, 114.	2.6	12
52	A systematic comparison of the MetaCyc and KEGG pathway databases. BMC Bioinformatics, 2013, 14, 112.	2.6	123
53	Data Mining in the MetaCyc Family of Pathway Databases. Methods in Molecular Biology, 2013, 939, 183-200.	0.9	9
54	The challenge of constructing, classifying, and representing metabolic pathways. FEMS Microbiology Letters, 2013, 345, 85-93.	1.8	82

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55	Groups: knowledge spreadsheets for symbolic biocomputing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat061.	3.0	19
56	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
57	EcoCyc: fusing model organism databases with systems biology. Nucleic Acids Research, 2013, 41, D605-D612.	14.5	505
58	Dead End Metabolites - Defining the Known Unknowns of the E. coli Metabolic Network. PLoS ONE, 2013, 8, e75210.	2.5	23
59	Construction and completion of flux balance models from pathway databases. Bioinformatics, 2012, 28, 388-396.	4.1	86
60	Accurate Atom-Mapping Computation for Biochemical Reactions. Journal of Chemical Information and Modeling, 2012, 52, 2970-2982.	5.4	67
61	Regulatory network operations in the Pathway Tools software. BMC Bioinformatics, 2012, 13, 243.	2.6	13
62	Metabolomics Reveals Amino Acids Contribute to Variation in Response to Simvastatin Treatment. PLoS ONE, 2012, 7, e38386.	2.5	90
63	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Research, 2012, 40, D742-D753.	14.5	561
64	Browsing Metabolic and Regulatory Networks with BioCyc. Methods in Molecular Biology, 2012, 804, 197-216.	0.9	27
65	The Pathway Tools Pathway Prediction Algorithm. Standards in Genomic Sciences, 2011, 5, 424-429.	1.5	109
66	Using cellular network diagrams to interpret large-scale datasets: past progress and future challenges. Proceedings of SPIE, 2011, , .	0.8	1
67	A survey of metabolic databases emphasizing the MetaCyc family. Archives of Toxicology, 2011, 85, 1015-1033.	4.2	72
68	Web-based metabolic network visualization with a zooming user interface. BMC Bioinformatics, 2011, 12, 176.	2.6	30
69	EcoCyc: a comprehensive database of Escherichia coli biology. Nucleic Acids Research, 2011, 39, D583-D590.	14.5	444
70	Discovering novel subsystems using comparative genomics. Bioinformatics, 2011, 27, 2478-2485.	4.1	6
71	Machine learning methods for metabolic pathway prediction. BMC Bioinformatics, 2010, 11, 15.	2.6	131
72	A systematic study of genome context methods: calibration, normalization and combination. BMC Bioinformatics, 2010, 11, 493.	2.6	26

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73	The BioPAX community standard for pathway data sharing. <i>Nature Biotechnology</i> , 2010, 28, 935-942.	17.5	613
74	Creation of a Genome-Wide Metabolic Pathway Database for <i>Populus trichocarpa</i> Using a New Approach for Reconstruction and Curation of Metabolic Pathways for Plants. <i>Plant Physiology</i> , 2010, 153, 1479-1491.	4.8	115
75	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2010, 38, D473-D479.	14.5	403
76	An advanced web query interface for biological databases. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq006-baq006.	3.0	10
77	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2010, 11, 40-79.	6.5	551
78	Beyond the genome (BTG) is a (PGDB) pathway genome database: HumanCyc. <i>Genome Biology</i> , 2010, 11, O12.	9.6	28
79	EcoCyc: A comprehensive view of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2009, 37, D464-D470.	14.5	320
80	What we can learn about <i>Escherichia coli</i> through application of Gene Ontology. <i>Trends in Microbiology</i> , 2009, 17, 269-278.	7.7	16
81	The Multiple Scientific Disciplines Served by EcoCyc. , 2009, , 99-112.		0
82	Changes to NIH Grant System May Backfire. <i>Science</i> , 2008, 322, 1187-1188.	12.6	0
83	Annotation-based inference of transporter function. <i>Bioinformatics</i> , 2008, 24, i259-i267.	4.1	36
84	BioWarehouse: Relational Integration of Eleven Bioinformatics Databases and Formats. <i>Lecture Notes in Computer Science</i> , 2008, , 5-7.	1.3	1
85	Multidimensional annotation of the <i>Escherichia coli</i> K-12 genome. <i>Nucleic Acids Research</i> , 2007, 35, 7577-7590.	14.5	168
86	Using genome-context data to identify specific types of functional associations in pathway/genome databases. <i>Bioinformatics</i> , 2007, 23, i205-i211.	4.1	24
87	A genome-scale metabolic reconstruction for <i>Escherichia coli</i> K12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121.	7.2	1,234
88	The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. <i>Nucleic Acids Research</i> , 2007, 36, D623-D631.	14.5	600
89	Using the MetaCyc Pathway Database and the BioCyc Database Collection. <i>Current Protocols in Bioinformatics</i> , 2007, 20, Unit1.17.	25.8	25
90	A survey of orphan enzyme activities. <i>BMC Bioinformatics</i> , 2007, 8, 244.	2.6	36

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91	BioWarehouse: a bioinformatics database warehouse toolkit. BMC Bioinformatics, 2006, 7, 170.	2.6	133
92	The comprehensive updated regulatory network of Escherichia coli K-12. BMC Bioinformatics, 2006, 7, 5.	2.6	63
93	Evidence supporting predicted metabolic pathways for Vibrio cholerae: gene expression data and clinical tests. Nucleic Acids Research, 2006, 34, 2438-2444.	14.5	27
94	Creating Fungal Pathway/Genome Databases Using Pathway Tools. Applied Mycology and Biotechnology, 2006, 6, 209-225.	0.3	0
95	The Pathway Tools cellular overview diagram and Omics Viewer. Nucleic Acids Research, 2006, 34, 3771-3778.	14.5	170
96	The outcomes of pathway database computations depend on pathway ontology. Nucleic Acids Research, 2006, 34, 3687-3697.	14.5	73
97	MetaCyc: a multiorganism database of metabolic pathways and enzymes. Nucleic Acids Research, 2006, 34, D511-D516.	14.5	436
98	The complete genome sequence of Francisella tularensis, the causative agent of tularemia. Nature Genetics, 2005, 37, 153-159.	21.4	436
99	Bioinformatics pathway representations, databases, and algorithms. , 2005, , .		0
100	Querying and computing with BioCyc databases. Bioinformatics, 2005, 21, 3454-3455.	4.1	79
101	MetaCyc and AraCyc. Metabolic Pathway Databases for Plant Research. Plant Physiology, 2005, 138, 27-37.	4.8	227
102	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Research, 2005, 33, 6083-6089.	14.5	570
103	EcoCyc: a comprehensive database resource for Escherichia coli. Nucleic Acids Research, 2004, 33, D334-D337.	14.5	597
104	A Bayesian method for identifying missing enzymes in predicted metabolic pathway databases. BMC Bioinformatics, 2004, 5, 76.	2.6	209
105	Computational Analysis of Plasmodium falciparum Metabolism: Organizing Genomic Information to Facilitate Drug Discovery. Genome Research, 2004, 14, 917-924.	5.5	206
106	MetaCyc: a multiorganism database of metabolic pathways and enzymes. Nucleic Acids Research, 2004, 32, 438D-442.	14.5	250
107	Computational prediction of human metabolic pathways from the complete human genome. Genome Biology, 2004, 6, R2.	9.6	462
108	Call for an enzyme genomics initiative. Genome Biology, 2004, 5, 401.	9.6	67

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109	PseudoCyc, A Pathway-Genome Database for <i>Pseudomonas aeruginosa</i> . Journal of Molecular Microbiology and Biotechnology, 2003, 5, 230-239.	1.0	38
110	Knowledge acquisition, consistency checking and concurrency control for Gene Ontology (GO). Bioinformatics, 2003, 19, 241-248.	4.1	81
111	What Database Management System(s) Should Be Employed in Bioinformatics Applications?. OMICS A Journal of Integrative Biology, 2003, 7, 35-36.	2.0	3
112	AN EVIDENCE ONTOLOGY FOR USE IN PATHWAY/GENOME DATABASES. , 2003, , 190-201.		26
113	The Pathway Tools Software and Its Role in Antimicrobial Drug Discovery. , 2003, , 43-54.		1
114	The Pathway Tools software. Bioinformatics, 2002, 18, S225-S232.	4.1	603
115	The MetaCyc Database. Nucleic Acids Research, 2002, 30, 59-61.	14.5	345
116	The EcoCyc Database. Nucleic Acids Research, 2002, 30, 56-58.	14.5	386
117	EcoCyc: The Resource and the Lessons Learned. , 2002, , 47-62.		7
118	The past, present and future of genome-wide re-annotation. Genome Biology, 2002, 3, comment2001.1.	9.6	86
119	Evaluation of computational metabolic-pathway predictions for Helicobacter pylori. Bioinformatics, 2002, 18, 715-724.	4.1	88
120	Pathway Databases: A Case Study in Computational Symbolic Theories. Science, 2001, 293, 2040-2044.	12.6	200
121	Many Genbank Entries for Complete Microbial Genomes Violate the Genbank Standard. Comparative and Functional Genomics, 2001, 2, 25-27.	2.0	8
122	The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. Science, 2001, 294, 2317-2323.	12.6	741
123	Database verification studies of SWISS-PROT and GenBank. Bioinformatics, 2001, 17, 526-532.	4.1	30
124	Global Properties of the Metabolic Map of Escherichia coli. Genome Research, 2000, 10, 568-576.	5.5	88
125	The EcoCyc and MetaCyc databases. Nucleic Acids Research, 2000, 28, 56-59.	14.5	234
126	An ontology for biological function based on molecular interactions. Bioinformatics, 2000, 16, 269-285.	4.1	164



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127	A Collaborative Environment for Authoring Large Knowledge Bases. <i>Journal of Intelligent Information Systems</i> , 1999, 13, 155-194.	3.9	25
128	Integrated pathway genome databases and their role in drug discovery. <i>Trends in Biotechnology</i> , 1999, 17, 275-281.	9.3	154
129	Metabolic databases. <i>Trends in Biochemical Sciences</i> , 1998, 23, 114-116.	7.5	42
130	Estimation of equilibrium constants using automated group contribution methods. <i>Bioinformatics</i> , 1997, 13, 537-543.	4.1	6
131	EcoCyc: Encyclopedia of Escherichia coli Genes and Metabolism. <i>Nucleic Acids Research</i> , 1997, 25, 43-50.	14.5	46
132	The complete genome sequence of the gastric pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 1997, 388, 539-547.	27.8	3,405
133	Using the EcoCyc Database. , 1997, , 269-280.		3
134	Adapting EcoCyc for use on the World Wide Web. <i>Gene</i> , 1996, 172, GC43-GC50.	2.2	3
135	Integrated Access to Metabolic and Genomic Data. <i>Journal of Computational Biology</i> , 1996, 3, 191-212.	1.6	47
136	Database links are a foundation for interoperability. <i>Trends in Biotechnology</i> , 1996, 14, 273-279.	9.3	48
137	A Strategy for Database Interoperation. <i>Journal of Computational Biology</i> , 1995, 2, 573-586.	1.6	87
138	The Grasper-CL graph management system. <i>Higher-Order and Symbolic Computation</i> , 1994, 7, 251-290.	0.6	5
139	Design Methods for Scientific Hypothesis Formation and Their Application to Molecular Biology. <i>Machine Learning</i> , 1993, 12, 89-116.	5.4	7
140	A knowledge base of the chemical compounds of intermediary metabolism. <i>Bioinformatics</i> , 1992, 8, 347-357.	4.1	9