Peter D Karp

List of Publications by Year
in descending order

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	The complete genome sequence of the gastric pathogen Helicobacter pylori. Nature, 1997, 388, 539-547.	27.8	3,405
2	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
3	A genomeâ€scale metabolic reconstruction for Escherichia coli Kâ€12 MG1655 that accounts for 1260 ORFs and thermodynamic information. Molecular Systems Biology, 2007, 3, 121.	7.2	1,234
4	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
5	The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. Science, 2001, 294, 2317-2323.	12.6	741
6	The MetaCyc database of metabolic pathways and enzymes. Nucleic Acids Research, 2018, 46, D633-D639.	14.5	658
7	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
8	The MetaCyc database of metabolic pathways and enzymes - a 2019 update. Nucleic Acids Research, 2020, 48, D445-D453.	14.5	606
9	The Pathway Tools software. Bioinformatics, 2002, 18, S225-S232.	4.1	603
10	The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. Nucleic Acids Research, 2007, 36, D623-D631.	14.5	600
11	EcoCyc: a comprehensive database resource for Escherichia coli. Nucleic Acids Research, 2004, 33, D334-D337.	14.5	597
12	The BioCyc collection of microbial genomes and metabolic pathways. Briefings in Bioinformatics, 2019, 20, 1085-1093.	6.5	582
13	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Research, 2005, 33, 6083-6089.	14.5	570
14	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
15	Pathway Tools version 13.0: integrated software for pathway/genome informatics and systems biology. Briefings in Bioinformatics, 2010, 11, 40-79.	6.5	551
16	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. Nucleic Acids Research, 2017, 45, D543-D550.	14.5	541
17	EcoCyc: fusing model organism databases with systems biology. Nucleic Acids Research, 2013, 41, D605-D612.	14.5	505
18	Computational prediction of human metabolic pathways from the complete human genome. Genome Biology, 2004, 6, R2.	9.6	462

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19	EcoCyc: a comprehensive database of Escherichia coli biology. Nucleic Acids Research, 2011, 39, D583-D590.	14.5	444
20	The complete genome sequence of Francisella tularensis, the causative agent of tularemia. Nature Genetics, 2005, 37, 153-159.	21.4	436
21	MetaCyc: a multiorganism database of metabolic pathways and enzymes. Nucleic Acids Research, 2006, 34, D511-D516.	14.5	436
22	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Research, 2010, 38, D473-D479.	14.5	403
23	The EcoCyc Database. Nucleic Acids Research, 2002, 30, 56-58.	14.5	386
24	The MetaCyc Database. Nucleic Acids Research, 2002, 30, 59-61.	14.5	345
25	EcoCyc: A comprehensive view of Escherichia coli biology. Nucleic Acids Research, 2009, 37, D464-D470.	14.5	320
26	MetaCyc: a multiorganism database of metabolic pathways and enzymes. Nucleic Acids Research, 2004, 32, 438D-442.	14.5	250
27	Pathway Tools version 19.0 update: software for pathway/genome informatics and systems biology. Briefings in Bioinformatics, 2016, 17, 877-890.	6.5	250
28	The EcoCyc and MetaCyc databases. Nucleic Acids Research, 2000, 28, 56-59.	14.5	234
29	MetaCyc and AraCyc. Metabolic Pathway Databases for Plant Research. Plant Physiology, 2005, 138, 27-37.	4.8	227
30	A Bayesian method for identifying missing enzymes in predicted metabolic pathway databases. BMC Bioinformatics, 2004, 5, 76.	2.6	209
31	Computational Analysis of Plasmodium falciparum Metabolism: Organizing Genomic Information to Facilitate Drug Discovery. Genome Research, 2004, 14, 917-924.	5.5	206
32	Pathway Databases: A Case Study in Computational Symbolic Theories. Science, 2001, 293, 2040-2044.	12.6	200
33	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
34	The Pathway Tools cellular overview diagram and Omics Viewer. Nucleic Acids Research, 2006, 34, 3771-3778.	14.5	170
35	Multidimensional annotation of the Escherichia coli K-12 genome. Nucleic Acids Research, 2007, 35, 7577-7590.	14.5	168
36	An ontology for biological function based on molecular interactions. Bioinformatics, 2000, 16, 269-285.	4.1	164

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37	Pathway size matters: the influence of pathway granularity on over-representation (enrichment) Tj ETQq1 1 0.784314 rgBT /Overlock	2.8	158
38	Integrated pathway–genome databases and their role in drug discovery. Trends in Biotechnology, 1999, 17, 275-281.	9.3	154
39	BioWarehouse: a bioinformatics database warehouse toolkit. BMC Bioinformatics, 2006, 7, 170.	2.6	133
40	Machine learning methods for metabolic pathway prediction. BMC Bioinformatics, 2010, 11, 15.	2.6	131
41	A systematic comparison of the MetaCyc and KEGG pathway databases. BMC Bioinformatics, 2013, 14, 112.	2.6	123
42	The EcoCyc Database in 2021. Frontiers in Microbiology, 2021, 12, 711077.	3.5	122
43	Pathway Tools version 23.0 update: software for pathway/genome informatics and systems biology. Briefings in Bioinformatics, 2021, 22, 109-126.	6.5	117
44	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 Â. Plant Physiology, 2010, 153, 1479-1491.	4.8	115
45	Plant Metabolic Network 15: A resource of genome–wide metabolism databases for 126 plants and algae. Journal of Integrative Plant Biology, 2021, 63, 1888-1905.	8.5	114
46	The Pathway Tools Pathway Prediction Algorithm. Standards in Genomic Sciences, 2011, 5, 424-429.	1.5	109
47	Simultaneous cross-evaluation of heterogeneous <i>E. coli</i> datasets via mechanistic simulation. Science, 2020, 369, .	12.6	105
48	The EcoCyc Database. EcoSal Plus, 2014, 6, .	5.4	101
49	Metabolomics Reveals Amino Acids Contribute to Variation in Response to Simvastatin Treatment. PLoS ONE, 2012, 7, e38386.	2.5	90
50	Global Properties of the Metabolic Map of Escherichia coli. Genome Research, 2000, 10, 568-576.	5.5	88
51	Evaluation of computational metabolic-pathway predictions for Helicobacter pylori. Bioinformatics, 2002, 18, 715-724.	4.1	88
52	A Strategy for Database Interoperation. Journal of Computational Biology, 1995, 2, 573-586.	1.6	87
53	The past, present and future of genome-wide re-annotation. Genome Biology, 2002, 3, comment2001.1.	9.6	86
54	Construction and completion of flux balance models from pathway databases. Bioinformatics, 2012, 28, 388-396.	4.1	86

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55	The challenge of constructing, classifying, and representing metabolic pathways. FEMS Microbiology Letters, 2013, 345, 85-93.	1.8	82
56	Knowledge acquisition, consistency checking and concurrency control for Gene Ontology (GO). Bioinformatics, 2003, 19, 241-248.	4.1	81
57	Querying and computing with BioCyc databases. Bioinformatics, 2005, 21, 3454-3455.	4.1	79
58	The EcoCyc Database. EcoSal Plus, 2018, 8, .	5.4	75
59	The outcomes of pathway database computations depend on pathway ontology. Nucleic Acids Research, 2006, 34, 3687-3697.	14.5	73
60	A survey of metabolic databases emphasizing the MetaCyc family. Archives of Toxicology, 2011, 85, 1015-1033.	4.2	72
61	Call for an enzyme genomics initiative. Genome Biology, 2004, 5, 401.	9.6	67
62	Accurate Atom-Mapping Computation for Biochemical Reactions. Journal of Chemical Information and Modeling, 2012, 52, 2970-2982.	5.4	67
63	The comprehensive updated regulatory network of Escherichia coli K-12. BMC Bioinformatics, 2006, 7, 5.	2.6	63
64	The Time Is Right to Focus on Model Organism Metabolomes. Metabolites, 2016, 6, 8.	2.9	63
65	The Omics Dashboard for interactive exploration of gene-expression data. Nucleic Acids Research, 2017, 45, 12113-12124.	14.5	57
66	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	5.6	54
67	Metabolic pathways for the whole community. BMC Genomics, 2014, 15, 619.	2.8	50
68	Database links are a foundation for interoperability. Trends in Biotechnology, 1996, 14, 273-279.	9.3	48
69	Integrated Access to Metabolic and Genomic Data. Journal of Computational Biology, 1996, 3, 191-212.	1.6	47
70	Optimal metabolic route search based on atom mappings. Bioinformatics, 2014, 30, 2043-2050.	4.1	47
71	EcoCyc: Enyclopedia of Escherichia coli Genes and Metabolism. Nucleic Acids Research, 1997, 25, 43-50.	14.5	46
72	How much does curation cost?. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw110.	3.0	43

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73	Metabolic databases. Trends in Biochemical Sciences, 1998, 23, 114-116.	7.5	42
74	A genome-scale metabolic flux model of Escherichia coli Kâ€"12 derived from the EcoCyc database. BMC Systems Biology, 2014, 8, 79.	3.0	42
75	PseudoCyc, A Pathway-Genome Database for <i>Pseudomonas aeruginosa</i>. Journal of Molecular Microbiology and Biotechnology, 2003, 5, 230-239.	1.0	38
76	A survey of orphan enzyme activities. BMC Bioinformatics, 2007, 8, 244.	2.6	36
77	Annotation-based inference of transporter function. Bioinformatics, 2008, 24, i259-i267.	4.1	36
78	How accurate is automated gap filling of metabolic models?. BMC Systems Biology, 2018, 12, 73.	3.0	33
79	Database verification studies of SWISS-PROT and GenBank. Bioinformatics, 2001, 17, 526-532.	4.1	30
80	Web-based metabolic network visualization with a zooming user interface. BMC Bioinformatics, 2011, 12, 176.	2.6	30
81	Beyond the genome (BTG) is a (PGDB) pathway genome database: HumanCyc. Genome Biology, 2010, 11, O12.	9.6	28
82	Evidence supporting predicted metabolic pathways for Vibrio cholerae: gene expression data and clinical tests. Nucleic Acids Research, 2006, 34, 2438-2444.	14.5	27
83	Browsing Metabolic and Regulatory Networks with BioCyc. Methods in Molecular Biology, 2012, 804, 197-216.	0.9	27
84	Curation accuracy of model organism databases. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau058-bau058.	3.0	27
85	A systematic study of genome context methods: calibration, normalization and combination. BMC Bioinformatics, 2010, 11, 493.	2.6	26
86	Computational Metabolomics Operations at BioCyc.org. Metabolites, 2015, 5, 291-310.	2.9	26
87	AN EVIDENCE ONTOLOGY FOR USE IN PATHWAY/GENOME DATABASES. , 2003, , 190-201.		26
88	A Collaborative Environment for Authoring Large Knowledge Bases. Journal of Intelligent Information Systems, 1999, 13, 155-194.	3.9	25
89	Using the MetaCyc Pathway Database and the BioCyc Database Collection. Current Protocols in Bioinformatics, 2007, 20, Unit1.17.	25.8	25
90	PortEco: a resource for exploring bacterial biology through high-throughput data and analysis tools. Nucleic Acids Research, 2014, 42, D677-D684.	14.5	25

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91	Using genome-context data to identify specific types of functional associations in pathway/genome databases. Bioinformatics, 2007, 23, i205-i211.	4.1	24
92	Dead End Metabolites - Defining the Known Unknowns of the E. coli Metabolic Network. PLoS ONE, 2013, 8, e75210.	2.5	23
93	Can we replace curation with information extraction software?. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw150.	3.0	23
94	A Comparison of Microbial Genome Web Portals. Frontiers in Microbiology, 2019, 10, 208.	3.5	22
95	Gene Dispensability in Escherichia coli Grown in Thirty Different Carbon Environments. MBio, 2020, 11, .	4.1	21
96	Groups: knowledge spreadsheets for symbolic biocomputing. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat061.	3.0	19
97	Pathway collages: personalized multi-pathway diagrams. BMC Bioinformatics, 2016, 17, 529.	2.6	19
98	What we can learn about Escherichia coli through application of Gene Ontology. Trends in Microbiology, 2009, 17, 269-278.	7.7	16
99	Evaluation of reaction gap-filling accuracy by randomization. BMC Bioinformatics, 2018, 19, 53.	2.6	14
100	Crowd-sourcing and author submission as alternatives to professional curation. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw149.	3.0	14
101	Regulatory network operations in the Pathway Tools software. BMC Bioinformatics, 2012, 13, 243.	2.6	13
102	Computing minimal nutrient sets from metabolic networks via linear constraint solving. BMC Bioinformatics, 2013, 14, 114.	2.6	12
103	Update notifications for the BioCyc collection of databases. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	11
104	An advanced web query interface for biological databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq006-baq006.	3.0	10
105	A knowledge base of the chemical compounds of intermediary metabolism. Bioinformatics, 1992, 8, 347-357.	4.1	9
106	Data Mining in the MetaCyc Family of Pathway Databases. Methods in Molecular Biology, 2013, 939, 183-200.	0.9	9
107	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
108	Pathway Tools Visualization of Organism-Scale Metabolic Networks. Metabolites, 2021, 11, 64.	2.9	9

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109	The BioCyc Metabolic Network Explorer. BMC Bioinformatics, 2021, 22, 208.	2.6	9
110	Many Genbank Entries for Complete Microbial Genomes Violate the Genbank Standard. Comparative and Functional Genomics, 2001, 2, 25-27.	2.0	8
111	Design Methods for Scientific Hypothesis Formation and Their Application to Molecular Biology. Machine Learning, 1993, 12, 89-116.	5.4	7
112	EcoCyc: The Resource and the Lessons Learned. , 2002, , 47-62.		7
113	Estimation of equilibrium constants using automated group contribution methods. Bioinformatics, 1997, 13, 537-543.	4.1	6
114	Discovering novel subsystems using comparative genomics. Bioinformatics, 2011, 27, 2478-2485.	4.1	6
115	The Grasper-CL graph management system. Higher-Order and Symbolic Computation, 1994, 7, 251-290.	0.6	5
116	The MultiOmics Explainer: explaining omics results in the context of a pathway/genome database. BMC Bioinformatics, 2019, 20, 399.	2.6	5
117	Metabolic route computation in organism communities. Microbiome, 2019, 7, 89.	11.1	4
118	Pathway Tools Management of Pathway/Genome Data for Microbial Communities. Frontiers in Bioinformatics, 2022, 2, .	2.1	4
119	Adapting EcoCyc for use on the World Wide Web. Gene, 1996, 172, GC43-GC50.	2.2	3
120	What Database Management System(s) Should Be Employed in Bioinformatics Applications?. OMICS A Journal of Integrative Biology, 2003, 7, 35-36.	2.0	3
121	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
122	How the strengths of Lisp-family languages facilitate building complex and flexible bioinformatics applications. Briefings in Bioinformatics, 2016, 19, bbw130.	6.5	3
123	Using Pathway Covering to Explore Connections among Metabolites. Metabolites, 2019, 9, 88.	2.9	3
124	Taxonomic weighting improves the accuracy of a gap-filling algorithm for metabolic models. Bioinformatics, 2020, 36, 1823-1830.	4.1	3
125	Leveraging Curation Among Escherichia coli Pathway/Genome Databases Using Ortholog-Based Annotation Propagation. Frontiers in Microbiology, 2021, 12, 614355.	3.5	3
126	Using the EcoCyc Database. , 1997, , 269-280.		3

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127	Metabolic Modeling with MetaFlux. Methods in Molecular Biology, 2022, 2349, 259-289.	0.9	3
128	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. PLoS Computational Biology, 2015, 11, e1004087.	3.2	2
129	Using cellular network diagrams to interpret large-scale datasets: past progress and future challenges. Proceedings of SPIE, 2011, , .	0.8	1
130	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
131	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. F1000Research, 2015, 4, 12.	1.6	1
132	The Pathway Tools Software and Its Role in Antimicrobial Drug Discovery. , 2003, , 43-54.		1
133	BioWarehouse: Relational Integration of Eleven Bioinformatics Databases and Formats. Lecture Notes in Computer Science, 2008, , 5-7.	1.3	1
134	Bioinformatics pathway representations, databases, and algorithms. , 2005, , .		0
135	Creating Fungal Pathway/Genome Databases Using Pathway Tools. Applied Mycology and Biotechnology, 2006, 6, 209-225.	0.3	0
136	Changes to NIH Grant System May Backfire. Science, 2008, 322, 1187-1188.	12.6	0
137	Representation and inference of cellular architecture for metabolic reconstruction and modeling. Bioinformatics, 2016, 32, 1074-1079.	4.1	0
138	The Multiple Scientific Disciplines Served by EcoCyc. , 2009, , 99-112.		0
139	Computing Metabolic Routes in the Human Microbiome. FASEB Journal, 2018, 32, .	0.5	0
140	Computing Metabolic Routes in the Human Microbiome. FASEB Journal, 2018, 32, lb121.	0.5	0