

Mario Latendresse

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

8,912
citations

257450

24
h-index

377865

34
g-index

34
all docs

34
docs citations

34
times ranked

12667
citing authors

#	ARTICLE	IF	CITATIONS
1	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2016, 44, D471-D480.	14.5	1,788
2	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases. <i>Nucleic Acids Research</i> , 2014, 42, D459-D471.	14.5	1,023
3	The MetaCyc database of metabolic pathways and enzymes. <i>Nucleic Acids Research</i> , 2018, 46, D633-D639.	14.5	658
4	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
5	The BioCyc collection of microbial genomes and metabolic pathways. <i>Briefings in Bioinformatics</i> , 2019, 20, 1085-1093.	6.5	582
6	The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. <i>Nucleic Acids Research</i> , 2012, 40, D742-D753.	14.5	561
7	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
8	The EcoCyc database: reflecting new knowledge about <i>Escherichia coli</i> K-12. <i>Nucleic Acids Research</i> , 2017, 45, D543-D550.	14.5	541
9	EcoCyc: fusing model organism databases with systems biology. <i>Nucleic Acids Research</i> , 2013, 41, D605-D612.	14.5	505
10	EcoCyc: a comprehensive database of <i>Escherichia coli</i> biology. <i>Nucleic Acids Research</i> , 2011, 39, D583-D590.	14.5	444
11	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
12	Pathway Tools version 19.0 update: software for pathway/genome informatics and systems biology. <i>Briefings in Bioinformatics</i> , 2016, 17, 877-890.	6.5	250
13	Multidimensional annotation of the <i>Escherichia coli</i> K-12 genome. <i>Nucleic Acids Research</i> , 2007, 35, 7577-7590.	14.5	168
14	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
15	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
16	The Pathway Tools Pathway Prediction Algorithm. <i>Standards in Genomic Sciences</i> , 2011, 5, 424-429.	1.5	109
17	Construction and completion of flux balance models from pathway databases. <i>Bioinformatics</i> , 2012, 28, 388-396.	4.1	86
18	The EcoCyc Database. <i>EcoSal Plus</i> , 2018, 8, .	5.4	75

#	ARTICLE	IF	CITATIONS
19	Accurate Atom-Mapping Computation for Biochemical Reactions. Journal of Chemical Information and Modeling, 2012, 52, 2970-2982.	5.4	67
20	Optimal metabolic route search based on atom mappings. Bioinformatics, 2014, 30, 2043-2050.	4.1	47
21	Efficiently gap-filling reaction networks. BMC Bioinformatics, 2014, 15, 225.	2.6	33
22	How accurate is automated gap filling of metabolic models?. BMC Systems Biology, 2018, 12, 73.	3.0	33
23	Web-based metabolic network visualization with a zooming user interface. BMC Bioinformatics, 2011, 12, 176.	2.6	30
24	Browsing Metabolic and Regulatory Networks with BioCyc. Methods in Molecular Biology, 2012, 804, 197-216.	0.9	27
25	Computational Metabolomics Operations at BioCyc.org. Metabolites, 2015, 5, 291-310.	2.9	26
26	Masquerade Detection via Customized Grammars. Lecture Notes in Computer Science, 2005, , 141-159.	1.3	21
27	Evaluation of reaction gap-filling accuracy by randomization. BMC Bioinformatics, 2018, 19, 53.	2.6	14
28	Regulatory network operations in the Pathway Tools software. BMC Bioinformatics, 2012, 13, 243.	2.6	13
29	An advanced web query interface for biological databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq006-baq006.	3.0	10
30	Generation of fast interpreters for Huffman compressed bytecode. Science of Computer Programming, 2005, 57, 295-317.	1.9	4
31	Metabolic route computation in organism communities. Microbiome, 2019, 7, 89.	11.1	4
32	Using Pathway Covering to Explore Connections among Metabolites. Metabolites, 2019, 9, 88.	2.9	3
33	Metabolic Modeling with MetaFlux. Methods in Molecular Biology, 2022, 2349, 259-289.	0.9	3
34	Using cellular network diagrams to interpret large-scale datasets: past progress and future challenges. Proceedings of SPIE, 2011, , .	0.8	1