

Alex Gavryushkin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/622030/publications.pdf>

Version: 2024-02-01

24
papers

701
citations

1163117

8
h-index

752698

20
g-index

38
all docs

38
docs citations

38
times ranked

974
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbiome interactions shape host fitness. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11951-E11960.	7.1	426
2	The space of ultrametric phylogenetic trees. Journal of Theoretical Biology, 2016, 403, 197-208.	1.7	32
3	Inferring genetic interactions from comparative fitness data. ELife, 2017, 6, .	6.0	32
4	How well can the exponential-growth coalescent approximate constant-rate birth-death population dynamics?. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150420.	2.6	29
5	Reducibilities among equivalence relations induced by recursively enumerable structures. Theoretical Computer Science, 2016, 612, 137-152.	0.9	20
6	Graphs realised by r.e. equivalence relations. Annals of Pure and Applied Logic, 2014, 165, 1263-1290.	0.5	18
7	Toward Analysis of Structural Changes Common for Alkaline Carbonates and Binary Compounds: Prediction of High-Pressure Structures of Li_2CO_3 , Na_2CO_3 , and K_2CO_3 . Crystal Growth and Design, 2016, 16, 5612-5617.	3.0	15
8	The combinatorics of discrete time-trees: theory and open problems. Journal of Mathematical Biology, 2018, 76, 1101-1121.	1.9	14
9	Computing nearest neighbour interchange distances between ranked phylogenetic trees. Journal of Mathematical Biology, 2021, 82, 8.	1.9	11
10	Stability of B-type FeS at Earth's inner core pressures. Geophysical Research Letters, 2016, 43, 8435-8440.	4.0	10
11	The geometry of partial fitness orders and an efficient method for detecting genetic interactions. Journal of Mathematical Biology, 2018, 77, 951-970.	1.9	8
12	Sustained software development, not number of citations or journal choice, is indicative of accurate bioinformatic software. Genome Biology, 2022, 23, 56.	8.8	8
13	Learning epistatic gene interactions from perturbation screens. PLoS ONE, 2021, 16, e0254491.	2.5	5
14	Accounting for Errors in Data Improves Divergence Time Estimates in Single-cell Cancer Evolution. Molecular Biology and Evolution, 2022, 39, .	8.9	5
15	Spectra of computable models for Ehrenfeucht theories. Algebra and Logic, 2007, 46, 149-157.	0.3	4
16	Tiling algebra for constraint-based layout editing. Journal of Logical and Algebraic Methods in Programming, 2017, 89, 67-94.	0.5	4
17	Discrete coalescent trees. Journal of Mathematical Biology, 2021, 83, 60.	1.9	4
18	Unbiased crystal structure prediction of NiSi under high pressure. Journal of Applied Crystallography, 2015, 48, 906-908.	4.5	3

#	ARTICLE	IF	CITATIONS
19	Dynamic Algorithms for Multimachine Interval Scheduling Through Analysis of Idle Intervals. <i>Algorithmica</i> , 2016, 76, 1160-1180.	1.3	2
20	Universality for left-computably enumerable metric spaces. <i>Lobachevskii Journal of Mathematics</i> , 2014, 35, 292-294.	0.9	1
21	Microbiome interactions shape host fitness. , 0, , .		1
22	Tuberous sclerosis complex: a complex case.. <i>Cold Spring Harbor Molecular Case Studies</i> , 2022, 8, .	1.0	1
23	Decidable models of small theories. <i>Lobachevskii Journal of Mathematics</i> , 2015, 36, 446-449.	0.9	0
24	THE SPACE OF SAMPLED ANCESTOR TREES. , 2016, , .		0