

Mile Sikic

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6400742/publications.pdf>

Version: 2024-02-01

30
papers

5,148
citations

471509

17
h-index

610901

24
g-index

41
all docs

41
docs citations

41
times ranked

10366
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct identification of A-to-I editing sites with nanopore native RNA sequencing. <i>Nature Methods</i> , 2022, 19, 833-844.	19.0	35
2	Time- and memory-efficient genome assembly with Raven. <i>Nature Computational Science</i> , 2021, 1, 332-336.	8.0	173
3	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. <i>Nature Biotechnology</i> , 2019, 37, 937-944.	17.5	216
4	Disentangling Sources of Influence in Online Social Networks. <i>IEEE Access</i> , 2019, 7, 131692-131704.	4.2	2
5	Yet another de novo genome assembler. , 2019, , .		18
6	Evaluation of tools for long read RNA-seq splice-aware alignment. <i>Bioinformatics</i> , 2018, 34, 748-754.	4.1	78
7	Fast and accurate de novo genome assembly from long uncorrected reads. <i>Genome Research</i> , 2017, 27, 737-746.	5.5	2,071
8	Unsupervised Learning of Sequencing Read Types. , 2017, , .		2
9	Edlib: a C/C++ library for fast, exact sequence alignment using edit distance. <i>Bioinformatics</i> , 2017, 33, 1394-1395.	4.1	159
10	Fast and sensitive mapping of nanopore sequencing reads with GraphMap. <i>Nature Communications</i> , 2016, 7, 11307.	12.8	331
11	Evaluation of hybrid and non-hybrid methods for <i>de novo</i> assembly of nanopore reads. <i>Bioinformatics</i> , 2016, 32, 2582-2589.	4.1	53
12	SWORD—a highly efficient protein database search. <i>Bioinformatics</i> , 2016, 32, i680-i684.	4.1	21
13	SIFT missense predictions for genomes. <i>Nature Protocols</i> , 2016, 11, 1-9.	12.0	1,053
14	SW#db: GPU-Accelerated Exact Sequence Similarity Database Search. <i>PLoS ONE</i> , 2015, 10, e0145857.	2.5	7
15	Some new results on assessment of Q-gram filter efficiency. , 2015, , .		0
16	Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations. <i>Physical Review Letters</i> , 2015, 114, 248701.	7.8	76
17	ExoLocator—an online view into genetic makeup of vertebrate proteins. <i>Nucleic Acids Research</i> , 2014, 42, D879-D881.	14.5	8
18	Statistical Inference Framework for Source Detection of Contagion Processes on Arbitrary Network Structures. , 2014, , .		12

#	ARTICLE	IF	CITATIONS
19	FastSIR algorithm: A fast algorithm for the simulation of the epidemic spread in large networks by using the susceptibleâ€“infectedâ€“recovered compartment model. Information Sciences, 2013, 239, 226-240.	6.9	17
20	Epidemic centrality â€” is there an underestimated epidemic impact of network peripheral nodes?. European Physical Journal B, 2013, 86, 1.	1.5	26
21	SW#â€“GPU-enabled exact alignments on genome scale. Bioinformatics, 2013, 29, 2494-2495.	4.1	50
22	BioMe: biologically relevant metals. Nucleic Acids Research, 2012, 40, W352-W357.	14.5	30
23	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	6.4	102
24	Prediction of Interacting Protein Residues Using Sequence and Structure Data. Methods in Molecular Biology, 2012, 819, 233-251.	0.9	3
25	Phase diagram of epidemic spreading â€” unimodal vs. bimodal probability distributions. Physica A: Statistical Mechanics and Its Applications, 2011, 390, 65-76.	2.6	7
26	Prediction of Proteinâ€“Protein Interaction Sites in Sequences and 3D Structures by Random Forests. PLoS Computational Biology, 2009, 5, e1000278.	3.2	140
27	PSAIA â€” Protein Structure and Interaction Analyzer. BMC Structural Biology, 2008, 8, 21.	2.3	152
28	Metals in proteins: correlation between the metal-ion type, coordination number and the amino-acid residues involved in the coordination. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 257-263.	2.5	182
29	Comparison of the RADIUS and Diameter protocols. , 2008, , .		6
30	Protecting and controlling virtual LANs by Linux router-firewall. , 0, , .		0