Mile Sikic

List of Publications by Year
in descending order

30 papers	5,148 citations	17 h-index (471509)
41 all docs	41 docs citations	41 times ranked

24 g-index (610901)
10366 citing authors

#	Article	IF	Citations
1	Fast and accurate de novo genome assembly from long uncorrected reads. Genome Research, 2017, 27, 737-746.	5.5	2,071
2	SIFT missense predictions for genomes. Nature Protocols, 2016, 11, 1-9.	12.0	1,053
3	Fast and sensitive mapping of nanopore sequencing reads with GraphMap. Nature Communications, 2016, 7, 11307.	12.8	331
4	Hybrid metagenomic assembly enables high-resolution analysis of resistance determinants and mobile elements in human microbiomes. Nature Biotechnology, 2019, 37, 937-944.	17.5	216
5	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
6	Time- and memory-efficient genome assembly with Raven. Nature Computational Science, 2021, 1, 332-336.	8.0	173
7	Edlib: a C/C‰++ library for fast, exact sequence alignment using edit distance. Bioinformatics, 2017, 33, 1394-1395.	4.1	159
8	PSAIA â€" Protein Structure and Interaction Analyzer. BMC Structural Biology, 2008, 8, 21.	2.3	152
9	Prediction of Proteinâ€"Protein Interaction Sites in Sequences and 3D Structures by Random Forests. PLoS Computational Biology, 2009, 5, e1000278.	3.2	140
10	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	6.4	102
11	Evaluation of tools for long read RNA-seq splice-aware alignment. Bioinformatics, 2018, 34, 748-754.	4.1	78
12	Identification of Patient Zero in Static and Temporal Networks: Robustness and Limitations. Physical Review Letters, 2015, 114, 248701.	7.8	76
13	Evaluation of hybrid and non-hybrid methods for <i>de novo</i> assembly of nanopore reads. Bioinformatics, 2016, 32, 2582-2589.	4.1	53
14	SW#â€"GPU-enabled exact alignments on genome scale. Bioinformatics, 2013, 29, 2494-2495.	4.1	50
15	Direct identification of A-to-I editing sites with nanopore native RNA sequencing. Nature Methods, 2022, 19, 833-844.	19.0	35
16	BioMe: biologically relevant metals. Nucleic Acids Research, 2012, 40, W352-W357.	14.5	30
17	Epidemic centrality â€" is there an underestimated epidemic impact of network peripheral nodes?. European Physical Journal B, 2013, 86, 1.	1.5	26
18	SWORDâ€"a highly efficient protein database search. Bioinformatics, 2016, 32, i680-i684.	4.1	21

#	ARTICLE	IF	CITATIONS
19	Yet another de novo genome assembler. , 2019, , .		18
20	FastSIR algorithm: A fast algorithm for the simulation of the epidemic spread in large networks by using the susceptible–infected–recovered compartment model. Information Sciences, 2013, 239, 226-240.	6.9	17
21	Statistical Inference Framework for Source Detection of Contagion Processes on Arbitrary Network Structures. , 2014, , .		12
22	ExoLocator—an online view into genetic makeup of vertebrate proteins. Nucleic Acids Research, 2014, 42, D879-D881.	14.5	8
23	Phase diagram of epidemic spreading – unimodal vs. bimodal probability distributions. Physica A: Statistical Mechanics and Its Applications, 2011, 390, 65-76.	2.6	7
24	SW#db: GPU-Accelerated Exact Sequence Similarity Database Search. PLoS ONE, 2015, 10, e0145857.	2.5	7
25	Comparison of the RADIUS and Diameter protocols. , 2008, , .		6
26	Prediction of Interacting Protein Residues Using Sequence and Structure Data. Methods in Molecular Biology, 2012, 819, 233-251.	0.9	3
27	Unsupervised Learning of Sequencing Read Types. , 2017, , .		2
28	Disentangling Sources of Influence in Online Social Networks. IEEE Access, 2019, 7, 131692-131704.	4.2	2
29	Protecting and controlling virtual LANs by Linux router-firewall. , 0, , .		0
30	Some new results on assessment of Q-gram filter efficiency. , 2015, , .		0