

Sergey Knyazev

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

405
citations

840776

11
h-index

839539

18
g-index

30
all docs

30
docs citations

30
times ranked

508
citing authors

#	ARTICLE	IF	CITATIONS
1	Correction for Rando et al., "Pathogenesis, Symptomatology, and Transmission of SARS-CoV-2 through Analysis of Viral Genomics and Structure". <i>MSystems</i> , 2022, , e0144721.	3.8	2
2	Unlocking capacities of genomics for the COVID-19 response and future pandemics. <i>Nature Methods</i> , 2022, 19, 374-380.	19.0	35
3	Epidemiological data analysis of viral quasispecies in the next-generation sequencing era. <i>Briefings in Bioinformatics</i> , 2021, 22, 96-108.	6.5	54
4	Clustering Based Identification of SARS-CoV-2 Subtypes. <i>Lecture Notes in Computer Science</i> , 2021, , 127-141.	1.3	9
5	Molecular Epidemiological Analysis of the Origin and Transmission Dynamics of the HIV-1 CRF01_AE Sub-Epidemic in Bulgaria. <i>Viruses</i> , 2021, 13, 116.	3.3	7
6	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. <i>Nucleic Acids Research</i> , 2021, 49, e102-e102.	14.5	36
7	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.	8.8	51
8	Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. <i>Journal of Computational Biology</i> , 2021, 28, 842-855.	1.6	2
9	MicrobeTrace: Retooling molecular epidemiology for rapid public health response. <i>PLoS Computational Biology</i> , 2021, 17, e1009300.	3.2	25
10	From Alpha to Zeta: Identifying Variants and Subtypes of SARS-CoV-2 Via Clustering. <i>Journal of Computational Biology</i> , 2021, 28, 1113-1129.	1.6	14
11	Scalable Reconstruction of SARS-CoV-2 Phylogeny with Recurrent Mutations. <i>Journal of Computational Biology</i> , 2021, 28, 1130-1141.	1.6	2
12	Using earth mover's distance for viral outbreak investigations. <i>BMC Genomics</i> , 2020, 21, 582.	2.8	12
13	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , 2020, 21, 71.	8.8	26
14	Molecular Epidemiology of the HIV-1 Subtype B Sub-Epidemic in Bulgaria. <i>Viruses</i> , 2020, 12, 441.	3.3	6
15	Benchmarking of computational error-correction methods for next-generation sequencing data. , 2020, , .		0
16	Repeat-aware evaluation of scaffolding tools. <i>Bioinformatics</i> , 2018, 34, 2530-2537.	4.1	6
17	QUENTIN: reconstruction of disease transmissions from viral quasispecies genomic data. <i>Bioinformatics</i> , 2018, 34, 163-170.	4.1	54
18	Metabolic Analysis of Metatranscriptomic Data from Planktonic Communities. <i>Lecture Notes in Computer Science</i> , 2017, , 396-402.	1.3	1

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19	Inference of genetic relatedness between viral quasispecies from sequencing data. BMC Genomics, 2017, 18, 918.	2.8	26
20	A New Approach for Modeling of Conformational Changes of Multi Chain Proteins. Procedia Computer Science, 2016, 101, 58-67.	2.0	0
21	Prediction of protein conformational mobility with validation using small-angle X-ray scattering. Biophysics (Russian Federation), 2015, 60, 886-892.	0.7	0
22	Modeling conformational redox switch modulation of human succinic semialdehyde dehydrogenase. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2217-2229.	2.6	13
23	Coarse-grained model of protein interaction for bio-inspired nano-communication. , 2014, , .		2
24	Protein Conformation Motion Modeling Using Sep-CMA-ES. , 2014, , .		0