

Anton I Korobeynikov

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

9,076
citations

172457

29
h-index

223800

46
g-index

61
all docs

61
docs citations

61
times ranked

12502
citing authors

#	ARTICLE	IF	CITATIONS
1	The lineage of coronavirus SARS-CoV-2 of Russian origin: Genetic characteristics and correlations with clinical parameters and severity of coronavirus infection. <i>Sibirskij Åžurnal Kliničeskoj I Åšperimental'noj Mediciny</i> , 2022, 36, 132-143.	0.4	1
2	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	17.5	99
3	Petabase-scale sequence alignment catalyses viral discovery. <i>Nature</i> , 2022, 602, 142-147.	27.8	213
4	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
5	Metagenomic Data Assembly â€“ The Way of Decoding Unknown Microorganisms. <i>Frontiers in Microbiology</i> , 2021, 12, 613791.	3.5	67
6	coronaSPAdes: from biosynthetic gene clusters to RNA viral assemblies. <i>Bioinformatics</i> , 2021, 38, 1-8.	4.1	30
7	Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. <i>Metabolites</i> , 2021, 11, 693.	2.9	11
8	Graph-Based Approaches Significantly Improve the Recovery of Antibiotic Resistance Genes From Complex Metagenomic Datasets. <i>Frontiers in Microbiology</i> , 2021, 12, 714836.	3.5	7
9	Hi-C Metagenomics in the ICU: Exploring Clinically Relevant Features of Gut Microbiome in Chronically Critically Ill Patients. <i>Frontiers in Microbiology</i> , 2021, 12, 770323.	3.5	12
10	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	14.5	296
11	SPAligner: alignment of long diverged molecular sequences to assembly graphs. <i>BMC Bioinformatics</i> , 2020, 21, 306.	2.6	13
12	CDSnake: Snakemake pipeline for retrieval of annotated OTUs from paired-end reads using CD-HIT utilities. <i>BMC Bioinformatics</i> , 2020, 21, 303.	2.6	2
13	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e102.	25.8	1,113
14	Sequence Analysis. , 2019, , 292-322.		8
15	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019, 9, 600-608.e4.	6.2	46
16	PathRacer: Racing Profile HMM Paths on Assembly Graph. <i>Lecture Notes in Computer Science</i> , 2019, , 80-94.	1.3	10
17	BiosyntheticSPAdes: reconstructing biosynthetic gene clusters from assembly graphs. <i>Genome Research</i> , 2019, 29, 1352-1362.	5.5	55
18	lonHammer: Homopolymer-Space Hamming Clustering for IonTorrent Read Error Correction. <i>Journal of Computational Biology</i> , 2019, 26, 124-127.	1.6	5

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19	Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. <i>Nature Microbiology</i> , 2018, 3, 319-327.	13.3	71
20	Ketoreductase Domain Dysfunction Expands Chemodiversity: Malyngamide Biosynthesis in the Cyanobacterium <i>Okeania hirsuta</i> . <i>ACS Chemical Biology</i> , 2018, 13, 3385-3395.	3.4	25
21	Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018, 9, 4035.	12.8	220
22	Autoprotobiotics as an Approach for Restoration of Personalised Microbiota. <i>Frontiers in Microbiology</i> , 2018, 9, 1869.	3.5	28
23	Introduction: Overview. <i>Use R!</i> , 2018, , 1-30.	0.2	0
24	Parameter Estimation, Forecasting, Gap Filling. <i>Use R!</i> , 2018, , 121-188.	0.2	0
25	SSA for Multivariate Time Series. <i>Use R!</i> , 2018, , 189-229.	0.2	1
26	Singular Spectrum Analysis with R. <i>Use R!</i> , 2018, , .	0.2	65
27	Comparative genomics uncovers the prolific and distinctive metabolic potential of the cyanobacterial genus <i>Moorea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3198-3203.	7.1	77
28	A Maldii isotopic Approach to Discover Natural Products: Cryptomaldamide, a Hybrid Tripeptide from the Marine Cyanobacterium <i>Moorea producens</i> . <i>Journal of Natural Products</i> , 2017, 80, 1514-1521.	3.0	30
29	metaSPAdes: a new versatile metagenomic assembler. <i>Genome Research</i> , 2017, 27, 824-834.	5.5	2,779
30	Sequencing rare marine actinomycete genomes reveals high density of unique natural product biosynthetic gene clusters. <i>Microbiology (United Kingdom)</i> , 2016, 162, 2075-2086.	1.8	61
31	A novel uncultured heterotrophic bacterial associate of the cyanobacterium <i>Moorea producens</i> JHB. <i>BMC Microbiology</i> , 2016, 16, 198.	3.3	13
32	The Phormidolide Biosynthetic Gene Cluster: A <i>trans</i> - β -CAT PKS Pathway Encoding a Toxic Macrocylic Polyketide. <i>ChemBioChem</i> , 2016, 17, 164-173.	2.6	36
33	<i>hybrid</i> SPA <i>des</i> : an algorithm for hybrid assembly of short and long reads. <i>Bioinformatics</i> , 2016, 32, 1009-1015.	4.1	463
34	Expanding the Described Metabolome of the Marine Cyanobacterium <i>Moorea producens</i> JHB through Orthogonal Natural Products Workflows. <i>PLoS ONE</i> , 2015, 10, e0133297.	2.5	40
35	Assembling short reads from jumping libraries with large insert sizes. <i>Bioinformatics</i> , 2015, 31, 3262-3268.	4.1	40
36	Spongiosine Production by a <i>Vibrio harveyi</i> Strain Associated with the Sponge <i>Tectitethya crypta</i> . <i>Journal of Natural Products</i> , 2015, 78, 493-499.	3.0	28

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37	Combining Mass Spectrometric Metabolic Profiling with Genomic Analysis: A Powerful Approach for Discovering Natural Products from Cyanobacteria. <i>Journal of Natural Products</i> , 2015, 78, 1671-1682.	3.0	156
38	Multivariate and 2D Extensions of Singular Spectrum Analysis with the <code>Rssa</code> Package. <i>Journal of Statistical Software</i> , 2015, 67, .	3.7	71
39	Discovery of novel chlorinated acyl amides from a marine cyanobacterium using integrated technologies. <i>Planta Medica</i> , 2015, 81, .	1.3	0
40	Characterization of Cyanobacterial Hydrocarbon Composition and Distribution of Biosynthetic Pathways. <i>PLoS ONE</i> , 2014, 9, e85140.	2.5	190
41	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	4.1	103
42	Basic Singular Spectrum Analysis and forecasting with R. <i>Computational Statistics and Data Analysis</i> , 2014, 71, 934-954.	1.2	148
43	Single cell genome analysis of an uncultured heterotrophic stramenopile. <i>Scientific Reports</i> , 2014, 4, 4780.	3.3	59
44	BayesHammer: Bayesian clustering for error correction in single-cell sequencing. <i>BMC Genomics</i> , 2013, 14, S7.	2.8	429
45	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.3	439
46	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	1.6	1,235
47	Consistency of Parametric MLE Under Mixed Case Interval Censoring. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2012, 41, 1083-1092.	1.2	0
48	Computation- and space-efficient implementation of SSA. <i>Statistics and Its Interface</i> , 2010, 3, 357-368.	0.3	63
49	Estimation of ion-site association constants in ion-selective electrode membranes by modified segmented sandwich membrane method. <i>Electrochimica Acta</i> , 2008, 53, 5819-5826.	5.2	31
50	Improving Switch Lowering for the LLVM Compiler System. , 2007, , .		3