

Alexey A Gurevich

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

33,008
citations

304368

22
h-index

525886

27
g-index

34
all docs

34
docs citations

34
times ranked

35254
citing authors

#	ARTICLE	IF	CITATIONS
1	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. <i>Journal of Computational Biology</i> , 2012, 19, 455-477.	0.8	20,193
2	QUAST: quality assessment tool for genome assemblies. <i>Bioinformatics</i> , 2013, 29, 1072-1075.	1.8	6,983
3	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	0.8	1,235
4	Versatile genome assembly evaluation with QUAST-LG. <i>Bioinformatics</i> , 2018, 34, i142-i150.	1.8	732
5	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	9.0	650
6	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
7	MetaQUAST: evaluation of metagenome assemblies. <i>Bioinformatics</i> , 2016, 32, 1088-1090.	1.8	447
8	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.0	439
9	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	9.0	430
10	Dereplication of microbial metabolites through database search of mass spectra. <i>Nature Communications</i> , 2018, 9, 4035.	5.8	220
11	Dereplication of peptidic natural products through database search of mass spectra. <i>Nature Chemical Biology</i> , 2017, 13, 30-37.	3.9	184
12	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
13	Icarus: visualizer for <i>de novo</i> assembly evaluation. <i>Bioinformatics</i> , 2016, 32, 3321-3323.	1.8	115
14	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	1.8	103
15	Increased diversity of peptidic natural products revealed by modification-tolerant database search of mass spectra. <i>Nature Microbiology</i> , 2018, 3, 319-327.	5.9	71
16	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.	2.9	46
17	MolDiscovery: learning mass spectrometry fragmentation of small molecules. <i>Nature Communications</i> , 2021, 12, 3718.	5.8	44
18	Assembling short reads from jumping libraries with large insert sizes. <i>Bioinformatics</i> , 2015, 31, 3262-3268.	1.8	40

#	ARTICLE	IF	CITATIONS
19	TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats. <i>Bioinformatics</i> , 2020, 36, i75-i83.	1.8	40
20	Spatial Molecular Architecture of the Microbial Community of a <i>Peltigera</i> Lichen. <i>MSystems</i> , 2016, 1, .	1.7	36
21	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	5.5	36
22	Integrating genomics and metabolomics for scalable non-ribosomal peptide discovery. <i>Nature Communications</i> , 2021, 12, 3225.	5.8	31
23	Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules. <i>MSystems</i> , 2017, 2, .	1.7	30
24	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. <i>Cell Systems</i> , 2020, 10, 99-108.e5.	2.9	28
25	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
26	Nerpa: A Tool for Discovering Biosynthetic Gene Clusters of Bacterial Nonribosomal Peptides. <i>Metabolites</i> , 2021, 11, 693.	1.3	11
27	NPS: scoring and evaluating the statistical significance of peptidic natural productâ€“spectrum matches. <i>Bioinformatics</i> , 2019, 35, i315-i323.	1.8	5