

Alexander Sczyrba

List of Publications by Year in descending order

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76
papers

9,069
citations

101543
36
h-index

79698
73
g-index

82
all docs

82
docs citations

82
times ranked

11526
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
3	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	3.3	12
4	Identification of Beneficial Microbial Consortia and Bioactive Compounds with Potential as Plant Biostimulants for a Sustainable Agriculture. <i>Microorganisms</i> , 2021, 9, 426.	3.6	37
5	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. <i>Nature Protocols</i> , 2021, 16, 1785-1801.	12.0	36
6	Going to extremes – a metagenomic journey into the dark matter of life. <i>FEMS Microbiology Letters</i> , 2021, 368, .	1.8	16
7	Haploflow: strain-resolved de novo assembly of viral genomes. <i>Genome Biology</i> , 2021, 22, 212.	8.8	16
8	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. <i>Viruses</i> , 2021, 13, 1870.	3.3	7
9	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
10	ConCysFind: a pipeline tool to predict conserved amino acids of protein sequences across the plant kingdom. <i>BMC Bioinformatics</i> , 2020, 21, 490.	2.6	3
11	The Role of <i>Petrimonas mucosa</i> ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. <i>Microorganisms</i> , 2020, 8, 2024.	3.6	23
12	Importance of <i>Defluviitalea raffinosedens</i> for Hydrolytic Biomass Degradation in Co-Culture with <i>Hungateiclostridium thermocellum</i> . <i>Microorganisms</i> , 2020, 8, 915.	3.6	13
13	Impact of process temperature and organic loading rate on cellulolytic / hydrolytic biofilm microbiomes during biomethanation of ryegrass silage revealed by genome-centered metagenomics and metatranscriptomics. <i>Environmental Microbiomes</i> , 2020, 15, 7.	5.0	13
14	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. <i>Cell Reports</i> , 2020, 30, 2909-2922.e6.	6.4	85
15	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. <i>Genes</i> , 2019, 10, 424.	2.4	61
16	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	11.1	117
17	de.NBI Cloud federation through ELIXIR AAI. <i>F1000Research</i> , 2019, 8, 842.	1.6	13
18	Analyzing large scale genomic data on the cloud with Sparkhit. <i>Bioinformatics</i> , 2018, 34, 1457-1465.	4.1	14

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19	Targeted <i>in situ</i> metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. <i>Microbial Biotechnology</i> , 2018, 11, 667-679.	4.2	43
20	Invasion ecology applied to inoculation of plant growth promoting bacteria through a novel SIMPER-PCA approach. <i>Plant and Soil</i> , 2018, 422, 467-478.	3.7	7
21	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018, 7, .	6.4	16
22	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. <i>Biotechnology for Biofuels</i> , 2018, 11, 167.	6.2	38
23	AMBER: Assessment of Metagenome BinnERs. <i>GigaScience</i> , 2018, 7, .	6.4	72
24	Common ELIXIR Service for Researcher Authentication and Authorisation. <i>F1000Research</i> , 2018, 7, 1199.	1.6	23
25	Rapid protein alignment in the cloud: HAMOND combines fast DIAMOND alignments with Hadoop parallelism. <i>Journal of Biotechnology</i> , 2017, 257, 58-60.	3.8	5
26	Critical Assessment of Metagenome Interpretation – a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
27	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017, 261, 10-23.	3.8	84
28	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. <i>Biotechnology for Biofuels</i> , 2017, 10, 264.	6.2	50
29	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	3.5	120
30	Proteotyping of biogas plant microbiomes separates biogas plants according to process temperature and reactor type. <i>Biotechnology for Biofuels</i> , 2016, 9, 155.	6.2	80
31	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. <i>Biotechnology for Biofuels</i> , 2016, 9, 171.	6.2	134
32	acdc – Automated Contamination Detection and Confidence estimation for single-cell genome data. <i>BMC Bioinformatics</i> , 2016, 17, 543.	2.6	22
33	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. <i>Biotechnology for Biofuels</i> , 2016, 9, 156.	6.2	120
34	miRNA profiling of high, low and non-producing CHO cells during biphasic fed-batch cultivation reveals process relevant targets for host cell engineering. <i>Journal of Biotechnology</i> , 2016, 225, 31-43.	3.8	19
35	Finished genome sequence and methylome of the cyanide-degrading <i>Pseudomonas pseudoalcaligenes</i> strain CECT5344 as resolved by single-molecule real-time sequencing. <i>Journal of Biotechnology</i> , 2016, 232, 61-68.	3.8	20
36	Genomic characterization of <i>Defluviitoga tunisiensis</i> L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. <i>Journal of Biotechnology</i> , 2016, 232, 50-60.	3.8	53

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37	MeCorS: Metagenome-enabled error correction of single cell sequencing reads. <i>Bioinformatics</i> , 2016, 32, 2199-2201.	4.1	8
38	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. <i>Journal of Biotechnology</i> , 2016, 231, 268-279.	3.8	33
39	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. <i>GigaScience</i> , 2015, 4, 33.	6.4	68
40	Bioboxes: standardised containers for interchangeable bioinformatics software. <i>GigaScience</i> , 2015, 4, 47.	6.4	84
41	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. <i>Proteomics</i> , 2015, 15, 3585-3589.	2.2	14
42	Automatic discovery of metagenomic structure. , 2015, , .		5
43	Targeted diversity generation by intraterrestrial archaea and archaeal viruses. <i>Nature Communications</i> , 2015, 6, 6585.	12.8	63
44	Genomic insights into the uncultivated marine <i>Zetaproteobacteria</i> at Loihi Seamount. <i>ISME Journal</i> , 2015, 9, 857-870.	9.8	69
45	Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. <i>Frontiers in Microbiology</i> , 2014, 5, 307.	3.5	78
46	Comparative single-cell genomics reveals potential ecological niches for the freshwater <i>Actinobacteria</i> lineage. <i>ISME Journal</i> , 2014, 8, 2503-2516.	9.8	137
47	Complete genome sequence of the cyanide-degrading bacterium <i>Pseudomonas pseudoalcaligenes</i> CECT5344. <i>Journal of Biotechnology</i> , 2014, 175, 67-68.	3.8	28
48	Phylogenomically Guided Identification of Industrially Relevant GH1 β -Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. <i>ACS Chemical Biology</i> , 2014, 9, 2082-2091.	3.4	78
49	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. <i>PLoS ONE</i> , 2014, 9, e87353.	2.5	79
50	<i>Mycoplasma salivarium</i> as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. <i>PLoS ONE</i> , 2014, 9, e92297.	2.5	32
51	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. <i>PLoS ONE</i> , 2014, 9, e95380.	2.5	95
52	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
53	Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton. <i>ISME Journal</i> , 2013, 7, 137-147.	9.8	94
54	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5540-5545.	7.1	290

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55	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. ISME Journal, 2013, 7, 2287-2300.	9.8	113
56	Nonlinear Dimensionality Reduction for Cluster Identification in Metagenomic Samples. , 2013, , .		18
57	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11463-11468.	7.1	328
58	Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. PLoS ONE, 2013, 8, e59361.	2.5	44
59	Personalized cloud-based bioinformatics services for research and education: use cases and the elasticHPC package. BMC Bioinformatics, 2012, 13, S22.	2.6	20
60	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. Science, 2011, 333, 1296-1300.	12.6	510
61	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. Science, 2011, 331, 463-467.	12.6	1,135
62	Titelbild: High-Throughput Inâ€¦Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery (Angew. Chem. 47/2011). Angewandte Chemie, 2011, 123, 11205-11205.	2.0	0
63	Highâ€¦Throughput Inâ€¦Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery. Angewandte Chemie - International Edition, 2011, 50, 11215-11218.	13.8	23
64	Cover Picture: Highâ€¦Throughput Inâ€¦Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery (Angew. Chem. Int. Ed. 47/2011). Angewandte Chemie - International Edition, 2011, 50, 11013-11013.	13.8	0
65	Genome Sequence of the 1,4-Dioxane-Degrading Pseudonocardia dioxanivorans Strain CB1190. Journal of Bacteriology, 2011, 193, 4549-4550.	2.2	56
66	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. PLoS ONE, 2011, 6, e26161.	2.5	163
67	Meeting Report: The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project. Standards in Genomic Sciences, 2010, 3, 243-248.	1.5	228
68	IsoSVM--distinguishing isoforms and paralogs on the protein level. BMC Bioinformatics, 2006, 7, 110.	2.6	16
69	XenDB: Full length cDNA prediction and cross species mapping in Xenopus laevis. BMC Genomics, 2005, 6, 123.	2.8	5
70	AGenDA: gene prediction by cross-species sequence comparison. Nucleic Acids Research, 2004, 32, W305-W308.	14.5	15
71	e2g: an interactive web-based server for efficiently mapping large EST and cDNA sets to genomic sequences. Nucleic Acids Research, 2004, 32, W301-W304.	14.5	10
72	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	3.8	100

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73	AltAVisT: Comparing alternative multiple sequence alignments. Bioinformatics, 2003, 19, 425-426.	4.1	24
74	RNA-related tools on the Bielefeld Bioinformatics Server. Nucleic Acids Research, 2003, 31, 3767-3770.	14.5	17
75	AGenDA: homology-based gene prediction. Bioinformatics, 2003, 19, 1575-1577.	4.1	30
76	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	21.4	58