Alexander Sczyrba

List of Publications by Year
in descending order

76 papers	9,069 citations	101496 36 h-index	79644 73 g-index
82 all docs	82 docs citations	82 times ranked	11526 citing authors

#	Article	IF	Citations
1	Insights into the phylogeny and coding potential of microbial dark matter. Nature, 2013, 499, 431-437.	13.7	2,239
2	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. Science, 2011, 331, 463-467.	6.0	1,135
3	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
4	Potential for Chemolithoautotrophy Among Ubiquitous Bacteria Lineages in the Dark Ocean. Science, 2011, 333, 1296-1300.	6.0	510
5	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
6	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.	3.3	328
7	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5540-5545.	3.3	290
8	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
9	Decontamination of MDA Reagents for Single Cell Whole Genome Amplification. PLoS ONE, 2011, 6, e26161.	1.1	163
10	Comparative single-cell genomics reveals potential ecological niches for the freshwater acI Actinobacteria lineage. ISME Journal, 2014, 8, 2503-2516.	4.4	137
11	Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. Biotechnology for Biofuels, 2016, 9, 171.	6.2	134
12	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	9.0	133
13	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	1.5	120
14	Identification and genome reconstruction of abundant distinct taxa in microbiomes from one thermophilic and three mesophilic production-scale biogas plants. Biotechnology for Biofuels, 2016, 9, 156.	6.2	120
15	CAMISIM: simulating metagenomes and microbial communities. Microbiome, 2019, 7, 17.	4.9	117
16	Single-cell genomics reveals complex carbohydrate degradation patterns in poribacterial symbionts of marine sponges. ISME Journal, 2013, 7, 2287-2300.	4.4	113
17	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	1.9	100
18	Genomic and Metabolic Diversity of Marine Group I Thaumarchaeota in the Mesopelagic of Two Subtropical Gyres. PLoS ONE, 2014, 9, e95380.	1.1	95

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19	Metabolic potential of a single cell belonging to one of the most abundant lineages in freshwater bacterioplankton. ISME Journal, 2013, 7, 137-147.	4.4	94
20	An Integrated Metagenome Catalog Reveals New Insights into the Murine Gut Microbiome. Cell Reports, 2020, 30, 2909-2922.e6.	2.9	85
21	Bioboxes: standardised containers for interchangeable bioinformatics software. GigaScience, 2015, 4, 47.	3.3	84
22	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	1.9	84
23	Proteotyping of biogas plant microbiomes separates biogas plants according to process temperature and reactor type. Biotechnology for Biofuels, 2016, 9, 155.	6.2	80
24	The Candidate Phylum Poribacteria by Single-Cell Genomics: New Insights into Phylogeny, Cell-Compartmentation, Eukaryote-Like Repeat Proteins, and Other Genomic Features. PLoS ONE, 2014, 9, e87353.	1.1	79
25	Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. Frontiers in Microbiology, 2014, 5, 307.	1.5	78
26	Phylogenomically Guided Identification of Industrially Relevant GH1 Î²-Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. ACS Chemical Biology, 2014, 9, 2082-2091.	1.6	78
27	AMBER: Assessment of Metagenome BinnERs. GigaScience, 2018, 7, .	3.3	72
28	Genomic insights into the uncultivated marine *Zetaproteobacteria* at Loihi Seamount. ISME Journal, 2015, 9, 857-870.	4.4	69
29	Deeply sequenced metagenome and metatranscriptome of a biogas-producing microbial community from an agricultural production-scale biogas plant. GigaScience, 2015, 4, 33.	3.3	68
30	Targeted diversity generation by intraterrestrial archaea and archaeal viruses. Nature Communications, 2015, 6, 6585.	5.8	63
31	Effect of Long-Term Farming Practices on Agricultural Soil Microbiome Members Represented by Metagenomically Assembled Genomes (MAGs) and Their Predicted Plant-Beneficial Genes. Genes, 2019, 10, 424.	1.0	61
32	Homology-based annotation yields 1,042 new candidate genes in the Drosophila melanogaster genome. Nature Genetics, 2001, 27, 337-340.	9.4	58
33	Genome Sequence of the 1,4-Dioxane-Degrading Pseudonocardia dioxanivoransStrain CB1190. Journal of Bacteriology, 2011, 193, 4549-4550.	1.0	56
34	Genomic characterization of Defluviitoga tunisiensis L3, a key hydrolytic bacterium in a thermophilic biogas plant and its abundance as determined by metagenome fragment recruitment. Journal of Biotechnology, 2016, 232, 50-60.	1.9	53
35	Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. Biotechnology for Biofuels, 2017, 10, 264.	6.2	50
36	Multiple Single-Cell Genomes Provide Insight into Functions of Uncultured Deltaproteobacteria in the Human Oral Cavity. PLoS ONE, 2013, 8, e59361.	1.1	44

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37	Targeted *insitu* metatranscriptomics for selected taxa from mesophilic and thermophilic biogas plants. Microbial Biotechnology, 2018, 11, 667-679.	2.0	43
38	Characterization of Bathyarchaeota genomes assembled from metagenomes of biofilms residing in mesophilic and thermophilic biogas reactors. Biotechnology for Biofuels, 2018, 11, 167.	6.2	38
39	Identification of Beneficial Microbial Consortia and Bioactive Compounds with Potential as Plant Biostimulants for a Sustainable Agriculture. Microorganisms, 2021, 9, 426.	1.6	37
40	Tutorial: assessing metagenomics software with the CAMI benchmarking toolkit. Nature Protocols, 2021, 16, 1785-1801.	5.5	36
41	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	5.8	34
42	An integrated metagenome and -proteome analysis of the microbial community residing in a biogas production plant. Journal of Biotechnology, 2016, 231, 268-279.	1.9	33
43	Mycoplasma salivarium as a Dominant Coloniser of Fanconi Anaemia Associated Oral Carcinoma. PLoS ONE, 2014, 9, e92297.	1.1	32
44	AGenDA: homology-based gene prediction. Bioinformatics, 2003, 19, 1575-1577.	1.8	30
45	Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344. Journal of Biotechnology, 2014, 175, 67-68.	1.9	28
46	AltAVisT: Comparing alternative multiple sequence alignments. Bioinformatics, 2003, 19, 425-426.	1.8	24
47	High‐Throughput In‐Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery. Angewandte Chemie - International Edition, 2011, 50, 11215-11218.	7.2	23
48	The Role of Petrimonas mucosa ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. Microorganisms, 2020, 8, 2024.	1.6	23
49	Common ELIXIR Service for Researcher Authentication and Authorisation. F1000Research, 2018, 7, 1199.	0.8	23
50	acdc – Automated Contamination Detection and Confidence estimation for single-cell genome data. BMC Bioinformatics, 2016, 17, 543.	1.2	22
51	Personalized cloud-based bioinformatics services for research and education: use cases and the elasticHPC package. BMC Bioinformatics, 2012, 13, S22.	1.2	20
52	Finished genome sequence and methylome of the cyanide-degrading Pseudomonas pseudoalcaligenes strain CECT5344 as resolved by single-molecule real-time sequencing. Journal of Biotechnology, 2016, 232, 61-68.	1.9	20
53	miRNA profiling of high, low and non-producing CHO cells during biphasic fed-batch cultivation reveals process relevant targets for host cell engineering. Journal of Biotechnology, 2016, 225, 31-43.	1.9	19
54	Nonlinear Dimensionality Reduction for Cluster Identification in Metagenomic Samples. , 2013, , .		18

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55	RNA-related tools on the Bielefeld Bioinformatics Server. Nucleic Acids Research, 2003, 31, 3767-3770.	6.5	17
56	IsoSVM--distinguishing isoforms and paralogs on the protein level. BMC Bioinformatics, 2006, 7, 110.	1.2	16
57	Binning enables efficient host genome reconstruction in cnidarian holobionts. GigaScience, 2018, 7, .	3.3	16
58	Going to extremes â€" a metagenomic journey into the dark matter of life. FEMS Microbiology Letters, 2021, 368, .	0.7	16
59	Haploflow: strain-resolved de novo assembly of viral genomes. Genome Biology, 2021, 22, 212.	3.8	16
60	AGenDA: gene prediction by cross-species sequence comparison. Nucleic Acids Research, 2004, 32, W305-W308.	6.5	15
61	Fractionation of biogas plant sludge material improves metaproteomic characterization to investigate metabolic activity of microbial communities. Proteomics, 2015, 15, 3585-3589.	1.3	14
62	Analyzing large scale genomic data on the cloud with Sparkhit. Bioinformatics, 2018, 34, 1457-1465.	1.8	14
63	Importance of Defluviitalea raffinosedens for Hydrolytic Biomass Degradation in Co-Culture with Hungateiclostridium thermocellum. Microorganisms, 2020, 8, 915.	1.6	13
64	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. Environmental Microbiomes, 2020, 15, 7.	2.2	13
65	de.NBI Cloud federation through ELIXIR AAI. F1000Research, 2019, 8, 842.	0.8	13
66	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of Botryococcus consortia. Scientific Reports, 2021, 11, 1726.	1.6	12
67	e2g: an interactive web-based server for efficiently mapping large EST and cDNA sets to genomic sequences. Nucleic Acids Research, 2004, 32, W301-W304.	6.5	10
68	MeCorS: Metagenome-enabled error correction of single cell sequencing reads. Bioinformatics, 2016, 32, 2199-2201.	1.8	8
69	Invasion ecology applied to inoculation of plant growth promoting bacteria through a novel SIMPER-PCA approach. Plant and Soil, 2018, 422, 467-478.	1.8	7
70	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. Viruses, 2021, 13, 1870.	1.5	7
71	XenDB: Full length cDNA prediction and cross species mapping in Xenopus laevis. BMC Genomics, 2005, 6, 123.	1.2	5
72	Automatic discovery of metagenomic structure. , 2015, , .		5

#	Article	IF	Citations
73	Rapid protein alignment in the cloud: HAMOND combines fast DIAMOND alignments with Hadoop parallelism. Journal of Biotechnology, 2017, 257, 58-60.	1.9	5
74	ConCysFind: a pipeline tool to predict conserved amino acids of protein sequences across the plant kingdom. BMC Bioinformatics, 2020, 21, 490.	1.2	3
75	Titelbild: High-Throughput In–…Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery (Angew. Chem. 47/2011). Angewandte Chemie, 2011, 123, 11205-11205.	1.6	0
76	Cover Picture: High–Throughput In–…Vitro Glycoside Hydrolase (HIGH) Screening for Enzyme Discovery (Angew. Chem. Int. Ed. 47/2011). Angewandte Chemie - International Edition, 2011, 50, 11013-11013.	7.2	0