

# Alexander Goesmann

## List of Publications by Year in descending order

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207  
papers

15,671  
citations

18479

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213  
docs citations

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times ranked

18626  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. <i>Nucleic Acids Research</i> , 2005, 33, 5691-5702.	14.5	1,806
2	GenDB—an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003, 31, 2187-2195.	14.5	644
3	The genome of the recently domesticated crop plant sugar beet ( <i>Beta vulgaris</i> ). <i>Nature</i> , 2014, 505, 546-549.	27.8	569
4	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013, 31, 294-296.	17.5	423
5	An RNAi-Based Control of <i>Fusarium graminearum</i> Infections Through Spraying of Long dsRNAs Involves a Plant Passage and Is Controlled by the Fungal Silencing Machinery. <i>PLoS Pathogens</i> , 2016, 12, e1005901.	4.7	409
6	EDGAR: A software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , 2009, 10, 154.	2.6	401
7	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. <i>Nucleic Acids Research</i> , 2016, 44, W22-W28.	14.5	398
8	Complete Genome Sequence of the Prototype Lactic Acid Bacterium <i>Lactococcus lactis</i> subsp. <i>cremoris</i> MG1363. <i>Journal of Bacteriology</i> , 2007, 189, 3256-3270.	2.2	362
9	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007, 25, 1281-1289.	17.5	354
10	The metagenome of a biogas-producing microbial community of a production-scale biogas plant fermenter analysed by the 454-pyrosequencing technology. <i>Journal of Biotechnology</i> , 2008, 136, 77-90.	3.8	329
11	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	2.2	321
12	Phylogenetic characterization of a biogas plant microbial community integrating clone library 16S-rDNA sequences and metagenome sequence data obtained by 454-pyrosequencing. <i>Journal of Biotechnology</i> , 2009, 142, 38-49.	3.8	248
13	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	14.5	246
14	The genome of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 and its use for the reconstruction of metabolic pathways involved in xanthan biosynthesis. <i>Journal of Biotechnology</i> , 2008, 134, 33-45.	3.8	238
15	Reassessment of the <i>Listeria monocytogenes</i> pan-genome reveals dynamic integration hotspots and mobile genetic elements as major components of the accessory genome. <i>BMC Genomics</i> , 2013, 14, 47.	2.8	212
16	Comparative and Joint Analysis of Two Metagenomic Datasets from a Biogas Fermenter Obtained by 454-Pyrosequencing. <i>PLoS ONE</i> , 2011, 6, e14519.	2.5	208
17	Taxonomic composition and gene content of a methane-producing microbial community isolated from a biogas reactor. <i>Journal of Biotechnology</i> , 2008, 136, 91-101.	3.8	202
18	Profiling of the metabolically active community from a production-scale biogas plant by means of high-throughput metatranscriptome sequencing. <i>Journal of Biotechnology</i> , 2012, 158, 248-258.	3.8	198

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19	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. <i>Microbial Genomics</i> , 2021, 7, .	2.0	168
20	TACO A “ Taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. <i>BMC Bioinformatics</i> , 2009, 10, 56.	2.6	160
21	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013, 31, 694-695.	17.5	160
22	Whole-genome comparison of disease and carriage strains provides insights into virulence evolution in <i>Neisseria meningitidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3473-3478.	7.1	159
23	Complete Genome Sequence of the Fire Blight Pathogen <i>Erwinia amylovora</i> CFBP 1430 and Comparison to Other <i>Erwinia</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 384-393.	2.6	156
24	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011, 154, 312-320.	3.8	146
25	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
26	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model alga-associated bacterium <i>Zobellia galactanivorans</i> Dsij <sup>T</sup> . <i>Environmental Microbiology</i> , 2016, 18, 4610-4627.	3.8	131
27	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. <i>FEMS Microbiology Ecology</i> , 2012, 79, 785-799.	2.7	130
28	Antibiotic multiresistance plasmid pRSB101 isolated from a wastewater treatment plant is related to plasmids residing in phytopathogenic bacteria and carries eight different resistance determinants including a multidrug transport system. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3613-3630.	1.8	128
29	ReadXplorer visualization and analysis of mapped sequences. <i>Bioinformatics</i> , 2014, 30, 2247-2254.	4.1	127
30	Insect pathogenicity in plant-beneficial pseudomonads: phylogenetic distribution and comparative genomics. <i>ISME Journal</i> , 2016, 10, 2527-2542.	9.8	127
31	Bacterial Community Shift in Treated Periodontitis Patients Revealed by Ion Torrent 16S rRNA Gene Amplicon Sequencing. <i>PLoS ONE</i> , 2012, 7, e41606.	2.5	116
32	Bioinformatic Analysis Reveals High Diversity of Bacterial Genes for Laccase-Like Enzymes. <i>PLoS ONE</i> , 2011, 6, e25724.	2.5	115
33	Interclonal gradient of virulence in the <i>Pseudomonas aeruginosa</i> pangenome from disease and environment. <i>Environmental Microbiology</i> , 2015, 17, 29-46.	3.8	113
34	Complete genome sequencing of <i>Agrobacterium</i> sp. H13-3, the former <i>Rhizobium lupini</i> H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. <i>Journal of Biotechnology</i> , 2011, 155, 50-62.	3.8	112
35	Comparative Analysis of Plasmids in the Genus <i>Listeria</i> . <i>PLoS ONE</i> , 2010, 5, e12511.	2.5	110
36	Circulation of clonal populations of fluoroquinolone-resistant CTX-M-15-producing <i>Escherichia coli</i> ST410 in humans and animals in Germany. <i>International Journal of Antimicrobial Agents</i> , 2016, 47, 457-465.	2.5	107

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37	The Waddlia Genome: A Window into Chlamydial Biology. PLoS ONE, 2010, 5, e10890.	2.5	104
38	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. Journal of Biotechnology, 2011, 153, 62-75.	3.8	102
39	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	3.8	100
40	MeltDB: a software platform for the analysis and integration of metabolomics experiment data. Bioinformatics, 2008, 24, 2726-2732.	4.1	100
41	Microbial diversity in different compartments of an aquaponics system. Archives of Microbiology, 2017, 199, 613-620.	2.2	99
42	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. Journal of Biotechnology, 2011, 156, 227-235.	3.8	96
43	ReadXplorer 2â€™ detailed read mapping analysis and visualization from one single source. Bioinformatics, 2016, 32, 3702-3708.	4.1	96
44	A reference genome of the Chinese hamster based on a hybrid assembly strategy. Biotechnology and Bioengineering, 2018, 115, 2087-2100.	3.3	95
45	Genome Sequence of the Biocontrol Agent <i>Pantoea vagans</i> Strain C9-1. Journal of Bacteriology, 2010, 192, 6486-6487.	2.2	93
46	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. Journal of Biotechnology, 2013, 167, 142-155.	3.8	93
47	Non-pathogenic <i>Rhizobium radiobacter</i> F4 deploys plant beneficial activity independent of its host <i>Piriformospora indica</i> . ISME Journal, 2016, 10, 871-884.	9.8	93
48	Whole-Genome Sequence of <i>Listeria welshimeri</i> Reveals Common Steps in Genome Reduction with <i>Listeria innocua</i> as Compared to <i>Listeria monocytogenes</i> . Journal of Bacteriology, 2006, 188, 7405-7415.	2.2	89
49	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . BMC Genomics, 2012, 13, 144.	2.8	88
50	Platon: identification and characterization of bacterial plasmid contigs in short-read draft assemblies exploiting protein sequence-based replicon distribution scores. Microbial Genomics, 2020, 6, .	2.0	87
51	The missing link: <i>Bordetella petrii</i> is endowed with both the metabolic versatility of environmental bacteria and virulence traits of pathogenic <i>Bordetellae</i> . BMC Genomics, 2008, 9, 449.	2.8	85
52	Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. Journal of Biotechnology, 2012, 161, 153-166.	3.8	85
53	Reconstruction of the lipid metabolism for the microalga <i>Monoraphidium neglectum</i> from its genome sequence reveals characteristics suitable for biofuel production. BMC Genomics, 2013, 14, 926.	2.8	84
54	Bioinformatics for NGS-based metagenomics and the application to biogas research. Journal of Biotechnology, 2017, 261, 10-23.	3.8	84

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55	Comparative Genomics of 12 Strains of <i>Erwinia amylovora</i> Identifies a Pan-Genome with a Large Conserved Core. <i>PLoS ONE</i> , 2013, 8, e55644.	2.5	80
56	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. <i>BMC Bioinformatics</i> , 2009, 10, 430.	2.6	78
57	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , 2011, 27, 1351-1358.	4.1	78
58	MeltDB 2.0“advances of the metabolomics software system. <i>Bioinformatics</i> , 2013, 29, 2452-2459.	4.1	75
59	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , 2004, 20, 1622-1631.	4.1	72
60	Genomic sequence of chorioallantois vaccinia virus Ankara, the ancestor of modified vaccinia virus Ankara. <i>Journal of General Virology</i> , 2007, 88, 3249-3259.	2.9	71
61	Chromosomal Locations of <i>mcr-1</i> and <i>bla</i> CTX-M-15 in Fluoroquinolone-Resistant <i>Escherichia coli</i> ST410. <i>Emerging Infectious Diseases</i> , 2016, 22, 1689-1691.	4.3	70
62	EMMA 2 “ A MAGE-compliant system for the collaborative analysis and integration of microarray data. <i>BMC Bioinformatics</i> , 2009, 10, 50.	2.6	68
63	Symbiotic properties and first analyses of the genomic sequence of the fast growing model strain <i>Sinorhizobium fredii</i> HH103 nodulating soybean. <i>Journal of Biotechnology</i> , 2011, 155, 11-19.	3.8	67
64	Identification and Characterization of Microcin S, a New Antibacterial Peptide Produced by Probiotic <i>Escherichia coli</i> G3/10. <i>PLoS ONE</i> , 2012, 7, e33351.	2.5	65
65	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. <i>Nucleic Acids Research</i> , 2021, 49, W185-W192.	14.5	65
66	Virulence Evolution of the Human Pathogen <i>Neisseria meningitidis</i> by Recombination in the Core and Accessory Genome. <i>PLoS ONE</i> , 2011, 6, e18441.	2.5	65
67	The pan-genome of <i>Lactobacillus reuteri</i> strains originating from the pig gastrointestinal tract. <i>BMC Genomics</i> , 2015, 16, 1023.	2.8	64
68	Changes in Root Bacterial Communities Associated to Two Different Development Stages of Canola ( <i>Brassica napus</i> L. var <i>oleifera</i> ) Evaluated through Next-Generation Sequencing Technology. <i>Microbial Ecology</i> , 2013, 65, 593-601.	2.8	62
69	Complete genome of a new <i>F</i> irmicutes species belonging to the dominant human colonic microbiota (“ <i>Ruminococcus bicirculans</i> ” <sup>TM</sup> ) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014, 16, 2879-2890.	3.8	62
70	Visualizing post genomics data-sets on customized pathway maps by ProMeTra “ aeration-dependent gene expression and metabolism of <i>Corynebacterium glutamicum</i> as an example. <i>BMC Systems Biology</i> , 2009, 3, 82.	3.0	61
71	<i>Enterobacter bugandensis</i> : a novel enterobacterial species associated with severe clinical infection. <i>Scientific Reports</i> , 2018, 8, 5392.	3.3	61
72	Genomic Avenue to Avian Colisepticemia. <i>MBio</i> , 2015, 6, .	4.1	59

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73	ASA3P: An automatic and scalable pipeline for the assembly, annotation and higher-level analysis of closely related bacterial isolates. <i>PLoS Computational Biology</i> , 2020, 16, e1007134.	3.2	59
74	Pan-genome analysis of <i>Aeromonas hydrophila</i> , <i>Aeromonas veronii</i> and <i>Aeromonas caviae</i> indicates phylogenomic diversity and greater pathogenic potential for <i>Aeromonas hydrophila</i> . <i>Antonie Van Leeuwenhoek</i> , 2016, 109, 945-956.	1.7	58
75	Complete genome sequence of the fire blight pathogen <i>Erwinia pyrifoliae</i> DSM 12163T and comparative genomic insights into plant pathogenicity. <i>BMC Genomics</i> , 2010, 11, 2.	2.8	57
76	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. <i>PLoS ONE</i> , 2014, 9, e85568.	2.5	57
77	Genomics of the Proteorhodopsin-Containing Marine Flavobacterium <i>Dokdonia</i> sp. Strain MED134. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8676-8686.	3.1	56
78	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus <i>Rana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 657-670.	2.7	56
79	The <i>Sinorhizobium fredii</i> HH103 Genome: A Comparative Analysis With <i>S. fredii</i> Strains Differing in Their Symbiotic Behavior With Soybean. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 811-824.	2.6	56
80	Metabolic Versatility and Antibacterial Metabolite Biosynthesis Are Distinguishing Genomic Features of the Fire Blight Antagonist <i>Pantoea vagans</i> C9-1. <i>PLoS ONE</i> , 2011, 6, e22247.	2.5	56
81	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B-13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015, 17, 91-104.	3.8	52
82	Complete genome sequence of <i>Pseudomonas</i> sp. strain VLB120 a solvent tolerant, styrene degrading bacterium, isolated from forest soil. <i>Journal of Biotechnology</i> , 2013, 168, 729-730.	3.8	51
83	Comparative Genome Biology of a Serogroup B Carriage and Disease Strain Supports a Polygenic Nature of Meningococcal Virulence. <i>Journal of Bacteriology</i> , 2010, 192, 5363-5377.	2.2	50
84	New insights into <i>Chlamydomonas reinhardtii</i> hydrogen production processes by combined microarray/RNA-seq transcriptomics. <i>Plant Biotechnology Journal</i> , 2013, 11, 717-733.	8.3	47
85	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. <i>Journal of Biotechnology</i> , 2012, 158, 151-155.	3.8	46
86	Multilineage murine stem cells generate complex organoids to model distal lung development and disease. <i>EMBO Journal</i> , 2020, 39, e103476.	7.8	44
87	Genomics and Physiology of a Marine Flavobacterium Encoding a Proteorhodopsin and a Xanthorhodopsin-Like Protein. <i>PLoS ONE</i> , 2013, 8, e57487.	2.5	42
88	Complete Genome Sequence of Clinical Isolate <i>Pantoea ananatis</i> LMG 5342. <i>Journal of Bacteriology</i> , 2012, 194, 1615-1616.	2.2	41
89	Intraclonal genome diversity of the major <i>Pseudomonas aeruginosa</i> clones C and PA14. <i>Environmental Microbiology Reports</i> , 2016, 8, 227-234.	2.4	41
90	Effect of UV irradiation on <i>Sulfolobus acidocaldarius</i> and involvement of the general transcription factor TFB3 in the early UV response. <i>Nucleic Acids Research</i> , 2018, 46, 7179-7192.	14.5	38

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91	The Sequence Analysis and Management System “SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	3.8	37
92	Conveyor: a workflow engine for bioinformatic analyses. <i>Bioinformatics</i> , 2011, 27, 903-911.	4.1	37
93	A detailed view of the intracellular transcriptome of <i>Listeria monocytogenes</i> in murine macrophages using RNA-seq. <i>Frontiers in Microbiology</i> , 2015, 6, 1199.	3.5	36
94	Time-resolved transcriptome analysis and lipid pathway reconstruction of the oleaginous green microalga <i>Monoraphidium neglectum</i> reveal a model for triacylglycerol and lipid hyperaccumulation. <i>Biotechnology for Biofuels</i> , 2017, 10, 197.	6.2	35
95	Complete Genome Sequence of the Probiotic <i>Enterococcus faecalis</i> Symbioflor 1 Clone DSM 16431. <i>Genome Announcements</i> , 2013, 1, .	0.8	33
96	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015, 16, 175.	2.8	33
97	<i>Erwinia gerundensis</i> sp. nov., a cosmopolitan epiphyte originally isolated from pome fruit trees. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 1583-1592.	1.7	33
98	BACCardl—a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005, 21, 853-859.	4.1	32
99	Transcriptome analysis of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). <i>Fungal Biology</i> , 2014, 118, 800-813.	2.5	32
100	Development of a <i>Rhizoctonia solani</i> AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic <i>R. solani</i> AG1-IA, AG1-IB, AG3 and AG8 Isolates. <i>PLoS ONE</i> , 2015, 10, e0144769.	2.5	32
101	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	3.5	32
102	Expansion and re-classification of the extracytoplasmic function (ECF) Ïf factor family. <i>Nucleic Acids Research</i> , 2021, 49, 986-1005.	14.5	32
103	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003, 106, 147-156.	3.8	31
104	Complete Genome Sequence of <i>Lactobacillus johnsonii</i> FI9785, a Competitive Exclusion Agent against Pathogens in Poultry. <i>Journal of Bacteriology</i> , 2009, 191, 7142-7143.	2.2	31
105	Genome sequence of the endophytic strain <i>Enterobacter</i> sp. J49, a potential biofertilizer for peanut and maize. <i>Genomics</i> , 2019, 111, 913-920.	2.9	30
106	Qupe—a Rich Internet Application to take a step forward in the analysis of mass spectrometry-based quantitative proteomics experiments. <i>Bioinformatics</i> , 2009, 25, 3128-3134.	4.1	29
107	GABenchToB: A Genome Assembly Benchmark Tuned on Bacteria and Benchtop Sequencers. <i>PLoS ONE</i> , 2014, 9, e107014.	2.5	29
108	Metabolite profiling on wheat grain to enable a distinction of samples from organic and conventional farming systems. <i>Journal of the Science of Food and Agriculture</i> , 2014, 94, 2605-2612.	3.5	29

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109	Draft Genome Sequence of the Commercial Biocontrol Strain <i>Pantoea agglomerans</i> P10c. <i>Genome Announcements</i> , 2015, 3, .	0.8	29
110	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018, 6, 76.	11.1	29
111	Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume <i>Medicago truncatula</i> . <i>Functional Plant Biology</i> , 2006, 33, 737.	2.1	29
112	ALlocator: An Interactive Web Platform for the Analysis of Metabolomic LC-ESI-MS Datasets, Enabling Semi-Automated, User-Revised Compound Annotation and Mass Isotopomer Ratio Analysis. <i>PLoS ONE</i> , 2014, 9, e113909.	2.5	28
113	Strain <i>Serratia</i> sp. S119: A potential biofertilizer for peanut and maize and a model bacterium to study phosphate solubilization mechanisms. <i>Applied Soil Ecology</i> , 2018, 126, 107-112.	4.3	28
114	Cyclophilin inhibitors restrict Middle East respiratory syndrome coronavirus <i>via</i> interferon- $\lambda$ <i>in vitro</i> and in mice. <i>European Respiratory Journal</i> , 2020, 56, 1901826.	6.7	28
115	Improved genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. <i>Journal of Biotechnology</i> , 2015, 203, 19-21.	3.8	27
116	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in <i>Neisseria meningitidis</i> during Invasive Disease. <i>PLoS ONE</i> , 2017, 12, e0169892.	2.5	26
117	Taxonomic analyses of members of the <i>Streptomyces cinnabarinus</i> cluster, description of <i>Streptomyces cinnabarigriseus</i> sp. nov. and <i>Streptomyces davaonensis</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 382-393.	1.7	26
118	Apparent vector-mediated parent-offspring transmission in an avian malaria-like parasite. <i>Molecular Ecology</i> , 2015, 24, 1355-1363.	3.9	25
119	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted by <i>Lucilia sericata</i> Medical Maggots. <i>BioMed Research International</i> , 2016, 2016, 1-27.	1.9	24
120	The Genome of the Toluene-Degrading <i>Pseudomonas veronii</i> Strain 1YdBTEX2 and Its Differential Gene Expression in Contaminated Sand. <i>PLoS ONE</i> , 2016, 11, e0165850.	2.5	24
121	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974 <sup>T</sup> (ATCC 19319 <sup>T</sup> ). <i>Genome Announcements</i> , 2016, 4, .	0.8	24
122	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017, 18, 35.	2.8	24
123	ADAR1 Is Required for Dendritic Cell Subset Homeostasis and Alveolar Macrophage Function. <i>Journal of Immunology</i> , 2019, 202, 1099-1111.	0.8	24
124	Construction and evaluation of a whole genome microarray of <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2011, 12, 579.	2.8	23
125	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> T $\frac{1}{4}$ 365 consisting of a linear chromosome and two linear plasmids. <i>Journal of Biotechnology</i> , 2013, 168, 739-740.	3.8	23
126	Learning to Classify Organic and Conventional Wheat $\tilde{c}$ A Machine Learning Driven Approach Using the MeltDB 2.0 Metabolomics Analysis Platform. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 35.	4.1	23



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127	CRISPR System Acquisition and Evolution of an Obligate Intracellular <i>Chlamydia</i> -Related Bacterium. <i>Genome Biology and Evolution</i> , 2016, 8, 2376-2386.	2.5	23
128	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	3.8	22
129	Metabolic and evolutionary patterns in the extremely acidophilic archaeon <i>Ferroplasma acidiphilum</i> YT. <i>Scientific Reports</i> , 2017, 7, 3682.	3.3	21
130	mRNA Inventory of Extracellular Vesicles from <i>Ustilago maydis</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 562.	3.5	21
131	Whole-Genome Sequence of the Transformable <i>Neisseria meningitidis</i> Serogroup A Strain WUE2594. <i>Journal of Bacteriology</i> , 2011, 193, 2064-2065.	2.2	20
132	Carbohydrate-active enzymes identified by metagenomic analysis of deep-sea sediment bacteria. <i>Extremophiles</i> , 2014, 18, 853-863.	2.3	20
133	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016, 222, 11-12.	3.8	20
134	<i>Acinetobacter baumannii</i> in manure and anaerobic digestates of German biogas plants. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	19
135	<i>Pseudomonas carnis</i> sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1528-1540.	1.7	19
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