

Alexander Goesmann

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205
papers

11,808
citations

58
h-index

104
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213
ext. papers

14,297
ext. citations

5.9
avg, IF

5.7
L-index

#	Paper	IF	Citations
205	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 5691-702	20.1	1485
204	GenDB--an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003 , 31, 2187-95	20.1	587
203	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014 , 505, 546-50	30.4	365
202	EDGAR: a software framework for the comparative analysis of prokaryotic genomes. <i>BMC Bioinformatics</i> , 2009 , 10, 154	3.6	317
201	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, 3256-70	3.5	314
200	Complete genome sequence of the myxobacterium <i>Sorangium cellulosum</i> . <i>Nature Biotechnology</i> , 2007 , 25, 1281-9	44.5	307
199	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, 7254-66	3.5	286
198	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	3.7	280
197	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013 , 31, 294-6	44.5	255
196	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	7.6	255
195	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. <i>Nucleic Acids Research</i> , 2016 , 44, W22-8	20.1	245
194	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008 , 36, 2230-9	11	222
193	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	3.7	209
192	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	3.7	202
191	Comparative and joint analysis of two metagenomic datasets from a biogas fermenter obtained by 454-pyrosequencing. <i>PLoS ONE</i> , 2011 , 6, e14519	3.7	187
190	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	3.7	177
189	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, 248-58	3.7	170

188	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	4.5	145
187	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, 3473-8	11.5	144
186	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013 , 31, 694-5	44.5	141
185	TACOA: taxonomic classification of environmental genomic fragments using a kernelized nearest neighbor approach. <i>BMC Bioinformatics</i> , 2009 , 10, 56	3.6	137
184	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, 384-93	3.6	136
183	High-quality genome sequence of <i>Pichia pastoris</i> CBS7435. <i>Journal of Biotechnology</i> , 2011 , 154, 312-20	3.7	123
182	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	2.9	120
181	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	7.8	102
180	Characterization of microbial biofilms in a thermophilic biogas system by high-throughput metagenome sequencing. <i>FEMS Microbiology Ecology</i> , 2012 , 79, 785-99	4.3	101
179	Bacterial community shift in treated periodontitis patients revealed by ion torrent 16S rRNA gene amplicon sequencing. <i>PLoS ONE</i> , 2012 , 7, e41606	3.7	100
178	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003 , 106, 135-46	3.7	99
177	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. <i>Journal of Biotechnology</i> , 2011 , 153, 62-75	3.7	95
176	Bioinformatic analysis reveals high diversity of bacterial genes for laccase-like enzymes. <i>PLoS ONE</i> , 2011 , 6, e25724	3.7	95
175	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	3.7	90
174	MeltDB: a software platform for the analysis and integration of metabolomics experiment data. <i>Bioinformatics</i> , 2008 , 24, 2726-32	7.2	89
173	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , 2011 , 156, 227-35	3.7	88
172	ReadXplorer--visualization and analysis of mapped sequences. <i>Bioinformatics</i> , 2014 , 30, 2247-54	7.2	85
171	Insect pathogenicity in plant-beneficial pseudomonads: phylogenetic distribution and comparative genomics. <i>ISME Journal</i> , 2016 , 10, 2527-42	11.9	82

170	The Waddlia genome: a window into chlamydial biology. <i>PLoS ONE</i> , 2010 , 5, e10890	3.7	82
169	Comparative analysis of plasmids in the genus <i>Listeria</i> . <i>PLoS ONE</i> , 2010 , 5, e12511	3.7	82
168	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> . <i>Journal of Bacteriology</i> , 2006 , 188, 7405-15	3.5	77
167	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, 457-65 ^{14.3}	14.3	76
166	Interclonal gradient of virulence in the <i>Pseudomonas aeruginosa</i> pangenome from disease and environment. <i>Environmental Microbiology</i> , 2015 , 17, 29-46	5.2	75
165	Insights into the completely annotated genome of <i>Lactobacillus buchneri</i> CD034, a strain isolated from stable grass silage. <i>Journal of Biotechnology</i> , 2012 , 161, 153-66	3.7	73
164	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsij. <i>Environmental Microbiology</i> , 2016 , 18, 4610-4627	5.2	72
163	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , 2011 , 27, 1351-8	7.2	71
162	Development of joint application strategies for two microbial gene finders. <i>Bioinformatics</i> , 2004 , 20, 1622-31	7.2	71
161	Genome sequence of the biocontrol agent <i>Pantoea vagans</i> strain C9-1. <i>Journal of Bacteriology</i> , 2010 , 192, 6486-7	3.5	70
160	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. <i>Journal of Biotechnology</i> , 2013 , 167, 142-55	3.7	68
159	WebCARMA: a web application for the functional and taxonomic classification of unassembled metagenomic reads. <i>BMC Bioinformatics</i> , 2009 , 10, 430	3.6	67
158	Genomic sequence of chorioallantois vaccinia virus Ankara, the ancestor of modified vaccinia virus Ankara. <i>Journal of General Virology</i> , 2007 , 88, 3249-3259	4.9	67
157	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> . <i>BMC Genomics</i> , 2008 , 9, 449	4.5	65
156	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	3.7	64
155	Non-pathogenic <i>Rhizobium radiobacter</i> F4 deploys plant beneficial activity independent of its host <i>Piriformospora indica</i> . <i>ISME Journal</i> , 2016 , 10, 871-84	11.9	63
154	Reconstruction of the lipid metabolism for the microalga <i>Monoraphidium neglectum</i> from its genome sequence reveals characteristics suitable for biofuel production. <i>BMC Genomics</i> , 2013 , 14, 926	4.5	63
153	MeltDB 2.0-advances of the metabolomics software system. <i>Bioinformatics</i> , 2013 , 29, 2452-9	7.2	63

152	Microbial diversity in different compartments of an aquaponics system. <i>Archives of Microbiology</i> , 2017 , 199, 613-620	3	62
151	EMMA 2--a MAGE-compliant system for the collaborative analysis and integration of microarray data. <i>BMC Bioinformatics</i> , 2009 , 10, 50	3.6	62
150	Chromosomal Locations of mcr-1 and bla CTX-M-15 in Fluoroquinolone-Resistant Escherichia coli ST410. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1689-91	10.2	62
149	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2012 , 13, 144	4.5	60
148	ReadXplorer 2-detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016 , 32, 3702-3708	7.2	59
147	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	3.5	56
146	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	3.7	56
145	A reference genome of the Chinese hamster based on a hybrid assembly strategy. <i>Biotechnology and Bioengineering</i> , 2018 , 115, 2087-2100	4.9	55
144	Construction of a public CHO cell line transcript database using versatile bioinformatics analysis pipelines. <i>PLoS ONE</i> , 2014 , 9, e85568	3.7	52
143	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	3.7	50
142	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, 11-9	3.7	50
141	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	4.5	45
140	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, 5363-77	3.5	43
139	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	3.7	43
138	New insights into <i>Chlamydomonas reinhardtii</i> hydrogen production processes by combined microarray/RNA-seq transcriptomics. <i>Plant Biotechnology Journal</i> , 2013 , 11, 717-33	11.6	42
137	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017 , 261, 10-23	3.7	41
136	Genomics of the proteorhodopsin-containing marine flavobacterium <i>Dokdonia</i> sp. strain MED134. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 8676-86	4.8	41
135	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, 729-30	3.7	40

134	Complete genome of a new Firmicutes species belonging to the dominant human colonic microbiota (<i>Ruminococcus bicirculans</i>) reveals two chromosomes and a selective capacity to utilize plant glucans. <i>Environmental Microbiology</i> , 2014 , 16, 2879-90	5.2	40
133	Genomic avenue to avian colisepticemia. <i>MBio</i> , 2015 , 6,	7.8	39
132	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, 811-24	3.6	39
131	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, 945-56	2.1	39
130	Genomics and physiology of a marine flavobacterium encoding a proteorhodopsin and a xanthorhodopsin-like protein. <i>PLoS ONE</i> , 2013 , 8, e57487	3.7	38
129	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. <i>Journal of Biotechnology</i> , 2012 , 158, 151-5	3.7	37
128	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, 657-70	4.1	37
127	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	3.7	36
126	Conveyor: a workflow engine for bioinformatic analyses. <i>Bioinformatics</i> , 2011 , 27, 903-11	7.2	32
125	BACCardI--a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005 , 21, 853-9	7.2	32
124	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	4.4	31
123	Complete genome sequence of clinical isolate <i>Pantoea ananatis</i> LMG 5342. <i>Journal of Bacteriology</i> , 2012 , 194, 1615-6	3.5	31
122	Intraclonal genome diversity of the major <i>Pseudomonas aeruginosa</i> clones C and PA14. <i>Environmental Microbiology Reports</i> , 2016 , 8, 227-34	3.7	31
121	Comparative genome analysis of <i>Pseudomonas knackmussii</i> B13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015 , 17, 91-104	5.2	30
120	<i>Enterobacter bugandensis</i> : a novel enterobacterial species associated with severe clinical infection. <i>Scientific Reports</i> , 2018 , 8, 5392	4.9	29
119	Bioinformatics support for high-throughput proteomics. <i>Journal of Biotechnology</i> , 2003 , 106, 147-56	3.7	29
118	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, 737-748	2.7	29
117	The pan-genome of <i>Lactobacillus reuteri</i> strains originating from the pig gastrointestinal tract. <i>BMC Genomics</i> , 2015 , 16, 1023	4.5	28

116	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	3.7	28
115	Complete Genome Sequence of the Probiotic <i>Enterococcus faecalis</i> Symbioflor 1 Clone DSM 16431. <i>Genome Announcements</i> , 2013 , 1,		28
114	Time-resolved transcriptome analysis and lipid pathway reconstruction of the oleaginous green microalga reveal a model for triacylglycerol and lipid hyperaccumulation. <i>Biotechnology for Biofuels</i> , 2017 , 10, 197	7.8	27
113	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, 800-13	2.8	27
112	Complete genome sequence of <i>Lactobacillus johnsonii</i> FI9785, a competitive exclusion agent against pathogens in poultry. <i>Journal of Bacteriology</i> , 2009 , 191, 7142-3	3.5	27
111	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	5	25
110	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, 3128-34	7.2	24
109	GABenchToB: a genome assembly benchmark tuned on bacteria and benchtop sequencers. <i>PLoS ONE</i> , 2014 , 9, e107014	3.7	23
108	Comprehensive molecular, genomic and phenotypic analysis of a major clone of <i>Enterococcus faecalis</i> MLST ST40. <i>BMC Genomics</i> , 2015 , 16, 175	4.5	22
107	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, 2605-12	4.3	22
106	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	3.7	22
105	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, 157-67	3.7	22
104	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	5.7	21
103	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in <i>Neisseria meningitidis</i> during Invasive Disease. <i>PLoS ONE</i> , 2017 , 12, e0169892	3.7	21
102	Complete genome sequence of the kirromycin producer <i>Streptomyces collinus</i> TB65 consisting of a linear chromosome and two linear plasmids. <i>Journal of Biotechnology</i> , 2013 , 168, 739-40	3.7	21
101	Construction and evaluation of a whole genome microarray of <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2011 , 12, 579	4.5	21
100	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	3.7	20
99	Whole-genome sequence of the transformable <i>Neisseria meningitidis</i> serogroup A strain WUE2594. <i>Journal of Bacteriology</i> , 2011 , 193, 2064-5	3.5	20

98	Learning to Classify Organic and Conventional Wheat - A Machine Learning Driven Approach Using the MeltDB 2.0 Metabolomics Analysis Platform. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015 , 3, 35	5.8	19
97	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	5	19
96	Carbohydrate-active enzymes identified by metagenomic analysis of deep-sea sediment bacteria. <i>Extremophiles</i> , 2014 , 18, 853-63	3	19
95	Apparent vector-mediated parent-to-offspring transmission in an avian malaria-like parasite. <i>Molecular Ecology</i> , 2015 , 24, 1355-63	5.7	18
94	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	5.7	18
93	MetaSAMS--a novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. <i>Journal of Biotechnology</i> , 2013 , 167, 156-65	3.7	17
92	Multilineage murine stem cells generate complex organoids to model distal lung development and disease. <i>EMBO Journal</i> , 2020 , 39, e103476	13	17
91	Comparative genomics of host adaptive traits in <i>Xanthomonas translucens</i> pv. <i>graminis</i> . <i>BMC Genomics</i> , 2017 , 18, 35	4.5	16
90	Comparative analysis of the Hrp pathogenicity island of <i>Rubus</i> - and <i>Spiraeoideae</i> -infecting <i>Erwinia amylovora</i> strains identifies the IT region as a remnant of an integrative conjugative element. <i>Gene</i> , 2012 , 504, 6-12	3.8	16
89	sp. nov., a cosmopolitan epiphyte originally isolated from pome fruit trees. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016 , 66, 1583-1592	2.2	16
88	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, 8285428	3	16
87	Complete Genome Sequence of the Barley Pathogen <i>Xanthomonas translucens</i> pv. <i>translucens</i> DSM 18974T (ATCC 19319T). <i>Genome Announcements</i> , 2016 , 4,		15
86	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	20.1	15
85	Whole-Genome Sequencing of <i>Erwinia amylovora</i> Strains from Mexico Detects Single Nucleotide Polymorphisms in <i>rpsL</i> Conferring Streptomycin Resistance and in the <i>avrRpt2</i> Effector Altering Host Interactions. <i>Genome Announcements</i> , 2014 , 2,		15
84	Phylogenetic position and virulence apparatus of the pear flower necrosis pathogen <i>Erwinia piriflorinigrans</i> CFBP 5888T as assessed by comparative genomics. <i>Systematic and Applied Microbiology</i> , 2013 , 36, 449-56	4.2	15
83	Platon: identification and characterization of bacterial plasmid contigs in short-read draft assemblies exploiting protein sequence-based replicon distribution scores. <i>Microbial Genomics</i> , 2020 , 6,	4.4	15
82	Complete genome sequence of the porcine isolate <i>Enterococcus faecalis</i> D32. <i>Journal of Bacteriology</i> , 2012 , 194, 5490-1	3.5	14
81	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018 , 6, 76	16.6	13

80	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016 , 222, 11-2	3.7	13
79	Complete genome sequence of the actinobacterium <i>Actinoplanes friuliensis</i> HAG 010964, producer of the lipopeptide antibiotic friulimycin. <i>Journal of Biotechnology</i> , 2014 , 178, 41-2	3.7	13
78	Lipopolysaccharide biosynthesis genes discriminate between <i>Rubus</i> - and <i>Spiraeoideae</i> -infective genotypes of <i>Erwinia amylovora</i> . <i>Molecular Plant Pathology</i> , 2012 , 13, 975-84	5.7	13
77	Whole Genome Sequencing of 39 Invasive <i>Streptococcus pneumoniae</i> Sequence Type 199 Isolates Revealed Switches from Serotype 19A to 15B. <i>PLoS ONE</i> , 2017 , 12, e0169370	3.7	13
76	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	2.2	13
75	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	3.7	13
74	Transcriptome analyses of CHO cells with the next-generation microarray CHO41K: development and validation by analysing the influence of the growth stimulating substance IGF-1 substitute LongR(3.). <i>Journal of Biotechnology</i> , 2014 , 178, 23-31	3.7	12
73	Expansion and re-classification of the extracytoplasmic function (ECF) σ -factor family. <i>Nucleic Acids Research</i> , 2021 , 49, 986-1005	20.1	12
72	Cellular Gene Expression during Hepatitis C Virus Replication as Revealed by Ribosome Profiling. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	11
71	Complete Sequence of Probiotic Symbioflor 2 <i>Escherichia coli</i> Strain G3/10 and Draft Sequences of Symbioflor 2 <i>E. coli</i> Strains G1/2, G4/9, G5, G6/7, and G8. <i>Genome Announcements</i> , 2015 , 3,		11
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