

Alexander Goesmann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

205
papers

11,808
citations

58
h-index

104
g-index

213
ext. papers

14,297
ext. citations

5.9
avg, IF

5.7
L-index

#	Paper	IF	Citations
205	CRP-Like Transcriptional Regulator MrpC Curbs c-di-GMP and 3 β -TcGAMP Nucleotide Levels during Development in <i>Myxococcus xanthus</i> . <i>MBio</i> , 2022 , e0004422	7.8	1
204	What goes around comes around: artificial circular RNAs bypass cellular antiviral responses.. <i>Molecular Therapy - Nucleic Acids</i> , 2022 ,	10.7	1
203	Evolutionarily stable gene clusters shed light on the common grounds of pathogenicity in the <i>Acinetobacter calcoaceticus-baumannii</i> complex. <i>PLoS Genetics</i> , 2022 , 18, e1010020	6	0
202	Bakta: rapid and standardized annotation of bacterial genomes via alignment-free sequence identification. <i>Microbial Genomics</i> , 2021 , 7,	4.4	8
201	Genome Analyses of the Less Aggressive AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	2
200	WASP: a versatile, web-accessible single cell RNA-Seq processing platform. <i>BMC Genomics</i> , 2021 , 22, 195	4.5	0
199	Incipient genome erosion and metabolic streamlining for antibiotic production in a defensive symbiont. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
198	EDGAR3.0: comparative genomics and phylogenomics on a scalable infrastructure. <i>Nucleic Acids Research</i> , 2021 , 49, W185-W192	20.1	8
197	How animals distribute themselves in space: energy landscapes of Antarctic avian predators. <i>Movement Ecology</i> , 2021 , 9, 24	4.6	4
196	Genomic analysis of novel <i>Yarrowia</i> -like yeast symbionts associated with the carrion-feeding burying beetle <i>Nicrophorus vespilloides</i> . <i>BMC Genomics</i> , 2021 , 22, 323	4.5	0
195	mRNA Inventory of Extracellular Vesicles from. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	5
194	Expansion and re-classification of the extracytoplasmic function (ECF) Tfactor family. <i>Nucleic Acids Research</i> , 2021 , 49, 986-1005	20.1	12
193	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	4.9	3
192	Countering reproducibility issues in mathematical models with software engineering techniques: A case study using a one-dimensional mathematical model of the atrioventricular node. <i>PLoS ONE</i> , 2021 , 16, e0254749	3.7	0
191	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
190	Cyclophilin inhibitors restrict Middle East respiratory syndrome coronavirus interferon- λ and in mice. <i>European Respiratory Journal</i> , 2020 , 56,	13.6	9
189	Multilineage murine stem cells generate complex organoids to model distal lung development and disease. <i>EMBO Journal</i> , 2020 , 39, e103476	13	17

188	ReferenceSeeker: rapid determination of appropriate reference genomes. <i>Journal of Open Source Software</i> , 2020 , 5, 1994	5.2	2
187	sp. nov., isolated from beef. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 292-301	2.2	1
186	sp. nov., isolated from meat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 1528-1540	2.2	4
185	The status of the genus (Pot 1992) and the species (Pot 1992). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020 , 70, 5165-5171	2.2	4
184	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
183	High diversity of <i>Vibrio</i> spp. associated with different ecological niches in a marine aquaria system and description of <i>Vibrio aquimaris</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2020 , 43, 126123	4.2	3
182	iCLIP analysis of RNA substrates of the archaeal exosome. <i>BMC Genomics</i> , 2020 , 21, 797	4.5	1
181	<i>Acinetobacter baumannii</i> in manure and anaerobic digestates of German biogas plants. <i>FEMS Microbiology Ecology</i> , 2020 , 96,	4.3	5
180	Whole-Genome Sequences of Clinical <i>Enterobacter bugandensis</i> Isolates from Germany. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	2
179	EDGAR: A Versatile Tool for Phylogenomics 2019 , 1-15		1
178	Complete Genome Sequence of the Corallopyronin A-Producing Myxobacterium <i>Coralloccoccus coralloides</i> B035. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
177	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
176	Fabry disease: Detection of Alu-mediated exon duplication by NGS. <i>Molecular and Cellular Probes</i> , 2019 , 45, 79-83	3.3	1
175	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	4.3	11
174	Complete Genome Sequence of the Plant Growth-Promoting Bacterium Strain E19. <i>International Journal of Genomics</i> , 2019 , 2019, 7586430	2.5	6
173	ADAR1 Is Required for Dendritic Cell Subset Homeostasis and Alveolar Macrophage Function. <i>Journal of Immunology</i> , 2019 , 202, 1099-1111	5.3	5
172	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
171	Flexible metagenome analysis using the MGX framework. <i>Microbiome</i> , 2018 , 6, 76	16.6	13

170	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
169	<i>Enterobacter bugandensis</i> : a novel enterobacterial species associated with severe clinical infection. <i>Scientific Reports</i> , 2018 , 8, 5392	4.9	29
168	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
167	Distinct Nitrogen Provisioning From Organic Amendments in Soil as Influenced by Farming System and Water Regime. <i>Frontiers in Environmental Science</i> , 2018 , 6,	4.8	9
166	<i>Streptomyces ciscaucasicus</i> Sveshnikova et al. 1983 is a later subjective synonym of <i>Streptomyces canus</i> Heinemann et al. 1953. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 42-46	2.2	2
165	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
164	Temporal variation in brain transcriptome is associated with the expression of female mimicry as a sequential male alternative reproductive tactic in fish. <i>Molecular Ecology</i> , 2018 , 27, 789-803	5.7	4
163	Microbial diversity in different compartments of an aquaponics system. <i>Archives of Microbiology</i> , 2017 , 199, 613-620	3	62
162	Massive parallel insertion site sequencing of an arrayed <i>Sinorhizobium meliloti</i> signature-tagged mini-Tn 5 transposon mutant library. <i>Journal of Biotechnology</i> , 2017 , 257, 9-12	3.7	3
161	Rapid protein alignment in the cloud: HAMOND combines fast DIAMOND alignments with Hadoop parallelism. <i>Journal of Biotechnology</i> , 2017 , 257, 58-60	3.7	3
160	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
159	Detection and Characterization of Endobacteria in the Fungal Endophyte <i>Piriformospora indica</i> 2017 , 237-250		1
158	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017 , 199, 1065-1068	3	8
157	Whole-Genome Sequence of the Fruiting Myxobacterium DSM 52655. <i>Genome Announcements</i> , 2017 , 5,		1
156	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
155	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
154	Bioinformatics for NGS-based metagenomics and the application to biogas research. <i>Journal of Biotechnology</i> , 2017 , 261, 10-23	3.7	41
153	Metabolic and evolutionary patterns in the extremely acidophilic archaeon <i>Ferroplasma acidiphilum</i> Y. <i>Scientific Reports</i> , 2017 , 7, 3682	4.9	11

152	Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. <i>BMC Genomics</i> , 2017 , 18, 282	4.5	11
151	Draft genome sequence of pectic polysaccharide-degrading moderate thermophilic bacterium <i>Geobacillus thermodenitrificans</i> DSM 101594. <i>Brazilian Journal of Microbiology</i> , 2017 , 48, 7-8	2.2	6
150	Complete Genome Sequence of the Fruiting Myxobacterium Strain DSM 14697, Generated by PacBio Sequencing. <i>Genome Announcements</i> , 2017 , 5,		6
149	Complete Genome Sequence of the Fruiting Myxobacterium DSM 14713. <i>Genome Announcements</i> , 2017 , 5,		2
148	Induces a Virulence-Dependent microRNA Signature That Regulates the Immune Response in. <i>Frontiers in Microbiology</i> , 2017 , 8, 2463	5.7	10
147	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
146	<i>Streptomyces phaeopurpureus</i> Shinobu 1957 (Approved Lists 1980) and <i>Streptomyces griseorubiginosus</i> (Ryabova and Preobrazhenskaya 1957) Pridham et al. 1958 (Approved Lists 1980) are heterotypic subjective synonyms. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017 , 67, 3111-3116	2.2	3
145	Systems and synthetic biology perspective of the versatile plant-pathogenic and polysaccharide-producing bacterium <i>Xanthomonas campestris</i> . <i>Microbiology (United Kingdom)</i> , 2017 , 163, 1117-1144	2.9	7
144	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
143	Habitat and taxon as driving forces of carbohydrate catabolism in marine heterotrophic bacteria: example of the model algae-associated bacterium <i>Zobellia galactanivorans</i> Dsj. <i>Environmental Microbiology</i> , 2016 , 18, 4610-4627	5.2	72
142	CRISPR System Acquisition and Evolution of an Obligate Intracellular Chlamydia-Related Bacterium. <i>Genome Biology and Evolution</i> , 2016 , 8, 2376-86	3.9	10
141	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
140	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	76
139	Complete Chloroplast and Mitochondrial Genome Sequences of the Hydrocarbon Oil-Producing Green Microalga <i>Botryococcus braunii</i> Race B (Showa). <i>Genome Announcements</i> , 2016 , 4,		4
138	Presence of a widely disseminated <i>Listeria monocytogenes</i> serotype 4b clone in India. <i>Emerging Microbes and Infections</i> , 2016 , 5, e55	18.9	10
137	Insect pathogenicity in plant-beneficial pseudomonads: phylogenetic distribution and comparative genomics. <i>ISME Journal</i> , 2016 , 10, 2527-42	11.9	82
136	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
135	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

134	Complete Genome Sequence of <i>Bacteroides ovatus</i> V975. <i>Genome Announcements</i> , 2016 , 4,		2
133	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, 1689-91	10.2	62
132	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
131	Comparison of Acceleration Techniques for Selected Low-Level Bioinformatics Operations. <i>Frontiers in Genetics</i> , 2016 , 7, 5	4.5	2
130	DistAMo: A Web-Based Tool to Characterize DNA-Motif Distribution on Bacterial Chromosomes. <i>Frontiers in Microbiology</i> , 2016 , 7, 283	5.7	9
129	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
128	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
127	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
126	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
125	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
124	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. <i>Nucleic Acids Research</i> , 2016 , 44, W22-8	20.1	245
123	ReadXplorer 2-detailed read mapping analysis and visualization from one single source. <i>Bioinformatics</i> , 2016 , 32, 3702-3708	7.2	59
122	Apparent vector-mediated parent-to-offspring transmission in an avian malaria-like parasite. <i>Molecular Ecology</i> , 2015 , 24, 1355-63	5.7	18
121	The structure of the <i>Cyberlindnera jadinii</i> genome and its relation to <i>Candida utilis</i> analyzed by the occurrence of single nucleotide polymorphisms. <i>Journal of Biotechnology</i> , 2015 , 211, 20-30	3.7	6
120	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
119	Genome Sequence of the Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH19. <i>Genome Announcements</i> , 2015 , 3,		2
118	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
117	Genomic avenue to avian colisepticemia. <i>MBio</i> , 2015 , 6,	7.8	39

116	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
115	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
114	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
113	Phylogenomic grouping of <i>Listeria monocytogenes</i> . <i>Canadian Journal of Microbiology</i> , 2015 , 61, 637-46	3.2	10
112	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
111	De novo assembly of the dual transcriptomes of a polymorphic raptor species and its malarial parasite. <i>BMC Genomics</i> , 2015 , 16, 1038	4.5	11
110	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
109	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
108	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
107	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS136, a Highly Cytotoxic ExoS-Positive Wound Isolate Recovered from Pyoderma Gangrenosum. <i>Genome Announcements</i> , 2015 , 3,		2
106	Genome Sequence of the Urethral Isolate <i>Pseudomonas aeruginosa</i> RN21. <i>Genome Announcements</i> , 2015 , 3,		2
105	Draft Genome Sequence of the Commercial Biocontrol Strain <i>Pantoea agglomerans</i> P10c. <i>Genome Announcements</i> , 2015 , 3,		9
104	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
103	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
102	Modeling Biology in Modelica: The Human Baroreflex 2015 ,		3
101	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
100	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014 , 505, 546-50.4	5.4	365
99	Carbohydrate-active enzymes identified by metagenomic analysis of deep-sea sediment bacteria. <i>Extremophiles</i> , 2014 , 18, 853-63	3	19

98	Elucidation of insertion elements carried on plasmids and in vitro construction of shuttle vectors from the toxic cyanobacterium <i>Planktothrix</i> . <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4887-97	4.8	11
97	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
96	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
95	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
94	Construction of a public CHO cell line transcript database using versatile bioinformatics analysis pipelines. <i>PLoS ONE</i> , 2014 , 9, e85568	3.7	52
93	GABenchToB: a genome assembly benchmark tuned on bacteria and benchtop sequencers. <i>PLoS ONE</i> , 2014 , 9, e107014	3.7	23
92	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
91	Genome Sequence of the Small-Colony Variant <i>Pseudomonas aeruginosa</i> MH27, Isolated from a Chronic Urethral Catheter Infection. <i>Genome Announcements</i> , 2014 , 2,		7
90	Genome Sequence of the Acute Urethral Catheter Isolate <i>Pseudomonas aeruginosa</i> MH38. <i>Genome Announcements</i> , 2014 , 2,		4
89	Draft Genome Sequence of <i>Pseudomonas aeruginosa</i> Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. <i>Genome Announcements</i> , 2014 , 2,		1
88	AKE - the Accelerated k-mer Exploration web-tool for rapid taxonomic classification and visualization. <i>BMC Bioinformatics</i> , 2014 , 15, 384	3.6	6
87	Discovery of transcription start sites in the Chinese hamster genome by next-generation RNA sequencing. <i>Journal of Biotechnology</i> , 2014 , 190, 64-75	3.7	7
86	<i>Criblamydia sequanensis</i> Harbors a Megaplasmid Encoding Arsenite Resistance. <i>Genome Announcements</i> , 2014 , 2,		9
85	ReadXplorer--visualization and analysis of mapped sequences. <i>Bioinformatics</i> , 2014 , 30, 2247-54	7.2	85
84	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
83	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
82	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013 , 31, 694-5	44.5	141
81	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

80	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
79	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
78	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
77	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
76	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
75	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
74	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
73	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
72	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
71	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013 , 31, 294-6	44.5	255
70	Complete Genome Sequence of the Probiotic <i>Enterococcus faecalis</i> Symbioflor 1 Clone DSM 16431. <i>Genome Announcements</i> , 2013 , 1,		28
69	MeltDB 2.0--advances of the metabolomics software system. <i>Bioinformatics</i> , 2013 , 29, 2452-9	7.2	63
68	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
67	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
66	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
65	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
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