

Thomas Rattei

List of Publications by Citations

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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.

170 papers	17,238 citations	58 h-index	130 g-index
181 ext. papers	23,204 ext. citations	9.7 avg, IF	6.72 L-index



#	Paper	IF	Citations
170	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010 , 463, 763-850.4	50.4	1399
169	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
168	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015 , 528, 504-9	50.4	1148
167	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006 , 440, 790-4	50.4	861
166	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019 , 47, D309-D314	20.1	850
165	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017 , 35, 725-731	44.5	648
164	The dynamic genome of <i>Hydra</i> . <i>Nature</i> , 2010 , 464, 592-6	50.4	613
163	A <i>Nitrospira</i> metagenome illuminates the physiology and evolution of globally important nitrite-oxidizing bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 13479-84	11.5	488
162	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007 , 23, 1026-8.2	8.2	444
161	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , 2017 , 14, 1063-1071	21.6	412
160	amoA-based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of amoA genes from soils of four different geographic regions. <i>Environmental Microbiology</i> , 2012 , 14, 525-39	5.2	402
159	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. <i>Trends in Microbiology</i> , 2010 , 18, 331-40	12.4	390
158	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014 , 42, D23129.1	20.1	387
157	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012 , 40, D284-9	20.1	387
156	Illuminating the evolutionary history of chlamydiae. <i>Science</i> , 2004 , 304, 728-30	33.3	333
155	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010 , 12, 2070-82	5.2	298
154	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D169-72	20.1	278

153	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. <i>Environmental Microbiology</i> , 2012 , 14, 3122-45	5.2	239
152	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013 , 14, R11	18.3	205
151	Sequence-based prediction of type III secreted proteins. <i>PLoS Pathogens</i> , 2009 , 5, e1000376	7.6	194
150	NxrB encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing <i>Nitrospira</i> . <i>Environmental Microbiology</i> , 2014 , 16, 3055-71	5.2	193
149	Independent evolution of the core domain and its flanking sequences in small heat shock proteins. <i>FASEB Journal</i> , 2010 , 24, 3633-42	0.9	180
148	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
147	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , 2015 , 9, 1152-65	11.9	176
146	The genome of <i>Desulfotalea psychrophila</i> , a sulfate-reducing bacterium from permanently cold Arctic sediments. <i>Environmental Microbiology</i> , 2004 , 6, 887-902	5.2	171
145	The Genome of <i>Nitrospina gracilis</i> Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. <i>Frontiers in Microbiology</i> , 2013 , 4, 27	5.7	158
144	Unity in variety--the pan-genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3253-70	8.3	157
143	probeCheck--a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008 , 10, 2894-8	5.2	154
142	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016 , 351, 162-165	33.3	152
141	The <i>Prevotella copri</i> Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , 2019 , 26, 666-679.e7	23.4	141
140	Identification of enzymes involved in anaerobic benzene degradation by a strictly anaerobic iron-reducing enrichment culture. <i>Environmental Microbiology</i> , 2010 , 12, 2783-96	5.2	128
139	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D196-201	10.1	123
138	Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018 , 20, 1041-1063	5.2	120
137	probeBase--an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D586-9	20.1	119
136	The genome of the amoeba symbiont " <i>Candidatus Amoebophilus asiaticus</i> " reveals common mechanisms for host cell interaction among amoeba-associated bacteria. <i>Journal of Bacteriology</i> , 2010 , 192, 1045-57	3.5	113

135	Impact of natural genetic variation on the transcriptome of autotetraploid <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17809-14	11.5	113
134	Functionally relevant diversity of closely related <i>Nitrospira</i> in activated sludge. <i>ISME Journal</i> , 2015 , 9, 643-55	11.9	112
133	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011 , 27, 919-24	7.2	112
132	The genome of the obligate intracellular parasite <i>Trachipleistophora hominis</i> : new insights into microsporidian genome dynamics and reductive evolution. <i>PLoS Pathogens</i> , 2012 , 8, e1002979	7.6	105
131	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012 , 14, 1308-24	5.2	102
130	Effects of season and experimental warming on the bacterial community in a temperate mountain forest soil assessed by 16S rRNA gene pyrosequencing. <i>FEMS Microbiology Ecology</i> , 2012 , 82, 551-62	4.3	101
129	The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , 2010 , 38, D540-4	20.1	90
128	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , 2017 , 2,	7.6	88
127	Distinct signatures of host-microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. <i>ISME Journal</i> , 2014 , 8, 2380-96	11.9	87
126	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014 , 5, 5497	17.4	86
125	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009 , 37, D408-11	20.1	85
124	Combined genomic and proteomic approaches identify gene clusters involved in anaerobic 2-methylnaphthalene degradation in the sulfate-reducing enrichment culture N47. <i>Journal of Bacteriology</i> , 2010 , 192, 295-306	3.5	83
123	Internalization of <i>Pseudomonas aeruginosa</i> Strain PAO1 into Epithelial Cells Is Promoted by Interaction of a T6SS Effector with the Microtubule Network. <i>MBio</i> , 2015 , 6, e00712	7.8	82
122	Deep metagenome and metatranscriptome analyses of microbial communities affiliated with an industrial biogas fermenter, a cow rumen, and elephant feces reveal major differences in carbohydrate hydrolysis strategies. <i>Biotechnology for Biofuels</i> , 2016 , 9, 121	7.8	82
121	Transcriptome Profiling of the Endophyte <i>Burkholderia phytofirmans</i> PsJN Indicates Sensing of the Plant Environment and Drought Stress. <i>MBio</i> , 2015 , 6, e00621-15	7.8	80
120	Effective--a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011 , 39, D591-5	20.1	78
119	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019 , 10, 968	17.4	78
118	EffectiveDB--updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. <i>Nucleic Acids Research</i> , 2016 , 44, D669-74	20.1	74

117	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the Chlamydiae. <i>ISME Journal</i> , 2014 , 8, 115-25	11.9	68
116	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011 , 39, D220-4	20.1	65
115	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing Deltaproteobacterium N47. <i>Environmental Microbiology</i> , 2011 , 13, 1125-37	5.2	59
114	Complete genome sequence of Cronobacter turicensis LMG 23827, a food-borne pathogen causing deaths in neonates. <i>Journal of Bacteriology</i> , 2011 , 193, 309-10	3.5	59
113	Peatland Acidobacteria with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018 , 12, 1729-1742	11.9	58
112	Sulfonolipids as novel metabolite markers of Alistipes and Odoribacter affected by high-fat diets. <i>Scientific Reports</i> , 2017 , 7, 11047	4.9	52
111	A comparative metagenome survey of the fecal microbiota of a breast- and a plant-fed Asian elephant reveals an unexpectedly high diversity of glycoside hydrolase family enzymes. <i>PLoS ONE</i> , 2014 , 9, e106707	3.7	50
110	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010 , 78, 1539-55	4.1	48
109	Comparative analysis of benzoxazinoid biosynthesis in monocots and dicots: independent recruitment of stabilization and activation functions. <i>Plant Cell</i> , 2012 , 24, 915-28	11.6	47
108	pH as a Driver for Ammonia-Oxidizing Archaea in Forest Soils. <i>Microbial Ecology</i> , 2015 , 69, 879-83	4.4	46
107	Complete genome sequences of Desulfosporosinus orientis DSM765T, Desulfosporosinus youngiae DSM17734T, Desulfosporosinus meridiei DSM13257T, and Desulfosporosinus acidiphilus DSM22704T. <i>Journal of Bacteriology</i> , 2012 , 194, 6300-1	3.5	46
106	The genomes of closely related Pantoea ananatis maize seed endophytes having different effects on the host plant differ in secretion system genes and mobile genetic elements. <i>Frontiers in Microbiology</i> , 2015 , 6, 440	5.7	44
105	Phage morphology recapitulates phylogeny: the comparative genomics of a new group of myoviruses. <i>PLoS ONE</i> , 2012 , 7, e40102	3.7	43
104	A distinct microbiota composition is associated with protection from food allergy in an oral mouse immunization model. <i>Clinical Immunology</i> , 2016 , 173, 10-18	9	42
103	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006 , 34, D252-6	20.1	39
102	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015 , 3, 62	16.6	38
101	The evolutionary dynamics of protein-protein interaction networks inferred from the reconstruction of ancient networks. <i>PLoS ONE</i> , 2013 , 8, e58134	3.7	38
100	SIMAP--a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , 2010 , 38, D223-6	20.1	36

99	Challenges in RNA virus bioinformatics. <i>Bioinformatics</i> , 2014 , 30, 1793-9	7.2	34
98	Cellulose as an extracellular matrix component present in <i>Enterobacter sakazakii</i> biofilms. <i>Journal of Food Protection</i> , 2008 , 71, 13-8	2.5	31
97	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , 2016 , 7, 822	5.7	31
96	Molecular characterization of the alpha-glucosidase activity in <i>Enterobacter sakazakii</i> reveals the presence of a putative gene cluster for palatinose metabolism. <i>Systematic and Applied Microbiology</i> , 2006 , 29, 609-25	4.2	30
95	Viruses comprise an extensive pool of mobile genetic elements in eukaryote cell cultures and human clinical samples. <i>FASEB Journal</i> , 2017 , 31, 1987-2000	0.9	29
94	Development of a human vasopressin V-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , 2017 , 7, 41002	4.9	28
93	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. <i>Research in Microbiology</i> , 2013 , 164, 425-38	4	28
92	SIMAP--the similarity matrix of proteins. <i>Bioinformatics</i> , 2005 , 21 Suppl 2, ii42-6	7.2	28
91	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018 , 12, 1964-1976	11.9	28
90	Ultra deep sequencing of <i>Listeria monocytogenes</i> sRNA transcriptome revealed new antisense RNAs. <i>PLoS ONE</i> , 2014 , 9, e83979	3.7	27
89	Massive expansion of Ubiquitination-related gene families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2890-904	8.3	26
88	Comprehensive in silico prediction and analysis of chlamydial outer membrane proteins reflects evolution and life style of the Chlamydiae. <i>BMC Genomics</i> , 2009 , 10, 634	4.5	26
87	Metagenomic analysis reveals presence of <i>Treponema denticola</i> in a tissue biopsy of the Iceman. <i>PLoS ONE</i> , 2014 , 9, e99994	3.7	26
86	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018 , 28, 2348-2355.e8.3	5.3	25
85	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. <i>Current Opinion in Biotechnology</i> , 2016 , 39, 174-181	11.4	25
84	Reef invertebrate viromics: diversity, host specificity and functional capacity. <i>Environmental Microbiology</i> , 2018 , 20, 2125-2141	5.2	24
83	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Ianthella basta</i> . <i>Environmental Microbiology</i> , 2019 , 21, 3831-3854	5.2	23
82	Cloning and characterization of <i>Enterobacter sakazakii</i> pigment genes and in situ spectroscopic analysis of the pigment. <i>FEMS Microbiology Letters</i> , 2006 , 265, 244-8	2.9	23

81	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019 , 10,	7.8	22
80	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019 , 10, 1313	6.2	22
79	Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 14, S1	3.6	22
78	SIMAP--structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2008 , 36, D289-92	20.1	22
77	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <i>MBio</i> , 2016 , 7,	7.8	21
76	In vitro inhibition activity of different bacteriocin-producing <i>Escherichia coli</i> against <i>Salmonella</i> strains isolated from clinical cases. <i>Letters in Applied Microbiology</i> , 2009 , 49, 31-8	2.9	21
75	Genetic diversity of the obligate intracellular bacterium <i>Chlamydomonas pneumoniae</i> by genome-wide analysis of single nucleotide polymorphisms: evidence for highly clonal population structure. <i>BMC Genomics</i> , 2007 , 8, 355	4.5	21
74	The Intraperitoneal Transcriptome of the Opportunistic Pathogen <i>Enterococcus faecalis</i> in Mice. <i>PLoS ONE</i> , 2015 , 10, e0126143	3.7	20
73	Phenotypic and transcriptomic analyses of Sigma L-dependent characteristics in <i>Listeria monocytogenes</i> EGD-e. <i>Food Microbiology</i> , 2012 , 32, 152-64	6	20
72	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010 , 12, 346-58	9.3	20
71	Unraveling the microbial processes of black band disease in corals through integrated genomics. <i>Scientific Reports</i> , 2017 , 7, 40455	4.9	19
70	Signature protein of the PVC superphylum. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 440-5	4.8	18
69	Complete Genome Sequence of <i>Listeria monocytogenes</i> LL195, a Serotype 4b Strain from the 1983-1987 Listeriosis Epidemic in Switzerland. <i>Genome Announcements</i> , 2013 , 1,		18
68	Bacteriocyte-associated gammaproteobacterial symbionts of the <i>Adelges nordmannianae/piceae</i> complex (Hemiptera: Adelgidae). <i>ISME Journal</i> , 2012 , 6, 384-96	11.9	18
67	Great Cause-Small Effect: Undeclared Genetically Engineered Orange Petunias Harbor an Inefficient Dihydroflavonol 4-Reductase. <i>Frontiers in Plant Science</i> , 2018 , 9, 149	6.2	17
66	Critical Assessment of Metagenome Interpretation  benchmark of computational metagenomics software		17
65	Shotgun sequencing of <i>Yersinia enterocolitica</i> strain W22703 (biotype 2, serotype O:9): genomic evidence for oscillation between invertebrates and mammals. <i>BMC Genomics</i> , 2011 , 12, 168	4.5	16
64	The morphology, systematic position and inferred biology of <i>Spiromatosperrum</i>  An extinct genus of Zingiberales. <i>Review of Palaeobotany and Palynology</i> , 2009 , 157, 391-426	1.7	16

63	Draft genome sequence of <i>Lactobacillus casei</i> W56. <i>Journal of Bacteriology</i> , 2012 , 194, 6638	3.5	16
62	SIMAP--the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , 2014 , 42, D279-84	20.1	15
61	Coral-associated viral communities show high levels of diversity and host auxiliary functions. <i>PeerJ</i> , 2017 , 5, e4054	3.1	15
60	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018 , 3,	5	15
59	Characterization of a community-acquired-MRSA USA300 isolate from a river sample in Austria and whole genome sequence based comparison to a diverse collection of USA300 isolates. <i>Scientific Reports</i> , 2018 , 8, 9467	4.9	15
58	The Mouse Functional Genome Database (MfunGD): functional annotation of proteins in the light of their cellular context. <i>Nucleic Acids Research</i> , 2006 , 34, D568-71	20.1	14
57	Exploring Actinobacteria Associated With Rhizosphere and Endosphere of the Native Alpine Medicinal Plant Subspecies. <i>Frontiers in Microbiology</i> , 2019 , 10, 2531	5.7	14
56	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018 , 49, 90-93	2.5	13
55	Peripheral blood vessels are a niche for blood-borne meningococci. <i>Virulence</i> , 2017 , 8, 1808-1819	4.7	13
54	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019 , 9, 6095	4.9	12
53	Prebiotic Effects of Partially Hydrolyzed Guar Gum on the Composition and Function of the Human Microbiota-Results from the PAGODA Trial. <i>Nutrients</i> , 2020 , 12,	6.7	12
52	Growth of Is Enhanced in Cells with Impaired Mitochondrial Function. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 499	5.9	12
51	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021 , 15, 3159-3180	11.9	12
50	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019 , 11,	6.2	11
49	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. <i>Environmental Microbiology</i> , 2019 , 21, 3873-3884	5.2	11
48	Variant profiling of evolving prokaryotic populations. <i>PeerJ</i> , 2017 , 5, e2997	3.1	11
47	Transcriptomic and Proteomic Analysis of <i>Arion vulgaris</i> --Proteins for Probably Successful Survival Strategies?. <i>PLoS ONE</i> , 2016 , 11, e0150614	3.7	11
46	Recombination drives evolution of the <i>Clostridium difficile</i> 16S-23S rRNA intergenic spacer region. <i>PLoS ONE</i> , 2014 , 9, e106545	3.7	10

45	Oxytocin-like signaling in ants influences metabolic gene expression and locomotor activity. <i>FASEB Journal</i> , 2018 , 32, fj201800443	0.9	9
44	MScDB: a mass spectrometry-centric protein sequence database for proteomics. <i>Journal of Proteome Research</i> , 2013 , 12, 2386-98	5.6	9
43	Beyond the BestSmatch: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , 2008 , 24, 621-8	7.2	9
42	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , 2019 , 9, 1652	4.9	9
41	Hybrid de novo transcriptome assembly of poinsettia (<i>Euphorbia pulcherrima</i> Willd. Ex Klotsch) bracts. <i>BMC Genomics</i> , 2019 , 20, 900	4.5	8
40	Assessment of urban microbiome assemblies with the help of targeted in silico gold standards. <i>Biology Direct</i> , 2018 , 13, 22	7.2	8
39	Thermal stress modifies the marine sponge virome. <i>Environmental Microbiology Reports</i> , 2019 , 11, 690-697	3.7	7
38	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , 2016 , 32, 3327-3329	7.2	7
37	A promiscuous beta-glucosidase is involved in benzoxazinoid deglycosylation in <i>Lamium galeobdolon</i> . <i>Phytochemistry</i> , 2018 , 156, 224-233	4	7
36	Genomic factors related to tissue tropism in <i>Chlamydia pneumoniae</i> infection. <i>BMC Genomics</i> , 2015 , 16, 268	4.5	6
35	A proteotranscriptomic study of silk-producing glands from the orb-weaving spiders. <i>Molecular Omics</i> , 2019 , 15, 256-270	4.4	6
34	The <i>Prevotella copri</i> complex comprises four distinct clades that are underrepresented in Westernised populations		6
33	Viral ecogenomics across the Porifera. <i>Microbiome</i> , 2020 , 8, 144	16.6	6
32	Functional analysis of the finO distal region of plasmid R1. <i>Plasmid</i> , 2011 , 65, 159-68	3.3	5
31	in ancient human remains. <i>World Journal of Gastroenterology</i> , 2019 , 25, 6289-6298	5.6	5
30	Novel taxa of Acidobacteriota involved in seafloor sulfur cycling		5
29	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. <i>Frontiers in Microbiology</i> , 2020 , 11, 584222	5.7	5
28	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , 2021 , 15, 2779-2791	11.9	5

27	Learning From Limited Data: Towards Best Practice Techniques for Antimicrobial Resistance Prediction From Whole Genome Sequencing Data. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 610348	5.9	5
26	DeepNOG: Fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , 2020 ,	7.2	4
25	DNA-foraging bacteria in the seafloor		4
24	NVT: a fast and simple tool for the assessment of RNA-seq normalization strategies. <i>Bioinformatics</i> , 2016 , 32, 3682-3684	7.2	4
23	Characterization of 19 new microsatellite loci for the Omani barb <i>Garra barreimiae</i> from 454 sequences. <i>BMC Research Notes</i> , 2014 , 7, 522	2.3	3
22	Genome sequencing of <i>Chlamydia trachomatis</i> serovars E and F reveals substantial genetic variation. <i>Pathogens and Disease</i> , 2017 , 75,	4.2	3
21	Draft Genome Sequence of the Growth-Promoting Endophyte <i>Paenibacillus</i> sp. P22, Isolated from <i>Populus</i> . <i>Genome Announcements</i> , 2014 , 2,		3
20	Hallstatt miners consumed blue cheese and beer during the Iron Age and retained a non-Westernized gut microbiome until the Baroque period. <i>Current Biology</i> , 2021 , 31, 5149-5162.e6	6.3	3
19	Molecular causes of an evolutionary shift along the parasitism-mutualism continuum in a bacterial symbiont. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21658-21666	11.5	3
18	Regulation of the Mitochondrion-Fatty Acid Axis for the Metabolic Reprogramming of <i>Chlamydia trachomatis</i> during Treatment with β -Lactam Antimicrobials. <i>MBio</i> , 2021 , 12,	7.8	3
17	Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. <i>Biomedicine</i> , 2021 , 9,	4.8	3
16	Insecticidal Toxicity of Involves the Novel Enterotoxin YacT. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 392	5.9	3
15	Revealing the Venomous Secrets of the Spider's Web. <i>Journal of Proteome Research</i> , 2020 , 19, 3044-3059.	3.6	2
14	Complete Genome Sequence of <i>Listeria monocytogenes</i> Lm60, a Strain with an Enhanced Cold Adaptation Capacity. <i>Genome Announcements</i> , 2014 , 2,		2
13	Using Public Resource Computing and Systematic Pre-calculation for Large Scale Sequence Analysis. <i>Lecture Notes in Computer Science</i> , 2007 , 11-18	0.9	2
12	Growth arrest in the active rare biosphere		2
11	Isolate-Based Surveillance of <i>Bordetella pertussis</i> , Austria, 2018-2020. <i>Emerging Infectious Diseases</i> , 2021 , 27, 862-871	10.2	2
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7	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical spongelanthella basta		1
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