

# Thomas Rattei

## List of Publications by Year in descending order

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166  
papers

26,492  
citations

16411

64  
h-index

7333

152  
g-index

181  
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181  
docs citations

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times ranked

32817  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	6.5	2,575
2	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-D293.	6.5	1,937
3	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	13.7	1,878
4	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
5	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.	9.4	1,512
6	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	13.7	1,075
7	The dynamic genome of <i>Hydra</i> . <i>Nature</i> , 2010, 464, 592-596.	13.7	743
8	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, 13479-13484.	3.3	732
9	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007, 23, 1026-1028.	1.8	639
10	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
11	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
12	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
13	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, 525-539.	1.8	485
14	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. <i>Trends in Microbiology</i> , 2010, 18, 331-340.	3.5	431
15	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
16	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010, 12, 2070-2082.	1.8	394
17	Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730.	6.0	373
18	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	6.5	348

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19	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. <i>Environmental Microbiology</i> , 2012, 14, 3122-3145.	1.8	332
20	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , 2015, 9, 1152-1165.	4.4	331
21	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.	13.9	296
22	<i>NxrB</i> encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing <i>Nitrospira</i> . <i>Environmental Microbiology</i> , 2014, 16, 3055-3071.	1.8	280
23	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.	5.1	274
24	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.	1.5	243
25	Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376.	2.1	230
26	Genomic insights into the <i>Acidobacteria</i> reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , 2018, 20, 1041-1063.	1.8	228
27	Independent evolution of the core domain and its flanking sequences in small heat shock proteins. <i>FASEB Journal</i> , 2010, 24, 3633-3642.	0.2	219
28	The genome of <i>Desulfotalea psychrophila</i> , a sulfate-reducing bacterium from permanently cold Arctic sediments. <i>Environmental Microbiology</i> , 2004, 6, 887-902.	1.8	204
29	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165.	6.0	200
30	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	3.5	184
31	Functionally relevant diversity of closely related <i>Nitrospira</i> in activated sludge. <i>ISME Journal</i> , 2015, 9, 643-655.	4.4	172
32	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-D674.	6.5	172
33	probeCheck - a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898.	1.8	170
34	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168
35	probeBase - an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Research</i> , 2016, 44, D586-D589.	6.5	163
36	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201.	6.5	156

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37	Identification of enzymes involved in anaerobic benzene degradation by a strictly anaerobic iron-reducing enrichment culture. <i>Environmental Microbiology</i> , 2010, 12, 2783-2796.	1.8	152
38	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of <i>Mucispirillum schaedleri</i> , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , 2017, 2, .	1.7	148
39	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.	6.2	141
40	The Genome of the Amoeba Symbiont <i>Candidatus</i> <i>Amoebophilus asiaticus</i> Reveals Common Mechanisms for Host Cell Interaction among Amoeba-Associated Bacteria. <i>Journal of Bacteriology</i> , 2010, 192, 1045-1057.	1.0	138
41	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	1.8	137
42	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, 17809-17814.	3.3	136
43	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.	1.8	132
44	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, 551-562.	1.3	128
45	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019, 10, 968.	5.8	128
46	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.	2.1	127
47	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012, 14, 1308-1324.	1.8	124
48	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.	1.8	121
49	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	5.8	119
50	The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , 2010, 38, D540-D544.	6.5	114
51	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, 2380-2396.	4.4	106
52	Effective—a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011, 39, D591-D595.	6.5	102
53	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.	1.0	101
54	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	6.5	97

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55	pH as a Driver for Ammonia-Oxidizing Archaea in Forest Soils. <i>Microbial Ecology</i> , 2015, 69, 879-883.	1.4	95
56	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i> . <i>ISME Journal</i> , 2014, 8, 115-125.	4.4	94
57	The genomes of closely related <i>Pantoea ananatis</i> 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.	1.5	85
58	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.	1.1	80
59	Sulfonolipids as novel metabolite markers of <i>Alistipes</i> and <i>Odoribacter</i> affected by high-fat diets. <i>Scientific Reports</i> , 2017, 7, 11047.	1.6	78
60	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	6.5	77
61	Complete Genome Sequence of <i>Cronobacter turicensis</i> LMG 23827, a Food-Borne Pathogen Causing Deaths in Neonates. <i>Journal of Bacteriology</i> , 2011, 193, 309-310.	1.0	76
62	Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765, <i>Desulfosporosinus youngiae</i> DSM17734, <i>Desulfosporosinus meridiei</i> DSM13257, and <i>Desulfosporosinus acidiphilus</i> DSM22704. <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301.	1.0	73
63	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.	0.2	69
64	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing <i>Deltaproteobacterium</i> N47. <i>Environmental Microbiology</i> , 2011, 13, 1125-1137.	1.8	66
65	Comparative Analysis of Benzoxazinoid Biosynthesis in Monocots and Dicots: Independent Recruitment of Stabilization and Activation Functions. <i>Plant Cell</i> , 2012, 24, 915-928.	3.1	58
66	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010, 78, 1539-1555.	1.2	57
67	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	4.9	56
68	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313.	1.7	54
69	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180.	4.4	54
70	Phage Morphology Recapitulates Phylogeny: The Comparative Genomics of a New Group of Myoviruses. <i>PLoS ONE</i> , 2012, 7, e40102.	1.1	52
71	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.	1.4	52
72	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.	1.8	50

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73	Bacteriocyte-associated gammaproteobacterial symbionts of the <i>Adelges nordmannianae/piceae</i> complex (Hemiptera: Adelgidae). <i>ISME Journal</i> , 2012, 6, 384-396.	4.4	49
74	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , 2016, 7, 822.	1.5	49
75	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018, 12, 1964-1976.	4.4	48
76	The Evolutionary Dynamics of Protein-Protein Interaction Networks Inferred from the Reconstruction of Ancient Networks. <i>PLoS ONE</i> , 2013, 8, e58134.	1.1	47
77	Challenges in RNA virus bioinformatics. <i>Bioinformatics</i> , 2014, 30, 1793-1799.	1.8	47
78	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. <i>Research in Microbiology</i> , 2013, 164, 425-438.	1.0	46
79	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006, 34, D252-D256.	6.5	44
80	Phenotypic and transcriptomic analyses of Sigma L-dependent characteristics in <i>Listeria monocytogenes</i> EGD-e. <i>Food Microbiology</i> , 2012, 32, 152-164.	2.1	43
81	Massive Expansion of Ubiquitination-Related Gene Families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2014, 31, 2890-2904.	3.5	43
82	Reef invertebrate viromics: diversity, host specificity and functional capacity. <i>Environmental Microbiology</i> , 2018, 20, 2125-2141.	1.8	41
83	SIMAP—a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , 2010, 38, D223-D226.	6.5	40
84	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
85	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
86	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, 1257.	1.7	39
87	Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , 2015, 16, S1.	1.2	38
88	Molecular characterization of the Î±-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, 609-625.	1.2	37
89	Cellulose as an Extracellular Matrix Component Present in <i>Enterobacter sakazakii</i> Biofilms. <i>Journal of Food Protection</i> , 2008, 71, 13-18.	0.8	37
90	The Intraperitoneal Transcriptome of the Opportunistic Pathogen <i>Enterococcus faecalis</i> in Mice. <i>PLoS ONE</i> , 2015, 10, e0126143.	1.1	36

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91	Unraveling the microbial processes of black band disease in corals through integrated genomics. <i>Scientific Reports</i> , 2017, 7, 40455.	1.6	36
92	SIMAP--The similarity matrix of proteins. <i>Bioinformatics</i> , 2005, 21, ii42-ii46.	1.8	35
93	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019, 10, .	1.8	35
94	Coral-associated viral communities show high levels of diversity and host auxiliary functions. <i>PeerJ</i> , 2017, 5, e4054.	0.9	34
95	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.	1.2	33
96	Development of a human vasopressin V1a-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , 2017, 7, 41002.	1.6	33
97	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93.	0.6	32
98	Ultra Deep Sequencing of <i>Listeria monocytogenes</i> sRNA Transcriptome Revealed New Antisense RNAs. <i>PLoS ONE</i> , 2014, 9, e83979.	1.1	31
99	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, 244-248.	0.7	30
100	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, .	0.8	30
101	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.	3.3	30
102	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.	4.4	30
103	Metagenomic Analysis Reveals Presence of <i>Treponema denticola</i> in a Tissue Biopsy of the Iceman. <i>PLoS ONE</i> , 2014, 9, e99994.	1.1	30
104	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , 2021, 6, 885-898.	5.9	29
105	Great Cause- Small Effect: Undeclared Genetically Engineered Orange Petunias Harbor an Inefficient Dihydroflavonol 4-Reductase. <i>Frontiers in Plant Science</i> , 2018, 9, 149.	1.7	28
106	Exploring Actinobacteria Associated With Rhizosphere and Endosphere of the Native Alpine Medicinal Plant <i>Leontopodium nivale</i> Subspecies <i>alpinum</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2531.	1.5	28
107	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.	1.2	27
108	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, 31-38.	1.0	27

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109	SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292.	6.5	24
110	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-D284.	6.5	24
111	Genetic diversity of the obligate intracellular bacterium <i>Chlamydomonas reinhardtii</i> by genome-wide analysis of single nucleotide polymorphisms: evidence for highly clonal population structure. <i>BMC Genomics</i> , 2007, 8, 355.	1.2	23
112	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010, 12, 346-358.	1.0	23
113	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	1.3	23
114	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <i>MBio</i> , 2016, 7, .	1.8	22
115	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.	1.6	22
116	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019, 11, 401.	1.5	22
117	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.	1.8	22
118	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. <i>Environmental Microbiology</i> , 2019, 21, 3873-3884.	1.8	21
119	Viral ecogenomics across the Porifera. <i>Microbiome</i> , 2020, 8, 144.	4.9	21
120	Signature Protein of the PVC Superphylum. <i>Applied and Environmental Microbiology</i> , 2014, 80, 440-445.	1.4	20
121	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , 2019, 9, 1652.	1.6	20
122	Peripheral blood vessels are a niche for blood-borne meningococci. <i>Virulence</i> , 2017, 8, 1808-1819.	1.8	19
123	The morphology, systematic position and inferred biology of <i>SpiromatospERMUM</i> – An extinct genus of Zingiberales. <i>Review of Palaeobotany and Palynology</i> , 2009, 157, 391-426.	0.8	18
124	Draft Genome Sequence of <i>Lactobacillus casei</i> W56. <i>Journal of Bacteriology</i> , 2012, 194, 6638-6638.	1.0	18
125	Growth of <i>Chlamydia pneumoniae</i> Is Enhanced in Cells with Impaired Mitochondrial Function. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 499.	1.8	18
126	Oxytocin-like signaling in ants influences metabolic gene expression and locomotor activity. <i>FASEB Journal</i> , 2018, 32, 6808-6821.	0.2	17



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127	DeepNOG: fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , 2021, 36, 5304-5312.	1.8	16
128	Variant profiling of evolving prokaryotic populations. <i>PeerJ</i> , 2017, 5, e2997.	0.9	16
129	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-D571.	6.5	15
130	Insecticidal Toxicity of <i>Yersinia frederiksenii</i> Involves the Novel Enterotoxin YacT. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 392.	1.8	14
131	Hybrid de novo transcriptome assembly of poinsettia ( <i>Euphorbia pulcherrima</i> Willd. Ex Klotsch) bracts. <i>BMC Genomics</i> , 2019, 20, 900.	1.2	14
132	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.	1.8	14
133	A time-resolved multi-omics atlas of <i>Acanthamoeba castellanii</i> encystment. <i>Nature Communications</i> , 2022, 13, .	5.8	14
134	Genomic factors related to tissue tropism in <i>Chlamydia pneumoniae</i> infection. <i>BMC Genomics</i> , 2015, 16, 268.	1.2	13
135	Thermal stress modifies the marine sponge virome. <i>Environmental Microbiology Reports</i> , 2019, 11, 690-698.	1.0	13
136	<i>Helicobacter pylori</i> in ancient human remains. <i>World Journal of Gastroenterology</i> , 2019, 25, 6289-6298.	1.4	13
137	Beyond the "best" match: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , 2008, 24, 621-628.	1.8	12
138	Transcriptomic and Proteomic Analysis of <i>Arion vulgaris</i> Proteins for Probably Successful Survival Strategies?. <i>PLoS ONE</i> , 2016, 11, e0150614.	1.1	12
139	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.	3.3	12
140	Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. <i>Biomedicines</i> , 2021, 9, 910.	1.4	12
141	MScDB: A Mass Spectrometry-centric Protein Sequence Database for Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2386-2398.	1.8	11
142	Recombination Drives Evolution of the <i>Clostridium difficile</i> 16S-23S rRNA Intergenic Spacer Region. <i>PLoS ONE</i> , 2014, 9, e106545.	1.1	11
143	A promiscuous beta-glucosidase is involved in benzoxazinoid deglycosylation in <i>Lamium galeobdolon</i> . <i>Phytochemistry</i> , 2018, 156, 224-233.	1.4	11
144	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , 2016, 32, 3327-3329.	1.8	10

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145	Assessment of urban microbiome assemblies with the help of targeted in silico gold standards. <i>Biology Direct</i> , 2018, 13, 22.	1.9	10
146	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. <i>Frontiers in Microbiology</i> , 2020, 11, 584222.	1.5	9
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