

Thomas Rattei

List of Publications by Year in descending order

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Version: 2024-02-01

166
papers

26,492
citations

16451

64
h-index

7348

152
g-index

181
all docs

181
docs citations

181
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. | 14.5 | 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. | 14.5 | 1,937 |
| 3 | Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509. | 27.8 | 1,878 |
| 4 | Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768. | 27.8 | 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. | 17.5 | 1,512 |
| 6 | Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794. | 27.8 | 1,075 |
| 7 | The dynamic genome of <i>Hydra</i> . <i>Nature</i> , 2010, 464, 592-596. | 27.8 | 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. | 7.1 | 732 |
| 9 | Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007, 23, 1026-1028. | 4.1 | 639 |
| 10 | Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071. | 19.0 | 635 |
| 11 | eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239. | 14.5 | 526 |
| 12 | eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289. | 14.5 | 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. | 3.8 | 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. | 7.7 | 431 |
| 15 | Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37. | 17.5 | 414 |
| 16 | Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010, 12, 2070-2082. | 3.8 | 394 |
| 17 | Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730. | 12.6 | 373 |
| 18 | MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172. | 14.5 | 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. | 3.8 | 332 |
| 20 | Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , 2015, 9, 1152-1165. | 9.8 | 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. | 9.6 | 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. | 3.8 | 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. | 11.0 | 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. | 3.5 | 243 |
| 25 | Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376. | 4.7 | 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. | 3.8 | 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. | 0.5 | 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. | 3.8 | 204 |
| 29 | The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165. | 12.6 | 200 |
| 30 | Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270. | 8.9 | 184 |
| 31 | Functionally relevant diversity of closely related <i>Nitrospira</i> in activated sludge. <i>ISME Journal</i> , 2015, 9, 643-655. | 9.8 | 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. | 14.5 | 172 |
| 33 | probeCheck - a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898. | 3.8 | 170 |
| 34 | Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742. | 9.8 | 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. | 14.5 | 163 |
| 36 | MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201. | 14.5 | 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. | 3.8 | 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, . | 3.8 | 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. | 2.2 | 138 |
| 41 | B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924. | 4.1 | 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. | 7.1 | 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. | 4.1 | 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. | 2.7 | 128 |
| 45 | Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019, 10, 968. | 12.8 | 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. | 4.7 | 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. | 3.8 | 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. | 4.1 | 121 |
| 49 | Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497. | 12.8 | 119 |
| 50 | The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , 2010, 38, D540-D544. | 14.5 | 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. | 9.8 | 106 |
| 52 | Effective—a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011, 39, D591-D595. | 14.5 | 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. | 2.2 | 101 |
| 54 | PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411. | 14.5 | 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. | 2.8 | 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. | 9.8 | 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. | 3.5 | 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. | 2.5 | 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. | 3.3 | 78 |
| 60 | MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224. | 14.5 | 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. | 2.2 | 76 |
| 62 | Complete Genome Sequences of <i>Desulfosporosinus orientis</i> DSM765 ^T , <i>Desulfosporosinus youngiae</i> DSM17734 ^T , <i>Desulfosporosinus meridiei</i> DSM13257 ^T , and <i>Desulfosporosinus acidiphilus</i> DSM22704 ^T . <i>Journal of Bacteriology</i> , 2012, 194, 6300-6301. | 2.2 | 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. | 0.5 | 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. | 3.8 | 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. | 6.6 | 58 |
| 66 | Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010, 78, 1539-1555. | 2.5 | 57 |
| 67 | A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62. | 11.1 | 56 |
| 68 | A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313. | 3.6 | 54 |
| 69 | Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180. | 9.8 | 54 |
| 70 | Phage Morphology Recapitulates Phylogeny: The Comparative Genomics of a New Group of Myoviruses. <i>PLoS ONE</i> , 2012, 7, e40102. | 2.5 | 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. | 3.2 | 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. | 3.8 | 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. | 9.8 | 49 |
| 74 | HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , 2016, 7, 822. | 3.5 | 49 |
| 75 | Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018, 12, 1964-1976. | 9.8 | 48 |
| 76 | The Evolutionary Dynamics of Protein-Protein Interaction Networks Inferred from the Reconstruction of Ancient Networks. <i>PLoS ONE</i> , 2013, 8, e58134. | 2.5 | 47 |
| 77 | Challenges in RNA virus bioinformatics. <i>Bioinformatics</i> , 2014, 30, 1793-1799. | 4.1 | 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. | 2.1 | 46 |
| 79 | SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006, 34, D252-D256. | 14.5 | 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. | 4.2 | 43 |
| 81 | Massive Expansion of Ubiquitination-Related Gene Families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2014, 31, 2890-2904. | 8.9 | 43 |
| 82 | Reef invertebrate viromics: diversity, host specificity and functional capacity. <i>Environmental Microbiology</i> , 2018, 20, 2125-2141. | 3.8 | 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. | 14.5 | 40 |
| 84 | The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9. | 3.9 | 39 |
| 85 | The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095. | 3.3 | 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. | 4.1 | 39 |
| 87 | Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , 2015, 16, S1. | 2.6 | 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. | 2.8 | 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. | 1.7 | 37 |
| 90 | The Intraperitoneal Transcriptome of the Opportunistic Pathogen <i>Enterococcus faecalis</i> in Mice. <i>PLoS ONE</i> , 2015, 10, e0126143. | 2.5 | 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. | 3.3 | 36 |
| 92 | SIMAP--The similarity matrix of proteins. <i>Bioinformatics</i> , 2005, 21, ii42-ii46. | 4.1 | 35 |
| 93 | Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019, 10, . | 4.1 | 35 |
| 94 | Coral-associated viral communities show high levels of diversity and host auxiliary functions. <i>PeerJ</i> , 2017, 5, e4054. | 2.0 | 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. | 2.8 | 33 |
| 96 | Development of a human vasopressin V1a-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , 2017, 7, 41002. | 3.3 | 33 |
| 97 | Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93. | 1.7 | 32 |
| 98 | Ultra Deep Sequencing of <i>Listeria monocytogenes</i> sRNA Transcriptome Revealed New Antisense RNAs. <i>PLoS ONE</i> , 2014, 9, e83979. | 2.5 | 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. | 1.8 | 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. | 6.6 | 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. | 9.8 | 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. | 2.5 | 30 |
| 104 | Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , 2021, 6, 885-898. | 13.3 | 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. | 3.6 | 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. | 3.5 | 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. | 2.8 | 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. | 2.2 | 27 |

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|-----|---|------|-----------|
| 109 | SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292. | 14.5 | 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. | 14.5 | 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. | 2.8 | 23 |
| 112 | Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010, 12, 346-358. | 1.9 | 23 |
| 113 | The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, . | 2.9 | 23 |
| 114 | Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <i>MBio</i> , 2016, 7, . | 4.1 | 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. | 3.3 | 22 |
| 116 | Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019, 11, 401. | 3.3 | 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. | 3.9 | 22 |
| 118 | Highly variable mRNA half-life time within marine bacterial taxa and functional genes. <i>Environmental Microbiology</i> , 2019, 21, 3873-3884. | 3.8 | 21 |
| 119 | Viral ecogenomics across the Porifera. <i>Microbiome</i> , 2020, 8, 144. | 11.1 | 21 |
| 120 | Signature Protein of the PVC Superphylum. <i>Applied and Environmental Microbiology</i> , 2014, 80, 440-445. | 3.1 | 20 |
| 121 | Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , 2019, 9, 1652. | 3.3 | 20 |
| 122 | Peripheral blood vessels are a niche for blood-borne meningococci. <i>Virulence</i> , 2017, 8, 1808-1819. | 4.4 | 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. | 1.5 | 18 |
| 124 | Draft Genome Sequence of <i>Lactobacillus casei</i> W56. <i>Journal of Bacteriology</i> , 2012, 194, 6638-6638. | 2.2 | 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. | 3.9 | 18 |
| 126 | Oxytocin-like signaling in ants influences metabolic gene expression and locomotor activity. <i>FASEB Journal</i> , 2018, 32, 6808-6821. | 0.5 | 17 |

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|-----|--|------|-----------|
| 127 | DeepNOG: fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , 2021, 36, 5304-5312. | 4.1 | 16 |
| 128 | Variant profiling of evolving prokaryotic populations. <i>PeerJ</i> , 2017, 5, e2997. | 2.0 | 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. | 14.5 | 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. | 3.9 | 14 |
| 131 | Hybrid de novo transcriptome assembly of poinsettia (<i>Euphorbia pulcherrima</i> Willd. Ex Klotsch) bracts. <i>BMC Genomics</i> , 2019, 20, 900. | 2.8 | 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. | 3.9 | 14 |
| 133 | A time-resolved multi-omics atlas of <i>Acanthamoeba castellanii</i> encystment. <i>Nature Communications</i> , 2022, 13, . | 12.8 | 14 |
| 134 | Genomic factors related to tissue tropism in <i>Chlamydia pneumoniae</i> infection. <i>BMC Genomics</i> , 2015, 16, 268. | 2.8 | 13 |
| 135 | Thermal stress modifies the marine sponge virome. <i>Environmental Microbiology Reports</i> , 2019, 11, 690-698. | 2.4 | 13 |
| 136 | <i>Helicobacter pylori</i> in ancient human remains. <i>World Journal of Gastroenterology</i> , 2019, 25, 6289-6298. | 3.3 | 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. | 4.1 | 12 |
| 138 | Transcriptomic and Proteomic Analysis of <i>Arion vulgaris</i> Proteins for Probably Successful Survival Strategies?. <i>PLoS ONE</i> , 2016, 11, e0150614. | 2.5 | 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. | 7.1 | 12 |
| 140 | Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. <i>Biomedicines</i> , 2021, 9, 910. | 3.2 | 12 |
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