

Thomas Rattei

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2678456/publications.pdf>

Version: 2024-02-01

166
papers

26,492
citations

16411

64
h-index

7333

152
g-index

181
all docs

181
docs citations

181
times ranked

32817
citing authors

#	ARTICLE	IF	CITATIONS
1	A time-resolved multi-omics atlas of <i>Acanthamoeba castellanii</i> encystment. <i>Nature Communications</i> , 2022, 13, .	5.8	14
2	<i>Dahlia variabilis</i> cultivar "Seattle"™ as a model plant for anthochlor biosynthesis. <i>Plant Physiology and Biochemistry</i> , 2021, 159, 193-201.	2.8	7
3	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
4	Isolate-Based Surveillance of <i>Bordetella pertussis</i> , Austria, 2018–2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 862-871.	2.0	3
5	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
6	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, .	1.8	9
7	ITN–VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
8	Tamock: simulation of habitat-specific benchmark data in metagenomics. <i>BMC Bioinformatics</i> , 2021, 22, 227.	1.2	1
9	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , 2021, 15, 3159-3180.	4.4	54
10	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , 2021, 6, 885-898.	5.9	29
11	Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. <i>Biomedicines</i> , 2021, 9, 910.	1.4	12
12	Alteration of the phenylpropanoid pathway by watercore disorder in apple (<i>Malus x domestica</i>). <i>Scientia Horticulturae</i> , 2021, 289, 110438.	1.7	9
13	DeepNOG: fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , 2021, 36, 5304-5312.	1.8	16
14	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
15	Genome-Wide Mutation Scoring for Machine-Learning-Based Antimicrobial Resistance Prediction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13049.	1.8	8
16	Viral ecogenomics across the Porifera. <i>Microbiome</i> , 2020, 8, 144.	4.9	21
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Revealing the Venomous Secrets of the Spider's Web. <i>Journal of Proteome Research</i> , 2020, 19, 3044-3059.	1.8	5
20	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
21	scikit-hubness: Hubness Reduction and Approximate Neighbor Search. <i>Journal of Open Source Software</i> , 2020, 5, 1957.	2.0	2
22	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. <i>Environmental Microbiology</i> , 2019, 21, 3873-3884.	1.8	21
23	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Lanthella basta</i> . <i>Environmental Microbiology</i> , 2019, 21, 3831-3854.	1.8	50
24	Thermal stress modifies the marine sponge virome. <i>Environmental Microbiology Reports</i> , 2019, 11, 690-698.	1.0	13
25	A proteotranscriptomic study of silk-producing glands from the orb-weaving spiders. <i>Molecular Omics</i> , 2019, 15, 256-270.	1.4	8
26	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , 2019, 10, 1313.	1.7	54
27	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
28	P034 A dietary fibre intervention shapes the microbiome towards an anti-inflammatory tone. <i>Journal of Crohn's and Colitis</i> , 2019, 13, S103-S103.	0.6	0
29	Proteome Changes Paralleling the Olfactory Conditioning in the Forager Honey Bee and Provision of a Brain Proteomics Dataset. <i>Proteomics</i> , 2019, 19, e1900094.	1.3	2
30	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , 2019, 9, 6095.	1.6	39
31	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019, 11, 401.	1.5	22
32	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , 2019, 10, .	1.8	35
33	Man-made microbial resistances in built environments. <i>Nature Communications</i> , 2019, 10, 968.	5.8	128
34	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , 2019, 9, 1652.	1.6	20
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
38	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
39	<i>Helicobacter pylori</i> in ancient human remains. <i>World Journal of Gastroenterology</i> , 2019, 25, 6289-6298.	1.4	13
40	Auswirkung von PHGG auf Zusammensetzung und Funktion des intestinalen Mikrobioms – Ergebnisse der PAGODA Studie. , 2019, 57, .		0
41	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168
42	Reef invertebrate viromics: diversity, host specificity and functional capacity. <i>Environmental Microbiology</i> , 2018, 20, 2125-2141.	1.8	41
43	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , 2018, 49, 90-93.	0.6	32
44	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
45	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
46	Assessment of urban microbiome assemblies with the help of targeted in silico gold standards. <i>Biology Direct</i> , 2018, 13, 22.	1.9	10
47	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , 2018, 3, .	1.3	23
48	A promiscuous beta-glucosidase is involved in benzoxazinoid deglycosylation in <i>Lamium galeobdolon</i> . <i>Phytochemistry</i> , 2018, 156, 224-233.	1.4	11
49	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , 2018, 12, 1964-1976.	4.4	48
50	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
51	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
52	The Iceman’s Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
53	Oxytocin-like signaling in ants influences metabolic gene expression and locomotor activity. <i>FASEB Journal</i> , 2018, 32, 6808-6821.	0.2	17
54	Unraveling the microbial processes of black band disease in corals through integrated genomics. <i>Scientific Reports</i> , 2017, 7, 40455.	1.6	36

#	ARTICLE	IF	CITATIONS
55	Development of a human vasopressin V1a-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , 2017, 7, 41002.	1.6	33
56	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
57	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
58	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	9.0	635
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	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
61	Peripheral blood vessels are a niche for blood-borne meningococci. <i>Virulence</i> , 2017, 8, 1808-1819.	1.8	19
62	Genome sequencing of <i>Chlamydia trachomatis</i> serovars E and F reveals substantial genetic variation. <i>Pathogens and Disease</i> , 2017, 75, .	0.8	6
63	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
64	Variant profiling of evolving prokaryotic populations. <i>PeerJ</i> , 2017, 5, e2997.	0.9	16
65	Coral-associated viral communities show high levels of diversity and host auxiliary functions. <i>PeerJ</i> , 2017, 5, e4054.	0.9	34
66	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
67	Transcriptomic and Proteomic Analysis of <i>Arion vulgaris</i> â€”Proteins for Probably Successful Survival Strategies?. <i>PLoS ONE</i> , 2016, 11, e0150614.	1.1	12
68	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , 2016, 32, 3327-3329.	1.8	10
69	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
70	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
71	NVT: a fast and simple tool for the assessment of RNA-seq normalization strategies. <i>Bioinformatics</i> , 2016, 32, 3682-3684.	1.8	6
72	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <i>MBio</i> , 2016, 7, .	1.8	22

#	ARTICLE	IF	CITATIONS
73	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
74	probeBaseâ€”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
75	The 5300-year-old <i>Helicobacter pylori</i> genome of the Iceman. <i>Science</i> , 2016, 351, 162-165.	6.0	200
76	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
77	EffectiveDBâ€”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
78	Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , 2015, 16, S1.	1.2	38
79	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , 2015, 3, 62.	4.9	56
80	The Intraperitoneal Transcriptome of the Opportunistic Pathogen <i>Enterococcus faecalis</i> in Mice. <i>PLoS ONE</i> , 2015, 10, e0126143.	1.1	36
81	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
82	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
83	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , 2015, 9, 1152-1165.	4.4	331
84	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
85	Genomic factors related to tissue tropism in <i>Chlamydia pneumoniae</i> infection. <i>BMC Genomics</i> , 2015, 16, 268.	1.2	13
86	Complete nitrification by <i>Nitrospira</i> bacteria. <i>Nature</i> , 2015, 528, 504-509.	13.7	1,878
87	Functionally relevant diversity of closely related <i>Nitrospira</i> in activated sludge. <i>ISME Journal</i> , 2015, 9, 643-655.	4.4	172
88	pH as a Driver for Ammonia-Oxidizing Archaea in Forest Soils. <i>Microbial Ecology</i> , 2015, 69, 879-883.	1.4	95
89	Ultra Deep Sequencing of <i>Listeria monocytogenes</i> sRNA Transcriptome Revealed New Antisense RNAs. <i>PLoS ONE</i> , 2014, 9, e83979.	1.1	31
90	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

#	ARTICLE	IF	CITATIONS
91	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the <i>Chlamydiae</i> . ISME Journal, 2014, 8, 115-125.	4.4	94
92	Draft Genome Sequence of the Growth-Promoting Endophyte <i>Paenibacillus</i> sp. P22, Isolated from <i>Populus</i> . Genome Announcements, 2014, 2, .	0.8	4
93	Complete Genome Sequence of <i>Listeria monocytogenes</i> Lm60, a Strain with an Enhanced Cold Adaptation Capacity. Genome Announcements, 2014, 2, .	0.8	2
94	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. Nature Communications, 2014, 5, 5497.	5.8	119
95	<i>ncpN</i> encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing <i>Nitrospira</i> . Environmental Microbiology, 2014, 16, 3055-3071.	1.8	280
96	Massive Expansion of Ubiquitination-Related Gene Families within the <i>Chlamydiae</i> . Molecular Biology and Evolution, 2014, 31, 2890-2904.	3.5	43
97	SIMAP—the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. Nucleic Acids Research, 2014, 42, D279-D284.	6.5	24
98	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
99	Challenges in RNA virus bioinformatics. Bioinformatics, 2014, 30, 1793-1799.	1.8	47
100	Signature Protein of the PVC Superphylum. Applied and Environmental Microbiology, 2014, 80, 440-445.	1.4	20
101	Characterization of 19 new microsatellite loci for the Omani barb <i>Garra barreimiae</i> from 454 sequences. BMC Research Notes, 2014, 7, 522.	0.6	4
102	Distinct signatures of host-microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. ISME Journal, 2014, 8, 2380-2396.	4.4	106
103	Metagenomic Analysis Reveals Presence of <i>Treponema denticola</i> in a Tissue Biopsy of the Iceman. PLoS ONE, 2014, 9, e99994.	1.1	30
104	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. PLoS ONE, 2014, 9, e106707.	1.1	80
105	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. Research in Microbiology, 2013, 164, 425-438.	1.0	46
106	MScDB: A Mass Spectrometry-centric Protein Sequence Database for Proteomics. Journal of Proteome Research, 2013, 12, 2386-2398.	1.8	11
107	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 2013, 14, R11.	13.9	296
108	Complete Genome Sequence of <i>Listeria monocytogenes</i> LL195, a Serotype 4b Strain from the 1983-1987 Listeriosis Epidemic in Switzerland. Genome Announcements, 2013, 1, .	0.8	30

#	ARTICLE	IF	CITATIONS
109	The Evolutionary Dynamics of Protein-Protein Interaction Networks Inferred from the Reconstruction of Ancient Networks. PLoS ONE, 2013, 8, e58134.	1.1	47
110	The Genome of Nitrospina gracilis Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. Frontiers in Microbiology, 2013, 4, 27.	1.5	243
111	The Genome of the Obligate Intracellular Parasite Trachipleistophora hominis: New Insights into Microsporidian Genome Dynamics and Reductive Evolution. PLoS Pathogens, 2012, 8, e1002979.	2.1	127
112	Bacteriocyte-associated gammaproteobacterial symbionts of the <i>Adelges nordmannianae/piceae</i> complex (Hemiptera: Adelgidae). ISME Journal, 2012, 6, 384-396.	4.4	49
113	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. Journal of Bacteriology, 2012, 194, 6300-6301.	1.0	73
114	Comparative Analysis of Benzoxazinoid Biosynthesis in Monocots and Dicots: Independent Recruitment of Stabilization and Activation Functions. Plant Cell, 2012, 24, 915-928.	3.1	58
115	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	6.5	490
116	Draft Genome Sequence of <i>Lactobacillus casei</i> W56. Journal of Bacteriology, 2012, 194, 6638-6638.	1.0	18
117	Phenotypic and transcriptomic analyses of Sigma L-dependent characteristics in <i>Listeria monocytogenes</i> EGD-e. Food Microbiology, 2012, 32, 152-164.	2.1	43
118	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. Environmental Microbiology, 2012, 14, 3122-3145.	1.8	332
119	Phage Morphology Recapitulates Phylogeny: The Comparative Genomics of a New Group of Myoviruses. PLoS ONE, 2012, 7, e40102.	1.1	52
120	Effects of season and experimental warming on the bacterial community in a temperate mountain forest soil assessed by 16S rRNA gene pyrosequencing. FEMS Microbiology Ecology, 2012, 82, 551-562.	1.3	128
121	<i>amoA</i> -based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of <i>amoA</i> genes from soils of four different geographic regions. Environmental Microbiology, 2012, 14, 525-539.	1.8	485
122	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. Environmental Microbiology, 2012, 14, 1308-1324.	1.8	124
123	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing <i>Deltaproteobacterium</i> N47. Environmental Microbiology, 2011, 13, 1125-1137.	1.8	66
124	Functional analysis of the <i>finO</i> distal region of plasmid R1. Plasmid, 2011, 65, 159-168.	0.4	6
125	Shotgun sequencing of <i>Yersinia enterocolitica</i> strain W22703 (biotype 2, serotype O:9): genomic evidence for oscillation between invertebrates and mammals. BMC Genomics, 2011, 12, 168.	1.2	33
126	MIPS: curated databases and comprehensive secondary data resources in 2010. Nucleic Acids Research, 2011, 39, D220-D224.	6.5	77

#	ARTICLE	IF	CITATIONS
127	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	1.8	137
128	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
129	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	3.5	184
130	Effective--a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011, 39, D591-D595.	6.5	102
131	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010, 12, 2070-2082.	1.8	394
132	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010, 12, 346-358.	1.0	23
133	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010, 78, 1539-1555.	1.2	57
134	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	13.7	1,685
135	The dynamic genome of Hydra. <i>Nature</i> , 2010, 464, 592-596.	13.7	743
136	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
137	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
138	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
139	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
140	The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , 2010, 38, D540-D544.	6.5	114
141	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
142	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
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	6.5	97
146	Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376.	2.1	230
147	The morphology, systematic position and inferred biology of <i>Spirematospermum</i> " An extinct genus of Zingiberales. <i>Review of Palaeobotany and Palynology</i> , 2009, 157, 391-426.	0.8	18
148	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
149	<i>In vitro</i> 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
150	probeCheck " a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898.	1.8	170
151	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
152	Modification of the In Vitro Release Profile of Cetrorelix by Complexation with Biophilic Partners. <i>Current Drug Delivery</i> , 2008, 5, 319-323.	0.8	1
153	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
154	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201.	6.5	156
155	SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292.	6.5	24
156	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007, 23, 1026-1028.	1.8	639
157	Genetic diversity of the obligate intracellular bacterium <i>Chlamydophila pneumoniae</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
158	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
159	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	13.7	1,075
160	Molecular characterization of the α -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
161	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
162	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006, 34, D252-D256.	6.5	44

#	ARTICLE	IF	CITATIONS
163	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	6.5	348
164	SIMAP--The similarity matrix of proteins. <i>Bioinformatics</i> , 2005, 21, ii42-ii46.	1.8	35
165	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
166	Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730.	6.0	373