

# Thomas Rattei

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/2678456/thomas-rattei-publications-by-year.pdf>

**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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> , <b>2021</b> , 31, 5149-5162.e6	6.3	3
169	Sulfoquinovose is a select nutrient of prominent bacteria and a source of hydrogen sulfide in the human gut. <i>ISME Journal</i> , <b>2021</b> , 15, 2779-2791	11.9	5
168	Regulation of the Mitochondrion-Fatty Acid Axis for the Metabolic Reprogramming of Chlamydia trachomatis during Treatment with Lactam Antimicrobials. <i>MBio</i> , <b>2021</b> , 12,	7.8	3
167	ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , <b>2021</b> , 13,	6.2	1
166	Tamock: simulation of habitat-specific benchmark data in metagenomics. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 227	3.6	
165	Novel taxa of Acidobacteriota implicated in seafloor sulfur cycling. <i>ISME Journal</i> , <b>2021</b> , 15, 3159-3180	11.9	12
164	Genomic insights into diverse bacterial taxa that degrade extracellular DNA in marine sediments. <i>Nature Microbiology</i> , <b>2021</b> , 6, 885-898	26.6	1
163	Predictive Antibiotic Susceptibility Testing by Next-Generation Sequencing for Periprosthetic Joint Infections: Potential and Limitations. <i>Biomedicines</i> , <b>2021</b> , 9,	4.8	3
162	Dahlia variabilis cultivar SeattleSas a model plant for anthochlor biosynthesis. <i>Plant Physiology and Biochemistry</i> , <b>2021</b> , 159, 193-201	5.4	1
161	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> , <b>2021</b> , 11, 610348	5.9	5
160	Isolate-Based Surveillance of Bordetella pertussis, Austria, 2018-2020. <i>Emerging Infectious Diseases</i> , <b>2021</b> , 27, 862-871	10.2	2
159	Alteration of the phenylpropanoid pathway by watercore disorder in apple (Malus x domestica). <i>Scientia Horticulturae</i> , <b>2021</b> , 289, 110438	4.1	1
158	Revealing the Venomous Secrets of the Spider's Web. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 3044-3059.	3.6	2
157	Prebiotic Effects of Partially Hydrolyzed Guar Gum on the Composition and Function of the Human Microbiota-Results from the PAGODA Trial. <i>Nutrients</i> , <b>2020</b> , 12,	6.7	12
156	scikit-hubness: Hubness Reduction and Approximate Neighbor Search. <i>Journal of Open Source Software</i> , <b>2020</b> , 5, 1957	5.2	1
155	DeepNOG: Fast and accurate protein orthologous group assignment. <i>Bioinformatics</i> , <b>2020</b> ,	7.2	4
154	Viral ecogenomics across the Porifera. <i>Microbiome</i> , <b>2020</b> , 8, 144	16.6	6

153	Functional Seasonality of Free-Living and Particle-Associated Prokaryotic Communities in the Coastal Adriatic Sea. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 584222	5.7	5
152	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> , <b>2020</b> , 117, 21658-21666	11.5	3
151	P034 A dietary fibre intervention shapes the microbiome towards an anti-inflammatory tone. <i>Journal of Crohns and Colitis</i> , <b>2019</b> , 13, S103-S103	1.5	
150	Proteome Changes Paralleling the Olfactory Conditioning in the Forager Honey Bee and Provision of a Brain Proteomics Dataset. <i>Proteomics</i> , <b>2019</b> , 19, e1900094	4.8	1
149	The horse Y chromosome as an informative marker for tracing sire lines. <i>Scientific Reports</i> , <b>2019</b> , 9, 60954.9	4.9	12
148	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , <b>2019</b> , 11,	6.2	11
147	Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. <i>MBio</i> , <b>2019</b> , 10,	7.8	22
146	Highly variable mRNA half-life time within marine bacterial taxa and functional genes. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 3873-3884	5.2	11
145	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>lanthella basta</i> . <i>Environmental Microbiology</i> , <b>2019</b> , 21, 3831-3854	5.2	23
144	Thermal stress modifies the marine sponge virome. <i>Environmental Microbiology Reports</i> , <b>2019</b> , 11, 690-698	5.7	7
143	A proteotranscriptomic study of silk-producing glands from the orb-weaving spiders. <i>Molecular Omics</i> , <b>2019</b> , 15, 256-270	4.4	6
142	A Bioinformatics Guide to Plant Microbiome Analysis. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 1313	6.2	22
141	The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations. <i>Cell Host and Microbe</i> , <b>2019</b> , 26, 666-679.e7	23.4	141
140	in ancient human remains. <i>World Journal of Gastroenterology</i> , <b>2019</b> , 25, 6289-6298	5.6	5
139	Man-made microbial resistances in built environments. <i>Nature Communications</i> , <b>2019</b> , 10, 968	17.4	78
138	Plasmid DNA contaminant in molecular reagents. <i>Scientific Reports</i> , <b>2019</b> , 9, 1652	4.9	9
137	Hybrid de novo transcriptome assembly of poinsettia ( <i>Euphorbia pulcherrima</i> Willd. Ex Klotzsch) bracts. <i>BMC Genomics</i> , <b>2019</b> , 20, 900	4.5	8
136	Exploring Actinobacteria Associated With Rhizosphere and Endosphere of the Native Alpine Medicinal Plant Subspecies. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2531	5.7	14

135	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , <b>2019</b> , 37, 29-37	44.5	180
134	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D309-D314	20.1	850
133	Peatland Acidobacteria with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , <b>2018</b> , 12, 1729-1742	11.9	58
132	Reef invertebrate viromics: diversity, host specificity and functional capacity. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 2125-2141	5.2	24
131	Asian horses deepen the MSY phylogeny. <i>Animal Genetics</i> , <b>2018</b> , 49, 90-93	2.5	13
130	Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 1041-1063	5.2	120
129	Great Cause-Small Effect: Undeclared Genetically Engineered Orange Petunias Harbor an Inefficient Dihydroflavonol 4-Reductase. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 149	6.2	17
128	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , <b>2018</b> , 28, 2348-2355.e63	6.3	25
127	Oxytocin-like signaling in ants influences metabolic gene expression and locomotor activity. <i>FASEB Journal</i> , <b>2018</b> , 32, fj201800443	0.9	9
126	Insecticidal Toxicity of Involves the Novel Enterotoxin YacT. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2018</b> , 8, 392	5.9	3
125	Assessment of urban microbiome assemblies with the help of targeted in silico gold standards. <i>Biology Direct</i> , <b>2018</b> , 13, 22	7.2	8
124	The Genetic Transformation of <i>Chlamydia pneumoniae</i> . <i>MSphere</i> , <b>2018</b> , 3,	5	15
123	A promiscuous beta-glucosidase is involved in benzoxazinoid deglycosylation in <i>Lamium galeobdolon</i> . <i>Phytochemistry</i> , <b>2018</b> , 156, 224-233	4	7
122	Interplay between gut microbiota metabolism and inflammation in HIV infection. <i>ISME Journal</i> , <b>2018</b> , 12, 1964-1976	11.9	28
121	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> , <b>2018</b> , 8, 9467	4.9	15
120	Unraveling the microbial processes of black band disease in corals through integrated genomics. <i>Scientific Reports</i> , <b>2017</b> , 7, 40455	4.9	19
119	Development of a human vasopressin V-receptor antagonist from an evolutionary-related insect neuropeptide. <i>Scientific Reports</i> , <b>2017</b> , 7, 41002	4.9	28
118	Viruses comprise an extensive pool of mobile genetic elements in eukaryote cell cultures and human clinical samples. <i>FASEB Journal</i> , <b>2017</b> , 31, 1987-2000	0.9	29

117	Lifestyle and Horizontal Gene Transfer-Mediated Evolution of , a Core Member of the Murine Gut Microbiota. <i>MSystems</i> , <b>2017</b> , 2,	7.6	88
116	Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. <i>Nature Methods</i> , <b>2017</b> , 14, 1063-1071	21.6	412
115	Sulfonolipids as novel metabolite markers of Alistipes and Odoribacter affected by high-fat diets. <i>Scientific Reports</i> , <b>2017</b> , 7, 11047	4.9	52
114	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 725-731	44.5	648
113	Peripheral blood vessels are a niche for blood-borne meningococci. <i>Virulence</i> , <b>2017</b> , 8, 1808-1819	4.7	13
112	Genome sequencing of Chlamydia trachomatis serovars E and F reveals substantial genetic variation. <i>Pathogens and Disease</i> , <b>2017</b> , 75,	4.2	3
111	Growth of Is Enhanced in Cells with Impaired Mitochondrial Function. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2017</b> , 7, 499	5.9	12
110	Variant profiling of evolving prokaryotic populations. <i>PeerJ</i> , <b>2017</b> , 5, e2997	3.1	11
109	Coral-associated viral communities show high levels of diversity and host auxiliary functions. <i>PeerJ</i> , <b>2017</b> , 5, e4054	3.1	15
108	Comprehensive Identification of Meningococcal Genes and Small Noncoding RNAs Required for Host Cell Colonization. <i>MBio</i> , <b>2016</b> , 7,	7.8	21
107	A distinct microbiota composition is associated with protection from food allergy in an oral mouse immunization model. <i>Clinical Immunology</i> , <b>2016</b> , 173, 10-18	9	42
106	probeBase--an online resource for rRNA-targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D586-9	20.1	119
105	The 5300-year-old Helicobacter pylori genome of the Iceman. <i>Science</i> , <b>2016</b> , 351, 162-165	33.3	152
104	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D286-93	20.1	1211
103	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> , <b>2016</b> , 44, D669-74	20.1	74
102	HoloVir: A Workflow for Investigating the Diversity and Function of Viruses in Invertebrate Holobionts. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 822	5.7	31
101	Transcriptomic and Proteomic Analysis of Arion vulgaris--Proteins for Probably Successful Survival Strategies?. <i>PLoS ONE</i> , <b>2016</b> , 11, e0150614	3.7	11
100	ConsPred: a rule-based (re-)annotation framework for prokaryotic genomes. <i>Bioinformatics</i> , <b>2016</b> , 32, 3327-3329	7.2	7

99	High definition for systems biology of microbial communities: metagenomics gets genome-centric and strain-resolved. <i>Current Opinion in Biotechnology</i> , <b>2016</b> , 39, 174-181	11.4	25
98	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> , <b>2016</b> , 9, 121	7.8	82
97	NVT: a fast and simple tool for the assessment of RNA-seq normalization strategies. <i>Bioinformatics</i> , <b>2016</b> , 32, 3682-3684	7.2	4
96	Transcriptome Profiling of the Endophyte Burkholderia phytofirmans PsJN Indicates Sensing of the Plant Environment and Drought Stress. <i>MBio</i> , <b>2015</b> , 6, e00621-15	7.8	80
95	Genomic factors related to tissue tropism in Chlamydia pneumoniae infection. <i>BMC Genomics</i> , <b>2015</b> , 16, 268	4.5	6
94	Complete nitrification by Nitrospira bacteria. <i>Nature</i> , <b>2015</b> , 528, 504-9	50.4	1148
93	Functionally relevant diversity of closely related Nitrospira in activated sludge. <i>ISME Journal</i> , <b>2015</b> , 9, 643-55	11.9	112
92	pH as a Driver for Ammonia-Oxidizing Archaea in Forest Soils. <i>Microbial Ecology</i> , <b>2015</b> , 69, 879-83	4.4	46
91	Prediction of microbial phenotypes based on comparative genomics. <i>BMC Bioinformatics</i> , <b>2015</b> , 16 Suppl 14, S1	3.6	22
90	A viability-linked metagenomic analysis of cleanroom environments: eukarya, prokaryotes, and viruses. <i>Microbiome</i> , <b>2015</b> , 3, 62	16.6	38
89	The Intraperitoneal Transcriptome of the Opportunistic Pathogen Enterococcus faecalis in Mice. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126143	3.7	20
88	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> , <b>2015</b> , 6, 440	5.7	44
87	Internalization of Pseudomonas aeruginosa Strain PAO1 into Epithelial Cells Is Promoted by Interaction of a T6SS Effector with the Microtubule Network. <i>MBio</i> , <b>2015</b> , 6, e00712	7.8	82
86	Phylogenetic and environmental diversity of DsrAB-type dissimilatory (bi)sulfite reductases. <i>ISME Journal</i> , <b>2015</b> , 9, 1152-65	11.9	176
85	Challenges in RNA virus bioinformatics. <i>Bioinformatics</i> , <b>2014</b> , 30, 1793-9	7.2	34
84	Signature protein of the PVC superphylum. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 440-5	4.8	18
83	Characterization of 19 new microsatellite loci for the Omani barb Garra barreimiae from 454 sequences. <i>BMC Research Notes</i> , <b>2014</b> , 7, 522	2.3	3
82	Distinct signatures of host-microbial meta-metabolome and gut microbiome in two C57BL/6 strains under high-fat diet. <i>ISME Journal</i> , <b>2014</b> , 8, 2380-96	11.9	87

81	Ultra deep sequencing of <i>Listeria monocytogenes</i> sRNA transcriptome revealed new antisense RNAs. <i>PLoS ONE</i> , <b>2014</b> , 9, e83979	3.7	27
80	Recombination drives evolution of the <i>Clostridium difficile</i> 16S-23S rRNA intergenic spacer region. <i>PLoS ONE</i> , <b>2014</b> , 9, e106545	3.7	10
79	Integrating metagenomic and amplicon databases to resolve the phylogenetic and ecological diversity of the Chlamydiae. <i>ISME Journal</i> , <b>2014</b> , 8, 115-25	11.9	68
78	Draft Genome Sequence of the Growth-Promoting Endophyte <i>Paenibacillus</i> sp. P22, Isolated from <i>Populus</i> . <i>Genome Announcements</i> , <b>2014</b> , 2,		3
77	Complete Genome Sequence of <i>Listeria monocytogenes</i> Lm60, a Strain with an Enhanced Cold Adaptation Capacity. <i>Genome Announcements</i> , <b>2014</b> , 2,		2
76	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , <b>2014</b> , 5, 5497	17.4	86
75	NxrB encoding the beta subunit of nitrite oxidoreductase as functional and phylogenetic marker for nitrite-oxidizing Nitrospira. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 3055-71	5.2	193
74	Massive expansion of Ubiquitination-related gene families within the Chlamydiae. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 2890-904	8.3	26
73	SIMAP--the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D279-84	20.1	15
72	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D23120-1	20.1	387
71	Metagenomic analysis reveals presence of <i>Treponema denticola</i> in a tissue biopsy of the Iceman. <i>PLoS ONE</i> , <b>2014</b> , 9, e99994	3.7	26
70	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> , <b>2014</b> , 9, e106707	3.7	50
69	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. <i>Research in Microbiology</i> , <b>2013</b> , 164, 425-38	4	28
68	MScDB: a mass spectrometry-centric protein sequence database for proteomics. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 2386-98	5.6	9
67	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , <b>2013</b> , 14, R11	18.3	205
66	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> , <b>2013</b> , 1,		18
65	The evolutionary dynamics of protein-protein interaction networks inferred from the reconstruction of ancient networks. <i>PLoS ONE</i> , <b>2013</b> , 8, e58134	3.7	38
64	The Genome of <i>Nitrospina gracilis</i> Illuminates the Metabolism and Evolution of the Major Marine Nitrite Oxidizer. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 27	5.7	158




63	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> , <b>2012</b> , 82, 551-62	4.3	101
62	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> , <b>2012</b> , 14, 525-39	5.2	402
61	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 1308-24	5.2	102
60	Phenotypic and transcriptomic analyses of Sigma L-dependent characteristics in <i>Listeria monocytogenes</i> EGD-e. <i>Food Microbiology</i> , <b>2012</b> , 32, 152-64	6	20
59	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. <i>Environmental Microbiology</i> , <b>2012</b> , 14, 3122-45	5.2	239
58	Phage morphology recapitulates phylogeny: the comparative genomics of a new group of myoviruses. <i>PLoS ONE</i> , <b>2012</b> , 7, e40102	3.7	43
57	The genome of the obligate intracellular parasite <i>Trachipleistophora hominis</i> : new insights into microsporidian genome dynamics and reductive evolution. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002979	7.6	105
56	Bacteriocyte-associated gammaproteobacterial symbionts of the <i>Adelges nordmannianae/piceae</i> complex (Hemiptera: Adelgidae). <i>ISME Journal</i> , <b>2012</b> , 6, 384-96	11.9	18
55	Complete genome sequences of <i>Desulfosporosinus orientis</i> DSM765T, <i>Desulfosporosinus youngiae</i> DSM17734T, <i>Desulfosporosinus meridiei</i> DSM13257T, and <i>Desulfosporosinus acidiphilus</i> DSM22704T. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6300-1	3.5	46
54	Comparative analysis of benzoxazinoid biosynthesis in monocots and dicots: independent recruitment of stabilization and activation functions. <i>Plant Cell</i> , <b>2012</b> , 24, 915-28	11.6	47
53	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D284-9	20.1	387
52	Draft genome sequence of <i>Lactobacillus casei</i> W56. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 6638	3.5	16
51	Genomic insights into the metabolic potential of the polycyclic aromatic hydrocarbon degrading sulfate-reducing <i>Deltaproteobacterium</i> N47. <i>Environmental Microbiology</i> , <b>2011</b> , 13, 1125-37	5.2	59
50	Functional analysis of the <i>finO</i> distal region of plasmid R1. <i>Plasmid</i> , <b>2011</b> , 65, 159-68	3.3	5
49	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> , <b>2011</b> , 12, 168	4.5	16
48	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D220-4	20.1	65
47	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , <b>2011</b> , 27, 919-24	7.2	112
46	Complete genome sequence of <i>Cronobacter turicensis</i> LMG 23827, a food-borne pathogen causing deaths in neonates. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 309-10	3.5	59



45	Unity in variety--the pan-genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 3253-70	8.3	157
44	Effective--a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D591-5	20.1	78
43	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , <b>2010</b> , 78, 1539-55	4.1	48
42	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , <b>2010</b> , 463, 763-8	50.4	1399
41	The dynamic genome of <i>Hydra</i> . <i>Nature</i> , <b>2010</b> , 464, 592-6	50.4	613
40	Identification of enzymes involved in anaerobic benzene degradation by a strictly anaerobic iron-reducing enrichment culture. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 2783-96	5.2	128
39	SIMAP--a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D223-6	20.1	36
38	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> , <b>2010</b> , 192, 295-306	3.5	83
37	Independent evolution of the core domain and its flanking sequences in small heat shock proteins. <i>FASEB Journal</i> , <b>2010</b> , 24, 3633-42	0.9	180
36	The Negatome database: a reference set of non-interacting protein pairs. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D540-4	20.1	90
35	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> , <b>2010</b> , 192, 1045-57	3.5	113
34	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. <i>Trends in Microbiology</i> , <b>2010</b> , 18, 331-40	12.4	390
33	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> , <b>2010</b> , 107, 17809-14	11.5	113
32	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> , <b>2010</b> , 107, 13479-84	11.5	488
31	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , <b>2010</b> , 12, 2070-82	5.2	298
30	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , <b>2010</b> , 12, 346-58	9.3	20
29	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D408-11	20.1	85
28	Sequence-based prediction of type III secreted proteins. <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000376	7.6	194

27	The morphology, systematic position and inferred biology of <i>Spirematospermum</i> [An extinct genus of Zingiberales. <i>Review of Palaeobotany and Palynology</i> , <b>2009</b> , 157, 391-426	1.7	16
26	Comprehensive in silico prediction and analysis of chlamydial outer membrane proteins reflects evolution and life style of the Chlamydiae. <i>BMC Genomics</i> , <b>2009</b> , 10, 634	4.5	26
25	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> , <b>2009</b> , 49, 31-8	2.9	21
24	probeCheck--a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , <b>2008</b> , 10, 2894-8	5.2	154
23	Beyond the \$best\$match: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , <b>2008</b> , 24, 621-8	7.2	9
22	Modification of the in vitro release profile of Cetrorelix by complexation with biophilic partners. <i>Current Drug Delivery</i> , <b>2008</b> , 5, 319-23	3.2	1
21	Cellulose as an extracellular matrix component present in <i>Enterobacter sakazakii</i> biofilms. <i>Journal of Food Protection</i> , <b>2008</b> , 71, 13-8	2.5	31
20	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D196-201	10.1	123
19	SIMAP--structuring the network of protein similarities. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D289-92	20.1	22
18	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> , <b>2007</b> , 8, 355	4.5	21
17	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , <b>2007</b> , 23, 1026-8	8.2	444
16	Using Public Resource Computing and Systematic Pre-calculation for Large Scale Sequence Analysis. <i>Lecture Notes in Computer Science</i> , <b>2007</b> , 11-18	0.9	2
15	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> , <b>2006</b> , 29, 609-25	4.2	30
14	The Mouse Functional Genome Database (MfunGD): functional annotation of proteins in the light of their cellular context. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D568-71	20.1	14
13	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D252-6	20.1	39
12	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D169-72	20.1	278
11	Cloning and characterization of <i>Enterobacter sakazakii</i> pigment genes and in situ spectroscopic analysis of the pigment. <i>FEMS Microbiology Letters</i> , <b>2006</b> , 265, 244-8	2.9	23
10	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , <b>2006</b> , 440, 790-4	50.4	861

9	SIMAP--the similarity matrix of proteins. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 2, ii42-6	7.2	28
8	The genome of <i>Desulfotalea psychrophila</i> , a sulfate-reducing bacterium from permanently cold Arctic sediments. <i>Environmental Microbiology</i> , <b>2004</b> , 6, 887-902	5.2	171
7	Illuminating the evolutionary history of chlamydiae. <i>Science</i> , <b>2004</b> , 304, 728-30	33.3	333
6	Critical Assessment of Metagenome Interpretation  benchmark of computational metagenomics software		17
5	Novel taxa of Acidobacteriota involved in seafloor sulfur cycling		5
4	Growth arrest in the active rare biosphere		2
3	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical spongelanthella basta		1
2	DNA-foraging bacteria in the seafloor		4
1	The <i>Prevotella copri</i> complex comprises four distinct clades that are underrepresented in Westernised populations		6