

Bas E Dutilh

List of Publications by Year in descending order

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Version: 2024-02-01

147
papers

16,982
citations

28274

55
h-index

18130

120
g-index

181
all docs

181
docs citations

181
times ranked

20920
citing authors

#	ARTICLE	IF	CITATIONS
1	High viral abundance and low diversity are associated with increased CRISPR-Cas prevalence across microbial ecosystems. <i>Current Biology</i> , 2022, 32, 220-227.e5.	3.9	23
2	Differentiating between viruses and virus species by writing their names correctly. <i>Archives of Virology</i> , 2022, 167, 1231-1234.	2.1	33
3	A metagenomic portrait of the microbial community responsible for two decades of bioremediation of poly-contaminated groundwater. <i>Water Research</i> , 2022, 221, 118767.	11.3	11
4	Gut virome profiling identifies a widespread bacteriophage family associated with metabolic syndrome. <i>Nature Communications</i> , 2022, 13, .	12.8	32
5	The bacterial sulfur cycle in expanding dysoxic and euxinic marine waters. <i>Environmental Microbiology</i> , 2021, 23, 2834-2857.	3.8	145
6	Ecogenomics and metabolic potential of the South Atlantic Ocean microbiome. <i>Science of the Total Environment</i> , 2021, 765, 142758.	8.0	16
7	<i>Virus Bioinformatics</i> . , 2021, , 124-132.		12
8	OGRE: Overlap Graph-based metagenomic Read clustEring. <i>Bioinformatics</i> , 2021, 37, 905-912.	4.1	6
9	Bridging the membrane lipid divide: bacteria of the FCB group superphylum have the potential to synthesize archaeal ether lipids. <i>ISME Journal</i> , 2021, 15, 168-182.	9.8	62
10	<i>Metagenomics in Virology</i> . , 2021, , 133-140.		23
11	Lifestyle of sponge symbiont phages by host prediction and correlative microscopy. <i>ISME Journal</i> , 2021, 15, 2001-2011.	9.8	19
12	ITNâ€™VIRIINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	3.3	5
13	Production of inactivated gram-positive and gram-negative species with preserved cellular morphology and integrity. <i>Journal of Microbiological Methods</i> , 2021, 184, 106208.	1.6	12
14	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	6.4	34
15	Identical sequences found in distant genomes reveal frequent horizontal transfer across the bacterial domain. <i>ELife</i> , 2021, 10, .	6.0	23
16	Optimized bacterial DNA isolation method for microbiome analysis of human tissues. <i>MicrobiologyOpen</i> , 2021, 10, e1191.	3.0	21
17	The human gut microbiome and health inequities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	82
18	RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. <i>Patterns</i> , 2021, 2, 100274.	5.9	53

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19	Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). Archives of Virology, 2021, 166, 2633-2648.	2.1	219
20	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. Archives of Virology, 2021, 166, 3239-3244.	2.1	24
21	Quantifying the Impact of Human Leukocyte Antigen on the Human Gut Microbiota. MSphere, 2021, 6, e0047621.	2.9	12
22	A Prioritized and Validated Resource of Mitochondrial Proteins in <i>Plasmodium</i> Identifies Unique Biology. MSphere, 2021, 6, e0061421.	2.9	16
23	Finding functional associations between prokaryotic virus orthologous groups: a proof of concept. BMC Bioinformatics, 2021, 22, 438.	2.6	2
24	Perspective on taxonomic classification of uncultivated viruses. Current Opinion in Virology, 2021, 51, 207-215.	5.4	31
25	Novel high-resolution targeted sequencing of the cervicovaginal microbiome. BMC Biology, 2021, 19, 267.	3.8	11
26	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. Systematic Biology, 2020, 69, 110-123.	5.6	89
27	Microsatellite instability screening in colorectal adenomas to detect Lynch syndrome patients? A systematic review and meta-analysis. European Journal of Human Genetics, 2020, 28, 277-286.	2.8	22
28	Binomial nomenclature for virus species: a consultation. Archives of Virology, 2020, 165, 519-525.	2.1	51
29	Impact of phosphate dosing on the microbial ecology of drinking water distribution systems: Fieldwork studies in chlorinated networks. Water Research, 2020, 187, 116416.	11.3	19
30	Adsorption Sequencing as a Rapid Method to Link Environmental Bacteriophages to Hosts. IScience, 2020, 23, 101439.	4.1	23
31	Prophages are associated with extensive CRISPR-Cas auto-immunity. Nucleic Acids Research, 2020, 48, 12074-12084.	14.5	35
32	Evolutionary Study of the Crassphage Virus at Gene Level. Viruses, 2020, 12, 1035.	3.3	8
33	Development of Styrene Maleic Acid Lipid Particles as a Tool for Studies of Phage-Host Interactions. Journal of Virology, 2020, 94, .	3.4	3
34	Growth rate alterations of human colorectal cancer cells by 157 gut bacteria. Gut Microbes, 2020, 12, 1799733.	9.8	26
35	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	2.1	202
36	Editorial: Computational Methods for Microbiome Analysis. Frontiers in Genetics, 2020, 11, 623897.	2.3	0

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37	Genome reconstruction of the non-culturable spinach downy mildew <i>Peronospora effusa</i> by metagenome filtering. <i>PLoS ONE</i> , 2020, 15, e0225808.	2.5	14
38	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	2.1	144
39	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
40	Metabolic models predict bacterial passengers in colorectal cancer. <i>Cancer & Metabolism</i> , 2020, 8, 3.	5.0	28
41	Ecogenomics of the Marine Benthic Filamentous Cyanobacterium <i>Adonisia</i> . <i>Microbial Ecology</i> , 2020, 80, 249-265.	2.8	4
42	Microbial diversity, ecological networks and functional traits associated to materials used in drinking water distribution systems. <i>Water Research</i> , 2020, 173, 115586.	11.3	45
43	The new scope of virus taxonomy: partitioning the virosphere into 15 hierarchical ranks. <i>Nature Microbiology</i> , 2020, 5, 668-674.	13.3	198
44	Genome-wide association studies of <i>Shigella</i> spp. and Enteroinvasive <i>Escherichia coli</i> isolates demonstrate an absence of genetic markers for prediction of disease severity. <i>BMC Genomics</i> , 2020, 21, 138.	2.8	11
45	Using the structure of genome data in the design of deep neural networks for predicting amyotrophic lateral sclerosis from genotype. <i>Bioinformatics</i> , 2019, 35, i538-i547.	4.1	35
46	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
47	Drug Discovery and Repurposing Inhibits a Major Gut Pathogen-Derived Oncogenic Toxin. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 364.	3.9	10
48	Robust taxonomic classification of uncharted microbial sequences and bins with CAT and BAT. <i>Genome Biology</i> , 2019, 20, 217.	8.8	269
49	A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. <i>Cell Host and Microbe</i> , 2019, 26, 542-550.e5.	11.0	94
50	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). <i>Archives of Virology</i> , 2019, 164, 943-946.	2.1	102
51	Use of whole-genome sequencing to predict <i>Mycobacterium tuberculosis</i> drug resistance in Indonesia. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 170-177.	2.2	13
52	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). <i>Archives of Virology</i> , 2019, 164, 2417-2429.	2.1	257
53	Modelling the influence of environmental parameters over marine planktonic microbial communities using artificial neural networks. <i>Science of the Total Environment</i> , 2019, 677, 205-214.	8.0	21
54	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	28.9	541

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55	Reply to: Caution in inferring viral strategies from abundance correlations in marine metagenomes. <i>Nature Communications</i> , 2019, 10, 502.	12.8	2
56	Evolution of BACON Domain Tandem Repeats in crAssphage and Novel Gut Bacteriophage Lineages. <i>Viruses</i> , 2019, 11, 1085.	3.3	20
57	Molecular and Evolutionary Determinants of Bacteriophage Host Range. <i>Trends in Microbiology</i> , 2019, 27, 51-63.	7.7	277
58	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
59	Integrating Computational Methods to Investigate the Macroecology of Microbiomes. <i>Frontiers in Genetics</i> , 2019, 10, 1344.	2.3	7
60	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
61	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	2.1	172
62	Towards predicting the environmental metabolome from metagenomics with a mechanistic model. <i>Nature Microbiology</i> , 2018, 3, 456-460.	13.3	79
63	Temporal dynamics of uncultured viruses: a new dimension in viral diversity. <i>ISME Journal</i> , 2018, 12, 199-211.	9.8	44
64	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018, 1681, 231-238.	0.9	64
65	The gill-associated microbiome is the main source of wood plant polysaccharide hydrolases and secondary metabolite gene clusters in the mangrove shipworm <i>Neoteredo reynei</i> . <i>PLoS ONE</i> , 2018, 13, e0200437.	2.5	18
66	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018, 163, 2601-2631.	2.1	567
67	Establishing normal metabolism and differentiation in hepatocellular carcinoma cells by culturing in adult human serum. <i>Scientific Reports</i> , 2018, 8, 11685.	3.3	20
68	Metagenomic Characterization of the Human Intestinal Microbiota in Fecal Samples from STEC-Infected Patients. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 25.	3.9	47
69	Bioinformatics Meets Virology: The European Virus Bioinformatics Center's Second Annual Meeting. <i>Viruses</i> , 2018, 10, 256.	3.3	6
70	Large-scale genomic analysis shows association between homoplasmic genetic variation in <i>Mycobacterium tuberculosis</i> genes and meningeal or pulmonary tuberculosis. <i>BMC Genomics</i> , 2018, 19, 122.	2.8	18
71	Targeting mechanisms of tailed bacteriophages. <i>Nature Reviews Microbiology</i> , 2018, 16, 760-773.	28.6	310
72	Draft Genome of <i>Scalindua rubra</i> , Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. <i>Microbial Ecology</i> , 2017, 74, 1-5.	2.8	73

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73	Preservation of bacterial DNA in 10-year-old guaiac FOBT cards and FIT tubes. <i>Journal of Clinical Pathology</i> , 2017, 70, 994-996.	2.0	4
74	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	2.1	57
75	Marine viruses discovered via metagenomics shed light on viral strategies throughout the oceans. <i>Nature Communications</i> , 2017, 8, 15955.	12.8	231
76	Characterization and Temperature Dependence of Arctic <i>Micromonas polaris</i> Viruses. <i>Viruses</i> , 2017, 9, 134.	3.3	59
77	Insights of Phage-Host Interaction in Hypersaline Ecosystem through Metagenomics Analyses. <i>Frontiers in Microbiology</i> , 2017, 8, 352.	3.5	28
78	Editorial: Virus Discovery by Metagenomics: The (Im)possibilities. <i>Frontiers in Microbiology</i> , 2017, 8, 1710.	3.5	32
79	Ecogenomics and Taxonomy of Cyanobacteria Phylum. <i>Frontiers in Microbiology</i> , 2017, 8, 2132.	3.5	99
80	Ultrastructure and Viral Metagenome of Bacteriophages from an Anaerobic Methane Oxidizing <i>Methylospirillum</i> Bioreactor Enrichment Culture. <i>Frontiers in Microbiology</i> , 2016, 7, 1740.	3.5	13
81	Metagenomic and metaproteomic analyses of <i>Accumulibacter phosphatis</i> -enriched floccular and granular biofilm. <i>Environmental Microbiology</i> , 2016, 18, 273-287.	3.8	51
82	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	27.8	629
83	Genome-based microbial ecology of anammox granules in a full-scale wastewater treatment system. <i>Nature Communications</i> , 2016, 7, 11172.	12.8	373
84	Proposal of fifteen new species of <i>Parasynecococcus</i> based on genomic, physiological and ecological features. <i>Archives of Microbiology</i> , 2016, 198, 973-986.	2.2	10
85	Computational approaches to predict bacteriophage-host relationships. <i>FEMS Microbiology Reviews</i> , 2016, 40, 258-272.	8.6	394
86	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	2.1	83
87	SUPER-FOCUS: a tool for agile functional analysis of shotgun metagenomic data. <i>Bioinformatics</i> , 2016, 32, 354-361.	4.1	161
88	Sequence specificity between interacting and non-interacting homologs identifies interface residues - a homodimer and monomer use case. <i>BMC Bioinformatics</i> , 2015, 16, 325.	2.6	18
89	Genomic Comparison of the Closely-Related <i>Salmonella enterica</i> Serovars Enteritidis, Dublin and Gallinarum. <i>PLoS ONE</i> , 2015, 10, e0126883.	2.5	39
90	Dispersion of the HIV-1 Epidemic in Men Who Have Sex with Men in the Netherlands: A Combined Mathematical Model and Phylogenetic Analysis. <i>PLoS Medicine</i> , 2015, 12, e1001898.	8.4	69

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91	Copper tolerance and distribution of epibiotic bacteria associated with giant kelp <i>Macrocystis pyrifera</i> in southern California. <i>Ecotoxicology</i> , 2015, 24, 1131-1140.	2.4	7
92	Microbial community diversity and physical–chemical features of the Southwestern Atlantic Ocean. <i>Archives of Microbiology</i> , 2015, 197, 165-179.	2.2	34
93	Draft Genome Sequence of Anammox Bacterium – <i>Candidatus Scalindua brodae</i> , –Obtained Using Differential Coverage Binning of Sequencing Data from Two Reactor Enrichments. <i>Genome Announcements</i> , 2015, 3, .	0.8	46
94	Beyond research: a primer for considerations on using viral metagenomics in the field and clinic. <i>Frontiers in Microbiology</i> , 2015, 6, 224.	3.5	21
95	Immunoglobulin rearrangement analysis from multiple lesions in the same patient using next–generation sequencing. <i>Histopathology</i> , 2015, 67, 843-858.	2.9	5
96	From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. <i>Cellular and Molecular Life Sciences</i> , 2015, 72, 4287-4308.	5.4	114
97	Microbial taxonomy in the post-genomic era: Rebuilding from scratch?. <i>Archives of Microbiology</i> , 2015, 197, 359-370.	2.2	144
98	Microbial Metabolism Shifts Towards an Adverse Profile with Supplementary Iron in the TIM-2 In vitro Model of the Human Colon. <i>Frontiers in Microbiology</i> , 2015, 6, 1481.	3.5	55
99	Niche distribution and influence of environmental parameters in marine microbial communities: a systematic review. <i>PeerJ</i> , 2015, 3, e1008.	2.0	36
100	Metagenomic ventures into outer sequence space. <i>Bacteriophage</i> , 2014, 4, e979664.	1.9	27
101	Pharmacomicrobiomics: The Impact of Human Microbiome Variations on Systems Pharmacology and Personalized Therapeutics. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 402-414.	2.0	122
102	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. <i>Nature Communications</i> , 2014, 5, 4498.	12.8	617
103	Comparative genomics of 274 <i>Vibrio cholerae</i> genomes reveals mobile functions structuring three niche dimensions. <i>BMC Genomics</i> , 2014, 15, 654.	2.8	24
104	Cell Wall Modifications during Conidial Maturation of the Human Pathogenic Fungus <i>Pseudallescheria boydii</i> . <i>PLoS ONE</i> , 2014, 9, e100290.	2.5	23
105	FOCUS: an alignment-free model to identify organisms in metagenomes using non-negative least squares. <i>PeerJ</i> , 2014, 2, e425.	2.0	89
106	Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. <i>PeerJ</i> , 2014, 2, e520.	2.0	19
107	The metagenome of the marine anammox bacterium – <i>Candidatus</i> – <i>Scalindua profunda</i> ™ illustrates the versatility of this globally important nitrogen cycle bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1275-1289.	3.8	246
108	Screening metatranscriptomes for toxin genes as functional drivers of human colorectal cancer. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2013, 27, 85-99.	2.4	36

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109	Combining de novo and reference-guided assembly with scaffold_builder. Source Code for Biology and Medicine, 2013, 8, 23.	1.7	59
110	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. Briefings in Functional Genomics, 2013, 12, 366-380.	2.7	57
111	Identification of a Novel Human Papillomavirus by Metagenomic Analysis of Samples from Patients with Febrile Respiratory Illness. PLoS ONE, 2013, 8, e58404.	2.5	58
112	Colorectal Cancer-Associated Microbiota. , 2013, , 1-8.		0
113	Bacterial Responses to a Simulated Colon Tumor Microenvironment. Molecular and Cellular Proteomics, 2012, 11, 851-862.	3.8	43
114	Reference-independent comparative metagenomics using cross-assembly: crAss. Bioinformatics, 2012, 28, 3225-3231.	4.1	87
115	Metagenomics and future perspectives in virus discovery. Current Opinion in Virology, 2012, 2, 63-77.	5.4	493
116	Genome Sequences of the Ethanol-Tolerant Lactobacillus vini Strains LMG 23202 T and JP7.8.9. Journal of Bacteriology, 2012, 194, 3018-3018.	2.2	9
117	Oxygen minimum zones harbour novel viral communities with low diversity. Environmental Microbiology, 2012, 14, 3043-3065.	3.8	68
118	Genome-Wide Study of the Defective Sucrose Fermenter Strain of Vibrio cholerae from the Latin American Cholera Epidemic. PLoS ONE, 2012, 7, e37283.	2.5	13
119	Taxonomic and Functional Microbial Signatures of the Endemic Marine Sponge Arenosclera brasiliensis. PLoS ONE, 2012, 7, e39905.	2.5	56
120	A bacterial driverâ€ passenger model for colorectal cancer: beyond the usual suspects. Nature Reviews Microbiology, 2012, 10, 575-582.	28.6	672
121	Discovery of a hapE Mutation That Causes Azole Resistance in Aspergillus fumigatus through Whole Genome Sequencing and Sexual Crossing. PLoS ONE, 2012, 7, e50034.	2.5	168
122	FACIL: Fast and Accurate Genetic Code Inference and Logo. Bioinformatics, 2011, 27, 1929-1933.	4.1	42
123	The Organellar Genome and Metabolic Potential of the Hydrogen-Producing Mitochondrion of Nyctotherus ovalis. Molecular Biology and Evolution, 2011, 28, 2379-2391.	8.9	82
124	Ultra-deep pyrosequencing of pmoA amplicons confirms the prevalence of Methylomonas and Methylocystis in Sphagnum mosses from a Dutch peat bog. Environmental Microbiology Reports, 2011, 3, 667-673.	2.4	58
125	Mass Spectrometry Analysis of Hepcidin Peptides in Experimental Mouse Models. PLoS ONE, 2011, 6, e16762.	2.5	25
126	Towards the Human Colorectal Cancer Microbiome. PLoS ONE, 2011, 6, e20447.	2.5	470

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127	Pyrosequencing of 16S rRNA gene amplicons to study the microbiota in the gastrointestinal tract of carp (<i>Cyprinus carpio</i> L.). <i>AMB Express</i> , 2011, 1, 41.	3.0	186
128	Genome Sequence of the Human Pathogen <i>Vibrio cholerae</i> Amazonia. <i>Journal of Bacteriology</i> , 2011, 193, 5877-5878.	2.2	8
129	Genome-wide screening in human growth plates during puberty in one patient suggests a role for RUNX2 in epiphyseal maturation. <i>Journal of Endocrinology</i> , 2011, 209, 245-254.	2.6	6
130	Nitrite-driven anaerobic methane oxidation by oxygenic bacteria. <i>Nature</i> , 2010, 464, 543-548.	27.8	1,521
131	Genome-Wide Profiling of p63 DNA-Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. <i>PLoS Genetics</i> , 2010, 6, e1001065.	3.5	169
132	Increasing the coverage of a metapopulation consensus genome by iterative read mapping and assembly. <i>Bioinformatics</i> , 2009, 25, 2878-2881.	4.1	29
133	The mitochondrial genomes of the ciliates <i>Euplotes minuta</i> and <i>Euplotes crassus</i> . <i>BMC Genomics</i> , 2009, 10, 514.	2.8	36
134	Asymmetric relationships between proteins shape genome evolution. <i>Genome Biology</i> , 2009, 10, R19.	9.6	39
135	Macronuclear genome structure of the ciliate <i>Nyctotherus ovalis</i> : Single-gene chromosomes and tiny introns. <i>BMC Genomics</i> , 2008, 9, 587.	2.8	33
136	Conservation of divergent transcription in fungi. <i>Trends in Genetics</i> , 2008, 24, 207-211.	6.7	48
137	Practical and theoretical advances in predicting the function of a protein by its phylogenetic distribution. <i>Journal of the Royal Society Interface</i> , 2008, 5, 151-170.	3.4	97
138	Signature, a web server for taxonomic characterization of sequence samples using signature genes. <i>Nucleic Acids Research</i> , 2008, 36, W470-W474.	14.5	14
139	Signature Genes as a Phylogenomic Tool. <i>Molecular Biology and Evolution</i> , 2008, 25, 1659-1667.	8.9	72
140	Assessment of phylogenomic and orthology approaches for phylogenetic inference. <i>Bioinformatics</i> , 2007, 23, 815-824.	4.1	87
141	Development of the first marmoset-specific DNA microarray (EUMAMA): a new genetic tool for large-scale expression profiling in a non-human primate. <i>BMC Genomics</i> , 2007, 8, 190.	2.8	22
142	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	27.8	1,075
143	A global definition of expression context is conserved between orthologs, but does not correlate with sequence conservation. <i>BMC Genomics</i> , 2006, 7, 10.	2.8	28
144	Horizontal gene transfer from Bacteria to rumen Ciliates indicates adaptation to their anaerobic, carbohydrates-rich environment. <i>BMC Genomics</i> , 2006, 7, 22.	2.8	138

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145	GENOME TREES AND THE NATURE OF GENOME EVOLUTION. Annual Review of Microbiology, 2005, 59, 191-209.	7.3	184
146	The Consistent Phylogenetic Signal in Genome Trees Revealed by Reducing the Impact of Noise. Journal of Molecular Evolution, 2004, 58, 527-539.	1.8	88
147	Decline in excision circles requires homeostatic renewal or homeostatic death of naive T cells. Journal of Theoretical Biology, 2003, 224, 351-358.	1.7	46