

Denis Baurain

List of Publications by Year in descending order

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65
papers

5,346
citations

136950

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h-index

106344

65
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81
all docs

81
docs citations

81
times ranked

7877
citing authors

#	ARTICLE	IF	CITATIONS
1	Lower Statistical Support with Larger Data Sets: Insights from the Ochrophyta Radiation. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	7
2	A Fast-Growing Oleaginous Strain of <i>Coelastrella</i> Capable of Astaxanthin and Canthaxanthin Accumulation in Phototrophy and Heterotrophy. <i>Life</i> , 2022, 12, 334.	2.4	7
3	Contamination detection in genomic data: more is not enough. <i>Genome Biology</i> , 2022, 23, 60.	8.8	37
4	Was the Last Bacterial Common Ancestor a Monoderm after All?. <i>Genes</i> , 2022, 13, 376.	2.4	6
5	An Extended Reservoir of Class-D Beta-Lactamases in Non-Clinical Bacterial Strains. <i>Microbiology Spectrum</i> , 2022, 10, e0031522.	3.0	4
6	Phylogenomic Analyses of <i>Snodgrassella</i> Isolates from Honeybees and Bumblebees Reveal Taxonomic and Functional Diversity. <i>MSystems</i> , 2022, 7, .	3.8	19
7	Broadly sampled orthologous groups of eukaryotic proteins for the phylogenetic study of plastid-bearing lineages. <i>BMC Research Notes</i> , 2021, 14, 143.	1.4	5
8	De Novo Transcriptome Meta-Assembly of the Mixotrophic Freshwater Microalga <i>Euglena gracilis</i> . <i>Genes</i> , 2021, 12, 842.	2.4	9
9	ToRQuEMaDA: tool for retrieving queried Eubacteria, metadata and dereplicating assemblies. <i>PeerJ</i> , 2021, 9, e11348.	2.0	5
10	Decontamination, pooling and dereplication of the 678 samples of the Marine Microbial Eukaryote Transcriptome Sequencing Project. <i>BMC Research Notes</i> , 2021, 14, 306.	1.4	13
11	Exploring syntenic conservation across genomes for phylogenetic studies of organisms subjected to horizontal gene transfers: A case study with Cyanobacteria and cyanolichens. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107100.	2.7	8
12	Trophic state alters the mechanism whereby energetic coupling between photosynthesis and respiration occurs in <i>Euglena gracilis</i> . <i>New Phytologist</i> , 2021, 232, 1603-1617.	7.3	11
13	Contamination in Reference Sequence Databases: Time for Divide-and-Rule Tactics. <i>Frontiers in Microbiology</i> , 2021, 12, 755101.	3.5	25
14	ORPER: A Workflow for Constrained SSU rRNA Phylogenies. <i>Genes</i> , 2021, 12, 1741.	2.4	2
15	The taxonomy of the <i>Trichophyton rubrum</i> complex: a phylogenomic approach. <i>Microbial Genomics</i> , 2021, 7, .	2.0	11
16	Bryophytes are predicted to lag behind future climate change despite their high dispersal capacities. <i>Nature Communications</i> , 2020, 11, 5601.	12.8	47
17	Palantir: a springboard for the analysis of secondary metabolite gene clusters in large-scale genome mining projects. <i>Bioinformatics</i> , 2020, 36, 4345-4347.	4.1	16
18	Nonribosomal peptides in fungal cell factories: from genome mining to optimized heterologous production. <i>Biotechnology Advances</i> , 2019, 37, 107449.	11.7	24

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19	Cyanobacteria evolution: Insight from the fossil record. <i>Free Radical Biology and Medicine</i> , 2019, 140, 206-223.	2.9	116
20	Evaluating the usefulness of alignment filtering methods to reduce the impact of errors on evolutionary inferences. <i>BMC Evolutionary Biology</i> , 2019, 19, 21.	3.2	96
21	A constrained SSU-rRNA phylogeny reveals the unsequenced diversity of photosynthetic Cyanobacteria (Oxyphotobacteria). <i>BMC Research Notes</i> , 2018, 11, 435.	1.4	9
22	Consensus assessment of the contamination level of publicly available cyanobacterial genomes. <i>PLoS ONE</i> , 2018, 13, e0200323.	2.5	41
23	High-Throughput Sequencing Analysis of the Actinobacterial Spatial Diversity in Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 27.	3.7	22
24	Isolation, Characterization, and Antibacterial Activity of Hard-to-Culture Actinobacteria from Cave Moonmilk Deposits. <i>Antibiotics</i> , 2018, 7, 28.	3.7	68
25	Complete Genome Sequence of <i>Streptomyces lunaelactis</i> MM109 T , Isolated from Cave Moonmilk Deposits. <i>Genome Announcements</i> , 2018, 6, .	0.8	8
26	Metagenomic assembly of new (sub)polar Cyanobacteria and their associated microbiome from non-axenic cultures. <i>Microbial Genomics</i> , 2018, 4, .	2.0	23
27	Draft Genome Sequence of the Axenic Strain <i>Phormidesmis priestleyi</i> ULC007, a Cyanobacterium Isolated from Lake Bruehwiler (Larsemann Hills, Antarctica). <i>Genome Announcements</i> , 2017, 5, .	0.8	12
28	High-throughput sequencing analysis reveals the genetic diversity of different regions of the murine norovirus genome during in vitro replication. <i>Archives of Virology</i> , 2017, 162, 1019-1023.	2.1	8
29	Human Chitotriosidase: Catalytic Domain or Carbohydrate Binding Module, Who's Leading HCHT's Biological Function. <i>Scientific Reports</i> , 2017, 7, 2768.	3.3	14
30	A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. <i>Current Biology</i> , 2017, 27, 958-967.	3.9	423
31	Inferring the shallow phylogeny of true salamanders (<i>Salamandra</i>) by multiple phylogenomic approaches. <i>Molecular Phylogenetics and Evolution</i> , 2017, 115, 16-26.	2.7	44
32	Phylotranscriptomic consolidation of the jawed vertebrate timetree. <i>Nature Ecology and Evolution</i> , 2017, 1, 1370-1378.	7.8	247
33	Number of inadvertent RNA targets for morpholino knockdown in <i>Danio rerio</i> is largely underestimated: evidence from the study of Ser/Arg-rich splicing factors. <i>Nucleic Acids Research</i> , 2017, 45, 9547-9557.	14.5	29
34	Assessment of the Potential Role of <i>Streptomyces</i> in Cave Moonmilk Formation. <i>Frontiers in Microbiology</i> , 2017, 8, 1181.	3.5	63
35	Pitfalls in supermatrix phylogenomics. <i>European Journal of Taxonomy</i> , 2017, , .	0.6	50
36	A Phenotypic and Genotypic Analysis of the Antimicrobial Potential of Cultivable <i>Streptomyces</i> Isolated from Cave Moonmilk Deposits. <i>Frontiers in Microbiology</i> , 2016, 7, 1455.	3.5	64

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37	On the use of high-throughput sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. <i>Journal of Phycology</i> , 2016, 52, 356-368.	2.3	36
38	Coding and noncoding variants in <i>HFM1</i> , <i>MLH3</i> , <i>MSH4</i> , <i>MSH5</i> , <i>RNF212</i> , and <i>RNF212B</i> affect recombination rate in cattle. <i>Genome Research</i> , 2016, 26, 1323-1332.	5.5	77
39	Gram-Negative Bacteria- Inner vs. Cytoplasmic or Plasma Membrane- A Question of Clarity rather than Vocabulary. <i>Journal of Microbial & Biochemical Technology</i> , 2016, 8, .	0.2	3
40	Rooting the tree of life: the phylogenetic jury is still out. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140329.	4.0	77
41	<i>Chromera velia</i> , Endosymbioses and the Rhodoplex Hypothesis—Plastid Evolution in Cryptophytes, Alveolates, Stramenopiles, and Haptophytes (CASH Lineages). <i>Genome Biology and Evolution</i> , 2014, 6, 666-684.	2.5	93
42	The mitochondrial respiratory chain of the secondary green alga <i>Euglena gracilis</i> shares many additional subunits with parasitic Trypanosomatidae. <i>Mitochondrion</i> , 2014, 19, 338-349.	3.4	59
43	Impact of Missing Data on Phylogenies Inferred from Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2013, 30, 197-214.	8.9	275
44	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013, 496, 311-316.	27.8	612
45	Origin and evolution of metal P-type ATPases in Plantae (Archaeplastida). <i>Frontiers in Plant Science</i> , 2013, 4, 544.	3.6	39
46	The unusual Gasteromycetes <i>Lycogalopsis solmsii</i> belongs to the gomphoid-phalloid group. <i>Acta Mycologica</i> , 2013, 48, 13-20.	0.3	2
47	A Single Ancient Origin for Prototypical Serine/Arginine-Rich Splicing Factors. <i>Plant Physiology</i> , 2012, 158, 546-560.	4.8	28
48	Variants modulating the expression of a chromosome domain encompassing <i>PLAG1</i> influence bovine stature. <i>Nature Genetics</i> , 2011, 43, 405-413.	21.4	300
49	Resolving Difficult Phylogenetic Questions: Why More Sequences Are Not Enough. <i>PLoS Biology</i> , 2011, 9, e1000602.	5.6	932
50	Phylogenomic Evidence for Separate Acquisition of Plastids in Cryptophytes, Haptophytes, and Stramenopiles. <i>Molecular Biology and Evolution</i> , 2010, 27, 1698-1709.	8.9	248
51	Assessing the effect of the CLPG mutation on the microRNA catalog of skeletal muscle using high-throughput sequencing. <i>Genome Research</i> , 2010, 20, 1651-1662.	5.5	38
52	Patrocles: a database of polymorphic miRNA-mediated gene regulation in vertebrates. <i>Nucleic Acids Research</i> , 2010, 38, D640-D651.	14.5	126
53	Atypical Subunit Composition of the Chlorophycean Mitochondrial F1FO-ATP Synthase and Role of <i>Asa7</i> Protein in Stability and Oligomycin Resistance of the Enzyme. <i>Molecular Biology and Evolution</i> , 2010, 27, 1630-1644.	8.9	47
54	Lack of Resolution in the Animal Phylogeny: Closely Spaced Cladogeneses or Undetected Systematic Errors?. <i>Molecular Biology and Evolution</i> , 2007, 24, 6-9.	8.9	150

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55	Origin and Distribution of Calvin Cycle Fructose and Sedoheptulose Bisphosphatases in Plantae and Complex Algae: A Single Secondary Origin of Complex Red Plastids and Subsequent Propagation via Tertiary Endosymbioses. <i>Protist</i> , 2007, 158, 263-276.	1.5	55
56	A Comparative Inventory of Metal Transporters in the Green Alga <i>Chlamydomonas reinhardtii</i> and the Red Alga <i>Cyanidioschyzon merolae</i> . <i>Plant Physiology</i> , 2005, 137, 428-446.	4.8	157
57	The Mitochondrial Oxidative Phosphorylation Proteome of <i>Chlamydomonas reinhardtii</i> Deduced from the Genome Sequencing Project: Table I.. <i>Plant Physiology</i> , 2005, 137, 447-459.	4.8	78
58	Regulation of the Alternative Oxidase Aox1 Gene in <i>Chlamydomonas reinhardtii</i> . Role of the Nitrogen Source on the Expression of a Reporter Gene under the Control of the Aox1 Promoter. <i>Plant Physiology</i> , 2003, 131, 1418-1430.	4.8	50
59	REMARKABLE CONSERVATION OF INTERNALLY TRANSCRIBED SPACER SEQUENCES OF <i>ARTHROSPIRA</i> (= <i>SPIRULINA</i>) (CYANOPHYCEAE, CYANOBACTERIA) STRAINS FROM FOUR CONTINENTS AND OF RECENT AND 30-YEAR-OLD DRIED SAMPLES FROM AFRICA1. <i>Journal of Phycology</i> , 2002, 38, 384-393.		44
60	Characterization of two genes encoding the mitochondrial alternative oxidase in <i>Chlamydomonas reinhardtii</i> . <i>Current Genetics</i> , 2001, 39, 101-108.	1.7	60
61	A mutation in the GTPase domain of the large subunit rRNA is involved in the suppression of a 1T frameshift mutation affecting a mitochondrial gene in <i>Chlamydomonas reinhardtii</i> . <i>Molecular Genetics and Genomics</i> , 2001, 266, 103-108.	2.1	4
62	Mutants of <i>Chlamydomonas reinhardtii</i> Deficient in Mitochondrial Complex I: Characterization of Two Mutations Affecting the Coding Sequence. <i>Genetics</i> , 2001, 158, 1051-1060.	2.9	47
63	<i>Arthrospira</i> (= <i>Spirulina</i>) strains from four continents are resolved into only two clusters, based on amplified ribosomal DNA restriction analysis of the internally transcribed spacer. <i>FEMS Microbiology Letters</i> , 1999, 172, 213-222.	1.8	79
64	<i>Arthrospira</i> (' <i>Spirulina</i> ') strains from four continents are resolved into only two clusters, based on amplified ribosomal DNA restriction analysis of the internally transcribed spacer. <i>FEMS Microbiology Letters</i> , 1999, 172, 213-222.	1.8	3
65	Phylogenomics: how far back in the past can we go?. , 0, , 149-177.		0