

Oliver Rupp

List of Publications by Year in descending order

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64
papers

4,848
citations

201385

27
h-index

110170

64
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66
all docs

66
docs citations

66
times ranked

6184
citing authors

#	ARTICLE	IF	CITATIONS
1	The complete <i>Corynebacterium glutamicum</i> ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. <i>Journal of Biotechnology</i> , 2003, 104, 5-25.	1.9	844
2	GenDB—an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003, 31, 2187-2195.	6.5	644
3	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
4	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium <i>Alcanivorax borkumensis</i> . <i>Nature Biotechnology</i> , 2006, 24, 997-1004.	9.4	417
5	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Revealed by the Complete Genome Sequence. <i>Journal of Bacteriology</i> , 2005, 187, 7254-7266.	1.0	321
6	Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen <i>Corynebacterium jeikeium</i> K411, a Lipid-Requiring Bacterium of the Human Skin Flora. <i>Journal of Bacteriology</i> , 2005, 187, 4671-4682.	1.0	189
7	Chinese hamster genome sequenced from sorted chromosomes. <i>Nature Biotechnology</i> , 2013, 31, 694-695.	9.4	160
8	Complete genome sequencing of <i>Agrobacterium</i> sp. H13-3, the former <i>Rhizobium lupini</i> H13-3, reveals a tripartite genome consisting of a circular and a linear chromosome and an accessory plasmid but lacking a tumor-inducing Ti-plasmid. <i>Journal of Biotechnology</i> , 2011, 155, 50-62.	1.9	112
9	EMMA: a platform for consistent storage and efficient analysis of microarray data. <i>Journal of Biotechnology</i> , 2003, 106, 135-146.	1.9	100
10	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. <i>Journal of Biotechnology</i> , 2011, 156, 227-235.	1.9	96
11	A reference genome of the Chinese hamster based on a hybrid assembly strategy. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2087-2100.	1.7	95
12	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. <i>Journal of Biotechnology</i> , 2013, 167, 142-155.	1.9	93
13	Reconstruction of the lipid metabolism for the microalga <i>Monoraphidium neglectum</i> from its genome sequence reveals characteristics suitable for biofuel production. <i>BMC Genomics</i> , 2013, 14, 926.	1.2	84
14	Genome analysis of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. <i>BMC Genomics</i> , 2016, 17, 245.	1.2	69
15	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. <i>PLoS ONE</i> , 2014, 9, e85568.	1.1	57
16	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus <i>Rana</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 657-670.	1.2	56
17	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. <i>Journal of Biotechnology</i> , 2012, 158, 151-155.	1.9	46
18	Utilization and evaluation of CHO-specific sequence databases for mass spectrometry based proteomics. <i>Biotechnology and Bioengineering</i> , 2012, 109, 1386-1394.	1.7	46

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19	The more the better – polyandry and genetic similarity are positively linked to reproductive success in a natural population of terrestrial salamanders (<i>Salamandra atra</i>). <i>Molecular Ecology</i> , 2014, 23, 239-250.	2.0	45
20	Seed plant specific gene lineages involved in carpel development. <i>Molecular Biology and Evolution</i> , 2017, 34, msw297.	3.5	42
21	Genome sequence of <i>Wickerhamomyces anomalus</i> DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. <i>FEMS Yeast Research</i> , 2012, 12, 382-386.	1.1	40
22	The Sequence Analysis and Management System – SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. <i>Journal of Biotechnology</i> , 2009, 140, 3-12.	1.9	37
23	Pathogen recognition in compatible plant-microbe interactions. <i>Scientific Reports</i> , 2017, 7, 6383.	1.6	34
24	Transcriptome analysis of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). <i>Fungal Biology</i> , 2014, 118, 800-813.	1.1	32
25	Development of a <i>Rhizoctonia solani</i> AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic <i>R. solani</i> AG1-IA, AG1-IB, AG3 and AG8 Isolates. <i>PLoS ONE</i> , 2015, 10, e0144769.	1.1	32
26	The DNA methylation landscape of Chinese hamster ovary (CHO) DP-12 cells. <i>Journal of Biotechnology</i> , 2015, 199, 38-46.	1.9	32
27	Genome sequence of the endophytic strain <i>Enterobacter</i> sp. J49, a potential biofertilizer for peanut and maize. <i>Genomics</i> , 2019, 111, 913-920.	1.3	30
28	Strain <i>Serratia</i> sp. S119: A potential biofertilizer for peanut and maize and a model bacterium to study phosphate solubilization mechanisms. <i>Applied Soil Ecology</i> , 2018, 126, 107-112.	2.1	28
29	Metagenomics-Guided Survey, Isolation, and Characterization of Uranium Resistant Microbiota from the Savannah River Site, USA. <i>Genes</i> , 2019, 10, 325.	1.0	28
30	What remains from a 454 run: estimation of success rates of microsatellite loci development in selected newt species (<i>Ambystoma macrodactylum</i> , <i>Ambystoma macrodactylum</i> , and <i>Ambystoma macrodactylum</i>). <i>Evolution</i> , 2013, 3, 3947-3957.	0.8	27
31	Improved genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. <i>Journal of Biotechnology</i> , 2015, 203, 19-21.	1.9	27
32	Establishment of a CpG island microarray for analyses of genome-wide DNA methylation in Chinese hamster ovary cells. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 579-589.	1.7	25
33	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted by <i>Lucilia sericata</i> Medical Maggots. <i>BioMed Research International</i> , 2016, 2016, 1-27.	0.9	24
34	ADAR1 Is Required for Dendritic Cell Subset Homeostasis and Alveolar Macrophage Function. <i>Journal of Immunology</i> , 2019, 202, 1099-1111.	0.4	24
35	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. <i>Journal of Biotechnology</i> , 2003, 106, 157-167.	1.9	22
36	Integrative analysis of DNA methylation and gene expression in butyrate-treated CHO cells. <i>Journal of Biotechnology</i> , 2017, 257, 150-161.	1.9	22

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37	A review of bioinformatics platforms for comparative genomics. Recent developments of the EDGAR 2.0 platform and its utility for taxonomic and phylogenetic studies. <i>Journal of Biotechnology</i> , 2017, 261, 2-9.	1.9	22
38	mRNA Inventory of Extracellular Vesicles from <i>Ustilago maydis</i> . <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 562.	1.5	21
39	Draft genome sequence of the sugar beet pathogen <i>Rhizoctonia solani</i> AG2-2IIIB strain BBA69670. <i>Journal of Biotechnology</i> , 2016, 222, 11-12.	1.9	20
40	Deep sequencing of naupliar-, cyprid- and adult-specific normalised Expressed Sequence Tag (EST) libraries of the acorn barnacle <i>Balanus amphitrite</i> . <i>Biofouling</i> , 2011, 27, 367-374.	0.8	19
41	An Evolutionary Framework for Carpel Developmental Control Genes. <i>Molecular Biology and Evolution</i> , 2016, 34, msw229.	3.5	18
42	MetaSAMS – A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. <i>Journal of Biotechnology</i> , 2013, 167, 156-165.	1.9	17
43	<i>Listeria monocytogenes</i> Induces a Virulence-Dependent microRNA Signature That Regulates the Immune Response in <i>Galleria mellonella</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2463.	1.5	17
44	Binning enables efficient host genome reconstruction in cnidarian holobionts. <i>GigaScience</i> , 2018, 7, .	3.3	16
45	De novo assembly of the dual transcriptomes of a polymorphic raptor species and its malarial parasite. <i>BMC Genomics</i> , 2015, 16, 1038.	1.2	15
46	Transcriptome analyses of CHO cells with the next-generation microarray CHO41K: Development and validation by analysing the influence of the growth stimulating substance IGF-1 substitute LongR3. <i>Journal of Biotechnology</i> , 2014, 178, 23-31.	1.9	14
47	Assembly of the <i>Lactuca sativa</i> , L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. <i>Journal of Biotechnology</i> , 2018, 267, 12-18.	1.9	13
48	Draft genome sequence of the potato pathogen <i>Rhizoctonia solani</i> AG3-PT isolate Ben3. <i>Archives of Microbiology</i> , 2017, 199, 1065-1068.	1.0	12
49	Nuclear factor of activated T-cells, NFATC1, governs FLT3ITD-driven hematopoietic stem cell transformation and a poor prognosis in AML. <i>Journal of Hematology and Oncology</i> , 2019, 12, 72.	6.9	12
50	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of <i>Botryococcus</i> consortia. <i>Scientific Reports</i> , 2021, 11, 1726.	1.6	12
51	Next-generation sequencing of the CHO cell transcriptome. <i>BMC Proceedings</i> , 2011, 5, P6.	1.8	11
52	The structure of the <i>Cyberlindnera jadinii</i> genome and its relation to <i>Candida utilis</i> analyzed by the occurrence of single nucleotide polymorphisms. <i>Journal of Biotechnology</i> , 2015, 211, 20-30.	1.9	10
53	Transcriptome analysis reveals major transcriptional changes during regrowth after mowing of red clover (<i>Trifolium pratense</i>). <i>BMC Plant Biology</i> , 2021, 21, 95.	1.6	10
54	Refined annotation of the complete genome of the phytopathogenic and xanthan producing <i>Xanthomonas campestris</i> pv. <i>campestris</i> strain B100 based on RNA sequence data. <i>Journal of Biotechnology</i> , 2017, 253, 55-61.	1.9	7

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55	Complete Genome Sequence of the Fruiting Myxobacterium <i>Myxococcus macrosporus</i> Strain DSM 14697, Generated by PacBio Sequencing. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
56	Massive parallel insertion site sequencing of an arrayed <i>Sinorhizobium meliloti</i> signature-tagged mini-Tn 5 transposon mutant library. <i>Journal of Biotechnology</i> , 2017, 257, 9-12.	1.9	5
57	Genome Analyses of the Less Aggressive <i>Rhizoctonia solani</i> AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, 832.	1.5	5
58	Whole-Genome Sequence of the Fruiting Myxobacterium <i>Cystobacter fuscus</i> DSM 52655. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
59	Complete Genome Sequence of the Corallopyronin A-Producing Myxobacterium <i>Coralloccoccus coralloides</i> B035. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
60	Genomic analysis of novel <i>Yarrowia</i> -like yeast symbionts associated with the carrion-feeding burying beetle <i>Nicrophorus vespilloides</i> . <i>BMC Genomics</i> , 2021, 22, 323.	1.2	3
61	Complete Genome Sequence of the Fruiting Myxobacterium <i>Melittangium boletus</i> DSM 14713. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
62	iCLIP analysis of RNA substrates of the archaeal exosome. <i>BMC Genomics</i> , 2020, 21, 797.	1.2	2
63	First CpG island microarray for genome-wide analyses of DNA methylation in Chinese hamster ovary cells: new insights into the epigenetic answer to butyrate treatment. <i>BMC Proceedings</i> , 2013, 7, .	1.8	1
64	Draft Genome Sequence of the Fruiting Myxobacterium <i>Nannocystis exedens</i> DSM 71. <i>Genome Announcements</i> , 2017, 5, .	0.8	1