Oliver Rupp

List of Publications by Year
in descending order

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64
papers

4,848
citations

201385

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110170

64
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all docs

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docs citations

66
times ranked

6184
citing authors

#	Article	IF	Citations
1	Phytoplankton consortia as a blueprint for mutually beneficial eukaryote-bacteria ecosystems based on the biocoenosis of Botryococcus consortia. Scientific Reports, 2021, 11, 1726.	1.6	12
2	Transcriptome analysis reveals major transcriptional changes during regrowth after mowing of red clover (Trifolium pratense). BMC Plant Biology, 2021, 21, 95.	1.6	10
3	Genomic analysis of novel Yarrowia-like yeast symbionts associated with the carrion-feeding burying beetle Nicrophorus vespilloides. BMC Genomics, 2021, 22, 323.	1.2	3
4	mRNA Inventory of Extracellular Vesicles from Ustilago maydis. Journal of Fungi (Basel, Switzerland), 2021, 7, 562.	1.5	21
5	Genome Analyses of the Less Aggressive Rhizoctonia solani AG1-IB Isolates 1/2/21 and O8/2 Compared to the Reference AG1-IB Isolate 7/3/14. Journal of Fungi (Basel, Switzerland), 2021, 7, 832.	1.5	5
6	iCLIP analysis of RNA substrates of the archaeal exosome. BMC Genomics, 2020, 21, 797.	1.2	2
7	Genome sequence of the endophytic strain Enterobacter sp. J49, a potential biofertilizer for peanut and maize. Genomics, 2019, 111, 913-920.	1.3	30
8	Nuclear factor of activated T-cells, NFATC1, governs FLT3ITD-driven hematopoietic stem cell transformation and a poor prognosis in AML. Journal of Hematology and Oncology, 2019, 12, 72.	6.9	12
9	Complete Genome Sequence of the Corallopyronin A-Producing Myxobacterium Corallococcus coralloides B035. Microbiology Resource Announcements, 2019, 8, .	0.3	3
10	Metagenomics-Guided Survey, Isolation, and Characterization of Uranium Resistant Microbiota from the Savannah River Site, USA. Genes, 2019, 10, 325.	1.0	28
11	ADAR1 Is Required for Dendritic Cell Subset Homeostasis and Alveolar Macrophage Function. Journal of Immunology, 2019, 202, 1099-1111.	0.4	24
12	Strain Serratia sp. S119: A potential biofertilizer for peanut and maize and a model bacterium to study phosphate solubilization mechanisms. Applied Soil Ecology, 2018, 126, 107-112.	2.1	28
13	Assembly of the Lactuca sativa, L. cv. Tizian draft genome sequence reveals differences within major resistance complex 1 as compared to the cv. Salinas reference genome. Journal of Biotechnology, 2018, 267, 12-18.	1.9	13
14	A reference genome of the Chinese hamster based on a hybrid assembly strategy. Biotechnology and Bioengineering, 2018, 115, 2087-2100.	1.7	95
15	Binning enables efficient host genome reconstruction in cnidarian holobionts. GigaScience, 2018, 7, .	3.3	16
16	Seed plant specific gene lineages involved in carpel development. Molecular Biology and Evolution, 2017, 34, msw297.	3.5	42
17	Massive parallel insertion site sequencing of an arrayed Sinorhizobium meliloti signature-tagged mini-Tn 5 transposon mutant library. Journal of Biotechnology, 2017, 257, 9-12.	1.9	5
18	Integrative analysis of DNA methylation and gene expression in butyrate-treated CHO cells. Journal of Biotechnology, 2017, 257, 150-161.	1.9	22

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19	Refined annotation of the complete genome of the phytopathogenic and xanthan producing Xanthomonas campestris pv. campestris strain B100 based on RNA sequence data. Journal of Biotechnology, 2017, 253, 55-61.	1.9	7
20	Draft genome sequence of the potato pathogen Rhizoctonia solani AG3-PT isolate Ben3. Archives of Microbiology, 2017, 199, 1065-1068.	1.0	12
21	Whole-Genome Sequence of the Fruiting Myxobacterium Cystobacter fuscus DSM 52655. Genome Announcements, 2017, 5, .	0.8	3
22	A review of bioinformatics platforms for comparative genomics. Recent developments of the EDGAR 2.0 platform and its utility for taxonomic and phylogenetic studies. Journal of Biotechnology, 2017, 261, 2-9.	1.9	22
23	Pathogen recognition in compatible plant-microbe interactions. Scientific Reports, 2017, 7, 6383.	1.6	34
24	Complete Genome Sequence of the Fruiting Myxobacterium Myxococcus macrosporus Strain DSM 14697, Generated by PacBio Sequencing. Genome Announcements, 2017, 5, .	0.8	6
25	Complete Genome Sequence of the Fruiting Myxobacterium Melittangium boletus DSM 14713. Genome Announcements, 2017, 5, .	0.8	2
26	Listeria monocytogenes Induces a Virulence-Dependent microRNA Signature That Regulates the Immune Response in Galleria mellonella. Frontiers in Microbiology, 2017, 8, 2463.	1.5	17
27	Draft Genome Sequence of the Fruiting Myxobacterium Nannocystis exedens DSM 71. Genome Announcements, 2017, 5, .	0.8	1
28	Next Generation Sequencing Identifies Five Major Classes of Potentially Therapeutic Enzymes Secreted byLucilia sericataMedical Maggots. BioMed Research International, 2016, 2016, 1-27.	0.9	24
29	Genome analysis of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB revealed high numbers in secreted proteins and cell wall degrading enzymes. BMC Genomics, 2016, 17, 245.	1.2	69
30	An Evolutionary Framework for Carpel Developmental Control Genes. Molecular Biology and Evolution, 2016, 34, msw229.	3.5	18
31	Draft genome sequence of the sugar beet pathogen Rhizoctonia solani AG2-2IIIB strain BBA69670. Journal of Biotechnology, 2016, 222, 11-12.	1.9	20
32	De novo assembly of the dual transcriptomes of a polymorphic raptor species and its malarial parasite. BMC Genomics, 2015, 16, 1038.	1.2	15
33	Development of a Rhizoctonia solani AG1-IB Specific Gene Model Enables Comparative Genome Analyses between Phytopathogenic R. solani AG1-IA, AG1-IB, AG3 and AG8 Isolates. PLoS ONE, 2015, 10, e0144769.	1.1	32
34	The DNA methylation landscape of Chinese hamster ovary (CHO) DP-12 cells. Journal of Biotechnology, 2015, 199, 38-46.	1.9	32
35	The structure of the Cyberlindnera jadinii genome and its relation to Candida utilis analyzed by the occurrence of single nucleotide polymorphisms. Journal of Biotechnology, 2015, 211, 20-30.	1.9	10
36	Improved genome sequence of the phytopathogenic fungus Rhizoctonia solani AG1-IB 7/3/14 as established by deep mate-pair sequencing on the MiSeq (Illumina) system. Journal of Biotechnology, 2015, 203, 19-21.	1.9	27

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37	Construction of a Public CHO Cell Line Transcript Database Using Versatile Bioinformatics Analysis Pipelines. PLoS ONE, 2014, 9, e85568.	1.1	57
38	The more the better â€“ polyandry and genetic similarity are positively linked to reproductive success in a natural population of terrestrial salamanders <i>(<scp>S</scp>alamandra salamandra)</i>. Molecular Ecology, 2014, 23, 239-250.	2.0	45
39	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. Journal of Biotechnology, 2014, 178, 23-31.	1.9	14
40	Establishment of a CpG island microarray for analyses of genome-wide DNA methylation in Chinese hamster ovary cells. Applied Microbiology and Biotechnology, 2014, 98, 579-589.	1.7	25
41	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature, 2014, 505, 546-549.	13.7	569
42	Transcriptome analysis of the phytopathogenic fungus Rhizoctonia solani AG1-IB 7/3/14 applying high-throughput sequencing of expressed sequence tags (ESTs). Fungal Biology, 2014, 118, 800-813.	1.1	32
43	Chinese hamster genome sequenced from sorted chromosomes. Nature Biotechnology, 2013, 31, 694-695.	9.4	160
44	MetaSAMSâ€"A novel software platform for taxonomic classification, functional annotation and comparative analysis of metagenome datasets. Journal of Biotechnology, 2013, 167, 156-165.	1.9	17
45	Reconstruction of the lipid metabolism for the microalga Monoraphidium neglectum from its genome sequence reveals characteristics suitable for biofuel production. BMC Genomics, 2013, 14, 926.	1.2	84
46	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. BMC Proceedings, 2013, 7, .	1.8	1
47	Establishment and interpretation of the genome sequence of the phytopathogenic fungus Rhizoctonia solani AG1-IB isolate 7/3/14. Journal of Biotechnology, 2013, 167, 142-155.	1.9	93
48	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus Rana. Molecular Phylogenetics and Evolution, 2013, 68, 657-670.	1.2	56
49	What remains from a 454 run: estimation of success rates of microsatellite loci development in selected newt species (<i><scp>C</scp>alotriton asper, <scp>L</scp>issotriton helveticus</i>, and) Tj ETQq1 1 0.784314 rgBT /Over Evolution, 2013, 3, 3947-3957.	0.8	27
50	Computational identification of microRNA gene loci and precursor microRNA sequences in CHO cell lines. Journal of Biotechnology, 2012, 158, 151-155.	1.9	46
51	Utilization and evaluation of CHOâ€specific sequence databases for mass spectrometry based proteomics. Biotechnology and Bioengineering, 2012, 109, 1386-1394.	1.7	46
52	Genome sequence of Wickerhamomyces anomalus DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. FEMS Yeast Research, 2012, 12, 382-386.	1.1	40
53	Unraveling the Chinese hamster ovary cell line transcriptome by next-generation sequencing. Journal of Biotechnology, 2011, 156, 227-235.	1.9	96
54	Next-generation sequencing of the CHO cell transcriptome. BMC Proceedings, 2011, 5, P6.	1.8	11

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55	Complete genome sequencing of Agrobacterium sp. H13-3, the former Rhizobium lupini 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. Journal of Biotechnology, 2011, 155, 50-62.	1.9	112
56	Deep sequencing of naupliar-, cyprid- and adult-specific normalised Expressed Sequence Tag (EST) libraries of the acorn barnacleBalanus amphitrite. Biofouling, 2011, 27, 367-374.	0.8	19
57	The Sequence Analysis and Management System â€“ SAMS-2.0: Data management and sequence analysis adapted to changing requirements from traditional sanger sequencing to ultrafast sequencing technologies. Journal of Biotechnology, 2009, 140, 3-12.	1.9	37
58	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium Alcanivorax borkumensis. Nature Biotechnology, 2006, 24, 997-1004.	9.4	417
59	Complete Genome Sequence and Analysis of the Multiresistant Nosocomial Pathogen Corynebacterium jeikeium K411, a Lipid-Requiring Bacterium of the Human Skin Flora. Journal of Bacteriology, 2005, 187, 4671-4682.	1.0	189
60	Insights into Genome Plasticity and Pathogenicity of the Plant Pathogenic Bacterium Xanthomonas campestris pv. vesicatoria Revealed by the Complete Genome Sequence. Journal of Bacteriology, 2005, 187, 7254-7266.	1.0	321
61	The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of l-aspartate-derived amino acids and vitamins. Journal of Biotechnology, 2003, 104, 5-25.	1.9	844
62	GenDB--an open source genome annotation system for prokaryote genomes. Nucleic Acids Research, 2003, 31, 2187-2195.	6.5	644
63	Building a BRIDGE for the integration of heterogeneous data from functional genomics into a platform for systems biology. Journal of Biotechnology, 2003, 106, 157-167.	1.9	22
64	EMMA: a platform for consistent storage and efficient analysis of microarray data. Journal of Biotechnology, 2003, 106, 135-146.	1.9	100