

Mark A Arick, Ii

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5844952/publications.pdf>

Version: 2024-02-01

29
papers

581
citations

623188

14
h-index

676716

22
g-index

38
all docs

38
docs citations

38
times ranked

738
citing authors

#	ARTICLE	IF	CITATIONS
1	Homoeologous gene expression and co-expression network analyses and evolutionary inference in allopolyploids. <i>Briefings in Bioinformatics</i> , 2021, 22, 1819-1835.	3.2	23
2	TALEN-Based HvMPK3 Knock-Out Attenuates Proteome and Root Hair Phenotypic Responses to flg22 in Barley. <i>Frontiers in Plant Science</i> , 2021, 12, 666229.	1.7	11
3	The <i>Gossypium stocksii</i> genome as a novel resource for cotton improvement. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	8
4	Transcriptomic response patterns of hornyhead turbot (<i>Pleuronichthys verticalis</i>) dosed with polychlorinated biphenyls and polybrominated diphenyl ethers. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100822.	0.4	1
5	Genome assembly of two nematode-resistant cotton lines (<i>Gossypium hirsutum</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
6	The <i>Gossypium anomalum</i> genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	13
7	Transcriptomic Analysis of <i>Listeria monocytogenes</i> in Response to Bile Under Aerobic and Anaerobic Conditions. <i>Frontiers in Microbiology</i> , 2021, 12, 754748.	1.5	2
8	Identification of Antimicrobial Resistance Determinants in <i>Aeromonas veronii</i> Strain MS-17-88 Recovered From Channel Catfish (<i>Ictalurus punctatus</i>). <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 348.	1.8	30
9	Complete genome sequence of multidrug-resistant avian pathogenic <i>Escherichia coli</i> strain APEC-O2-MS1170. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 23, 401-403.	0.9	3
10	The <i>Gossypium longicalyx</i> Genome as a Resource for Cotton Breeding and Evolution. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1457-1467.	0.8	32
11	Molecular evolution in immune genes across the avian tree of life. <i>Parasitology Open</i> , 2019, 5, .	0.9	3
12	Therapeutic potential of N-acetylcysteine in acrylamide acute neurotoxicity in adult zebrafish. <i>Scientific Reports</i> , 2019, 9, 16467.	1.6	17
13	The Genome Sequence of <i>Gossypioides kirkii</i> Illustrates a Descending Dysploidy in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1541.	1.7	41
14	Multimiomic Analysis of Zebrafish Models of Acute Organophosphorus Poisoning With Different Severity. <i>Toxicological Sciences</i> , 2019, 171, 211-220.	1.4	4
15	Keanu: a novel visualization tool to explore biodiversity in metagenomes. <i>BMC Bioinformatics</i> , 2019, 20, 103.	1.2	4
16	<i>De Novo</i> Genome Sequence Assemblies of <i>Gossypium raimondii</i> and <i>Gossypium turneri</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3079-3085.	0.8	72
17	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i>), Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 107 Td 53-71.	1.1	45
18	Quack: A quality assurance tool for high throughput sequence data. <i>Analytical Biochemistry</i> , 2018, 548, 38-43.	1.1	24

#	ARTICLE	IF	CITATIONS
19	Exploring the loblolly pine (<i>Pinus taeda</i> L.) genome by BAC sequencing and Cot analysis. <i>Gene</i> , 2018, 663, 165-177.	1.0	13
20	Differential Gene Expression Analysis of Plants. <i>Methods in Molecular Biology</i> , 2018, 1783, 279-298.	0.4	2
21	Complete Genome Sequence of Multidrug-Resistant <i>Edwardsiella ictaluri</i> Strain MS-17-156. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
22	Complete Genome Sequence of Multidrug-Resistant <i>Plesiomonas shigelloides</i> Strain MS-17-188. <i>Genome Announcements</i> , 2018, 6, .	0.8	15
23	The genome of the cotton bacterial blight pathogen <i>Xanthomonas citri</i> pv. <i>malvacearum</i> strain MSCT1. <i>Standards in Genomic Sciences</i> , 2017, 12, 42.	1.5	7
24	Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (<i>Gossypieae</i>) Yields Insights into Genome Downsizing. <i>Genome Biology and Evolution</i> , 2017, 9, 3328-3344.	1.1	26
25	Independent Domestication of Two Old World Cotton Species. <i>Genome Biology and Evolution</i> , 2016, 8, 1940-1947.	1.1	40
26	Zebrafish Models for Human Acute Organophosphorus Poisoning. <i>Scientific Reports</i> , 2015, 5, 15591.	1.6	63
27	Transcriptomic dissection of the rice – <i>Burkholderia glumae</i> interaction. <i>BMC Genomics</i> , 2014, 15, 755.	1.2	21
28	Genome comparison of <i>Listeria monocytogenes</i> serotype 4a strain HCC23 with selected lineage I and lineage II <i>L. monocytogenes</i> strains and other <i>Listeria</i> strains. <i>Genomics Data</i> , 2014, 2, 219-225.	1.3	14
29	Computational prediction of disease microRNAs in domestic animals. <i>BMC Research Notes</i> , 2014, 7, 403.	0.6	18