

Scott A Givan

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

9,341
citations

126858

33
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206029

48
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all docs

49
docs citations

49
times ranked

12519
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in nucleus accumbens gene expression accompany sex-specific suppression of spontaneous physical activity in aromatase knockout mice. <i>Hormones and Behavior</i> , 2020, 121, 104719.	1.0	8
2	Sexual dimorphism in brain transcriptomes of Amami spiny rats (<i>Tokudaia osimensis</i>): a rodent species where males lack the Y chromosome. <i>BMC Genomics</i> , 2019, 20, 87.	1.2	4
3	Draft Genome Sequence of <i>Bradyrhizobium</i> sp. Strain LVM 105, a Nitrogen-Fixing Symbiont of <i>Chamaecrista fasciculata</i> (Michx.) Greene. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	0
4	The influence of caging, bedding, and diet on the composition of the microbiota in different regions of the mouse gut. <i>Scientific Reports</i> , 2018, 8, 4065.	1.6	137
5	Transcriptomic alterations in the brain of painted turtles (<i>Chrysemys picta</i>) developmentally exposed to bisphenol A or ethinyl estradiol. <i>Physiological Genomics</i> , 2017, 49, 201-215.	1.0	18
6	Bisphenol A (BPA) in the serum of pet dogs following short-term consumption of canned dog food and potential health consequences of exposure to BPA. <i>Science of the Total Environment</i> , 2017, 579, 1804-1814.	3.9	43
7	Consumption of a high-fat diet alters the seminal fluid and gut microbiomes in male mice. <i>Reproduction, Fertility and Development</i> , 2017, 29, 1602.	0.1	38
8	Gut Dysbiosis and Neurobehavioral Alterations in Rats Exposed to Silver Nanoparticles. <i>Scientific Reports</i> , 2017, 7, 2822.	1.6	91
9	Hypothalamic transcriptomic alterations in male and female California mice (<i>Peromyscus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2017, 5, e13133.	0.7	27
10	Effects of exposure to bisphenol A and ethinyl estradiol on the gut microbiota of parents and their offspring in a rodent model. <i>Gut Microbes</i> , 2016, 7, 471-485.	4.3	121
11	Discovery of a Novel Seminal Fluid Microbiome and Influence of Estrogen Receptor Alpha Genetic Status. <i>Scientific Reports</i> , 2016, 6, 23027.	1.6	59
12	Intermittent severe hypoxia induces plasticity within serotonergic and catecholaminergic neurons in the neonatal rat ventrolateral medulla. <i>Journal of Applied Physiology</i> , 2016, 120, 1277-1287.	1.2	9
13	Short-Stalked <i>Prosthecomicrobium hirschii</i> Cells Have a Caulobacter-Like Cell Cycle. <i>Journal of Bacteriology</i> , 2016, 198, 1149-1159.	1.0	40
14	Draft Genome Sequence of <i>Prosthecomicrobium hirschii</i> ATCC 27832 T. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
15	Genome Sequences of <i>Pseudoalteromonas</i> Strains ATCC BAA-314, ATCC 70018, and ATCC 70019. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
16	Effects of Vendor and Genetic Background on the Composition of the Fecal Microbiota of Inbred Mice. <i>PLoS ONE</i> , 2015, 10, e0116704.	1.1	268
17	Analysis of Genome Sequences from Plant Pathogenic <i>Rhodococcus</i> Reveals Genetic Novelty in Virulence Loci. <i>PLoS ONE</i> , 2014, 9, e101996.	1.1	54
18	Discovery of novel transcripts and gametophytic functions via RNA-seq analysis of maize gametophytic transcriptomes. <i>Genome Biology</i> , 2014, 15, 414.	3.8	74

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19	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419
20	Characterization of the rat developmental liver transcriptome. <i>Physiological Genomics</i> , 2013, 45, 301-311.	1.0	21
21	High-throughput sequence analysis reveals structural diversity and improved potency among RNA inhibitors of HIV reverse transcriptase. <i>Nucleic Acids Research</i> , 2013, 41, 1873-1884.	6.5	57
22	Assembly and Characterization of the European Hazelnut "Jefferson"™ Transcriptome. <i>Crop Science</i> , 2012, 52, 2679-2686.	0.8	35
23	Computational Analysis of RNA-seq. <i>Methods in Molecular Biology</i> , 2012, 883, 201-219.	0.4	11
24	Genome sequencing and comparative analysis of the carrot bacterial blight pathogen, <i>Xanthomonas hortorum</i> pv. <i>carotae</i> M081, for insights into pathogenicity and applications in molecular diagnostics. <i>Molecular Plant Pathology</i> , 2011, 12, 580-594.	2.0	18
25	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
26	An improved, high-quality draft genome sequence of the Germination-Arrest Factor-producing <i>Pseudomonas fluorescens</i> WH6. <i>BMC Genomics</i> , 2010, 11, 522.	1.2	54
27	MicroRNA Gene Evolution in <i>Arabidopsis lyrata</i> and <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2010, 22, 1074-1089.	3.1	234
28	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2010, 20, 45-58.	2.4	825
29	Computational and analytical framework for small RNA profiling by high-throughput sequencing. <i>Rna</i> , 2009, 15, 992-1002.	1.6	112
30	The small genome of an abundant coastal ocean methylotroph. <i>Environmental Microbiology</i> , 2008, 10, 1771-1782.	1.8	197
31	Network Discovery Pipeline Elucidates Conserved Time-of-Day-Specific cis-Regulatory Modules. <i>PLoS Genetics</i> , 2008, 4, e14.	1.5	474
32	Genome-Wide Analysis of the RNA-DEPENDENT RNA POLYMERASE6/DICER-LIKE4 Pathway in <i>Arabidopsis</i> Reveals Dependency on miRNA- and tasiRNA-Directed Targeting. <i>Plant Cell</i> , 2007, 19, 926-942.	3.1	381
33	Update of ASRP: the <i>Arabidopsis</i> Small RNA Project database. <i>Nucleic Acids Research</i> , 2007, 36, D982-D985.	6.5	70
34	High-Throughput Sequencing of <i>Arabidopsis</i> microRNAs: Evidence for Frequent Birth and Death of miRNA Genes. <i>PLoS ONE</i> , 2007, 2, e219.	1.1	1,100
35	The Diurnal Project: Diurnal and Circadian Expression Profiling, Model-based Pattern Matching, and Promoter Analysis. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2007, 72, 353-363.	2.0	358
36	Natural variation in SAR11 marine bacterioplankton genomes inferred from metagenomic data. <i>Biology Direct</i> , 2007, 2, 27.	1.9	95

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37	Genome-Wide Profiling and Analysis of Arabidopsis siRNAs. PLoS Biology, 2007, 5, e57.	2.6	473
38	Polyphyletic photosynthetic reaction centre genes in oligotrophic marine Gammaproteobacteria. Environmental Microbiology, 2007, 9, 1456-1463.	1.8	76
39	The Personal Sequence Database: a suite of tools to create and maintain web-accessible sequence databases. BMC Bioinformatics, 2007, 8, 479.	1.2	3
40	Toxicogenomic Profiling of the Hepatic Tumor Promoters Indole-3-Carbinol, 17 β -Estradiol and β -Naphthoflavone in Rainbow Trout. Toxicological Sciences, 2006, 90, 61-72.	1.4	68
41	Use of a Rainbow Trout Oligonucleotide Microarray to Determine Transcriptional Patterns in Aflatoxin B1-Induced Hepatocellular Carcinoma Compared to Adjacent Liver. Toxicological Sciences, 2005, 88, 319-330.	1.4	61
42	Expression of Arabidopsis MIRNA Genes. Plant Physiology, 2005, 138, 2145-2154.	2.3	626
43	Genome Streamlining in a Cosmopolitan Oceanic Bacterium. Science, 2005, 309, 1242-1245.	6.0	1,034
44	ASRP: the Arabidopsis Small RNA Project Database. Nucleic Acids Research, 2004, 33, D637-D640.	6.5	173
45	Ctf3p, the Mis6 budding yeast homolog, interacts with Mcm22p and Mcm16p at the yeast outer kinetochore. Genes and Development, 2002, 16, 101-113.	2.7	111
46	GTPase-Activating Proteins for Cdc42. Eukaryotic Cell, 2002, 1, 469-480.	3.4	109
47	Genetic mapping with dispersed repeated sequences in the rice blast fungus: Mapping the SMO locus. Molecular Genetics and Genomics, 1990, 223, 487-495.	2.4	47