

Sorel T Fitz-Gibbon

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,573
citations

393982

19
h-index

500791

28
g-index

30
all docs

30
docs citations

30
times ranked

4281
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct Shifts in Microbiota Composition during <i>Drosophila</i> Aging Impair Intestinal Function and Drive Mortality. <i>Cell Reports</i> , 2015, 12, 1656-1667.	2.9	382
2	An Indexed, Mapped Mutant Library Enables Reverse Genetics Studies of Biological Processes in <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2016, 28, 367-387.	3.1	336
3	Genome sequence of the hyperthermophilic crenarchaeon <i>Pyrobaculum aerophilum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 984-989.	3.3	206
4	Genomic landscape of the global oak phylogeny. <i>New Phytologist</i> , 2020, 226, 1198-1212.	3.5	186
5	Systems-Level Analysis of Nitrogen Starvation-Induced Modifications of Carbon Metabolism in a <i>Chlamydomonas reinhardtii</i> Starchless Mutant. <i>Plant Cell</i> , 2013, 25, 4305-4323.	3.1	176
6	Species-wide patterns of <i>scp</i> DNA methylation variation in <i>Quercus lobata</i> and their association with climate gradients. <i>Molecular Ecology</i> , 2016, 25, 1665-1680.	2.0	159
7	CRISPR/Cas9-Mediated Correction of the Sickie Mutation in Human CD34+ cells. <i>Molecular Therapy</i> , 2016, 24, 1561-1569.	3.7	157
8	Site-Specific Gene Editing of Human Hematopoietic Stem Cells for X-Linked Hyper-IgM Syndrome. <i>Cell Reports</i> , 2018, 23, 2606-2616.	2.9	119
9	<i>Chlamydomonas</i> Genome Resource for Laboratory Strains Reveals a Mosaic of Sequence Variation, Identifies True Strain Histories, and Enables Strain-Specific Studies. <i>Plant Cell</i> , 2015, 27, 2335-2352.	3.1	102
10	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017, 18, 54-67.	2.9	100
11	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	0.8	95
12	High-throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved <i>de novo</i> assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. <i>Plant Journal</i> , 2018, 93, 545-565.	2.8	90
13	Adaptational lag to temperature in valley oak (<i>Quercus lobata</i>) can be mitigated by genome-informed assisted gene flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25179-25185.	3.3	89
14	An epigenetic gene silencing pathway selectively acting on transgenic DNA in the green alga <i>Chlamydomonas</i> . <i>Nature Communications</i> , 2020, 11, 6269.	5.8	58
15	Dynamic changes in the transcriptome and methylome of <i>Chlamydomonas reinhardtii</i> throughout its life cycle. <i>Plant Physiology</i> , 2015, 169, pp.00861.2015.	2.3	51
16	Phylogenomic inferences from reference-mapped and <i>de novo</i> assembled short-read sequence data using RADseq sequencing of California white oaks (<i>Quercus</i> section <i>Quercus</i>). <i>Genome</i> , 2017, 60, 743-755.	0.9	50
17	RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (<i>Quercus</i> sect. <i>Quercus</i> : Fagaceae). <i>Molecular Ecology</i> , 2018, 27, 4556-4571.	2.0	33
18	Landscape genomics of <i>Quercus lobata</i> reveals genes involved in local climate adaptation at multiple spatial scales. <i>Molecular Ecology</i> , 2021, 30, 406-423.	2.0	30

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19	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. <i>Nature Communications</i> , 2022, 13, 2047.	5.8	30
20	Ni induces the CRR1-dependent regulon revealing overlap and distinction between hypoxia and Cu deficiency responses in <i>Chlamydomonas reinhardtii</i> . <i>Metallomics</i> , 2016, 8, 679-691.	1.0	27
21	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. <i>Metabolic Engineering</i> , 2018, 49, 153-163.	3.6	22
22	Metabolic repair through emergence of new pathways in <i>Escherichia coli</i> . <i>Nature Chemical Biology</i> , 2018, 14, 1005-1009.	3.9	20
23	Complete genomic sequences of <i>Propionibacterium freudenreichii</i> phages from Swiss cheese reveal greater diversity than <i>Cutibacterium</i> (formerly <i>Propionibacterium</i>) <i>acnes</i> phages. <i>BMC Microbiology</i> , 2018, 18, 19.	1.3	13
24	An in situ high-throughput screen identifies inhibitors of intracellular <i>Burkholderia pseudomallei</i> with therapeutic efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18597-18606.	3.3	13
25	Epigenetic changes mediated by polycomb repressive complex 2 and E2a are associated with drug resistance in a mouse model of lymphoma. <i>Genome Medicine</i> , 2016, 8, 54.	3.6	12
26	Genome-Wide Variation in DNA Methylation Predicts Variation in Leaf Traits in an Ecosystem-Foundational Oak Species. <i>Forests</i> , 2021, 12, 569.	0.9	8
27	Ancient Introgression Between Distantly Related White Oaks (<i>Quercus</i> sect. <i>Quercus</i>) Shows Evidence of Climate-Associated Asymmetric Gene Exchange. <i>Journal of Heredity</i> , 2021, 112, 663-670.	1.0	3
28	Genome-wide gene order distances support clustering the gram-positive bacteria. <i>Frontiers in Microbiology</i> , 2015, 5, 785.	1.5	2