

Sorel T Fitz-Gibbon

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29
papers

1,669
citations

17
h-index

30
g-index

30
ext. papers

2,229
ext. citations

8.6
avg, IF

4.44
L-index

#	Paper	IF	Citations
29	Distinct Shifts in Microbiota Composition during <i>Drosophila</i> Aging Impair Intestinal Function and Drive Mortality. <i>Cell Reports</i> , 2015 , 12, 1656-67	10.6	258
28	An Indexed, Mapped Mutant Library Enables Reverse Genetics Studies of Biological Processes in <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2016 , 28, 367-87	11.6	226
27	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, 984-9	11.5	197
26	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, 4305-23	11.6	145
25	CRISPR/Cas9-Mediated Correction of the Sickie Mutation in Human CD34+ cells. <i>Molecular Therapy</i> , 2016 , 24, 1561-9	11.7	118
24	Species-wide patterns of DNA methylation variation in <i>Quercus lobata</i> and their association with climate gradients. <i>Molecular Ecology</i> , 2016 , 25, 1665-80	5.7	88
23	Genomic landscape of the global oak phylogeny. <i>New Phytologist</i> , 2020 , 226, 1198-1212	9.8	83
22	Human Embryonic Stem Cells Do Not Change Their X Inactivation Status during Differentiation. <i>Cell Reports</i> , 2017 , 18, 54-67	10.6	72
21	Site-Specific Gene Editing of Human Hematopoietic Stem Cells for X-Linked Hyper-IgM Syndrome. <i>Cell Reports</i> , 2018 , 23, 2606-2616	10.6	66
20	<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, 2335-52	11.6	63
19	First Draft Assembly and Annotation of the Genome of a California Endemic Oak NB (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3485-3495	3.2	57
18	High-throughput sequencing of the chloroplast and mitochondrion of <i>Chlamydomonas reinhardtii</i> to generate improved de novo assemblies, analyze expression patterns and transcript speciation, and evaluate diversity among laboratory strains and wild isolates. <i>Plant Journal</i> , 2018 , 93, 545-565	6.9	54
17	Adaptational lag to temperature in valley oak () 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	11.5	44
16	Phylogenomic inferences from reference-mapped and de novo 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	2.4	35
15	Dynamic Changes in the Transcriptome and Methylome of <i>Chlamydomonas reinhardtii</i> throughout Its Life Cycle. <i>Plant Physiology</i> , 2015 , 169, 2730-43	6.6	34
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	17.4	24
13	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	5.7	22

12	Directed strain evolution restructures metabolism for 1-butanol production in minimal media. <i>Metabolic Engineering</i> , 2018 , 49, 153-163	9.7	16
11	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, 679-91	4.5	16
10	Metabolic repair through emergence of new pathways in <i>Escherichia coli</i> . <i>Nature Chemical Biology</i> , 2018 , 14, 1005-1009	11.7	14
9	An in situ high-throughput screen identifies inhibitors of intracellular with therapeutic efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 18597-18606	11.5	8
8	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	4.5	8
7	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	14.4	7
6	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	5.7	6
5	Genome-wide gene order distances support clustering the gram-positive bacteria. <i>Frontiers in Microbiology</i> , 2014 , 5, 785	5.7	2
4	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks		2
3	High-quality genome and methylomes illustrate features underlying evolutionary success of oaks.. <i>Nature Communications</i> , 2022 , 13, 2047	17.4	2
2	Genome-Wide Variation in DNA Methylation Predicts Variation in Leaf Traits in an Ecosystem-Foundational Oak Species. <i>Forests</i> , 2021 , 12, 569	2.8	1
1	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 ,	2.4	1