

Joshua S Bloom

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,511
citations

394421

19
h-index

454955

30
g-index

50
all docs

50
docs citations

50
times ranked

3115
citing authors

#	ARTICLE	IF	CITATIONS
1	Retrospective Detection of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in Symptomatic Patients Prior to Widespread Diagnostic Testing in Southern California. <i>Clinical Infectious Diseases</i> , 2022, 74, 271-277.	5.8	4
2	Genomic epidemiology of the Los Angeles COVID-19 outbreak and the early history of the B.1.43 strain in the USA. <i>BMC Genomics</i> , 2022, 23, 260.	2.8	0
3	Island-specific evolution of a sex-primed autosome in a sexual planarian. <i>Nature</i> , 2022, 606, 329-334.	27.8	19
4	Metabolic reprogramming and epigenetic changes of vital organs in SARS-CoV-2-induced systemic toxicity. <i>JCI Insight</i> , 2021, 6, .	5.0	57
5	Ancient balancing selection maintains incompatible versions of the galactose pathway in yeast. <i>Science</i> , 2021, 371, 415-419.	12.6	27
6	Whole-organism eQTL mapping at cellular resolution with single-cell sequencing. <i>ELife</i> , 2021, 10, .	6.0	24
7	Genetics of white color and iridophoroma in "Lemon Frost" leopard geckos. <i>PLoS Genetics</i> , 2021, 17, e1009580.	3.5	13
8	Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples. <i>Nature Biomedical Engineering</i> , 2021, 5, 657-665.	22.5	46
9	Pooled analysis of radiation hybrids identifies loci for growth and drug action in mammalian cells. <i>Genome Research</i> , 2020, 30, 1458-1467.	5.5	6
10	Reliable and accurate diagnostics from highly multiplexed sequencing assays. <i>Scientific Reports</i> , 2020, 10, 21759.	3.3	13
11	Modeling epistasis in mice and yeast using the proportion of two or more distinct genetic backgrounds: Evidence for "polygenic epistasis". <i>PLoS Genetics</i> , 2020, 16, e1009165.	3.5	7
12	Analysis of the genetic basis of height in large Jewish nuclear families. <i>PLoS Genetics</i> , 2019, 15, e1008082.	3.5	1
13	A Scalable, Multiplexed Assay for Decoding GPCR-Ligand Interactions with RNA Sequencing. <i>Cell Systems</i> , 2019, 8, 254-260.e6.	6.2	22
14	The Genetic Basis of Mutation Rate Variation in Yeast. <i>Genetics</i> , 2019, 211, 731-740.	2.9	39
15	Rare variants contribute disproportionately to quantitative trait variation in yeast. <i>ELife</i> , 2019, 8, .	6.0	70
16	Highly parallel genome variant engineering with CRISPR-Cas9. <i>Nature Genetics</i> , 2018, 50, 510-514.	21.4	73
17	Shared Genomic Regions Underlie Natural Variation in Diverse Toxin Responses. <i>Genetics</i> , 2018, 210, 1509-1525.	2.9	39
18	Genetics of trans-regulatory variation in gene expression. <i>ELife</i> , 2018, 7, .	6.0	146

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19	Accounting for genetic interactions improves modeling of individual quantitative trait phenotypes in yeast. <i>Nature Genetics</i> , 2017, 49, 497-503.	21.4	141
20	Genetic variation in adaptability and pleiotropy in budding yeast. <i>ELife</i> , 2017, 6, .	6.0	62
21	CRISPR-directed mitotic recombination enables genetic mapping without crosses. <i>Science</i> , 2016, 352, 1113-1116.	12.6	90
22	Genetic interactions contribute less than additive effects to quantitative trait variation in yeast. <i>Nature Communications</i> , 2015, 6, 8712.	12.8	139
23	Genetics of Intraspecies Variation in Avoidance Behavior Induced by a Thermal Stimulus in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2015, 200, 1327-1339.	2.9	9
24	A Powerful New Quantitative Genetics Platform, Combining <i>Caenorhabditis elegans</i> High-Throughput Fitness Assays with a Large Collection of Recombinant Strains. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 911-920.	1.8	106
25	Genetic Mapping of MAPK-Mediated Complex Traits Across <i>S. cerevisiae</i> . <i>PLoS Genetics</i> , 2015, 11, e1004913.	3.5	46
26	A Variant in the Neuropeptide Receptor <i>npr-1</i> is a Major Determinant of <i>Caenorhabditis elegans</i> Growth and Physiology. <i>PLoS Genetics</i> , 2014, 10, e1004156.	3.5	174
27	Genetics of single-cell protein abundance variation in large yeast populations. <i>Nature</i> , 2014, 506, 494-497.	27.8	134
28	Finding the sources of missing heritability in a yeast cross. <i>Nature</i> , 2013, 494, 234-237.	27.8	427
29	Genetic Architecture of Highly Complex Chemical Resistance Traits across Four Yeast Strains. <i>PLoS Genetics</i> , 2012, 8, e1002570.	3.5	85
30	Chromosome-scale selective sweeps shape <i>Caenorhabditis elegans</i> genomic diversity. <i>Nature Genetics</i> , 2012, 44, 285-290.	21.4	366
31	Fine mapping of regulatory loci for mammalian gene expression using radiation hybrids. <i>Nature Genetics</i> , 2008, 40, 421-429.	21.4	29