

David Burstein

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

5,499
citations

185998

28
h-index

329751

37
g-index

41
all docs

41
docs citations

41
times ranked

6912
citing authors

#	ARTICLE	IF	CITATIONS
1	Chimeric CRISPR-CasX enzymes and guide RNAs for improved genome editing activity. <i>Molecular Cell</i> , 2022, 82, 1199-1209.e6.	4.5	29
2	Engineered B cells expressing an anti-HIV antibody enable memory retention, isotype switching and clonal expansion. <i>Nature Communications</i> , 2020, 11, 5851.	5.8	42
3	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	4.5	49
4	Tiny Hidden Genes within Our Microbiome. <i>Cell</i> , 2019, 178, 1034-1035.	13.5	1
5	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	5.8	112
6	A Functional Mini-Integrase in a Two-Protein Type V-C CRISPR System. <i>Molecular Cell</i> , 2019, 73, 727-737.e3.	4.5	22
7	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	5.8	87
8	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. <i>Nature Microbiology</i> , 2019, 4, 1356-1367.	5.9	170
9	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	6.0	757
10	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
11	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. <i>Genome Research</i> , 2017, 27, 601-612.	2.4	99
12	RNA Targeting by Functionally Orthogonal Type VI-A CRISPR-Cas Enzymes. <i>Molecular Cell</i> , 2017, 66, 373-383.e3.	4.5	229
13	Potential for microbial H ₂ and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	4.4	137
14	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	5.9	62
15	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	13.7	471
16	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82
17	Identification of novel <i>Xanthomonas euvesicatoria</i> type III effector proteins by a machine learning approach. <i>Molecular Plant Pathology</i> , 2016, 17, 398-411.	2.0	66
18	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. <i>Nature</i> , 2016, 538, 270-273.	13.7	854

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19	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
20	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	9.4	235
21	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. <i>PeerJ</i> , 2016, 4, e1607.	0.9	57
22	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	2.4	121
23	Novel Type III Effectors in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015, 6, e00161.	1.8	37
24	Identification of Novel <i>Coxiella burnetii</i> Icm/Dot Effectors and Genetic Analysis of Their Involvement in Modulating a Mitogen-Activated Protein Kinase Pathway. <i>Infection and Immunity</i> , 2014, 82, 3740-3752.	1.0	55
25	Computational modeling and experimental validation of the <i>Legionella</i> and <i>Coxiella</i> virulence-related type-IVB secretion signal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E707-15.	3.3	166
26	DNA motifs determining the efficiency of adaptation into the <i>Escherichia coli</i> CRISPR array. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14396-14401.	3.3	62
27	CoPAP: Coevolution of Presence-Absence Patterns. <i>Nucleic Acids Research</i> , 2013, 41, W232-W237.	6.5	30
28	Changes in exon-intron structure during vertebrate evolution affect the splicing pattern of exons. <i>Genome Research</i> , 2012, 22, 35-50.	2.4	88
29	A Machine Learning Approach To Identify Hydrogenosomal Proteins in <i>Trichomonas vaginalis</i> . <i>Eukaryotic Cell</i> , 2012, 11, 217-228.	3.4	24
30	Uncovering the co-evolutionary network among prokaryotic genes. <i>Bioinformatics</i> , 2012, 28, i389-i394.	1.8	36
31	Differential GC Content between Exons and Introns Establishes Distinct Strategies of Splice-Site Recognition. <i>Cell Reports</i> , 2012, 1, 543-556.	2.9	249
32	Native homing endonucleases can target conserved genes in humans and in animal models. <i>Nucleic Acids Research</i> , 2011, 39, 6646-6659.	6.5	27
33	Genome-Scale Identification of <i>Legionella pneumophila</i> Effectors Using a Machine Learning Approach. <i>PLoS Pathogens</i> , 2009, 5, e1000508.	2.1	236
34	Large-scale comparative analysis of splicing signals and their corresponding splicing factors in eukaryotes. <i>Genome Research</i> , 2008, 18, 88-103.	2.4	161
35	The Average Common Substring Approach to Phylogenomic Reconstruction. <i>Journal of Computational Biology</i> , 2006, 13, 336-350.	0.8	184
36	Information Theoretic Approaches to Whole Genome Phylogenies. <i>Lecture Notes in Computer Science</i> , 2005, , 283-295.	1.0	6