

David Burstein

List of Publications by Year in descending order

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36
papers

5,499
citations

186265

28
h-index

330143

37
g-index

41
all docs

41
docs citations

41
times ranked

6912
citing authors

#	ARTICLE	IF	CITATIONS
1	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. <i>Nature</i> , 2016, 538, 270-273.	27.8	854
2	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. <i>Science</i> , 2018, 362, 839-842.	12.6	757
3	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	27.8	471
4	Differential GC Content between Exons and Introns Establishes Distinct Strategies of Splice-Site Recognition. <i>Cell Reports</i> , 2012, 1, 543-556.	6.4	249
5	Genome-Scale Identification of <i>Legionella pneumophila</i> Effectors Using a Machine Learning Approach. <i>PLoS Pathogens</i> , 2009, 5, e1000508.	4.7	236
6	Genomic analysis of 38 <i>Legionella</i> species identifies large and diverse effector repertoires. <i>Nature Genetics</i> , 2016, 48, 167-175.	21.4	235
7	RNA Targeting by Functionally Orthogonal Type VI-A CRISPR-Cas Enzymes. <i>Molecular Cell</i> , 2017, 66, 373-383.e3.	9.7	229
8	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
9	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.	3.8	212
10	The Average Common Substring Approach to Phylogenomic Reconstruction. <i>Journal of Computational Biology</i> , 2006, 13, 336-350.	1.6	184
11	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.	13.3	170
12	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.	7.1	166
13	Large-scale comparative analysis of splicing signals and their corresponding splicing factors in eukaryotes. <i>Genome Research</i> , 2008, 18, 88-103.	5.5	161
14	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.	9.8	137
15	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
16	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	12.8	112
17	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.	5.5	99
18	Changes in exon-intron structure during vertebrate evolution affect the splicing pattern of exons. <i>Genome Research</i> , 2012, 22, 35-50.	5.5	88

#	ARTICLE	IF	CITATIONS
19	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
20	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	3.9	82
21	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.	4.2	66
22	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.	7.1	62
23	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	13.3	62
24	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.	2.0	57
25	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.	2.2	55
26	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	9.7	49
27	Engineered B cells expressing an anti-HIV antibody enable memory retention, isotype switching and clonal expansion. <i>Nature Communications</i> , 2020, 11, 5851.	12.8	42
28	Novel Type III Effectors in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2015, 6, e00161.	4.1	37
29	Uncovering the co-evolutionary network among prokaryotic genes. <i>Bioinformatics</i> , 2012, 28, i389-i394.	4.1	36
30	CoPAP: Coevolution of Presence-Absence Patterns. <i>Nucleic Acids Research</i> , 2013, 41, W232-W237.	14.5	30
31	Chimeric CRISPR-CasX enzymes and guide RNAs for improved genome editing activity. <i>Molecular Cell</i> , 2022, 82, 1199-1209.e6.	9.7	29
32	Native homing endonucleases can target conserved genes in humans and in animal models. <i>Nucleic Acids Research</i> , 2011, 39, 6646-6659.	14.5	27
33	A Machine Learning Approach To Identify Hydrogenosomal Proteins in <i>Trichomonas vaginalis</i> . <i>Eukaryotic Cell</i> , 2012, 11, 217-228.	3.4	24
34	A Functional Mini-Integrase in a Two-Protein Type V-C CRISPR System. <i>Molecular Cell</i> , 2019, 73, 727-737.e3.	9.7	22
35	Information Theoretic Approaches to Whole Genome Phylogenies. <i>Lecture Notes in Computer Science</i> , 2005, , 283-295.	1.3	6
36	Tiny Hidden Genes within Our Microbiome. <i>Cell</i> , 2019, 178, 1034-1035.	28.9	1