

Ruth Hershberg

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

4,256
citations

361413

20
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414414

32
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37
all docs

37
docs citations

37
times ranked

5666
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of Adaptation During Three Years of Evolution Under Long-Term Stationary Phase. <i>Molecular Biology and Evolution</i> , 2021, 38, 2778-2790.	8.9	22
2	Culture Volume Influences the Dynamics of Adaptation under Long-Term Stationary Phase. <i>Genome Biology and Evolution</i> , 2020, 12, 2292-2301.	2.5	12
3	Adaptations Accumulated under Prolonged Resource Exhaustion Are Highly Transient. <i>MSphere</i> , 2020, 5, .	2.9	11
4	The Codon Usage of Lowly Expressed Genes Is Subject to Natural Selection. <i>Genome Biology and Evolution</i> , 2018, 10, 1237-1246.	2.5	45
5	Characterization of Factors Affecting the Detection Limit of EGFR p.T790M in Circulating Tumor DNA. <i>Technology in Cancer Research and Treatment</i> , 2018, 17, 153303381879365.	1.9	3
6	Antibiotic-Independent Adaptive Effects of Antibiotic Resistance Mutations. <i>Trends in Genetics</i> , 2017, 33, 521-528.	6.7	47
7	Rapid Genetic Adaptation during the First Four Months of Survival under Resource Exhaustion. <i>Molecular Biology and Evolution</i> , 2017, 34, 1758-1769.	8.9	64
8	Horizontally Acquired Genes Are Often Shared between Closely Related Bacterial Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1536.	3.5	19
9	Similar levels of gene content variation observed for <i>Pseudomonas syringae</i> populations extracted from single and multiple host species. <i>PLoS ONE</i> , 2017, 12, e0184195.	2.5	8
10	Human host range of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2016, 48, 1453-1454.	21.4	3
11	Variation in KRAS driver substitution distributions between tumor types is determined by both mutation and natural selection. <i>Scientific Reports</i> , 2016, 6, 21927.	3.3	11
12	Bacterial intra-species gene loss occurs in a largely clocklike manner mostly within a pool of less conserved and constrained genes. <i>Scientific Reports</i> , 2016, 6, 35168.	3.3	24
13	Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains. <i>Microbiome</i> , 2016, 4, 18.	11.1	58
14	The Somatic Nature of Cancer Allows It to Affect Highly Constrained Genes. <i>Genome Biology and Evolution</i> , 2016, 8, 1614-1620.	2.5	3
15	Prokaryotic Nucleotide Composition Is Shaped by Both Phylogeny and the Environment. <i>Genome Biology and Evolution</i> , 2015, 7, 1380-1389.	2.5	82
16	Alarmingly High Segregation Frequencies of Quinolone Resistance Alleles within Human and Animal Microbiomes Are Not Explained by Direct Clinical Antibiotic Exposure. <i>Genome Biology and Evolution</i> , 2015, 7, 1743-1757.	2.5	18
17	Gene Loss Dominates As a Source of Genetic Variation within Clonal Pathogenic Bacterial Species. <i>Genome Biology and Evolution</i> , 2015, 7, 2173-2187.	2.5	69
18	Mutation – The Engine of Evolution: Studying Mutation and Its Role in the Evolution of Bacteria: Figure 1.. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015, 7, a018077.	5.5	66

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19	Cancer Evolution Is Associated with Pervasive Positive Selection on Globally Expressed Genes. <i>PLoS Genetics</i> , 2014, 10, e1004239.	3.5	93
20	POGO-DB—a database of pairwise-comparisons of genomes and conserved orthologous genes. <i>Nucleic Acids Research</i> , 2014, 42, D625-D632.	14.5	22
21	Strong Purifying Selection at Synonymous Sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003527.	3.5	187
22	Elevated Mutagenesis Does Not Explain the Increased Frequency of Antibiotic Resistant Mutants in Starved Aging Colonies. <i>PLoS Genetics</i> , 2013, 9, e1003968.	3.5	30
23	On the Limitations of Using Ribosomal Genes as References for the Study of Codon Usage: A Rebuttal. <i>PLoS ONE</i> , 2012, 7, e49060.	2.5	17
24	Evidence That Mutation Is Universally Biased towards AT in Bacteria. <i>PLoS Genetics</i> , 2010, 6, e1001115.	3.5	386
25	General Rules for Optimal Codon Choice. <i>PLoS Genetics</i> , 2009, 5, e1000556.	3.5	203
26	Selection on Codon Bias. <i>Annual Review of Genetics</i> , 2008, 42, 287-299.	7.6	827
27	High Functional Diversity in <i>Mycobacterium tuberculosis</i> Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311.	5.6	507
28	Small RNAs encoded within genetic islands of <i>Salmonella typhimurium</i> show host-induced expression and role in virulence. <i>Nucleic Acids Research</i> , 2008, 36, 1913-1927.	14.5	212
29	Chromosomal organization is shaped by the transcription regulatory network. <i>Trends in Genetics</i> , 2005, 21, 138-142.	6.7	69
30	A survey of small RNA-encoding genes in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2003, 31, 1813-1820.	14.5	223
31	Molecular Basis for Expression of Common and Rare Fragile Sites. <i>Molecular and Cellular Biology</i> , 2003, 23, 7143-7151.	2.3	211
32	Novel small RNA-encoding genes in the intergenic regions of <i>Escherichia coli</i> . <i>Current Biology</i> , 2001, 11, 941-950.	3.9	695