

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
h-index

414414

32
g-index

37
all docs

37
docs citations

37
times ranked

5666
citing authors

#	ARTICLE	IF	CITATIONS
1	Selection on Codon Bias. Annual Review of Genetics, 2008, 42, 287-299.	7.6	827
2	Novel small RNA-encoding genes in the intergenic regions of Escherichia coli. Current Biology, 2001, 11, 941-950.	3.9	695
3	High Functional Diversity in Mycobacterium tuberculosis Driven by Genetic Drift and Human Demography. PLoS Biology, 2008, 6, e311.	5.6	507
4	Evidence That Mutation Is Universally Biased towards AT in Bacteria. PLoS Genetics, 2010, 6, e1001115.	3.5	386
5	A survey of small RNA-encoding genes in Escherichia coli. Nucleic Acids Research, 2003, 31, 1813-1820.	14.5	223
6	Small RNAs encoded within genetic islands of Salmonella typhimurium show host-induced expression and role in virulence. Nucleic Acids Research, 2008, 36, 1913-1927.	14.5	212
7	Molecular Basis for Expression of Common and Rare Fragile Sites. Molecular and Cellular Biology, 2003, 23, 7143-7151.	2.3	211
8	General Rules for Optimal Codon Choice. PLoS Genetics, 2009, 5, e1000556.	3.5	203
9	Strong Purifying Selection at Synonymous Sites in D. melanogaster. PLoS Genetics, 2013, 9, e1003527.	3.5	187
10	Cancer Evolution Is Associated with Pervasive Positive Selection on Globally Expressed Genes. PLoS Genetics, 2014, 10, e1004239.	3.5	93
11	Prokaryotic Nucleotide Composition Is Shaped by Both Phylogeny and the Environment. Genome Biology and Evolution, 2015, 7, 1380-1389.	2.5	82
12	Chromosomal organization is shaped by the transcription regulatory network. Trends in Genetics, 2005, 21, 138-142.	6.7	69
13	Gene Loss Dominates As a Source of Genetic Variation within Clonal Pathogenic Bacterial Species. Genome Biology and Evolution, 2015, 7, 2173-2187.	2.5	69
14	Mutationâ€”The Engine of Evolution: Studying Mutation and Its Role in the Evolution of Bacteria: Figure 1.. Cold Spring Harbor Perspectives in Biology, 2015, 7, a018077.	5.5	66
15	Rapid Genetic Adaptation during the First Four Months of Survival under Resource Exhaustion. Molecular Biology and Evolution, 2017, 34, 1758-1769.	8.9	64
16	Marker genes that are less conserved in their sequences are useful for predicting genome-wide similarity levels between closely related prokaryotic strains. Microbiome, 2016, 4, 18.	11.1	58
17	Antibiotic-Independent Adaptive Effects of Antibiotic Resistance Mutations. Trends in Genetics, 2017, 33, 521-528.	6.7	47
18	The Codon Usage of Lowly Expressed Genes Is Subject to Natural Selection. Genome Biology and Evolution, 2018, 10, 1237-1246.	2.5	45

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19	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
20	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
21	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
22	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
23	Horizontally Acquired Genes Are Often Shared between Closely Related Bacterial Species. <i>Frontiers in Microbiology</i> , 2017, 8, 1536.	3.5	19
24	Alarming 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
25	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
26	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
27	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
28	Adaptations Accumulated under Prolonged Resource Exhaustion Are Highly Transient. <i>MSphere</i> , 2020, 5, .	2.9	11
29	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
30	Human host range of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2016, 48, 1453-1454.	21.4	3
31	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
32	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