

Tal Dagan

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

6,150
citations

81900

39
h-index

79698

73
g-index

102
all docs

102
docs citations

102
times ranked

7134
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene sharing among plasmids and chromosomes reveals barriers for antibiotic resistance gene transfer. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022, 377, 20200467.	4.0	23
2	Denitrification in foraminifera has an ancient origin and is complemented by associated bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	9
3	Pangenome Evolution in Environmentally Transmitted Symbionts of Deep-Sea Mussels Is Governed by Vertical Inheritance. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5
4	Natural Competence in the Filamentous, Heterocystous Cyanobacterium <i>Chlorogloeopsis fritschii</i> PCC 6912. <i>MSphere</i> , 2022, 7, .	2.9	1
5	Darwinian individuality of extrachromosomal genetic elements calls for population genetics tinkering. <i>Environmental Microbiology Reports</i> , 2021, 13, 22-26.	2.4	6
6	Two novel heteropolymer-forming proteins maintain the multicellular shape of the cyanobacterium <i>Anabaena</i> sp. PCC 7120. <i>FEBS Journal</i> , 2021, 288, 3197-3216.	4.7	7
7	Colonization dynamics of <i>Pantoea agglomerans</i> in the wheat root habitat. <i>Environmental Microbiology</i> , 2021, 23, 2260-2273.	3.8	14
8	Essential gene acquisition destabilizes plasmid inheritance. <i>PLoS Genetics</i> , 2021, 17, e1009656.	3.5	19
9	Segregational Drift Constrains the Evolutionary Rate of Prokaryotic Plasmids. <i>Molecular Biology and Evolution</i> , 2021, 38, 5610-5624.	8.9	14
10	The Order of Trait Emergence in the Evolution of Cyanobacterial Multicellularity. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	26
11	Antibiotics Interfere with the Evolution of Plasmid Stability. <i>Current Biology</i> , 2020, 30, 3841-3847.e4.	3.9	37
12	Plasmid evolution. <i>Current Biology</i> , 2020, 30, R1158-R1163.	3.9	23
13	A novel septal protein of multicellular heterocystous cyanobacteria is associated with the divisome. <i>Molecular Microbiology</i> , 2020, 113, 1140-1154.	2.5	22
14	Discovery of multi-operon colinear syntenic blocks in microbial genomes. <i>Bioinformatics</i> , 2020, 36, i21-i29.	4.1	15
15	Intracellular Competitions Reveal Determinants of Plasmid Evolutionary Success. <i>Frontiers in Microbiology</i> , 2020, 11, 2062.	3.5	13
16	Somatic genetic drift and multilevel selection in a clonal seagrass. <i>Nature Ecology and Evolution</i> , 2020, 4, 952-962.	7.8	86
17	Identification and characterization of novel filament-forming proteins in cyanobacteria. <i>Scientific Reports</i> , 2020, 10, 1894.	3.3	22
18	Seed-Derived Microbial Colonization of Wild Emmer and Domesticated Bread Wheat (<i>Triticum</i>) and Composition. <i>MBio</i> , 2020, 11, .	4.1	40

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19	Insertion and deletion evolution reflects antibiotics selection pressure in a Mycobacterium tuberculosis outbreak. <i>PLoS Pathogens</i> , 2020, 16, e1008357.	4.7	22
20	Rates of Molecular Evolution in a Marine Synechococcus Phage Lineage. <i>Viruses</i> , 2019, 11, 720.	3.3	12
21	Interactions and Coadaptation in Plant Metaorganisms. <i>Annual Review of Phytopathology</i> , 2019, 57, 483-503.	7.8	28
22	Currency, Exchange, and Inheritance in the Evolution of Symbiosis. <i>Trends in Microbiology</i> , 2019, 27, 836-849.	7.7	29
23	Horizontally transmitted symbiont populations in deep-sea mussels are genetically isolated. <i>ISME Journal</i> , 2019, 13, 2954-2968.	9.8	42
24	Comparative analysis of amplicon and metagenomic sequencing methods reveals key features in the evolution of animal metaorganisms. <i>Microbiome</i> , 2019, 7, 133.	11.1	141
25	Emergence of plasmid stability under non-selective conditions maintains antibiotic resistance. <i>Nature Communications</i> , 2019, 10, 2595.	12.8	141
26	Evolthon: A community endeavor to evolve lab evolution. <i>PLoS Biology</i> , 2019, 17, e3000182.	5.6	10
27	Metabolic preference of nitrate over oxygen as an electron acceptor in foraminifera from the Peruvian oxygen minimum zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2860-2865.	7.1	73
28	The effect of population bottleneck size and selective regime on genetic diversity and evolvability in bacteria. <i>Genome Biology and Evolution</i> , 2019, 11, 3283-3290.	2.5	27
29	Quantification of Plasmid-Mediated Antibiotic Resistance in an Experimental Evolution Approach. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	3
30	CSBFinder: discovery of colinear syntenic blocks across thousands of prokaryotic genomes. <i>Bioinformatics</i> , 2019, 35, 1634-1643.	4.1	11
31	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. <i>Molecular Biology and Evolution</i> , 2019, 36, 472-486.	8.9	46
32	Rates of Mutation and Recombination in Siphoviridae Phage Genome Evolution over Three Decades. <i>Molecular Biology and Evolution</i> , 2018, 35, 1147-1159.	8.9	61
33	Metaorganisms in extreme environments: do microbes play a role in organismal adaptation?. <i>Zoology</i> , 2018, 127, 1-19.	1.2	194
34	A Novel Eukaryotic Denitrification Pathway in Foraminifera. <i>Current Biology</i> , 2018, 28, 2536-2543.e5.	3.9	75
35	Carrying Capacity and Colonization Dynamics of <i>Curvibacter</i> in the Hydra Host Habitat. <i>Frontiers in Microbiology</i> , 2018, 9, 443.	3.5	39
36	Recombination Signal in <i>Mycobacterium tuberculosis</i> Stems from Reference-guided Assemblies and Alignment Artefacts. <i>Genome Biology and Evolution</i> , 2018, 10, 1920-1926.	2.5	27

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37	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. <i>Nature Plants</i> , 2017, 3, 17066.	9.3	26
38	Phylogenetic rooting using minimal ancestor deviation. <i>Nature Ecology and Evolution</i> , 2017, 1, 193.	7.8	152
39	An evolutionary perspective on plasmid lifestyle modes. <i>Current Opinion in Microbiology</i> , 2017, 38, 74-80.	5.1	113
40	Phylogenomic networks reveal limited phylogenetic range of lateral gene transfer by transduction. <i>ISME Journal</i> , 2017, 11, 543-554.	9.8	81
41	Evolution of Chaperonin Gene Duplication in Stigonematalean Cyanobacteria (Subsection V). <i>Genome Biology and Evolution</i> , 2017, 9, evw287.	2.5	13
42	Plasticity first: molecular signatures of a complex morphological trait in filamentous cyanobacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 209.	3.2	19
43	DnaK-Dependent Accelerated Evolutionary Rate in Prokaryotes. <i>Genome Biology and Evolution</i> , 2016, 8, 1590-1599.	2.5	23
44	Phylogenomic Networks of Microbial Genome Evolution. , 2015, , 4.1.1-1-4.1.1-18.		0
45	The Contribution of Genetic Recombination to CRISPR Array Evolution. <i>Genome Biology and Evolution</i> , 2015, 7, 1925-1939.	2.5	31
46	Integration of Two Ancestral Chaperone Systems into One: The Evolution of Eukaryotic Molecular Chaperones in Light of Eukaryogenesis. <i>Molecular Biology and Evolution</i> , 2014, 31, 410-418.	8.9	17
47	Application and comparative performance of network modularity algorithms to ecological communities classification. <i>Acta Societatis Botanicorum Poloniae</i> , 2014, 83, 93-102.	0.8	2
48	Genomes of Stigonematalean Cyanobacteria (Subsection V) and the Evolution of Oxygenic Photosynthesis from Prokaryotes to Plastids. <i>Genome Biology and Evolution</i> , 2013, 5, 31-44.	2.5	234
49	Cyanobacterial defense mechanisms against foreign DNA transfer and their impact on genetic engineering. <i>Biological Research</i> , 2013, 46, 373-382.	3.4	44
50	The Genome of the Obligate Intracellular Parasite <i>Trachipleistophora hominis</i> : New Insights into Microsporidian Genome Dynamics and Reductive Evolution. <i>PLoS Pathogens</i> , 2012, 8, e1002979.	4.7	127
51	An Evolutionary Network of Genes Present in the Eukaryote Common Ancestor Polls Genomes on Eukaryotic and Mitochondrial Origin. <i>Genome Biology and Evolution</i> , 2012, 4, 466-485.	2.5	119
52	A Machine Learning Approach To Identify Hydrogenosomal Proteins in <i>Trichomonas vaginalis</i> . <i>Eukaryotic Cell</i> , 2012, 11, 217-228.	3.4	24
53	Chaperones Divide Yeast Proteins into Classes of Expression Level and Evolutionary Rate. <i>Genome Biology and Evolution</i> , 2012, 4, 618-625.	2.5	22
54	<i>Plasmodium falciparum</i> -encoded exported hsp70/hsp40 chaperone/co-chaperone complexes within the host erythrocyte. <i>Cellular Microbiology</i> , 2012, 14, 1784-1795.	2.1	137

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55	Cumulative Impact of Chaperone-Mediated Folding on Genome Evolution. <i>Biochemistry</i> , 2012, 51, 9941-9953.	2.5	52
56	Transformation and Conjugal Transfer of Foreign Genes into the Filamentous Multicellular Cyanobacteria (Subsection V) <i>Fischerella</i> and <i>Chlorogloeopsis</i> . <i>Current Microbiology</i> , 2012, 65, 552-560.	2.2	43
57	Acquisition of 1,000 eubacterial genes physiologically transformed a methanogen at the origin of Haloarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20537-20542.	7.1	211
58	Transcriptomic Evidence That Longevity of Acquired Plastids in the Photosynthetic Slugs <i>Elysia timida</i> and <i>Plakobranthus ocellatus</i> Does Not Entail Lateral Transfer of Algal Nuclear Genes. <i>Molecular Biology and Evolution</i> , 2011, 28, 699-706.	8.9	119
59	Trends and barriers to lateral gene transfer in prokaryotes. <i>Current Opinion in Microbiology</i> , 2011, 14, 615-623.	5.1	214
60	Phylogenomic networks. <i>Trends in Microbiology</i> , 2011, 19, 483-491.	7.7	66
61	Red and Problematic Green Phylogenetic Signals among Thousands of Nuclear Genes from the Photosynthetic and Apicomplexa-Related <i>Chromera velia</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 1220-1230.	2.5	75
62	Networks uncover hidden lexical borrowing in Indo-European language evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 1794-1803.	2.6	63
63	Directed networks reveal genomic barriers and DNA repair bypasses to lateral gene transfer among prokaryotes. <i>Genome Research</i> , 2011, 21, 599-609.	5.5	215
64	Networks of Gene Sharing among 329 Proteobacterial Genomes Reveal Differences in Lateral Gene Transfer Frequency at Different Phylogenetic Depths. <i>Molecular Biology and Evolution</i> , 2011, 28, 1057-1074.	8.9	147
65	Chaperonin-Dependent Accelerated Substitution Rates in Prokaryotes. <i>Genome Biology and Evolution</i> , 2010, 2, 602-608.	2.5	48
66	Genome Networks Root the Tree of Life between Prokaryotic Domains. <i>Genome Biology and Evolution</i> , 2010, 2, 379-392.	2.5	80
67	Evolution of spliceosomal introns following endosymbiotic gene transfer. <i>BMC Evolutionary Biology</i> , 2010, 10, 57.	3.2	23
68	Seeing Green and Red in Diatom Genomes. <i>Science</i> , 2009, 324, 1651-1652.	12.6	26
69	Getting a better picture of microbial evolution en route to a network of genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2009, 364, 2187-2196.	4.0	71
70	A Machine-Learning Approach Reveals That Alignment Properties Alone Can Accurately Predict Inference of Lateral Gene Transfer from Discordant Phylogenies. <i>Molecular Biology and Evolution</i> , 2009, 26, 1931-1939.	8.9	11
71	A Proteomic Survey of <i>Chlamydomonas reinhardtii</i> Mitochondria Sheds New Light on the Metabolic Plasticity of the Organelle and on the Nature of the α -Proteobacterial Mitochondrial Ancestor. <i>Molecular Biology and Evolution</i> , 2009, 26, 1533-1548.	8.9	172
72	Prokaryotic evolution and the tree of life are two different things. <i>Biology Direct</i> , 2009, 4, 34.	4.6	188

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73	Modular networks and cumulative impact of lateral transfer in prokaryote genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10039-10044.	7.1	366
74	Genes of Cyanobacterial Origin in Plant Nuclear Genomes Point to a Heterocyst-Forming Plastid Ancestor. Molecular Biology and Evolution, 2008, 25, 748-761.	8.9	197
75	Ancestral genome sizes specify the minimum rate of lateral gene transfer during prokaryote evolution. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 870-875.	7.1	186
76	Evolutionary Dynamics of Introns in Plastid-Derived Genes in Plants: Saturation Nearly Reached but Slow Intron Gain Continues. Molecular Biology and Evolution, 2007, 25, 111-119.	8.9	27
77	The Evolution of Eukaryotes. Science, 2007, 316, 542c-543c.	12.6	24
78	The origin of mitochondria in light of a fluid prokaryotic chromosome model. Biology Letters, 2007, 3, 180-184.	2.3	86
79	Genome history in the symbiotic hybrid <i>Euglena gracilis</i> . Gene, 2007, 402, 35-39.	2.2	43
80	Testing hypotheses without considering predictions. BioEssays, 2007, 29, 500-503.	2.5	16
81	The tree of one percent. Genome Biology, 2006, 7, 118.	9.6	313
82	The "Domino Theory" of Gene Death: Gradual and Mass Gene Extinction Events in Three Lineages of Obligate Symbiotic Bacterial Pathogens. Molecular Biology and Evolution, 2006, 23, 310-316.	8.9	70
83	The Comparative Method Rules! Codon Volatility Cannot Detect Positive Darwinian Selection Using a Single Genome Sequence. Molecular Biology and Evolution, 2005, 22, 496-500.	8.9	14
84	GC Composition of the Human Genome: In Search of Isochores. Molecular Biology and Evolution, 2005, 22, 1260-1272.	8.9	71
85	AluGene: a database of Alu elements incorporated within protein-coding genes. Nucleic Acids Research, 2004, 32, 489D-492.	14.5	64
86	Minimal Conditions for Exonization of Intronic Sequences. Molecular Cell, 2004, 14, 221-231.	9.7	160
87	pANT: A Method for the Pairwise Assessment of Nonfunctionalization Times of Processed Pseudogenes. Molecular Biology and Evolution, 2003, 20, 1876-1880.	8.9	9
88	Ratios of Radical to Conservative Amino Acid Replacement are Affected by Mutational and Compositional Factors and May Not Be Indicative of Positive Darwinian Selection. Molecular Biology and Evolution, 2002, 19, 1022-1025.	8.9	110