

Giddy Landan

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

5,090
citations

218677

26
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330143

37
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44
all docs

44
docs citations

44
times ranked

7234
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	27.8	1,255
2	GUIDANCE: a web server for assessing alignment confidence scores. <i>Nucleic Acids Research</i> , 2010, 38, W23-W28.	14.5	560
3	An Alignment Confidence Score Capturing Robustness to Guide Tree Uncertainty. <i>Molecular Biology and Evolution</i> , 2010, 27, 1759-1767.	8.9	313
4	Endosymbiotic origin and differential loss of eukaryotic genes. <i>Nature</i> , 2015, 524, 427-432.	27.8	251
5	Origins of major archaeal clades correspond to gene acquisitions from bacteria. <i>Nature</i> , 2015, 517, 77-80.	27.8	238
6	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
7	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
8	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
9	Early bioenergetic evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130088.	4.0	199
10	Genes of Cyanobacterial Origin in Plant Nuclear Genomes Point to a Heterocyst-Forming Plastid Ancestor. <i>Molecular Biology and Evolution</i> , 2008, 25, 748-761.	8.9	197
11	Heads or Tails: A Simple Reliability Check for Multiple Sequence Alignments. <i>Molecular Biology and Evolution</i> , 2007, 24, 1380-1383.	8.9	177
12	Phylogenetic rooting using minimal ancestor deviation. <i>Nature Ecology and Evolution</i> , 2017, 1, 193.	7.8	152
13	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
14	Estimates of Positive Darwinian Selection Are Inflated by Errors in Sequencing, Annotation, and Alignment. <i>Genome Biology and Evolution</i> , 2009, 1, 114-118.	2.5	101
15	Phylogenomic networks reveal limited phylogenetic range of lateral gene transfer by transduction. <i>ISME Journal</i> , 2017, 11, 543-554.	9.8	81
16	Deep sequencing of <i>Trichomonas vaginalis</i> during the early infection of vaginal epithelial cells and amoeboid transition. <i>International Journal for Parasitology</i> , 2013, 43, 707-719.	3.1	76
17	Concatenated alignments and the case of the disappearing tree. <i>BMC Evolutionary Biology</i> , 2014, 14, 266.	3.2	54
18	Evolution of isopenicillin N synthase genes may have involved horizontal gene transfer.. <i>Molecular Biology and Evolution</i> , 1990, 7, 399-406.	8.9	53

#	ARTICLE	IF	CITATIONS
19	Local reliability measures from sets of co-optimal multiple sequence alignments. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 15-24.	0.7	53
20	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. Molecular Biology and Evolution, 2019, 36, 472-486.	8.9	46
21	LOCAL RELIABILITY MEASURES FROM SETS OF CO-OPTIMAL MULTIPLE SEQUENCE ALIGNMENTS. , 2007, , .		43
22	A Method for the Simultaneous Estimation of Selection Intensities in Overlapping Genes. PLoS ONE, 2008, 3, e3996.	2.5	38
23	Characterization of pairwise and multiple sequence alignment errors. Gene, 2009, 441, 141-147.	2.2	37
24	Can GC Content at Third-Codon Positions Be Used as a Proxy for Isochore Composition?. Molecular Biology and Evolution, 2009, 26, 1829-1833.	8.9	35
25	Late Mitochondrial Origin Is an Artifact. Genome Biology and Evolution, 2017, 9, 373-379.	2.5	34
26	The parasite <i>Trichomonas</i> vaginalis expresses thousands of pseudogenes and long non-coding RNAs independently from functional neighbouring genes. BMC Genomics, 2014, 15, 906.	2.8	33
27	The Contribution of Genetic Recombination to CRISPR Array Evolution. Genome Biology and Evolution, 2015, 7, 1925-1939.	2.5	31
28	Evolution of the sarafotoxin/endothelin superfamily of proteins. Toxicon, 1991, 29, 237-244.	1.6	29
29	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. Nature Plants, 2017, 3, 17066.	9.3	26
30	The Order of Trait Emergence in the Evolution of Cyanobacterial Multicellularity. Genome Biology and Evolution, 2021, 13, .	2.5	26
31	Same-strand overlapping genes in bacteria: compositional determinants of phase bias. Biology Direct, 2008, 3, 36.	4.6	25
32	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. Systematic Biology, 2019, 68, 117-130.	5.6	24
33	DnaK-Dependent Accelerated Evolutionary Rate in Prokaryotes. Genome Biology and Evolution, 2016, 8, 1590-1599.	2.5	23
34	Chaperones Divide Yeast Proteins into Classes of Expression Level and Evolutionary Rate. Genome Biology and Evolution, 2012, 4, 618-625.	2.5	22
35	Integration of Two Ancestral Chaperone Systems into One: The Evolution of Eukaryotic Molecular Chaperones in Light of Eukaryogenesis. Molecular Biology and Evolution, 2014, 31, 410-418.	8.9	17
36	New views on an old enzyme: allosteric regulation and evolution of archaeal pyruvate kinases. FEBS Journal, 2019, 286, 2471-2489.	4.7	17

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37	Identifying compositionally homogeneous and nonhomogeneous domains within the human genome using a novel segmentation algorithm. <i>Nucleic Acids Research</i> , 2010, 38, e158-e158.	14.5	16
38	Detecting negative selection on recurrent mutations using gene genealogy. <i>BMC Genetics</i> , 2013, 14, 37.	2.7	5
39	Phylogenomic Networks of Microbial Genome Evolution. , 2015, , 4.1.1-1-4.1.1-18.		0