Giddy Landan

List of Publications by Year
in descending order

39 papers	5,090 citations	218677 26 h-index	330143 37 g-index
44 all docs	44 docs citations	44 times ranked	7234 citing authors

#	Article	IF	Citations
1	The Order of Trait Emergence in the Evolution of Cyanobacterial Multicellularity. Genome Biology and Evolution, 2021, 13, .	2.5	26
2	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. Systematic Biology, 2019, 68, 117-130.	5.6	24
3	New views on an old enzyme: allosteric regulation and evolution of archaeal pyruvate kinases. FEBS Journal, 2019, 286, 2471-2489.	4.7	17
4	Segregational Drift and the Interplay between Plasmid Copy Number and Evolvability. Molecular Biology and Evolution, 2019, 36, 472-486.	8.9	46
5	Expansion of the redox-sensitive proteome coincides with the plastid endosymbiosis. Nature Plants, 2017, 3, 17066.	9.3	26
6	Phylogenetic rooting using minimal ancestor deviation. Nature Ecology and Evolution, 2017, 1, 193.	7.8	152
7	Phylogenomic networks reveal limited phylogenetic range of lateral gene transfer by transduction. ISME Journal, 2017, 11, 543-554.	9.8	81
8	Late Mitochondrial Origin Is an Artifact. Genome Biology and Evolution, 2017, 9, 373-379.	2.5	34
9	DnaK-Dependent Accelerated Evolutionary Rate in Prokaryotes. Genome Biology and Evolution, 2016, 8, 1590-1599.	2.5	23
10	Phylogenomic Networks of Microbial Genome Evolution. , 2015, , 4.1.1-1-4.1.1-18.		0
11	The Contribution of Genetic Recombination to CRISPR Array Evolution. Genome Biology and Evolution, 2015, 7, 1925-1939.	2.5	31
12	Endosymbiotic origin and differential loss of eukaryotic genes. Nature, 2015, 524, 427-432.	27.8	251
13	Origins of major archaeal clades correspond to gene acquisitions from bacteria. Nature, 2015, 517, 77-80.	27.8	238
14	The parasite TrichomonasÂvaginalis expresses thousands of pseudogenes and long non-coding RNAs independently from functional neighbouring genes. BMC Genomics, 2014, 15, 906.	2.8	33
15	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
16	Concatenated alignments and the case of the disappearing tree. BMC Evolutionary Biology, 2014, 14, 266.	3.2	54
17	Detecting negative selection on recurrent mutations using gene genealogy. BMC Genetics, 2013, 14, 37.	2.7	5
18	Deep sequencing of Trichomonas vaginalis during the early infection of vaginal epithelial cells and amoeboid transition. International Journal for Parasitology, 2013, 43, 707-719.	3.1	76

#	ARTICLE	IF	CITATIONS
19	Genomes of Stigonematalean Cyanobacteria (Subsection V) and the Evolution of Oxygenic Photosynthesis from Prokaryotes to Plastids. Genome Biology and Evolution, 2013, 5, 31-44.	2.5	234
20	Early bioenergetic evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130088.	4.0	199
21	An Evolutionary Network of Genes Present in the Eukaryote Common Ancestor Polls Genomes on Eukaryotic and Mitochondrial Origin. Genome Biology and Evolution, 2012, 4, 466-485.	2.5	119
22	Chaperones Divide Yeast Proteins into Classes of Expression Level and Evolutionary Rate. Genome Biology and Evolution, 2012, 4, 618-625.	2.5	22
23	Acquisition of 1,000 eubacterial genes physiologically transformed a methanogen at the origin of Haloarchaea. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20537-20542.	7.1	211
24	Directed networks reveal genomic barriers and DNA repair bypasses to lateral gene transfer among prokaryotes. Genome Research, 2011, 21, 599-609.	5.5	215
25	Identifying compositionally homogeneous and nonhomogeneous domains within the human genome using a novel segmentation algorithm. Nucleic Acids Research, 2010, 38, e158-e158.	14.5	16
26	GUIDANCE: a web server for assessing alignment confidence scores. Nucleic Acids Research, 2010, 38, W23-W28.	14.5	560
27	An Alignment Confidence Score Capturing Robustness to Guide Tree Uncertainty. Molecular Biology and Evolution, 2010, 27, 1759-1767.	8.9	313
28	Estimates of Positive Darwinian Selection Are Inflated by Errors in Sequencing, Annotation, and Alignment. Genome Biology and Evolution, 2009, 1, 114-118.	2.5	101
29	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
30	Characterization of pairwise and multiple sequence alignment errors. Gene, 2009, 441, 141-147.	2.2	37
31	The genome of the model beetle and pest Tribolium castaneum. Nature, 2008, 452, 949-955.	27.8	1,255
32	Same-strand overlapping genes in bacteria: compositional determinants of phase bias. Biology Direct, 2008, 3, 36.	4.6	25
33	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
34	A Method for the Simultaneous Estimation of Selection Intensities in Overlapping Genes. PLoS ONE, 2008, 3, e3996.	2.5	38
35	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
36	Heads or Tails: A Simple Reliability Check for Multiple Sequence Alignments. Molecular Biology and Evolution, 2007, 24, 1380-1383.	8.9	177

#	Article	IF	Citations
37	LOCAL RELIABILITY MEASURES FROM SETS OF CO-OPTIMAL MULTIPLE SEQUENCE ALIGNMENTS. , 2007, , .		43
38	Evolution of the sarafotoxin/endothelin superfamily of proteins. Toxicon, 1991, 29, 237-244.	1.6	29
39	Evolution of isopenicillin N synthase genes may have involved horizontal gene transfer.. Molecular Biology and Evolution, 1990, 7, 399-406.	8.9	53