

Geoffrey Brian Golding

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

2,981
citations

201674

27
h-index

175258

52
g-index

72
all docs

72
docs citations

72
times ranked

4538
citing authors

#	ARTICLE	IF	CITATIONS
1	The Closest BLAST Hit Is Often Not the Nearest Neighbor. <i>Journal of Molecular Evolution</i> , 2001, 52, 540-542.	1.8	429
2	Transcriptional Profiling Implicates Novel Interactions between Abiotic Stress and Hormonal Responses in <i>Thellungiella</i> , a Close Relative of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2006, 140, 1437-1450.	4.8	227
3	Massively parallel multiplex DNA sequencing for specimen identification using an Illumina MiSeq platform. <i>Scientific Reports</i> , 2015, 5, 9687.	3.3	217
4	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	3.9	197
5	The fate of laterally transferred genes: Life in the fast lane to adaptation or death. <i>Genome Research</i> , 2006, 16, 636-643.	5.5	164
6	Eighteenth century <i>Yersinia pestis</i> genomes reveal the long-term persistence of an historical plague focus. <i>ELife</i> , 2016, 5, e12994.	6.0	139
7	Examination of Prokaryotic Multipartite Genome Evolution through Experimental Genome Reduction. <i>PLoS Genetics</i> , 2014, 10, e1004742.	3.5	89
8	Simple sequences are rare in the Protein Data Bank. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 48, 134-140.	2.6	84
9	A Step Toward Barcoding Life: A Model-Based, Decision-Theoretic Method to Assign Genes to Preexisting Species Groups. <i>Systematic Biology</i> , 2007, 56, 44-56.	5.6	79
10	Gene Gain and Gene Loss in <i>Streptococcus</i> : Is It Driven by Habitat?. <i>Molecular Biology and Evolution</i> , 2006, 23, 2379-2391.	8.9	78
11	Evolution of Simple Sequence in Proteins. <i>Journal of Molecular Evolution</i> , 2000, 51, 131-140.	1.8	77
12	An Integrated Approach to Functional Genomics: Construction of a Novel Reporter Gene Fusion Library for <i>Sinorhizobium meliloti</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 7156-7167.	3.1	70
13	A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150330.	4.0	67
14	DELPHI: accurate deep ensemble model for protein interaction sites prediction. <i>Bioinformatics</i> , 2021, 37, 896-904.	4.1	63
15	Low-complexity sequences and single amino acid repeats: not just "junk" peptide sequences. <i>Genome</i> , 2010, 53, 753-762.	2.0	62
16	Prediction of plant lncRNA by ensemble machine learning classifiers. <i>BMC Genomics</i> , 2018, 19, 316.	2.8	53
17	Rapid and accurate taxonomic classification of insect (class Insecta) cytochrome c oxidase subunit 1 () Tj ETQq1 1 0.784314 rgBT /Over 929-942.	4.8	50
18	Assigning sequences to species in the absence of large interspecific differences. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 187-194.	2.7	48

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19	A molecular portrait of maternal sepsis from Byzantine Troy. <i>ELife</i> , 2017, 6, .	6.0	46
20	Shotgun metagenomic sequencing reveals freshwater beach sands as reservoir of bacterial pathogens. <i>Water Research</i> , 2017, 115, 360-369.	11.3	41
21	RNA-Seq effectively monitors gene expression in <i>Eutrema salsugineum</i> plants growing in an extreme natural habitat and in controlled growth cabinet conditions. <i>BMC Genomics</i> , 2013, 14, 578.	2.8	40
22	Genome-wide evidence for selection acting on single amino acid repeats. <i>Genome Research</i> , 2010, 20, 755-760.	5.5	35
23	The effect of sampling from subdivided populations on species identification with DNA barcodes using a Bayesian statistical approach. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 765-773.	2.7	35
24	Selection and Slippage Creating Serine Homopolymers. <i>Molecular Biology and Evolution</i> , 2006, 23, 2017-2025.	8.9	33
25	The Evolution of the Scavenger Receptor Cysteine-Rich Domain of the Class A Scavenger Receptors. <i>Frontiers in Immunology</i> , 2015, 6, 342.	4.8	31
26	The role of introgression and ecotypic parallelism in delineating intraspecific conservation units. <i>Molecular Ecology</i> , 2020, 29, 2793-2809.	3.9	31
27	A phylogenetic analysis of the pSymB replicon from the <i>Sinorhizobium meliloti</i> genome reveals a complex evolutionary history. <i>Canadian Journal of Microbiology</i> , 2003, 49, 269-280.	1.7	30
28	Uncovering rate variation of lateral gene transfer during bacterial genome evolution. <i>BMC Genomics</i> , 2008, 9, 235.	2.8	29
29	The Caribou (<i>Rangifer tarandus</i>) Genome. <i>Genes</i> , 2019, 10, 540.	2.4	24
30	The origins and genomic diversity of American Civil War Era smallpox vaccine strains. <i>Genome Biology</i> , 2020, 21, 175.	8.8	22
31	Asymmetrical Evolution of Cytochrome bd Subunits. <i>Journal of Molecular Evolution</i> , 2006, 62, 132-142.	1.8	21
32	Phylogenetic Gaussian Process Model for the Inference of Functionally Important Regions in Protein Tertiary Structures. <i>PLoS Computational Biology</i> , 2014, 10, e1003429.	3.2	21
33	Increased Substitution Rates Surrounding Low-Complexity Regions within Primate Proteins. <i>Genome Biology and Evolution</i> , 2014, 6, 655-665.	2.5	21
34	The LysR-type PcaQ protein regulates expression of a protocatechuate-inducible ABC-type transport system in <i>Sinorhizobium meliloti</i> . <i>Microbiology (United Kingdom)</i> , 2011, 157, 2522-2533.	1.8	20
35	FuncPatch: a web server for the fast Bayesian inference of conserved functional patches in protein 3D structures. <i>Bioinformatics</i> , 2015, 31, 523-531.	4.1	20
36	Genetic Discontinuity between the Maritime Archaic and Beothuk Populations in Newfoundland, Canada. <i>Current Biology</i> , 2017, 27, 3149-3156.e11.	3.9	17

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37	Dinucleotide compositional analysis of <i>Sinorhizobium meliloti</i> using the genome signature: distinguishing chromosomes and plasmids. <i>Functional and Integrative Genomics</i> , 2002, 2, 274-281.	3.5	16
38	fingerprint: visual depiction of variation in multiple sequence alignments. <i>Molecular Ecology Notes</i> , 2007, 7, 908-914.	1.7	16
39	Spatial Patterns of Gene Expression in Bacterial Genomes. <i>Journal of Molecular Evolution</i> , 2020, 88, 510-520.	1.8	16
40	Ribosomal DNA and Plastid Markers Used to Sample Fungal and Plant Communities from Wetland Soils Reveals Complementary Biotas. <i>PLoS ONE</i> , 2016, 11, e0142759.	2.5	16
41	The advantage of recombination when selection is acting at many genetic Loci. <i>Journal of Theoretical Biology</i> , 2018, 442, 123-128.	1.7	15
42	Genetic resiliency and the Black Death: No apparent loss of mitogenomic diversity due to the Black Death in medieval London and Denmark. <i>American Journal of Physical Anthropology</i> , 2019, 169, 240-252.	2.1	15
43	Inter-replicon Gene Flow Contributes to Transcriptional Integration in the <i>Sinorhizobium meliloti</i> Multipartite Genome. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1711-1720.	1.8	14
44	Molecular Traits of Long Non-protein Coding RNAs from Diverse Plant Species Show Little Evidence of Phylogenetic Relationships. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2511-2520.	1.8	14
45	Does Gene Translocation Accelerate the Evolution of Laterally Transferred Genes?. <i>Genetics</i> , 2009, 182, 1365-1375.	2.9	13
46	Divergent subgenome evolution after allopolyploidization in African clawed frogs (<i>Xenopus</i>). <i>Journal of Evolutionary Biology</i> , 2018, 31, 1945-1958.	1.7	13
47	Neurological Proteins Are Not Enriched For Repetitive Sequences. <i>Genetics</i> , 2004, 166, 1141-1154.	2.9	12
48	Inferring Bacterial Genome Flux While Considering Truncated Genes. <i>Genetics</i> , 2010, 186, 411-426.	2.9	12
49	Increased Polymorphism Near Low-Complexity Sequences across the Genomes of <i>Plasmodium falciparum</i> Isolates. <i>Genome Biology and Evolution</i> , 2011, 3, 539-550.	2.5	12
50	Human-Specific Mutations and Positively Selected Sites in MARCO Confer Functional Changes. <i>Molecular Biology and Evolution</i> , 2018, 35, 440-450.	8.9	11
51	A Guide to Bioinformatics for Immunologists. <i>Frontiers in Immunology</i> , 2013, 4, 416.	4.8	10
52	American mastodon mitochondrial genomes suggest multiple dispersal events in response to Pleistocene climate oscillations. <i>Nature Communications</i> , 2020, 11, 4048.	12.8	9
53	Coding and long non-coding RNAs provide evidence of distinct transcriptional reprogramming for two ecotypes of the extremophile plant <i>Eutrema salsugineum</i> undergoing water deficit stress. <i>BMC Genomics</i> , 2020, 21, 396.	2.8	9
54	Substitution rate variation in closely related rodent species. <i>Heredity</i> , 1997, 78, 21-31.	2.6	7

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55	High rates of lateral gene transfer are not due to false diagnosis of gene absence. <i>Gene</i> , 2008, 421, 27-31.	2.2	7
56	DNA and the revolutions of molecular evolution, computational biology, and bioinformatics. <i>Genome</i> , 2003, 46, 930-935.	2.0	5
57	LANDMark: an ensemble approach to the supervised selection of biomarkers in high-throughput sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, 110.	2.6	5
58	Low Complexity Regions in Mammalian Proteins are Associated with Low Protein Abundance and High Transcript Abundance. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	5
59	markophylo: Markov chain analysis on phylogenetic trees. <i>Bioinformatics</i> , 2016, 32, 130-132.	4.1	3
60	Estimation of Gene Insertion/Deletion Rates with Missing Data. <i>Genetics</i> , 2016, 204, 513-529.	2.9	3
61	Sex solves Haldane's dilemma. <i>Genome</i> , 2019, 62, 761-768.	2.0	3
62	Probe design for simultaneous, targeted capture of diverse metagenomic targets. <i>Cell Reports Methods</i> , 2021, 1, 100069.	2.9	3
63	Identification of Conflicting Selective Effects on Highly Expressed Genes. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	1.2	2
64	The Location of Substitutions and Bacterial Genome Arrangements. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	2
65	Genomic inversions in <i>Escherichia coli</i> alter gene expression and are associated with nucleoid protein binding sites. <i>Genome</i> , 2022, 65, 287-299.	2.0	2
66	Resampling the pool of genotypic possibilities: an adaptive function of sexual reproduction. <i>Bmc Ecology and Evolution</i> , 2021, 21, 119.	1.6	1
67	Population biology and bioinformatics. , 2004, , 94-103.		0
68	Reconstructing the Prior Probabilities of Allelic Phylogenies. <i>Genetics</i> , 2002, 161, 889-896.	2.9	0