

Jonathan Arnold

List of Publications by Year in descending order

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134
papers

8,231
citations

81743

39
h-index

48187

88
g-index

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all docs

136
docs citations

136
times ranked

7395
citing authors

#	ARTICLE	IF	CITATIONS
1	Intraspecific Phylogeography: The Mitochondrial DNA Bridge Between Population Genetics and Systematics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1987, 18, 489-522.	6.7	2,444
2	Quality of service for workflows and web service processes. <i>Web Semantics</i> , 2004, 1, 281-308.	2.2	723
3	Demographic influences on mitochondrial DNA lineage survivorship in animal populations. <i>Journal of Molecular Evolution</i> , 1984, 20, 99-105.	0.8	576
4	Next-Generation Sequencing. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-2.	3.0	437
5	Chromosome-specific recombinant DNA libraries from the fungus <i>Aspergillus nidulans</i> . <i>Nucleic Acids Research</i> , 1991, 19, 3105-3109.	6.5	231
6	Current versus historical population sizes in vertebrate species with high gene flow: a comparison based on mitochondrial DNA lineages and inbreeding theory for neutral mutations.. <i>Molecular Biology and Evolution</i> , 1988, 5, 331-44.	3.5	230
7	Definition and Properties of Disequilibrium Statistics for Associations Between Nuclear and Cytoplasmic Genotypes. <i>Genetics</i> , 1987, 115, 755-768.	1.2	190
8	Comparison of the nucleotide sequence of soybean 18S rRNA with the sequences of other small-subunit rRNAs. <i>Journal of Molecular Evolution</i> , 1985, 21, 259-269.	0.8	168
9	Cytonuclear Disequilibria in Hybrid Zones. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1993, 24, 521-553.	6.7	128
10	THE EVOLUTIONARY GENETIC STATUS OF ICELANDIC EELS. <i>Evolution; International Journal of Organic Evolution</i> , 1990, 44, 1254-1262.	1.1	118
11	An ensemble method for identifying regulatory circuits with special reference to the qa gene cluster of <i>Neurospora crassa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16904-16909.	3.3	110
12	The effects of assortative mating and migration on cytonuclear associations in hybrid zones.. <i>Genetics</i> , 1989, 122, 923-934.	1.2	105
13	Mono-through hexanucleotide composition of the <i>Escherichia coli</i> genome: a Markov chain analysis. <i>Nucleic Acids Research</i> , 1987, 15, 2611-2626.	6.5	102
14	A genetic network for the clock of <i>Neurospora crassa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2809-2814.	3.3	93
15	Systems Biology of the Clock in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2008, 3, e3105.	1.1	86
16	Telomere maintenance genes SIRT1 and XRCC6 impact age-related decline in telomere length but only SIRT1 is associated with human longevity. <i>Biogerontology</i> , 2012, 13, 119-131.	2.0	85
17	Selection for resistance to <i>Bacillus thuringiensis</i> subspecies <i>israelensis</i> in field and laboratory populations of the mosquito <i>Aedes aegypti</i> . <i>Journal of Invertebrate Pathology</i> , 1986, 47, 317-324.	1.5	83
18	<i>HRAS1</i> and <i>LASS1</i> with <i>APOE</i> are associated with human longevity and healthy aging. <i>Aging Cell</i> , 2010, 9, 698-708.	3.0	75

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19	Characterization of Agglutinin-like Sequence Genes From Non- <i>Candida albicans</i> and Phylogenetic Analysis of the ALS Family. <i>Genetics</i> , 2001, 157, 1555-1567.	1.2	75
20	An epistatic mating system model can produce permanent cytonuclear disequilibria in a hybrid zone.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 1893-1896.	3.3	73
21	Methodological Considerations in Studying Centenarians: Lessons Learned From the Georgia Centenarian Studies. <i>Annual Review of Gerontology and Geriatrics</i> , 2007, 27, 231-264.	0.5	73
22	Genetics and the origin of a vector population: <i>Aedes aegypti</i> , a case study. <i>Science</i> , 1980, 208, 1385-1387.	6.0	71
23	Towards understanding the evolution of the human commensal yeast <i>Candida albicans</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 1137-1143.	0.7	71
24	A NARROW HYBRID ZONE BETWEEN CLOSELY RELATED CRICKET SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 1982, 36, 535-552.	1.1	68
25	IntelliGEN: A Distributed Workflow System for Discovering Protein-Protein Interactions. <i>Distributed and Parallel Databases</i> , 2003, 13, 43-72.	1.0	67
26	The effect of codon usage on the oligonucleotide composition of the <i>E.coli</i> genome and identification of over-and underrepresented sequences by Markov chain analysis. <i>Nucleic Acids Research</i> , 1987, 15, 2627-2638.	6.5	65
27	In vitro reconstruction of the <i>Aspergillus (= Emericella) nidulans</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14564-14569.	3.3	62
28	The effects of admixture and population subdivision on cytonuclear disequilibria. <i>Theoretical Population Biology</i> , 1991, 39, 273-300.	0.5	61
29	Transcriptome of <i>Pneumocystis carinii</i> during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. <i>PLoS ONE</i> , 2007, 2, e423.	1.1	58
30	Understanding Dementia Prevalence Among Centenarians. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2012, 67A, 358-365.	1.7	52
31	Mono- through hexanucleotide composition of the sense strand of yeast DNA: a Markov chain analysis. <i>Nucleic Acids Research</i> , 1988, 16, 7145-7158.	6.5	51
32	The <i>Neurospora crassa</i> Genome: Cosmid Libraries Sorted by Chromosome. <i>Genetics</i> , 2001, 157, 979-990.	1.2	51
33	The Evolutionary Genetic Status of Icelandic Eels. <i>Evolution; International Journal of Organic Evolution</i> , 1990, 44, 1254.	1.1	48
34	The human commensal yeast, <i>Candida albicans</i> , has an ancient origin. <i>Fungal Genetics and Biology</i> , 2005, 42, 444-451.	0.9	47
35	Cognitive Performance in Centenarians and the Oldest Old: Norms from the Georgia Centenarian Study. <i>Aging, Neuropsychology, and Cognition</i> , 2010, 17, 575-590.	0.7	47
36	The use of simulated annealing in chromosome reconstruction experiments based on binary scoring.. <i>Genetics</i> , 1992, 132, 591-601.	1.2	46

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37	Predicting Successful Aging in a Population-Based Sample of Georgia Centenarians. <i>Current Gerontology and Geriatrics Research</i> , 2010, 2010, 1-9.	1.6	45
38	Recognizing the forest for the trees: testing temporal patterns of cladogenesis using a null model of stochastic diversification. <i>Molecular Biology and Evolution</i> , 1996, 13, 833-849.	3.5	44
39	Genetic relatedness in open-pollinated families of two leguminous tree species, <i>Robinia pseudoacacia</i> L. and <i>Gleditsia triacanthos</i> L.. <i>Theoretical and Applied Genetics</i> , 1990, 80, 49-56.	1.8	43
40	A fast random cost algorithm for physical mapping.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11094-11098.	3.3	43
41	Continuous in vivo Metabolism by NMR. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 26.	1.6	41
42	KINSOLVER: A simulator for computing large ensembles of biochemical and gene regulatory networks. <i>Computers and Mathematics With Applications</i> , 2009, 57, 420-435.	1.4	38
43	Frequency-dependent viabilities of <i>Drosophila pseudoobscura</i> karyotypes. <i>Heredity</i> , 1986, 56, 7-17.	1.2	32
44	Population structure of <i>Candida albicans</i> , a member of the human flora, as determined by microsatellite loci. <i>Infection, Genetics and Evolution</i> , 2002, 2, 57-68.	1.0	32
45	On the Consistency of a Physical Mapping Method to Reconstruct a Chromosome <i>in Vitro</i> . <i>Genetics</i> , 1996, 142, 267-284.	1.2	30
46	A Narrow Hybrid Zone Between Closely Related Cricket Species. <i>Evolution; International Journal of Organic Evolution</i> , 1982, 36, 535.	1.1	28
47	Density-Regulated Selection with Genotypic Interactions. <i>American Naturalist</i> , 1983, 121, 649-655.	1.0	28
48	Dynamics of cytonuclear disequilibria in finite populations and comparison with a two-locus nuclear system. <i>Theoretical Population Biology</i> , 1992, 41, 1-25.	0.5	28
49	Recombination within a subclass of restriction fragment length polymorphisms may help link classical and molecular genetics.. <i>Genetics</i> , 1988, 120, 809-818.	1.2	26
50	A Table of Exact Sample Sizes for Use with Fisher's Exact Test for 2 x 2 Tables. <i>Biometrics</i> , 1992, 48, 1103.	0.8	24
51	Systems Biology of the qa Gene Cluster in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2011, 6, e20671.	1.1	24
52	Proposal for a <i>Pneumocystis</i> Genome Project. <i>Journal of Eukaryotic Microbiology</i> , 1997, 44, 7s-7s.	0.8	23
53	Generalized linear modeling methods for selection component experiments. <i>Theoretical Population Biology</i> , 1990, 37, 389-423.	0.5	20
54	ODS: ordering DNA sequences—a physical mapping algorithm based on simulated annealing. <i>Bioinformatics</i> , 1993, 9, 215-219.	1.8	20

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55	Solving Large Nonlinear Systems of First-Order Ordinary Differential Equations With Hierarchical Structure Using Multi-GPGPUs and an Adaptive Runge Kutta ODE Solver. IEEE Access, 2013, 1, 770-777.	2.6	20
56	Dynamics and Equilibrium Behavior of Cytonuclear Disequilibria under Genetic Drift, Mutation, and Migration. Theoretical Population Biology, 1996, 50, 298-324.	0.5	17
57	Synchronizing stochastic circadian oscillators in single cells of Neurospora crassa. Scientific Reports, 2016, 6, 35828.	1.6	17
58	“How Do We Do This at a Distance?” A Descriptive Study of Remote Undergraduate Research Programs during COVID-19. CBE Life Sciences Education, 2022, 21, ar1.	1.1	17
59	Statistics of Natural Populations. I: Estimating an Allele Probability in Cryptic Fathers with a Fixed Number of Offspring. Biometrics, 1981, 37, 495.	0.8	16
60	On the Design of Genome Mapping Experiments Using Short Synthetic Oligonucleotides. Biometrics, 1992, 48, 337.	0.8	16
61	Competitive coexistence of two Pneumocystis species. Infection, Genetics and Evolution, 2006, 6, 177-186.	1.0	16
62	The aging biological clock in Neurospora crassa. Ecology and Evolution, 2014, 4, 3494-3507.	0.8	16
63	Discovering Regulatory Network Topologies Using Ensemble Methods on GPGPUs With Special Reference to the Biological Clock of <i>Neurospora crassa</i> . IEEE Access, 2015, 3, 27-42.	2.6	16
64	Density-Regulated Selection in a Heterogeneous Environment. American Naturalist, 1983, 121, 656-668.	1.0	16
65	A comprehensive package for DNA sequence analysis in FORTRAN IV for the PDP-11. Nucleic Acids Research, 1986, 14, 239-254.	6.5	15
66	The application of markov chain analysis to oligonucleotide frequency prediction and physical mapping of <i>Drosophila melanogaster</i> . Nucleic Acids Research, 1992, 20, 3651-3657.	6.5	15
67	Constructing a Physical Map of the Pneumocystis Genome. Journal of Eukaryotic Microbiology, 1997, 44, 8s-8s.	0.8	15
68	Secondary structural entropy in RNA switch (Riboswitch) identification. BMC Bioinformatics, 2015, 16, 133.	1.2	15
69	Genomics for Fungi. , 2001, , 267-297.		15
70	A Statistical Test of a Neutral Model Using the Dynamics of Cytonuclear Disequilibria. Genetics, 1996, 144, 1985-1992.	1.2	15
71	An analysis of gene-finding programs for Neurospora crassa. Bioinformatics, 2001, 17, 901-912.	1.8	14
72	Revelations from a bread mould. Nature, 2003, 422, 821-822.	13.7	13

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73	On the association of restriction fragment length polymorphisms across species boundaries.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 3967-3971.	3.3	12
74	ODS_BOOTSTRAP: assessing the statistical reliability of physical maps by bootstrap resampling. Bioinformatics, 1994, 10, 625-634.	1.8	12
75	STATISTICS OF NATURAL POPULATIONS. II. ESTIMATING AN ALLELE PROBABILITY IN FAMILIES DESCENDED FROM CRYPTIC MOTHERS. Genetics, 1985, 109, 785-798.	1.2	11
76	The effects of cytoplasmic male sterility on cytonuclear disequilibria in hybrid zones. Genetica, 1993, 88, 37-50.	0.5	10
77	Diagnostics and a Statistical Test of Neutrality Hypotheses Using the Dynamics of Cytonuclear Disequilibria. Biometrics, 1996, 52, 1042.	0.8	10
78	Editorial. Fungal Genetics and Biology, 1997, 21, 254-257.	0.9	10
79	Exact Sample Size Needed to Detect Dependence in 2 \times 2 Tables. Biometrics, 2007, 63, 1245-1252.	0.8	10
80	Solving Nonlinear Systems of First Order Ordinary Differential Equations Using a Galerkin Finite Element Method. IEEE Access, 2013, 1, 408-417.	2.6	10
81	Mapping by Sequencing the Pneumocystis Genome Using the Ordering DNA Sequences V3 Tool. Genetics, 2003, 163, 1299-1313.	1.2	10
82	Symbiont Survival and Host-Symbiont Disequilibria Under Differential Vertical Transmission. Genetics, 2000, 154, 1347-1365.	1.2	10
83	APOE ϵ 4, rated life experiences, and affect among centenarians. Aging and Mental Health, 2014, 18, 240-247.	1.5	9
84	Ensemble methods for stochastic networks with special reference to the biological clock of Neurospora crassa. PLoS ONE, 2018, 13, e0196435.	1.1	9
85	Using Workflow to Build an Information Management System for a Geographically Distributed Genome Sequencing Initiative. , 2003, , .		9
86	PCAP: probe choice and analysis package—a set of programs to aid in choosing synthetic oligomers for contig mapping. Bioinformatics, 1993, 9, 201-203.	1.8	8
87	ESSENTIAL EUKARYOTIC CORE. Evolution; International Journal of Organic Evolution, 2004, 58, 441-446.	1.1	8
88	RTEExtract: time-series NMR spectra quantification based on 3D surface ridge tracking. Bioinformatics, 2020, 36, 5068-5075.	1.8	7
89	FATE MAPPING MULTI-FOCUS PHENOTYPES. Genetics, 1981, 99, 211-229.	1.2	7
90	Small sample properties for estimators of cytonuclear disequilibria. Heredity, 1996, 77, 396-399.	1.2	6

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91	Parallel Computing of Physical Maps— A Comparative Study in SIMD and MIMD Parallelism. <i>Journal of Computational Biology</i> , 1996, 3, 503-528.	0.8	6
92	The effects of unidirectional incompatibility on cytonuclear disequilibria in a hybrid zone. <i>Genetica</i> , 1997, 101, 215-224.	0.5	6
93	Parallel computing for chromosome reconstruction via ordering of DNA sequences. <i>Parallel Computing</i> , 1998, 24, 1177-1204.	1.3	6
94	Title is missing!. <i>Genetica</i> , 1999, 105, 101-108.	0.5	6
95	Physical mapping with automatic capture of hybridization data. <i>Bioinformatics</i> , 2001, 17, 205-213.	1.8	6
96	Systems biology of the <i>Neurospora</i> biological clock. <i>IET Systems Biology</i> , 2007, 1, 257-265.	0.8	6
97	$lac^{\Delta 1}$ and $lag^{\Delta 1}$ with $ras^{\Delta 1}$ affect aging and the biological clock in <i>Neurospora crassa</i> . <i>Ecology and Evolution</i> , 2016, 6, 8341-8351.	0.8	6
98	Discovering Regulators in Post-Transcriptional Control of the Biological Clock of <i>Neurospora crassa</i> Using Variable Topology Ensemble Methods on GPUs. <i>IEEE Access</i> , 2018, 6, 54582-54594.	2.6	6
99	Single Cells of <i>Neurospora Crassa</i> Show Circadian Oscillations, Light Entrainment, Temperature Compensation, and Phase Synchronization. <i>IEEE Access</i> , 2019, 7, 49403-49417.	2.6	6
100	Measuring synchronization of stochastic oscillators in biology. <i>Journal of Physics: Conference Series</i> , 2016, 750, 012001.	0.3	5
101	Aging and the Biological Clock. <i>Healthy Ageing and Longevity</i> , 2017, , 211-234.	0.2	5
102	SOME COMPARISONS OF CLUSTERING AND CLASSIFICATION TECHNIQUES APPLIED TO TRANSCRIPTIONAL PROFILING DATA. , 2002, , .		5
103	A MINE Alternative to D-Optimal Designs for the Linear Model. <i>PLoS ONE</i> , 2014, 9, e110234.	1.1	5
104	Dynamics of Cytonuclear Disequilibria in Subdivided Populations. <i>Journal of Theoretical Biology</i> , 1998, 192, 99-111.	0.8	4
105	Exact sample sizes needed to detect dependence in 2 \times 3 tables. <i>Theoretical Population Biology</i> , 2006, 69, 111-120.	0.5	4
106	Genome-wide expression analysis of genetic networks in <i>Neurospora crassa</i> . <i>Bioinformatics</i> , 2007, 1, 390-395.	0.2	4
107	Statistics of Natural Populations. III. Sequential Sampling Plans for the Estimation of Gene Frequencies. <i>Biometrics</i> , 1986, 42, 45.	0.8	3
108	Cytonuclear Disequilibria in Hybrid Zones Using RAPD Markers. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1702.	1.1	3

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109	Parallel Monte Carlo methods for physical mapping of chromosomes. , 0, , .		3
110	J3DV: A Java-based 3D database visualization tool. <i>Software - Practice and Experience</i> , 2002, 32, 443-463.	2.5	3
111	Identifying a stochastic clock network with light entrainment for single cells of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2020, 10, 15168.	1.6	3
112	CCSDB: an integrated database system for the Georgia Centenarian Study. <i>Bioinformatics</i> , 2006, 1, 214-9.	0.2	3
113	What is Phase in Cellular Clocks?. <i>Yale Journal of Biology and Medicine</i> , 2019, 92, 169-178.	0.2	3
114	Ensemble Methods for Identifying RNA Operons and Regulons in the Clock Network of <i>Neurospora Crassa</i> . <i>IEEE Access</i> , 2022, 10, 32510-32524.	2.6	3
115	Uncovering in vivo biochemical patterns from time-series metabolic dynamics. <i>PLoS ONE</i> , 2022, 17, e0268394.	1.1	3
116	An Analysis of Density-Dependent Viability Selection. <i>Journal of the American Statistical Association</i> , 1989, 84, 662-668.	1.8	2
117	CMAP: contig mapping and analysis package, a relational database for chromosome reconstruction. <i>Bioinformatics</i> , 1992, 8, 467-474.	1.8	2
118	PARODSâ€”a study of parallel algorithms for ordering DNA sequences. <i>Bioinformatics</i> , 1996, 12, 269-280.	1.8	2
119	Wild Isolates of <i>Neurospora crassa</i> Reveal Three Conidiophore Architectural Phenotypes. <i>Microorganisms</i> , 2020, 8, 1760.	1.6	2
120	Foreword to the Special Section on Fungal Genomics. <i>Genetics</i> , 2001, 157, 933-933.	1.2	2
121	An Analysis of Density-Dependent Viability Selection. , 0, .		2
122	Characterizing the geneâ€”environment interaction underlying natural morphological variation in <i>Neurospora crassa</i> conidiophores using high-throughput phenomics and transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
123	A neural network model based on differential-algebraic equations for nonlinear programming. , 0, , .		1
124	CYTONUCLEAR DISEQUILIBRIA IN HYBRID ZONES USING RAPD MARKERS. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1702-1705.	1.1	1
125	Parallel computation for chromosome reconstruction on a cluster of workstations. , 0, , .		1
126	DESIGN AND ANALYSIS OF AN EFFICIENT RECURSIVE LINKING ALGORITHM FOR CONSTRUCTING LIKELIHOOD BASED GENETIC MAPS FOR A LARGE NUMBER OF MARKERS. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 201-250.	0.3	1

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127	LIKELIHOOD OF A PARTICULAR ORDER OF GENETIC MARKERS AND THE CONSTRUCTION OF GENETIC MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 125-162.	0.3	1
128	Metabolomics. Mycology, 2004, , 597-633.	0.5	1
129	The macroscopic limit to synchronization of cellular clocks in single cells of Neurospora crassa. Scientific Reports, 2022, 12, 6750.	1.6	1
130	A parallel genetic algorithm for physical mapping of chromosomes. , 0, , .		0
131	ESSENTIAL EUKARYOTIC CORE. Evolution; International Journal of Organic Evolution, 2004, 58, 441.	1.1	0
132	EFFICIENT RECURSIVE LINKING ALGORITHM FOR COMPUTING THE LIKELIHOOD OF AN ORDER OF A LARGE NUMBER OF GENETIC MARKERS. , 2006, , .		0
133	Mapping Contingency Tables. , 1983, , 140-149.		0
134	Are we there yet? A machine learning architecture to predict organotropic metastases. BMC Medical Genomics, 2021, 14, 281.	0.7	0