

Gavin C Conant

List of Publications by Year in descending order

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84
papers

7,608
citations

136740

32
h-index

62479

80
g-index

93
all docs

93
docs citations

93
times ranked

9441
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
2	Turning a hobby into a job: How duplicated genes find new functions. <i>Nature Reviews Genetics</i> , 2008, 9, 938-950.	7.7	1,042
3	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	3.3	458
4	GenomeVx: simple web-based creation of editable circular chromosome maps. <i>Bioinformatics</i> , 2008, 24, 861-862.	1.8	308
5	Dosage, duplication, and diploidization: clarifying the interplay of multiple models for duplicate gene evolution over time. <i>Current Opinion in Plant Biology</i> , 2014, 19, 91-98.	3.5	261
6	Asymmetric Sequence Divergence of Duplicate Genes. <i>Genome Research</i> , 2003, 13, 2052-2058.	2.4	222
7	Independent sorting-out of thousands of duplicated gene pairs in two yeast species descended from a whole-genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8397-8402.	3.3	210
8	Increased glycolytic flux as an outcome of whole-genome duplication in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 129.	3.2	197
9	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	3.3	196
10	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. <i>New Phytologist</i> , 2012, 196, 596-605.	3.5	178
11	Convergent evolution of gene circuits. <i>Nature Genetics</i> , 2003, 34, 264-266.	9.4	177
12	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	1.2	163
13	Duplicate genes and robustness to transient gene knock-downs in <i>Caenorhabditis elegans</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2004, 271, 89-96.	1.2	139
14	Molecular Evolution in Large Genetic Networks: Does Connectivity Equal Constraint?. <i>Journal of Molecular Evolution</i> , 2004, 58, 203-211.	0.8	138
15	Two-Phase Resolution of Polyploidy in the <i>Arabidopsis</i> Metabolic Network Gives Rise to Relative and Absolute Dosage Constraints. <i>Plant Cell</i> , 2011, 23, 1719-1728.	3.1	137
16	Functional Partitioning of Yeast Co-Expression Networks after Genome Duplication. <i>PLoS Biology</i> , 2006, 4, e109.	2.6	129
17	The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity. <i>Nucleic Acids Research</i> , 2015, 43, gkv973.	6.5	98
18	Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. <i>PLoS Genetics</i> , 2018, 14, e1007267.	1.5	78

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19	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019, 10, 2878.	5.8	78
20	GenomeHistory: a software tool and its application to fully sequenced genomes. <i>Nucleic Acids Research</i> , 2002, 30, 3378-3386.	6.5	69
21	Effects of Nucleotide Composition Bias on the Success of the Parsimony Criterion in Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2001, 18, 1024-1033.	3.5	65
22	Solvent Exposure Imparts Similar Selective Pressures across a Range of Yeast Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 1155-1161.	3.5	60
23	Altered patterns of gene duplication and differential gene gain and loss in fungal pathogens. <i>BMC Genomics</i> , 2008, 9, 147.	1.2	59
24	Diet and feed efficiency status affect rumen microbial profiles of sheep. <i>Small Ruminant Research</i> , 2017, 156, 12-19.	0.6	52
25	Probabilistic Cross-Species Inference of Orthologous Genomic Regions Created by Whole-Genome Duplication in Yeast. <i>Genetics</i> , 2008, 179, 1681-1692.	1.2	50
26	Nonrandom Survival of Gene Conversions among Yeast Ribosomal Proteins Duplicated through Genome Doubling. <i>Genome Biology and Evolution</i> , 2010, 2, 826-834.	1.1	44
27	Long identical multispecies elements in plant and animal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1183-91.	3.3	43
28	Integrating Networks, Phylogenomics, and Population Genomics for the Study of Polyploidy. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 253-278.	3.8	42
29	Comparative Genomics as a Time Machine: How Relative Gene Dosage and Metabolic Requirements Shaped the Time-dependent Resolution of Yeast Polyploidy. <i>Molecular Biology and Evolution</i> , 2014, 31, 3184-3193.	3.5	38
30	Diet shifts provoke complex and variable changes in the metabolic networks of the ruminal microbiome. <i>Microbiome</i> , 2017, 5, 60.	4.9	38
31	Watching the grin fade: Tracing the effects of polyploidy on different evolutionary time scales. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 320-331.	2.3	37
32	Diet Alters Both the Structure and Taxonomy of the Ovine Gut Microbial Ecosystem. <i>DNA Research</i> , 2014, 21, 115-125.	1.5	37
33	Modeling amino acid substitution patterns in orthologous and paralogous genes. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 298-307.	1.2	36
34	Genome-wide association for milk production and lactation curve parameters in Holstein dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 292-304.	0.8	36
35	Expression level, cellular compartment and metabolic network position all influence the average selective constraint on mammalian enzymes. <i>BMC Evolutionary Biology</i> , 2011, 11, 89.	3.2	34
36	Convergent Evolution and the Origin of Complex Phenotypes in the Age of Systems Biology. <i>International Journal of Plant Sciences</i> , 2016, 177, 305-318.	0.6	33

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37	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	32
38	Robust Yet Fragile: Expression Noise, Protein Misfolding, and Gene Dosage in the Evolution of Genomes. <i>Annual Review of Genetics</i> , 2016, 50, 113-131.	3.2	29
39	Patterns of indirect protein interactions suggest a spatial organization to metabolism. <i>Molecular BioSystems</i> , 2011, 7, 3056.	2.9	27
40	Selection for Higher Gene Copy Number after Different Types of Plant Gene Duplications. <i>Genome Biology and Evolution</i> , 2011, 3, 1369-1380.	1.1	27
41	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27
42	The lasting after-effects of an ancient polyploidy on the genomes of teleosts. <i>PLoS ONE</i> , 2020, 15, e0231356.	1.1	27
43	Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2021, 230, 372-386.	3.5	26
44	Very Low Rate of Gene Conversion in the Yeast Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 3817-3826.	3.5	25
45	Copy Number Alterations among Mammalian Enzymes Cluster in the Metabolic Network. <i>Molecular Biology and Evolution</i> , 2011, 28, 1111-1121.	3.5	24
46	Secondary Structure Analyses of the Nuclear rRNA Internal Transcribed Spacers and Assessment of Its Phylogenetic Utility across the Brassicaceae (Mustards). <i>PLoS ONE</i> , 2014, 9, e101341.	1.1	24
47	Neutral evolution on mammalian protein surfaces. <i>Trends in Genetics</i> , 2009, 25, 377-381.	2.9	23
48	Rapid reorganization of the transcriptional regulatory network after genome duplication in yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 869-876.	1.2	23
49	Tiny but mighty: The role of the rumen microbes in livestock production. <i>Journal of Animal Science</i> , 2018, 96, 752-770.	0.2	23
50	Patterns of Gene Conversion in Duplicated Yeast Histones Suggest Strong Selection on a Coadapted Macromolecular Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 3249-3258.	1.1	22
51	Patterns of Population Variation in Two Paleopolyploid Eudicot Lineages Suggest That Dosage-Based Selection on Homeologs Is Long-Lived. <i>Genome Biology and Evolution</i> , 2018, 10, 999-1011.	1.1	21
52	The contributions from the progenitor genomes of the mesopolyploid Brassicaceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
53	Identification and characterization of RING-finger ubiquitin ligase UBR7 in mammalian spermatozoa. <i>Cell and Tissue Research</i> , 2014, 356, 261-278.	1.5	20
54	Polyploidy and the Evolution of Complex Traits. <i>International Journal of Evolutionary Biology</i> , 2012, 1-12.	1.0	19

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55	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
56	The rarity of gene shuffling in conserved genes. <i>Genome Biology</i> , 2005, 6, R50.	13.9	16
57	Convergent evolution of polyploid genomes from across the eukaryotic tree of life. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	16
58	Poor feed efficiency in sheep is associated with several structural abnormalities in the community metabolic network of their ruminal microbes ¹ . <i>Journal of Animal Science</i> , 2018, 96, 2113-2124.	0.2	15
59	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
60	Extreme Evolutionary Conservation of Functionally Important Regions in H1N1 Influenza Proteome. <i>PLoS ONE</i> , 2013, 8, e81027.	1.1	15
61	Parallel Genehunter: implementation of a linkage analysis package for distributed-memory architectures. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 674-682.	2.7	14
62	Predicting residual feed intake status using rumen microbial profiles in ewe lambs ¹ . <i>Journal of Animal Science</i> , 2019, 97, 2878-2888.	0.2	13
63	A Single, Shared Triploidy in Three Species of Parasitic Nematodes. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 225-233.	0.8	13
64	Baby Genomics: Tracing the Evolutionary Changes That Gave Rise to Placentation. <i>Genome Biology and Evolution</i> , 2020, 12, 35-47.	1.1	11
65	A Conserved Mammalian Protein Interaction Network. <i>PLoS ONE</i> , 2013, 8, e52581.	1.1	10
66	Gene Duplication and Phenotypic Changes in the Evolution of Mammalian Metabolic Networks. <i>PLoS ONE</i> , 2014, 9, e87115.	1.1	10
67	Functional characterization of SMN evolution in mouse models of SMA. <i>Scientific Reports</i> , 2019, 9, 9472.	1.6	8
68	Cloning and Characterization of the Peptidoglycan Recognition Protein Genes in the Mosquito, <i>Armigeres subalbatus</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 2012, 49, 656-671.	0.9	7
69	Some assembly required: evolutionary and systems perspectives on the mammalian reproductive system. <i>Cell and Tissue Research</i> , 2016, 363, 267-278.	1.5	6
70	A distributed CPU-GPU framework for pairwise alignments on large-scale sequence datasets. , 2013, , .		5
71	Parallel Gene Upstream Comparison via Multi-Level Hash Tables on GPU. , 2016, , .		5
72	A Second-Generation Genome Screen for Linkage to Type 1 Diabetes in a Bedouin Arab Family. <i>Annals of the New York Academy of Sciences</i> , 2004, 1037, 157-160.	1.8	4

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73	Transcriptional robustness and protein interactions are associated in yeast. BMC Systems Biology, 2011, 5, 62.	3.0	4
74	Yeast as a Window into Changes in Genome Complexity Due to Polyploidization. , 2012, , 293-308.		4
75	The yeast protein interaction network has a capacity for self-organization. FEBS Journal, 2014, 281, 3420-3432.	2.2	4
76	Distinct C ₄ subtypes and C ₃ bundle sheath isolation in the Paniceae grasses. Plant Direct, 2021, 5, e373.	0.8	4
77	The T box regulatory element controlling expression of the class I lysyl-tRNA synthetase of Bacillus cereus strain 14579 is functional and can be partially induced by reduced charging of asparaginyl-tRNA ^{Asn} . BMC Microbiology, 2010, 10, 196.	1.3	3
78	Large-Scale Pairwise Alignments on GPU Clusters: Exploring the Implementation Space. Journal of Signal Processing Systems, 2014, 77, 131-149.	1.4	3
79	A metagenomic analysis of the effect of antibiotic feed additives on the ovine rumen metabolism. Small Ruminant Research, 2021, 205, 106539.	0.6	3
80	A fast algorithm for determining the best combination of local alignments to a query sequence. BMC Bioinformatics, 2004, 5, 62.	1.2	2
81	POInT: A Tool for Modeling Ancient Polyploidies Using Multiple Polyploid Genomes. Methods in Molecular Biology, 2022, , 81-91.	0.4	1
82	Increased glycolytic flux as an outcome of whole-genome duplication in yeast. Molecular Systems Biology, 2008, 4, .	3.2	0
83	Structure, Interaction, and Evolution: Reflections on the Natural History of Proteins. , 2015, , 187-201.		0
84	Effects of evolutionary pressure on histone modifications. , 2017, , .		0