

# Gavin C Conant

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Convergent evolution of polyploid genomes from across the eukaryotic tree of life. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	16
2	POInT: A Tool for Modeling Ancient Polyploidies Using Multiple Polyploid Genomes. <i>Methods in Molecular Biology</i> , 2022, , 81-91.	0.4	1
3	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
4	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	2.4	21
5	Comparative phylogenetics of repetitive elements in a diverse order of flowering plants (Brassicales). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	15
6	A metagenomic analysis of the effect of antibiotic feed additives on the ovine rumen metabolism. <i>Small Ruminant Research</i> , 2021, 205, 106539.	0.6	3
7	Distinct C <sub>4</sub> subtypes and C <sub>3</sub> bundle sheath isolation in the Paniceae grasses. <i>Plant Direct</i> , 2021, 5, e373.	0.8	4
8	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
9	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	0.8	32
10	Baby Genomics: Tracing the Evolutionary Changes That Gave Rise to Placentation. <i>Genome Biology and Evolution</i> , 2020, 12, 35-47.	1.1	11
11	The lasting after-effects of an ancient polyploidy on the genomes of teleosts. <i>PLoS ONE</i> , 2020, 15, e0231356.	1.1	27
12	A Single, Shared Triploidy in Three Species of Parasitic Nematodes. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 225-233.	0.8	13
13	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
14	Functional characterization of SMN evolution in mouse models of SMA. <i>Scientific Reports</i> , 2019, 9, 9472.	1.6	8
15	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
16	Predicting residual feed intake status using rumen microbial profiles in ewe lambs <sup>1</sup> . <i>Journal of Animal Science</i> , 2019, 97, 2878-2888.	0.2	13
17	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
18	Poor feed efficiency in sheep is associated with several structural abnormalities in the community metabolic network of their ruminal microbes <sup>1</sup> . <i>Journal of Animal Science</i> , 2018, 96, 2113-2124.	0.2	15

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19	Integrating Networks, Phylogenomics, and Population Genomics for the Study of Polyploidy. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 253-278.	3.8	42
20	Patterns of Population Variation in Two Paleopolyploid Eudicot Lineages Suggest That Dosage-Based Selection on Homeologs Is Long-Lived. Genome Biology and Evolution, 2018, 10, 999-1011.	1.1	21
21	Preferential retention of genes from one parental genome after polyploidy illustrates the nature and scope of the genomic conflicts induced by hybridization. PLoS Genetics, 2018, 14, e1007267.	1.5	78
22	Diet shifts provoke complex and variable changes in the metabolic networks of the ruminal microbiome. Microbiome, 2017, 5, 60.	4.9	38
23	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	1.6	27
24	Diet and feed efficiency status affect rumen microbial profiles of sheep. Small Ruminant Research, 2017, 156, 12-19.	0.6	52
25	Effects of evolutionary pressure on histone modifications. , 2017, , .		0
26	Parallel Gene Upstream Comparison via Multi-Level Hash Tables on GPU. , 2016, , .		5
27	Robust Yet Fragile: Expression Noise, Protein Misfolding, and Gene Dosage in the Evolution of Genomes. Annual Review of Genetics, 2016, 50, 113-131.	3.2	29
28	Convergent Evolution and the Origin of Complex Phenotypes in the Age of Systems Biology. International Journal of Plant Sciences, 2016, 177, 305-318.	0.6	33
29	Some assembly required: evolutionary and systems perspectives on the mammalian reproductive system. Cell and Tissue Research, 2016, 363, 267-278.	1.5	6
30	Patterns of Gene Conversion in Duplicated Yeast Histones Suggest Strong Selection on a Coadapted Macromolecular Complex. Genome Biology and Evolution, 2015, 7, 3249-3258.	1.1	22
31	The players may change but the game remains: network analyses of ruminal microbiomes suggest taxonomic differences mask functional similarity. Nucleic Acids Research, 2015, 43, gkv973.	6.5	98
32	The butterfly plant arms-race escalated by gene and genome duplications. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8362-8366.	3.3	458
33	Structure, Interaction, and Evolution: Reflections on the Natural History of Proteins. , 2015, , 187-201.		0
34	Secondary Structure Analyses of the Nuclear rRNA Internal Transcribed Spacers and Assessment of Its Phylogenetic Utility across the Brassicaceae (Mustards). PLoS ONE, 2014, 9, e101341.	1.1	24
35	The yeast protein interaction network has a capacity for self-organization. FEBS Journal, 2014, 281, 3420-3432.	2.2	4
36	Identification and characterization of RING-finger ubiquitin ligase UBR7 in mammalian spermatozoa. Cell and Tissue Research, 2014, 356, 261-278.	1.5	20

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37	Diet Alters Both the Structure and Taxonomy of the Ovine Gut Microbial Ecosystem. <i>DNA Research</i> , 2014, 21, 115-125.	1.5	37
38	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
39	Large-Scale Pairwise Alignments on GPU Clusters: Exploring the Implementation Space. <i>Journal of Signal Processing Systems</i> , 2014, 77, 131-149.	1.4	3
40	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
41	Gene Duplication and Phenotypic Changes in the Evolution of Mammalian Metabolic Networks. <i>PLoS ONE</i> , 2014, 9, e87115.	1.1	10
42	A distributed CPU-GPU framework for pairwise alignments on large-scale sequence datasets. , 2013, , .		5
43	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
44	A Conserved Mammalian Protein Interaction Network. <i>PLoS ONE</i> , 2013, 8, e52581.	1.1	10
45	Extreme Evolutionary Conservation of Functionally Important Regions in H1N1 Influenza Proteome. <i>PLoS ONE</i> , 2013, 8, e81027.	1.1	15
46	Polyploidy and the Evolution of Complex Traits. <i>International Journal of Evolutionary Biology</i> , 2012, 2012, 1-12.	1.0	19
47	Very Low Rate of Gene Conversion in the Yeast Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 3817-3826.	3.5	25
48	Metabolic and evolutionary costs of herbivory defense: systems biology of glucosinolate synthesis. <i>New Phytologist</i> , 2012, 196, 596-605.	3.5	178
49	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
50	Yeast as a Window into Changes in Genome Complexity Due to Polyploidization. , 2012, , 293-308.		4
51	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
52	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
53	Patterns of indirect protein interactions suggest a spatial organization to metabolism. <i>Molecular BioSystems</i> , 2011, 7, 3056.	2.9	27
54	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

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55	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
56	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
57	Transcriptional robustness and protein interactions are associated in yeast. <i>BMC Systems Biology</i> , 2011, 5, 62.	3.0	4
58	Copy Number Alterations among Mammalian Enzymes Cluster in the Metabolic Network. <i>Molecular Biology and Evolution</i> , 2011, 28, 1111-1121.	3.5	24
59	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
60	The T box regulatory element controlling expression of the class I lysyl-tRNA synthetase of <i>Bacillus cereus</i> strain 14579 is functional and can be partially induced by reduced charging of asparaginyl-tRNAAsn. <i>BMC Microbiology</i> , 2010, 10, 196.	1.3	3
61	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
62	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
63	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
64	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
65	Neutral evolution on mammalian protein surfaces. <i>Trends in Genetics</i> , 2009, 25, 377-381.	2.9	23
66	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
67	Altered patterns of gene duplication and differential gene gain and loss in fungal pathogens. <i>BMC Genomics</i> , 2008, 9, 147.	1.2	59
68	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
69	GenomeVx: simple web-based creation of editable circular chromosome maps. <i>Bioinformatics</i> , 2008, 24, 861-862.	1.8	308
70	Increased glycolytic flux as an outcome of whole-genome duplication in yeast. <i>Molecular Systems Biology</i> , 2008, 4, .	3.2	0
71	Increased glycolytic flux as an outcome of whole-genome duplication in yeast. <i>Molecular Systems Biology</i> , 2007, 3, 129.	3.2	197
72	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

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73	Modeling amino acid substitution patterns in orthologous and paralogous genes. <i>Molecular Phylogenetics and Evolution</i> , 2007, 42, 298-307.	1.2	36
74	Functional Partitioning of Yeast Co-Expression Networks after Genome Duplication. <i>PLoS Biology</i> , 2006, 4, e109.	2.6	129
75	The rarity of gene shuffling in conserved genes. <i>Genome Biology</i> , 2005, 6, R50.	13.9	16
76	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
77	A fast algorithm for determining the best combination of local alignments to a query sequence. <i>BMC Bioinformatics</i> , 2004, 5, 62.	1.2	2
78	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
79	Molecular Evolution in Large Genetic Networks: Does Connectivity Equal Constraint?. <i>Journal of Molecular Evolution</i> , 2004, 58, 203-211.	0.8	138
80	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
81	Convergent evolution of gene circuits. <i>Nature Genetics</i> , 2003, 34, 264-266.	9.4	177
82	Asymmetric Sequence Divergence of Duplicate Genes. <i>Genome Research</i> , 2003, 13, 2052-2058.	2.4	222
83	GenomeHistory: a software tool and its application to fully sequenced genomes. <i>Nucleic Acids Research</i> , 2002, 30, 3378-3386.	6.5	69
84	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