

Brandon S Gaut

List of Publications by Year in descending order

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138
papers

22,704
citations

16411

64
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11288

136
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docs citations

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times ranked

19641
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene Body Methylation in Plants: Mechanisms, Functions, and Important Implications for Understanding Evolutionary Processes. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	39
2	The 3D architecture of the pepper genome and its relationship to function and evolution. <i>Nature Communications</i> , 2022, 13, .	5.8	28
3	Structural variation and parallel evolution of apomixis in citrus during domestication and diversification. <i>National Science Review</i> , 2022, 9, .	4.6	19
4	Gene capture by transposable elements leads to epigenetic conflict in maize. <i>Molecular Plant</i> , 2021, 14, 237-252.	3.9	17
5	Gene body methylation is under selection in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2021, 218, .	1.2	10
6	CHH Methylation Islands: A Nonconserved Feature of Grass Genomes That Is Positively Associated with Transposable Elements but Negatively Associated with Gene-Body Methylation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	25
7	The evolutionary genomics of species'™ responses to climate change. <i>Nature Ecology and Evolution</i> , 2021, 5, 1350-1360.	3.4	63
8	Introgression among North American wild grapes (<i>Vitis</i>) fuels biotic and abiotic adaptation. <i>Genome Biology</i> , 2021, 22, 254.	3.8	25
9	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. <i>BMC Bioinformatics</i> , 2021, 22, 9.	1.2	9
10	Phylogenetic Shifts in Gene Body Methylation Correlate with Gene Expression and Reflect Trait Conservation. <i>Molecular Biology and Evolution</i> , 2020, 37, 31-43.	3.5	29
11	Large chromosomal variants drive adaptation in sunflowers. <i>Nature Plants</i> , 2020, 6, 734-735.	4.7	2
12	Evolutionary Genomics of Structural Variation in Asian Rice (<i>Oryza sativa</i>) Domestication. <i>Molecular Biology and Evolution</i> , 2020, 37, 3507-3524.	3.5	58
13	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (<i>Olea europaea</i> L.). <i>BMC Biology</i> , 2020, 18, 148.	1.7	39
14	Sahara mustard as a major threat to desert biodiversity in the southwest United States and the need to integrate contemporary methods to understand its biology. <i>Ecology and Evolution</i> , 2020, 10, 14453-14455.	0.8	0
15	The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020, 11, 2902.	5.8	118
16	Genetic Mutations That Drive Evolutionary Rescue to Lethal Temperature in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2029-2044.	1.1	3
17	Multiple introductions and population structure during the rapid expansion of the invasive Sahara mustard (<i>Brassica tournefortii</i>). <i>Ecology and Evolution</i> , 2019, 9, 7928-7941.	0.8	13
18	Living with Two Genomes: Grafting and Its Implications for Plant Genome-to-Genome Interactions, Phenotypic Variation, and Evolution. <i>Annual Review of Genetics</i> , 2019, 53, 195-215.	3.2	46

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19	The genome-wide dynamics of purging during selfing in maize. <i>Nature Plants</i> , 2019, 5, 980-990.	4.7	42
20	The population genetics of structural variants in grapevine domestication. <i>Nature Plants</i> , 2019, 5, 965-979.	4.7	229
21	EvoChromo: towards a synthesis of chromatin biology and evolution. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	16
22	Divergence with gene flow is driven by local adaptation to temperature and soil phosphorus concentration in teosinte subspecies (<i>Zea mays parviglumis</i> and <i>Zea mays mexicana</i>). <i>Molecular Ecology</i> , 2019, 28, 2814-2830.	2.0	48
23	Maize transposable elements contribute to long non-coding RNAs that are regulatory hubs for abiotic stress response. <i>BMC Genomics</i> , 2019, 20, 864.	1.2	47
24	The genomic diversification of grapevine clones. <i>BMC Genomics</i> , 2019, 20, 972.	1.2	66
25	Loss of Gene Body Methylation in <i>Eutrema salsugineum</i> Is Associated with Reduced Gene Expression. <i>Molecular Biology and Evolution</i> , 2019, 36, 155-158.	3.5	29
26	Evolutionary Genomics and the Domestication of Grapes. <i>Compendium of Plant Genomes</i> , 2019, , 39-55.	0.3	17
27	Modeling Interactions between Transposable Elements and the Plant Epigenetic Response: A Surprising Reliance on Element Retention. <i>Genome Biology and Evolution</i> , 2018, 10, 803-815.	1.1	35
28	Natural rubber and the Russian dandelion genome. <i>National Science Review</i> , 2018, 5, 88-89.	4.6	1
29	A convergent outcome: small genomes in mangroves. <i>New Phytologist</i> , 2018, 217, 5-7.	3.5	2
30	Demography and its effects on genomic variation in crop domestication. <i>Nature Plants</i> , 2018, 4, 512-520.	4.7	173
31	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	68
32	The Evolutionary Dynamics of Orthologs That Shift in Gene Body Methylation between Arabidopsis Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1479-1491.	3.5	29
33	Considerations and complications of mapping small RNA high-throughput data to transposable elements. <i>Mobile DNA</i> , 2017, 8, 3.	1.3	11
34	Evolutionary genomics of grape (<i>Vitis vinifera</i> ssp. <i>vinifera</i>) domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11715-11720.	3.3	236
35	Adaptive Mutations in RNA Polymerase and the Transcriptional Terminator Rho Have Similar Effects on <i>Escherichia coli</i> Gene Expression. <i>Molecular Biology and Evolution</i> , 2017, 34, 2839-2855.	3.5	27
36	How Single Molecule Real-Time Sequencing and Haplotype Phasing Have Enabled Reference-Grade Diploid Genome Assembly of Wine Grapes. <i>Frontiers in Plant Science</i> , 2017, 8, 826.	1.7	55

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37	Seasonal Changes in a Maize-Based Polyculture of Central Mexico Reshape the Co-occurrence Networks of Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2017, 8, 2478.	1.5	36
38	The jury may be out, but it is important that it deliberates: a response to Besnard and Rubio de Casas about olive domestication. <i>New Phytologist</i> , 2016, 209, 471-473.	3.5	11
39	Evolutionary patterns of genic DNA methylation vary across land plants. <i>Nature Plants</i> , 2016, 2, 15222.	4.7	178
40	A role for palindromic structures in the cis-region of maize Sirevirus LTRs in transposable element evolution and host epigenetic response. <i>Genome Research</i> , 2016, 26, 226-237.	2.4	22
41	Mechanistic and evolutionary questions about epigenetic conflicts between transposable elements and their plant hosts. <i>Current Opinion in Plant Biology</i> , 2016, 30, 123-133.	3.5	39
42	First-Step Mutations during Adaptation Restore the Expression of Hundreds of Genes. <i>Molecular Biology and Evolution</i> , 2016, 33, 25-39.	3.5	60
43	CG Methylation Covaries with Differential Gene Expression between Leaf and Floral Bud Tissues of <i>Brachypodium distachyon</i> . <i>PLoS ONE</i> , 2016, 11, e0150002.	1.1	25
44	The phenotypic signature of adaptation to thermal stress in <i>Escherichia coli</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 177.	3.2	24
45	Evolution Is an Experiment: Assessing Parallelism in Crop Domestication and Experimental Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 1661-1671.	3.5	41
46	Genomics and the Contrasting Dynamics of Annual and Perennial Domestication. <i>Trends in Genetics</i> , 2015, 31, 709-719.	2.9	145
47	Olive domestication and diversification in the Mediterranean Basin. <i>New Phytologist</i> , 2015, 206, 436-447.	3.5	227
48	Three Groups of Transposable Elements with Contrasting Copy Number Dynamics and Host Responses in the Maize (<i>Zea mays ssp. mays</i>) Genome. <i>PLoS Genetics</i> , 2014, 10, e1004298.	1.5	52
49	Different tradeoffs result from alternate genetic adaptations to a common environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12121-12126.	3.3	89
50	Epigenetics and plant genome evolution. <i>Current Opinion in Plant Biology</i> , 2014, 18, 1-8.	3.5	90
51	The complex domestication history of the common bean. <i>Nature Genetics</i> , 2014, 46, 663-664.	9.4	17
52	Gene body methylation is conserved between plant orthologs and is of evolutionary consequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1797-1802.	3.3	206
53	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	9.4	374
54	Genome size variation in wild and cultivated maize along altitudinal gradients. <i>New Phytologist</i> , 2013, 199, 264-276.	3.5	107

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55	Recent Retrotransposon Insertions Are Methylated and Phylogenetically Clustered in Japonica Rice (<i>Oryza sativa</i> spp. japonica). <i>Molecular Biology and Evolution</i> , 2012, 29, 3193-3203.	3.5	22
56	Body-Methylated Genes in <i>Arabidopsis thaliana</i> Are Functionally Important and Evolve Slowly. <i>Molecular Biology and Evolution</i> , 2012, 29, 219-227.	3.5	222
57	The Molecular Diversity of Adaptive Convergence. <i>Science</i> , 2012, 335, 457-461.	6.0	688
58	<i>Arabidopsis thaliana</i> as a model for the genetics of local adaptation. <i>Nature Genetics</i> , 2012, 44, 115-116.	9.4	22
59	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012, 44, 803-807.	9.4	577
60	Inferences from the Historical Distribution of Wild and Domesticated Maize Provide Ecological and Evolutionary Insight. <i>PLoS ONE</i> , 2012, 7, e47659.	1.1	79
61	The Patterns and Causes of Variation in Plant Nucleotide Substitution Rates. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2011, 42, 245-266.	3.8	136
62	Genome Size and Transposable Element Content as Determined by High-Throughput Sequencing in Maize and <i>Zea luxurians</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 219-229.	1.1	167
63	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	9.4	814
64	Retrogenes in Rice (<i>Oryza sativa</i> L. ssp. japonica) Exhibit Correlated Expression with Their Source Genes. <i>Genome Biology and Evolution</i> , 2011, 3, 1357-1368.	1.1	62
65	Transposable elements and small RNAs contribute to gene expression divergence between <i>Arabidopsis thaliana</i> and <i>Arabidopsis lyrata</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2322-2327.	3.3	308
66	Factors that Contribute to Variation in Evolutionary Rate among <i>Arabidopsis</i> Genes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2359-2369.	3.5	149
67	Mapping Salinity Tolerance during <i>Arabidopsis thaliana</i> Germination and Seedling Growth. <i>PLoS ONE</i> , 2011, 6, e22832.	1.1	66
68	Lowly Expressed Genes in <i>Arabidopsis thaliana</i> Bear the Signature of Possible Pseudogenization by Promoter Degradation. <i>Molecular Biology and Evolution</i> , 2011, 28, 1193-1203.	3.5	59
69	The evolution of transposable elements in natural populations of self-fertilizing <i>Arabidopsis thaliana</i> and its outcrossing relative <i>Arabidopsis lyrata</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 10.	3.2	84
70	Genetic diversity in domesticated soybean (<i>Glycine max</i>) and its wild progenitor (<i>Glycine</i>) <i>TJ ETQq0 0 0 rgBT /Overlock 10 Tf 5</i> 188, 242-253.	3.5	181
71	Fine scale genetic structure in the wild ancestor of maize (<i>Zea mays</i> ssp. <i>parviglumis</i>). <i>Molecular Ecology</i> , 2010, 19, 1162-1173.	2.0	37
72	Indel-Associated Mutation Rate Varies with Mating System in Flowering Plants. <i>Molecular Biology and Evolution</i> , 2010, 27, 409-416.	3.5	47

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73	A triptych of the evolution of plant transposable elements. <i>Trends in Plant Science</i> , 2010, 15, 471-478.	4.3	254
74	Epigenetic silencing of transposable elements: A trade-off between reduced transposition and deleterious effects on neighboring gene expression. <i>Genome Research</i> , 2009, 19, 1419-1428.	2.4	569
75	Historical Divergence and Gene Flow in the Genus <i>Zea</i> . <i>Genetics</i> , 2009, 181, 1399-1413.	1.2	175
76	Do genetic recombination and gene density shape the pattern of DNA elimination in rice long terminal repeat retrotransposons?. <i>Genome Research</i> , 2009, 19, 2221-2230.	2.4	169
77	The Contribution of Transposable Elements to Expressed Coding Sequence in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2009, 68, 80-89.	0.8	68
78	Selection on grain shattering genes and rates of rice domestication. <i>New Phytologist</i> , 2009, 184, 708-720.	3.5	140
79	Selection on Amino Acid Substitutions in <i>Arabidopsis</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1375-1383.	3.5	71
80	Selection on Major Components of Angiosperm Genomes. <i>Science</i> , 2008, 320, 484-486.	6.0	62
81	Demography and weak selection drive patterns of transposable element diversity in natural populations of <i>Arabidopsis lyrata</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13965-13970.	3.3	99
82	Patterns of Polymorphism and Demographic History in Natural Populations of <i>Arabidopsis lyrata</i> . <i>PLoS ONE</i> , 2008, 3, e2411.	1.1	163
83	Empirical Analysis of Selection Screens for Domestication and Improvement Loci in Maize by Extended DNA Sequencing. <i>Plant Genome</i> , 2008, 1, .	1.6	5
84	Linkage Mapping of Domestication Loci in a Large Maize Teosinte Backcross Resource. <i>Genetics</i> , 2007, 177, 1915-1928.	1.2	97
85	Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. <i>Plant Physiology</i> , 2007, 144, 1642-1653.	2.3	17
86	Multilocus Analysis of Nucleotide Variation of <i>Oryza sativa</i> and Its Wild Relatives: Severe Bottleneck during Domestication of Rice. <i>Molecular Biology and Evolution</i> , 2007, 24, 875-888.	3.5	329
87	A Weak Effect of Background Selection on Trinucleotide Microsatellites in Maize. <i>Journal of Heredity</i> , 2007, 99, 45-55.	1.0	3
88	Population and Evolutionary Dynamics of Helitron Transposable Elements in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2007, 24, 2515-2524.	3.5	64
89	Plant domestication, a unique opportunity to identify the genetic basis of adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8641-8648.	3.3	385
90	Phylogenetic analysis, genome evolution and the rate of gene gain in the Herpesviridae. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 1066-1075.	1.2	22

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91	Recombination: an underappreciated factor in the evolution of plant genomes. <i>Nature Reviews Genetics</i> , 2007, 8, 77-84.	7.7	223
92	Spatial scale of local adaptation and population genetic structure in a miniature succulent, <i>Argyroderma pearsonii</i> . <i>New Phytologist</i> , 2007, 174, 904-914.	3.5	15
93	The Molecular Genetics of Crop Domestication. <i>Cell</i> , 2006, 127, 1309-1321.	13.5	1,701
94	Adaptive selection of mitochondrial complex I subunits during primate radiation. <i>Gene</i> , 2006, 378, 11-18.	1.0	85
95	EVOLUTIONARY RADIATION OF "STONE PLANTS" IN THE GENUS ARGYRODERMA (AIZOACEAE): UNRAVELING THE EFFECTS OF LANDSCAPE, HABITAT, AND FLOWERING TIME. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 39-55.	1.1	65
96	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006, 38, 203-208.	9.4	3,622
97	Molecular and functional diversity of maize. <i>Current Opinion in Plant Biology</i> , 2006, 9, 172-176.	3.5	201
98	Striking Similarities in the Genomic Distribution of Tandemly Arrayed Genes in Arabidopsis and Rice. <i>PLoS Computational Biology</i> , 2006, 2, e115.	1.5	265
99	Variation in Mutation Dynamics Across the Maize Genome as a Function of Regional and Flanking Base Composition. <i>Genetics</i> , 2006, 172, 569-577.	1.2	70
100	Testing for Effects of Recombination Rate on Nucleotide Diversity in Natural Populations of <i>Arabidopsis lyrata</i> . <i>Genetics</i> , 2006, 174, 1421-1430.	1.2	64
101	Timing and rate of speciation in Agave (Agavaceae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9124-9129.	3.3	230
102	Plant conserved non-coding sequences and paralogue evolution. <i>Trends in Genetics</i> , 2005, 21, 60-65.	2.9	147
103	Molecular Population Genetics and the Search for Adaptive Evolution in Plants. <i>Molecular Biology and Evolution</i> , 2005, 22, 506-519.	3.5	301
104	A Large-Scale Screen for Artificial Selection in Maize Identifies Candidate Agronomic Loci for Domestication and Crop Improvement. <i>Plant Cell</i> , 2005, 17, 2859-2872.	3.1	234
105	Uneven distribution of expressed sequence tag loci on maize pachytene chromosomes. <i>Genome Research</i> , 2005, 16, 115-122.	2.4	56
106	The Effects of Artificial Selection on the Maize Genome. <i>Science</i> , 2005, 308, 1310-1314.	6.0	742
107	Gene Conversion and the Evolution of Three Leucine-Rich Repeat Gene Families in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 2444-2456.	3.5	131
108	Population Genetic Evidence for Rapid Changes in Intraspecific Diversity and Allelic Cycling of a Specialist Defense Gene in <i>Zea</i> —Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY320258, AY320280, AY52550, AY52551, AY52552, AY52553, AY52554, AY52555, AY52556, AY52557, AY52558, AY52559, and AY549598, AY549599, AY549600, AY549601, AY549602, AY549603, AY549604, AY549605, AY549606, AY549607, AY549608, AY549609, AY549610, AY549611, AY549612, AY549613, AY5. <i>Genetics</i> , 2004, 168, 425-434.	1.2	34

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109	Selection Versus Demography: A Multilocus Investigation of the Domestication Process in Maize. <i>Molecular Biology and Evolution</i> , 2004, 21, 1214-1225.	3.5	251
110	Extensive gene gain associated with adaptive evolution of poxviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15655-15660.	3.3	161
111	The Lowdown on Linkage Disequilibrium. <i>Plant Cell</i> , 2003, 15, 1502-1506.	3.1	217
112	Does Recombination Shape the Distribution and Evolution of Tandemly Arrayed Genes (TAGs) in the <i>Arabidopsis thaliana</i> Genome?. <i>Genome Research</i> , 2003, 13, 2533-2540.	2.4	79
113	LineUp: Statistical Detection of Chromosomal Homology With Application to Plant Comparative Genomics. <i>Genome Research</i> , 2003, 13, 999-1010.	2.4	45
114	Patterns of Positive Selection in the Complete NBS-LRR Gene Family of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2002, 12, 1305-1315.	2.4	278
115	Genetic diversity and selection in the maize starch pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12959-12962.	3.3	298
116	Patterns of Nucleotide Substitution Among Simultaneously Duplicated Gene Pairs in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2002, 19, 1464-1473.	3.5	117
117	Evolutionary dynamics of grass genomes. <i>New Phytologist</i> , 2002, 154, 15-28.	3.5	376
118	Population Genetics of Duplicated Disease-Defense Genes, <i>hm1</i> and <i>hm2</i> , in Maize (<i>Zea mays</i> ssp. <i>indica</i>). <i>Genetics</i> , 2002, 162, 851-860.	1.2	53
119	Patterns of Diversity and Recombination Along Chromosome 1 of Maize (<i>Zea mays</i> ssp. <i>indica</i>). <i>Genetics</i> , 2002, 162, 851-860.	1.2	86
120	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , 2001, 12, 84-86.	0.3	39
121	Genetic Diversity in Seven Perennial Ryegrass (<i>Lolium perenne</i> L.) Cultivars Based on SSR Markers. <i>Crop Science</i> , 2001, 41, 1565-1572.	0.8	124
122	A Survey of the Molecular Evolutionary Dynamics of Twenty-Five Multigene Families from Four Grass Taxa. <i>Journal of Molecular Evolution</i> , 2001, 52, 144-156.	0.8	49
123	The Interaction of Protein Structure, Selection, and Recombination on the Evolution of the Type-1 Fimbrial Major Subunit (<i>fimA</i>) from <i>Escherichia coli</i> . <i>Journal of Molecular Evolution</i> , 2001, 52, 193-204.	0.8	34
124	Molecular Evolution of the Wound-Induced Serine Protease Inhibitor <i>wip1</i> in <i>Zea</i> and Related Genera. <i>Molecular Biology and Evolution</i> , 2001, 18, 2092-2101.	3.5	61
125	Sequence Diversity in the Tetraploid <i>Zea perennis</i> and the Closely Related Diploid <i>Z. diploperennis</i> : Insights From Four Nuclear Loci. <i>Genetics</i> , 2001, 158, 401-412.	1.2	41
126	Neutral and Nonneutral Mitochondrial Genetic Variation in Deep-Sea Clams from the Family Vesicomyidae. <i>Journal of Molecular Evolution</i> , 2000, 50, 141-153.	0.8	43

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127	Assesing the Abundance and Polymorphism of Simple Sequence Repeats in Perennial Ryegrass. <i>Crop Science</i> , 1999, 39, 1136-1141.	0.8	51
128	The paleontology of intergene retrotransposons of maize. <i>Nature Genetics</i> , 1998, 20, 43-45.	9.4	953
129	Xa21D Encodes a Receptor-like Molecule with a Leucine-Rich Repeat Domain That Determines Race-Specific Recognition and Is Subject to Adaptive Evolution. <i>Plant Cell</i> , 1998, 10, 765-779.	3.1	304
130	Receptor-like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998, 10, 1833-1846.	3.1	288
131	Receptor-Like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998, 10, 1833.	3.1	15
132	Speciation and Domestication in Maize and Its Wild Relatives: Evidence From the Globulin-1 Gene. <i>Genetics</i> , 1998, 150, 863-872.	1.2	112
133	Comparing Patterns of Nucleotide Substitution Rates Among Chloroplast Loci Using the Relative Ratio Test. <i>Genetics</i> , 1997, 146, 393-399.	1.2	79
134	Evolution in the Genus <i>Zea</i> : Lessons from Studies of Nucleotide Polymorphism. <i>Plant Species Biology</i> , 1996, 11, 1-11.	0.6	4
135	Evolution of Anthocyanin Biosynthesis in Maize Kernels: The Role of Regulatory and Enzymatic Loci. <i>Genetics</i> , 1996, 143, 1395-1407.	1.2	144
136	Relative Rates of Nucleotide Substitution in the Chloroplast Genome. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 89-96.	1.2	62
137	Inferring plant evolutionary history from molecular data. <i>New Zealand Journal of Botany</i> , 1993, 31, 307-315.	0.8	10
138	Relative rates of nucleotide substitution at the <i>rbcl</i> locus of monocotyledonous plants. <i>Journal of Molecular Evolution</i> , 1992, 35, 292-303.	0.8	276