

Brandon S Gaut

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143
papers

17,231
citations

60
h-index

131
g-index

150
ext. papers

20,774
ext. citations

9.7
avg, IF

6.78
L-index

#	Paper	IF	Citations
143	A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. <i>Nature Genetics</i> , 2006 , 38, 203-8	36.3	2595
142	The molecular genetics of crop domestication. <i>Cell</i> , 2006 , 127, 1309-21	56.2	1247
141	The paleontology of intergene retrotransposons of maize. <i>Nature Genetics</i> , 1998 , 20, 43-5	36.3	816
140	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011 , 43, 476-81	36.3	638
139	The effects of artificial selection on the maize genome. <i>Science</i> , 2005 , 308, 1310-4	33.3	634
138	The molecular diversity of adaptive convergence. <i>Science</i> , 2012 , 335, 457-61	33.3	511
137	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
136	Epigenetic silencing of transposable elements: a trade-off between reduced transposition and deleterious effects on neighboring gene expression. <i>Genome Research</i> , 2009 , 19, 1419-28	9.7	429
135	Evolutionary dynamics of grass genomes. <i>New Phytologist</i> , 2002 , 154, 15-28	9.8	336
134	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 Suppl 1, 8641-8	11.5	284
133	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013 , 45, 831-5	36.3	274
132	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, 875-88	8.3	270
131	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, 765-79	11.6	268
130	Molecular population genetics and the search for adaptive evolution in plants. <i>Molecular Biology and Evolution</i> , 2005 , 22, 506-19	8.3	267
129	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, 12959-62	11.5	252
128	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, 2322-7	11.5	247
127	Relative rates of nucleotide substitution at the <i>rbcl</i> locus of monocotyledonous plants. <i>Journal of Molecular Evolution</i> , 1992 , 35, 292-303	3.1	242

126	Receptor-like genes in the major resistance locus of lettuce are subject to divergent selection. <i>Plant Cell</i> , 1998 , 10, 1833-46	11.6	239
125	Patterns of positive selection in the complete NBS-LRR gene family of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2002 , 12, 1305-15	9.7	231
124	Selection versus demography: a multilocus investigation of the domestication process in maize. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1214-25	8.3	220
123	A large-scale screen for artificial selection in maize identifies candidate agronomic loci for domestication and crop improvement. <i>Plant Cell</i> , 2005 , 17, 2859-72	11.6	202
122	A triptych of the evolution of plant transposable elements. <i>Trends in Plant Science</i> , 2010 , 15, 471-8	13.1	193
121	Striking similarities in the genomic distribution of tandemly arrayed genes in <i>Arabidopsis</i> and rice. <i>PLoS Computational Biology</i> , 2006 , 2, e115	5	193
120	Timing and rate of speciation in <i>Agave</i> (Agavaceae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 9124-9	11.5	184
119	Recombination: an underappreciated factor in the evolution of plant genomes. <i>Nature Reviews Genetics</i> , 2007 , 8, 77-84	30.1	183
118	The lowdown on linkage disequilibrium. <i>Plant Cell</i> , 2003 , 15, 1502-6	11.6	179
117	Molecular and functional diversity of maize. <i>Current Opinion in Plant Biology</i> , 2006 , 9, 172-6	9.9	168
116	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, 1797-802	11.5	163
115	Body-methylated genes in <i>Arabidopsis thaliana</i> are functionally important and evolve slowly. <i>Molecular Biology and Evolution</i> , 2012 , 29, 219-27	8.3	155
114	Patterns of polymorphism and demographic history in natural populations of <i>Arabidopsis lyrata</i> . <i>PLoS ONE</i> , 2008 , 3, e2411	3.7	144
113	Evolutionary genomics of grape (<i>ssp.</i>) domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11715-11720	11.5	142
112	Genetic diversity in domesticated soybean (<i>Glycine max</i>) and its wild progenitor (<i>Glycine soja</i>) for simple sequence repeat and single-nucleotide polymorphism loci. <i>New Phytologist</i> , 2010 , 188, 242-53	9.8	140
111	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, 219-29	3.9	136
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, 15655-60	11.5	134
109	Olive domestication and diversification in the Mediterranean Basin. <i>New Phytologist</i> , 2015 , 206, 436-447	9.8	133

108	Evolutionary patterns of genic DNA methylation vary across land plants. <i>Nature Plants</i> , 2016 , 2, 15222	11.5	133
107	Historical divergence and gene flow in the genus <i>Zea</i> . <i>Genetics</i> , 2009 , 181, 1399-413	4	133
106	Plant conserved non-coding sequences and paralogue evolution. <i>Trends in Genetics</i> , 2005 , 21, 60-5	8.5	125
105	Do genetic recombination and gene density shape the pattern of DNA elimination in rice long terminal repeat retrotransposons?. <i>Genome Research</i> , 2009 , 19, 2221-30	9.7	123
104	Factors that contribute to variation in evolutionary rate among <i>Arabidopsis</i> genes. <i>Molecular Biology and Evolution</i> , 2011 , 28, 2359-69	8.3	123
103	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, 2444-56	8.3	120
102	Genetic Diversity in Seven Perennial Ryegrass (<i>Lolium perenne</i> L.) Cultivars Based on SSR Markers. <i>Crop Science</i> , 2001 , 41, 1565-1572	2.4	114
101	Evolution of anthocyanin biosynthesis in maize kernels: the role of regulatory and enzymatic loci. <i>Genetics</i> , 1996 , 143, 1395-407	4	113
100	The population genetics of structural variants in grapevine domestication. <i>Nature Plants</i> , 2019 , 5, 965-979	11.5	110
99	Patterns of nucleotide substitution among simultaneously duplicated gene pairs in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2002 , 19, 1464-73	8.3	109
98	Selection on grain shattering genes and rates of rice domestication. <i>New Phytologist</i> , 2009 , 184, 708-720	9.8	107
97	The Patterns and Causes of Variation in Plant Nucleotide Substitution Rates. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2011 , 42, 245-266	13.5	103
96	Speciation and domestication in maize and its wild relatives: evidence from the globulin-1 gene. <i>Genetics</i> , 1998 , 150, 863-72	4	89
95	Demography and its effects on genomic variation in crop domestication. <i>Nature Plants</i> , 2018 , 4, 512-520	11.5	86
94	Linkage mapping of domestication loci in a large maize teosinte backcross resource. <i>Genetics</i> , 2007 , 177, 1915-28	4	86
93	Adaptive selection of mitochondrial complex I subunits during primate radiation. <i>Gene</i> , 2006 , 378, 11-8	3.8	76
92	Genome size variation in wild and cultivated maize along altitudinal gradients. <i>New Phytologist</i> , 2013 , 199, 264-276	9.8	75
91	Epigenetics and plant genome evolution. <i>Current Opinion in Plant Biology</i> , 2014 , 18, 1-8	9.9	74

90	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, 13965-70	11.5	74
89	Patterns of diversity and recombination along chromosome 1 of maize (<i>Zea mays</i> ssp. <i>mays</i> L.). <i>Genetics</i> , 2002 , 162, 1401-13	4	74
88	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	73
87	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, 2533-40	9.7	72
86	Genomics and the Contrasting Dynamics of Annual and Perennial Domestication. <i>Trends in Genetics</i> , 2015 , 31, 709-719	8.5	71
85	Selection on amino acid substitutions in <i>Arabidopsis</i> . <i>Molecular Biology and Evolution</i> , 2008 , 25, 1375-83	8.3	66
84	Comparing patterns of nucleotide substitution rates among chloroplast loci using the relative ratio test. <i>Genetics</i> , 1997 , 146, 393-9	4	66
83	Population and evolutionary dynamics of Helitron transposable elements in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2007 , 24, 2515-24	8.3	60
82	Selection on major components of angiosperm genomes. <i>Science</i> , 2008 , 320, 484-6	33.3	56
81	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, 12121-6	11.5	55
80	The contribution of transposable elements to expressed coding sequence in <i>Arabidopsis thaliana</i> . <i>Journal of Molecular Evolution</i> , 2009 , 68, 80-9	3.1	55
79	Testing for effects of recombination rate on nucleotide diversity in natural populations of <i>Arabidopsis lyrata</i> . <i>Genetics</i> , 2006 , 174, 1421-30	4	55
78	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	3.8	54
77	Molecular evolution of the wound-induced serine protease inhibitor wip1 in <i>Zea</i> and related genera. <i>Molecular Biology and Evolution</i> , 2001 , 18, 2092-101	8.3	54
76	Mapping salinity tolerance during <i>Arabidopsis thaliana</i> germination and seedling growth. <i>PLoS ONE</i> , 2011 , 6, e22832	3.7	53
75	Relative rates of nucleotide substitution in the chloroplast genome. <i>Molecular Phylogenetics and Evolution</i> , 1993 , 2, 89-96	4.1	53
74	Inferences from the historical distribution of wild and domesticated maize provide ecological and evolutionary insight. <i>PLoS ONE</i> , 2012 , 7, e47659	3.7	53
73	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, 1193-203	8.3	51

72	Deleterious Variants in Asian Rice and the Potential Cost of Domestication. <i>Molecular Biology and Evolution</i> , 2017 , 34, 908-924	8.3	50
71	Variation in mutation dynamics across the maize genome as a function of regional and flanking base composition. <i>Genetics</i> , 2006 , 172, 569-77	4	50
70	The genetic basis of sex determination in grapes. <i>Nature Communications</i> , 2020 , 11, 2902	17.4	46
69	Assesing the Abundance and Polymorphism of Simple Sequence Repeats in Perennial Ryegrass. <i>Crop Science</i> , 1999 , 39, 1136-1141	2.4	45
68	Population genetics of duplicated disease-defense genes, hm1 and hm2, in maize (<i>Zea mays</i> ssp. <i>mays</i> L.) and its wild ancestor (<i>Zea mays</i> ssp. <i>parviglumis</i>). <i>Genetics</i> , 2002 , 162, 851-60	4	45
67	Uneven distribution of expressed sequence tag loci on maize pachytene chromosomes. <i>Genome Research</i> , 2006 , 16, 115-22	9.7	44
66	Retrogenes in rice (<i>Oryza sativa</i> L. ssp. <i>japonica</i>) exhibit correlated expression with their source genes. <i>Genome Biology and Evolution</i> , 2011 , 3, 1357-68	3.9	43
65	A survey of the molecular evolutionary dynamics of twenty-five multigene families from four grass taxa. <i>Journal of Molecular Evolution</i> , 2001 , 52, 144-56	3.1	41
64	LineUp: statistical detection of chromosomal homology with application to plant comparative genomics. <i>Genome Research</i> , 2003 , 13, 999-1010	9.7	39
63	Neutral and nonneutral mitochondrial genetic variation in deep-sea clams from the family vesicomidae. <i>Journal of Molecular Evolution</i> , 2000 , 50, 141-53	3.1	38
62	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	6.2	36
61	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, 401-12	4	36
60	First-Step Mutations during Adaptation Restore the Expression of Hundreds of Genes. <i>Molecular Biology and Evolution</i> , 2016 , 33, 25-39	8.3	35
59	Genetic Evidence and the Origin of Maize. <i>Latin American Antiquity</i> , 2001 , 12, 84-86	0.5	34
58	Evolution Is an Experiment: Assessing Parallelism in Crop Domestication and Experimental Evolution: (Nei Lecture, SMCB 2014, Puerto Rico). <i>Molecular Biology and Evolution</i> , 2015 , 32, 1661-71	8.3	33
57	Indel-associated mutation rate varies with mating system in flowering plants. <i>Molecular Biology and Evolution</i> , 2010 , 27, 409-16	8.3	33
56	Three groups of transposable elements with contrasting copy number dynamics and host responses in the maize (<i>Zea mays</i> ssp. <i>mays</i>) genome. <i>PLoS Genetics</i> , 2014 , 10, e1004298	6	32
55	The genomic diversification of grapevine clones. <i>BMC Genomics</i> , 2019 , 20, 972	4.5	32

54	Population genetic evidence for rapid changes in intraspecific diversity and allelic cycling of a specialist defense gene in Zea. <i>Genetics</i> , 2004 , 168, 425-34	4	31
53	Fine scale genetic structure in the wild ancestor of maize (<i>Zea mays</i> ssp. <i>parviglumis</i>). <i>Molecular Ecology</i> , 2010 , 19, 1162-73	5.7	30
52	The interaction of protein structure, selection, and recombination on the evolution of the type-1 fimbrial major subunit (fimA) from <i>Escherichia coli</i> . <i>Journal of Molecular Evolution</i> , 2001 , 52, 193-204	3.1	30
51	Maize transposable elements contribute to long non-coding RNAs that are regulatory hubs for abiotic stress response. <i>BMC Genomics</i> , 2019 , 20, 864	4.5	27
50	Mechanistic and evolutionary questions about epigenetic conflicts between transposable elements and their plant hosts. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 123-33	9.9	24
49	The genome-wide dynamics of purging during selfing in maize. <i>Nature Plants</i> , 2019 , 5, 980-990	11.5	23
48	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	3.7	22
47	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	5.7	21
46	Phylogenetic analysis, genome evolution and the rate of gene gain in the Herpesviridae. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 43, 1066-75	4.1	21
45	The Evolutionary Dynamics of Orthologs That Shift in Gene Body Methylation between <i>Arabidopsis</i> Species. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1479-1491	8.3	20
44	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	3.9	20
43	Evolutionary Genomics of Structural Variation in Asian Rice (<i>Oryza sativa</i>) Domestication. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3507-3524	8.3	19
42	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	14.5	18
41	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	8.3	18
40	Recent retrotransposon insertions are methylated and phylogenetically clustered in japonica rice (<i>Oryza sativa</i> spp. <i>japonica</i>). <i>Molecular Biology and Evolution</i> , 2012 , 29, 3193-203	8.3	17
39	Patterns of selection and tissue-specific expression among maize domestication and crop improvement loci. <i>Plant Physiology</i> , 2007 , 144, 1642-53	6.6	17
38	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, 226-37	9.7	16
37	Phylogenetic Shifts in Gene Body Methylation Correlate with Gene Expression and Reflect Trait Conservation. <i>Molecular Biology and Evolution</i> , 2020 , 37, 31-43	8.3	16

36	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	5.7	14
35	The phenotypic signature of adaptation to thermal stress in <i>Escherichia coli</i> . <i>BMC Evolutionary Biology</i> , 2015 , 15, 177	3	14
34	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	7.3	14
33	Evolutionary Genomics and the Domestication of Grapes. <i>Compendium of Plant Genomes</i> , 2019 , 39-55	0.8	13
32	The complex domestication history of the common bean. <i>Nature Genetics</i> , 2014 , 46, 663-4	36.3	12
31	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	9.8	11
30	Structural variants, clonal propagation, and genome evolution in grapevine (<i>Vitis vinifera</i>)		11
29	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	8.3	10
28	The evolutionary genomics of species' responses to climate change. <i>Nature Ecology and Evolution</i> , 2021 , 5, 1350-1360	12.3	9
27	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, 471-3	9.8	8
26	EvoChromo: towards a synthesis of chromatin biology and evolution. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	7
25	Inferring plant evolutionary history from molecular data. <i>New Zealand Journal of Botany</i> , 1993 , 31, 307-315		7
24	Considerations and complications of mapping small RNA high-throughput data to transposable elements. <i>Mobile DNA</i> , 2017 , 8, 3	4.4	6
23	Multiple introductions and population structure during the rapid expansion of the invasive Sahara mustard (<i>Sisymbrium</i>). <i>Ecology and Evolution</i> , 2019 , 9, 7928-7941	2.8	6
22	The genomic diversification of clonally propagated grapevines		6
21	Gene capture by transposable elements leads to epigenetic conflict in maize. <i>Molecular Plant</i> , 2021 , 14, 237-252	14.4	6
20	Receptor-Like Genes in the Major Resistance Locus of Lettuce Are Subject to Divergent Selection. <i>Plant Cell</i> , 1998 , 10, 1833	11.6	4
19	Evolution in the Genus <i>Zea</i> : Lessons from Studies of Nucleotide Polymorphism. <i>Plant Species Biology</i> , 1996 , 11, 1-11	1.3	4

18	Empirical Analysis of Selection Screens for Domestication and Improvement Loci in Maize by Extended DNA Sequencing. <i>Plant Genome</i> , 2008 , 1,	4.4	4
17	The genetic basis of sex determination in grapevines (<i>Vitis</i> spp.)		4
16	A weak effect of background selection on trinucleotide microsatellites in maize. <i>Journal of Heredity</i> , 2008 , 99, 45-55	2.4	3
15	The Evolutionary Genomics of Grape (<i>Vitis vinifera</i> ssp. <i>vinifera</i>) Domestication		3
14	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,	3.9	3
13	Introgression among North American wild grapes (<i>Vitis</i>) fuels biotic and abiotic adaptation. <i>Genome Biology</i> , 2021 , 22, 254	18.3	3
12	Phylogenetic shifts in gene body methylation correlate with gene expression and reflect trait conservation		2
11	Evolutionary genomics of structural variation in Asian rice (<i>Oryza sativa</i>) and its wild progenitor (<i>O. rufipogon</i>)		2
10	Large chromosomal variants drive adaptation in sunflowers. <i>Nature Plants</i> , 2020 , 6, 734-735	11.5	2
9	A convergent outcome: small genomes in mangroves. <i>New Phytologist</i> , 2018 , 217, 5-7	9.8	2
8	Genomic evidence for recurrent genetic admixture during domestication mediterranean olive trees (<i>Olea europaea</i>)		1
7	Gene capture by transposable elements leads to epigenetic conflict in maize		1
6	Gene body methylation is under selection in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2021 , 218,	4	1
5	Extensive introgression among North American wild grapes (<i>Vitis</i>) fuels biotic and abiotic adaptation		1
4	Natural rubber and the Russian dandelion genome. <i>National Science Review</i> , 2018 , 5, 88-89	10.8	0
3	Genetic Mutations That Drive Evolutionary Rescue to Lethal Temperature in <i>Escherichia coli</i> . <i>Genome Biology and Evolution</i> , 2020 , 12, 2029-2044	3.9	0
2	HapSolo: an optimization approach for removing secondary haplotigs during diploid genome assembly and scaffolding. <i>BMC Bioinformatics</i> , 2021 , 22, 9	3.6	0
1	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	2.8	

