

A genomic variation map provides insights into the gen
domestication and diversity

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Analysis of the bZIP Transcription Factors in Cucumber. PLoS ONE, 2014, 9, e96014.	1.1	191
2	Fastq_clean: An optimized pipeline to clean the Illumina sequencing data with quality control. , 2014, , .		51
3	What lies beyond the eye: the molecular mechanisms regulating tomato fruit weight and shape. Frontiers in Plant Science, 2014, 5, 227.	1.7	167
4	Genome-wide variation within and between wild and domestic yak. Molecular Ecology Resources, 2014, 14, 794-801.	2.2	40
5	Biosynthesis, regulation, and domestication of bitterness in cucumber. Science, 2014, 346, 1084-1088.	6.0	388
6	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in cucumber using specific-length amplified fragment (SLAF) sequencing. BMC Genomics, 2014, 15, 1158.	1.2	127
7	The contribution of genetic and genomic approaches to plant domestication studies. Current Opinion in Plant Biology, 2014, 18, 51-59.	3.5	93
8	Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 2014, 46, 1220-1226.	9.4	801
9	The complex domestication history of the common bean. Nature Genetics, 2014, 46, 663-664.	9.4	17
10	QTL-seq identifies an early flowering QTL located near Flowering Locus T in cucumber. Theoretical and Applied Genetics, 2014, 127, 1491-1499.	1.8	267
11	Investment in plant research and development bears fruit in China. Plant Cell Reports, 2014, 33, 541-550.	2.8	7
12	Transcriptome comparison reveals the patterns of selection in domesticated and wild ramie (<i>Boehmeria nivea</i> L. Gaud). Plant Molecular Biology, 2014, 86, 85-92.	2.0	43
13	A transposable element insertion in the susceptibility gene CsaMLO8 results in hypocotyl resistance to powdery mildew in cucumber. BMC Plant Biology, 2015, 15, 243.	1.6	104
15	QTL mapping of cucumber fruit flesh thickness by SLAF-seq. Scientific Reports, 2015, 5, 15829.	1.6	70
16	Bitter but tasty cucumber. National Science Review, 2015, 2, 129-130.	4.6	2
17	Transgenic cucumber lines expressing the chimeric <sc>pGT</sc>::<i>Dhn24</i> gene do not show enhanced chilling tolerance in phytotron conditions. Plant Breeding, 2015, 134, 468-476.	1.0	3
18	Development of genomewide simple sequence repeat fingerprints and highly polymorphic markers in cucumbers based on next-generation sequence data. Plant Breeding, 2015, 134, 605-611.	1.0	10
19	Genome-Wide Identification, Characterization and Evolutionary Analysis of Long Intergenic Noncoding RNAs in Cucumber. PLoS ONE, 2015, 10, e0121800.	1.1	98

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20	High-Throughput Sequencing Identifies Novel and Conserved Cucumber (<i>Cucumis sativus</i> L.) microRNAs in Response to Cucumber Green Mottle Mosaic Virus Infection. <i>PLoS ONE</i> , 2015, 10, e0129002.	1.1	26
21	Loss-of-Function Mutations in <i>CsMLO1</i> Confer Durable Powdery Mildew Resistance in Cucumber (<i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1155.	1.7	65
22	Taxonomy and Genetic Differentiation among Wild and Cultivated Germplasm of <i>Solanum</i> sect. <i>Petota</i> . <i>Plant Genome</i> , 2015, 8, eplantgenome2014.06.0025.	1.6	52
23	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. <i>Plant Cell</i> , 2015, 27, 1595-1604.	3.1	125
24	A Sequencing-Based Linkage Map of Cucumber. <i>Molecular Plant</i> , 2015, 8, 961-963.	3.9	28
25	Epidemiology and Population Biology of <i>Pseudoperonospora cubensis</i> : A Model System for Management of Downy Mildews. <i>Annual Review of Phytopathology</i> , 2015, 53, 223-246.	3.5	84
26	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
27	Differential proteomic analysis of dwarf characteristics in cucumber (<i>Cucumis sativus</i> Linn.) stems. <i>Acta Physiologiae Plantarum</i> , 2015, 37, 1.	1.0	3
28	Patterns of genomic changes with crop domestication and breeding. <i>Current Opinion in Plant Biology</i> , 2015, 24, 47-53.	3.5	83
29	Molecular mapping and candidate gene analysis for yellow fruit flesh in cucumber. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	36
30	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. <i>Nature Biotechnology</i> , 2015, 33, 408-414.	9.4	1,023
31	Identification and fine mapping of <i>pm5.1</i> : a recessive gene for powdery mildew resistance in cucumber (<i>Cucumis sativus</i> L.). <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	46
32	QTL mapping in multiple populations and development stages reveals dynamic quantitative trait loci for fruit size in cucumbers of different market classes. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1747-1763.	1.8	128
33	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2760-2774.	3.5	80
34	Resurgence of Cucurbit Downy Mildew in the United States: A Watershed Event for Research and Extension. <i>Plant Disease</i> , 2015, 99, 428-441.	0.7	117
35	Sequencing consolidates molecular markers with plant breeding practice. <i>Theoretical and Applied Genetics</i> , 2015, 128, 779-795.	1.8	96
36	An <i>ACCUMULATION AND REPLICATION OF CHLOROPLASTS 5</i> gene mutation confers light green peel in cucumber. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 936-942.	4.1	53
37	Genetic diversity and evolutionary relationship analyses within and among <i>Raphanus</i> species using EST-SSR markers. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	26

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38	Transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2015, 5, 8031.	1.6	89
39	Genetic analysis and gene mapping of papaya ring spot virus resistance in cucumber. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	22
40	Fine genetic mapping of target leaf spot resistance gene <i>cca-3</i> in cucumber, <i>Cucumis sativus</i> L.. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2495-2506.	1.8	38
41	A Rare SNP Identified a TCP Transcription Factor Essential for Tendril Development in Cucumber. <i>Molecular Plant</i> , 2015, 8, 1795-1808.	3.9	58
42	Combining niche modelling and landscape genetics to study local adaptation: A novel approach illustrated using alpine plants. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2015, 17, 491-499.	1.1	13
43	Genomics and the Contrasting Dynamics of Annual and Perennial Domestication. <i>Trends in Genetics</i> , 2015, 31, 709-719.	2.9	145
44	Phylogeography of Chinese cherry (<i>Prunus pseudocerasus</i> Lindl.) inferred from chloroplast and nuclear DNA: insights into evolutionary patterns and demographic history. <i>Plant Biology</i> , 2015, 17, 787-797.	1.8	17
45	Molecular mapping reveals structural rearrangements and quantitative trait loci underlying traits with local adaptation in semi-wild Xishuangbanna cucumber (<i>Cucumis sativus</i> L. var.) Tj ETQq1 1 0.784314 rgBT / Overlock 10.1155/2015/457	1.0	1
46	Genome-wide identification and evolutionary analysis of positively selected miRNA genes in domesticated rice. <i>Molecular Genetics and Genomics</i> , 2015, 290, 593-602.	1.0	13
47	Hierarchical Map of Orthologous Genomic Regions Reconstructed from Two Closely Related Genomes: Cucumber Case Study. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0099.	1.6	1
48	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. <i>PLoS Genetics</i> , 2016, 12, e1006433.	1.5	136
49	Genome-Wide Association Study Provides Insight into the Genetic Control of Plant Height in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1102.	1.7	49
50	A Detailed Analysis of the BR1 Locus Suggests a New Mechanism for Bolting after Winter in Sugar Beet (<i>Beta vulgaris</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1662.	1.7	26
51	Coverage recommendation for genotyping analysis of highly heterologous species using next-generation sequencing technology. <i>Scientific Reports</i> , 2016, 6, 35736.	1.6	46
52	Identification and characterisation of Dof transcription factors in the cucumber genome. <i>Scientific Reports</i> , 2016, 6, 23072.	1.6	73
53	Landscape and Fruit Developmental Regulation of Alternative Splicing in Tomato by Genome-Wide Analysis. <i>Horticultural Plant Journal</i> , 2016, 2, 338-350.	2.3	11
54	The Cucumber Genome. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 183-197.	0.3	5
55	Databases and Bioinformatics for Cucurbit Species. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 253-267.	0.3	2

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58	Genetic Resources of Cucumber. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 61-86.	0.3	12
59	The Melon Genome. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 173-181.	0.3	3
60	Genomic Analysis of Cucurbit Fruit Growth. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 321-344.	0.3	7
61	Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. <i>Journal of Experimental Botany</i> , 2017, 68, erw433.	2.4	118
62	Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants (<i>Cucumis sativus</i>). <i>Plant Physiology</i> , 2016, 172, 603-618.	2.3	99
63	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. <i>Plant Physiology</i> , 2016, 172, pp.00501.2016.	2.3	22
64	How the truffle got its mate: insights from genetic structure in spontaneous and planted Mediterranean populations of <i>Tuber melanosporum</i> . <i>Molecular Ecology</i> , 2016, 25, 5611-5627.	2.0	44
65	Genetic analysis and fine mapping of Watermelon mosaic virus resistance gene in cucumber. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	21
66	CsSNP: A Web-Based Tool for the Detecting of Comparative Segments SNPs. <i>Journal of Computational Biology</i> , 2016, 23, 597-602.	0.8	0
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70	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. <i>BMC Genomics</i> , 2016, 17, 110.	1.2	43
71	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. <i>Plant Science</i> , 2016, 242, 47-64.	1.7	60
72	A proposed regulatory framework for genome-edited crops. <i>Nature Genetics</i> , 2016, 48, 109-111.	9.4	184
73	Phloem transcriptome signatures underpin the physiological differentiation of the pedicel, stalk and fruit of cucumber (<i>Cucumis sativus</i> L.). <i>Plant and Cell Physiology</i> , 2016, 57, 19-34.	1.5	27

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75	A Truncated F-Box Protein Confers the Dwarfism in Cucumber. <i>Journal of Genetics and Genomics</i> , 2016, 43, 223-226.	1.7	27
76	Integrated analysis in bi-parental and natural populations reveals CsCLAVATA3 (CsCLV3) underlying carpel number variations in cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1007-1022.	1.8	43
77	Map-based cloning, identification and characterization of the w gene controlling white immature fruit color in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2016, 129, 1247-1256.	1.8	87
78	Databases for Solanaceae and Cucurbitaceae Research. <i>Biotechnology in Agriculture and Forestry</i> , 2016, , 31-42.	0.2	1
79	DNA Markers in Cucurbitaceae Breeding. <i>Biotechnology in Agriculture and Forestry</i> , 2016, , 59-74.	0.2	1
80	The complete chloroplast genome sequence of <i>Cucumis sativus</i> var. <i>Hardwickii</i> , the wild progenitor of cultivated cucumber. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4627-4628.	0.7	8
81	The complete chloroplast genome sequence of wild cucumber (<i>Cucumis sativus</i> var. <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>) 4524-4525.	0.7	3
82	Next generation sequencing and omics in cucumber (<i>Cucumis sativus</i> L.) breeding directed research. <i>Plant Science</i> , 2016, 242, 77-88.	1.7	35
83	Genomics of crop wild relatives: expanding the gene pool for crop improvement. <i>Plant Biotechnology Journal</i> , 2016, 14, 1070-1085.	4.1	303
84	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. <i>Nature Genetics</i> , 2017, 49, 765-772.	9.4	316
85	Domestication rewired gene expression and nucleotide diversity patterns in tomato. <i>Plant Journal</i> , 2017, 91, 631-645.	2.8	34
86	The association of changes in DNA methylation with temperature-dependent sex determination in cucumber. <i>Journal of Experimental Botany</i> , 2017, 68, 2899-2912.	2.4	53
87	Variation in cucumber (<i>Cucumis sativus</i> L.) fruit size and shape results from multiple components acting pre-anthesis and post-pollination. <i>Planta</i> , 2017, 246, 641-658.	1.6	53
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90	Quantitative trait loci analysis of melon (<i>Cucumis melo</i> L.) domestication-related traits. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1837-1856.	1.8	37
91	Genome-wide sequence variations between wild and cultivated tomato species revisited by whole genome sequence mapping. <i>BMC Genomics</i> , 2017, 18, 430.	1.2	24

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92	Transcriptomic and metabolomic analyses of cucumber fruit peels reveal a developmental increase in terpenoid glycosides associated with age-related resistance to <i>Phytophthora capsici</i> . <i>Horticulture Research</i> , 2017, 4, 17022.	2.9	54
93	Footprints of domestication revealed by RAD-tag resequencing in loquat: SNP data reveals a non-significant domestication bottleneck and a single domestication event. <i>BMC Genomics</i> , 2017, 18, 354.	1.2	13
94	Comparative Genomics of the Cucurbitaceae. <i>Plant Genetics and Genomics: Crops and Models</i> , 2017, , 229-240.	0.3	3
95	Genome diversity of tuber-bearing <i>Solanum</i> uncovers complex evolutionary history and targets of domestication in the cultivated potato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9999-E10008.	3.3	271
96	Genetics and Genomics of Cucurbitaceae. <i>Plant Genetics and Genomics: Crops and Models</i> , 2017, , .	0.3	22
97	A high-density linkage map and QTL mapping of fruit-related traits in pumpkin (<i>Cucurbita moschata</i>) Tj ETQq1 1 0.784314 rgBT /Over 1.6 55	1.6	55
98	The Genetics and Genomics of Plant Domestication. <i>BioScience</i> , 2017, 67, 971-982.	2.2	83
99	A genome-wide survey with different rapeseed ecotypes uncovers footprints of domestication and breeding. <i>Journal of Experimental Botany</i> , 2017, 68, 4791-4801.	2.4	52
100	Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. <i>Plant Physiology</i> , 2017, 175, 786-801.	2.3	98
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102	Genome-wide analysis of microRNA targeting impacted by SNPs in cucumber genome. <i>BMC Genomics</i> , 2017, 18, 275.	1.2	12
103	Functional characterization of cucumber (<i>Cucumis sativus</i> L.) Clade V MLO genes. <i>BMC Plant Biology</i> , 2017, 17, 80.	1.6	29
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108	Genome-wide association study identified genetic variations and candidate genes for plant architecture component traits in Chinese upland cotton. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1299-1314.	1.8	62
109	Multiple R genes and phenolic compounds synthesis involved in the durable resistance to <i>Phytophthora infestans</i> in potato cv. Cooperation 88. <i>Agri Gene</i> , 2018, 8, 28-36.	1.9	6
110	Long distance <i>scp</i> RNA movement. <i>New Phytologist</i> , 2018, 218, 29-40.	3.5	137

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111	Genetic mapping reveals a candidate gene (ClFS1) for fruit shape in watermelon (<i>Citrullus lanatus</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 947-958.	1.8	94
112	Development of Bi gene-based SNP markers for genotyping for bitter-free cucumber lines. <i>Horticulture Environment and Biotechnology</i> , 2018, 59, 231-238.	0.7	4
113	Development of cost-effective single nucleotide polymorphism marker assays for genetic diversity analysis in <i>Brassica rapa</i> . <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	21
114	Exploiting natural variation for accelerating discoveries in plant specialized metabolism. <i>Phytochemistry Reviews</i> , 2018, 17, 17-36.	3.1	9
115	Transcriptome Comparison Reveals Distinct Selection Patterns in Domesticated and Wild Agave Species, the Important CAM Plants. <i>International Journal of Genomics</i> , 2018, 2018, 1-12.	0.8	29
116	Temperature and photoperiod changes affect cucumber sex expression by different epigenetic regulations. <i>BMC Plant Biology</i> , 2018, 18, 268.	1.6	35
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118	Genetic mapping of psl locus and quantitative trait loci for angular leaf spot resistance in cucumber (<i>Cucumis sativus</i> L.). <i>Molecular Breeding</i> , 2018, 38, 111.	1.0	13
119	Genetic analysis and identification of a candidate gene associated with in vitro regeneration ability of cucumber. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2663-2675.	1.8	11
120	Genetic mapping reveals a marker for yellow skin in watermelon (<i>Citrullus lanatus</i> L.). <i>PLoS ONE</i> , 2018, 13, e0200617.	1.1	47
121	Construction of A High-Density Genetic Map and Mapping of Fruit Traits in Watermelon (<i>Citrullus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 19, 3268.	1.8	43
122	The USDA cucumber (<i>Cucumis sativus</i> L.) collection: genetic diversity, population structure, genome-wide association studies, and core collection development. <i>Horticulture Research</i> , 2018, 5, 64.	2.9	102
123	Carotenoid Accumulation and Its Contribution to Flower Coloration of <i>Osmanthus fragrans</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1499.	1.7	43
124	Unraveling the Roles of Regulatory Genes during Domestication of Cultivated <i>Camellia</i> : Evidence and Insights from Comparative and Evolutionary Genomics. <i>Genes</i> , 2018, 9, 488.	1.0	11
125	DNA methylation footprints during soybean domestication and improvement. <i>Genome Biology</i> , 2018, 19, 128.	3.8	61
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127	The evolutionary road from wild moth to domestic silkworm. <i>Nature Ecology and Evolution</i> , 2018, 2, 1268-1279.	3.4	112
128	Signatures of Selection in the Genomes of Chinese Chestnut (<i>Castanea mollissima</i> Blume): The Roots of Nut Tree Domestication. <i>Frontiers in Plant Science</i> , 2018, 9, 810.	1.7	18

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130	Genome-Wide Identification and Expression Analyses of the Fibrillin Family Genes Suggest Their Involvement in Photoprotection in Cucumber. <i>Plants</i> , 2018, 7, 50.	1.6	6
131	Genome of Wild Mandarin and Domestication History of Mandarin. <i>Molecular Plant</i> , 2018, 11, 1024-1037.	3.9	130
132	Genetic analysis and QTL mapping of fruit-related traits in wax gourd (<i>Benincasa hispida</i>). <i>Euphytica</i> , 2018, 214, 1.	0.6	13
133	Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. <i>Nature Genetics</i> , 2018, 50, 796-802.	9.4	401
134	Genomics of Cucurbits. , 2018, , 413-432.		5
135	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 433-456.	3.8	143
136	<i>LITTLELEAF</i> (<i>LL</i>) encodes a WD40 repeat domain-containing protein associated with organ size variation in cucumber. <i>Plant Journal</i> , 2018, 95, 834-847.	2.8	58
137	The Evolutionary Consequences of Transposon-Related Pericentromer Expansion in Melon. <i>Genome Biology and Evolution</i> , 2018, 10, 1584-1595.	1.1	20
138	Identification of QTLs controlling low-temperature tolerance during the germination stage in cucumber (<i>Cucumis sativus</i> L.). <i>Plant Breeding</i> , 2018, 137, 629-637.	1.0	16
139	STAYGREEN, STAY HEALTHY: a loss-of-susceptibility mutation in the <i>STAYGREEN</i> gene provides durable, broad-spectrum disease resistances for over 50 years of US cucumber production. <i>New Phytologist</i> , 2019, 221, 415-430.	3.5	72
140	CsBRC1 inhibits axillary bud outgrowth by directly repressing the auxin efflux carrier <i>CsPIN3</i> in cucumber. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17105-17114.	3.3	91
141	Genome-wide association analysis of nutrient traits in the oyster <i>Crassostrea gigas</i> : genetic effect and interaction network. <i>BMC Genomics</i> , 2019, 20, 625.	1.2	31
142	Genome Resequencing Reveals Congenital Causes of Embryo and Nestling Death in Crested Ibis (<i>Nipponia nippon</i>). <i>Genome Biology and Evolution</i> , 2019, 11, 2125-2135.	1.1	4
143	Combination of multi-locus genome-wide association study and QTL mapping reveals genetic basis of tassel architecture in maize. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1421-1440.	1.0	12
144	Two types of mutations in the HEUKCHEEM gene functioning in cucumber spine color development can be used as signatures for cucumber domestication. <i>Planta</i> , 2019, 250, 1491-1504.	1.6	7
145	Genetic Diversity in Horticultural Plants. <i>Sustainable Development and Biodiversity</i> , 2019, , .	1.4	2
147	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. <i>Nature Genetics</i> , 2019, 51, 1607-1615.	9.4	153

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148	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. <i>Nature Communications</i> , 2019, 10, 5158.	5.8	94
149	Natural Variation and Domestication Selection of ZmPGP1 Affects Plant Architecture and Yield-Related Traits in Maize. <i>Genes</i> , 2019, 10, 664.	1.0	21
150	Whole-Genome Resequencing of Seven Eggplant (<i>Solanum melongena</i>) and One Wild Relative (<i>S. Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>) in <i>Plant Science</i> , 2019, 10, 1220.	1.7	46
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152	A chromosome-scale genome assembly of cucumber (<i>Cucumis sativus</i> L.). <i>GigaScience</i> , 2019, 8, .	3.3	138
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253	A mutation in <i>CsHY2</i> encoding a phytochromobilin (P ₁ B) synthase leads to an elongated hypocotyl 1(<i>elh1</i>) phenotype in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2639-2652.	1.8	8
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304	Molecular Research Progress on Xishuangbanna Cucumber (<i>Cucumis sativus</i> L. var. <i>Xishuangbannensis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.3	10
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