

The *Brassica oleracea* genome reveals the asymmetrical

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Complex Recombination Pattern in the Genome of Allotetraploid <i>Brassica napus</i> as Revealed by a High-Density Genetic Map. <i>PLoS ONE</i> , 2014, 9, e109910.	2.5	41
2	Functional Analysis of the <i>Brassica napus</i> L. Phytoene Synthase (PSY) Gene Family. <i>PLoS ONE</i> , 2014, 9, e114878.	2.5	26
3	Identification of three FLOWERING LOCUS C genes responsible for vernalization response in radish (<i>Raphanus sativus</i> L.). <i>Horticulture Environment and Biotechnology</i> , 2014, 55, 548-556.	2.1	22
4	Integration of a constraint-based metabolic model of <i>Brassica napus</i> developing seeds with ¹³ C-metabolic flux analysis. <i>Frontiers in Plant Science</i> , 2014, 5, 724.	3.6	32
5	Neofunctionalization of Duplicated <i>Tic40</i> Genes Caused a Gain-of-Function Variation Related to Male Fertility in <i>Brassica oleracea</i> Lineages. <i>Plant Physiology</i> , 2014, 166, 1403-1419.	4.8	17
6	Quantitative trait loci analyses for resistance to <i>Sclerotinia sclerotiorum</i> and flowering time in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2014, 34, 1797-1804.	2.1	84
7	Mapping and analysis of a novel candidate <i>Fusarium</i> wilt resistance gene FOC1 in <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2014, 15, 1094.	2.8	74
8	A high-throughput SNP array in the amphidiploid species <i>Brassica napus</i> shows diversity in resistance genes. <i>Functional and Integrative Genomics</i> , 2014, 14, 643-655.	3.5	43
9	Analysis of global gene expression profiles to identify differentially expressed genes critical for embryo development in <i>Brassica rapa</i> . <i>Plant Molecular Biology</i> , 2014, 86, 425-442.	3.9	18
10	<i>BrassicaTED</i> - a public database for utilization of miniature transposable elements in <i>Brassica</i> species. <i>BMC Research Notes</i> , 2014, 7, 379.	1.4	18
11	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
12	Polyploid Evolution of the Brassicaceae during the Cenozoic Era. <i>Plant Cell</i> , 2014, 26, 2777-2791.	6.6	165
13	Genome triplication drove the diversification of <i>Brassica</i> plants. <i>Horticulture Research</i> , 2014, 1, 14024.	6.3	288
14	Comparative miRNAs analysis of Two contrasting broccoli inbred lines with divergent head-forming capacity under temperature stress. <i>BMC Genomics</i> , 2015, 16, 1026.	2.8	22
15	Genome expansion of <i>Arabidopsis thaliana</i> linked with retrotransposition and reduced symmetric DNA methylation. <i>Nature Plants</i> , 2015, 1, 14023.	9.3	156
16	Linkage and regional association analysis reveal two new tightly-linked major-QTLs for pod number and seed number per pod in rapeseed (<i>Brassica napus</i> L.). <i>Scientific Reports</i> , 2015, 5, 14481.	3.3	79
17	The power of single molecule real-time sequencing technology in the de novo assembly of a eukaryotic genome. <i>Scientific Reports</i> , 2015, 5, 16780.	3.3	73
18	Comparative quantitative trait loci for silique length and seed weight in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2015, 5, 14407.	3.3	65

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19	Diversification and evolution of the SDG gene family in <i>Brassica rapa</i> after the whole genome triplication. <i>Scientific Reports</i> , 2015, 5, 16851.	3.3	9
20	Species-wide genome sequence and nucleotide polymorphisms from the model allopolyploid plant <i>Brassica napus</i> . <i>Scientific Data</i> , 2015, 2, 150072.	5.3	79
21	Generation and characterization of <i>Brassica rapa</i> ssp. <i>pekinensis</i> "B. oleracea var. capitata monosomic and disomic alien addition lines. <i>Journal of Genetics</i> , 2015, 94, 435-444.	0.7	4
22	PTGBase: an integrated database to study tandem duplicated genes in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	46
23	<i>Brassica</i> database (BRAD) version 2.0: integrating and mining Brassicaceae species genomic resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav093.	3.0	58
24	Identification and Expression Analysis of Glucosinolate Biosynthetic Genes and Estimation of Glucosinolate Contents in Edible Organs of <i>Brassica oleracea</i> Subspecies. <i>Molecules</i> , 2015, 20, 13089-13111.	3.8	61
25	Improving the Annotation of <i>Arabidopsis lyrata</i> Using RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0137391.	2.5	82
26	Recent progress in the use of "omics technologies in brassicaceous vegetables. <i>Frontiers in Plant Science</i> , 2015, 6, 244.	3.6	30
27	Genome-wide gene expression perturbation induced by loss of C2 chromosome in allotetraploid <i>Brassica napus</i> L.. <i>Frontiers in Plant Science</i> , 2015, 6, 763.	3.6	27
28	Comparative genomic analysis of duplicated homoeologous regions involved in the resistance of <i>Brassica napus</i> to stem canker. <i>Frontiers in Plant Science</i> , 2015, 6, 772.	3.6	38
29	Genome-wide DNA methylation profiling by modified reduced representation bisulfite sequencing in <i>Brassica rapa</i> suggests that epigenetic modifications play a key role in polyploid genome evolution. <i>Frontiers in Plant Science</i> , 2015, 6, 836.	3.6	52
30	Molecular evolution, characterization, and expression analysis of SnRK2 gene family in Pak-choi (<i>Brassica rapa</i> ssp. <i>chinensis</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 879.	3.6	29
31	Genome-specific differential gene expressions in resynthesized <i>Brassica</i> allotetraploids from pair-wise crosses of three cultivated diploids revealed by RNA-seq. <i>Frontiers in Plant Science</i> , 2015, 6, 957.	3.6	31
32	Genotyping-by-sequencing map permits identification of clubroot resistance QTLs and revision of the reference genome assembly in cabbage (<i>Brassica oleracea</i> L.). <i>DNA Research</i> , 2016, 23, dsv034.	3.4	94
33	Three genes encoding AOP2, a protein involved in aliphatic glucosinolate biosynthesis, are differentially expressed in <i>Brassica rapa</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 6205-6218.	4.8	29
34	Transfer of sclerotinia stem rot resistance from wild <i>Brassica oleracea</i> into <i>B. rapa</i> . <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	12
35	Generation and characterization of tribenuron-methyl herbicide-resistant rapeseed (<i>Brassica napus</i>) for hybrid seed production using chemically induced male sterility. <i>Theoretical and Applied Genetics</i> , 2015, 128, 107-118.	3.6	41
36	Susceptibility to <i>Verticillium longisporum</i> is linked to monoterpene production by TPS23/27 in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 81, 572-585.	5.7	19

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37	Disruption of a <i>CAROTENOID CLEAVAGE DIOXYGENASE</i> gene converts flower colour from white to yellow in <i>Brassica</i> species. <i>New Phytologist</i> , 2015, 206, 1513-1526.	7.3	155
38	Nanoparticle-Mediated Expression of a Wnt Pathway Inhibitor Ameliorates Ocular Neovascularization. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 855-864.	2.4	32
39	Lineage-specific evolution of Methylthioalkylmalate synthases (MAMs) involved in glucosinolates biosynthesis. <i>Frontiers in Plant Science</i> , 2015, 6, 18.	3.6	18
40	Association mapping of seed quality traits in <i>Brassica napus</i> L. using GWAS and candidate QTL approaches. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	51
41	Sequencing of allotetraploid cotton (<i>Gossypium hirsutum</i> L. acc. TM-1) provides a resource for fiber improvement. <i>Nature Biotechnology</i> , 2015, 33, 531-537.	17.5	1,560
42	Development of genic cleavage markers in association with seed glucosinolate content in canola. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1029-1037.	3.6	14
43	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in <i>Cicer arietinum</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1039-1047.	3.6	76
44	Dynamic and comparative QTL analysis for plant height in different developmental stages of <i>Brassica napus</i> L. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1175-1192.	3.6	56
45	New insights into the genetic networks affecting seed fatty acid concentrations in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2015, 15, 91.	3.6	73
46	Mapping QTLs of resistance to head splitting in cabbage (<i>Brassica oleracea</i> L.var. capitata L.). <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	11
47	Identification and expression analysis of BoMF25, a novel polygalacturonase gene involved in pollen development of <i>Brassica oleracea</i> . <i>Plant Reproduction</i> , 2015, 28, 121-132.	2.2	9
48	Genome-wide identification of aquaporin encoding genes in <i>Brassica oleracea</i> and their phylogenetic sequence comparison to <i>Brassica</i> crops and <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 166.	3.6	51
49	A draft genome of field pennycress (<i>Thlaspi arvense</i>) provides tools for the domestication of a new winter biofuel crop. <i>DNA Research</i> , 2015, 22, 121-131.	3.4	86
50	Beyond the thale: comparative genomics and genetics of <i>Arabidopsis</i> relatives. <i>Nature Reviews Genetics</i> , 2015, 16, 285-298.	16.3	84
51	Polyploidy and Plant Breeding. , 2015, , 201-223.		0
52	DNA Sequencing, Other Omics and Synthetic Biology. , 2015, , 125-140.		0
53	Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7241-7253.	4.8	44
54	BnaC9.SMG7b functions as a positive regulator of number of seeds per silique in rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314 rgBT /Overbo pp.01040.2015.	4.8	70

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55	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. BMC Plant Biology, 2015, 15, 32.	3.6	63
56	Widespread and evolutionary analysis of a MITE family Monkey King in Brassicaceae. BMC Plant Biology, 2015, 15, 149.	3.6	9
57	A bi-filtering method for processing single nucleotide polymorphism array data improves the quality of genetic map and accuracy of quantitative trait locus mapping in doubled haploid populations of polyploid Brassica napus. BMC Genomics, 2015, 16, 409.	2.8	27
58	Miniature Transposable Elements (mTEs): Impacts and Uses in the Brassica Genome. Compendium of Plant Genomes, 2015, , 65-81.	0.5	3
59	Comparative Analysis of Gene Conversion Between Duplicated Regions in Brassica rapa and B. oleracea Genomes. Compendium of Plant Genomes, 2015, , 121-129.	0.5	3
60	Genomics-Assisted Breeding. , 2015, , 145-173.		1
61	Sequence and expression variation in SUPPRESSOR of OVEREXPRESSION of CONSTANS 1 (SOC1): homeolog evolution in Indian Brassicas. Development Genes and Evolution, 2015, 225, 287-303.	0.9	14
62	Genome-wide identification and Phylogenic analysis of kelch motif containing ACBP in Brassica napus. BMC Genomics, 2015, 16, 512.	2.8	26
63	Inheritance and InDel markers closely linked to petal color gene (cpc-1) in Brassica oleracea. Molecular Breeding, 2015, 35, 1.	2.1	30
65	The gap in research on polyploidization between plants and vertebrates: model systems and strategic challenges. Science Bulletin, 2015, 60, 1471-1478.	9.0	4
66	Identification, characterization and diversification of non-autonomous hAT transposons and unknown insertions in Brassica. Genes and Genomics, 2015, 37, 945-958.	1.4	6
67	Novel glucosinolate composition lacking 4-methylthio-3-butenyl glucosinolate in Japanese white radish (Raphanus sativus L.). Theoretical and Applied Genetics, 2015, 128, 2037-2046.	3.6	20
68	Genome-wide identification and comparative expression analysis reveal a rapid expansion and functional divergence of duplicated genes in the WRKY gene family of cabbage, Brassica oleracea var. capitata. Gene, 2015, 557, 35-42.	2.2	51
69	Reverse Genetics and High Throughput Sequencing Methodologies for Plant Functional Genomics. Current Genomics, 2016, 17, 460-475.	1.6	27
70	Genome-Wide Identification and Characterization of bZIP Transcription Factors in Brassica oleracea under Cold Stress. BioMed Research International, 2016, 2016, 1-18.	1.9	20
71	Molecular and Genomic Tools Provide Insights on Crop Domestication and Evolution. Advances in Agronomy, 2016, 135, 181-223.	5.2	4
72	Glutathione Transferases Superfamily: Cold-Inducible Expression of Distinct GST Genes in Brassica oleracea. International Journal of Molecular Sciences, 2016, 17, 1211.	4.1	47
73	Transcriptome and Metabolome Analyses of Glucosinolates in Two Broccoli Cultivars Following Jasmonate Treatment for the Induction of Glucosinolate Defense to Trichoplusia ni (H ₄ Bner). International Journal of Molecular Sciences, 2016, 17, 1135.	4.1	30

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74	Exogenous Methyl Jasmonate and Salicylic Acid Induce Subspecies-Specific Patterns of Glucosinolate Accumulation and Gene Expression in <i>Brassica oleracea</i> L.. <i>Molecules</i> , 2016, 21, 1417.	3.8	54
75	Evaluation of Linkage Disequilibrium Pattern and Association Study on Seed Oil Content in <i>Brassica napus</i> Using ddRAD Sequencing. <i>PLoS ONE</i> , 2016, 11, e0146383.	2.5	63
76	Transcriptome Profiling of Resistance to <i>Fusarium oxysporum</i> f. sp. <i>conglutinans</i> in Cabbage (<i>Brassica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.5	36
77	Genome-Wide Identification of QTL for Seed Yield and Yield-Related Traits and Construction of a High-Density Consensus Map for QTL Comparison in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 17.	3.6	80
78	Characterizing Variation of Branch Angle and Genome-Wide Association Mapping in Rapeseed (<i>Brassica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	44
79	De novo Transcriptome Analysis of <i>Sinapis alba</i> in Revealing the Glucosinolate and Phytochelatin Pathways. <i>Frontiers in Plant Science</i> , 2016, 7, 259.	3.6	19
80	Comparative Leaves Transcriptome Analysis Emphasizing on Accumulation of Anthocyanins in <i>Brassica</i> : Molecular Regulation and Potential Interaction with Photosynthesis. <i>Frontiers in Plant Science</i> , 2016, 7, 311.	3.6	63
81	Influence of Light and Temperature on Gene Expression Leading to Accumulation of Specific Flavonol Glycosides and Hydroxycinnamic Acid Derivatives in Kale (<i>Brassica oleracea</i> var. <i>sabellica</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 326.	3.6	61
82	Genome-Wide Single-Nucleotide Polymorphisms Discovery and High-Density Genetic Map Construction in Cauliflower Using Specific-Locus Amplified Fragment Sequencing. <i>Frontiers in Plant Science</i> , 2016, 7, 334.	3.6	49
83	Conservation and Expression Patterns Divergence of Ascorbic Acid d-mannose/l-galactose Pathway Genes in <i>Brassica rapa</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 778.	3.6	14
84	Whole-Genome Mapping Reveals Novel QTL Clusters Associated with Main Agronomic Traits of Cabbage (<i>Brassica oleracea</i> var. <i>capitata</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 989.	3.6	48
85	Multigenic Control of Pod Shattering Resistance in Chinese Rapeseed Germplasm Revealed by Genome-Wide Association and Linkage Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 1058.	3.6	25
86	Origination, Expansion, Evolutionary Trajectory, and Expression Bias of AP2/ERF Superfamily in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1186.	3.6	36
87	Vacuolar Iron Transporter BnMEB2 Is Involved in Enhancing Iron Tolerance of <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1353.	3.6	25
88	Genome-Wide Gene/Genome Dosage Imbalance Regulates Gene Expressions in Synthetic <i>Brassica napus</i> and Derivatives (AC, AAC, CCA, CCAA). <i>Frontiers in Plant Science</i> , 2016, 7, 1432.	3.6	25
89	Genome-Wide Analysis and Expression Profiling of the SUC and SWEET Gene Families of Sucrose Transporters in Oilseed Rape (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1464.	3.6	80
90	A Genome-Wide Association Study Reveals New Loci for Resistance to Clubroot Disease in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1483.	3.6	74
91	Fire and Brimstone: Molecular Interactions between Sulfur and Glucosinolate Biosynthesis in Model and Crop Brassicaceae. <i>Frontiers in Plant Science</i> , 2016, 7, 1735.	3.6	35

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92	Single R Gene Introgression Lines for Accurate Dissection of the Brassica - Leptosphaeria Pathosystem. <i>Frontiers in Plant Science</i> , 2016, 7, 1771.	3.6	69
93	Genome-Wide Identification, Localization, and Expression Analysis of Proanthocyanidin-Associated Genes in Brassica. <i>Frontiers in Plant Science</i> , 2016, 7, 1831.	3.6	14
94	Expression Profiling of Glucosinolate Biosynthetic Genes in Brassica oleracea L. var. capitata Inbred Lines Reveals Their Association with Glucosinolate Content. <i>Molecules</i> , 2016, 21, 787.	3.8	37
95	Identification of a novel MLPK homologous gene MLPKn1 and its expression analysis in Brassica oleracea. <i>Plant Reproduction</i> , 2016, 29, 239-250.	2.2	11
96	Identification of Polymorphisms Associated with Drought Adaptation QTL in <i>Brassica napus</i> by Resequencing. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 793-803.	1.8	39
97	SHORT HYPOCOTYL UNDER BLUE 1 or HAIKU 2 mixexpression alters canola and Arabidopsis seed development. <i>New Phytologist</i> , 2016, 209, 636-649.	7.3	15
98	Comparative mitochondrial genome analysis reveals the evolutionary rearrangement mechanism in <i>Brassica</i> . <i>Plant Biology</i> , 2016, 18, 527-536.	3.8	35
99	Narrowing down the single homoeologous <i>FaPFRU</i> locus controlling flowering in cultivated octoploid strawberry using a selective mapping strategy. <i>Plant Biotechnology Journal</i> , 2016, 14, 2176-2189.	8.3	48
100	Increased diversification rates follow shifts to bisexuality in liverworts. <i>New Phytologist</i> , 2016, 210, 1121-1129.	7.3	34
101	Oilseed rape: learning about ancient and recent polyploid evolution from a recent crop species. <i>Plant Biology</i> , 2016, 18, 883-892.	3.8	46
102	Multi-environment QTL studies suggest a role for cysteine-rich protein kinase genes in quantitative resistance to blackleg disease in Brassica napus. <i>BMC Plant Biology</i> , 2016, 16, 183.	3.6	81
103	Quantitative genetic analysis of grain yield in an Australian Brassica napus doubled-haploid population. <i>Crop and Pasture Science</i> , 2016, 67, 298.	1.5	42
104	Global DNA methylation variations after short-term heat shock treatment in cultured microspores of Brassica napus cv. Topas. <i>Scientific Reports</i> , 2016, 6, 38401.	3.3	58
105	Can genomics assist the phenological adaptation of canola to new and changing environments?. <i>Crop and Pasture Science</i> , 2016, 67, 284.	1.5	17
106	Genome resequencing and comparative variome analysis in a Brassica rapa and Brassica oleracea collection. <i>Scientific Data</i> , 2016, 3, 160119.	5.3	57
107	Characterization of a recently evolved flavonol-phenylacyltransferase gene provides signatures of natural light selection in Brassicaceae. <i>Nature Communications</i> , 2016, 7, 12399.	12.8	145
108	Interspecific hybridization, polyploidization and backcross of Brassica oleracea var. alboglabra with B. rapa var. purpurea morphologically recapitulate the evolution of Brassica vegetables. <i>Scientific Reports</i> , 2016, 6, 18618.	3.3	33
109	Biofortification of oilseed Brassica juncea with the anti-cancer compound glucoraphanin by suppressing GSL-ALK gene family. <i>Scientific Reports</i> , 2016, 5, 18005.	3.3	72

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110	Turnip Time Travels: Age Estimates in Brassicaceae. Trends in Plant Science, 2016, 21, 554-561.	8.8	36
111	Elucidating the triplicated ancestral genome structure of radish based on chromosome-level comparison with the Brassica genomes. Theoretical and Applied Genetics, 2016, 129, 1357-1372.	3.6	110
112	<i>MS5</i> Mediates Early Meiotic Progression and Its Natural Variants May Have Applications for Hybrid Production in <i>Brassica napus</i> . Plant Cell, 2016, 28, 1263-1278.	6.6	26
113	Genome of Plant Maca (<i>Lepidium meyenii</i>) Illuminates Genomic Basis for High-Altitude Adaptation in the Central Andes. Molecular Plant, 2016, 9, 1066-1077.	8.3	69
114	High-throughput multiplex cpDNA resequencing clarifies the genetic diversity and genetic relationships among <i>Brassica napus</i> , <i>Brassica rapa</i> and <i>Brassica oleracea</i> . Plant Biotechnology Journal, 2016, 14, 409-418.	8.3	30
115	Comparative paleogenomics of crucifers: ancestral genomic blocks revisited. Current Opinion in Plant Biology, 2016, 30, 108-115.	7.1	84
116	Evolution by gene loss. Nature Reviews Genetics, 2016, 17, 379-391.	16.3	597
117	Pooled mapping: an efficient method of calling variations for population samples with low-depth resequencing data. Molecular Breeding, 2016, 36, 1.	2.1	13
118	Microsynteny and phylogenetic analysis of tandemly organised miRNA families across five members of Brassicaceae reveals complex retention and loss history. Plant Science, 2016, 247, 35-48.	3.6	19
119	The genome sequence of allopolyploid Brassica juncea and analysis of differential homoeolog gene expression influencing selection. Nature Genetics, 2016, 48, 1225-1232.	21.4	479
120	Evolution of TWIN SISTER of FT (TSF) Genes in Brassicaceae. Horticultural Plant Journal, 2016, 2, 16-25.	5.0	4
121	Spreading Winge and flying high: The evolutionary importance of polyploidy after a century of study. American Journal of Botany, 2016, 103, 1139-1145.	1.7	81
122	Altered Transcription and Neofunctionalization of Duplicated Genes Rescue the Harmful Effects of a Chimeric Gene in <i>Brassica napus</i> . Plant Cell, 2016, 28, 2060-2078.	6.6	28
123	Profiles of Glucosinolates, Their Hydrolysis Products, and Quinone Reductase Inducing Activity from 39 <i>Arugula</i> (<i>Eruca sativa</i> Mill.) Accessions. Journal of Agricultural and Food Chemistry, 2016, 64, 6524-6532.	5.2	37
124	Subgenome parallel selection is associated with morphotype diversification and convergent crop domestication in <i>Brassica rapa</i> and <i>Brassica oleracea</i> . Nature Genetics, 2016, 48, 1218-1224.	21.4	297
125	Genome-wide analysis of RNA-interference pathway in <i>Brassica napus</i> , and the expression profile of BnAGOs in response to <i>Sclerotinia sclerotiorum</i> infection. European Journal of Plant Pathology, 2016, 146, 565-579.	1.7	10
126	Comparative transcriptomic analysis uncovers the complex genetic network for resistance to <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . Scientific Reports, 2016, 6, 19007.	3.3	126
127	Extraction of the Constituent Subgenomes of the Natural Allopolyploid Rapeseed (<i>Brassica</i>) Tj ETQq1 1 0.784314rgBT /Overlock 10	2.9	32

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128	Hybrid lethality caused by two complementary dominant genes in cabbage (<i>Brassica oleracea</i> L.). <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	7
129	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
130	Fine mapping of a dominant gene conferring chlorophyll-deficiency in <i>Brassica napus</i> . <i>Scientific Reports</i> , 2016, 6, 31419.	3.3	30
131	Genetic Engineering for Insect Resistance in Economically Important Vegetable Crops. , 2016, , 343-378.		7
132	Physiological importance and possible applications of β^2 -substituted alanine synthase in plants. <i>Applied Biological Chemistry</i> , 2016, 59, 631-647.	1.9	2
133	A Recent Whole-Genome Duplication Divides Populations of a Globally Distributed Microsporidian. <i>Molecular Biology and Evolution</i> , 2016, 33, 2002-2015.	8.9	16
134	Development of INDELs markers in oilseed rape (<i>Brassica napus</i> L.) using re-sequencing data. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	20
135	Genetics and fine mapping of a yellow-green leaf gene (<i>ygl-1</i>) in cabbage (<i>Brassica oleracea</i> var. <i>capitata</i>) Tj ETQq1 1 0.784314 rgBT /Over	2.1	23
136	A global study of transcriptome dynamics in canola (<i>Brassica napus</i> L.) responsive to <i>Sclerotinia sclerotiorum</i> infection using RNA-Seq. <i>Gene</i> , 2016, 590, 57-67.	2.2	41
137	Quantitative trait loci analysis and genome-wide comparison for silique related traits in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2016, 16, 71.	3.6	64
138	Evolution of plant genome architecture. <i>Genome Biology</i> , 2016, 17, 37.	8.8	331
139	Genetic analysis and QTL mapping of traits related to head shape in cabbage (<i>Brassica oleracea</i> var.) Tj ETQq1 1 0.784314 rgBT /Over	3.6	14
140	Small RNA changes in synthetic <i>Brassica napus</i> . <i>Planta</i> , 2016, 244, 607-622.	3.2	13
141	Major Chromosomal Rearrangements Distinguish Willow and Poplar After the Ancestral "Salicoid" Genome Duplication. <i>Genome Biology and Evolution</i> , 2016, 8, 1868-1875.	2.5	30
142	Genome-Wide Classification and Abiotic Stress-Responsive Expression Profiling of Carotenoid Oxygenase Genes in <i>Brassica rapa</i> and <i>Brassica oleracea</i> . <i>Journal of Plant Growth Regulation</i> , 2016, 35, 202-214.	5.1	24
143	Genomic incompatibilities in the diploid and tetraploid offspring of the goldfish \times common carp cross. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1327-1332.	7.1	119
144	Identification, duplication, evolution and expression analyses of caleosins in <i>Brassica</i> plants and <i>Arabidopsis</i> subspecies. <i>Molecular Genetics and Genomics</i> , 2016, 291, 971-988.	2.1	15
145	Genome-wide association analyses reveal complex genetic architecture underlying natural variation for flowering time in canola. <i>Plant, Cell and Environment</i> , 2016, 39, 1228-1239.	5.7	82

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146	Molecular and systems approaches towards drought-tolerant canola crops. <i>New Phytologist</i> , 2016, 210, 1169-1189.	7.3	70
147	Quantitative trait loci controlling leaf appearance and curd initiation of cauliflower in relation to temperature. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1273-1288.	3.6	21
148	Ensembl Genomes 2016: more genomes, more complexity. <i>Nucleic Acids Research</i> , 2016, 44, D574-D580.	14.5	530
149	Characterization and abiotic stress-responsive expression analysis of <i>SGT1</i> genes in <i>Brassica oleracea</i> . <i>Genome</i> , 2016, 59, 243-251.	2.0	17
150	Genome-wide identification, classification, and analysis of NADP-ME family members from 12 crucifer species. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1167-1180.	2.1	10
151	Genome-wide identification and homeolog-specific expression analysis of the SnRK2 genes in <i>Brassica napus</i> guard cells. <i>Plant Molecular Biology</i> , 2016, 91, 211-227.	3.9	20
152	Natural genetic variation in <i>Brassica</i> homologs of FLOWERING LOCUS T and characterization of its expression domains. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2016, 25, 270-277.	1.7	4
153	Mapping of Pi, a gene conferring pink leaf in ornamental kale (<i>Brassica oleracea</i> L. var. <i>acephala</i> DC). <i>Euphytica</i> , 2016, 207, 377-385.	1.2	12
154	Resolution of Brassicaceae Phylogeny Using Nuclear Genes Uncovers Nested Radiations and Supports Convergent Morphological Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 394-412.	8.9	259
155	A Systems Genetics Approach Identifies Gene Regulatory Networks Associated with Fatty Acid Composition in <i>Brassica rapa</i> Seed. <i>Plant Physiology</i> , 2016, 170, 568-585.	4.8	34
156	Map-based cloning reveals the complex organization of the BnRf locus and leads to the identification of BnRf b, a male sterility gene, in <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2016, 129, 53-64.	3.6	15
157	<i>Brassica napus</i> DS-3, encoding a DELLA protein, negatively regulates stem elongation through gibberellin signaling pathway. <i>Theoretical and Applied Genetics</i> , 2017, 130, 727-741.	3.6	62
158	Assessment of DNA markers for seed contamination testing and selection of disease resistance in cabbage. <i>Euphytica</i> , 2017, 213, 1.	1.2	8
159	A user guide to the <i>Brassica</i> 60K Illumina Infinium [®] SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633.	3.6	90
160	Genome sequencing supports a multi-vertex model for Brassicaceae species. <i>Current Opinion in Plant Biology</i> , 2017, 36, 79-87.	7.1	45
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162	Recessive male sterility in cabbage (<i>Brassica oleracea</i> var. <i>capitata</i>) caused by loss of function of BoCYP704B1 due to the insertion of a LTR-retrotransposon. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1441-1451.	3.6	29
163	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610.	8.3	150

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165	Regulation of Glucosinolate Metabolism: From Model Plant <i>Arabidopsis thaliana</i> to Brassica Crops. Reference Series in Phytochemistry, 2017, , 163-199.	0.4	14
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167	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . Molecular Ecology, 2017, 26, 3373-3388.	3.9	66
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171	Genetics and fine mapping of a purple leaf gene, BoPr, in ornamental kale (<i>Brassica oleracea</i> L. var.) Tj ETQq1 1 0.784314 rgBT /Overlock 63	2.8	63
172	Identification of different cytoplasm based on newly developed mitotype-specific markers for marker-assisted selection breeding in <i>Brassica napus</i> L.. Plant Cell Reports, 2017, 36, 901-909.	5.6	17
173	Korean <i>Brassica oleracea</i> germplasm offers a novel source of qualitative resistance to blackleg disease. European Journal of Plant Pathology, 2017, 149, 611-623.	1.7	16
174	Ensembl Plants: Integrating Tools for Visualizing, Mining, and Analyzing Plant Genomic Data. Methods in Molecular Biology, 2017, 1533, 1-31.	0.9	189
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176	Proposed Method for Estimating Health-Promoting Glucosinolates and Hydrolysis Products in Broccoli (<i>Brassica oleracea</i> var. <i>italica</i>) Using Relative Transcript Abundance. Journal of Agricultural and Food Chemistry, 2017, 65, 301-308.	5.2	6
177	Genome-wide characterization and stress-responsive expression profiling of MCM genes in <i>Brassica oleracea</i> and <i>Brassica rapa</i> . Journal of Plant Biology, 2017, 60, 472-484.	2.1	3
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179	Comparative Analysis of the Radish Genome with Brassica Genomes. Compendium of Plant Genomes, 2017, , 53-69.	0.5	1
180	Development of <i>Brassica oleracea-nigra</i> monosomic alien addition lines: genotypic, cytological and morphological analyses. Theoretical and Applied Genetics, 2017, 130, 2491-2504.	3.6	6
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183	The high-quality genome of <i>Brassica napus</i> cultivar ‘ZS11’ reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	5.7	233
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185	Impact of transposable elements on polyploid plant genomes. <i>Annals of Botany</i> , 2017, 120, 195-207.	2.9	228
186	Papain-like cysteine protease encoding genes in rubber (<i>Hevea brasiliensis</i>): comparative genomics, phylogenetic, and transcriptional profiling analysis. <i>Planta</i> , 2017, 246, 999-1018.	3.2	41
188	Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common <i>Brassica rapa</i> Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2259-2270.	1.8	15
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190	RapaNet: A Web Tool for the Co-Expression Analysis of <i>Brassica rapa</i> Genes. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431771542.	1.2	9
191	Omics Meets Phytonutrients in Vegetable Brassicas: For Nutritional Quality Breeding. <i>Horticultural Plant Journal</i> , 2017, 3, 247-254.	5.0	12
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196	OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. <i>BMC Genomics</i> , 2017, 18, 390.	2.8	23
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199	A multiplex PCR for rapid identification of <i>Brassica</i> species in the triangle of U. <i>Plant Methods</i> , 2017, 13, 49.	4.3	20
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202	The poor lonesome A subgenome of <i>Brassica napus</i> var. Darmor (AACC) may not survive without its mate. <i>New Phytologist</i> , 2017, 213, 1886-1897.	7.3	12
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210	Genome-Wide Identification and Characterization of SPX Domain-Containing Members and Their Responses to Phosphate Deficiency in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 35.	3.6	31
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214	Fine-Mapping and Analysis of Cgl1, a Gene Conferring Glossy Trait in Cabbage (<i>Brassica oleracea</i> L. var.) Tj ETQq1 1,0,784314 rgBT /Ove	3.6	20
215	Genetic Transformation and Genomic Resources for Next-Generation Precise Genome Engineering in Vegetable Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 241.	3.6	50
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217	Whole-Genome Identification and Expression Pattern of the Vicinal Oxygen Chelate Family in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 745.	3.6	16
218	Genome-Wide Association Study Reveals Candidate Genes for Control of Plant Height, Branch Initiation Height and Branch Number in Rapeseed (<i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1246.	3.6	63

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220	Genome-Wide Identification and Characterization of the Aquaporin Gene Family and Transcriptional Responses to Boron Deficiency in Brassica napus. <i>Frontiers in Plant Science</i> , 2017, 8, 1336.	3.6	54
221	Leptosphaeria maculans Alters Glucosinolate Profiles in Blackleg Disease-Resistant and -Susceptible Cabbage Lines. <i>Frontiers in Plant Science</i> , 2017, 8, 1769.	3.6	19
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223	Cultivar-Specific Changes in Primary and Secondary Metabolites in Pak Choi (Brassica Rapa, Chinensis) Tj ETQq0 0 0 rgBT /Overlock 10 T	4.1	39
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234	Amplifying recombination genome-wide and reshaping crossover landscapes in Brassicas. <i>PLoS Genetics</i> , 2017, 13, e1006794.	3.5	43
235	Genome-wide identification, characterization, and evolutionary analysis of flowering genes in radish (Raphanus sativus L.). <i>BMC Genomics</i> , 2017, 18, 981.	2.8	17
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340	Genome sequences of horticultural plants: past, present, and future. <i>Horticulture Research</i> , 2019, 6, 112.	6.3	108
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361	Overexpression of the MYB29 transcription factor affects aliphatic glucosinolate synthesis in <i>Brassica oleracea</i> . <i>Plant Molecular Biology</i> , 2019, 101, 65-79.	3.9	28
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363	Towards the new normal: Transcriptomic convergence and genomic legacy of the two subgenomes of an allopolyploid weed (<i>Capsella bursa-pastoris</i>). <i>PLoS Genetics</i> , 2019, 15, e1008131.	3.5	27

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366	Uneven selection pressure accelerating divergence of <i>Populus</i> and <i>Salix</i> . <i>Horticulture Research</i> , 2019, 6, 37.	6.3	15
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377	Tea Plant Information Archive: a comprehensive genomics and bioinformatics platform for tea plant. <i>Plant Biotechnology Journal</i> , 2019, 17, 1938-1953.	8.3	220
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379	Map-based cloning and characterization of BoCCD4, a gene responsible for white/yellow petal color in <i>B. oleracea</i> . <i>BMC Genomics</i> , 2019, 20, 242.	2.8	30
380	Unbiased subgenome evolution following a recent whole-genome duplication in pear (<i>Pyrus</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>	6.3	54
381	Whole-genome resequencing reveals <i>Brassica napus</i> origin and genetic loci involved in its improvement. <i>Nature Communications</i> , 2019, 10, 1154.	12.8	249

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383	Genome wide analysis of MADS-box gene family in <i>Brassica oleracea</i> reveals conservation and variation in flower development. <i>BMC Plant Biology</i> , 2019, 19, 106.	3.6	30
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388	Fine-mapping of a gene for the lobed leaf, BoLL, in ornamental kale (<i>Brassica oleracea</i> L. var. <i>acephala</i>). <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	19
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394	Distinguishing successive ancient polyploidy levels based on genome-internal syntenic alignment. <i>BMC Bioinformatics</i> , 2019, 20, 635.	2.6	3
395	Complex Horticultural Quality Traits in Broccoli Are Illuminated by Evaluation of the Immortal BoLTBDH Mapping Population. <i>Frontiers in Plant Science</i> , 2019, 10, 1104.	3.6	12
396	Identification, Evolution, and Expression Profiling of Histone Lysine Methylation Moderators in <i>Brassica rapa</i> . <i>Plants</i> , 2019, 8, 526.	3.5	8
397	Circadian Regulation of the Plant Transcriptome Under Natural Conditions. <i>Frontiers in Genetics</i> , 2019, 10, 1239.	2.3	35
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402	Mapping loci controlling fatty acid profiles, oil and protein content by genome-wide association study in <i>Brassica napus</i> . <i>Crop Journal</i> , 2019, 7, 217-226.	5.2	19
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407	Synchronous improvement of subgenomes in allopolyploid: a case of <i>Sclerotinia</i> resistance improvement in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	7
408	Genome-wide analysis of the Hsf gene family in <i>Brassica oleracea</i> and a comparative analysis of the Hsf gene family in <i>B. oleracea</i> , <i>B. rapa</i> and <i>B. napus</i> . <i>Functional and Integrative Genomics</i> , 2019, 19, 515-531.	3.5	44
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