

# Graham J King

## List of Publications by Year in descending order

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188  
papers

15,919  
citations

25014

57  
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18633

119  
g-index

194  
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194  
docs citations

194  
times ranked

11573  
citing authors

#	ARTICLE	IF	CITATIONS
1	BRAD V3.0: an upgraded Brassicaceae database. <i>Nucleic Acids Research</i> , 2022, 50, D1432-D1441.	6.5	89
2	Transposable element insertion: a hidden major source of domesticated phenotypic variation in <i>Brassica rapa</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1298-1310.	4.1	29
3	Genetic Control of Seed Phytate Accumulation and the Development of Low-Phytate Crops: A Review and Perspective. <i>Journal of Agricultural and Food Chemistry</i> , 2022, 70, 3375-3390.	2.4	3
4	Development of Selection Indices for Improvement of Seed Yield and Lipid Composition in Bambara Groundnut ( <i>Vigna subterranea</i> (L.) Verdc.). <i>Foods</i> , 2022, 11, 86.	1.9	3
5	Systematic trait dissection in oilseed rape provides a comprehensive view, further insight, and exact roadmap for yield determination. , 2022, 15, 38.		1
6	Challenges for FAIR-compliant description and comparison of crop phenotype data with standardized controlled vocabularies. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	4
7	On the Role of Transposable Elements in the Regulation of Gene Expression and Subgenomic Interactions in Crop Genomes. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 157-189.	2.7	28
8	Magnesium and calcium overaccumulate in the leaves of a <i>schengen3</i> mutant of <i>Brassica rapa</i> . <i>Plant Physiology</i> , 2021, 186, 1616-1631.	2.3	11
9	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21
10	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	4.7	31
11	Functional homoeologous alleles of <i>CONSTANS</i> contribute to seasonal crop type in rapeseed. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3287-3303.	1.8	6
12	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
13	Integrating a genome-wide association study with transcriptomic data to predict candidate genes and favourable haplotypes influencing <i>Brassica napus</i> seed phytate. <i>DNA Research</i> , 2021, 28, .	1.5	14
14	A Systematic Approach to Defining Nutritional Quality of Underutilised Crops. <i>Proceedings (mdpi)</i> , 2020, 36, .	0.2	0
15	Genetic Elucidation of Glucosinolates in a Diverse Collection of Indian Mustard ( <i>Brassica juncea</i> L.). <i>Proceedings (mdpi)</i> , 2020, 36, .	0.2	0
16	Characteristics of the Underutilised Pulse Bambara Groundnut ( <i>Vigna subterranea</i> (L.) Verdc.) Relevant to Food & Nutritional Security. <i>Proceedings (mdpi)</i> , 2020, 36, .	0.2	4
17	Genetic and signalling pathways of dry fruit size: targets for genome editing-based crop improvement. <i>Plant Biotechnology Journal</i> , 2020, 18, 1124-1140.	4.1	40
18	Bridging the food security gap: an information-enabled approach to connect dietary nutrition, food composition and crop production. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 1495-1504.	1.7	10

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19	Chromosome-Scale Assembly and Annotation of the Macadamia Genome ( <i>Macadamia integrifolia</i> ) Tj ETQq1, 1, 0.784314 rgBT /O	0.8	26
20	An extreme-phenotype genome-wide association study identifies candidate cannabinoid pathway genes in Cannabis. Scientific Reports, 2020, 10, 18643.	1.6	17
21	Alternatively Spliced BnaPAP2.A7 Isoforms Play Opposing Roles in Anthocyanin Biosynthesis of Brassica napus L.. Frontiers in Plant Science, 2020, 11, 983.	1.7	23
22	Transposon insertions within alleles of BnaFLC.A10 and BnaFLC.A2 are associated with seasonal crop type in rapeseed. Journal of Experimental Botany, 2020, 71, 4729-4741.	2.4	32
23	Abundant expression of maternal siRNAs is a conserved feature of seed development. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15305-15315.	3.3	49
24	Maximising recombination across macadamia populations to generate linkage maps for genome anchoring. Scientific Reports, 2020, 10, 5048.	1.6	8
25	Knowledge representation and data sharing to unlock crop variation for nutritional food security. Crop Science, 2020, 60, 516-529.	0.8	7
26	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	3.5	84
27	Identification, characterization and epitope mapping of proteins encoded by putative allergenic napin genes from <i>Brassica rapa</i> . Clinical and Experimental Allergy, 2020, 50, 848-868.	1.4	13
28	Complex Patterns of Cannabinoid Alkyl Side-Chain Inheritance in Cannabis. Scientific Reports, 2019, 9, 11421.	1.6	14
29	Identification of SNP loci and candidate genes related to four important fatty acid composition in Brassica napus using genome wide association study. PLoS ONE, 2019, 14, e0221578.	1.1	20
30	Oilseed rape ( <i>Brassica napus</i> ) resistance to growth of <i>Leptosphaeria maculans</i> in leaves of young plants contributes to quantitative resistance in stems of adult plants. PLoS ONE, 2019, 14, e0222540.	1.1	15
31	A <i>CACTA</i> -like transposable element in the upstream region of <i>BnaA9</i> . <i>CYP78A9</i> acts as an enhancer to increase silique length and seed weight in rapeseed. Plant Journal, 2019, 98, 524-539.	2.8	77
32	Remobilization and fate of sulphur in mustard. Annals of Botany, 2019, 124, 471-480.	1.4	14
33	DNA paternity testing indicates unexpectedly high levels of self-fertilisation in macadamia. Tree Genetics and Genomes, 2019, 15, 1.	0.6	16
34	Developing Robust Standardised Analytical Procedures for Cannabinoid Quantification: Laying the Foundations for an Emerging Cannabis-Based Pharmaceutical Industry. Medical Cannabis and Cannabinoids, 2019, 2, 1-13.	1.2	8
35	Seed glucosinolate yield is maximized by higher rates of sulfur nutrition than required for seed yield in condiment mustard ( <i>Brassica juncea</i> L.). PLoS ONE, 2019, 14, e0213429.	1.1	6
36	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. Plant Biotechnology Journal, 2019, 17, 1998-2010.	4.1	54

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37	Remobilisation and Fate of Sulphur in Indian Mustard ( <i>Brassica juncea</i> . L). Proceedings (mdpi), 2019, 36, 26.	0.2	0
38	The potential of the underutilized pulse bambara groundnut ( <i>Vigna subterranea</i> (L.) Verdc.) for nutritional food security. Journal of Food Composition and Analysis, 2019, 77, 47-59.	1.9	81
39	Black salve composition: An evaluation of the potential for normal tissue toxicity and treatment failure from black salve products. Journal of Herbal Medicine, 2019, 15, 100246.	1.0	2
40	An auxin signaling gene <i>BnaA3</i> . <i>IAA7</i> contributes to improved plant architecture and yield heterosis in rapeseed. New Phytologist, 2019, 222, 837-851.	3.5	80
41	Maternal components of <i>RNA</i> -directed <i>DNA</i> methylation are required for seed development in <i>Brassica rapa</i> . Plant Journal, 2018, 94, 575-582.	2.8	72
42	Assessing the risk of epidemic dropsy from black salve use. Journal of Applied Toxicology, 2018, 38, 1274-1281.	1.4	5
43	Dissection of the genetic architecture of three seed-quality traits and consequences for breeding in <i>Brassica napus</i> . Plant Biotechnology Journal, 2018, 16, 1336-1348.	4.1	91
44	Sequence variation and functional analysis of a FRIGIDA orthologue ( <i>BnaA3.FRI</i> ) in <i>Brassica napus</i> . BMC Plant Biology, 2018, 18, 32.	1.6	24
45	A sibling pair with cardiofaciocutaneous syndrome (CFC) secondary to BRAF mutation with unaffected parents—the first cases of gonadal mosaicism in CFC?. American Journal of Medical Genetics, Part A, 2018, 176, 1637-1640.	0.7	2
46	Annotation of the <i>Corymbia</i> terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to <i>Eucalyptus</i> . Heredity, 2018, 121, 87-104.	1.2	17
47	Genetic Properties of a Nested Association Mapping Population Constructed With Semi-Winter and Spring Oilseed Rapes. Frontiers in Plant Science, 2018, 9, 1740.	1.7	29
48	Developmental Plasticity of the Major Alkyl Cannabinoid Chemotypes in a Diverse Cannabis Genetic Resource Collection. Frontiers in Plant Science, 2018, 9, 1510.	1.7	16
49	<i>Brassica napus</i> Genomic Resources. Compendium of Plant Genomes, 2018, , 233-244.	0.3	3
50	A comprehensive and precise set of intervarietal substitution lines to identify candidate genes and quantitative trait loci in oilseed rape ( <i>Brassica napus</i> L.). Theoretical and Applied Genetics, 2018, 131, 2117-2129.	1.8	5
51	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . Plant Biotechnology Journal, 2018, 16, 1265-1274.	4.1	217
52	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. Plant Biotechnology Journal, 2017, 15, 1602-1610.	4.1	150
53	Breeding histories and selection criteria for oilseed rape in Europe and China identified by genome wide pedigree dissection. Scientific Reports, 2017, 7, 1916.	1.6	16
54	Carcinogenic potential of sanguinarine, a phytochemical used in “therapeutic” black salve and mouthwash. Mutation Research - Reviews in Mutation Research, 2017, 774, 46-56.	2.4	29

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55	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	1.2	17
56	Genome-Wide Identification and Characterization of the Aquaporin Gene Family and Transcriptional Responses to Boron Deficiency in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1336.	1.7	54
57	Genotypic Variation in Wheat Flour Lysophospholipids. <i>Molecules</i> , 2017, 22, 909.	1.7	4
58	Development of a Statistical Crop Model to Explain the Relationship between Seed Yield and Phenotypic Diversity within the <i>Brassica napus</i> Genepool. <i>Agronomy</i> , 2017, 7, 31.	1.3	13
59	A Review of Black Salve: Cancer Specificity, Cure, and Cosmesis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2017, 2017, 1-11.	0.5	12
60	Geospatial binding for transdisciplinary research in crop science: the GRASPGfs initiative. <i>Open Geospatial Data, Software and Standards</i> , 2017, 2, .	4.3	5
61	Genome-wide analysis of the auxin/indoleacetic acid (Aux/IAA) gene family in allotetraploid rapeseed ( <i>Brassica napus</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 204.	1.6	32
62	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. <i>F1000Research</i> , 2017, 6, 465.	0.8	16
63	Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data. <i>F1000Research</i> , 2017, 6, 465.	0.8	10
64	<i>Sanguinaria canadensis</i> : Traditional Medicine, Phytochemical Composition, Biological Activities and Current Uses. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1414.	1.8	72
65	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.	1.1	63
66	A Belated Green Revolution for Cannabis: Virtual Genetic Resources to Fast-Track Cultivar Development. <i>Frontiers in Plant Science</i> , 2016, 7, 1113.	1.7	65
67	Fire and Brimstone: Molecular Interactions between Sulfur and Glucosinolate Biosynthesis in Model and Crop Brassicaceae. <i>Frontiers in Plant Science</i> , 2016, 7, 1735.	1.7	35
68	QTL meta-analysis of root traits in <i>Brassica napus</i> under contrasting phosphorus supply in two growth systems. <i>Scientific Reports</i> , 2016, 6, 33113.	1.6	55
69	Genome and transcriptome sequencing characterises the gene space of <i>Macadamia integrifolia</i> (Proteaceae). <i>BMC Genomics</i> , 2016, 17, 937.	1.2	45
70	Identification of environmentally stable QTL for resistance against <i>Leptosphaeria maculans</i> in oilseed rape ( <i>Brassica napus</i> ). <i>Theoretical and Applied Genetics</i> , 2016, 129, 169-180.	1.8	60
71	Characterisation of cannabinoid composition in a diverse <i>Cannabis sativa</i> L. germplasm collection. <i>Euphytica</i> , 2016, 208, 463-475.	0.6	68
72	Perturbation of nutrient source-sink relationships by post-anthesis stresses results in differential accumulation of nutrients in wheat grain. <i>Journal of Plant Nutrition and Soil Science</i> , 2015, 178, 89-98.	1.1	30

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73	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.	1.7	52
74	Crop epigenetics and the molecular hardware of genotype × environment interactions. <i>Frontiers in Plant Science</i> , 2015, 6, 968.	1.7	20
75	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.	1.8	41
76	Disruption of a <i>CAROTENOID CLEAVAGE DIOXYGENASE 4</i> gene converts flower colour from white to yellow in <i>Brassica</i> species. <i>New Phytologist</i> , 2015, 206, 1513-1526.	3.5	155
77	Assessing Quantitative Resistance against <i>Leptosphaeria maculans</i> (Phoma Stem Canker) in <i>Brassica napus</i> (Oilseed Rape) in Young Plants. <i>PLoS ONE</i> , 2014, 9, e84924.	1.1	40
78	Complete chloroplast genome of <i>Macadamia integrifolia</i> confirms the position of the Gondwanan early-diverging eudicot family Proteaceae. <i>BMC Genomics</i> , 2014, 15, S13.	1.2	39
79	Genetical and Comparative Genomics of <i>Brassica</i> under Altered Ca Supply Identifies <i>Arabidopsis</i> Ca-Transporter Orthologs. <i>Plant Cell</i> , 2014, 26, 2818-2830.	3.1	40
80	Sustainable harvest: managing plasticity for resilient crops. <i>Plant Biotechnology Journal</i> , 2014, 12, 517-533.	4.1	34
81	Whole genome shotgun sequences for microsatellite discovery and application in cultivated and wild <i>Macadamia</i> ( <i>Proteaceae</i> ). <i>Applications in Plant Sciences</i> , 2014, 2, 1300089.	0.8	29
82	Genome-wide investigation of genetic changes during modern breeding of <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 1817-1829.	1.8	60
83	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
84	Determination of Starch Lysophospholipids in Rice Using Liquid Chromatography–Mass Spectrometry (LC-MS). <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 6600-6607.	2.4	53
85	Genotypic Variation in Lysophospholipids of Milled Rice. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 9353-9361.	2.4	17
86	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
87	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	13.9	456
88	Phospholipids in rice: Significance in grain quality and health benefits: A review. <i>Food Chemistry</i> , 2013, 139, 1133-1145.	4.2	108
89	High-Throughput Sequencing and Mutagenesis to Accelerate the Domestication of <i>Microlaena stipoides</i> as a New Food Crop. <i>PLoS ONE</i> , 2013, 8, e82641.	1.1	43
90	Genome Analysis. , 2013, , 91-109.		0

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91	Seed colour loci, homoeology and linkage groups of the C genome chromosomes revealed in Brassica rapa-B. oleracea monosomic alien addition lines. <i>Annals of Botany</i> , 2012, 109, 1227-1242.	1.4	29
92	High-Resolution Mapping of a Fruit Firmness-Related Quantitative Trait Locus in Tomato Reveals Epistatic Interactions Associated with a Complex Combinatorial Locus. <i>Plant Physiology</i> , 2012, 159, 1644-1657.	2.3	83
93	Distribution of calcium (Ca) and magnesium (Mg) in the leaves of Brassica rapa under varying exogenous Ca and Mg supply. <i>Annals of Botany</i> , 2012, 109, 1081-1089.	1.4	43
94	Three-point appraisal of genetic linkage maps. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1393-1402.	1.8	1
95	A Hypomethylated population of Brassica rapa for forward and reverse Epi-genetics. <i>BMC Plant Biology</i> , 2012, 12, 193.	1.6	64
96	Assigning Brassica microsatellite markers to the nine C-genome chromosomes using Brassica rapa var. trilocularis and B. oleracea var. alboglabra monosomic alien addition lines. <i>Theoretical and Applied Genetics</i> , 2012, 125, 455-466.	1.8	20
97	Effects of R gene-mediated resistance in Brassica napus (oilseed rape) on asexual and sexual sporulation of Pyrenopeziza brassicae (light leaf spot). <i>Plant Pathology</i> , 2012, 61, 543-554.	1.2	12
98	InterStoreDB: A Generic Integration Resource for Genetic and Genomic Data. <i>Journal of Integrative Plant Biology</i> , 2012, 54, 345-355.	4.1	13
99	Parental genome imbalance in Brassica oleracea causes asymmetric triploid block. <i>Plant Journal</i> , 2012, 71, 503-516.	2.8	48
100	Promoter Variation and Transcript Divergence in Brassicaceae Lineages of FLOWERING LOCUS T. <i>PLoS ONE</i> , 2012, 7, e47127.	1.1	37
101	Effects of fungicide on growth of Leptosphaeria maculans and L. biglobosa in relation to development of phoma stem canker on oilseed rape (Brassica napus). <i>Plant Pathology</i> , 2011, 60, 607-620.	1.2	23
102	Generation of nonvernal obligate, faster cycling Noccea caerulescens lines through fast neutron mutagenesis. <i>New Phytologist</i> , 2011, 189, 409-414.	3.5	10
103	Integration of linkage maps for the Amphidiploid Brassica napus and comparative mapping with Arabidopsis and Brassica rapa. <i>BMC Genomics</i> , 2011, 12, 101.	1.2	125
104	The genome of the mesopolyploid crop species Brassica rapa. <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
105	Universal endogenous gene controls for bisulphite conversion in analysis of plant DNA methylation. <i>Plant Methods</i> , 2011, 7, 39.	1.9	15
106	High Resolution Melt (HRM) analysis is an efficient tool to genotype EMS mutants in complex crop genomes. <i>Plant Methods</i> , 2011, 7, 43.	1.9	79
107	Epigenetic QTL Mapping in Brassica napus. <i>Genetics</i> , 2011, 189, 1093-1102.	1.2	71
108	Regulatory Hotspots Are Associated with Plant Gene Expression under Varying Soil Phosphorus Supply in Brassica rapa. <i>Plant Physiology</i> , 2011, 156, 1230-1241.	2.3	60

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109	A SEPALLATA gene is involved in the development and ripening of strawberry ( <i>Fragaria ananassa</i> Duch.) fruit, a non-climacteric tissue*. <i>Journal of Experimental Botany</i> , 2011, 62, 1179-1188.	2.4	174
110	Tandem Quadruplication of HMA4 in the Zinc (Zn) and Cadmium (Cd) Hyperaccumulator <i>Noccaea caerulescens</i> . <i>PLoS ONE</i> , 2011, 6, e17814.	1.1	112
111	Shoot zinc (Zn) concentration varies widely within <i>Brassica oleracea</i> L. and is affected by soil Zn and phosphorus (P) levels. <i>Journal of Horticultural Science and Biotechnology</i> , 2010, 85, 375-380.	0.9	42
112	<i>Brassica</i> GLABRA2 genes: analysis of function related to seed oil content and development of functional markers. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1597-1610.	1.8	24
113	A FRUITFULL-like gene is associated with genetic variation for fruit flesh firmness in apple ( <i>Malus domestica</i> B.S.P.). <i>PLoS ONE</i> , 2010, 5, e12812.	0.6	56
114	Construction of an integrated genetic linkage map for the A genome of <i>Brassica napus</i> using SSR markers derived from sequenced BACs in <i>B. rapa</i> . <i>BMC Genomics</i> , 2010, 11, 594.	1.2	78
115	Origins of the amphiploid species <i>Brassica napus</i> L. investigated by chloroplast and nuclear molecular markers. <i>BMC Plant Biology</i> , 2010, 10, 54.	1.6	202
116	A rich TILLING resource for studying gene function in <i>Brassica rapa</i> . <i>BMC Plant Biology</i> , 2010, 10, 62.	1.6	149
117	The first meiosis of resynthesized <i>Brassica napus</i> , a genome blender. <i>New Phytologist</i> , 2010, 186, 102-112.	3.5	267
118	A <i>Brassica</i> Exon Array for Whole-Transcript Gene Expression Profiling. <i>PLoS ONE</i> , 2010, 5, e12812.	1.1	27
119	Exploring and exploiting epigenetic variation in crops This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 856-868.	0.9	35
120	Genetic analysis of potassium use efficiency in <i>Brassica oleracea</i> . <i>Annals of Botany</i> , 2010, 105, 1199-1210.	1.4	54
121	A SQUAMOSA MADS Box Gene Involved in the Regulation of Anthocyanin Accumulation in Bilberry Fruits. <i>Plant Physiology</i> , 2010, 153, 1619-1629.	2.3	232
122	The evolution of <i>Brassica napus</i> FLOWERING LOCUST paralogues in the context of inverted chromosomal duplication blocks. <i>BMC Evolutionary Biology</i> , 2009, 9, 271.	3.2	86
123	Quantitative resistance to symptomless growth of <i>Leptosphaeria maculans</i> (phoma stem canker) in <i>Brassica napus</i> (oilseed rape). <i>Plant Pathology</i> , 2009, 58, 314-323.	1.2	65
124	Rapeseed cytoplasm gives advantage in wild relatives and complicates genetically modified crop biocontainment. <i>New Phytologist</i> , 2009, 183, 1201-1211.	3.5	27
125	Shoot yield drives phosphorus use efficiency in <i>Brassica oleracea</i> and correlates with root architecture traits. <i>Journal of Experimental Botany</i> , 2009, 60, 1953-1968.	2.4	278
126	Double haploids, markers and QTL analysis in vegetable brassicas. <i>Euphytica</i> , 2008, 164, 509-514.	0.6	46

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127	A functional genomics resource for <i>Brassica napus</i> : development of an EMS mutagenized population and discovery of <i>FAE1</i> point mutations by TILLING. <i>New Phytologist</i> , 2008, 180, 751-765.	3.5	165
128	The CACTA transposon <i>Bot1</i> played a major role in <i>Brassica</i> genome divergence and gene proliferation. <i>Plant Journal</i> , 2008, 56, 1030-1044.	2.8	75
129	Genetics and epigenetics of fruit development and ripening. <i>Current Opinion in Plant Biology</i> , 2008, 11, 58-63.	3.5	136
130	Standardized gene nomenclature for the Brassica genus. <i>Plant Methods</i> , 2008, 4, 10.	1.9	130
131	A and C Genome Distinction and Chromosome Identification in <i>Brassica napus</i> by Sequential Fluorescence <i>In Situ</i> Hybridization and Genomic <i>In Situ</i> Hybridization. <i>Genetics</i> , 2008, 180, 1849-1857.	1.2	78
132	Shoot Calcium and Magnesium Concentrations Differ between Subtaxa, Are Highly Heritable, and Associate with Potentially Pleiotropic Loci in <i>Brassica oleracea</i> . <i>Plant Physiology</i> , 2008, 146, 1707-1720.	2.3	107
133	Novel Insights into Seed Fatty Acid Synthesis and Modification Pathways from Genetic Diversity and Quantitative Trait Loci Analysis of the Brassica C Genome. <i>Plant Physiology</i> , 2007, 144, 1827-1842.	2.3	78
134	Simple sequence repeats reveal uneven distribution of genetic diversity in chloroplast genomes of <i>Brassica oleracea</i> L. and (n=9) wild relatives. <i>Theoretical and Applied Genetics</i> , 2007, 114, 609-618.	1.8	55
135	Detection and resolution of genetic loci affecting circadian period in <i>Brassica oleracea</i> . <i>Theoretical and Applied Genetics</i> , 2007, 114, 683-692.	1.8	21
136	The reference genetic linkage map for the multinational Brassica rapa genome sequencing project. <i>Theoretical and Applied Genetics</i> , 2007, 115, 777-792.	1.8	160
137	Fitness of hybrids between rapeseed ( <i>Brassica napus</i> ) and wild <i>Brassica rapa</i> in natural habitats. <i>Molecular Ecology</i> , 2006, 15, 1175-1184.	2.0	65
138	A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. <i>Nature Genetics</i> , 2006, 38, 948-952.	9.4	1,076
139	A Sequence-Tagged Linkage Map of Brassica rapa. <i>Genetics</i> , 2006, 174, 29-39.	1.2	140
140	Utilization of Arabidopsis and Brassica Genomic Resources to Underpin Genetic Analysis and Improvement of Brassica Crops. , 2006, , 33-69.		1
141	Relationships between water-use traits and photosynthesis in Brassica oleracea resolved by quantitative genetic analysis. <i>Plant Breeding</i> , 2005, 124, 557-564.	1.0	59
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