

# Richard G F Visser

## List of Publications by Year in descending order

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504  
papers

29,789  
citations

5268

83  
h-index

10734

138  
g-index

527  
all docs

527  
docs citations

527  
times ranked

20750  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and analysis of the tuber crop potato. <i>Nature</i> , 2011, 475, 189-195.	27.8	1,912
2	Visualization of differential gene expression using a novel method of RNA fingerprinting based on AFLP: Analysis of gene expression during potato tuber development. <i>Plant Journal</i> , 1996, 9, 745-753.	5.7	764
3	If Homogalacturonan Were a Side Chain of Rhamnogalacturonan I. Implications for Cell Wall Architecture. <i>Plant Physiology</i> , 2003, 132, 1781-1789.	4.8	527
4	Anthocyanin Biosynthesis and Degradation Mechanisms in Solanaceous Vegetables: A Review. <i>Frontiers in Chemistry</i> , 2018, 6, 52.	3.6	456
5	Societal Costs of Late Blight in Potato and Prospects of Durable Resistance Through Cisgenic Modification. <i>Potato Research</i> , 2008, 51, 47-57.	2.7	381
6	Applied Biotechnology to Combat Late Blight in Potato Caused by <i>Phytophthora infestans</i> . <i>Potato Research</i> , 2009, 52, 249-264.	2.7	363
7	Effector Genomics Accelerates Discovery and Functional Profiling of Potato Disease Resistance and <i>Phytophthora infestans</i> Avirulence Genes. <i>PLoS ONE</i> , 2008, 3, e2875.	2.5	361
8	Comparative genomics enabled the isolation of the R3a late blight resistance gene in potato. <i>Plant Journal</i> , 2005, 42, 251-261.	5.7	355
9	A Next-Generation Sequencing Method for Genotyping-by-Sequencing of Highly Heterozygous Autotetraploid Potato. <i>PLoS ONE</i> , 2013, 8, e62355.	2.5	317
10	Naturally occurring allele diversity allows potato cultivation in northern latitudes. <i>Nature</i> , 2013, 495, 246-250.	27.8	313
11	Loss of susceptibility as a novel breeding strategy for durable and broad-spectrum resistance. <i>Molecular Breeding</i> , 2010, 25, 1-12.	2.1	300
12	The Tomato Yellow Leaf Curl Virus Resistance Genes Ty-1 and Ty-3 Are Allelic and Code for DFDGD-Class RNA-Dependent RNA Polymerases. <i>PLoS Genetics</i> , 2013, 9, e1003399.	3.5	299
13	Enhancing crop resilience to combined abiotic and biotic stress through the dissection of physiological and molecular crosstalk. <i>Frontiers in Plant Science</i> , 2014, 5, 207.	3.6	295
14	Inhibition of the expression of the gene for granule-bound starch synthase in potato by antisense constructs. <i>Molecular Genetics and Genomics</i> , 1991, 225, 289-296.	2.4	260
15	RECORD: a novel method for ordering loci on a genetic linkage map. <i>Theoretical and Applied Genetics</i> , 2005, 112, 30-40.	3.6	248
16	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2031-2047.	1.8	244
17	SMOOTH: a statistical method for successful removal of genotyping errors from high-density genetic linkage data. <i>Theoretical and Applied Genetics</i> , 2005, 112, 187-194.	3.6	239
18	Elicitin recognition confers enhanced resistance to <i>Phytophthora infestans</i> in potato. <i>Nature Plants</i> , 2015, 1, 15034.	9.3	229

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19	Construction of a 10,000-Marker Ultradense Genetic Recombination Map of Potato: Providing a Framework for Accelerated Gene Isolation and a Genomewide Physical Map. <i>Genetics</i> , 2006, 173, 1075-1087.	2.9	212
20	Towards F1 Hybrid Seed Potato Breeding. <i>Potato Research</i> , 2011, 54, 301-312.	2.7	204
21	Functional stacking of three resistance genes against <i>Phytophthora infestans</i> in potato. <i>Transgenic Research</i> , 2012, 21, 89-99.	2.4	198
22	Transcript Imaging with cDNA-AFLP: A Step-by-Step Protocol. <i>Plant Molecular Biology Reporter</i> , 1998, 16, 157-157.	1.8	194
23	Progress in understanding the biosynthesis of amylose. <i>Trends in Plant Science</i> , 1998, 3, 462-467.	8.8	193
24	Isolation of an amylose-free starch mutant of the potato ( <i>Solanum tuberosum</i> L.). <i>Theoretical and Applied Genetics</i> , 1987, 75, 217-221.	3.6	186
25	Exploiting Knowledge of <i>R/Avr</i> Genes to Rapidly Clone a New LZ-NBS-LRR Family of Late Blight Resistance Genes from Potato Linkage Group IV. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 630-641.	2.6	181
26	Tomato yellow leaf curl virus resistance by <i>Ty-1</i> involves increased cytosine methylation of viral genomes and is compromised by cucumber mosaic virus infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12942-12947.	7.1	180
27	Tools for Genetic Studies in Experimental Populations of Polyploids. <i>Frontiers in Plant Science</i> , 2018, 9, 513.	3.6	175
28	Durable Late Blight Resistance in Potato Through Dynamic Varieties Obtained by Cisgenesis: Scientific and Societal Advances in the DuRPh Project. <i>Potato Research</i> , 2016, 59, 35-66.	2.7	171
29	The potential of C4 grasses for cellulosic biofuel production. <i>Frontiers in Plant Science</i> , 2013, 4, 107.	3.6	170
30	EBP1 regulates organ size through cell growth and proliferation in plants. <i>EMBO Journal</i> , 2006, 25, 4909-4920.	7.8	169
31	Genetic Variation in Pea Seed Globulin Composition. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 425-433.	5.2	165
32	Development and analysis of a 20K SNP array for potato ( <i>Solanum tuberosum</i> ): an insight into the breeding history. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2387-2401.	3.6	165
33	Plant behaviour under combined stress: tomato responses to combined salinity and pathogen stress. <i>Plant Journal</i> , 2018, 93, 781-793.	5.7	163
34	Qualitative and Quantitative Late Blight Resistance in the Potato Cultivar Sarpo Mira Is Determined by the Perception of Five Distinct RXLR Effectors. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 910-919.	2.6	162
35	Evaluation of LD decay and various LD-decay estimators in simulated and SNP-array data of tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2017, 130, 123-135.	3.6	158
36	Secondary somatic embryogenesis and applications in plant breeding. <i>Euphytica</i> , 1995, 81, 93-107.	1.2	151

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37	Mapping and Cloning of Late Blight Resistance Genes from <i>Solanum venturii</i> Using an Interspecific Candidate Gene Approach. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 601-615.	2.6	148
38	<i>Rin4</i> Causes Hybrid Necrosis and Race-Specific Resistance in an Interspecific Lettuce Hybrid. <i>Plant Cell</i> , 2009, 21, 3368-3378.	6.6	146
39	Breeding drought tolerant cowpea: constraints, accomplishments, and future prospects. <i>Euphytica</i> , 2009, 167, 353-370.	1.2	145
40	Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. <i>New Phytologist</i> , 2017, 213, 1346-1362.	7.3	144
41	Pea powdery mildew <i>er1</i> resistance is associated to loss-of-function mutations at a MLO homologous locus. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1425-1431.	3.6	140
42	Source-Sink Regulation Is Mediated by Interaction of an FT Homolog with a SWEET Protein in Potato. <i>Current Biology</i> , 2019, 29, 1178-1186.e6.	3.9	137
43	The Role of Tomato WRKY Genes in Plant Responses to Combined Abiotic and Biotic Stresses. <i>Frontiers in Plant Science</i> , 2018, 9, 801.	3.6	135
44	Biochemical and molecular characterization of a novel starch synthase from potato tubers. <i>Plant Journal</i> , 1995, 8, 283-294.	5.7	134
45	Haplotype-resolved genome analyses of a heterozygous diploid potato. <i>Nature Genetics</i> , 2020, 52, 1018-1023.	21.4	134
46	The Late Blight Resistance Locus <i>Rpi-blb3</i> from <i>Solanum bulbocastanum</i> Belongs to a Major Late Blight R Gene Cluster on Chromosome 4 of Potato. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 722-729.	2.6	133
47	Sequence of the structural gene for granule-bound starch synthase of potato ( <i>Solanum tuberosum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl... 228, 240-248.	2.4	126
48	Association mapping of salt tolerance in barley ( <i>Hordeum vulgare</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 2335-2351.	3.6	124
49	<i>StGA2ox1</i> is induced prior to stolon swelling and controls GA levels during potato tuber development. <i>Plant Journal</i> , 2007, 52, 362-373.	5.7	122
50	Meiosis Drives Extraordinary Genome Plasticity in the Haploid Fungal Plant Pathogen <i>Mycosphaerella graminicola</i> . <i>PLoS ONE</i> , 2009, 4, e5863.	2.5	122
51	The R3 Resistance to <i>Phytophthora infestans</i> in Potato is Conferred by Two Closely Linked R Genes with Distinct Specificities. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 428-435.	2.6	121
52	The effects of auxin and strigolactones on tuber initiation and stolon architecture in potato. <i>Journal of Experimental Botany</i> , 2012, 63, 4539-4547.	4.8	121
53	Development of late blight resistant potatoes by cisgene stacking. <i>BMC Biotechnology</i> , 2014, 14, 50.	3.3	120
54	Untargeted Metabolic Quantitative Trait Loci Analyses Reveal a Relationship between Primary Metabolism and Potato Tuber Quality. <i>Plant Physiology</i> , 2012, 158, 1306-1318.	4.8	119

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55	<i>Phytophthora infestans</i> Isolates Lacking Class I <i>RpiO</i> Variants Are Virulent on <i>Rpi-blb1</i> Potato. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1535-1545.	2.6	118
56	Developmental changes of enzymes involved in conversion of sucrose to hexose-phosphate during early tuberisation of potato. <i>Planta</i> , 1997, 202, 220-226.	3.2	116
57	Implementation of two high through-put techniques in a novel application: detecting point mutations in large EMS mutated plant populations. <i>Plant Methods</i> , 2009, 5, 13.	4.3	116
58	Cloning and expression analysis of a potato cDNA that encodes branching enzyme evidence for co-expression of starch biosynthetic genes. <i>Molecular Genetics and Genomics</i> , 1991, 230, 39-44.	2.4	115
59	Expression of a chimaeric granule-bound starch synthase-GUS gene in transgenic potato plants. <i>Plant Molecular Biology</i> , 1991, 17, 691-699.	3.9	114
60	Genes driving potato tuber initiation and growth: identification based on transcriptional changes using the POCL array. <i>Functional and Integrative Genomics</i> , 2008, 8, 329-340.	3.5	114
61	CRISPR/Cas9-targeted mutagenesis of the tomato susceptibility gene <i>PMR4</i> for resistance against powdery mildew. <i>BMC Plant Biology</i> , 2020, 20, 284.	3.6	114
62	Cloning and Characterization of <i>R3b</i> ; Members of the <i>R3</i> Superfamily of Late Blight Resistance Genes Show Sequence and Functional Divergence. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1132-1142.	2.6	113
63	Loss of Function in <i>Mlo</i> Orthologs Reduces Susceptibility of Pepper and Tomato to Powdery Mildew Disease Caused by <i>Leveillula taurica</i> . <i>PLoS ONE</i> , 2013, 8, e70723.	2.5	113
64	Population structure and linkage disequilibrium unravelled in tetraploid potato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1151-1170.	3.6	107
65	The dosage effect of the wildtype GBSS allele is linear for GBSS activity but not for amylose content: absence of amylose has a distinct influence on the physico-chemical properties of starch. <i>Theoretical and Applied Genetics</i> , 1996, 92, 121-127.	3.6	106
66	Validation of the high-throughput marker technology DArT using the model plant <i>Arabidopsis thaliana</i> . <i>Molecular Genetics and Genomics</i> , 2005, 274, 30-39.	2.1	106
67	New broad-spectrum resistance to septoria tritici blotch derived from synthetic hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2012, 124, 125-142.	3.6	106
68	The effect of pyramiding <i>Phytophthora infestans</i> resistance genes <i>R Pi-mcd1</i> and <i>R Pi-ber</i> in potato. <i>Theoretical and Applied Genetics</i> , 2010, 121, 117-125.	3.6	104
69	The <i>Ph-3</i> gene from <i>Solanum pimpinellifolium</i> encodes CC-NBS-LRR protein conferring resistance to <i>Phytophthora infestans</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 1353-1364.	3.6	104
70	A transposable element insertion in the susceptibility gene <i>CsaMLO8</i> results in hypocotyl resistance to powdery mildew in cucumber. <i>BMC Plant Biology</i> , 2015, 15, 243.	3.6	104
71	The Double-Reduction Landscape in Tetraploid Potato as Revealed by a High-Density Linkage Map. <i>Genetics</i> , 2015, 201, 853-863.	2.9	100
72	polymap linkage analysis and genetic map construction from F1 populations of outcrossing polyploids. <i>Bioinformatics</i> , 2018, 34, 3496-3502.	4.1	99

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73	A new and versatile method for the successful conversion of AFLPTM markers into simple single locus markers. <i>Nucleic Acids Research</i> , 2003, 31, 55e-55.	14.5	98
74	Characterization of the MLO gene family in Rosaceae and gene expression analysis in <i>Malus domestica</i> . <i>BMC Genomics</i> , 2014, 15, 618.	2.8	97
75	Chromosomal rearrangements between tomato and <i>Solanum chilense</i> hamper mapping and breeding of the TYLCV resistance gene <i>Ty-1</i> . <i>Plant Journal</i> , 2011, 68, 1093-1103.	5.7	96
76	Broad spectrum late blight resistance in potato differential set plants MaR8 and MaR9 is conferred by multiple stacked R genes. <i>Theoretical and Applied Genetics</i> , 2012, 124, 923-935.	3.6	96
77	Complexes with Mixed Primary and Secondary Cellulose Synthases Are Functional in Arabidopsis Plants. <i>Plant Physiology</i> , 2012, 160, 726-737.	4.8	95
78	Fine mapping of the tomato yellow leaf curl virus resistance gene <i>Ty-2</i> on chromosome 11 of tomato. <i>Molecular Breeding</i> , 2014, 34, 749-760.	2.1	95
79	The <i>Bemisia tabaci</i> species complex: Additions from different parts of the world. <i>Insect Science</i> , 2013, 20, 723-733.	3.0	94
80	Resistance to <i>Bemisia tabaci</i> in tomato wild relatives. <i>Euphytica</i> , 2012, 187, 31-45.	1.2	93
81	Transformation of homozygous diploid potato with an <i>Agrobacterium tumefaciens</i> binary vector system by adventitious shoot regeneration on leaf and stem segments. <i>Plant Molecular Biology</i> , 1989, 12, 329-337.	3.9	92
82	Identification of Granule-Bound Starch Synthase in Potato Tubers. <i>Plant Physiology</i> , 1986, 82, 411-416.	4.8	90
83	An Online Potato Pedigree Database Resource. <i>Potato Research</i> , 2007, 50, 45-57.	2.7	90
84	MADMAX - Management and analysis database for multiple -omics experiments. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 160.	1.5	90
85	Silencing of six susceptibility genes results in potato late blight resistance. <i>Transgenic Research</i> , 2016, 25, 731-742.	2.4	89
86	Isolation and characterization of a cDNA encoding granule-bound starch synthase in cassava ( <i>Manihot esculenta</i> Crantz) and its antisense expression in potato. <i>Plant Molecular Biology</i> , 1993, 23, 947-962.	3.9	88
87	Sequencing the Potato Genome: Outline and First Results to Come from the Elucidation of the Sequence of the World's Third Most Important Food Crop. <i>American Journal of Potato Research</i> , 2009, 86, 417-429.	0.9	87
88	Beyond genomic variation - comparison and functional annotation of three Brassica rapagenomes: a turnip, a rapid cycling and a Chinese cabbage. <i>BMC Genomics</i> , 2014, 15, 250.	2.8	87
89	Responses to combined abiotic and biotic stress in tomato are governed by stress intensity and resistance mechanism. <i>Journal of Experimental Botany</i> , 2016, 67, 5119-5132.	4.8	87
90	In muro fragmentation of the rhamnogalacturonan I backbone in potato ( <i>Solanum tuberosum</i> L.) results in a reduction and altered location of the galactan and arabinan side-chains and abnormal periderm development. <i>Plant Journal</i> , 2002, 30, 403-413.	5.7	86

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91	Tuber on a chip: differential gene expression during potato tuber development. <i>Plant Biotechnology Journal</i> , 2005, 3, 505-519.	8.3	86
92	Tomato breeding in the genomics era: insights from a SNP array. <i>BMC Genomics</i> , 2013, 14, 354.	2.8	86
93	Bacterial Canker of Tomato: Current Knowledge of Detection, Management, Resistance, and Interactions. <i>Plant Disease</i> , 2015, 99, 4-13.	1.4	86
94	Impact of drought stress on growth and quality of miscanthus for biofuel production. <i>GCB Bioenergy</i> , 2017, 9, 770-782.	5.6	85
95	Resistance to Tomato Yellow Leaf Curl Virus in Tomato Germplasm. <i>Frontiers in Plant Science</i> , 2018, 9, 1198.	3.6	85
96	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	7.3	84
97	The <i>R<sub>Pi-mcd1</sub></i> Locus from <i>Solanum microdontum</i> Involved in Resistance to <i>Phytophthora infestans</i> , Causing a Delay in Infection, Maps on Potato Chromosome 4 in a Cluster of NBS-LRR Genes. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 909-918.	2.6	83
98	Identification of alleles of carotenoid pathway genes important for zeaxanthin accumulation in potato tubers. <i>Plant Molecular Biology</i> , 2010, 73, 659-671.	3.9	83
99	Induced point mutations in the phytoene synthase 1 gene cause differences in carotenoid content during tomato fruit ripening. <i>Molecular Breeding</i> , 2012, 29, 801-812.	2.1	79
100	Breeding Has Increased the Diversity of Cultivated Tomato in The Netherlands. <i>Frontiers in Plant Science</i> , 2019, 10, 1606.	3.6	79
101	Cross-Species Bacterial Artificial Chromosome Fluorescence in Situ Hybridization Painting of the Tomato and Potato Chromosome 6 Reveals Undescribed Chromosomal Rearrangements. <i>Genetics</i> , 2008, 180, 1319-1328.	2.9	78
102	The <i>Solanum demissum</i> R8 late blight resistance gene is an Sw-5 homologue that has been deployed worldwide in late blight resistant varieties. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1785-1796.	3.6	78
103	Genomic rearrangements and signatures of breeding in the allo-octoploid strawberry as revealed through an allele dose based SSR linkage map. <i>BMC Plant Biology</i> , 2014, 14, 55.	3.6	75
104	A detailed analysis of the recombination landscape of the button mushroom <i>Agaricus bisporus</i> var. <i>bisporus</i> . <i>Fungal Genetics and Biology</i> , 2016, 93, 35-45.	2.1	75
105	Untargeted metabolomic analysis of tomato pollen development and heat stress response. <i>Plant Reproduction</i> , 2017, 30, 81-94.	2.2	75
106	Outlook for coeliac disease patients: towards bread wheat with hypoimmunogenic gluten by gene editing of $\alpha$ - and $\beta$ -gliadin gene families. <i>BMC Plant Biology</i> , 2019, 19, 333.	3.6	75
107	Genetic analysis of metabolites in apple fruits indicates an mQTL hotspot for phenolic compounds on linkage group 16. <i>Journal of Experimental Botany</i> , 2012, 63, 2895-2908.	4.8	74
108	Powdery Mildew Resistance in Tomato by Impairment of SIPMR4 and SIDMR1. <i>PLoS ONE</i> , 2013, 8, e67467.	2.5	74



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109	A non-directed approach to the differential analysis of multiple LC-MS-derived metabolic profiles. <i>Metabolomics</i> , 2005, 1, 169-180.	3.0	73
110	Towards modifying plants for altered starch content and composition. <i>Trends in Biotechnology</i> , 1993, 11, 63-68.	9.3	72
111	Partial preferential chromosome pairing is genotype dependent in tetraploid rose. <i>Plant Journal</i> , 2017, 90, 330-343.	5.7	72
112	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. <i>Molecular Plant</i> , 2022, 15, 520-536.	8.3	72
113	Gene expression and carbohydrate content during stolon to tuber transition in potatoes ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBJ/Overload	3.2	71
114	Mapping of the <i>S. demissum</i> late blight resistance gene R8 to a new locus on chromosome IX. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1331-1340.	3.6	70
115	Evaluation of <i>Miscanthus sinensis</i> biomass quality as feedstock for conversion into different bioenergy products. <i>GCB Bioenergy</i> , 2017, 9, 176-190.	5.6	70
116	Molecular breeding for resistance to <i>Phytophthora infestans</i> (Mont.) de Bary in potato ( <i>Solanum tuberosum</i> L.): a perspective of cisgenesis. <i>Plant Breeding</i> , 2009, 128, 109-117.	1.9	69
117	Diversity, Distribution, and Evolution of <i>Solanum bulbocastanum</i> Late Blight Resistance Genes. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1206-1216.	2.6	69
118	Introduction of sense and antisense cDNA for branching enzyme in the amylose-free potato mutant leads to physico-chemical changes in the starch. <i>Planta</i> , 1996, 198, 340-347.	3.2	68
119	Interactions between membrane-bound cellulose synthases involved in the synthesis of the secondary cell wall. <i>FEBS Letters</i> , 2009, 583, 978-982.	2.8	68
120	A taste of sweet pepper: Volatile and non-volatile chemical composition of fresh sweet pepper ( <i>Capsicum annuum</i> ) in relation to sensory evaluation of taste. <i>Food Chemistry</i> , 2012, 132, 301-310.	8.2	68
121	Transformation of the potato variety Desiree with single or multiple resistance genes increases resistance to late blight under field conditions. <i>Crop Protection</i> , 2015, 77, 163-175.	2.1	67
122	Carbon partitioning mechanisms in POTATO under drought stress. <i>Plant Physiology and Biochemistry</i> , 2020, 146, 211-219.	5.8	67
123	Sucrose Metabolism in Plastids. <i>Plant Physiology</i> , 2001, 125, 926-934.	4.8	66
124	High-resolution Mapping and Analysis of the Resistance Locus Rpi-abpt Against <i>Phytophthora infestans</i> in Potato. <i>Molecular Breeding</i> , 2005, 16, 33-43.	2.1	66
125	Identification and QTL mapping of whitefly resistance components in <i>Solanum galapagense</i> . <i>Theoretical and Applied Genetics</i> , 2013, 126, 1487-1501.	3.6	66
126	Identification of agronomically important QTL in tetraploid potato cultivars using a marker-trait association analysis. <i>Theoretical and Applied Genetics</i> , 2014, 127, 731-748.	3.6	66



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127	Combined biotic and abiotic stress resistance in tomato. <i>Euphytica</i> , 2015, 202, 317-332.	1.2	66
128	Genetic dissection of drought tolerance and recovery potential by quantitative trait locus mapping of a diploid potato population. <i>Molecular Breeding</i> , 2012, 30, 1413-1429.	2.1	65
129	Genome composition of triploid lily cultivars derived from sexual polyploidization of <i>Longiflorum</i> — <i>Asiatic</i> hybrids ( <i>Lilium</i> ). <i>Euphytica</i> , 2008, 160, 207-215.	1.2	64
130	Chromosome evolution in <i>Solanum</i> traced by cross-species BAC-FISH. <i>New Phytologist</i> , 2012, 195, 688-698.	7.3	64
131	Screening for pollen tolerance to high temperatures in tomato. <i>Euphytica</i> , 2017, 213, 1.	1.2	64
132	Potato CYCLING DOF FACTOR1 and its lncRNA counterpart <i>StFLORE</i> link tuber development and drought response. <i>Plant Journal</i> , 2021, 105, 855-869.	5.7	64
133	Anthocyanin production as a potential visual selection marker during plant transformation. <i>Transgenic Research</i> , 2011, 20, 1253-1264.	2.4	63
134	Production of transgenic cassava ( <i>Manihot esculenta</i> Crantz) plants by particle bombardment using luciferase activity as selection marker. <i>Molecular Breeding</i> , 1996, 2, 339-349.	2.1	62
135	Genetic analysis of resistance to septoria tritici blotch in the French winter wheat cultivars Balance and Apache. <i>Theoretical and Applied Genetics</i> , 2011, 123, 741-754.	3.6	62
136	Generation and analysis of expressed sequence tags in the extreme large genomes <i>Lilium</i> and <i>Tulipa</i> . <i>BMC Genomics</i> , 2012, 13, 640.	2.8	62
137	Integration of multi-omics data for prediction of phenotypic traits using random forest. <i>BMC Bioinformatics</i> , 2016, 17, 180.	2.6	62
138	Fluorescence in situ hybridization on extended DNA fibres as a tool to analyse complex DNA loci in potato. <i>Plant Journal</i> , 1998, 13, 837-847.	5.7	61
139	A crosstalk of auxin and GA during tuber development. <i>Plant Signaling and Behavior</i> , 2012, 7, 1360-1363.	2.4	61
140	Genome-Wide Study of the Tomato SIMLO Gene Family and Its Functional Characterization in Response to the Powdery Mildew Fungus <i>Oidium neolycopersici</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 380.	3.6	61
141	QTL methodology for response curves on the basis of non-linear mixed models, with an illustration to senescence in potato. <i>Theoretical and Applied Genetics</i> , 2006, 113, 288-300.	3.6	60
142	The knock-down of the expression of <i>MdMLO19</i> reduces susceptibility to powdery mildew ( <i>Podosphaera leucotricha</i> ) in apple ( <i>Malus domestica</i> ). <i>Plant Biotechnology Journal</i> , 2016, 14, 2033-2044.	8.3	60
143	Drought response in field grown potatoes and the interactions between canopy growth and yield. <i>Agricultural Water Management</i> , 2018, 206, 20-30.	5.6	60
144	Improved Cassava Starch by Antisense Inhibition of Granule-bound Starch Synthase I. <i>Molecular Breeding</i> , 2005, 16, 163-172.	2.1	58

#	ARTICLE	IF	CITATIONS
145	Mapping and characterization of novel parthenocarp QTLs in tomato. <i>Theoretical and Applied Genetics</i> , 2008, 116, 755-767.	3.6	58
146	From QTL to candidate gene: Genetical genomics of simple and complex traits in potato using a pooling strategy. <i>BMC Genomics</i> , 2010, 11, 158.	2.8	58
147	Europe's Farm to Fork Strategy and Its Commitment to Biotechnology and Organic Farming: Conflicting or Complementary Goals?. <i>Trends in Plant Science</i> , 2021, 26, 600-606.	8.8	58
148	Title is missing!. <i>Euphytica</i> , 2002, 124, 13-22.	1.2	57
149	Intergenic recombination in <i>F<sub>1</sub></i> lily hybrids ( <i>Lilium</i> ) and its significance for genetic variation in the BC <sub>1</sub> progenies as revealed by GISH and FISH. <i>Genome</i> , 2005, 48, 884-894.	2.0	57
150	Design of a <i>Brassica rapa</i> core collection for association mapping studies 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, 884-898.	2.0	56
151	Environmental biosafety and transgenic potato in a centre of diversity for this crop. <i>Nature</i> , 2004, 432, 222-225.	27.8	55
152	Data integration and network reconstruction with omics data using Random Forest regression in potato. <i>Analytica Chimica Acta</i> , 2011, 705, 56-63.	5.4	55
153	Identification of candidate MLO powdery mildew susceptibility genes in cultivated Solanaceae and functional characterization of tobacco NtMLO1. <i>Transgenic Research</i> , 2015, 24, 847-858.	2.4	55
154	Differences in regulation of carbohydrate metabolism during early fruit development between domesticated tomato and two wild relatives. <i>Planta</i> , 2007, 226, 929-939.	3.2	54
155	Discrete Forms of Amylose Are Synthesized by Isoforms of GBSSI in Pea[W]. <i>Plant Cell</i> , 2002, 14, 1767-1785.	6.6	53
156	Enhancing pterin and para-aminobenzoate content is not sufficient to successfully biofortify potato tubers and <i>Arabidopsis thaliana</i> plants with folate. <i>Journal of Experimental Botany</i> , 2013, 64, 3899-3909.	4.8	53
157	Expression of <i>Escherichia coli</i> branching enzyme in tubers of amylose-free transgenic potato leads to an increased branching degree of the amylopectin. <i>Plant Journal</i> , 1996, 10, 83-90.	5.7	52
158	Genetic Positioning of Centromeres Using Half-Tetrad Analysis in a 4x2x Cross Population of Potato. <i>Genetics</i> , 2007, 176, 85-94.	2.9	52
159	Unravelling enzymatic discoloration in potato through a combined approach of candidate genes, QTL, and expression analysis. <i>Theoretical and Applied Genetics</i> , 2007, 115, 245-252.	3.6	52
160	An ultra-dense integrated linkage map for hexaploid chrysanthemum enables multi-allelic QTL analysis. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2527-2541.	3.6	52
161	A pipeline for high throughput detection and mapping of SNPs from EST databases. <i>Molecular Breeding</i> , 2010, 26, 65-75.	2.1	51
162	Genetic mapping in <i>Lilium</i> : mapping of major genes and quantitative trait loci for several ornamental traits and disease resistances. <i>Plant Breeding</i> , 2011, 130, 372-382.	1.9	51

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163	In vitro screening and QTL analysis for drought tolerance in diploid potato. <i>Euphytica</i> , 2011, 181, 357-369.	1.2	51
164	Field testing and exploitation of genetically modified cassava with low-amylose or amylose-free starch in Indonesia. <i>Transgenic Research</i> , 2012, 21, 39-50.	2.4	51
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166	Integrating haplotype-specific linkage maps in tetraploid species using SNP markers. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2211-2226.	3.6	51
167	Far-red radiation increases dry mass partitioning to fruits but reduces <i>Botrytis cinerea</i> resistance in tomato. <i>Environmental and Experimental Botany</i> , 2019, 168, 103889.	4.2	51
168	Microbial starch-binding domains as a tool for targeting proteins to granules during starch biosynthesis. <i>Plant Molecular Biology</i> , 2003, 51, 789-801.	3.9	50
169	Characterization and high-resolution mapping of a late blight resistance locus similar to R2 in potato. <i>Theoretical and Applied Genetics</i> , 2005, 111, 591-597.	3.6	50
170	Agroinfection-based high-throughput screening reveals specific recognition of INF elicitors in <i>Solanum</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 499-510.	4.2	50
171	Deciphering the genetic control of fruit texture in apple by multiple family-based analysis and genome-wide association. <i>Journal of Experimental Botany</i> , 2017, 68, 1451-1466.	4.8	50
172	Development of Wheat With Hypoimmunogenic Gluten Obstructed by the Gene Editing Policy in Europe. <i>Frontiers in Plant Science</i> , 2018, 9, 1523.	3.6	50
173	Gene expression and carbohydrate content during stolon to tuber transition in potatoes ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 3.2 49	3.2	49
174	A novel approach to locate <i>Phytophthora infestans</i> resistance genes on the potato genetic map. <i>Theoretical and Applied Genetics</i> , 2010, 120, 785-796.	3.6	49
175	Identification of quantitative trait loci for ion homeostasis and salt tolerance in barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 2.1 49	2.1	49
176	Developments in breeding of <i>Agaricus bisporus</i> var. <i>bisporus</i> : progress made and technical and legal hurdles to take. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1819-1829.	3.6	49
177	Two different <i>R</i> gene loci co-evolved with <i>Avr2</i> of <i>Phytophthora infestans</i> and confer distinct resistance specificities in potato. <i>Studies in Mycology</i> , 2018, 89, 105-115.	7.2	49
178	Folate Biofortification of Potato by Tuber-Specific Expression of Four Folate Biosynthesis Genes. <i>Molecular Plant</i> , 2018, 11, 175-188.	8.3	49
179	Efficient transformation of potato ( <i>Solanum tuberosum</i> L.) using a binary vector in <i>Agrobacterium rhizogenes</i> . <i>Theoretical and Applied Genetics</i> , 1989, 78, 594-600.	3.6	48
180	Quantitative Trait Locus Analysis of Seed Germination and Seedling Vigor in <i>Brassica rapa</i> Reveals QTL Hotspots and Epistatic Interactions. <i>Frontiers in Plant Science</i> , 2015, 6, 1032.	3.6	48

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181	Gapless Genome Assembly of the Potato and Tomato Early Blight Pathogen <i>Alternaria solani</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 692-694.	2.6	48
182	Three Combined Quantitative Trait Loci from Nonhost <i>Lactuca saligna</i> Are Sufficient to Provide Complete Resistance of Lettuce Against <i>Bremia lactucae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1160-1168.	2.6	47
183	Identification of markers associated with bacterial blight resistance loci in cowpea [ <i>Vigna unguiculata</i> (L.) Walp.]. <i>Euphytica</i> , 2010, 175, 215-226.	1.2	47
184	EU court casts new plant breeding techniques into regulatory limbo. <i>Nature Biotechnology</i> , 2018, 36, 799-800.	17.5	47
185	A Welcome Proposal to Amend the GMO Legislation of the EU. <i>Trends in Biotechnology</i> , 2018, 36, 1100-1103.	9.3	47
186	Developmental changes in enzymes involved in the conversion of hexose phosphate and its subsequent metabolites during early tuberization of potato. <i>Plant, Cell and Environment</i> , 1999, 22, 1085-1096.	5.7	46
187	Occurrence of 2n gametes in the F1 hybrids of Oriental Asiatic lilies ( <i>Lilium</i> ): Relevance to intergenomic recombination and backcrossing. <i>Euphytica</i> , 2005, 143, 67-73.	1.2	46
188	Screening of pepper accessions for resistance against two thrips species ( <i>Frankliniella occidentalis</i> ) and <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	1.2	46
189	Identification and mapping of quantitative resistance to late blight ( <i>Phytophthora infestans</i> ) in <i>Solanum habrochaites</i> LA1777. <i>Euphytica</i> , 2011, 179, 427-438.	1.2	46
190	A limited set of starch related genes explain several interrelated traits in potato. <i>Euphytica</i> , 2012, 186, 501-516.	1.2	46
191	Mapping in the era of sequencing: high density genotyping and its application for mapping TYLCV resistance in <i>Solanum pimpinellifolium</i> . <i>BMC Genomics</i> , 2014, 15, 1152.	2.8	46
192	Assessing the genetic variation of Ty-1 and Ty-3 alleles conferring resistance to tomato yellow leaf curl virus in a broad tomato germplasm. <i>Molecular Breeding</i> , 2015, 35, 132.	2.1	46
193	The ELR-SOBIR1 Complex Functions as a Two-Component Receptor-Like Kinase to Mount Defense Against <i>Phytophthora infestans</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018, 31, 795-802.	2.6	46
194	Reduction of starch granule size by expression of an engineered tandem starch-binding domain in potato plants. <i>Plant Biotechnology Journal</i> , 2004, 2, 251-260.	8.3	45
195	Hybridization between wild and cultivated potato species in the Peruvian Andes and biosafety implications for deployment of GM potatoes. <i>Euphytica</i> , 2008, 164, 881-892.	1.2	45
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197	Assignment of genetic linkage maps to diploid <i>Solanum tuberosum</i> pachytene chromosomes by BAC-FISH technology. <i>Chromosome Research</i> , 2009, 17, 899-915.	2.2	44
198	Potato starch synthases: Functions and relationships. <i>Biochemistry and Biophysics Reports</i> , 2017, 10, 7-16.	1.3	44

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200	A novel method for the construction of genome wide transcriptome maps. <i>Plant Journal</i> , 2002, 31, 211-222.	5.7	43
201	Progenies of allotriploids of Oriental $\tilde{\text{A}}$ – Asiatic lilies ( <i>Lilium</i> ) examined by GISH analysis. <i>Euphytica</i> , 2006, 151, 243-250.	1.2	43
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203	Molecular and Morphological Aspects of Annealing-Induced Stabilization of Starch Crystallites. <i>Biomacromolecules</i> , 2012, 13, 1361-1370.	5.4	43
204	Neofunctionalisation of the Sli gene leads to self-compatibility and facilitates precision breeding in potato. <i>Nature Communications</i> , 2021, 12, 4141.	12.8	43
205	The PIN family of proteins in potato and their putative role in tuberization. <i>Frontiers in Plant Science</i> , 2013, 4, 524.	3.6	42
206	High-density SNP-based genetic maps for the parents of an outcrossed and a selfed tetraploid garden rose cross, inferred from admixed progeny using the 68k rose SNP array. <i>Horticulture Research</i> , 2016, 3, 16052.	6.3	42
207	Cloning, partial sequencing and expression of a cDNA coding for branching enzyme in cassava. <i>Plant Molecular Biology</i> , 1992, 20, 809-819.	3.9	41
208	Dissection of foliage and tuber late blight resistance in mapping populations of potato. <i>Euphytica</i> , 2005, 143, 75-83.	1.2	41
209	Analysis of the meiosis in the F1 hybrids of Longiflorum $\tilde{\text{A}}$ – Asiatic (LA) of lilies ( <i>Lilium</i> ) using genomic in situ hybridization. <i>Journal of Genetics and Genomics</i> , 2008, 35, 687-695.	3.9	41
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211	KORRIGAN1 Interacts Specifically with Integral Components of the Cellulose Synthase Machinery. <i>PLoS ONE</i> , 2014, 9, e112387.	2.5	41
212	Genetic variation, heritability and genotype by environment interaction of morphological traits in a tetraploid rose population. <i>BMC Genetics</i> , 2014, 15, 146.	2.7	41
213	An updated conventional- and a novel GM potato late blight R gene differential set for virulence monitoring of <i>Phytophthora infestans</i> . <i>Euphytica</i> , 2015, 202, 219-234.	1.2	41
214	Down-regulation of Arabidopsis DND1 orthologs in potato and tomato leads to broad-spectrum resistance to late blight and powdery mildew. <i>Transgenic Research</i> , 2016, 25, 123-138.	2.4	41
215	Potential for analytic breeding in allopolyploids: an illustration from Longiflorum $\tilde{\text{A}}$ – $\tilde{\text{A}}$ Asiatic hybrid lilies ( <i>Lilium</i> ). <i>Euphytica</i> , 2009, 166, 399-409.	1.2	40
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218	Detection of an inversion in the Ty-2 region between <i>S. lycopersicum</i> and <i>S. habrochaites</i> by a combination of de novo genome assembly and BAC cloning. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1987-1997.	3.6	40
219	Solyntus, the New Highly Contiguous Reference Genome for Potato ( <i>Solanum tuberosum</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3489-3495.	1.8	40
220	In situ hybridization to somatic metaphase chromosomes of potato. <i>Theoretical and Applied Genetics</i> , 1988, 76, 420-424.	3.6	39
221	Field evaluation of transgenic potato plants expressing an antisense granule-bound starch synthase gene: increase of the antisense effect during tuber growth. <i>Plant Molecular Biology</i> , 1994, 26, 1759-1773.	3.9	39
222	Modulation of the cellulose content of tuber cell walls by antisense expression of different potato ( <i>Solanum tuberosum</i> L.) <i>CesA</i> clones. <i>Phytochemistry</i> , 2004, 65, 535-546.	2.9	39
223	How to effectively deploy plant resistances to pests and pathogens in crop breeding. <i>Euphytica</i> , 2013, 190, 321-334.	1.2	39
224	Pectic arabinan side chains are essential for pollen cell wall integrity during pollen development. <i>Plant Biotechnology Journal</i> , 2014, 12, 492-502.	8.3	39
225	Efficient development of highly polymorphic microsatellite markers based on polymorphic repeats in transcriptome sequences of multiple individuals. <i>Molecular Ecology Resources</i> , 2015, 15, 17-27.	4.8	39
226	Complementation of the amylose-free starch mutant of potato ( <i>Solanum tuberosum</i> .) by the gene encoding granule-bound starch synthase. <i>Theoretical and Applied Genetics</i> , 1991, 82, 289-295.	3.6	38
227	Factors affecting the inhibition by antisense RNA of granule-bound starch synthase gene expression in potato. <i>Molecular Genetics and Genomics</i> , 1995, 246, 745-755.	2.4	38
228	Efficiency of transcriptional gene silencing of GBSSI in potato depends on the promoter region that is used in an inverted repeat. <i>Molecular Genetics and Genomics</i> , 2006, 275, 437-449.	2.1	38
229	Characterization of Cassava Starch Attributes of Different Genotypes. <i>Starch/Staerke</i> , 2009, 61, 472-481.	2.1	38
230	SolRgene: an online database to explore disease resistance genes in tuber-bearing <i>Solanum</i> species. <i>BMC Plant Biology</i> , 2011, 11, 116.	3.6	38
231	Resistance factors in pepper inhibit larval development of thrips ( <i>Frankliniella</i> ) Tj ETQq1 1 0.784314 <sup>rgBT / Overlock 10 T</sup> 1.4 38	1.4	38
232	Identification of QTL markers contributing to plant growth, oil yield and fatty acid composition in the oilseed crop <i>Jatropha curcas</i> L.. <i>Biotechnology for Biofuels</i> , 2015, 8, 160.	6.2	38
233	Induction, germination and shoot development of somatic embryos in cassava. <i>Plant Cell, Tissue and Organ Culture</i> , 1993, 33, 151-156.	2.3	37
234	Microbial fructan production in transgenic potato plants and tubers. <i>Industrial Crops and Products</i> , 1996, 5, 35-46.	5.2	37

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235	Post-transcriptional Gene Silencing of GBSSI in Potato: Effects of Size and Sequence of the Inverted Repeats. <i>Plant Molecular Biology</i> , 2006, 60, 647-662.	3.9	37
236	Effect of Maize Biomass Composition on the Optimization of Dilute-Acid Pretreatments and Enzymatic Saccharification. <i>Bioenergy Research</i> , 2013, 6, 1038-1051.	3.9	37
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238	Future-proof crops: challenges and strategies for climate resilience improvement. <i>Current Opinion in Plant Biology</i> , 2016, 30, 47-56.	7.1	37
239	QTL mapping of insect resistance components of <i>Solanum galapagense</i> . <i>Theoretical and Applied Genetics</i> , 2019, 132, 531-541.	3.6	37
240	Development of a highly efficient, repetitive system of organogenesis in soybean ( <i>Glycine max</i> (L.)) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	5.6	36
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243	Expression and inheritance of inserted markers in binary vector carrying <i>Agrobacterium rhizogenes</i> -transformed potato ( <i>Solanum tuberosum</i> L.). <i>Theoretical and Applied Genetics</i> , 1989, 78, 705-714.	3.6	35
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245	Title is missing!. <i>Euphytica</i> , 2001, 120, 85-93.	1.2	35
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247	Conclusive evidence for hexasomic inheritance in chrysanthemum based on analysis of a 183k SNP array. <i>BMC Genomics</i> , 2017, 18, 585.	2.8	35
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249	The tuberization signal StSP6A represses flower bud development in potato. <i>Journal of Experimental Botany</i> , 2019, 70, 937-948.	4.8	35
250	The genetic and functional analysis of flavor in commercial tomato: the FLORAL4 gene underlies a QTL for floral aroma volatiles in tomato fruit. <i>Plant Journal</i> , 2020, 103, 1189-1204.	5.7	35
251	Identification of silverleaf whitefly resistance in pepper. <i>Plant Breeding</i> , 2011, 130, 708-714.	1.9	34
252	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



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254	Relevance of unilateral and bilateral sexual polyploidization in relation to intergenomic recombination and introgression in <i>Lilium</i> species hybrids. <i>Euphytica</i> , 2010, 171, 157-173.	1.2	33
255	Seedling salt tolerance in tomato. <i>Euphytica</i> , 2011, 178, 403-414.	1.2	33
256	Activation tagging of ATHB13 in <i>Arabidopsis thaliana</i> confers broad-spectrum disease resistance. <i>Plant Molecular Biology</i> , 2014, 86, 641-653.	3.9	33
257	Understanding the role of oat $\beta$ -glucan in oat-based dough systems. <i>Journal of Cereal Science</i> , 2015, 62, 1-7.	3.7	33
258	Impact of Different Lignin Fractions on Saccharification Efficiency in Diverse Species of the Bioenergy Crop <i>Miscanthus</i> . <i>Bioenergy Research</i> , 2016, 9, 146-156.	3.9	33
259	Plant regeneration from protoplasts isolated from friable embryogenic callus of cassava. <i>Plant Cell Reports</i> , 1998, 18, 159-165.	5.6	32
260	A potato tuber-expressed mRNA with homology to steroid dehydrogenases affects gibberellin levels and plant development. <i>Plant Journal</i> , 2001, 25, 595-604.	5.7	32
261	Towards a more versatile $\beta$ -glucan biosynthesis in plants. <i>Journal of Plant Physiology</i> , 2003, 160, 765-777.	3.5	32
262	Linked, if Not the Same, <i>Mi-1</i> Homologues Confer Resistance to Tomato Powdery Mildew and Root-Knot Nematodes. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 441-450.	2.6	32
263	Microsatellite allele dose and configuration establishment (MADCE): an integrated approach for genetic studies in allopolyploids. <i>BMC Plant Biology</i> , 2012, 12, 25.	3.6	32
264	Down regulation of <i>StGA3ox</i> genes in potato results in altered GA content and affect plant and tuber growth characteristics. <i>Journal of Plant Physiology</i> , 2013, 170, 1228-1234.	3.5	32
265	Capturing flavors from <i>Capsicum baccatum</i> by introgression in sweet pepper. <i>Theoretical and Applied Genetics</i> , 2014, 127, 373-390.	3.6	32
266	RLP/K enrichment sequencing; a novel method to identify receptor-like protein ( <i>RLP</i> ) and receptor-like kinase ( <i>RLK</i> ) genes. <i>New Phytologist</i> , 2020, 227, 1264-1276.	7.3	32
267	Exploitation of a marker dense linkage map of potato for positional cloning of a wart disease resistance gene. <i>Theoretical and Applied Genetics</i> , 2006, 112, 269-277.	3.6	31
268	A Bayesian analysis of gene flow from crops to their wild relatives: cultivated ( <i>Lactuca sativa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Molecular Ecology</i> , 2012, 21, 2640-2654.	3.9	31
269	Screening for new sources of resistance to <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> (Cmm) in tomato. <i>Euphytica</i> , 2013, 190, 309-317.	1.2	31
270	Large subclonal variation in <i>Phytophthora infestans</i> populations associated with <i>Andean</i> potato landraces. <i>Plant Pathology</i> , 2013, 62, 1081-1088.	2.4	31

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271	Genetics and molecular mechanisms of resistance to powdery mildews in tomato ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.7	31
272	Susceptibility reversed: modified plant susceptibility genes for resistance to bacteria. <i>Trends in Plant Science</i> , 2022, 27, 69-79.	8.8	31
273	Comparison of tuber and shoot formation from in vitro cultured potato explants. <i>Plant Cell, Tissue and Organ Culture</i> , 1998, 53, 197-204.	2.3	30
274	Physiological and genetic control of tuber formation. <i>Potato Research</i> , 1999, 42, 313-331.	2.7	30
275	An Accurate In Vitro Assay for High-Throughput Disease Testing of <i>Phytophthora infestans</i> in Potato. <i>Plant Disease</i> , 2005, 89, 1263-1267.	1.4	30
276	Multi-environment QTL analysis of plant and flower morphological traits in tetraploid rose. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2055-2069.	3.6	30
277	The European Union Court's Advocate General's Opinion and new plant breeding techniques. <i>Nature Biotechnology</i> , 2018, 36, 573-575.	17.5	30
278	Quantifying the Power and Precision of QTL Analysis in Autopolyploids Under Bivalent and Multivalent Genetic Models. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2107-2122.	1.8	30
279	Pinpointing towards improved transformation and regeneration of cassava ( <i>Manihot esculenta</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	3.6	29
280	Temporal dynamics of tuber formation and related processes in a crossing population of potato ( <i>Solanum tuberosum</i> ). <i>Annals of Applied Biology</i> , 2003, 143, 175-186.	2.5	29
281	Detection and Quantification of <i>Leveillula taurica</i> Growth in Pepper Leaves. <i>Phytopathology</i> , 2013, 103, 623-632.	2.2	29
282	“Schmidt's Antonovka”™ is identical to “Common Antonovka”™, an apple cultivar widely used in Russia in breeding for biotic and abiotic stresses. <i>Tree Genetics and Genomes</i> , 2014, 10, 261-271.	1.6	29
283	Graphical genotyping as a method to map <i>Ny (o,n)sto</i> and <i>Gpa5</i> using a reference panel of tetraploid potato cultivars. <i>Theoretical and Applied Genetics</i> , 2017, 130, 515-528.	3.6	29
284	Functional characterization of cucumber ( <i>Cucumis sativus</i> L.) Clade V MLO genes. <i>BMC Plant Biology</i> , 2017, 17, 80.	3.6	29
285	Expression Analysis of a Family of nsLTP Genes Tissue Specifically Expressed throughout the Plant and during Potato Tuber Life Cycle. <i>Plant Physiology</i> , 2002, 129, 1494-1506.	4.8	28
286	Dynamics of senescence-related QTLs in potato. <i>Euphytica</i> , 2012, 183, 289-302.	1.2	28
287	Abiotic stress QTL in lettuce crop “wild hybrids: comparing greenhouse and field experiments. <i>Ecology and Evolution</i> , 2014, 4, 2395-2409.	1.9	28
288	Quantitative trait locus mapping for bruising sensitivity and cap color of <i>Agaricus bisporus</i> (button) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	2.1	28

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290	Ethylene and Abscisic Acid Signaling Pathways Differentially Influence Tomato Resistance to Combined Powdery Mildew and Salt Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 2009.	3.6	28
291	Engineering Potato Starch with a Higher Phosphate Content. <i>PLoS ONE</i> , 2017, 12, e0169610.	2.5	28
292	Development of the GlutEnSeq capture system for sequencing gluten gene families in hexaploid bread wheat with deletions or mutations induced by $\gamma$ -irradiation or CRISPR/Cas9. <i>Journal of Cereal Science</i> , 2019, 88, 157-166.	3.7	28
293	Fusion proteins comprising the catalytic domain of mutansucrase and a starch-binding domain can alter the morphology of amylose-free potato starch granules during biosynthesis. <i>Transgenic Research</i> , 2007, 16, 645-656.	2.4	27
294	Promiscuous, non-catalytic, tandem carbohydrate-binding modules modulate the cell-wall structure and development of transgenic tobacco ( <i>Nicotiana tabacum</i> ) plants. <i>Journal of Plant Research</i> , 2007, 120, 605-617.	2.4	27
295	Comparative BAC end sequence analysis of tomato and potato reveals overrepresentation of specific gene families in potato. <i>BMC Plant Biology</i> , 2008, 8, 34.	3.6	27
296	Prediction of sweet pepper ( <i>Capsicum annuum</i> ) flavor over different harvests. <i>Euphytica</i> , 2012, 187, 117-131.	1.2	26
297	Genetic Diversity of Salt Tolerance in <i>Miscanthus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 187.	3.6	26
298	Shoot sodium exclusion in salt stressed barley ( <i>Hordeum vulgare</i> L.) is determined by allele specific increased expression of HKT1;5. <i>Journal of Plant Physiology</i> , 2019, 241, 153029.	3.5	26
299	The NLR Protein Encoded by the Resistance Gene Ty-2 Is Triggered by the Replication-Associated Protein Rep/C1 of Tomato Yellow Leaf Curl Virus. <i>Frontiers in Plant Science</i> , 2020, 11, 545306.	3.6	26
300	Pectin – the Hairy Thing. , 2003, , 47-59.		25
301	Genetic mapping and transcription analyses of resistance gene loci in potato using NBS profiling. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1379-1388.	3.6	25
302	Construction of chromosomal recombination maps of three genomes of lilies ( <i>Lilium</i> ) based on GISH analysis. <i>Genome</i> , 2009, 52, 238-251.	2.0	25
303	SNP markers retrieval for a non-model species: a practical approach. <i>BMC Research Notes</i> , 2012, 5, 79.	1.4	25
304	Cell Wall Diversity in Forage Maize: Genetic Complexity and Bioenergy Potential. <i>Bioenergy Research</i> , 2015, 8, 187-202.	3.9	25
305	Effect of kilning and milling on the dough-making properties of oat flour. <i>LWT - Food Science and Technology</i> , 2015, 63, 960-965.	5.2	25
306	Distribution of P1(D1) wart disease resistance in potato germplasm and GWAS identification of haplotype-specific SNP markers. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1859-1871.	3.6	25

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308	Map- vs. homology-based cloning for the recessive gene <i>ol-2</i> conferring resistance to tomato powdery mildew. <i>Euphytica</i> , 2008, 162, 91-98.	1.2	24
309	Genomic regions in crop-wild hybrids of lettuce are affected differently in different environments: implications for crop breeding. <i>Evolutionary Applications</i> , 2012, 5, 629-640.	3.1	24
310	Genome-wide analysis of coordinated transcript abundance during seed development in different <i>Brassica rapa</i> morphotypes. <i>BMC Genomics</i> , 2013, 14, 840.	2.8	24
311	Overexpression of <i>IRM1</i> Enhances Resistance to Aphids in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2013, 8, e70914.	2.5	24
312	Genome-wide association analysis in tetraploid potato reveals four QTLs for protein content. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	24
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314	Differential responses to salt stress in ion dynamics, growth and seed yield of European quinoa varieties. <i>Environmental and Experimental Botany</i> , 2020, 177, 104146.	4.2	24
315	The dosage effect of the wildtype <i>GBSS</i> allele is linear for <i>GBSS</i> activity but not for amylose content: absence of amylose has a distinct influence on the physico-chemical properties of starch. <i>Theoretical and Applied Genetics</i> , 1996, 92, 121-127.	3.6	24
316	Development of a plant regeneration system based on friable embryogenic callus in the ornamental <i>Alstroemeria</i> . <i>Plant Cell Reports</i> , 2000, 19, 529-534.	5.6	23
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318	High throughput phenotyping for aphid resistance in large plant collections. <i>Plant Methods</i> , 2012, 8, 33.	4.3	23
319	Genomic and environmental selection patterns in two distinct lettuce crop-wild hybrid crosses. <i>Evolutionary Applications</i> , 2013, 6, 569-584.	3.1	23
320	Transcriptome Analysis of <i>Gerbera hybrida</i> Including in silico Confirmation of Defense Genes Found. <i>Frontiers in Plant Science</i> , 2016, 7, 247.	3.6	23
321	Optimisation of droplet digital PCR for determining copy number variation of $\alpha$ -gliadin genes in mutant and gene-edited polyploid bread wheat. <i>Journal of Cereal Science</i> , 2020, 92, 102903.	3.7	23
322	Regeneration and transformation of potato by <i>Agrobacterium tumefaciens</i> . , 1991, , 301-309.		23
323	Crucial factors for the feasibility of commercial hybrid breeding in food crops. <i>Nature Plants</i> , 2022, 8, 463-473.	9.3	23
324	Blue light increases anthocyanin content and delays fruit ripening in purple pepper fruit. <i>Postharvest Biology and Technology</i> , 2022, 192, 112024.	6.0	23

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326	Azacytidine and miR156 promote rooting in adult but not in juvenile <i>Arabidopsis</i> tissues. <i>Journal of Plant Physiology</i> , 2017, 208, 52-60.	3.5	22
327	Genetic complexity of miscanthus cell wall composition and biomass quality for biofuels. <i>BMC Genomics</i> , 2017, 18, 406.	2.8	22
328	Stability of Cell Wall Composition and Saccharification Efficiency in <i>Miscanthus</i> across Diverse Environments. <i>Frontiers in Plant Science</i> , 2016, 7, 2004.	3.6	22
329	Genetic transformation of <i>Alstroemeria</i> using particle bombardment. <i>Molecular Breeding</i> , 2000, 6, 369-377.	2.1	21
330	In situ analysis of enzymes involved in sucrose to hexose-phosphate conversion during stolon-to-tuber transition of potato. <i>Physiologia Plantarum</i> , 2002, 115, 303-310.	5.2	21
331	Host plant resistance towards the cabbage whitefly in <i>Brassica oleracea</i> and its wild relatives. <i>Euphytica</i> , 2015, 202, 297-306.	1.2	21
332	Genetic mapping and QTL analysis of <i>Botrytis</i> resistance in <i>Gerbera hybrida</i> . <i>Molecular Breeding</i> , 2017, 37, 13.	2.1	21
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334	Genetic mapping of tuber size distribution and marketable tuber yield under drought stress in potatoes. <i>Euphytica</i> , 2019, 215, 1.	1.2	21
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336	Regeneration of Pea ( <i>Pisum sativum</i> L.) by a cyclic organogenic system. <i>Plant Cell Reports</i> , 2004, 23, 453-460.	5.6	20
337	GpaXI tar I originating from <i>Solanum tarijense</i> is a major resistance locus to <i>Globodera pallida</i> and is localised on chromosome 11 of potato. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1477-1487.	3.6	20
338	Crop to wild introgression in lettuce: following the fate of crop genome segments in backcross populations. <i>BMC Plant Biology</i> , 2012, 12, 43.	3.6	20
339	Characterization of polygenic resistance to powdery mildew in tomato at cytological, biochemical and gene expression level. <i>Molecular Plant Pathology</i> , 2012, 13, 148-159.	4.2	20
340	Phenotypic, Molecular, and Pathological Characterization of <i>Colletotrichum acutatum</i> Associated with Andean Lupine and Tamarillo in the Ecuadorian Andes. <i>Plant Disease</i> , 2013, 97, 819-827.	1.4	20
341	QTL mapping of thrips resistance in pepper. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1945-1956.	3.6	20
342	Silencing of DND1 in potato and tomato impedes conidial germination, attachment and hyphal growth of <i>Botrytis cinerea</i> . <i>BMC Plant Biology</i> , 2017, 17, 235.	3.6	20

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344	Isolation and functional characterization of a stolon specific promoter from potato ( <i>Solanum tuberosum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702	2.2	19
345	Influence of plant growth stage on resistance to anthracnose in Andean lupin ( <i>Lupinus mutabilis</i> ). <i>Crop and Pasture Science</i> , 2015, 66, 729.	1.5	19
346	Bioethanol from maize cell walls: genes, molecular tools, and breeding prospects. <i>GCB Bioenergy</i> , 2015, 7, 591-607.	5.6	19
347	Inheritance and QTL analysis of the determinants of flower color in tetraploid cut roses. <i>Molecular Breeding</i> , 2016, 36, 143.	2.1	19
348	Morphological and physiological responses of the potato stem transport tissues to dehydration stress. <i>Planta</i> , 2020, 251, 45.	3.2	19
349	Allelic variants of the NLR protein Rpi- <i>chc1</i> differentially recognize members of the <i>Phytophthora infestans</i> PexRD12/31 effector superfamily through the leucine-rich repeat domain. <i>Plant Journal</i> , 2021, 107, 182-197.	5.7	19
350	Fructan as a New Carbohydrate Sink in Transgenic Potato Plants. <i>Plant Cell</i> , 1994, 6, 561.	6.6	18
351	Targeted transcript mapping for agronomic traits in potato. <i>Journal of Experimental Botany</i> , 2007, 58, 2761-2774.	4.8	18
352	Accumulation of multiple-repeat starch-binding domains (SBD2-SBD5) does not reduce amylose content of potato starch granules. <i>Planta</i> , 2007, 225, 919-933.	3.2	18
353	A hybrid BAC physical map of potato: a framework for sequencing a heterozygous genome. <i>BMC Genomics</i> , 2011, 12, 594.	2.8	18
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355	Genetical genomics of quality related traits in potato tubers using proteomics. <i>BMC Plant Biology</i> , 2018, 18, 20.	3.6	18
356	Detecting quantitative trait loci and exploring chromosomal pairing in autopolyploids using polyqTLR. <i>Bioinformatics</i> , 2021, 37, 3822-3829.	4.1	18
357	Understanding the Effectiveness of Genomic Prediction in Tetraploid Potato. <i>Frontiers in Plant Science</i> , 2021, 12, 672417.	3.6	18
358	GBSS T-DNA inserts giving partial complementation of the amylose-free potato mutant can also cause co-suppression of the endogenous GBSS gene in a wild-type background. <i>Plant Molecular Biology</i> , 1996, 31, 731-739.	3.9	17
359	Production of dextran in transgenic potato plants. <i>Transgenic Research</i> , 2005, 14, 385-395.	2.4	17
360	Production of small starch granules by expression of a tandem-repeat of a family 20 starch-binding domain (SBD3-SBD5) in an amylose-free potato genetic background. <i>Functional Plant Biology</i> , 2012, 39, 146.	2.1	17

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362	Normal adult survival but reduced <i>Bemisia tabaci</i> oviposition rate on tomato lines carrying an introgression from <i>S. habrochaites</i> . <i>BMC Genetics</i> , 2014, 15, 142.	2.7	17
363	Down-regulation of acetolactate synthase compromises Ol-1-mediated resistance to powdery mildew in tomato. <i>BMC Plant Biology</i> , 2014, 14, 32.	3.6	17
364	Effects of stacked quantitative resistances to downy mildew in lettuce do not simply add up. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1805-1816.	3.6	17
365	Maize feedstocks with improved digestibility reduce the costs and environmental impacts of biomass pretreatment and saccharification. <i>Biotechnology for Biofuels</i> , 2016, 9, 63.	6.2	17
366	The assessment of field trials in GMO research around the world and their possible integration in field trials for variety registration. <i>Transgenic Research</i> , 2018, 27, 321-329.	2.4	17
367	Comparative Subsequence Sets Analysis (CoSSA) is a robust approach to identify haplotype specific SNPs; mapping and pedigree analysis of a potato wart disease resistance gene <i>Sen3</i> . <i>Plant Methods</i> , 2019, 15, 60.	4.3	17
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369	Patterns of Transmission Ratio Distortion in Interspecific Lettuce Hybrids Reveal a Sex-Independent Gametophytic Barrier. <i>Genetics</i> , 2019, 211, 263-276.	2.9	17
370	Genetic Variation and Combining Ability Analysis of Bruising Sensitivity in <i>Agaricus bisporus</i> . <i>PLoS ONE</i> , 2013, 8, e76826.	2.5	17
371	Characterization and localization of repetitive DNA sequences in the ornamental <i>Alstroemeria aurea</i> Graham. <i>Theoretical and Applied Genetics</i> , 1997, 94, 982-990.	3.6	16
372	Cloning and characterization of a tuberous root-specific promoter from cassava ( <i>Manihot esculenta</i> ) Tj ETQqO O O rgBT /Overlock 10 Tf 5	3.2	16
373	Organ specificity and transcriptional control of metabolic routes revealed by expression QTL profiling of source-sink tissues in a segregating potato population. <i>BMC Plant Biology</i> , 2012, 12, 17.	3.6	16
374	Chromosomal organizations of major repeat families on potato ( <i>Solanum tuberosum</i> ) and further exploring in its sequenced genome. <i>Molecular Genetics and Genomics</i> , 2014, 289, 1307-1319.	2.1	16
375	Genetic mapping of resistance to <i>Fusarium oxysporum</i> f. sp. <i>tulipae</i> in tulip. <i>Molecular Breeding</i> , 2015, 35, 122.	2.1	16
376	Simultaneous analysis of a series of phosphorylated sugars in small tissue samples by anion exchange chromatography and pulsed amperometric detection. <i>Phytochemical Analysis</i> , 1999, 10, 107-112.	2.4	15
377	Characterisation of distant <i>Alstroemeria</i> hybrids: application of highly repetitive DNA sequences from <i>A. ligtu</i> ssp. <i>ligtu</i> . <i>Annals of Applied Biology</i> , 2003, 142, 277-283.	2.5	15
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380	Efficient production of transgenic <i>Alstroemeria</i> plants by using <i>Agrobacterium tumefaciens</i> . <i>Annals of Applied Biology</i> , 2007, 151, 401-412.	2.5	15
381	Moderate abiotic stresses increase rhizome growth and outgrowth of axillary buds in <i>Alstroemeria</i> cultured in vitro. <i>Plant Cell, Tissue and Organ Culture</i> , 2012, 110, 395-400.	2.3	15
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383	Homologues of potato chromosome 5 show variable collinearity in the euchromatin, but dramatic absence of sequence similarity in the pericentromeric heterochromatin. <i>BMC Genomics</i> , 2015, 16, 374.	2.8	15
384	Aphid resistance in <i>Capsicum</i> maps to a locus containing LRR-RLK gene analogues. <i>Theoretical and Applied Genetics</i> , 2020, 133, 227-237.	3.6	15
385	Options to Reform the European Union Legislation on GMOs: Risk Governance. <i>Trends in Biotechnology</i> , 2020, 38, 349-351.	9.3	15
386	The protein composition of the cytoplasmic membrane of aerobically and anaerobically grown <i>Escherichia coli</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 1984, 16, 295-307.	2.3	14
387	Efficient Somatic Embryogenesis in <i>Alstroemeria</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2006, 86, 233-238.	2.3	14
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389	Development of a standard test for dough-making properties of oat cultivars. <i>Journal of Cereal Science</i> , 2014, 59, 56-61.	3.7	14
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392	Genetically engineering <i>Crambe abyssinica</i> – A potentially high-value oil crop for salt land improvement. <i>Land Degradation and Development</i> , 2018, 29, 1096-1106.	3.9	14
393	The <i>Synchytrium endobioticum</i> AvrSen1 Triggers a Hypersensitive Response in <i>Sen1</i> Potatoes While Natural Variants Evade Detection. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 1536-1546.	2.6	14
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395	Silencing susceptibility genes in potato hinders primary infection with <i>Phytophthora infestans</i> at different stages. <i>Horticulture Research</i> , 2022, 9, .	6.3	14
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398	Functional analysis of the omega-6 fatty acid desaturase ( <i>CaFAD2</i> ) gene family of the oil seed crop <i>Crambe abyssinica</i> . <i>BMC Plant Biology</i> , 2013, 13, 146.	3.6	13
399	Qualitative and Quantitative Resistance against Early Blight Introgressed in Potato. <i>Biology</i> , 2021, 10, 892.	2.8	13
400	Antisense suppression of a potato alpha-SNAP homologue leads to alterations in cellular development and assimilate distribution. <i>Plant Molecular Biology</i> , 2000, 43, 473-482.	3.9	12
401	Analysis of genes differentially expressed during potato tuber life cycle and isolation of their promoter regions. <i>Plant Science</i> , 2004, 166, 423-433.	3.6	12
402	Expression of alternansucrase in potato plants. <i>Biotechnology Letters</i> , 2007, 29, 1135-1142.	2.2	12
403	Fine mapping of two major QTLs conferring resistance to powdery mildew in tomato. <i>Euphytica</i> , 2012, 184, 223-234.	1.2	12
404	Fine mapping quantitative resistances to downy mildew in lettuce revealed multiple sub-QTLs with plant stage dependent effects reducing or even promoting the infection. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2995-3007.	3.6	12
405	Characterization of B chromosomes in <i>Lilium</i> hybrids through GISH and FISH. <i>Plant Systematics and Evolution</i> , 2014, 300, 1771-1777.	0.9	12
406	Multi-trait QTL analysis for agronomic and quality characters of <i>Agaricus bisporus</i> (button) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td	3.0	12
407	Breeding for postharvest performance in chrysanthemum by selection against storage-induced degreening of disk florets. <i>Postharvest Biology and Technology</i> , 2017, 124, 45-53.	6.0	12
408	Family-Based Haplotype Estimation and Allele Dosage Correction for Polyploids Using Short Sequence Reads. <i>Frontiers in Genetics</i> , 2019, 10, 335.	2.3	12
409	A rapid method to screen wild <i>Solanum</i> for resistance to early blight. <i>European Journal of Plant Pathology</i> , 2019, 154, 109-114.	1.7	12
410	Expression of an engineered granule-bound <i>Escherichia coli</i> maltose acetyltransferase in wild-type and amf potato plants. <i>Plant Biotechnology Journal</i> , 2007, 5, 134-145.	8.3	11
411	Frequency of a natural truncated allele of <i>MdMLO19</i> in the germplasm of <i>Malus domestica</i> . <i>Molecular Breeding</i> , 2017, 37, 7.	2.1	11
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414	Development of an <i>in vitro</i> protocol to screen <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> pathogenicity in different <i>Solanum</i> species. <i>Plant Pathology</i> , 2019, 68, 42-48.	2.4	11

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416	Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. <i>MBio</i> , 2020, 11, .	4.1	11
417	Differential expression of cellulose synthase (CesA) gene transcripts in potato as revealed by QRT-PCR. <i>Plant Physiology and Biochemistry</i> , 2009, 47, 1116-1118.	5.8	10
418	High-Resolution Mapping of Two Broad-Spectrum Late Blight Resistance Genes from Two Wild Species of the <i>Solanum tuberosum</i> Group. <i>Potato Research</i> , 2012, 55, 109-123.	2.7	10
419	Constitutive overexpression of the pollen specific gene SKS13 in leaves reduces aphid performance on <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2014, 14, 217.	3.6	10
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