

Peter Hedley

List of Publications by Year in descending order

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136
papers

10,017
citations

61984

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147
all docs

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docs citations

147
times ranked

10437
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#	ARTICLE	IF	CITATIONS
1	WHIRLY1 functions in the nucleus to regulate barley leaf development and associated metabolite profiles. <i>Biochemical Journal</i> , 2022, 479, 641-659.	3.7	2
2	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	12.8	44
3	Chitosan primes plant defence mechanisms against <i>Botrytis cinerea</i> , including expression of <i>Avr9/Cfâ€9</i> rapidly elicited genes. <i>Plant, Cell and Environment</i> , 2021, 44, 290-303.	5.7	29
4	Haustorium formation and a distinct biotrophic transcriptome characterize infection of <i>Nicotiana benthamiana</i> by the tree pathogen <i>Phytophthora kernoviae</i> . <i>Molecular Plant Pathology</i> , 2021, 22, 954-968.	4.2	5
5	Draft genome assemblies for tree pathogens <i>Phytophthora pseudosyringae</i> and <i>Phytophthora boehmeriae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4
6	Senescent sweetening in potato (<i>Solanum tuberosum</i>) tubers is associated with a reduction in plastidial glucose-6-phosphate/phosphate translocator transcripts. <i>Postharvest Biology and Technology</i> , 2021, 181, 111637.	6.0	5
7	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. <i>PeerJ</i> , 2021, 9, e12498.	2.0	12
8	A high-throughput genomic screen identifies a role for the plasmid-borne type II secretion system of <i>Escherichia coli</i> O157:H7 (Sakai) in plant-microbe interactions. <i>Genomics</i> , 2020, 112, 4242-4253.	2.9	2
9	<i>Phytophthora austrocedri</i> in Argentina and Co-Inhabiting <i>Phytophthoras</i> : Roles of Anthropogenic and Abiotic Factors in Species Distribution and Diversity. <i>Forests</i> , 2020, 11, 1223.	2.1	11
10	A footprint of plant eco-geographic adaptation on the composition of the barley rhizosphere bacterial microbiota. <i>Scientific Reports</i> , 2020, 10, 12916.	3.3	48
11	<i>Escherichia coli</i> O157:H7 F9 Fimbriae Recognize Plant Xyloglucan and Elicit a Response in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9720.	4.1	3
12	Detection and spread of <i>Phytophthora austrocedri</i> within infected <i>Juniperus communis</i> woodland and diversity of co-associated <i>Phytophthoras</i> as revealed by metabarcoding. <i>Forest Pathology</i> , 2020, 50, e12602.	1.1	8
13	TRA1: A Locus Responsible for Controlling Agrobacterium-Mediated Transformability in Barley. <i>Frontiers in Plant Science</i> , 2020, 11, 355.	3.6	12
14	Intact salicylic acid signalling is required for potato defence against the necrotrophic fungus <i>Alternaria solani</i> . <i>Plant Molecular Biology</i> , 2020, 104, 1-19.	3.9	32
15	Physiological, Biochemical, and Transcriptional Responses to Single and Combined Abiotic Stress in Stress-Tolerant and Stress-Sensitive Potato Genotypes. <i>Frontiers in Plant Science</i> , 2020, 11, 169.	3.6	79
16	TERMINAL FLOWERâ€1/CENTRORADIALIS inhibits tuberisation via protein interaction with the tuberigen activation complex. <i>Plant Journal</i> , 2020, 103, 2263-2278.	5.7	24
17	Light Regulation of Chlorophyll and Glycoalkaloid Biosynthesis During Tuber Greening of Potato <i>S. tuberosum</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 753.	3.6	14
18	Dataset of <i>Escherichia coli</i> O157: H7 genes enriched in adherence to spinach root tissue. <i>Data in Brief</i> , 2020, 31, 105769.	1.0	0

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19	Signatures of adaptation to a monocot host in the plant-parasitic cyst nematode <i>Heterodera sacchari</i> . <i>Plant Journal</i> , 2020, 103, 1263-1274.	5.7	9
20	Barley Anther and Meioocyte Transcriptome Dynamics in Meiotic Prophase I. <i>Frontiers in Plant Science</i> , 2020, 11, 619404.	3.6	19
21	Identification of TIMING OF CAB EXPRESSION 1 as a temperature-sensitive negative regulator of tuberization in potato. <i>Journal of Experimental Botany</i> , 2019, 70, 5703-5714.	4.8	21
22	A highly mutagenised barley (cv. Golden Promise) TILLING population coupled with strategies for screening-by-sequencing. <i>Plant Methods</i> , 2019, 15, 99.	4.3	39
23	Ancient barley landraces adapted to marginal soils demonstrate exceptional tolerance to manganese limitation. <i>Annals of Botany</i> , 2019, 123, 831-843.	2.9	29
24	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <i>Frontiers in Plant Science</i> , 2019, 10, 544.	3.6	66
25	Development and Quality of Barley Husk Adhesion Correlates With Changes in Caryopsis Cuticle Biosynthesis and Composition. <i>Frontiers in Plant Science</i> , 2019, 10, 672.	3.6	5
26	APETALA2 control of barley internode elongation. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	36
27	BaRTv1.0: an improved barley reference transcript dataset to determine accurate changes in the barley transcriptome using RNA-seq. <i>BMC Genomics</i> , 2019, 20, 968.	2.8	50
28	Exome Capture for Variant Discovery and Analysis in Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 283-310.	0.9	5
29	High-Resolution RT-PCR Analysis of Alternative Barley Transcripts. <i>Methods in Molecular Biology</i> , 2019, 1900, 269-281.	0.9	11
30	Microarrays for High-Throughput Gene Expression Analysis of Barley. <i>Methods in Molecular Biology</i> , 2019, 1900, 181-194.	0.9	0
31	Metabarcoding reveals a high diversity of woody host-associated <i>Phytophthora</i> spp. in soils at public gardens and amenity woodlands in Britain. <i>PeerJ</i> , 2019, 7, e6931.	2.0	40
32	A reversible light- and genotype-dependent acquired thermotolerance response protects the potato plant from damage due to excessive temperature. <i>Planta</i> , 2018, 247, 1377-1392.	3.2	19
33	The redox state of the apoplast influences the acclimation of photosynthesis and leaf metabolism to changing irradiance. <i>Plant, Cell and Environment</i> , 2018, 41, 1083-1097.	5.7	47
34	Enhancement of Glen Moy x Latham raspberry linkage map using GbS to further understand control of developmental processes leading to fruit ripening. <i>BMC Genetics</i> , 2018, 19, 59.	2.7	31
35	Gene Prediction in the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 73-88.	0.5	0
36	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 89-107.	0.5	0

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37	A Transcript and Metabolite Atlas of Blackcurrant Fruit Development Highlights Hormonal Regulation and Reveals the Role of Key Transcription Factors. <i>Frontiers in Plant Science</i> , 2018, 9, 1235.	3.6	11
38	RXLR Effector AVR2 Up-Regulates a Brassinosteroid-Responsive bHLH Transcription Factor to Suppress Immunity. <i>Plant Physiology</i> , 2017, 174, 356-369.	4.8	82
39	Barley transcriptome analyses upon interaction with different aphid species identify thionins contributing to resistance. <i>Plant, Cell and Environment</i> , 2017, 40, 2628-2643.	5.7	38
40	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
41	Redox Control of Aphid Resistance through Altered Cell Wall Composition and Nutritional Quality. <i>Plant Physiology</i> , 2017, 175, 259-271.	4.8	26
42	Fine mapping of a major QTL for awn length in barley using a multiparent mapping population. <i>Theoretical and Applied Genetics</i> , 2017, 130, 269-281.	3.6	46
43	Root Hair Mutations Displace the Barley Rhizosphere Microbiota. <i>Frontiers in Plant Science</i> , 2017, 8, 1094.	3.6	85
44	Association Mapping of Diastatic Power in UK Winter and Spring Barley by Exome Sequencing of Phenotypically Contrasting Variety Sets. <i>Frontiers in Plant Science</i> , 2017, 8, 1566.	3.6	6
45	Development and Evaluation of a Barley 50k iSelect SNP Array. <i>Frontiers in Plant Science</i> , 2017, 8, 1792.	3.6	257
46	A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. <i>BMC Plant Biology</i> , 2017, 17, 232.	3.6	21
47	Whole-Transcriptome Analysis of Verocytotoxigenic <i>Escherichia coli</i> O157:H7 (Sakai) Suggests Plant-Species-Specific Metabolic Responses on Exposure to Spinach and Lettuce Extracts. <i>Frontiers in Microbiology</i> , 2016, 7, 1088.	3.5	34
48	Molecular and Biochemical Examination of Spraing Disease in Potato Tuber in Response to Tobacco rattle virus Infection. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 822-828.	2.6	10
49	The Dynamics of Transcript Abundance during Cellularization of Developing Barley Endosperm. <i>Plant Physiology</i> , 2016, 170, 1549-1565.	4.8	47
50	Insight on Genes Affecting Tuber Development in Potato upon Potato spindle tuber viroid (PSTVd) Infection. <i>PLoS ONE</i> , 2016, 11, e0150711.	2.5	43
51	Gene expression changes in diapause or quiescent potato cyst nematode, <i>Globodera pallida</i> , eggs after hydration or exposure to tomato root diffusate. <i>PeerJ</i> , 2016, 4, e1654.	2.0	8
52	A transcriptional reference map of defence hormone responses in potato. <i>Scientific Reports</i> , 2015, 5, 15229.	3.3	28
53	WHIRLY1 Functions in the Control of Responses to Nitrogen Deficiency But Not Aphid Infestation in Barley. <i>Plant Physiology</i> , 2015, 168, 1140-1151.	4.8	20
54	Assessing the genetic diversity of rice originating from Bangladesh, Assam and West Bengal. <i>Rice</i> , 2015, 8, 35.	4.0	63

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55	The MORPH web server and software tool for predicting missing genes in biological pathways. <i>Physiologia Plantarum</i> , 2015, 155, 12-20.	5.2	3
56	Characterization of Arabidopsis Transcriptional Responses to Different Aphid Species Reveals Genes that Contribute to Host Susceptibility and Non-host Resistance. <i>PLoS Pathogens</i> , 2015, 11, e1004918.	4.7	47
57	Optimising ketocarotenoid production in potato tubers: Effect of genetic background, transgene combinations and environment. <i>Plant Science</i> , 2015, 234, 27-37.	3.6	33
58	Impacts on the metabolome of down-regulating polyphenol oxidase in potato tubers. <i>Transgenic Research</i> , 2015, 24, 447-461.	2.4	12
59	Towards an understanding of the control of crumbly™ fruit in red raspberry. <i>SpringerPlus</i> , 2015, 4, 223.	1.2	24
60	Nitrogen deficiency in barley (<i>Hordeum vulgare</i>) seedlings induces molecular and metabolic adjustments that trigger aphid resistance. <i>Journal of Experimental Botany</i> , 2015, 66, 3639-3655.	4.8	60
61	The effects of drought stress on leaf gene expression during flowering in blackcurrant (<i>Ribes nigrum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	4
62	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014, 14, 329.	3.6	42
63	Phosphite-induced changes of the transcriptome and secretome in <i>Solanum tuberosum</i> leading to resistance against <i>Phytophthora infestans</i> . <i>BMC Plant Biology</i> , 2014, 14, 254.	3.6	77
64	Effect of short-term exposure to high-temperature on total gene expression in the leaves of four raspberry (<i>Rubus idaeus</i> L.) cultivars. <i>Journal of Horticultural Science and Biotechnology</i> , 2014, 89, 532-541.	1.9	12
65	Day length dependent restructuring of the leaf transcriptome and metabolome in potato genotypes with contrasting tuberization phenotypes. <i>Plant, Cell and Environment</i> , 2014, 37, 1351-1363.	5.7	47
66	The low-recombining pericentromeric region of barley restricts gene diversity and evolution but not gene expression. <i>Plant Journal</i> , 2014, 79, 981-992.	5.7	30
67	The use of genotyping by sequencing in blackcurrant (<i>Ribes nigrum</i>): developing high-resolution linkage maps in species without reference genome sequences. <i>Molecular Breeding</i> , 2014, 33, 835-849.	2.1	53
68	An evaluation of genotyping by sequencing (GBS) to map the Breviaristatum-e (ari-e) locus in cultivated barley. <i>BMC Genomics</i> , 2014, 15, 104.	2.8	145
69	Physiological, biochemical and molecular responses of the potato (<i>Solanum tuberosum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	5.7	196
70	Quantitative proteomics and transcriptomics of potato in response to <i>Phytophthora infestans</i> in compatible and incompatible interactions. <i>BMC Genomics</i> , 2014, 15, 497.	2.8	77
71	Genome-wide QTL and bulked transcriptomic analysis reveals new candidate genes for the control of tuber carotenoid content in potato (<i>Solanum tuberosum</i> L.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 1917-1933.	3.6	53
72	Proteomics and transcriptomics of the BABA-induced resistance response in potato using a novel functional annotation approach. <i>BMC Genomics</i> , 2014, 15, 315.	2.8	67

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73	tropiTree: An NGS-Based EST-SSR Resource for 24 Tropical Tree Species. PLoS ONE, 2014, 9, e102502.	2.5	12
74	A Sequence-Ready Physical Map of Barley Anchored Genetically by Two Million Single-Nucleotide Polymorphisms. Plant Physiology, 2014, 164, 412-423.	4.8	77
75	The Barley Genome Sequence Assembly Reveals Three Additional Members of the CslF (1,3;1,4)- β -Glucan Synthase Gene Family. PLoS ONE, 2014, 9, e90888.	2.5	39
76	Identification of genes in the VirR regulon of <i>Pectobacterium atrosepticum</i> and characterization of their roles in quorum sensing-dependent virulence. Environmental Microbiology, 2013, 15, 687-701.	3.8	18
77	Phytophthora capsici-tomato interaction features dramatic shifts in gene expression associated with a hemi-biotrophic lifestyle. Genome Biology, 2013, 14, R63.	8.8	113
78	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. Plant Journal, 2013, 76, 494-505.	5.7	260
79	A Metabolic Regulator Modulates Virulence and Quorum Sensing Signal Production in <i>Pectobacterium atrosepticum</i> . Molecular Plant-Microbe Interactions, 2013, 26, 356-366.	2.6	14
80	Vitamin C and the Abscisic Acid-Insensitive 4 Transcription Factor Are Important Determinants of Aphid Resistance in <i>Arabidopsis</i> . Antioxidants and Redox Signaling, 2013, 18, 2091-2105.	5.4	68
81	Identification and Characterisation of CRN Effectors in <i>Phytophthora capsici</i> Shows Modularity and Functional Diversity. PLoS ONE, 2013, 8, e59517.	2.5	156
82	A physical, genetic and functional sequence assembly of the barley genome. Nature, 2012, 491, 711-716.	27.8	1,416
83	Natural variation in a homolog of <i>Antirrhinum CENTRORADIALIS</i> contributed to spring growth habit and environmental adaptation in cultivated barley. Nature Genetics, 2012, 44, 1388-1392.	21.4	477
84	Genetic characterization of the HrpL regulon of the fire blight pathogen <i>Erwinia amylovora</i> reveals novel virulence factors. Molecular Plant Pathology, 2012, 13, 160-173.	4.2	54
85	Comparison of transcript profiles in different life stages of the nematode <i>Globodera pallida</i> under different host potato genotypes. Molecular Plant Pathology, 2012, 13, 1120-1134.	4.2	14
86	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. Plant Cell, 2011, 23, 1249-1263.	6.6	448
87	Highly parallel gene-to-BAC addressing using microarrays. BioTechniques, 2011, 50, 165-174.	1.8	8
88	Pectin engineering to modify product quality in potato. Plant Biotechnology Journal, 2011, 9, 848-856.	8.3	19
89	An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4E resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. Molecular Ecology, 2011, 20, no-no.	3.9	48
90	Analysis of ESTs generated from inner bark tissue of an <i>Acacia auriculiformis</i> x <i>Acacia mangium</i> hybrid. Tree Genetics and Genomes, 2011, 7, 143-152.	1.6	18

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91	Combining genetical genomics and bulked segregant analysis-based differential expression: an approach to gene localization. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1375-1383.	3.6	20
92	Transcriptome sequencing of an ecologically important graminivorous sawfly: a resource for marker development. <i>Conservation Genetics Resources</i> , 2011, 3, 789-795.	0.8	10
93	Identification, utilisation and mapping of novel transcriptome-based markers from blackcurrant (<i>Ribes</i>) Tj ETQq1 1 0.784314 rsgBT /Ov	3.6	41
94	Early response mechanisms of perennial ryegrass (<i>Lolium perenne</i>) to phosphorus deficiency. <i>Annals of Botany</i> , 2011, 107, 243-254.	2.9	60
95	Allele Mining in Barley Genetic Resources Reveals Genes of Race-Non-Specific Powdery Mildew Resistance. <i>Frontiers in Plant Science</i> , 2011, 2, 113.	3.6	27
96	MICROARRAY CHARACTERIZATION OF THE HRPL REGULON OF THE FIRE BLIGHT PATHOGEN ERWINIA AMYLOVORA. <i>Acta Horticulturae</i> , 2011, , 263-270.	0.2	2
97	Differential gene expression in nearly isogenic lines with QTL for partial resistance to <i>Puccinia hordei</i> in barley. <i>BMC Genomics</i> , 2010, 11, 629.	2.8	17
98	Specific patterns of gene space organisation revealed in wheat by using the combination of barley and wheat genomic resources. <i>BMC Genomics</i> , 2010, 11, 714.	2.8	21
99	Candidate genes associated with bud dormancy release in blackcurrant (<i>Ribes nigrum</i> L.). <i>BMC Plant Biology</i> , 2010, 10, 202.	3.6	69
100	An eQTL Analysis of Partial Resistance to <i>Puccinia hordei</i> in Barley. <i>PLoS ONE</i> , 2010, 5, e8598.	2.5	77
101	Effect of salinity on water relations of wild barley plants differing in salt tolerance. <i>AoB PLANTS</i> , 2010, 2010, plq006-plq006.	2.3	53
102	Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21611-21616.	7.1	259
103	Flavonoid profiling and transcriptome analysis reveals new gene-metabolite correlations in tubers of <i>Solanum tuberosum</i> L.. <i>Journal of Experimental Botany</i> , 2010, 61, 1225-1238.	4.8	64
104	The Metabolic and Developmental Roles of Carotenoid Cleavage Dioxygenase4 from Potato \hat{A} . <i>Plant Physiology</i> , 2010, 154, 656-664.	4.8	143
105	Microarray Comparative Genomic Hybridisation Analysis Incorporating Genomic Organisation, and Application to Enterobacterial Plant Pathogens. <i>PLoS Computational Biology</i> , 2009, 5, e1000473.	3.2	9
106	Does biotechnology have a role in the promotion of underutilised crops?. <i>Food Policy</i> , 2009, 34, 319-328.	6.0	28
107	Molecular regulation of somatic embryogenesis in potato: an auxin led perspective. <i>Plant Molecular Biology</i> , 2008, 68, 185-201.	3.9	57
108	Quorum Sensing Coordinates Brute Force and Stealth Modes of Infection in the Plant Pathogen <i>Pectobacterium atrosepticum</i> . <i>PLoS Pathogens</i> , 2008, 4, e1000093.	4.7	216

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109	Expression profiling of potato germplasm differentiated in quality traits leads to the identification of candidate flavour and texture genes. <i>Journal of Experimental Botany</i> , 2008, 59, 4219-4231.	4.8	73
110	DsbA Plays a Critical and Multifaceted Role in the Production of Secreted Virulence Factors by the Phytopathogen <i>Erwinia carotovora</i> subsp. <i>atroseptica</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 23739-23753.	3.4	48
111	WHAT WILL A GENOME SEQUENCE DO FOR FIRE BLIGHT RESEARCH? <i>PECTOBACTERIUM ATROSEPTICUM</i> AND POTATO "A CASE STUDY". <i>Acta Horticulturae</i> , 2008, , 157-162.	0.2	0
112	Co-ordinated gene expression during phases of dormancy release in raspberry (<i>Rubus idaeus</i> L.) buds. <i>Journal of Experimental Botany</i> , 2007, 58, 1035-1045.	4.8	187
113	Efflux Pump Gene Expression in <i>Erwinia chrysanthemi</i> Is Induced by Exposure to Phenolic Acids. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 313-320.	2.6	43
114	The <i>Erwinia chrysanthemi</i> 3937 PhoQ Sensor Kinase Regulates Several Virulence Determinants. <i>Journal of Bacteriology</i> , 2006, 188, 3088-3098.	2.2	48
115	Characterisation and functional analysis of two barley caleosins expressed during barley caryopsis development. <i>Planta</i> , 2005, 221, 513-522.	3.2	27
116	Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. <i>Molecular Genetics and Genomics</i> , 2005, 274, 515-527.	2.1	250
117	A comparative analysis of transcript abundance using SAGE and Affymetrix arrays. <i>Functional and Integrative Genomics</i> , 2005, 5, 163-174.	3.5	36
118	Analysis of the distribution of marker classes in a genetic linkage map: a case study in Norway spruce (<i>Picea abies</i> karst). <i>Tree Genetics and Genomes</i> , 2005, 1, 93-102.	1.6	15
119	Single-feature polymorphism discovery in the barley transcriptome. <i>Genome Biology</i> , 2005, 6, R54.	9.6	130
120	Metabolic engineering of high carotenoid potato tubers containing enhanced levels of β -carotene and lutein. <i>Journal of Experimental Botany</i> , 2004, 56, 81-9.	4.8	265
121	Characterisation of early transcriptional changes involving multiple signalling pathways in the Mla13 barley interaction with powdery mildew (<i>Blumeria graminis</i> f. sp. <i>hordei</i>). <i>Planta</i> , 2004, 218, 803-813.	3.2	26
122	A comparison of sequence-based polymorphism and haplotype content in transcribed and anonymous regions of the barley genome. <i>Genome</i> , 2004, 47, 389-398.	2.0	120
123	Differential expression of invertase genes in internal and external phloem tissues of potato (<i>Solanum</i>) Tj ETQq1 1 0,784314 rgBT /Overl	4.8	18
124	Requirements for mini-exon inclusion in potato invertase mRNAs provides evidence for exon-scanning interactions in plants. <i>Rna</i> , 2000, 6, 422-433.	3.5	31
125	Differential expression of invertase genes in internal and external phloem tissues of potato (<i>Solanum</i>) Tj ETQq1 1 0,784314 rgBT /Overl	4.8	18
126	Microsatellite repeats are not randomly distributed within Norway spruce (<i>Picea abies</i> K.) expressed sequences. <i>Genome</i> , 2000, 43, 41-46.	2.0	33

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127	Expression of tandem invertase genes associated with sexual and vegetative growth cycles in potato. <i>Plant Molecular Biology</i> , 1999, 41, 741-752.	3.9	48
128	Organisation and expression of a potato (<i>Solanum tuberosum</i>) protein kinase gene. <i>Plant Science</i> , 1996, 118, 71-80.	3.6	3
129	Erratum to "Organisation and expression of a potato (<i>Solanum tuberosum</i>) protein kinase gene" [Plant Science 118 (1996) 77]. <i>Plant Science</i> , 1996, 120, 113.	3.6	0
130	Exon Skipping Induced by Cold Stress in a Potato Invertase Gene Transcript. <i>Nucleic Acids Research</i> , 1996, 24, 2347-2351.	14.5	85
131	Processing of a 58 Å— 103Mr invertase from potato tubers. <i>Phytochemistry</i> , 1994, 35, 579-582.	2.9	2
132	Characterisation of a complementary DNA encoding a novel plant enzyme with sucrolytic activity. <i>FEBS Letters</i> , 1994, 354, 123-127.	2.8	7
133	Potato (<i>Solanum tuberosum</i>) invertase-encoding cDNAs and their differential expression. <i>Gene</i> , 1994, 145, 211-214.	2.2	39
134	cDNA cloning and expression of a potato (<i>Solanum tuberosum</i>) invertase. <i>Plant Molecular Biology</i> , 1993, 22, 917-922.	3.9	38
135	Purification of soluble invertase from potato. <i>Phytochemistry</i> , 1992, 31, 1901-1904.	2.9	18
136	Developmental regulation of insulin like growth factor II gene expression in the pig. <i>Cell Biology International Reports</i> , 1989, 13, 857-862.	0.6	11