

Justin D Faris

List of Publications by Year in descending order

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145
papers

13,118
citations

20797

60
h-index

26591

107
g-index

150
all docs

150
docs citations

150
times ranked

6855
citing authors

#	ARTICLE	IF	CITATIONS
1	A triple threat: the <i>Parastagonospora nodorum</i> SnTox267 effector exploits three distinct host genetic factors to cause disease in wheat. <i>New Phytologist</i> , 2022, 233, 427-442.	3.5	22
2	The <i>Parastagonospora nodorum</i> necrotrophic effector SnTox5 targets the wheat gene <i>Snn5</i> and facilitates entry into the leaf mesophyll. <i>New Phytologist</i> , 2022, 233, 409-426.	3.5	28
3	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431.	9.4	102
4	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
5	Genetics of resistance to septoria nodorum blotch in wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3685-3707.	1.8	13
6	A conserved hypothetical gene is required but not sufficient for Ptr ToxC production in <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2022, , .	1.4	11
7	Genomic Analysis and Delineation of the Tan Spot Susceptibility Locus Tsc1 in Wheat. <i>Frontiers in Plant Science</i> , 2022, 13, 793925.	1.7	4
8	Disease Resistance. , 2022, , 341-360.		3
9	A wheat cysteine-rich receptor-like kinase confers broad-spectrum resistance against <i>Septoria tritici</i> blotch. <i>Nature Communications</i> , 2021, 12, 433.	5.8	55
10	A protein kinaseâ€‘major sperm protein gene hijacked by a necrotrophic fungal pathogen triggers disease susceptibility in wheat. <i>Plant Journal</i> , 2021, 106, 720-732.	2.8	31
11	Function and evolution of allelic variations of <i>Sr13</i> conferring resistance to stem rust in tetraploid wheat (<i>Triticum turgidum</i> L.). <i>Plant Journal</i> , 2021, 106, 1674-1691.	2.8	15
12	Characterization of synthetic wheat line Largo for resistance to stem rust. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
13	Characterization of Effectorâ€‘Target Interactions in Necrotrophic Pathosystems Reveals Trends and Variation in Host Manipulation. <i>Annual Review of Phytopathology</i> , 2021, 59, 77-98.	3.5	26
14	High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242.	2.0	14
15	Identification of a major dominant gene for race-nonspecific tan spot resistance in wild emmer wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 829-841.	1.8	26
16	QTL mapping of resistance to tan spot induced by race 2 of <i>Pyrenophora tritici-repentis</i> in tetraploid wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 433-442.	1.8	9
17	Comprehensive analysis of <i>Q</i> gene near-isogenic lines reveals key molecular pathways for wheat domestication and improvement. <i>Plant Journal</i> , 2020, 102, 299-310.	2.8	21
18	<i>Pyrenophora tritici-repentis</i> Race 4 Isolates Cause Disease on Tetraploid Wheat. <i>Phytopathology</i> , 2020, 110, 1781-1790.	1.1	12

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19	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. <i>Frontiers in Plant Science</i> , 2020, 11, 569905.	1.7	44
20	Meta-QTL analysis of tan spot resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2363-2375.	1.8	54
21	Plant genes hijacked by necrotrophic fungal pathogens. <i>Current Opinion in Plant Biology</i> , 2020, 56, 74-80.	3.5	79
22	Variation Analysis of Root System Development in Wheat Seedlings Using Root Phenotyping System. <i>Agronomy</i> , 2020, 10, 206.	1.3	14
23	Genome-wide association mapping of tan spot resistance in a worldwide collection of durum wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2227-2237.	1.8	14
24	Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2689-2705.	1.8	118
25	Local adaptation drives the diversification of effectors in the fungal wheat pathogen <i>Parastagonospora nodorum</i> in the United States. <i>PLoS Genetics</i> , 2019, 15, e1008223.	1.5	66
26	Mapping and characterization of two stem rust resistance genes derived from cultivated emmer wheat accession PI 193883. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3177-3189.	1.8	33
27	Genetic analysis of threshability and other spike traits in the evolution of cultivated emmer to fully domesticated durum wheat. <i>Molecular Genetics and Genomics</i> , 2019, 294, 757-771.	1.0	28
28	Genetics of Variable Disease Expression Conferred by Inverse Gene-For-Gene Interactions in the Wheat- <i>Parastagonospora nodorum</i> Pathosystem. <i>Plant Physiology</i> , 2019, 180, 420-434.	2.3	35
29	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
30	<i>Fusarium graminearum</i> KP4-like proteins possess root growth-inhibiting activity against wheat and potentially contribute to fungal virulence in seedling rot. <i>Fungal Genetics and Biology</i> , 2019, 123, 1-13.	0.9	19
31	Identification and Validation of a New Source of Low Grain Cadmium Accumulation in Durum Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 923-932.	0.8	19
32	Genetic Diversity and Resistance to <i>Fusarium</i> Head Blight in Synthetic Hexaploid Wheat Derived From <i>Aegilops tauschii</i> and Diverse <i>Triticum turgidum</i> Subspecies. <i>Frontiers in Plant Science</i> , 2018, 9, 1829.	1.7	20
33	Reference Quality Genome Assemblies of Three <i>Parastagonospora nodorum</i> Isolates Differing in Virulence on Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 393-399.	0.8	32
34	<i>ToxA</i> Is Present in the U.S. <i>Bipolaris sorokiniana</i> Population and Is a Significant Virulence Factor on Wheat Harboring <i>Tsn1</i> . <i>Plant Disease</i> , 2018, 102, 2446-2452.	0.7	53
35	Molecular Cloning and Comparative Analysis of a PR-1-RK Hybrid Gene from <i>Triticum urartu</i> , the A-Genome Progenitor of Hexaploid Wheat. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 469-483.	1.0	1
36	Identification, mapping, and marker development of stem rust resistance genes in durum wheat <i>Lebsock</i> . <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	19

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37	Molecular cloning and characterization of two novel genes from hexaploid wheat that encode double PR-1 domains coupled with a receptor-like protein kinase. <i>Molecular Genetics and Genomics</i> , 2017, 292, 435-452.	1.0	10
38	microRNA172 plays a critical role in wheat spike morphology and grain threshability. <i>Development (Cambridge)</i> , 2017, 144, 1966-1975.	1.2	125
39	Physical mapping of DNA markers linked to stem rust resistance gene Sr47 in durum wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1135-1154.	1.8	10
40	Inverse gene-for-gene interactions contribute additively to tan spot susceptibility in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1267-1276.	1.8	38
41	Molecular manipulation of the mating-type system and development of a new approach for characterizing pathogen virulence in <i>Pyrenophora tritici-repentis</i> . <i>Fungal Genetics and Biology</i> , 2017, 109, 16-25.	0.9	10
42	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
43	Discovery of a Novel Stem Rust Resistance Allele in Durum Wheat that Exhibits Differential Reactions to Ug99 Isolates. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3481-3490.	0.8	40
44	Genetic analysis of virulence in the <i>Pyrenophora teres</i> f. <i>teres</i> population BB25 – FGOH04Pt-21. <i>Fungal Genetics and Biology</i> , 2017, 107, 12-19.	0.9	27
45	Characterizing the <i>Pyrenophora teres</i> f. <i>maculata</i> Barley Interaction Using Pathogen Genetics. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2615-2626.	0.8	26
46	Fine mapping of the chromosome 5B region carrying closely linked rust resistance genes Yr47 and Lr52 in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 495-504.	1.8	34
47	Genetic Mapping of Major Effect Seed Dormancy Quantitative Trait Loci on Chromosome 2B using Recombinant Substitution Lines in Tetraploid Wheat. <i>Crop Science</i> , 2016, 56, 59-72.	0.8	5
48	New Insights into the Roles of Host Gene-Necrotrophic Effector Interactions in Governing Susceptibility of Durum Wheat to Tan Spot and <i>Septoria nodorum</i> Blotch. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4139-4150.	0.8	50
49	Validation of Genome-Wide Association Studies as a Tool to Identify Virulence Factors in <i>Parastagonospora nodorum</i> . <i>Phytopathology</i> , 2016, 106, 1177-1185.	1.1	74
50	The hijacking of a receptor kinase-driven pathway by a wheat fungal pathogen leads to disease. <i>Science Advances</i> , 2016, 2, e1600822.	4.7	188
51	SnTox1, a <i>Parastagonospora nodorum</i> necrotrophic effector, is a dual-function protein that facilitates infection while protecting from wheat-produced chitinases. <i>New Phytologist</i> , 2016, 211, 1052-1064.	3.5	76
52	Genetic relationships between race-nonspecific and race-specific interactions in the wheat <i>Pyrenophora tritici-repentis</i> pathosystem. <i>Theoretical and Applied Genetics</i> , 2016, 129, 897-908.	1.8	49
53	Marker development, saturation mapping, and high-resolution mapping of the <i>Septoria nodorum</i> blotch susceptibility gene Snn3-B1 in wheat. <i>Molecular Genetics and Genomics</i> , 2016, 291, 107-119.	1.0	41
54	Identification and Characterization of the SnTox6-Snn6 Interaction in the <i>Parastagonospora nodorum</i> Wheat Pathosystem. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 615-625.	1.4	85

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55	The Wheat <i>Snn1</i> Gene Confers Susceptibility on Recognition of the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox7. <i>Plant Genome</i> , 2015, 8, eplantgenome2015.02.0007.	1.6	52
56	A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. <i>Plant Biotechnology Journal</i> , 2015, 13, 648-663.	4.1	386
57	Development of a diagnostic co-dominant marker for stem rust resistance gene Sr47 introgressed from <i>Aegilops speltoides</i> into durum wheat. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2367-2374.	1.8	5
58	Necrotrophic effector-triggered susceptibility (NETS) underlies the barley <i>Pyrenophora teres</i> f. <i>teres</i> interaction specific to chromosome 6H. <i>Molecular Plant Pathology</i> , 2015, 16, 188-200.	2.0	55
59	Analysis of agronomic and domestication traits in a durum-cultivated emmer wheat population using a high-density single nucleotide polymorphism-based linkage map. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2333-2348.	1.8	64
60	Identification and molecular mapping of quantitative trait loci for Fusarium head blight resistance in emmer and durum wheat using a single nucleotide polymorphism-based linkage map. <i>Molecular Breeding</i> , 2014, 34, 1677-1687.	1.0	55
61	Map-based analysis of the tenacious glume gene Tg-B1 of wild emmer and its role in wheat domestication. <i>Gene</i> , 2014, 542, 198-208.	1.0	31
62	Evaluation of a <i>Pyrenophora teres</i> f. <i>teres</i> mapping population reveals multiple independent interactions with a region of barley chromosome 6H. <i>Fungal Genetics and Biology</i> , 2014, 70, 104-112.	0.9	53
63	A dimeric PR-1 type pathogenesis-related protein interacts with ToxA and potentially mediates ToxA-induced necrosis in sensitive wheat. <i>Molecular Plant Pathology</i> , 2014, 15, 650-663.	2.0	81
64	Molecular and comparative mapping of genes governing spike compactness from wild emmer wheat. <i>Molecular Genetics and Genomics</i> , 2014, 289, 641-651.	1.0	38
65	Rewiring the wheat reproductive system to harness heterosis for the next wave of yield improvement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9024-9025.	3.3	10
66	<i>Pyrenophora tritici-repentis</i> : A Plant Pathogenic Fungus with Global Impact. , 2014, , 1-39.		20
67	Wheat Domestication: Key to Agricultural Revolutions Past and Future. , 2014, , 439-464.		76
68	Genetics of tan spot resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2197-2217.	1.8	117
69	Dimerization and protease resistance: New insight into the function of PR-1. <i>Journal of Plant Physiology</i> , 2013, 170, 105-110.	1.6	20
70	The Cysteine Rich Necrotrophic Effector SnTox1 Produced by <i>Stagonospora nodorum</i> Triggers Susceptibility of Wheat Lines Harboring Snn1. <i>PLoS Pathogens</i> , 2012, 8, e1002467.	2.1	233
71	Genetic Mapping Analysis of Bread-Making Quality Traits in Spring Wheat. <i>Crop Science</i> , 2012, 52, 2182-2197.	0.8	40
72	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat. <i>Plant Physiology</i> , 2012, 161, 252-265.	2.3	113

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73	Introgression and Characterization of a Goatgrass Gene for a High Level of Resistance to Ug99 Stem Rust in Tetraploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 665-673.	0.8	81
74	Characterization of Plant-Fungal Interactions Involving Necrotrophic Effector-Producing Plant Pathogens. <i>Methods in Molecular Biology</i> , 2012, 835, 191-207.	0.4	33
75	Tan spot susceptibility governed by the <i>Tsn1</i> locus and race-nonspecific resistance quantitative trait loci in a population derived from the wheat lines Salamouni and Katepwa. <i>Molecular Breeding</i> , 2012, 30, 1669-1678.	1.0	42
76	Whole-Genome QTL Analysis of <i>Stagonospora nodorum</i> Blotch Resistance and Validation of the <i>SnTox4</i> – <i>Snn4</i> Interaction in Hexaploid Wheat. <i>Phytopathology</i> , 2012, 102, 94-104.	1.1	22
77	<i>Stagonospora nodorum</i> : From Pathology to Genomics and Host Resistance. <i>Annual Review of Phytopathology</i> , 2012, 50, 23-43.	3.5	182
78	Quantitative Variation in Effector Activity of <i>ToxA</i> Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 515-522.	1.4	70
79	<i>SnTox5</i> – <i>Snn5</i> : a novel <i>Stagonospora nodorum</i> effector–wheat gene interaction and its relationship with the <i>SnToxA</i> – <i>Tsn1</i> and <i>SnTox3</i> – <i>Snn3</i> – <i>B1</i> interactions. <i>Molecular Plant Pathology</i> , 2012, 13, 1101-1109.	2.0	78
80	New broad-spectrum resistance to septoria tritici blotch derived from synthetic hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2012, 124, 125-142.	1.8	106
81	Variable Expression of the <i>Stagonospora nodorum</i> Effector <i>SnToxA</i> Among Isolates Is Correlated with Levels of Disease in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1419-1426.	1.4	38
82	Two putatively homoeologous wheat genes mediate recognition of <i>SnTox3</i> to confer effector-triggered susceptibility to <i>Stagonospora nodorum</i> . <i>Plant Journal</i> , 2011, 65, 27-38.	2.8	65
83	Molecular characterization and genomic mapping of the pathogenesis-related protein 1 (PR-1) gene family in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Molecular Genetics and Genomics</i> , 2011, 285, 485-503.	1.0	66
84	Identification and molecular mapping of two QTLs with major effects for resistance to Fusarium head blight in wheat. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1107-1119.	1.8	65
85	Duplication and partitioning in evolution and function of homoeologous <i>Q</i> loci governing domestication characters in polyploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18737-18742.	3.3	168
86	Marker Development and Saturation Mapping of the Tan Spot Ptr <i>ToxB</i> Sensitivity Locus <i>Tsc2</i> in Hexaploid Wheat. <i>Plant Genome</i> , 2010, 3, .	1.6	48
87	Genetic analysis of disease susceptibility contributed by the compatible <i>Tsn1</i> – <i>SnToxA</i> and <i>Snn1</i> – <i>SnTox1</i> interactions in the wheat- <i>Stagonospora nodorum</i> pathosystem. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1451-1459.	1.8	42
88	Targeted mapping of <i>Cdu1</i> , a major locus regulating grain cadmium concentration in durum wheat (<i>Triticum turgidum</i> L. var durum). <i>Theoretical and Applied Genetics</i> , 2010, 121, 1047-1058.	1.8	76
89	Identification of novel tan spot resistance QTLs using an SSR-based linkage map of tetraploid wheat. <i>Molecular Breeding</i> , 2010, 25, 327-338.	1.0	66
90	Identification of Chromosome Locations of Genes Affecting Preharvest Sprouting and Seed Dormancy Using Chromosome Substitution Lines in Tetraploid Wheat (<i>Triticum turgidum</i> L.). <i>Crop Science</i> , 2010, 50, 1180-1187.	0.8	20

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91	A unique wheat disease resistance-like gene governs effector-triggered susceptibility to necrotrophic pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13544-13549.	3.3	450
92	Characterization of the wheat- <i>Stagonospora nodorum</i> disease system: what is the molecular basis of this quantitative necrotrophic disease interaction? Canadian Journal of Plant Pathology, 2010, 32, 20-28.	0.8	88
93	Development of Expressed Sequence Tag (EST)-based Markers for Genomic Analysis of a Barley 6H Region Harboring Multiple Net Form Net Blotch Resistance Genes. Plant Genome, 2010, 3, .	1.6	17
94	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. PLoS Pathogens, 2009, 5, e1000581.	2.1	175
95	Development, identification, and validation of markers for marker-assisted selection against the <i>Stagonospora nodorum</i> toxin sensitivity genes Tsn1 and Snn2 in wheat. Molecular Breeding, 2009, 23, 35-49.	1.0	80
96	Host-selective toxins produced by <i>Stagonospora nodorum</i> confer disease susceptibility in adult wheat plants under field conditions. Theoretical and Applied Genetics, 2009, 118, 1489-1497.	1.8	87
97	Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doubled haploid population. Theoretical and Applied Genetics, 2009, 119, 263-269.	1.8	59
98	Identification and characterization of a novel host-toxin interaction in the wheat- <i>Stagonospora nodorum</i> pathosystem. Theoretical and Applied Genetics, 2009, 120, 117-126.	1.8	112
99	Development and Characterization of Expressed Sequence Tag-Derived Microsatellite Markers for the Wheat Stem Rust Fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> . Phytopathology, 2009, 99, 282-289.	1.1	45
100	Reevaluation of a Tetraploid Wheat Population Indicates that the Tsn1-ToxA Interaction Is the Only Factor Governing <i>Stagonospora nodorum</i> Blotch Susceptibility. Phytopathology, 2009, 99, 906-912.	1.1	40
101	Molecular and cytogenetic characterization of a durum wheat <i>Aegilops speltoides</i> chromosome translocation conferring resistance to stem rust. Chromosome Research, 2008, 16, 1097-1105.	1.0	77
102	Whole genome mapping in a wheat doubled haploid population using SSRs and TRAPs and the identification of QTL for agronomic traits. Molecular Breeding, 2008, 22, 251-266.	1.0	97
103	Identification of novel tan spot resistance loci beyond the known host-selective toxin insensitivity genes in wheat. Theoretical and Applied Genetics, 2008, 117, 873-881.	1.8	77
104	A region of barley chromosome 6H harbors multiple major genes associated with net type net blotch resistance. Theoretical and Applied Genetics, 2008, 117, 1261-1270.	1.8	65
105	Micro-colinearity between rice, <i>Brachypodium</i> , and <i>Triticum monococcum</i> at the wheat domestication locus Q. Functional and Integrative Genomics, 2008, 8, 149-164.	1.4	53
106	Characterization of the Interaction of a Novel <i>Stagonospora nodorum</i> Host-Selective Toxin with a Wheat Susceptibility Gene. Plant Physiology, 2008, 146, 323-324.	2.3	149
107	Host-specific toxins: effectors of necrotrophic pathogenicity. Cellular Microbiology, 2008, 10, 1421-1428.	1.1	275
108	Emergence of Tan Spot Disease Caused by Toxigenic <i>Pyrenophora tritici-repentis</i> in Australia Is Not Associated with Increased Deployment of Toxin-Sensitive Cultivars. Phytopathology, 2008, 98, 488-491.	1.1	30

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109	<i>Acc</i> homoeoloci and the evolution of wheat genomes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9691-9696.	3.3	148
110	Molecular Mapping of the Leaf Rust Resistance Gene Lr17a in Wheat. Crop Science, 2008, 48, 1124-1128.	0.8	17
111	Genomic Analysis of the Snn1 Locus on Wheat Chromosome Arm 1BS and the Identification of Candidate Genes. Plant Genome, 2008, 1, .	1.6	31
112	Identification of a Novel Fusarium Head Blight Resistance Quantitative Trait Locus on Chromosome 7A in Tetraploid Wheat. Phytopathology, 2007, 97, 592-597.	1.1	69
113	Genetic mapping of Pyrenophora teres f. teres genes conferring avirulence on barley. Fungal Genetics and Biology, 2007, 44, 323-329.	0.9	33
114	Genetics and genomics of wheat domestication-driven evolution. Israel Journal of Plant Sciences, 2007, 55, 223-229.	0.3	21
115	The Stagonospora nodorum-wheat pathosystem involves multiple proteinaceous host-selective toxins and corresponding host sensitivity genes that interact in an inverse gene-for-gene manner. Plant Journal, 2007, 51, 681-692.	2.8	176
116	Saturation and comparative mapping of a major Fusarium head blight resistance QTL in tetraploid wheat. Molecular Breeding, 2007, 19, 113-124.	1.0	75
117	Identification and characterization of segregation distortion loci along chromosome 5B in tetraploid wheat. Molecular Genetics and Genomics, 2007, 278, 187-196.	1.0	52
118	Identification and characterization of segregation distortion loci along chromosome 5B in tetraploid wheat. , 2007, 278, 187.		1
119	Emergence of a new disease as a result of interspecific virulence gene transfer. Nature Genetics, 2006, 38, 953-956.	9.4	667
120	The <i>Tsn1</i> ToxA interaction in the wheat-Stagonospora nodorum pathosystem parallels that of the wheat-tan spot system. Genome, 2006, 49, 1265-1273.	0.9	149
121	Macro- and microcolinearity between the genomic region of wheat chromosome 5B containing the Tsn1 gene and the rice genome. Functional and Integrative Genomics, 2006, 6, 90-103.	1.4	35
122	Genomic analysis and marker development for the Tsn1 locus in wheat using bin-mapped ESTs and flanking BAC contigs. Theoretical and Applied Genetics, 2006, 112, 1132-1142.	1.8	54
123	Molecular mapping of hybrid necrosis genes Ne1 and Ne2 in hexaploid wheat using microsatellite markers. Theoretical and Applied Genetics, 2006, 112, 1374-1381.	1.8	74
124	Molecular Characterization of the Major Wheat Domestication Gene Q. Genetics, 2006, 172, 547-555.	1.2	535
125	Identification of quantitative trait loci for race-nonspecific resistance to tan spot in wheat. Theoretical and Applied Genetics, 2005, 111, 386-392.	1.8	99
126	A wheat intervarietal genetic linkage map based on microsatellite and target region amplified polymorphism markers and its utility for detecting quantitative trait loci. Theoretical and Applied Genetics, 2005, 111, 782-794.	1.8	123

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127	Genomic Targeting and High-Resolution Mapping of the Tsn1 Gene in Wheat. <i>Crop Science</i> , 2004, 44, 951-962.	0.8	42
128	Chromosomal location of genes for novel glutenin subunits and gliadins in wild emmer wheat (<i>Triticum turgidum</i> L. var. <i>dicoccoides</i>). <i>Theoretical and Applied Genetics</i> , 2004, 108, 1221-1228.	1.8	47
129	Molecular mapping of resistance to <i>Pyrenophora tritici-repentis</i> race 5 and sensitivity to Ptr ToxB in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 464-471.	1.8	140
130	Genetic and Physical Mapping of a Gene Conditioning Sensitivity in Wheat to a Partially Purified Host-Selective Toxin Produced by <i>Stagonospora nodorum</i> . <i>Phytopathology</i> , 2004, 94, 1056-1060.	1.1	191
131	Quantitative Trait Loci Analysis and Mapping of Seedling Resistance to <i>Stagonospora nodorum</i> Leaf Blotch in Wheat. <i>Phytopathology</i> , 2004, 94, 1061-1067.	1.1	106
132	Genomic Targeting and High-Resolution Mapping of the Gene in Wheat. <i>Crop Science</i> , 2004, 44, 951.	0.8	44
133	A Bacterial Artificial Chromosome Contig Spanning the Major Domestication Locus <i>Q</i> in Wheat and Identification of a Candidate Gene. <i>Genetics</i> , 2003, 164, 311-321.	1.2	182
134	Genes encoding plastid acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the <i>Triticum/Aegilops</i> complex and the evolutionary history of polyploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8133-8138.	3.3	630
135	Genomic targeting and high-resolution mapping of the domestication gene <i>Q</i> in wheat. <i>Genome</i> , 2002, 45, 706-718.	0.9	86
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137	Chromosome Mapping and Phylogenetic Analysis of the Cytosolic Acetyl-CoA Carboxylase Loci in Wheat. <i>Molecular Biology and Evolution</i> , 2001, 18, 1720-1733.	3.5	30
138	Isolation and characterization of novel cDNA clones of acidic chitinases and β -1,3-glucanases from wheat spikes infected by <i>Fusarium graminearum</i> . <i>Theoretical and Applied Genetics</i> , 2001, 102, 353-362.	1.8	119
139	Saturation Mapping of a Gene-Rich Recombination Hot Spot Region in Wheat. <i>Genetics</i> , 2000, 154, 823-835.	1.2	223
140	Candidate gene analysis of quantitative disease resistance in wheat. <i>Theoretical and Applied Genetics</i> , 1999, 98, 219-225.	1.8	183
141	Genomic mapping of defense response genes in wheat. <i>Theoretical and Applied Genetics</i> , 1999, 98, 226-233.	1.8	147
142	Genetic Analysis of Sensitivity to a <i>Pyrenophora tritici-repentis</i> Necrosis-Inducing Toxin in Durum and Common Wheat. <i>Phytopathology</i> , 1999, 89, 293-297.	1.1	84
143	Plastid-localized acetyl-CoA carboxylase of bread wheat is encoded by a single gene on each of the three ancestral chromosome sets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 14179-14184.	3.3	80
144	RFLP mapping of resistance to chlorosis induction by <i>Pyrenophora tritici-repentis</i> in wheat. <i>Theoretical and Applied Genetics</i> , 1997, 94, 98-103.	1.8	98

#	ARTICLE	IF	CITATIONS
145	Chromosomal Location of a Gene Conditioning Insensitivity in Wheat to a Necrosis-Inducing Culture Filtrate from <i>Pyrenophora tritici-repentis</i> . <i>Phytopathology</i> , 1996, 86, 459.	1.1	184