

# Justin D Faris

## List of Publications by Year in descending order

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145  
papers

13,118  
citations

20797

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26591

107  
g-index

150  
all docs

150  
docs citations

150  
times ranked

6855  
citing authors

#	ARTICLE	IF	CITATIONS
1	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. <i>Science</i> , 2017, 357, 93-97.	6.0	781
2	Emergence of a new disease as a result of interspecific virulence gene transfer. <i>Nature Genetics</i> , 2006, 38, 953-956.	9.4	667
3	Genes encoding plastid acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the Triticum/Aegilops 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
4	Durum wheat genome highlights past domestication signatures and future improvement targets. <i>Nature Genetics</i> , 2019, 51, 885-895.	9.4	576
5	Molecular Characterization of the Major Wheat Domestication Gene Q. <i>Genetics</i> , 2006, 172, 547-555.	1.2	535
6	A unique wheat disease resistance-like gene governs effector-triggered susceptibility to necrotrophic pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13544-13549.	3.3	450
7	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
8	Host-specific toxins: effectors of necrotrophic pathogenicity. <i>Cellular Microbiology</i> , 2008, 10, 1421-1428.	1.1	275
9	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
10	Saturation Mapping of a Gene-Rich Recombination Hot Spot Region in Wheat. <i>Genetics</i> , 2000, 154, 823-835.	1.2	223
11	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
12	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
13	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
14	Candidate gene analysis of quantitative disease resistance in wheat. <i>Theoretical and Applied Genetics</i> , 1999, 98, 219-225.	1.8	183
15	<i>Stagonospora nodorum</i> : From Pathology to Genomics and Host Resistance. <i>Annual Review of Phytopathology</i> , 2012, 50, 23-43.	3.5	182
16	A Bacterial Artificial Chromosome Contig Spanning the Major Domestication Locus Q in Wheat and Identification of a Candidate Gene. <i>Genetics</i> , 2003, 164, 311-321.	1.2	182
17	The <i>Stagonospora nodorum</i> -wheat pathosystem involves multiple proteinaceous host-selective toxins and corresponding host sensitivity genes that interact in an inverse gene-for-gene manner. <i>Plant Journal</i> , 2007, 51, 681-692.	2.8	176
18	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. <i>PLoS Pathogens</i> , 2009, 5, e1000581.	2.1	175

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19	Duplication and partitioning in evolution and function of homoeologous <i>Q</i> loci governing domestication characters in polyploid wheat. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18737-18742.	3.3	168
20	The <i>Tsn1</i> – <i>ToxA</i> interaction in the wheat– <i>Stagonospora nodorum</i> pathosystem parallels that of the wheat–tan spot system. Genome, 2006, 49, 1265-1273.	0.9	149
21	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
22	<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
23	Genomic mapping of defense response genes in wheat. Theoretical and Applied Genetics, 1999, 98, 226-233.	1.8	147
24	Molecular mapping of resistance to <i>Pyrenophora tritici-repentis</i> race 5 and sensitivity to Ptr ToxB in wheat. Theoretical and Applied Genetics, 2004, 109, 464-471.	1.8	140
25	Phylogenetic analysis of the acetyl-CoA carboxylase and 3-phosphoglycerate kinase loci in wheat and other grasses. Plant Molecular Biology, 2002, 48, 805-820.	2.0	135
26	microRNA172 plays a critical role in wheat spike morphology and grain threshability. Development (Cambridge), 2017, 144, 1966-1975.	1.2	125
27	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
28	Isolation and characterization of novel cDNA clones of acidic chitinases and $\beta$ -1,3-glucanases from wheat spikes infected by <i>Fusarium graminearum</i> . Theoretical and Applied Genetics, 2001, 102, 353-362.	1.8	119
29	Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. Theoretical and Applied Genetics, 2019, 132, 2689-2705.	1.8	118
30	Genetics of tan spot resistance in wheat. Theoretical and Applied Genetics, 2013, 126, 2197-2217.	1.8	117
31	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat. Plant Physiology, 2012, 161, 252-265.	2.3	113
32	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
33	Quantitative Trait Loci Analysis and Mapping of Seedling Resistance to <i>Stagonospora nodorum</i> Leaf Blotch in Wheat. Phytopathology, 2004, 94, 1061-1067.	1.1	106
34	New broad-spectrum resistance to septoria tritici blotch derived from synthetic hexaploid wheat. Theoretical and Applied Genetics, 2012, 124, 125-142.	1.8	106
35	Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. Nature Biotechnology, 2022, 40, 422-431.	9.4	102
36	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

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37	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
38	Whole genome mapping in a wheat doubled haploid population using SSRs and TRAPs and the identification of QTL for agronomic traits. <i>Molecular Breeding</i> , 2008, 22, 251-266.	1.0	97
39	Characterization of the wheat- <i>Stagonospora nodorum</i> disease system: what is the molecular basis of this quantitative necrotrophic disease interaction? <i>Canadian Journal of Plant Pathology</i> , 2010, 32, 20-28.	0.8	88
40	Host-selective toxins produced by <i>Stagonospora nodorum</i> confer disease susceptibility in adult wheat plants under field conditions. <i>Theoretical and Applied Genetics</i> , 2009, 118, 1489-1497.	1.8	87
41	Genomic targeting and high-resolution mapping of the domestication gene <i>Qin</i> in wheat. <i>Genome</i> , 2002, 45, 706-718.	0.9	86
42	Identification and Characterization of the <i>SnTox6-Snn6</i> Interaction in the <i>Parastagonospora nodorum</i> Wheat Pathosystem. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 615-625.	1.4	85
43	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
44	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
45	A dimeric <i>PR1</i> type pathogenesis-related protein interacts with <i>ToxA</i> and potentially mediates <i>ToxA</i> -induced necrosis in sensitive wheat. <i>Molecular Plant Pathology</i> , 2014, 15, 650-663.	2.0	81
46	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
47	Development, identification, and validation of markers for marker-assisted selection against the <i>Stagonospora nodorum</i> toxin sensitivity genes <i>Tsn1</i> and <i>Snn2</i> in wheat. <i>Molecular Breeding</i> , 2009, 23, 35-49.	1.0	80
48	Plant genes hijacked by necrotrophic fungal pathogens. <i>Current Opinion in Plant Biology</i> , 2020, 56, 74-80.	3.5	79
49	<i>SnTox5</i> : a novel <i>Stagonospora nodorum</i> effector-wheat gene interaction and its relationship with the <i>SnToxA</i> and <i>Tsn1</i> and <i>SnTox3</i> interactions. <i>Molecular Plant Pathology</i> , 2012, 13, 1101-1109.	2.0	78
50	Molecular and cytogenetic characterization of a durum wheat <i>Aegilops speltoides</i> chromosome translocation conferring resistance to stem rust. <i>Chromosome Research</i> , 2008, 16, 1097-1105.	1.0	77
51	Identification of novel tan spot resistance loci beyond the known host-selective toxin insensitivity genes in wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 873-881.	1.8	77
52	Targeted mapping of <i>Cdu1</i> , a major locus regulating grain cadmium concentration in durum wheat ( <i>Triticum turgidum</i> L. var <i>durum</i> ). <i>Theoretical and Applied Genetics</i> , 2010, 121, 1047-1058.	1.8	76
53	<i>SnTox1</i> , 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
54	Wheat Domestication: Key to Agricultural Revolutions Past and Future. , 2014, , 439-464.		76

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55	Saturation and comparative mapping of a major Fusarium head blight resistance QTL in tetraploid wheat. <i>Molecular Breeding</i> , 2007, 19, 113-124.	1.0	75
56	Molecular mapping of hybrid necrosis genes Ne1 and Ne2 in hexaploid wheat using microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1374-1381.	1.8	74
57	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
58	Quantitative Variation in Effector Activity of ToxA 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
59	Identification of a Novel Fusarium Head Blight Resistance Quantitative Trait Locus on Chromosome 7A in Tetraploid Wheat. <i>Phytopathology</i> , 2007, 97, 592-597.	1.1	69
60	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
61	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
62	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
63	A region of barley chromosome 6H harbors multiple major genes associated with net type net blotch resistance. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1261-1270.	1.8	65
64	Two putatively homoeologous wheat genes mediate recognition of SnTox3 to confer effector-triggered susceptibility to <i>Stagonospora nodorum</i> . <i>Plant Journal</i> , 2011, 65, 27-38.	2.8	65
65	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
66	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
67	Identification of novel QTLs for seedling and adult plant leaf rust resistance in a wheat doubled haploid population. <i>Theoretical and Applied Genetics</i> , 2009, 119, 263-269.	1.8	59
68	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
69	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
70	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
71	Genomic analysis and marker development for the Tsn1 locus in wheat using bin-mapped ESTs and flanking BAC contigs. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1132-1142.	1.8	54
72	Meta-QTL analysis of tan spot resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2363-2375.	1.8	54

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73	Micro-colinearity between rice, Brachypodium, and Triticum monococcum at the wheat domestication locus Q. Functional and Integrative Genomics, 2008, 8, 149-164.	1.4	53
74	Evaluation of a Pyrenophora teres f. teres mapping population reveals multiple independent interactions with a region of barley chromosome 6H. Fungal Genetics and Biology, 2014, 70, 104-112.	0.9	53
75	<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>. Plant Disease, 2018, 102, 2446-2452.	0.7	53
76	Identification and characterization of segregation distortion loci along chromosome 5B in tetraploid wheat. Molecular Genetics and Genomics, 2007, 278, 187-196.	1.0	52
77	The Wheat <i>Snn7</i> Gene Confers Susceptibility on Recognition of the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox7. Plant Genome, 2015, 8, eplantgenome2015.02.0007.	1.6	52
78	New Insights into the Roles of Host Gene-Necrotrophic Effector Interactions in Governing Susceptibility of Durum Wheat to Tan Spot and Septoria nodorum Blotch. G3: Genes, Genomes, Genetics, 2016, 6, 4139-4150.	0.8	50
79	Genetic relationships between race-nonspecific and race-specific interactions in the wheatâ€“Pyrenophora tritici-repentis pathosystem. Theoretical and Applied Genetics, 2016, 129, 897-908.	1.8	49
80	Marker Development and Saturation Mapping of the Tan Spot Ptr ToxB Sensitivity Locus<i>Tsc2</i> in Hexaploid Wheat. Plant Genome, 2010, 3, .	1.6	48
81	Chromosomal location of genes for novel glutenin subunits and gliadins in wild emmer wheat (Triticum turgidum L. var. dicocoides). Theoretical and Applied Genetics, 2004, 108, 1221-1228.	1.8	47
82	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
83	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. Frontiers in Plant Science, 2020, 11, 569905.	1.7	44
84	Genomic Targeting and High-Resolution Mapping of the Gene in Wheat. Crop Science, 2004, 44, 951.	0.8	44
85	Genomic Targeting and High-Resolution Mapping of the Tsn1 Gene in Wheat. Crop Science, 2004, 44, 951-962.	0.8	42
86	Genetic analysis of disease susceptibility contributed by the compatible Tsn1â€“SnToxA and Snn1â€“SnTox1 interactions in the wheat-Stagonospora nodorum pathosystem. Theoretical and Applied Genetics, 2010, 120, 1451-1459.	1.8	42
87	Tan spot susceptibility governed by the Tsn1 locus and race-nonspecific resistance quantitative trait loci in a population derived from the wheat lines Salamouni and Katepwa. Molecular Breeding, 2012, 30, 1669-1678.	1.0	42
88	Marker development, saturation mapping, and high-resolution mapping of the Septoria nodorum blotch susceptibility gene Snn3-B1 in wheat. Molecular Genetics and Genomics, 2016, 291, 107-119.	1.0	41
89	Reevaluation of a Tetraploid Wheat Population Indicates that the <i>Tsn1</i>â€“ToxA Interaction Is the Only Factor Governing Stagonospora nodorum Blotch Susceptibility. Phytopathology, 2009, 99, 906-912.	1.1	40
90	Genetic Mapping Analysis of Breadâ€“Making Quality Traits in Spring Wheat. Crop Science, 2012, 52, 2182-2197.	0.8	40

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91	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
92	Variable Expression of the <i>Stagonospora nodorum</i> Effector SnToxA Among Isolates Is Correlated with Levels of Disease in Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1419-1426.	1.4	38
93	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
94	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
95	Macro- and microcolinearity between the genomic region of wheat chromosome 5B containing the Tsn1 gene and the rice genome. <i>Functional and Integrative Genomics</i> , 2006, 6, 90-103.	1.4	35
96	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
97	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
98	Genetic mapping of <i>Pyrenophora teres</i> f. <i>teres</i> genes conferring avirulence on barley. <i>Fungal Genetics and Biology</i> , 2007, 44, 323-329.	0.9	33
99	Characterization of Plant-Fungal Interactions Involving Necrotrophic Effector-Producing Plant Pathogens. <i>Methods in Molecular Biology</i> , 2012, 835, 191-207.	0.4	33
100	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
101	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
102	Genomic Analysis of the Snn1 Locus on Wheat Chromosome Arm 1BS and the Identification of Candidate Genes. <i>Plant Genome</i> , 2008, 1, .	1.6	31
103	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
104	A protein kinase—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
105	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
106	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. <i>Phytopathology</i> , 2008, 98, 488-491.	1.1	30
107	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
108	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

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109	Genetic analysis of virulence in the <i>Pyrenophora teres</i> f. <i>teres</i> population BB25 – FGOH04Ptt-21. <i>Fungal Genetics and Biology</i> , 2017, 107, 12-19.	0.9	27
110	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
111	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
112	Characterization of Effector-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
113	Whole-Genome QTL Analysis of <i>Stagonospora nodorum</i> Blotch Resistance and Validation of the <i>SnTox4-Snn4</i> Interaction in Hexaploid Wheat. <i>Phytopathology</i> , 2012, 102, 94-104.	1.1	22
114	A triple threat: the <i>Parastagonospora nodorum</i> <i>SnTox267</i> effector exploits three distinct host genetic factors to cause disease in wheat. <i>New Phytologist</i> , 2022, 233, 427-442.	3.5	22
115	Genetics and genomics of wheat domestication-driven evolution. <i>Israel Journal of Plant Sciences</i> , 2007, 55, 223-229.	0.3	21
116	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
117	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
118	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
119	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
120	<i>Pyrenophora tritici-repentis</i> : A Plant Pathogenic Fungus with Global Impact. , 2014, , 1-39.		20
121	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
122	Identification, mapping, and marker development of stem rust resistance genes in durum wheat “Lebsock™. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	19
123	<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
124	Molecular Mapping of the Leaf Rust Resistance Gene <i>Lr17a</i> in Wheat. <i>Crop Science</i> , 2008, 48, 1124-1128.	0.8	17
125	Development of Expressed Sequence Tag (EST)-based Markers for Genomic Analysis of a Barley 6H Region Harboring Multiple Net Form Net Blotch Resistance Genes. <i>Plant Genome</i> , 2010, 3, .	1.6	17
126	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



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127	Variation Analysis of Root System Development in Wheat Seedlings Using Root Phenotyping System. <i>Agronomy</i> , 2020, 10, 206.	1.3	14
128	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
129	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
130	Genetics of resistance to septoria nodorum blotch in wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 3685-3707.	1.8	13
131	<i>Pyrenophora tritici-repentis</i> Race 4 Isolates Cause Disease on Tetraploid Wheat. <i>Phytopathology</i> , 2020, 110, 1781-1790.	1.1	12
132	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
133	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
134	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
135	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
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137	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
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139	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
140	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
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143	Disease Resistance. , 2022, , 341-360.		3
144	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

#	ARTICLE	IF	CITATIONS
145	Identification and characterization of segregation distortion loci along chromosome 5B in tetraploid wheat. , 2007, 278, 187.		1