

Frank F White

List of Publications by Year in descending order

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86
papers

10,605
citations

50276

46
h-index

54911

84
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126
all docs

126
docs citations

126
times ranked

7917
citing authors

#	ARTICLE	IF	CITATIONS
1	Redoxâ€engineering enhances maize thermotolerance and grain yield in the field. <i>Plant Biotechnology Journal</i> , 2022, 20, 1819-1832.	8.3	13
2	Ectopic Expression of a Heterologous Glutaredoxin Enhances Drought Tolerance and Grain Yield in Field Grown Maize. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5331.	4.1	8
3	The Xa7 resistance gene guards the rice susceptibility gene SWEET14 against exploitation by the bacterial blight pathogen. <i>Plant Communications</i> , 2021, 2, 100164.	7.7	30
4	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	8.8	32
5	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa075.	3.2	8
6	Big Genes, Small Effectors: Pea Aphid Cassette Effector Families Composed From Miniature Exons. <i>Frontiers in Plant Science</i> , 2020, 11, 1230.	3.6	8
7	Genomic Acquisitions in Emerging Populations of <i>Xanthomonas vasicola</i> pv. <i>vasculorum</i> Infecting Corn in the United States and Argentina. <i>Phytopathology</i> , 2020, 110, 1161-1173.	2.2	16
8	<i>Xanthomonas</i> diversity, virulence and plantâ€pathogen interactions. <i>Nature Reviews Microbiology</i> , 2020, 18, 415-427.	28.6	182
9	Early Drought-Responsive Genes Are Variable and Relevant to Drought Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1657-1670.	1.8	13
10	An efficient method to clone TAL effector genes from <i>Xanthomonas oryzae</i> using Gibson assembly. <i>Molecular Plant Pathology</i> , 2019, 20, 1453-1462.	4.2	12
11	A New TALE to Tell?. <i>Cell Host and Microbe</i> , 2019, 26, 573-574.	11.0	0
12	Broad-spectrum resistance to bacterial blight in rice using genome editing. <i>Nature Biotechnology</i> , 2019, 37, 1344-1350.	17.5	470
13	Diagnostic kit for rice blight resistance. <i>Nature Biotechnology</i> , 2019, 37, 1372-1379.	17.5	92
14	Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus. <i>PLoS Genetics</i> , 2019, 15, e1008272.	3.5	103
15	<i>Xanthomonas translucens</i> commandeers the host rate-limiting step in ABA biosynthesis for disease susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20938-20946.	7.1	58
16	Disease Resistance and Susceptibility Genes to Bacterial Blight of Rice. , 2019, , .		1
17	Recent advances in developing disease resistance in plants. <i>F1000Research</i> , 2019, 8, 1934.	1.6	11
18	One effector at a time. <i>Nature Plants</i> , 2018, 4, 134-135.	9.3	2

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19	Functional characterization of the citrus canker susceptibility gene <i>CsLOB1</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 1908-1916.	4.2	44
20	Genetic mapping of a major gene in triticale conferring resistance to bacterial leaf streak. <i>Theoretical and Applied Genetics</i> , 2018, 131, 649-658.	3.6	23
21	Sugar flux and signaling in plant-microbe interactions. <i>Plant Journal</i> , 2018, 93, 675-685.	5.7	180
22	Fast Evolution and Lineage-Specific Gene Family Expansions of Aphid Salivary Effectors Driven by Interactions with Host-Plants. <i>Genome Biology and Evolution</i> , 2018, 10, 1554-1572.	2.5	67
23	Analysis of Extreme Phenotype Bulk Copy Number Variation (XP-CNV) Identified the Association of <i>rp1</i> with Resistance to Goss's Wilt of Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 110.	3.6	23
24	Molecular characterization of XopAG effector <i>AvrGf2</i> from <i>Xanthomonas fuscans</i> ssp. <i>aurantifolii</i> in grapefruit. <i>Molecular Plant Pathology</i> , 2017, 18, 405-419.	4.2	12
25	Homologues of <i>CsLOB1</i> in citrus function as disease susceptibility genes in citrus canker. <i>Molecular Plant Pathology</i> , 2017, 18, 798-810.	4.2	38
26	A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in <i>Rhizoctonia solani</i> . <i>Phytobiomes Journal</i> , 2017, 1, 14-23.	2.7	24
27	Unbiased K-mer Analysis Reveals Changes in Copy Number of Highly Repetitive Sequences During Maize Domestication and Improvement. <i>Scientific Reports</i> , 2017, 7, 42444.	3.3	16
28	Glutaredoxins in plant development, abiotic stress response, and iron homeostasis: From model organisms to crops. <i>Environmental and Experimental Botany</i> , 2017, 139, 91-98.	4.2	38
29	Genome editing of the disease susceptibility gene <i>CsLOB1</i> in citrus confers resistance to citrus canker. <i>Plant Biotechnology Journal</i> , 2017, 15, 817-823.	8.3	371
30	Characterization of a unique copper resistance gene cluster in <i>Xanthomonas campestris</i> pv. <i>campestris</i> isolated in Trinidad, West Indies. <i>European Journal of Plant Pathology</i> , 2017, 147, 671-681.	1.7	21
31	Expression of a monothiol glutaredoxin, <i>AtGRXS17</i> , in tomato (<i>Solanum lycopersicum</i>) enhances drought tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 1034-1039.	2.1	37
32	Silencing of <i>OsGRXS17</i> in rice improves drought stress tolerance by modulating ROS accumulation and stomatal closure. <i>Scientific Reports</i> , 2017, 7, 15950.	3.3	64
33	The non-host pathogen <i>Puccinia triticina</i> elicits an active transcriptional response in rice. <i>European Journal of Plant Pathology</i> , 2017, 147, 553-569.	1.7	1
34	Complete Genome Sequencing and Targeted Mutagenesis Reveal Virulence Contributions of <i>Tal2</i> and <i>Tal4b</i> of <i>Xanthomonas translucens</i> pv. <i>undulosa</i> ICMP11055 in Bacterial Leaf Streak of Wheat. <i>Frontiers in Microbiology</i> , 2017, 8, 1488.	3.5	37
35	The broadly effective recessive resistance gene <i>xa5</i> of rice is a virulence effector-dependent quantitative trait for bacterial blight. <i>Plant Journal</i> , 2016, 86, 186-194.	5.7	64
36	Analysis of Sequenced Genomes of <i>Xanthomonas perforans</i> Identifies Candidate Targets for Resistance Breeding in Tomato. <i>Phytopathology</i> , 2016, 106, 1097-1104.	2.2	41

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37	Long read and single molecule DNA sequencing simplifies genome assembly and TAL effector gene analysis of <i>Xanthomonas translucens</i> . <i>BMC Genomics</i> , 2016, 17, 21.	2.8	97
38	<i>Xanthomonas</i> and the TAL Effectors: Nature's Molecular Biologist. <i>Methods in Molecular Biology</i> , 2016, 1338, 1-8.	0.9	5
39	Tomato expressing <i>Arabidopsis glutaredoxin</i> gene <i>AtGRXS17</i> confers tolerance to chilling stress via modulating cold responsive components. <i>Horticulture Research</i> , 2015, 2, 15051.	6.3	62
40	Phylogenomics of <i>Xanthomonas</i> field strains infecting pepper and tomato reveals diversity in effector repertoires and identifies determinants of host specificity. <i>Frontiers in Microbiology</i> , 2015, 6, 535.	3.5	156
41	TAL effectors and the executor R genes. <i>Frontiers in Plant Science</i> , 2015, 6, 641.	3.6	119
42	Genetic engineering of the <i>Xa10</i> promoter for broad-spectrum and durable resistance to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Plant Biotechnology Journal</i> , 2015, 13, 993-1001.	8.3	47
43	Gene targeting by the TAL effector <i>PthXo2</i> reveals cryptic resistance gene for bacterial blight of rice. <i>Plant Journal</i> , 2015, 82, 632-643.	5.7	409
44	Deciphering durable resistance one R gene at a time. <i>Nature Genetics</i> , 2015, 47, 1376-1377.	21.4	6
45	Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. <i>PLoS Pathogens</i> , 2014, 10, e1003972.	4.7	137
46	The Rice TAL Effector-Dependent Resistance Protein <i>XA10</i> Triggers Cell Death and Calcium Depletion in the Endoplasmic Reticulum. <i>Plant Cell</i> , 2014, 26, 497-515.	6.6	197
47	<i>Lateral organ boundaries 1</i> is a disease susceptibility gene for citrus bacterial canker disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E521-9.	7.1	268
48	Comparative genomic and transcriptome analyses of pathotypes of <i>Xanthomonas citri</i> subsp. <i>citri</i> provide insights into mechanisms of bacterial virulence and host range. <i>BMC Genomics</i> , 2013, 14, 551.	2.8	88
49	Genomic and Proteomic Analysis of <i>Schizaphis graminum</i> Reveals Cyclophilin Proteins Are Involved in the Transmission of Cereal Yellow Dwarf Virus. <i>PLoS ONE</i> , 2013, 8, e71620.	2.5	47
50	Parallel domestication of the <i>Shattering1</i> genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724.	21.4	401
51	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. <i>Journal of Bacteriology</i> , 2011, 193, 5450-5464.	2.2	189
52	Mutational analysis of type III effector genes from <i>Xanthomonas citri</i> subsp. <i>citri</i> . <i>European Journal of Plant Pathology</i> , 2011, 130, 339-347.	1.7	7
53	<i>Agrobacterium</i> -mediated transient expression in citrus leaves: a rapid tool for gene expression and functional gene assay. <i>Plant Cell Reports</i> , 2011, 30, 1339-1345.	5.6	34
54	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. <i>BMC Genomics</i> , 2011, 12, 146.	2.8	167

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55	Alien introgressions represent a rich source of genes for crop improvement. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7657-7658.	7.1	89
56	Sugar transporters for intercellular exchange and nutrition of pathogens. Nature, 2010, 468, 527-532.	27.8	1,258
57	Rice <i>xa13</i> Recessive Resistance to Bacterial Blight Is Defeated by Induction of the Disease Susceptibility Gene Os- <i>11N3</i> . Plant Cell, 2010, 22, 3864-3876.	6.6	401
58	Host and Pathogen Factors Controlling the Rice- <i>Xanthomonas oryzae</i> Interaction. Plant Physiology, 2009, 150, 1677-1686.	4.8	184
59	The type III effectors of <i>Xanthomonas</i> . Molecular Plant Pathology, 2009, 10, 749-766.	4.2	303
60	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 204.	2.8	327
61	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 534.	2.8	33
62	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . PLoS ONE, 2008, 3, e3828.	2.5	89
63	Two type III effector genes of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> control the induction of the host genes OsTFIIA1 and OsTFX1 during bacterial blight of rice. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10720-10725.	7.1	199
64	Inhibition of Resistance Gene-Mediated Defense in Rice by <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . Molecular Plant-Microbe Interactions, 2006, 19, 240-249.	2.6	58
65	Os8N3 is a host disease-susceptibility gene for bacterial blight of rice. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 10503-10508.	7.1	543
66	Avoidance of Host Recognition by Alterations in the Repetitive and C-Terminal Regions of AvrXa7, a Type III Effector of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . Molecular Plant-Microbe Interactions, 2005, 18, 142-149.	2.6	74
67	Characterization of the hrpF Pathogenicity Peninsula of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . Molecular Plant-Microbe Interactions, 2005, 18, 546-554.	2.6	63
68	R gene expression induced by a type-III effector triggers disease resistance in rice. Nature, 2005, 435, 1122-1125.	27.8	502
69	Diverse Members of the AvrBs3/PthA Family of Type III Effectors Are Major Virulence Determinants in Bacterial Blight Disease of Rice. Molecular Plant-Microbe Interactions, 2004, 17, 1192-1200.	2.6	183
70	Prospects for understanding avirulence gene function. Current Opinion in Plant Biology, 2000, 3, 291-298.	7.1	164
71	Identification of Two Novel hrp-Associated Genes in the hrp Gene Cluster of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . Journal of Bacteriology, 2000, 182, 1844-1853.	2.2	165
72	The C Terminus of AvrXa10 Can Be Replaced by the Transcriptional Activation Domain of VP16 from the Herpes Simplex Virus. Plant Cell, 1999, 11, 1665-1674.	6.6	80

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73	Insect resistance of transgenic tobacco expressing an insect chitinase gene. <i>Transgenic Research</i> , 1998, 7, 77-84.	2.4	151
74	The Corn Inhibitor of Activated Hageman Factor: Purification and Properties of Two Recombinant Forms of the Protein. <i>Protein Expression and Purification</i> , 1998, 13, 143-149.	1.3	14
75	AvrXa10 Contains an Acidic Transcriptional Activation Domain in the Functionally Conserved C Terminus. <i>Molecular Plant-Microbe Interactions</i> , 1998, 11, 824-832.	2.6	165
76	Differential Induction of a Peroxidase Gene Family During Infection of Rice by <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 1997, 10, 861-871.	2.6	169
77	BACTERIAL AVIRULENCE GENES. <i>Annual Review of Phytopathology</i> , 1996, 34, 153-179.	7.8	245
78	Expression of a corn bifunctional inhibitor of serine proteinases and insect α -amylases in transgenic tobacco plants. <i>Plant Science</i> , 1996, 115, 59-69.	3.6	11
79	Characterization of a 46 kda insect chitinase from transgenic tobacco. <i>Insect Biochemistry and Molecular Biology</i> , 1996, 26, 1055-1064.	2.7	59
80	Expression of a cysteine proteinase inhibitor (oryzacystatin-I) in transgenic tobacco plants. <i>Plant Molecular Biology</i> , 1993, 21, 655-663.	3.9	88
81	<i>Research Notes</i> Cloning of the Genes for Indoleacetic Acid Synthesis from <i>Pseudomonas syringae</i> pv. <i>syringae</i> . <i>Molecular Plant-Microbe Interactions</i> , 1991, 4, 207.	2.6	24
82	Reversion of Aberrant Plants Transformed with <i>Agrobacterium rhizogenes</i> Is Associated with the Transcriptional Inactivation of the TL-DNA Genes. <i>Plant Physiology</i> , 1988, 86, 584-590.	4.8	47
83	Molecular biology of Ri-plasmids—A review. <i>Journal of Biosciences</i> , 1987, 11, 47-57.	1.1	38
84	Transcription of <i>Agrobacterium rhizogenes</i> A4 T-DNA. <i>Molecular Genetics and Genomics</i> , 1985, 201, 546-553.	2.4	40
85	T-DNA analysis of plants regenerated from hairy root tumors. <i>Molecular Genetics and Genomics</i> , 1985, 201, 554-557.	2.4	67
86	Sequences homologous to <i>Agrobacterium rhizogenes</i> T-DNA in the genomes of uninfected plants. <i>Nature</i> , 1983, 301, 348-350.	27.8	173