

Frank F White

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7135790/publications.pdf>

Version: 2024-02-01

86
papers

10,605
citations

50276

46
h-index

54911

84
g-index

126
all docs

126
docs citations

126
times ranked

7917
citing authors

#	ARTICLE	IF	CITATIONS
1	Sugar transporters for intercellular exchange and nutrition of pathogens. <i>Nature</i> , 2010, 468, 527-532.	27.8	1,258
2	Os8N3 is a host disease-susceptibility gene for bacterial blight of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10503-10508.	7.1	543
3	R gene expression induced by a type-III effector triggers disease resistance in rice. <i>Nature</i> , 2005, 435, 1122-1125.	27.8	502
4	Broad-spectrum resistance to bacterial blight in rice using genome editing. <i>Nature Biotechnology</i> , 2019, 37, 1344-1350.	17.5	470
5	Gene targeting by the <i>TAL</i> effector PthXo2 reveals cryptic resistance gene for bacterial blight of rice. <i>Plant Journal</i> , 2015, 82, 632-643.	5.7	409
6	Rice <i>xa13</i> Recessive Resistance to Bacterial Blight Is Defeated by Induction of the Disease Susceptibility Gene <i>Os-11N3</i> . <i>Plant Cell</i> , 2010, 22, 3864-3876.	6.6	401
7	Parallel domestication of the <i>Shattering1</i> genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724.	21.4	401
8	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
9	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 204.	2.8	327
10	The type III effectors of <i>Xanthomonas</i> . <i>Molecular Plant Pathology</i> , 2009, 10, 749-766.	4.2	303
11	<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
12	BACTERIAL AVIRULENCE GENES. <i>Annual Review of Phytopathology</i> , 1996, 34, 153-179.	7.8	245
13	Two type III effector genes of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> control the induction of the host genes <i>OsTFIIA1</i> and <i>OsTFX1</i> during bacterial blight of rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10720-10725.	7.1	199
14	The Rice TAL Effector-Dependent Resistance Protein XA10 Triggers Cell Death and Calcium Depletion in the Endoplasmic Reticulum. <i>Plant Cell</i> , 2014, 26, 497-515.	6.6	197
15	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
16	Host and Pathogen Factors Controlling the Rice- <i>Xanthomonas oryzae</i> Interaction. <i>Plant Physiology</i> , 2009, 150, 1677-1686.	4.8	184
17	Diverse Members of the <i>AvrBs3/PthA</i> Family of Type III Effectors Are Major Virulence Determinants in Bacterial Blight Disease of Rice. <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 1192-1200.	2.6	183
18	<i>Xanthomonas</i> diversity, virulence and plant-pathogen interactions. <i>Nature Reviews Microbiology</i> , 2020, 18, 415-427.	28.6	182

#	ARTICLE	IF	CITATIONS
19	Sugar flux and signaling in plant-microbe interactions. <i>Plant Journal</i> , 2018, 93, 675-685.	5.7	180
20	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
21	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
22	Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. <i>BMC Genomics</i> , 2011, 12, 146.	2.8	167
23	<i>AvrXa10</i> 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
24	Identification of Two Novel <i>hrp</i> -Associated Genes in the <i>hrp</i> Gene Cluster of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Journal of Bacteriology</i> , 2000, 182, 1844-1853.	2.2	165
25	Prospects for understanding avirulence gene function. <i>Current Opinion in Plant Biology</i> , 2000, 3, 291-298.	7.1	164
26	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
27	Insect resistance of transgenic tobacco expressing an insect chitinase gene. <i>Transgenic Research</i> , 1998, 7, 77-84.	2.4	151
28	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
29	TAL effectors and the executor R genes. <i>Frontiers in Plant Science</i> , 2015, 6, 641.	3.6	119
30	Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus. <i>PLoS Genetics</i> , 2019, 15, e1008272.	3.5	103
31	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
32	Diagnostic kit for rice blight resistance. <i>Nature Biotechnology</i> , 2019, 37, 1372-1379.	17.5	92
33	Alien introgressions represent a rich source of genes for crop improvement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7657-7658.	7.1	89
34	Acquisition and Evolution of Plant Pathogenesis-Associated Gene Clusters and Candidate Determinants of Tissue-Specificity in <i>Xanthomonas</i> . <i>PLoS ONE</i> , 2008, 3, e3828.	2.5	89
35	Expression of a cysteine proteinase inhibitor (oryzacystatin-I) in transgenic tobacco plants. <i>Plant Molecular Biology</i> , 1993, 21, 655-663.	3.9	88
36	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

#	ARTICLE	IF	CITATIONS
37	The C Terminus of AvrXa10 Can Be Replaced by the Transcriptional Activation Domain of VP16 from the Herpes Simplex Virus. <i>Plant Cell</i> , 1999, 11, 1665-1674.	6.6	80
38	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> . <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 142-149.	2.6	74
39	T-DNA analysis of plants regenerated from hairy root tumors. <i>Molecular Genetics and Genomics</i> , 1985, 201, 554-557.	2.4	67
40	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
41	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
42	Silencing of OsGRXS17 in rice improves drought stress tolerance by modulating ROS accumulation and stomatal closure. <i>Scientific Reports</i> , 2017, 7, 15950.	3.3	64
43	Characterization of the hrpF Pathogenicity Peninsula of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 546-554.	2.6	63
44	Tomato expressing Arabidopsis glutaredoxin gene AtGRXS17 confers tolerance to chilling stress via modulating cold responsive components. <i>Horticulture Research</i> , 2015, 2, 15051.	6.3	62
45	Characterization of a 46 kda insect chitinase from transgenic tobacco. <i>Insect Biochemistry and Molecular Biology</i> , 1996, 26, 1055-1064.	2.7	59
46	Inhibition of Resistance Gene-Mediated Defense in Rice by <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 240-249.	2.6	58
47	<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
48	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
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	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
51	Functional characterization of the citrus canker susceptibility gene <i>CsLOB1</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 1908-1916.	4.2	44
52	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
53	Transcription of <i>Agrobacterium rhizogenes</i> A4 T-DNA. <i>Molecular Genetics and Genomics</i> , 1985, 201, 546-553.	2.4	40
54	Molecular biology of Ri-plasmids—A review. <i>Journal of Biosciences</i> , 1987, 11, 47-57.	1.1	38

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	Expression of a monothiol glutaredoxin, AtGRXS17, in tomato (<i>Solanum lycopersicum</i>) enhances drought tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2017, 491, 1034-1039.	2.1	37
58	Complete Genome Sequencing and Targeted Mutagenesis Reveal Virulence Contributions of Tal2 and Tal4b 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
59	<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
60	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. <i>BMC Genomics</i> , 2008, 9, 534.	2.8	33
61	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	8.8	32
62	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
63	A Dimorphic and Virulence-Enhancing Endosymbiont Bacterium Discovered in <i>Rhizoctonia solani</i> . <i>Phytobiomes Journal</i> , 2017, 1, 14-23.	2.7	24
64	<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
65	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
66	Analysis of Extreme Phenotype Bulk Copy Number Variation (XP-CNV) Identified the Association of rp1 with Resistance to Goss's Wilt of Maize. <i>Frontiers in Plant Science</i> , 2018, 9, 110.	3.6	23
67	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
68	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
69	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
70	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
71	Early Drought-Responsive Genes Are Variable and Relevant to Drought Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1657-1670.	1.8	13
72	Redox engineering enhances maize thermotolerance and grain yield in the field. <i>Plant Biotechnology Journal</i> , 2022, 20, 1819-1832.	8.3	13

#	ARTICLE	IF	CITATIONS
73	Molecular characterization of XopAG effector AvrGf2 from <i>Xanthomonas fuscans</i> ssp. <i>aurantifolii</i> in grapefruit. <i>Molecular Plant Pathology</i> , 2017, 18, 405-419.	4.2	12
74	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
75	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
76	Recent advances in developing disease resistance in plants. <i>F1000Research</i> , 2019, 8, 1934.	1.6	11
77	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
78	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
79	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
80	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
81	Deciphering durable resistance one R gene at a time. <i>Nature Genetics</i> , 2015, 47, 1376-1377.	21.4	6
82	<i>Xanthomonas</i> and the TAL Effectors: Nature's Molecular Biologist. <i>Methods in Molecular Biology</i> , 2016, 1338, 1-8.	0.9	5
83	One effector at a time. <i>Nature Plants</i> , 2018, 4, 134-135.	9.3	2
84	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
85	Disease Resistance and Susceptibility Genes to Bacterial Blight of Rice. , 2019, , .		1
86	A New TALE to Tell?. <i>Cell Host and Microbe</i> , 2019, 26, 573-574.	11.0	0