

David A Jones

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Optimized Production of Disulfide-Bonded Fungal Effectors in <i>Escherichia coli</i> Using CyDisCo and FunCyDisCo Coexpression Approaches. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 109-118.	2.6	3
2	Transcriptome Analysis of <i>Fusarium</i> –Tomato Interaction Based on an Updated Genome Annotation of <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> Identifies Novel Effector Candidates That Suppress or Induce Cell Death in <i>Nicotiana benthamiana</i> . <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 672.	3.5	8
3	The crystal structure of SnTox3 from the necrotrophic fungus <i>Parastagonospora nodorum</i> reveals a unique effector fold and provides insight into Snn3 recognition and prodomain protease processing of fungal effectors. <i>New Phytologist</i> , 2021, 231, 2282-2296.	7.3	24
4	Flax rust infection transcriptomics reveals a transcriptional profile that may be indicative for rust Avr genes. <i>PLoS ONE</i> , 2019, 14, e0226106.	2.5	14
5	Structural and functional insights into the modulation of the activity of a flax cytokinin oxidase by flax rust effector AvrL567. <i>Molecular Plant Pathology</i> , 2019, 20, 211-222.	4.2	15
6	Crystal structure of the <i>Melampsora lini</i> effector AvrP reveals insights into a possible nuclear function and recognition by the flax disease resistance protein P. <i>Molecular Plant Pathology</i> , 2018, 19, 1196-1209.	4.2	24
7	Evidence for horizontal gene transfer and separation of effector recognition from effector function revealed by analysis of effector genes shared between cape gooseberry and tomato infecting formae speciales of <i>Fusarium oxysporum</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 2302-2318.	4.2	36
8	Fungal phytopathogens encode functional homologues of plant rapid alkalization factor (RALF) peptides. <i>Molecular Plant Pathology</i> , 2017, 18, 811-824.	4.2	95
9	The tomato <i>WIPK</i> gene for <i>Fusarium</i> wilt resistance encodes an atypical leucine-rich repeat receptor-like protein whose function is nevertheless dependent on <i>SOBIR1</i> and <i>SERK3/BAK1</i> . <i>Plant Journal</i> , 2017, 89, 1195-1209.	5.7	103
10	Genome analysis and avirulence gene cloning using a high-density RADseq linkage map of the flax rust fungus, <i>Melampsora lini</i> . <i>BMC Genomics</i> , 2016, 17, 667.	2.8	59
11	Identification of <i>WIPK</i> expands the repertoire of genes for resistance to <i>Fusarium</i> wilt in tomato to three resistance gene classes. <i>Molecular Plant Pathology</i> , 2016, 17, 448-463.	4.2	125
12	A mutational analysis of the cytosolic domain of the tomato <i>CFR1</i> disease-resistance protein shows that membrane-proximal residues are important for <i>Avr9</i> -dependent necrosis. <i>Molecular Plant Pathology</i> , 2016, 17, 565-576.	4.2	12
13	The Full-Size ABCG Transporters Nb-ABCG1 and Nb-ABCG2 Function in Pre- and Postinvasion Defense against <i>Phytophthora infestans</i> in <i>Nicotiana benthamiana</i> . <i>Plant Cell</i> , 2016, 28, 1163-1181.	6.6	66
14	The tomato <i>WIPK</i> gene: a novel gene for resistance to <i>Fusarium</i> wilt disease. <i>New Phytologist</i> , 2015, 207, 106-118.	7.3	169
15	The genome sequence and effector complement of the flax rust pathogen <i>Melampsora lini</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 98.	3.6	126
16	Particle Bombardment-Mediated Transient Expression to Identify Localization Signals in Plant Disease Resistance Proteins and Target Sites for the Proteolytic Activity of Pathogen Effectors. <i>Methods in Molecular Biology</i> , 2014, 1127, 91-101.	0.9	4
17	Structures of the flax-rust effector AvrM reveal insights into the molecular basis of plant-cell entry and effector-triggered immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17594-17599.	7.1	75
18	N-Terminal Motifs in Some Plant Disease Resistance Proteins Function in Membrane Attachment and Contribute to Disease Resistance. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 379-392.	2.6	62

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19	Effector proteins of extracellular fungal plant pathogens that trigger host resistance. <i>Functional Plant Biology</i> , 2010, 37, 901.	2.1	14
20	Internalization of Flax Rust Avirulence Proteins into Flax and Tobacco Cells Can Occur in the Absence of the Pathogen. <i>Plant Cell</i> , 2010, 22, 2017-2032.	6.6	185
21	Lipid binding activities of flax rust AvrM and AvrL567 effectors. <i>Plant Signaling and Behavior</i> , 2010, 5, 1272-1275.	2.4	59
22	Effectors of biotrophic fungi and oomycetes: pathogenicity factors and triggers of host resistance. <i>New Phytologist</i> , 2009, 183, 993-1000.	7.3	153
23	The Major Specificity-Determining Amino Acids of the Tomato Cf-9 Disease Resistance Protein Are at Hypervariable Solvent-Exposed Positions in the Central Leucine-Rich Repeats. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1203-1213.	2.6	46
24	Recognition Specificity and Evolution in the Tomato- <i>Cladosporium fulvum</i> Pathosystem. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1191-1202.	2.6	48
25	Regions of the Cf-9B Disease Resistance Protein Able to Cause Spontaneous Necrosis in <i>Nicotiana benthamiana</i> Lie Within the Region Controlling Pathogen Recognition in Tomato. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 1214-1226.	2.6	17
26	High resolution genetic and physical mapping of the I-3 region of tomato chromosome 7 reveals almost continuous microsynteny with grape chromosome 12 but interspersed microsynteny with duplications on Arabidopsis chromosomes 1, 2 and 3. <i>Theoretical and Applied Genetics</i> , 2008, 118, 57-75.	3.6	23
27	Cytoskeleton and cell wall function in penetration resistance. <i>Current Opinion in Plant Biology</i> , 2007, 10, 342-348.	7.1	212
28	Development of PCR-based markers from the tomato glutamate oxaloacetate transaminase isozyme gene family as a means of revitalising old isozyme markers and recruiting new ones. <i>Molecular Breeding</i> , 2007, 19, 209-214.	2.1	3
29	Dominant negative interference with defence signalling by truncation mutations of the tomato Cf-9 disease resistance gene. <i>Plant Journal</i> , 2006, 46, 385-399.	5.7	6
30	A tomato mutant that shows stunting, wilting, progressive necrosis and constitutive expression of defence genes contains a recombinant Hcr9 gene encoding an autoactive protein. <i>Plant Journal</i> , 2006, 46, 369-384.	5.7	8
31	Re-organization of the cytoskeleton and endoplasmic reticulum in the Arabidopsis pen1-1 mutant inoculated with the non-adapted powdery mildew pathogen, <i>Blumeria graminis</i> f. sp. <i>hordei</i> . <i>Molecular Plant Pathology</i> , 2006, 7, 553-563.	4.2	62
32	Mapping the I-3 gene for resistance to Fusarium wilt in tomato: application of an I-3 marker in tomato improvement and progress towards the cloning of I-3. <i>Australasian Plant Pathology</i> , 2006, 35, 671.	1.0	37
33	Membrane Release and Destabilization of Arabidopsis RIN4 Following Cleavage by <i>Pseudomonas syringae</i> AvrRpt2. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 1258-1268.	2.6	54
34	ER retrieval of Avr9 compromises its elicitor activity consistent with perception of Avr9 at the plasma membrane. <i>Molecular Plant Pathology</i> , 2005, 6, 193-197.	4.2	4
35	Differences in Cell Death Induction by Phytophthora Elicitins Are Determined by Signal Components Downstream of MAP Kinase Kinase in Different Species of <i>Nicotiana</i> and Cultivars of <i>Brassica rapa</i> and <i>Raphanus sativus</i> . <i>Plant Physiology</i> , 2005, 138, 1491-1504.	4.8	41
36	Fine mapping of the tomato I-3 gene for fusarium wilt resistance and elimination of a co-segregating resistance gene analogue as a candidate for I-3. <i>Theoretical and Applied Genetics</i> , 2004, 109, 409-418.	3.6	56

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37	Plant innate immunity â€“ direct and indirect recognition of general and specific pathogen-associated molecules. <i>Current Opinion in Immunology</i> , 2004, 16, 48-62.	5.5	290
38	GFP-tagging of cell components reveals the dynamics of subcellular re-organization in response to infection of <i>Arabidopsis</i> by oomycete pathogens. <i>Plant Journal</i> , 2003, 33, 775-792.	5.7	240
39	Characterization and Evolutionary Analysis of a Large Polygalacturonase Gene Family in the Oomycete Plant Pathogen <i>Phytophthora cinnamomi</i> . <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 907-921.	2.6	135
40	The C-Terminal Dilysine Motif Confers Endoplasmic Reticulum Localization to Type I Membrane Proteins in Plants. <i>Plant Cell</i> , 2000, 12, 1179.	6.6	1
41	The C-Terminal Dilysine Motif Confers Endoplasmic Reticulum Localization to Type I Membrane Proteins in Plants. <i>Plant Cell</i> , 2000, 12, 1179-1201.	6.6	107
42	Homologues of the Cf-9 Disease Resistance Gene (Hcr9s) Are Present at Multiple Loci on the Short Arm of Tomato Chromosome 1. <i>Molecular Plant-Microbe Interactions</i> , 1999, 12, 93-102.	2.6	53
43	Instant diamond. <i>Nature</i> , 1999, 401, 544-544.	27.8	0
44	Structure and function of proteins controlling strain-specific pathogen resistance in plants. <i>Current Opinion in Plant Biology</i> , 1998, 1, 288-293.	7.1	153
45	A flax transposon identified in two spontaneous mutant alleles of the L6 rust resistance gene. <i>Plant Journal</i> , 1998, 16, 365-369.	5.7	31
46	The Tomato Cf-5 Disease Resistance Gene and Six Homologs Show Pronounced Allelic Variation in Leucine-Rich Repeat Copy Number. <i>Plant Cell</i> , 1998, 10, 1915-1925.	6.6	286
47	The Tomato Cf-5 Disease Resistance Gene and Six Homologs Show Pronounced Allelic Variation in Leucine-Rich Repeat Copy Number. <i>Plant Cell</i> , 1998, 10, 1915.	6.6	17
48	Characterization of the Tomato Cf-4 Gene for Resistance to <i>Cladosporium fulvum</i> Identifies Sequences That Determine Recognition Specificity in Cf-4 and Cf-9. <i>Plant Cell</i> , 1997, 9, 2209.	6.6	67
49	Novel Disease Resistance Specificities Result from Sequence Exchange between Tandemly Repeated Genes at the Cf-4/9 Locus of Tomato. <i>Cell</i> , 1997, 91, 821-832.	28.9	562
50	The Tomato Cf-2 Disease Resistance Locus Comprises Two Functional Genes Encoding Leucine-Rich Repeat Proteins. <i>Cell</i> , 1996, 84, 451-459.	28.9	591
51	Ensnaring microbes: the components of plant disease resistance. <i>New Phytologist</i> , 1996, 133, 11-34.	7.3	14
52	Identification of amplified restriction fragment polymorphism (AFLP) markers tightly linked to the tomato Cf-9 gene for resistance to <i>Cladosporium fulvum</i> . <i>Plant Journal</i> , 1995, 8, 785-794.	5.7	215
53	Identification of Two Genes Required in Tomato for Full Cf-9: Dependent Resistance to <i>Cladosporium fulvum</i> . <i>Plant Cell</i> , 1994, 6, 361.	6.6	48
54	Chloroplast targeting of spectinomycin adenyltransferase provides a cell-autonomous marker for monitoring transposon excision in tomato and tobacco. <i>Molecular Genetics and Genomics</i> , 1994, 244, 189-196.	2.4	6

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55	Analysis of the chromosomal distribution of transposon-carrying T-DNAs in tomato using the inverse polymerase chain reaction. <i>Molecular Genetics and Genomics</i> , 1994, 242, 573-585.	2.4	82
56	Isolation of the tomato Cf-9 gene for resistance to <i>Cladosporium fulvum</i> by transposon tagging. <i>Science</i> , 1994, 266, 789-793.	12.6	885
57	Use of the maize transposons Activator and Dissociation to show that phosphinothricin and spectinomycin resistance genes act non-cell-autonomously in tobacco and tomato seedlings. <i>Transgenic Research</i> , 1993, 2, 63-78.	2.4	19
58	The pTiC58 tzs gene promotes high-efficiency root induction by agropine strain 1855 of <i>Agrobacterium rhizogenes</i> . <i>Plant Molecular Biology</i> , 1990, 14, 785-792.	3.9	30
59	Characteristics of the nopaline catabolic plasmid in <i>Agrobacterium</i> strains K84 and K1026 used for biological control of crown gall disease. <i>Plasmid</i> , 1990, 23, 126-137.	1.4	48
60	Regeneration of Shoots on Root Explants of Flax. <i>Annals of Botany</i> , 1989, 63, 297-299.	2.9	16
61	Regeneration of flax plants transformed by <i>Agrobacterium rhizogenes</i> . <i>Plant Molecular Biology</i> , 1988, 11, 551-559.	3.9	54
62	Construction of a Tra ⁺ deletion mutant of pAgK84 to safeguard the biological control of crown gall. <i>Molecular Genetics and Genomics</i> , 1988, 212, 207-214.	2.4	77