

Peter N Dodds

List of Publications by Year in descending order

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123
papers

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15466

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#	ARTICLE	IF	CITATIONS
1	EffectorP 3.0: Prediction of Apoplastic and Cytoplasmic Effectors in Fungi and Oomycetes. <i>Molecular Plant-Microbe Interactions</i> , 2022, 35, 146-156.	1.4	179
2	The stem rust effector protein AvrSr50 escapes Sr50 recognition by a substitution in a single surface-exposed residue. <i>New Phytologist</i> , 2022, 234, 592-606.	3.5	32
3	Seeing is believing: Exploiting advances in structural biology to understand and engineer plant immunity. <i>Current Opinion in Plant Biology</i> , 2022, 67, 102210.	3.5	35
4	A chromosome-level, fully phased genome assembly of the oat crown rust fungus <i>Puccinia coronata</i> f. sp. <i>avenae</i> : a resource to enable comparative genomics in the cereal rusts. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	12
5	Direct recognition of pathogen effectors by plant NLR immune receptors and downstream signalling. <i>Essays in Biochemistry</i> , 2022, 66, 471-483.	2.1	21
6	A five-transgene cassette confers broad-spectrum resistance to a fungal rust pathogen in wheat. <i>Nature Biotechnology</i> , 2021, 39, 561-566.	9.4	94
7	A recombined Sr26 and Sr61 disease resistance gene stack in wheat encodes unrelated NLR genes. <i>Nature Communications</i> , 2021, 12, 3378.	5.8	39
8	Genomics accelerated isolation of a new stem rust avirulence gene-wheat resistance gene pair. <i>Nature Plants</i> , 2021, 7, 1220-1228.	4.7	67
9	Host Adaptation and Virulence in Heteroecious Rust Fungi. <i>Annual Review of Phytopathology</i> , 2021, 59, 403-422.	3.5	30
10	The stem rust fungus <i>Puccinia graminis</i> f. sp. <i>tritici</i> induces centromeric small RNAs during late infection that are associated with genome-wide DNA methylation. <i>BMC Biology</i> , 2021, 19, 203.	1.7	15
11	Induced proximity of a TIR signaling domain on a plant-mammalian NLR chimera activates defense in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18832-18839.	3.3	82
12	How Target-Sequence Enrichment and Sequencing (TEnSeq) Pipelines Have Catalyzed Resistance Gene Cloning in the Wheat-Rust Pathosystem. <i>Frontiers in Plant Science</i> , 2020, 11, 678.	1.7	38
13	Evolution of virulence in rust fungi – multiple solutions to one problem. <i>Current Opinion in Plant Biology</i> , 2020, 56, 20-27.	3.5	54
14	Increased virulence of <i>Puccinia coronata</i> f. sp. <i>avenae</i> populations through allele frequency changes at multiple putative Avr loci. <i>PLoS Genetics</i> , 2020, 16, e1009291.	1.5	34
15	The Plant ‘Resistosome’: Structural Insights into Immune Signaling. <i>Cell Host and Microbe</i> , 2019, 26, 193-201.	5.1	76
16	Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. <i>Nature Communications</i> , 2019, 10, 5068.	5.8	121
17	NAD ⁺ cleavage activity by animal and plant TIR domains in cell death pathways. <i>Science</i> , 2019, 365, 793-799.	6.0	357
18	De Novo Genome Assembly and Comparative Genomics of the Barley Leaf Rust Pathogen <i>Puccinia hordei</i> Identifies Candidates for Three Avirulence Genes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3263-3271.	0.8	25

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19	Flax rust infection transcriptomics reveals a transcriptional profile that may be indicative for rust Avr genes. PLoS ONE, 2019, 14, e0226106.	1.1	14
20	Structural and functional insights into the modulation of the activity of a flax cytokinin oxidase by flax rust effector AvrL567. Molecular Plant Pathology, 2019, 20, 211-222.	2.0	15
21	A Near-Complete Haplotype-Phased Genome of the Dikaryotic Wheat Stripe Rust Fungus <i>Puccinia striiformis</i> f. sp. <i>tritici</i> Reveals High Interhaplotype Diversity. MBio, 2018, 9, .	1.8	112
22	Improved prediction of fungal effector proteins from secretomes with EffectorP 2.0. Molecular Plant Pathology, 2018, 19, 2094-2110.	2.0	350
23	<i>De Novo</i> Assembly and Phasing of Dikaryotic Genomes from Two Isolates of <i>Puccinia coronata</i> f. sp. <i>avenae</i> , the Causal Agent of Oat Crown Rust. MBio, 2018, 9, .	1.8	57
24	ApoplastP: prediction of effectors and plant proteins in the apoplast using machine learning. New Phytologist, 2018, 217, 1764-1778.	3.5	180
25	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. Molecular Plant Pathology, 2018, 19, 1196-1209.	2.0	24
26	Plant NLR Origins Traced Back to Green Algae. Trends in Plant Science, 2018, 23, 651-654.	4.3	11
27	Production of small cysteine-rich effector proteins in <i>Escherichia coli</i> for structural and functional studies. Molecular Plant Pathology, 2017, 18, 141-151.	2.0	32
28	Multiple functional self-association interfaces in plant TIR domains. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2046-E2052.	3.3	103
29	What Do We Know About NOD-Like Receptors in Plant Immunity?. Annual Review of Phytopathology, 2017, 55, 205-229.	3.5	106
30	LOCALIZER: subcellular localization prediction of both plant and effector proteins in the plant cell. Scientific Reports, 2017, 7, 44598.	1.6	340
31	Dancing with the Stars: An Asterid NLR Family. Trends in Plant Science, 2017, 22, 1003-1005.	4.3	4
32	Loss of <i>AvrSr50</i> by somatic exchange in stem rust leads to virulence for <i>Sr50</i> resistance in wheat. Science, 2017, 358, 1607-1610.	6.0	206
33	Computational Methods for Predicting Effectors in Rust Pathogens. Methods in Molecular Biology, 2017, 1659, 73-83.	0.4	19
34	An overview of genetic rust resistance: From broad to specific mechanisms. PLoS Pathogens, 2017, 13, e1006380.	2.1	81
35	Genome analysis and avirulence gene cloning using a high-density RADseq linkage map of the flax rust fungus, <i>Melampsora lini</i> . BMC Genomics, 2016, 17, 667.	1.2	59
36	Changing the Game: Using Integrative Genomics to Probe Virulence Mechanisms of the Stem Rust Pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> . Frontiers in Plant Science, 2016, 7, 205.	1.7	45

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37	Starving the enemy. <i>Science</i> , 2016, 354, 1377-1378.	6.0	27
38	Cytosolic activation of cell death and stem rust resistance by cereal MLA-family NLR proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10204-10209.	3.3	97
39	The CC domain structure from the wheat stem rust resistance protein Sr33 challenges paradigms for dimerization in plant NLR proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12856-12861.	3.3	105
40	EffectorP: predicting fungal effector proteins from secretomes using machine learning. <i>New Phytologist</i> , 2016, 210, 743-761.	3.5	438
41	Comparative Analysis of the Flax Immune Receptors L6 and L7 Suggests an Equilibrium-Based Switch Activation Model. <i>Plant Cell</i> , 2016, 28, 146-159.	3.1	110
42	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. <i>Nature Plants</i> , 2015, 1, 15186.	4.7	209
43	Advances and Challenges in Computational Prediction of Effectors from Plant Pathogenic Fungi. <i>PLoS Pathogens</i> , 2015, 11, e1004806.	2.1	197
44	A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. <i>Nature Genetics</i> , 2015, 47, 1494-1498.	9.4	575
45	Epidemiological and Evolutionary Outcomes in Gene-for-Gene and Matching Allele Models. <i>Frontiers in Plant Science</i> , 2015, 6, 1084.	1.7	62
46	Genomic Analysis of <i>Xanthomonas translucens</i> Pathogenic on Wheat and Barley Reveals Cross-Kingdom Gene Transfer Events and Diverse Protein Delivery Systems. <i>PLoS ONE</i> , 2014, 9, e84995.	1.1	39
47	A Bacterial Type III Secretion-Based Delivery System for Functional Assays of Fungal Effectors in Cereals. <i>Methods in Molecular Biology</i> , 2014, 1127, 277-290.	0.4	15
48	The Ins and Outs of Rust Haustoria. <i>PLoS Pathogens</i> , 2014, 10, e1004329.	2.1	90
49	The past, present and future of breeding rust resistant wheat. <i>Frontiers in Plant Science</i> , 2014, 5, 641.	1.7	453
50	Diversifying selection in the wheat stem rust fungus acts predominantly on pathogen-associated gene families and reveals candidate effectors. <i>Frontiers in Plant Science</i> , 2014, 5, 372.	1.7	45
51	A novel conserved mechanism for plant NLR protein pairs: the integrated decoy hypothesis. <i>Frontiers in Plant Science</i> , 2014, 5, 606.	1.7	324
52	The genome sequence and effector complement of the flax rust pathogen <i>Melampsora lini</i> . <i>Frontiers in Plant Science</i> , 2014, 5, 98.	1.7	126
53	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. <i>Science</i> , 2014, 344, 299-303.	6.0	300
54	A Bacterial Type III Secretion Assay for Delivery of Fungal Effector Proteins into Wheat. <i>Molecular Plant-Microbe Interactions</i> , 2014, 27, 255-264.	1.4	111

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55	The <i>NB-LRR</i> proteins <i>RGA4</i> and <i>RGA5</i> interact functionally and physically to confer disease resistance. <i>EMBO Journal</i> , 2014, 33, 1941-1959.	3.5	310
56	Comparative genomics of Australian isolates of the wheat stem rust pathogen <i>Puccinia graminis</i> f. sp. <i>tritici</i> reveals extensive polymorphism in candidate effector genes. <i>Frontiers in Plant Science</i> , 2014, 5, 759.	1.7	98
57	The Gene <i>Sr33</i> , an Ortholog of Barley <i>Mla</i> Genes, Encodes Resistance to Wheat Stem Rust Race Ug99. <i>Science</i> , 2013, 341, 786-788.	6.0	370
58	Crystallization and preliminary X-ray diffraction analyses of the TIR domains of three <i>NB-LRR</i> proteins that are involved in disease resistance in <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1275-1280.	0.7	5
59	Structures of the flax-rust effector <i>AvrM</i> 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.	3.3	75
60	Crystallization and preliminary X-ray diffraction analysis of the flax cytokinin oxidase <i>LuCKX1.1</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1094-1096.	0.7	2
61	Strategies for Wheat Stripe Rust Pathogenicity Identified by Transcriptome Sequencing. <i>PLoS ONE</i> , 2013, 8, e67150.	1.1	110
62	Intramolecular Interaction Influences Binding of the Flax L5 and L6 Resistance Proteins to their <i>AvrL567</i> Ligands. <i>PLoS Pathogens</i> , 2012, 8, e1003004.	2.1	93
63	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.	1.4	62
64	Challenges and progress towards understanding the role of effectors in plant-fungal interactions. <i>Current Opinion in Plant Biology</i> , 2012, 15, 477-482.	3.5	166
65	Rapid genetic change underpins antagonistic coevolution in a natural host-pathogen metapopulation. <i>Ecology Letters</i> , 2012, 15, 425-435.	3.0	189
66	Plant Infection by Biotrophic Fungal and Oomycete Pathogens. <i>Signaling and Communication in Plants</i> , 2012, , 183-212.	0.5	7
67	Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9166-9171.	3.3	640
68	Showdown at the RXLR motif: Serious differences of opinion in how effector proteins from filamentous eukaryotic pathogens enter plant cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14381-14382.	3.3	76
69	Structural and Functional Analysis of a Plant Resistance Protein TIR Domain Reveals Interfaces for Self-Association, Signaling, and Autoregulation. <i>Cell Host and Microbe</i> , 2011, 9, 200-211.	5.1	301
70	An Autoactive Mutant of the M Flax Rust Resistance Protein Has a Preference for Binding ATP, Whereas Wild-Type M Protein Binds ADP. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 897-906.	1.4	141
71	The role of effectors of biotrophic and hemibiotrophic fungi in infection. <i>Cellular Microbiology</i> , 2011, 13, 1849-1857.	1.1	234
72	Variation in potential effector genes distinguishing Australian and non-Australian isolates of the cotton wilt pathogen <i>Fusarium oxysporum</i> f.sp. <i>vasinfectum</i> . <i>Plant Pathology</i> , 2011, 60, 232-243.	1.2	78

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73	Co-evolutionary interactions between host resistance and pathogen effector genes in flax rust disease. <i>Molecular Plant Pathology</i> , 2011, 12, 93-102.	2.0	106
74	Spatial variation in disease resistance: from molecules to metapopulations. <i>Journal of Ecology</i> , 2011, 99, 96-112.	1.9	162
75	New insights in plant immunity signaling activation. <i>Current Opinion in Plant Biology</i> , 2011, 14, 512-518.	3.5	114
76	Crystallization, X-ray diffraction analysis and preliminary structure determination of the TIR domain from the flax resistance protein L6. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 237-240.	0.7	3
77	Crystallization and X-ray diffraction analysis of the C-terminal domain of the flax rust effector protein AvrM. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1603-1607.	0.7	4
78	Constructing Haustorium-Specific cDNA Libraries from Rust Fungi. <i>Methods in Molecular Biology</i> , 2011, 712, 79-87.	0.4	5
79	TECHNICAL ADVANCE: Transformation of the flax rust fungus, <i>Melampsora lini</i> : selection via silencing of an avirulence gene. <i>Plant Journal</i> , 2010, 61, 364-369.	2.8	75
80	Effectors of biotrophic fungal plant pathogens. <i>Functional Plant Biology</i> , 2010, 37, 913.	1.1	17
81	The AvrM Effector from Flax Rust Has a Structured C-Terminal Domain and Interacts Directly with the M Resistance Protein. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 49-57.	1.4	113
82	Relationships between rust resistance genes at the <i>M</i> locus in flax. <i>Molecular Plant Pathology</i> , 2010, 11, 19-32.	2.0	39
83	Plant immunity: towards an integrated view of plant-pathogen interactions. <i>Nature Reviews Genetics</i> , 2010, 11, 539-548.	7.7	2,790
84	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.	3.1	185
85	Genome Evolution in Plant Pathogens. <i>Science</i> , 2010, 330, 1486-1487.	6.0	43
86	The interaction of avirulence and resistance gene products in flax rust disease – providing advances in rust research. <i>Canadian Journal of Plant Pathology</i> , 2010, 32, 11-19.	0.8	4
87	Lipid binding activities of flax rust AvrM and AvrL567 effectors. <i>Plant Signaling and Behavior</i> , 2010, 5, 1272-1275.	1.2	59
88	Diversity and Evolution of Effector Loci in Natural Populations of the Plant Pathogen <i>Melampsora lini</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 2499-2513.	3.5	130
89	Terrific Protein Traffic: The Mystery of Effector Protein Delivery by Filamentous Plant Pathogens. <i>Science</i> , 2009, 324, 748-750.	6.0	156
90	Positive selection in AvrP4 avirulence gene homologues across the genus <i>Melampsora</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 2913-2922.	1.2	33

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91	Recent progress in discovery and functional analysis of effector proteins of fungal and oomycete plant pathogens. <i>Current Opinion in Plant Biology</i> , 2009, 12, 399-405.	3.5	148
92	Effectors of biotrophic fungi and oomycetes: pathogenicity factors and triggers of host resistance. <i>New Phytologist</i> , 2009, 183, 993-1000.	3.5	153
93	In the trenches of plant pathogen recognition: Role of NB-LRR proteins. <i>Seminars in Cell and Developmental Biology</i> , 2009, 20, 1017-1024.	2.3	52
94	Recognition events and host-pathogen co-evolution in gene-for-gene resistance to flax rust. <i>Functional Plant Biology</i> , 2009, 36, 395.	1.1	49
95	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. <i>Plant Cell</i> , 2007, 19, 2898-2912.	3.1	143
96	The role of secreted proteins in diseases of plants caused by rust, powdery mildew and smut fungi. <i>Current Opinion in Microbiology</i> , 2007, 10, 326-331.	2.3	77
97	Flax Rust Resistance Gene Specificity is Based on Direct Resistance-Avirulence Protein Interactions. <i>Annual Review of Phytopathology</i> , 2007, 45, 289-306.	3.5	186
98	Wheat rust resistance research at CSIRO. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 507.	1.5	13
99	Avirulence proteins of rust fungi: penetrating the host - haustorium barrier. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 512.	1.5	4
100	The use of Co ²⁺ -for crystallization and structure determination, using a conventional monochromatic X-ray source, of flax rust avirulence protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 209-213.	0.7	14
101	Purification of the M flax-rust resistance protein expressed in <i>Pichia pastoris</i> . <i>Plant Journal</i> , 2007, 50, 1107-1117.	2.8	10
102	Further analysis of gene-for-gene disease resistance specificity in flax. <i>Molecular Plant Pathology</i> , 2007, 8, 103-109.	2.0	34
103	Rust of flax and linseed caused by <i>Melampsora lini</i> . <i>Molecular Plant Pathology</i> , 2007, 8, 349-364.	2.0	49
104	Avirulence proteins from haustoria-forming pathogens. <i>FEMS Microbiology Letters</i> , 2007, 269, 181-188.	0.7	99
105	The problem of how fungal and oomycete avirulence proteins enter plant cells. <i>Trends in Plant Science</i> , 2006, 11, 61-63.	4.3	116
106	Direct protein interaction underlies gene-for-gene specificity and coevolution of the flax resistance genes and flax rust avirulence genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8888-8893.	3.3	695
107	Autoactive Alleles of the Flax L6 Rust Resistance Gene Induce Non-Race-Specific Rust Resistance Associated with the Hypersensitive Response. <i>Molecular Plant-Microbe Interactions</i> , 2005, 18, 570-582.	1.4	110
108	Haustorially Expressed Secreted Proteins from Flax Rust Are Highly Enriched for Avirulence Elicitors. <i>Plant Cell</i> , 2005, 18, 243-256.	3.1	399

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109	The <i>Melampsora lini</i> AvrL567 Avirulence Genes Are Expressed in Haustoria and Their Products Are Recognized inside Plant Cells. <i>Plant Cell</i> , 2004, 16, 755-768.	3.1	365
110	Plant Pathology: Monitoring a Pathogen-Targeted Host Protein. <i>Current Biology</i> , 2003, 13, R400-R402.	1.8	14
111	New pollen-specific receptor kinases identified in tomato, maize and Arabidopsis: the tomato kinases show overlapping but distinct localization patterns on pollen tubes. <i>Plant Molecular Biology</i> , 2002, 50, 1-16.	2.0	65
112	Contrasting modes of evolution acting on the complex N locus for rust resistance in flax. <i>Plant Journal</i> , 2001, 27, 439-453.	2.8	83
113	Characterisation of a β -tubulin gene from <i>Melampsora lini</i> and comparison of fungal β -tubulin genes. <i>Mycological Research</i> , 2001, 105, 818-826.	2.5	40
114	Six Amino Acid Changes Confined to the Leucine-Rich Repeat β -Strand/ β -Turn Motif Determine the Difference between the P and P2 Rust Resistance Specificities in Flax. <i>Plant Cell</i> , 2001, 13, 163-178.	3.1	216
115	Structure, function and evolution of plant disease resistance genes. <i>Current Opinion in Plant Biology</i> , 2000, 3, 278-284.	3.5	514
116	A genetic map of the <i>Nicotiana glauca</i> S locus that includes three pollen-expressed genes. <i>Theoretical and Applied Genetics</i> , 2000, 100, 956-964.	1.8	28
117	Regions outside of the Leucine-Rich Repeats of Flax Rust Resistance Proteins Play a Role in Specificity Determination. <i>Plant Cell</i> , 2000, 12, 1367-1377.	3.1	180
118	The generation of plant disease resistance gene specificities. <i>Trends in Plant Science</i> , 2000, 5, 373-379.	4.3	149
119	Identification of Regions in Alleles of the Flax Rust Resistance Gene L That Determine Differences in Gene-for-Gene Specificity. <i>Plant Cell</i> , 1999, 11, 495-506.	3.1	463
120	Pollen-expressed S-RNases are not involved in self-incompatibility in <i>Lycopersicon peruvianum</i> . <i>Sexual Plant Reproduction</i> , 1999, 12, 76-87.	2.2	27
121	A Molecular Perspective on Pollination in Flowering Plants. <i>Cell</i> , 1996, 85, 141-144.	13.5	62
122	Molecular characterisation of an S-like RNase of <i>Nicotiana glauca</i> that is induced by phosphate starvation. <i>Plant Molecular Biology</i> , 1996, 31, 227-238.	2.0	82
123	Cloning and Nucleotide Sequence of the S7-RNase from <i>Nicotiana glauca</i> Link and Otto. <i>Plant Physiology</i> , 1995, 108, 427-428.	2.3	7