

# Daniel Croll

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/3387900/daniel-croll-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

130  
papers

4,217  
citations

40  
h-index

62  
g-index

171  
ext. papers

6,080  
ext. citations

6.8  
avg, IF

6.02  
L-index

#	Paper	IF	Citations
130	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. <i>New Phytologist</i> , <b>2012</b> , 193, 755-769	9.8	262
129	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . <i>BMC Biology</i> , <b>2016</b> , 14, 84	7.3	242
128	The accessory genome as a cradle for adaptive evolution in pathogens. <i>PLoS Pathogens</i> , <b>2012</b> , 8, e1002608	6.6	162
127	Genetic variability in a population of arbuscular mycorrhizal fungi causes variation in plant growth. <i>Ecology Letters</i> , <b>2006</b> , 9, 103-10	10	158
126	Nonsel self vegetative fusion and genetic exchange in the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> . <i>New Phytologist</i> , <b>2009</b> , 181, 924-937	9.8	141
125	A small secreted protein in <i>Zymoseptoria tritici</i> is responsible for avirulence on wheat cultivars carrying the <i>Stb6</i> resistance gene. <i>New Phytologist</i> , <b>2017</b> , 214, 619-631	9.8	122
124	Segregation in a mycorrhizal fungus alters rice growth and symbiosis-specific gene transcription. <i>Current Biology</i> , <b>2010</b> , 20, 1216-21	6.3	117
123	What if esca disease of grapevine were not a fungal disease?. <i>Fungal Diversity</i> , <b>2012</b> , 54, 51-67	17.6	114
122	Breakage-fusion-bridge cycles and large insertions contribute to the rapid evolution of accessory chromosomes in a fungal pathogen. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003567	6	109
121	A fungal wheat pathogen evolved host specialization by extensive chromosomal rearrangements. <i>ISME Journal</i> , <b>2017</b> , 11, 1189-1204	11.9	101
120	Genetic diversity and host plant preferences revealed by simple sequence repeat and mitochondrial markers in a population of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> . <i>New Phytologist</i> , <b>2008</b> , 178, 672-87	9.8	101
119	Arbuscular mycorrhiza: the challenge to understand the genetics of the fungal partner. <i>Annual Review of Genetics</i> , <b>2010</b> , 44, 271-92	14.5	90
118	The Evolution of Orphan Regions in Genomes of a Fungal Pathogen of Wheat. <i>MBio</i> , <b>2016</b> , 7,	7.8	85
117	The Impact of Recombination Hotspots on Genome Evolution of a Fungal Plant Pathogen. <i>Genetics</i> , <b>2015</b> , 201, 1213-28	4	84
116	Pangenome analyses of the wheat pathogen <i>Zymoseptoria tritici</i> reveal the structural basis of a highly plastic eukaryotic genome. <i>BMC Biology</i> , <b>2018</b> , 16, 5	7.3	84
115	Recombination in <i>Glomus intraradices</i> , a supposed ancient asexual arbuscular mycorrhizal fungus. <i>BMC Evolutionary Biology</i> , <b>2009</b> , 9, 13	3	78
114	The Genome Biology of Effector Gene Evolution in Filamentous Plant Pathogens. <i>Annual Review of Phytopathology</i> , <b>2018</b> , 56, 21-40	10.8	78

113	Coevolution and life cycle specialization of plant cell wall degrading enzymes in a hemibiotrophic pathogen. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1337-47	8.3	68
112	Highly recombinant VGII <i>Cryptococcus gattii</i> population develops clonal outbreak clusters through both sexual macroevolution and asexual microevolution. <i>MBio</i> , <b>2014</b> , 5, e01494-14	7.8	63
111	Wheat Blast: Past, Present, and Future. <i>Annual Review of Phytopathology</i> , <b>2018</b> , 56, 427-456	10.8	62
110	Introgression from domestic goat generated variation at the major histocompatibility complex of Alpine ibex. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004438	6	62
109	Gene copy number polymorphisms in an arbuscular mycorrhizal fungal population. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 366-9	4.8	62
108	Comparative transcriptomic analyses of <i>Zymoseptoria tritici</i> strains show complex lifestyle transitions and intraspecific variability in transcription profiles. <i>Molecular Plant Pathology</i> , <b>2016</b> , 17, 845-59	5.7	58
107	Significant genetic and phenotypic changes arising from clonal growth of a single spore of an arbuscular mycorrhizal fungus over multiple generations. <i>New Phytologist</i> , <b>2012</b> , 196, 853-861	9.8	57
106	Using Population and Comparative Genomics to Understand the Genetic Basis of Effector-Driven Fungal Pathogen Evolution. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 119	6.2	55
105	Quantitative trait locus mapping of melanization in the plant pathogenic fungus <i>Zymoseptoria tritici</i> . <i>G3: Genes, Genomes, Genetics</i> , <b>2014</b> , 4, 2519-33	3.2	51
104	The birth and death of effectors in rapidly evolving filamentous pathogen genomes. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 46, 34-42	7.9	50
103	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch. <i>New Phytologist</i> , <b>2018</b> , 219, 1048-1061	9.8	50
102	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex. <i>Nature Communications</i> , <b>2020</b> , 11, 1001	17.4	49
101	Evidence for extensive recent intron transposition in closely related fungi. <i>Current Biology</i> , <b>2011</b> , 21, 2017-22	6.3	49
100	Comparative Transcriptome Analyses in <i>Zymoseptoria tritici</i> Reveal Significant Differences in Gene Expression Among Strains During Plant Infection. <i>Molecular Plant-Microbe Interactions</i> , <b>2017</b> , 30, 231-244	2.6	47
99	Quantitative trait locus mapping reveals complex genetic architecture of quantitative virulence in the wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , <b>2018</b> , 19, 201-216	5.7	47
98	Distinct Trajectories of Massive Recent Gene Gains and Losses in Populations of a Microbial Eukaryotic Pathogen. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2808-2822	8.3	47
97	QTL mapping of fungicide sensitivity reveals novel genes and pleiotropy with melanization in the pathogen <i>Zymoseptoria tritici</i> . <i>Fungal Genetics and Biology</i> , <b>2015</b> , 80, 53-67	3.9	45
96	QTL mapping of temperature sensitivity reveals candidate genes for thermal adaptation and growth morphology in the plant pathogenic fungus <i>Zymoseptoria tritici</i> . <i>Heredity</i> , <b>2016</b> , 116, 384-94	3.6	43

95	Analysis of the Protein Kinase A-Regulated Proteome of <i>Cryptococcus neoformans</i> Identifies a Role for the Ubiquitin-Proteasome Pathway in Capsule Formation. <i>MBio</i> , <b>2016</b> , 7, e01862-15	7.8	42
94	The evolving fungal genome. <i>Fungal Biology Reviews</i> , <b>2014</b> , 28, 1-12	6.8	42
93	The genetic basis of local adaptation for pathogenic fungi in agricultural ecosystems. <i>Molecular Ecology</i> , <b>2017</b> , 26, 2027-2040	5.7	42
92	Wheat blast: from its origins in South America to its emergence as a global threat. <i>Molecular Plant Pathology</i> , <b>2019</b> , 20, 155-172	5.7	42
91	Can Evolution Supply What Ecology Demands?. <i>Trends in Ecology and Evolution</i> , <b>2017</b> , 32, 187-197	10.9	41
90	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , <b>2020</b> , 18, 12	7.3	37
89	Genome-wide evidence for divergent selection between populations of a major agricultural pathogen. <i>Molecular Ecology</i> , <b>2018</b> , 27, 2725-2741	5.7	37
88	Population genomics analyses of European ibex species show lower diversity and higher inbreeding in reintroduced populations. <i>Evolutionary Applications</i> , <b>2018</b> , 11, 123-139	4.8	37
87	Multilocus resistance evolution to azole fungicides in fungal plant pathogen populations. <i>Molecular Ecology</i> , <b>2016</b> , 25, 6124-6142	5.7	35
86	Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. <i>BMC Biology</i> , <b>2018</b> , 16, 78	7.3	35
85	Secretome profiling of <i>Cryptococcus neoformans</i> reveals regulation of a subset of virulence-associated proteins and potential biomarkers by protein kinase A. <i>BMC Microbiology</i> , <b>2015</b> , 15, 206	4.5	33
84	Stress-Driven Transposable Element De-repression Dynamics and Virulence Evolution in a Fungal Pathogen. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 221-239	8.3	33
83	Analysis of the nasal vestibule mycobiome in patients with allergic rhinitis. <i>Mycoses</i> , <b>2015</b> , 58, 167-72	5.2	32
82	: more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , <b>2021</b> , 98, 100116	22.2	28
81	A cryptic heterogametic transition revealed by sex-linked DNA markers in Palearctic green toads. <i>Journal of Evolutionary Biology</i> , <b>2011</b> , 24, 1064-70	2.3	27
80	Maize susceptibility to <i>Ustilago maydis</i> is influenced by genetic and chemical perturbation of carbohydrate allocation. <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 1222-1237	5.7	26
79	Rapid Parallel Evolution of Azole Fungicide Resistance in Australian Populations of the Wheat Pathogen. <i>Applied and Environmental Microbiology</i> , <b>2019</b> , 85,	4.8	26
78	The Monothiol Glutaredoxin Grx4 Regulates Iron Homeostasis and Virulence in <i>Cryptococcus neoformans</i> . <i>MBio</i> , <b>2018</b> , 9,	7.8	22

77	An assay for quantitative virulence in <i>Rhynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , <b>2014</b> , 63, 405-414	2.8	20
76	Strong reproductive isolation and narrow genomic tracts of differentiation among three woodpecker species in secondary contact. <i>Molecular Ecology</i> , <b>2016</b> , 25, 4247-66	5.7	20
75	Genomewide signatures of selection in <i>Epichloa</i> reveal candidate genes for host specialization. <i>Molecular Ecology</i> , <b>2018</b> , 27, 3070-3086	5.7	19
74	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 660	5.7	19
73	High-level molecular diversity of copper-zinc superoxide dismutase genes among and within species of arbuscular Mycorrhizal fungi. <i>Applied and Environmental Microbiology</i> , <b>2009</b> , 75, 1970-8	4.8	19
72	Population genetic structure of <i>Mycosphaerella graminicola</i> and Quinone Outside Inhibitor (Qoi) resistance in the Czech Republic. <i>European Journal of Plant Pathology</i> , <b>2013</b> , 135, 211-224	2.1	18
71	Intron gains and losses in the evolution of <i>Fusarium</i> and <i>Cryptococcus</i> fungi. <i>Genome Biology and Evolution</i> , <b>2012</b> , 4, 1148-61	3.9	18
70	The rise and fall of genes: origins and functions of plant pathogen pangenomes. <i>Current Opinion in Plant Biology</i> , <b>2020</b> , 56, 65-73	9.9	17
69	Meiosis Leads to Pervasive Copy-Number Variation and Distorted Inheritance of Accessory Chromosomes of the Wheat Pathogen <i>Zymoseptoria tritici</i> . <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 1416-1429 <sup>17</sup>	3.9	17
68	Multilocus genotyping of arbuscular mycorrhizal fungi and marker suitability for population genetics. <i>New Phytologist</i> , <b>2008</b> , 180, 564-568	9.8	17
67	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i> . <i>BMC Genomics</i> , <b>2020</b> , 21, 588	4.5	17
66	Cautionary Notes on Use of the MoT3 Diagnostic Assay for <i>Magnaporthe oryzae</i> Wheat and Rice Blast Isolates. <i>Phytopathology</i> , <b>2019</b> , 109, 504-508	3.8	16
65	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008652	7.6	15
64	A Chromosome-Scale Genome Assembly for the Strain Fo5176 To Establish a Model -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , <b>2020</b> , 10, 3549-3555	3.2	15
63	Genome-Wide Detection of Genes Under Positive Selection in Worldwide Populations of the Barley Scald Pathogen. <i>Genome Biology and Evolution</i> , <b>2018</b> , 10, 1315-1332	3.9	14
62	Nature's genetic screens: using genome-wide association studies for effector discovery. <i>Molecular Plant Pathology</i> , <b>2018</b> , 19, 3-6	5.7	14
61	Genome evolution in fungal plant pathogens: looking beyond the two-speed genome model. <i>Fungal Biology Reviews</i> , <b>2020</b> , 34, 136-143	6.8	11
60	Complex Evolutionary Origins of Specialized Metabolite Gene Cluster Diversity among the Plant Pathogenic Fungi of the <i>Fusarium graminearum</i> Species Complex. <i>Genome Biology and Evolution</i> , <b>2019</b> , 11, 3106-3122	3.9	11

59	Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. <i>ELife</i> , <b>2021</b> , 10,	8.9	11
58	The emergence of the multi-species NIP1 effector in <i>Rhynchosporium</i> was accompanied by high rates of gene duplications and losses. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 2677-2695	5.2	10
57	What the population genetic structures of host and pathogen tell us about disease evolution. <i>New Phytologist</i> , <b>2016</b> , 212, 537-539	9.8	10
56	Chloroplast-associated metabolic functions influence the susceptibility of maize to <i>Ustilago maydis</i> . <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 1210-1221	5.7	9
55	The era of reference genomes in conservation genomics.. <i>Trends in Ecology and Evolution</i> , <b>2022</b> ,	10.9	8
54	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen		8
53	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , <b>2020</b> , 12, 2231-2244	3.9	8
52	Comparative Genomics Analyses of Lifestyle Transitions at the Origin of an Invasive Fungal Pathogen in the Genus. <i>MSphere</i> , <b>2020</b> , 5,	5	8
51	Transcriptome plasticity underlying plant root colonization and insect invasion by <i>Pseudomonas protegens</i> . <i>ISME Journal</i> , <b>2020</b> , 14, 2766-2782	11.9	8
50	Chromosomal assembly and analyses of genome-wide recombination rates in the forest pathogenic fungus <i>Armillaria ostoyae</i> . <i>Heredity</i> , <b>2020</b> , 124, 699-713	3.6	7
49	Natural selection drives population divergence for local adaptation in a wheat pathogen. <i>Fungal Genetics and Biology</i> , <b>2020</b> , 141, 103398	3.9	7
48	The wheat blast pathogen <i>Pyricularia graminis-tritici</i> has complex origins and a disease cycle spanning multiple grass hosts		7
47	Acetate provokes mitochondrial stress and cell death in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , <b>2018</b> , 107, 488-507	4.1	7
46	Population-level deep sequencing reveals the interplay of clonal and sexual reproduction in the fungal wheat pathogen <i>Zymoseptoria tritici</i>		6
45	The complex genomic basis of rapid convergent adaptation to pesticides across continents in a fungal plant pathogen. <i>Molecular Ecology</i> , <b>2021</b> , 30, 5390-5405	5.7	6
44	Mapping the adaptive landscape of a major agricultural pathogen reveals evolutionary constraints across heterogeneous environments. <i>ISME Journal</i> , <b>2021</b> , 15, 1402-1419	11.9	6
43	The complex genomic basis of rapid convergent adaptation to pesticides across continents in a fungal plant pathogen		5
42	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , <b>2021</b> , 10,	8.9	5

41	The putative phospholipase Lip2 counteracts oxidative damage and influences the virulence of <i>Ustilago maydis</i> . <i>Molecular Plant Pathology</i> , <b>2017</b> , 18, 210-221	5.7	4
40	Hitchhiking selection is driving intron gain in a pathogenic fungus. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1741-9	8.3	4
39	Stress-driven transposable element de-repression dynamics in a fungal pathogen		4
38	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i>		4
37	Rapid sequence evolution driven by transposable elements at a virulence locus in a fungal wheat pathogen. <i>BMC Genomics</i> , <b>2021</b> , 22, 393	4.5	4
36	High-density genetic mapping identifies the genetic basis of a natural colony morphology mutant in the root rot pathogen <i>Armillaria ostoyae</i> . <i>Fungal Genetics and Biology</i> , <b>2017</b> , 108, 44-54	3.9	3
35	Population-level deep sequencing reveals the interplay of clonal and sexual reproduction in the fungal wheat pathogen. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	3
34	Emergence and diversification of a highly invasive chestnut pathogen lineage across south-eastern Europe		3
33	A chromosome-scale genome assembly for the <i>Fusarium oxysporum</i> strain Fo5176 to establish a model Arabidopsis-fungal pathosystem		3
32	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex		3
31	Natural selection drives population divergence for local adaptation in a wheat pathogen		3
30	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i>		3
29	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , <b>2021</b> , 12, 3551	17.4	3
28	Maintenance of variation in virulence and reproduction in populations of an agricultural plant pathogen. <i>Evolutionary Applications</i> , <b>2021</b> , 14, 335-347	4.8	3
27	Histone H3K27 methylation perturbs transcriptional robustness and underpins dispensability of highly conserved genes in fungi. <i>Molecular Biology and Evolution</i> , <b>2021</b> ,	8.3	2
26	Screening of grapevine red blotch virus in two European ampelographic collections. <i>Journal of Plant Pathology</i> , <b>2022</b> , 104, 9	1	2
25	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i>		2
24	The genetic architecture of emerging fungicide resistance in populations of a global wheat pathogen		2

23	Maintenance of variation in virulence and reproduction in populations of an agricultural plant pathogen		2
22	Evolution in the absence of sex: Ideas revisited in the post-genomics age (retrospective on DOI 10.1002/bies.201300155). <i>BioEssays</i> , <b>2016</b> , 38, 1191	4.1	1
21	Learn from the fungi: adaptive evolution without sex in fungal pathogens (comment on DOI 10.1002/bies.201300155). <i>BioEssays</i> , <b>2014</b> , 36, 334	4.1	1
20	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat.. <i>PLoS Pathogens</i> , <b>2022</b> , 18, e1010149	7.6	1
19	Meiosis leads to pervasive segregation distortion and copy-number variation in accessory chromosomes of the wheat pathogen <i>Zymoseptoria tritici</i>		1
18	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch		1
17	The MoT3 assay does not distinguish between <i>Magnaporthe oryzae</i> wheat and rice blast isolates from Bangladesh		1
16	Complex evolutionary origins of specialized metabolite gene cluster diversity among the plant pathogenic fungi of the <i>Fusarium graminearum</i> species complex		1
15	A transcriptome for the early-branching fern <i>Botrychium lunaria</i> enables fine-grained resolution of population structure		1
14	Genome-wide association study for septoria tritici blotch resistance reveals the occurrence and distribution of <i>Stb6</i> in a historic Swiss landrace collection. <i>Euphytica</i> , <b>2021</b> , 217, 1	2.1	1
13	Histone H3K27 methylation perturbs transcriptional robustness and underpins dispensability of highly conserved genes in fungi		1
12	Tackling microbial threats in agriculture with integrative imaging and computational approaches. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 372-383	6.8	1
11	Population genomics of transposable element activation in the highly repressive genome of an agricultural pathogen. <i>Microbial Genomics</i> , <b>2021</b> , 7,	4.4	1
10	Soil composition and plant genotype determine benzoxazinoid-mediated plant-soil feedbacks in cereals. <i>Plant, Cell and Environment</i> , <b>2021</b> , 44, 3502-3514	8.4	1
9	Transposable Elements in Fungi: Coevolution With the Host Genome Shapes, Genome Architecture, Plasticity and Adaptation <b>2021</b> , 142-155		0
8	Cryptic genetic structure and copy-number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , <b>2021</b> , 23, 6536-6556	5.2	0
7	High-quality genome assembly of <i>Pseudocercospora ulei</i> the main threat to natural rubber trees.. <i>Genetics and Molecular Biology</i> , <b>2022</b> , 45, e50510051	2	
6	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization <b>2020</b> , 16, e1008652		



- 5 A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization **2020**, 16, e1008652
- 4 A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization **2020**, 16, e1008652
- 3 A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization **2020**, 16, e1008652
- 2 A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization **2020**, 16, e1008652
- 1 A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization **2020**, 16, e1008652