

# Daniel Croll

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3387900/publications.pdf>

Version: 2024-02-01

119  
papers

7,211  
citations

46984

47  
h-index

79644

73  
g-index

171  
all docs

171  
docs citations

171  
times ranked

5864  
citing authors

#	ARTICLE	IF	CITATIONS
1	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i> . <i>BMC Biology</i> , 2016, 14, 84.	1.7	355
2	The transcriptome of the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> (DAOM 197198) reveals functional tradeoffs in an obligate symbiont. <i>New Phytologist</i> , 2012, 193, 755-769.	3.5	305
3	The Accessory Genome as a Cradle for Adaptive Evolution in Pathogens. <i>PLoS Pathogens</i> , 2012, 8, e1002608.	2.1	227
4	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> , 2017, 214, 619-631.	3.5	218
5	The Genome Biology of Effector Gene Evolution in Filamentous Plant Pathogens. <i>Annual Review of Phytopathology</i> , 2018, 56, 21-40.	3.5	195
6	Genetic variability in a population of arbuscular mycorrhizal fungi causes variation in plant growth. <i>Ecology Letters</i> , 2006, 9, 103-110.	3.0	185
7	What if esca disease of grapevine were not a fungal disease?. <i>Fungal Diversity</i> , 2012, 54, 51-67.	4.7	185
8	Breakage-fusion-bridge Cycles and Large Insertions Contribute to the Rapid Evolution of Accessory Chromosomes in a Fungal Pathogen. <i>PLoS Genetics</i> , 2013, 9, e1003567.	1.5	166
9	A fungal wheat pathogen evolved host specialization by extensive chromosomal rearrangements. <i>ISME Journal</i> , 2017, 11, 1189-1204.	4.4	166
10	Nonsel self vegetative fusion and genetic exchange in the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> . <i>New Phytologist</i> , 2009, 181, 924-937.	3.5	165
11	Pangenome analyses of the wheat pathogen <i>Zymoseptoria tritici</i> reveal the structural basis of a highly plastic eukaryotic genome. <i>BMC Biology</i> , 2018, 16, 5.	1.7	153
12	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex. <i>Nature Communications</i> , 2020, 11, 1001.	5.8	147
13	Segregation in a Mycorrhizal Fungus Alters Rice Growth and Symbiosis-Specific Gene Transcription. <i>Current Biology</i> , 2010, 20, 1216-1221.	1.8	140
14	The era of reference genomes in conservation genomics. <i>Trends in Ecology and Evolution</i> , 2022, 37, 197-202.	4.2	138
15	Using Population and Comparative Genomics to Understand the Genetic Basis of Effector-Driven Fungal Pathogen Evolution. <i>Frontiers in Plant Science</i> , 2017, 8, 119.	1.7	135
16	<i>Fusarium</i> : more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021, 98, 100116.	4.5	134
17	The Evolution of Orphan Regions in Genomes of a Fungal Pathogen of Wheat. <i>MBio</i> , 2016, 7, .	1.8	132
18	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> , 2017, 30, 231-244.	1.4	129

#	ARTICLE	IF	CITATIONS
19	The Impact of Recombination Hotspots on Genome Evolution of a Fungal Plant Pathogen. <i>Genetics</i> , 2015, 201, 1213-1228.	1.2	123
20	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> , 2008, 178, 672-687.	3.5	120
21	Wheat Blast: Past, Present, and Future. <i>Annual Review of Phytopathology</i> , 2018, 56, 427-456.	3.5	112
22	The birth and death of effectors in rapidly evolving filamentous pathogen genomes. <i>Current Opinion in Microbiology</i> , 2018, 46, 34-42.	2.3	106
23	Arbuscular Mycorrhiza: The Challenge to Understand the Genetics of the Fungal Partner. <i>Annual Review of Genetics</i> , 2010, 44, 271-292.	3.2	104
24	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch. <i>New Phytologist</i> , 2018, 219, 1048-1061.	3.5	103
25	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , 2020, 18, 12.	1.7	95
26	Wheat blast: from its origins in South America to its emergence as a global threat. <i>Molecular Plant Pathology</i> , 2019, 20, 155-172.	2.0	88
27	Introgression from Domestic Goat Generated Variation at the Major Histocompatibility Complex of Alpine Ibex. <i>PLoS Genetics</i> , 2014, 10, e1004438.	1.5	87
28	Distinct Trajectories of Massive Recent Gene Gains and Losses in Populations of a Microbial Eukaryotic Pathogen. <i>Molecular Biology and Evolution</i> , 2017, 34, 2808-2822.	3.5	87
29	Recombination in <i>Glomus intraradices</i> , a supposed ancient asexual arbuscular mycorrhizal fungus. <i>BMC Evolutionary Biology</i> , 2009, 9, 13.	3.2	86
30	Quantitative Trait Locus Mapping of Melanization in the Plant Pathogenic Fungus <i>Zymoseptoria tritici</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2519-2533.	0.8	86
31	Stress-Driven Transposable Element De-repression Dynamics and Virulence Evolution in a Fungal Pathogen. <i>Molecular Biology and Evolution</i> , 2020, 37, 221-239.	3.5	83
32	Comparative transcriptomic analyses of <i>Zymoseptoria tritici</i> strains show complex lifestyle transitions and intraspecific variability in transcription profiles. <i>Molecular Plant Pathology</i> , 2016, 17, 845-859.	2.0	82
33	Highly Recombinant <i>VGI Cryptococcus gattii</i> Population Develops Clonal Outbreak Clusters through both Sexual Macroevolution and Asexual Microevolution. <i>MBio</i> , 2014, 5, e01494-14.	1.8	81
34	The evolving fungal genome. <i>Fungal Biology Reviews</i> , 2014, 28, 1-12.	1.9	81
35	Coevolution and Life Cycle Specialization of Plant Cell Wall Degrading Enzymes in a Hemibiotrophic Pathogen. <i>Molecular Biology and Evolution</i> , 2013, 30, 1337-1347.	3.5	77
36	Quantitative trait locus mapping reveals complex genetic architecture of quantitative virulence in the wheat pathogen <i>Zymoseptoria tritici</i> . <i>Molecular Plant Pathology</i> , 2018, 19, 201-216.	2.0	76

#	ARTICLE	IF	CITATIONS
37	Genome-wide evidence for divergent selection between populations of a major agricultural pathogen. <i>Molecular Ecology</i> , 2018, 27, 2725-2741.	2.0	74
38	The genetic basis of local adaptation for pathogenic fungi in agricultural ecosystems. <i>Molecular Ecology</i> , 2017, 26, 2027-2040.	2.0	73
39	Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. <i>BMC Biology</i> , 2018, 16, 78.	1.7	70
40	Gene Copy Number Polymorphisms in an Arbuscular Mycorrhizal Fungal Population. <i>Applied and Environmental Microbiology</i> , 2007, 73, 366-369.	1.4	69
41	Can Evolution Supply What Ecology Demands?. <i>Trends in Ecology and Evolution</i> , 2017, 32, 187-197.	4.2	69
42	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> , 2016, 116, 384-394.	1.2	68
43	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> , 2012, 196, 853-861.	3.5	66
44	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> , 2015, 80, 53-67.	0.9	65
45	Genome evolution in fungal plant pathogens: looking beyond the two-speed genome model. <i>Fungal Biology Reviews</i> , 2020, 34, 136-143.	1.9	63
46	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> , 2016, 7, e01862-15.	1.8	62
47	Population genomics analyses of European ibex species show lower diversity and higher inbreeding in reintroduced populations. <i>Evolutionary Applications</i> , 2018, 11, 123-139.	1.5	62
48	Multilocus resistance evolution to azole fungicides in fungal plant pathogen populations. <i>Molecular Ecology</i> , 2016, 25, 6124-6142.	2.0	60
49	Evidence for Extensive Recent Intron Transposition in Closely Related Fungi. <i>Current Biology</i> , 2011, 21, 2017-2022.	1.8	57
50	The rise and fall of genes: origins and functions of plant pathogen pangenomes. <i>Current Opinion in Plant Biology</i> , 2020, 56, 65-73.	3.5	50
51	Rapid Parallel Evolution of Azole Fungicide Resistance in Australian Populations of the Wheat Pathogen <i>Zymoseptoria tritici</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	49
52	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021, 10, .	2.8	49
53	The Monothiol Glutaredoxin Grx4 Regulates Iron Homeostasis and Virulence in <i>Cryptococcus neoformans</i> . <i>MBio</i> , 2018, 9, .	1.8	48
54	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> , 2015, 15, 206.	1.3	47

#	ARTICLE	IF	CITATIONS
55	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. <i>PLoS Pathogens</i> , 2020, 16, e1008652.	2.1	44
56	Analysis of the nasal vestibule mycobiome in patients with allergic rhinitis. <i>Mycoses</i> , 2015, 58, 167-172.	1.8	43
57	Transcriptome plasticity underlying plant root colonization and insect invasion by <i>Pseudomonas protegens</i> . <i>ISME Journal</i> , 2020, 14, 2766-2782.	4.4	38
58	Maize susceptibility to <i>Ustilago maydis</i> is influenced by genetic and chemical perturbation of carbohydrate allocation. <i>Molecular Plant Pathology</i> , 2017, 18, 1222-1237.	2.0	35
59	Nature's genetic screens: using genome-wide association studies for effector discovery. <i>Molecular Plant Pathology</i> , 2018, 19, 3-6.	2.0	34
60	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i> . <i>BMC Genomics</i> , 2020, 21, 588.	1.2	34
61	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018, 9, 660.	1.5	33
62	An assay for quantitative virulence in <i>hynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , 2014, 63, 405-414.	1.2	30
63	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020, 12, 2231-2244.	1.1	29
64	Strong reproductive isolation and narrow genomic tracts of differentiation among three woodpecker species in secondary contact. <i>Molecular Ecology</i> , 2016, 25, 4247-4266.	2.0	28
65	Genomewide signatures of selection in <i>Epichloa</i> reveal candidate genes for host specialization. <i>Molecular Ecology</i> , 2018, 27, 3070-3086.	2.0	28
66	Genome-Wide Detection of Genes Under Positive Selection in Worldwide Populations of the Barley Scald Pathogen. <i>Genome Biology and Evolution</i> , 2018, 10, 1315-1332.	1.1	28
67	A Chromosome-Scale Genome Assembly for the <i>Fusarium oxysporum</i> Strain Fo5176 To Establish a Model <i>Arabidopsis</i> -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3549-3555.	0.8	28
68	A cryptic heterogametic transition revealed by sex-linked DNA markers in Palearctic green toads. <i>Journal of Evolutionary Biology</i> , 2011, 24, 1064-1070.	0.8	27
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> , 2018, 10, 1416-1429.	1.1	26
70	High-Level Molecular Diversity of Copper-Zinc Superoxide Dismutase Genes among and within Species of Arbuscular Mycorrhizal Fungi. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1970-1978.	1.4	25
71	A devil's bargain with transposable elements in plant pathogens. <i>Trends in Genetics</i> , 2022, 38, 222-230.	2.9	25
72	Mapping the adaptive landscape of a major agricultural pathogen reveals evolutionary constraints across heterogeneous environments. <i>ISME Journal</i> , 2021, 15, 1402-1419.	4.4	25

#	ARTICLE	IF	CITATIONS
73	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> , 2019, 11, 3106-3122.	1.1	24
74	Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. <i>ELife</i> , 2021, 10, .	2.8	24
75	Cautionary Notes on Use of the MoT3 Diagnostic Assay for <i>Magnaporthe oryzae</i> Wheat and Rice Blast Isolates. <i>Phytopathology</i> , 2019, 109, 504-508.	1.1	23
76	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> , 2013, 135, 211-224.	0.8	22
77	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , 2021, 12, 3551.	5.8	21
78	Population-level deep sequencing reveals the interplay of clonal and sexual reproduction in the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	21
79	Multilocus genotyping of arbuscular mycorrhizal fungi and marker suitability for population genetics. <i>New Phytologist</i> , 2008, 180, 564-568.	3.5	19
80	Intron Gains and Losses in the Evolution of <i>Fusarium</i> and <i>Cryptococcus</i> Fungi. <i>Genome Biology and Evolution</i> , 2012, 4, 1148-1161.	1.1	19
81	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> , 2019, 21, 2677-2695.	1.8	19
82	Maintenance of variation in virulence and reproduction in populations of an agricultural plant pathogen. <i>Evolutionary Applications</i> , 2021, 14, 335-347.	1.5	18
83	Rapid sequence evolution driven by transposable elements at a virulence locus in a fungal wheat pathogen. <i>BMC Genomics</i> , 2021, 22, 393.	1.2	18
84	The complex genomic basis of rapid convergent adaptation to pesticides across continents in a fungal plant pathogen. <i>Molecular Ecology</i> , 2021, 30, 5390-5405.	2.0	17
85	Comparative Genomics Analyses of Lifestyle Transitions at the Origin of an Invasive Fungal Pathogen in the Genus <i>Cryphonectria</i> . <i>MSphere</i> , 2020, 5, .	1.3	17
86	Chromosomal assembly and analyses of genome-wide recombination rates in the forest pathogenic fungus <i>Armillaria ostoyae</i> . <i>Heredity</i> , 2020, 124, 699-713.	1.2	17
87	Natural selection drives population divergence for local adaptation in a wheat pathogen. <i>Fungal Genetics and Biology</i> , 2020, 141, 103398.	0.9	16
88	What the population genetic structures of host and pathogen tell us about disease evolution. <i>New Phytologist</i> , 2016, 212, 537-539.	3.5	15
89	Acetate provokes mitochondrial stress and cell death in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2018, 107, 488-507.	1.2	15
90	Chloroplast-associated metabolic functions influence the susceptibility of maize to <i>Ustilago maydis</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 1210-1221.	2.0	14

#	ARTICLE	IF	CITATIONS
91	The population genetics of adaptation through copy number variation in a fungal plant pathogen. <i>Molecular Ecology</i> , 2023, 32, 2443-2460.	2.0	14
92	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. <i>PLoS Pathogens</i> , 2022, 18, e1010149.	2.1	9
93	Population genomics of transposable element activation in the highly repressive genome of an agricultural pathogen. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
94	Soil composition and plant genotype determine benzoxazinoidâ€‘mediated plantâ€‘soil feedbacks in cereals. <i>Plant, Cell and Environment</i> , 2021, 44, 3732-3744.	2.8	8
95	Screening of grapevine red blotch virus in two European ampelographic collections. <i>Journal of Plant Pathology</i> , 2022, 104, 9-15.	0.6	8
96	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> , 2017, 108, 44-54.	0.9	7
97	A robust sequencing assay of a thousand amplicons for the highâ€‘throughput population monitoring of Alpine ibex immunogenetics. <i>Molecular Ecology Resources</i> , 2022, 22, 66-85.	2.2	7
98	Temporal changes in pathogen diversity in a perennial plantâ€‘pathogenâ€‘hyperparasite system. <i>Molecular Ecology</i> , 2022, 31, 2073-2088.	2.0	7
99	Genome of <i>Malassezia arunalokei</i> and Its Distribution on Facial Skin. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	7
100	The putative phospholipase Lip2 counteracts oxidative damage and influences the virulence of <i>Ustilago maydis</i> . <i>Molecular Plant Pathology</i> , 2017, 18, 210-221.	2.0	6
101	Hitchhiking Selection Is Driving Intron Gain in a Pathogenic Fungus. <i>Molecular Biology and Evolution</i> , 2014, 31, 1741-1749.	3.5	5
102	Transposable Elements in Fungi: Coevolution With the Host Genome Shapes, Genome Architecture, Plasticity and Adaptation. , 2021, , 142-155.		5
103	A new method to determine the diet of pygmy hippopotamus in Taï National Park, CÃ´te d'Ivoire. <i>African Journal of Ecology</i> , 2021, 59, 809-825.	0.4	5
104	Cryptic genetic structure and copyâ€‘number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , 2021, 23, 6536-6556.	1.8	5
105	Organic acids and glucose prime late-stage fungal biotrophy in maize. <i>Science</i> , 2022, 376, 1187-1191.	6.0	5
106	Histone H3K27 Methylation Perturbs Transcriptional Robustness and Underpins Dispensability of Highly Conserved Genes in Fungi. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
107	Unraveling coevolutionary dynamics using ecological genomics. <i>Trends in Genetics</i> , 2022, 38, 1003-1012.	2.9	4
108	Genome-wide association study for septoria tritici blotch resistance reveals the occurrence and distribution of Stb6 in a historic Swiss landrace collection. <i>Euphytica</i> , 2021, 217, 1.	0.6	3

#	ARTICLE	IF	CITATIONS
109	Transcriptome-wide SNPs for <i>Botrychium lunaria</i> ferns enable fine-grained analysis of ploidy and population structure. <i>Molecular Ecology Resources</i> , 2022, 22, 254-271.	2.2	3
110	Learn from the fungi: Adaptive evolution without sex in fungal pathogens (comment on DOI) Tj ETQq0 0 0 rgBT /Overlock 10,Tf 50 702	1.2	1
111	Evolution in the absence of sex: Ideas revisited in the post-genomics age (retrospective on DOI) Tj ETQq1 1 0.784314 rgBT /Overlock	1.2	1
112	Tackling microbial threats in agriculture with integrative imaging and computational approaches. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 372-383.	1.9	1
113	High-quality genome assembly of <i>Pseudocercospora ulei</i> the main threat to natural rubber trees. <i>Genetics and Molecular Biology</i> , 2022, 45, e50510051.	0.6	1
114	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
115	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
116	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
117	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
118	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0
119	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. , 2020, 16, e1008652.		0