

Daniel Croll

List of Publications by Year in Descending Order

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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	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	2	
129	The era of reference genomes in conservation genomics.. <i>Trends in Ecology and Evolution</i> , 2022 ,	10.9	8
128	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	7.6	1
127	Screening of grapevine red blotch virus in two European ampelographic collections. <i>Journal of Plant Pathology</i> , 2022 , 104, 9	1	2
126	Histone H3K27 methylation perturbs transcriptional robustness and underpins dispensability of highly conserved genes in fungi. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	2
125	Population-level deep sequencing reveals the interplay of clonal and sexual reproduction in the fungal wheat pathogen. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
124	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	5.7	6
123	: more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021 , 98, 100116	22.2	28
122	Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. <i>ELife</i> , 2021 , 10,	8.9	11
121	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> , 2021 , 217, 1	2.1	1
120	Rapid sequence evolution driven by transposable elements at a virulence locus in a fungal wheat pathogen. <i>BMC Genomics</i> , 2021 , 22, 393	4.5	4
119	Machine-learning predicts genomic determinants of meiosis-driven structural variation in a eukaryotic pathogen. <i>Nature Communications</i> , 2021 , 12, 3551	17.4	3
118	Maintenance of variation in virulence and reproduction in populations of an agricultural plant pathogen. <i>Evolutionary Applications</i> , 2021 , 14, 335-347	4.8	3
117	Tackling microbial threats in agriculture with integrative imaging and computational approaches. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 372-383	6.8	1
116	Transposable Elements in Fungi: Coevolution With the Host Genome Shapes, Genome Architecture, Plasticity and Adaptation 2021 , 142-155		0
115	Population genomics of transposable element activation in the highly repressive genome of an agricultural pathogen. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
114	Soil composition and plant genotype determine benzoxazinoid-mediated plant-soil feedbacks in cereals. <i>Plant, Cell and Environment</i> , 2021 , 44, 3502-3514	8.4	1

113	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen. <i>ELife</i> , 2021 , 10,	8.9	5
112	Cryptic genetic structure and copy-number variation in the ubiquitous forest symbiotic fungus <i>Cenococcum geophilum</i> . <i>Environmental Microbiology</i> , 2021 , 23, 6536-6556	5.2	0
111	Mapping the adaptive landscape of a major agricultural pathogen reveals evolutionary constraints across heterogeneous environments. <i>ISME Journal</i> , 2021 , 15, 1402-1419	11.9	6
110	Genome evolution in fungal plant pathogens: looking beyond the two-speed genome model. <i>Fungal Biology Reviews</i> , 2020 , 34, 136-143	6.8	11
109	The rise and fall of genes: origins and functions of plant pathogen pangenomes. <i>Current Opinion in Plant Biology</i> , 2020 , 56, 65-73	9.9	17
108	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization. <i>PLoS Pathogens</i> , 2020 , 16, e1008652	7.6	15
107	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	3.6	7
106	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex. <i>Nature Communications</i> , 2020 , 11, 1001	17.4	49
105	A 19-isolate reference-quality global pangenome for the fungal wheat pathogen <i>Zymoseptoria tritici</i> . <i>BMC Biology</i> , 2020 , 18, 12	7.3	37
104	Natural selection drives population divergence for local adaptation in a wheat pathogen. <i>Fungal Genetics and Biology</i> , 2020 , 141, 103398	3.9	7
103	The Genetic Architecture of Emerging Fungicide Resistance in Populations of a Global Wheat Pathogen. <i>Genome Biology and Evolution</i> , 2020 , 12, 2231-2244	3.9	8
102	Comparative Genomics Analyses of Lifestyle Transitions at the Origin of an Invasive Fungal Pathogen in the Genus. <i>MSphere</i> , 2020 , 5,	5	8
101	Transcriptome plasticity underlying plant root colonization and insect invasion by <i>Pseudomonas protegens</i> . <i>ISME Journal</i> , 2020 , 14, 2766-2782	11.9	8
100	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i> . <i>BMC Genomics</i> , 2020 , 21, 588	4.5	17
99	A Chromosome-Scale Genome Assembly for the Strain Fo5176 To Establish a Model -Fungal Pathosystem. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3549-3555	3.2	15
98	Stress-Driven Transposable Element De-repression Dynamics and Virulence Evolution in a Fungal Pathogen. <i>Molecular Biology and Evolution</i> , 2020 , 37, 221-239	8.3	33
97	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization 2020 , 16, e1008652		
96	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization 2020 , 16, e1008652		

95	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization 2020 , 16, e1008652		
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93	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization 2020 , 16, e1008652		
92	A secreted LysM effector protects fungal hyphae through chitin-dependent homodimer polymerization 2020 , 16, e1008652		
91	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	5.2	10
90	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	3.9	11
89	Wheat blast: from its origins in South America to its emergence as a global threat. <i>Molecular Plant Pathology</i> , 2019 , 20, 155-172	5.7	42
88	Rapid Parallel Evolution of Azole Fungicide Resistance in Australian Populations of the Wheat Pathogen. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	26
87	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	3.8	16
86	The birth and death of effectors in rapidly evolving filamentous pathogen genomes. <i>Current Opinion in Microbiology</i> , 2018 , 46, 34-42	7.9	50
85	Genomewide signatures of selection in <i>Epichloa</i> reveal candidate genes for host specialization. <i>Molecular Ecology</i> , 2018 , 27, 3070-3086	5.7	19
84	Genome-wide evidence for divergent selection between populations of a major agricultural pathogen. <i>Molecular Ecology</i> , 2018 , 27, 2725-2741	5.7	37
83	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	9.8	50
82	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	5.7	47
81	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018 , 9, 660	5.7	19
80	Wheat Blast: Past, Present, and Future. <i>Annual Review of Phytopathology</i> , 2018 , 56, 427-456	10.8	62
79	Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. <i>BMC Biology</i> , 2018 , 16, 78	7.3	35
78	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	7.3	84

77	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	3.9	14
76	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 ¹⁷	3.9	17
75	Nature's genetic screens: using genome-wide association studies for effector discovery. <i>Molecular Plant Pathology</i> , 2018 , 19, 3-6	5.7	14
74	Acetate provokes mitochondrial stress and cell death in <i>Ustilago maydis</i> . <i>Molecular Microbiology</i> , 2018 , 107, 488-507	4.1	7
73	Population genomics analyses of European ibex species show lower diversity and higher inbreeding in reintroduced populations. <i>Evolutionary Applications</i> , 2018 , 11, 123-139	4.8	37
72	The Monothiol Glutaredoxin Grx4 Regulates Iron Homeostasis and Virulence in <i>Cryptococcus neoformans</i> . <i>MBio</i> , 2018 , 9,	7.8	22
71	The Genome Biology of Effector Gene Evolution in Filamentous Plant Pathogens. <i>Annual Review of Phytopathology</i> , 2018 , 56, 21-40	10.8	78
70	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	5.7	4
69	Can Evolution Supply What Ecology Demands?. <i>Trends in Ecology and Evolution</i> , 2017 , 32, 187-197	10.9	41
68	A fungal wheat pathogen evolved host specialization by extensive chromosomal rearrangements. <i>ISME Journal</i> , 2017 , 11, 1189-1204	11.9	101
67	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 ^{2.6}	2.6	47
66	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	9.8	122
65	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	3.9	3
64	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	8.3	47
63	Chloroplast-associated metabolic functions influence the susceptibility of maize to <i>Ustilago maydis</i> . <i>Molecular Plant Pathology</i> , 2017 , 18, 1210-1221	5.7	9
62	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	5.7	26
61	The genetic basis of local adaptation for pathogenic fungi in agricultural ecosystems. <i>Molecular Ecology</i> , 2017 , 26, 2027-2040	5.7	42
60	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	6.2	55

59	Evolution in the absence of sex: Ideas revisited in the post-genomics age (retrospective on DOI 10.1002/bies.201300155). <i>BioEssays</i> , 2016 , 38, 1191	4.1	1
58	Multilocus resistance evolution to azole fungicides in fungal plant pathogen populations. <i>Molecular Ecology</i> , 2016 , 25, 6124-6142	5.7	35
57	The Evolution of Orphan Regions in Genomes of a Fungal Pathogen of Wheat. <i>MBio</i> , 2016 , 7,	7.8	85
56	What the population genetic structures of host and pathogen tell us about disease evolution. <i>New Phytologist</i> , 2016 , 212, 537-539	9.8	10
55	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	7.8	42
54	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, 384-94	3.6	43
53	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, 845-59	5.7	58
52	Strong reproductive isolation and narrow genomic tracts of differentiation among three woodpecker species in secondary contact. <i>Molecular Ecology</i> , 2016 , 25, 4247-66	5.7	20
51	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	7.3	242
50	The Impact of Recombination Hotspots on Genome Evolution of a Fungal Plant Pathogen. <i>Genetics</i> , 2015 , 201, 1213-28	4	84
49	Analysis of the nasal vestibule mycobiome in patients with allergic rhinitis. <i>Mycoses</i> , 2015 , 58, 167-72	5.2	32
48	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	4.5	33
47	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	3.9	45
46	The evolving fungal genome. <i>Fungal Biology Reviews</i> , 2014 , 28, 1-12	6.8	42
45	Learn from the fungi: adaptive evolution without sex in fungal pathogens (comment on DOI 10.1002/bies.201300155). <i>BioEssays</i> , 2014 , 36, 334	4.1	1
44	Hitchhiking selection is driving intron gain in a pathogenic fungus. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1741-9	8.3	4
43	Quantitative trait locus mapping of melanization in the plant pathogenic fungus <i>Zymoseptoria tritici</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 2519-33	3.2	51
42	Introgression from domestic goat generated variation at the major histocompatibility complex of Alpine ibex. <i>PLoS Genetics</i> , 2014 , 10, e1004438	6	62

41	Highly recombinant VGII <i>Cryptococcus gattii</i> population develops clonal outbreak clusters through both sexual macroevolution and asexual microevolution. <i>MBio</i> , 2014 , 5, e01494-14	7.8	63
40	An assay for quantitative virulence in <i>Rhynchosporium commune</i> reveals an association between effector genotype and virulence. <i>Plant Pathology</i> , 2014 , 63, 405-414	2.8	20
39	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	2.1	18
38	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	6	109
37	Coevolution and life cycle specialization of plant cell wall degrading enzymes in a hemibiotrophic pathogen. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1337-47	8.3	68
36	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	9.8	57
35	What if esca disease of grapevine were not a fungal disease?. <i>Fungal Diversity</i> , 2012 , 54, 51-67	17.6	114
34	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	9.8	262
33	The accessory genome as a cradle for adaptive evolution in pathogens. <i>PLoS Pathogens</i> , 2012 , 8, e1002608	10.8	162
32	Intron gains and losses in the evolution of <i>Fusarium</i> and <i>Cryptococcus</i> fungi. <i>Genome Biology and Evolution</i> , 2012 , 4, 1148-61	3.9	18
31	A cryptic heterogametic transition revealed by sex-linked DNA markers in Palearctic green toads. <i>Journal of Evolutionary Biology</i> , 2011 , 24, 1064-70	2.3	27
30	Evidence for extensive recent intron transposition in closely related fungi. <i>Current Biology</i> , 2011 , 21, 2017-22	6.3	49
29	Arbuscular mycorrhiza: the challenge to understand the genetics of the fungal partner. <i>Annual Review of Genetics</i> , 2010 , 44, 271-92	14.5	90
28	Segregation in a mycorrhizal fungus alters rice growth and symbiosis-specific gene transcription. <i>Current Biology</i> , 2010 , 20, 1216-21	6.3	117
27	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, 1970-8	4.8	19
26	Recombination in <i>Glomus intraradices</i> , a supposed ancient asexual arbuscular mycorrhizal fungus. <i>BMC Evolutionary Biology</i> , 2009 , 9, 13	3	78
25	Nonsel self vegetative fusion and genetic exchange in the arbuscular mycorrhizal fungus <i>Glomus intraradices</i> . <i>New Phytologist</i> , 2009 , 181, 924-937	9.8	141
24	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, 672-87	9.8	101

23	Multilocus genotyping of arbuscular mycorrhizal fungi and marker suitability for population genetics. <i>New Phytologist</i> , 2008 , 180, 564-568	9.8	17
22	Gene copy number polymorphisms in an arbuscular mycorrhizal fungal population. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 366-9	4.8	62
21	Genetic variability in a population of arbuscular mycorrhizal fungi causes variation in plant growth. <i>Ecology Letters</i> , 2006 , 9, 103-10	10	158
20	Meiosis leads to pervasive segregation distortion and copy-number variation in accessory chromosomes of the wheat pathogen <i>Zymoseptoria tritici</i>		1
19	A fungal avirulence factor encoded in a highly plastic genomic region triggers partial resistance to septoria tritici blotch		1
18	The MoT3 assay does not distinguish between <i>Magnaporthe oryzae</i> wheat and rice blast isolates from Bangladesh		1
17	Complex evolutionary origins of specialized metabolite gene cluster diversity among the plant pathogenic fungi of the <i>Fusarium graminearum</i> species complex		1
16	A transcriptome for the early-branching fern <i>Botrychium lunaria</i> enables fine-grained resolution of population structure		1
15	Emergence of wheat blast in Bangladesh was caused by a South American lineage of <i>Magnaporthe oryzae</i>		2
14	A population-level invasion by transposable elements triggers genome expansion in a fungal pathogen		8
13	Emergence and diversification of a highly invasive chestnut pathogen lineage across south-eastern Europe		3
12	The genetic architecture of emerging fungicide resistance in populations of a global wheat pathogen		2
11	Maintenance of variation in virulence and reproduction in populations of an agricultural plant pathogen		2
10	A chromosome-scale genome assembly for the <i>Fusarium oxysporum</i> strain Fo5176 to establish a model <i>Arabidopsis</i> -fungal pathosystem		3
9	Population-level deep sequencing reveals the interplay of clonal and sexual reproduction in the fungal wheat pathogen <i>Zymoseptoria tritici</i>		6
8	The complex genomic basis of rapid convergent adaptation to pesticides across continents in a fungal plant pathogen		5
7	The wheat blast pathogen <i>Pyricularia graminis-tritici</i> has complex origins and a disease cycle spanning multiple grass hosts		7
6	Purging of highly deleterious mutations through severe bottlenecks in Alpine ibex		3

- 5 Stress-driven transposable element de-repression dynamics in a fungal pathogen 4
- 4 A 19-isolate reference-quality global pangenome for the fungal wheat pathogen *Zymoseptoria tritici* 4
- 3 Natural selection drives population divergence for local adaptation in a wheat pathogen 3
- 2 Genome compartmentalization predates species divergence in the plant pathogen genus *Zymoseptoria* 3
- 1 Histone H3K27 methylation perturbs transcriptional robustness and underpins dispensability of highly conserved genes in fungi 1