

# Minou Nowrousian

## List of Publications by Year in Descending Order

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**Version:** 2024-04-10

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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.

64 papers	2,097 citations	28 h-index	45 g-index
70 ext. papers	2,540 ext. citations	5.3 avg, IF	4.99 L-index

#	Paper	IF	Citations
64	Endoplasmic reticulum membrane receptors of the GET pathway are conserved throughout eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	5
63	A 20-kb lineage-specific genomic region tames virulence in pathogenic amphidiploid <i>Verticillium longisporum</i> . <i>Molecular Plant Pathology</i> , <b>2021</b> , 22, 939-953	5.7	2
62	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in Stramenopila-Alveolata-Rhizaria lineages. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008646	6	12
61	<i>Sordaria macrospora</i> : 25 years as a model organism for studying the molecular mechanisms of fruiting body development. <i>Applied Microbiology and Biotechnology</i> , <b>2020</b> , 104, 3691-3704	5.7	15
60	Degradative Capacity of Two Strains of : From Phenotype to Genotype. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1338	5.7	4
59	Convergent evolution of linked mating-type loci in basidiomycete fungi. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008365	15	
58	Genetic and Genomic Analyses Reveal Boundaries between Species Closely Related to Pathogens. <i>MBio</i> , <b>2019</b> , 10,	7.8	17
57	Combination of Proteogenomics with Peptide Sequencing Identifies New Genes and Hidden Posttranscriptional Modifications. <i>MBio</i> , <b>2019</b> , 10,	7.8	22
56	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. <i>Genetics</i> , <b>2019</b> , 213, 1545-1563	4	5
55	The secreted metabolome of and implications for bacterial chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 2490-2495	11.5	48
54	Genomics and transcriptomics to study fruiting body development: An update. <i>Fungal Biology Reviews</i> , <b>2018</b> , 32, 231-235	6.8	8
53	Visual tuning in the flashlight fish <i>Anomalops katoptron</i> to detect blue, bioluminescent light. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198765	3.7	6
52	Pezizomycetes genomes reveal the molecular basis of ectomycorrhizal truffle lifestyle. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 1956-1965	12.3	52
51	The transcription factor PRO44 and the histone chaperone ASF1 regulate distinct aspects of multicellular development in the filamentous fungus <i>Sordaria macrospora</i> . <i>BMC Genetics</i> , <b>2018</b> , 19, 112	2.6	8
50	Mating-type factor-specific regulation of the fumagillin/pseurotin secondary metabolite supercluster in <i>Aspergillus fumigatus</i> . <i>Molecular Microbiology</i> , <b>2018</b> , 110, 1045-1065	4.1	8
49	Innovation and constraint leading to complex multicellularity in the Ascomycota. <i>Nature Communications</i> , <b>2017</b> , 8, 14444	17.4	52
48	Simple discovery of bacterial biocatalysts from environmental samples through functional metaproteomics. <i>Microbiome</i> , <b>2017</b> , 5, 28	16.6	16

47	RNA Editing During Sexual Development Occurs in Distantly Related Filamentous Ascomycetes. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 855-868	3.9	28
46	New insights from an old mutant: SPADIX4 governs fruiting body development but not hyphal fusion in <i>Sordaria macrospora</i> . <i>Molecular Genetics and Genomics</i> , <b>2017</b> , 292, 93-104	3.1	8
45	Fungal genome and mating system transitions facilitated by chromosomal translocations involving intercentromeric recombination. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002527	9.7	44
44	Complete Mitochondrial Genome Sequence of the Pezizomycete <i>Pyronema confluens</i> . <i>Genome Announcements</i> , <b>2016</b> , 4,		5
43	Von Maxam-Gilbert und Sanger zur Next Generation-Sequenzierung. <i>BioSpektrum</i> , <b>2015</b> , 21, 25-27	0.1	1
42	Genomics and Transcriptomics Analyses of the Oil-Accumulating Basidiomycete Yeast <i>Trichosporon oleaginosus</i> : Insights into Substrate Utilization and Alternative Evolutionary Trajectories of Fungal Mating Systems. <i>MBio</i> , <b>2015</b> , 6, e00918	7.8	52
41	Microarray hybridization analysis of light-dependent gene expression in <i>Penicillium chrysogenum</i> identifies bZIP transcription factor PcAtfA. <i>Journal of Basic Microbiology</i> , <b>2015</b> , 55, 480-9	2.7	7
40	Functional Analysis of Developmentally Regulated Genes <i>chs7</i> and <i>sec22</i> in the Ascomycete <i>Sordaria macrospora</i> . <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 1233-45	3.2	8
39	Analysis of Circadian Rhythms in the Basal Filamentous Ascomycete <i>Pyronema confluens</i> . <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 2061-71	3.2	12
38	Laser-Mikrodissektion und RNA-Seq zur Analyse der Genexpression in Pilzen. <i>BioSpektrum</i> , <b>2014</b> , 20, 30-32	0.1	
37	The polyketide synthase gene <i>pkc4</i> is essential for sexual development and regulates fruiting body morphology in <i>Sordaria macrospora</i> . <i>Fungal Genetics and Biology</i> , <b>2014</b> , 68, 48-59	3.9	28
36	New insights into the roles of NADPH oxidases in sexual development and ascospore germination in <i>Sordaria macrospora</i> . <i>Genetics</i> , <b>2014</b> , 196, 729-44	4	65
35	Gene expansion shapes genome architecture in the human pathogen <i>Lichtheimia corymbifera</i> : an evolutionary genomics analysis in the ancient terrestrial mucorales (Mucoromycotina). <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004496	6	55
34	The filamentous fungus <i>Sordaria macrospora</i> as a genetic model to study fruiting body development. <i>Advances in Genetics</i> , <b>2014</b> , 87, 199-244	3.3	44
33	7 Genomics and Transcriptomics to Analyze Fruiting Body Development <b>2014</b> , 149-172		9
32	Genomsequenzierung zur Identifikation von Mutationen. <i>BioSpektrum</i> , <b>2013</b> , 19, 25-27	0.1	2
31	Fungal gene expression levels do not display a common mode of distribution. <i>BMC Research Notes</i> , <b>2013</b> , 6, 559	2.3	4
30	Suppression subtractive hybridization and comparative expression analysis to identify developmentally regulated genes in filamentous fungi. <i>Journal of Basic Microbiology</i> , <b>2013</b> , 53, 742-51	2.7	9

29	The genome and development-dependent transcriptomes of <i>Pyronema confluens</i> : a window into fungal evolution. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003820	6	65
28	The histone chaperone ASF1 is essential for sexual development in the filamentous fungus <i>Sordaria macrospora</i> . <i>Molecular Microbiology</i> , <b>2012</b> , 84, 748-65	4.1	15
27	Combining laser microdissection and RNA-seq to chart the transcriptional landscape of fungal development. <i>BMC Genomics</i> , <b>2012</b> , 13, 511	4.5	54
26	Deep sequencing uncovers numerous small RNAs on all four replicons of the plant pathogen <i>Agrobacterium tumefaciens</i> . <i>RNA Biology</i> , <b>2012</b> , 9, 446-57	4.8	66
25	Whole-Genome Sequencing of <i>Sordaria macrospora</i> Mutants Identifies Developmental Genes. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 261-70	3.2	70
24	10 Evolution of Genes for Secondary Metabolism in Fungi <b>2011</b> , 231-255		6
23	De novo assembly of a 40 Mb eukaryotic genome from short sequence reads: <i>Sordaria macrospora</i> , a model organism for fungal morphogenesis. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1000891	6	152
22	Next-generation sequencing techniques for eukaryotic microorganisms: sequencing-based solutions to biological problems. <i>Eukaryotic Cell</i> , <b>2010</b> , 9, 1300-10		106
21	<i>Sordaria macrospora</i> , a model organism to study fungal cellular development. <i>European Journal of Cell Biology</i> , <b>2010</b> , 89, 864-72	6.1	43
20	A novel polyketide biosynthesis gene cluster is involved in fruiting body morphogenesis in the filamentous fungi <i>Sordaria macrospora</i> and <i>Neurospora crassa</i> . <i>Current Genetics</i> , <b>2009</b> , 55, 185-98	2.9	24
19	<i>Sordaria macrospora</i> , a Model System for Fungal Development <b>2009</b> , 17-39		18
18	Three alpha-subunits of heterotrimeric G proteins and an adenylyl cyclase have distinct roles in fruiting body development in the homothallic fungus <i>Sordaria macrospora</i> . <i>Genetics</i> , <b>2008</b> , 180, 191-206 <sup>4</sup>		33
17	The Molecular Workings of the <i>Neurospora</i> Biological Clock. <i>Novartis Foundation Symposium</i> , <b>2008</b> , 184-202		4
16	The novel ER membrane protein PRO41 is essential for sexual development in the filamentous fungus <i>Sordaria macrospora</i> . <i>Molecular Microbiology</i> , <b>2007</b> , 64, 923-37	4.1	61
15	Regulation of melanin biosynthesis via the dihydroxynaphthalene pathway is dependent on sexual development in the ascomycete <i>Sordaria macrospora</i> . <i>FEMS Microbiology Letters</i> , <b>2007</b> , 275, 62-70	2.9	60
14	Of patterns and pathways: microarray technologies for the analysis of filamentous fungi. <i>Fungal Biology Reviews</i> , <b>2007</b> , 21, 171-178	6.8	14
13	The WW domain protein PRO40 is required for fungal fertility and associates with Woronin bodies. <i>Eukaryotic Cell</i> , <b>2007</b> , 6, 831-43		74
12	Multiple layers of temporal and spatial control regulate accumulation of the fruiting body-specific protein APP in <i>Sordaria macrospora</i> and <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , <b>2007</b> , 44, 602-14 <sup>9</sup>	2.9	29

11	Comparative gene expression analysis of fruiting body development in two filamentous fungi. <i>FEMS Microbiology Letters</i> , <b>2006</b> , 257, 328-35	2.9	21
10	The gene for a lectin-like protein is transcriptionally activated during sexual development, but is not essential for fruiting body formation in the filamentous fungus <i>Sordaria macrospora</i> . <i>BMC Microbiology</i> , <b>2005</b> , 5, 64	4.5	54
9	Cross-species microarray hybridization to identify developmentally regulated genes in the filamentous fungus <i>Sordaria macrospora</i> . <i>Molecular Genetics and Genomics</i> , <b>2005</b> , 273, 137-49	3.1	91
8	Comparative sequence analysis of <i>Sordaria macrospora</i> and <i>Neurospora crassa</i> as a means to improve genome annotation. <i>Fungal Genetics and Biology</i> , <b>2004</b> , 41, 285-92	3.9	44
7	The frequency gene is required for temperature-dependent regulation of many clock-controlled genes in <i>Neurospora crassa</i> . <i>Genetics</i> , <b>2003</b> , 164, 923-33	4	75
6	Analysis of expressed sequence tags from two starvation, time-of-day-specific libraries of <i>Neurospora crassa</i> reveals novel clock-controlled genes. <i>Genetics</i> , <b>2001</b> , 157, 1057-65	4	74
5	The fungal <i>acl1</i> and <i>acl2</i> genes encode two polypeptides with homology to the N- and C-terminal parts of the animal ATP citrate lyase polypeptide. <i>Current Genetics</i> , <b>2000</b> , 37, 189-93	2.9	34
4	Cell differentiation during sexual development of the fungus <i>Sordaria macrospora</i> requires ATP citrate lyase activity. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 450-60	4.8	85
3	An efficient procedure to isolate fungal genes from an indexed cosmid library. <i>Journal of Microbiological Methods</i> , <b>1997</b> , 29, 49-61	2.8	45
2	Genetic and genomic analyses reveal boundaries between species closely related to <i>Cryptococcus</i> pathogens		2
1	Convergent evolution of linked mating-type loci in basidiomycete fungi		1