James W Kronstad

List of Publications by Year
in descending order

146 papers	10,010 citations	36303 51 h-index	39675 94 g-index
153 all docs	153 docs citations	153 times ranked	7329 citing authors

#	Article	IF	Citations
1	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	27.8	1,113
2	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i>. Science, 2005, 307, 1321-1324.	12.6	664
3	Dandruff-associated <i>Malassezia</i> genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18730-18735.	7.1	396
4	Analysis of the Genome and Transcriptome of Cryptococcus neoformans var. grubii Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	3.5	336
5	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. MBio, 2020, 11, .	4.1	275
6	Expanding fungal pathogenesis: Cryptococcus breaks out of the opportunistic box. Nature Reviews Microbiology, 2011, 9, 193-203.	28.6	265
7	Spread of<i>Cryptococcus gattii</i>in British Columbia, Canada, and Detection in the Pacific Northwest, USA. Emerging Infectious Diseases, 2007, 13, 42-50.	4.3	252
8	Shared and distinct mechanisms of iron acquisition by bacterial and fungal pathogens of humans. Frontiers in Cellular and Infection Microbiology, 2013, 3, 80.	3.9	224
9	A yeast operator overlaps an upstream activation site. Cell, 1987, 50, 369-377.	28.9	216
10	Characterization of Environmental Sources of the Human and Animal Pathogen Cryptococcus gattii in British Columbia, Canada, and the Pacific Northwest of the United States. Applied and Environmental Microbiology, 2007, 73, 1433-1443.	3.1	209
11	Adenylyl Cyclase Functions Downstream of the GÎ± Protein Gpa1 and Controls Mating and Pathogenicity of Cryptococcus neoformans. Eukaryotic Cell, 2002, 1, 75-84.	3.4	196
12	Iron Regulation of the Major Virulence Factors in the AIDS-Associated Pathogen Cryptococcus neoformans. PLoS Biology, 2006, 4, e410.	5.6	192
13	OFSMUTS, BLASTS, MILDEWS,ANDBLIGHTS: cAMP Signaling in Phytopathogenic Fungi. Annual Review of Phytopathology, 2003, 41, 399-427.	7.8	171
14	Metabolic adaptation in <i>Cryptococcus neoformans</i> during early murine pulmonary infection. Molecular Microbiology, 2008, 69, 1456-1475.	2.5	147
15	Isolation of two alleles of the b locus of Ustilago maydis.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 978-982.	7.1	139
16	Iron Source Preference and Regulation of Iron Uptake in Cryptococcus neoformans. PLoS Pathogens, 2008, 4, e45.	4.7	139
17	Three classes of homologous Bacillus thuringiensis crystal-protein genes. Gene, 1986, 43, 29-40.	2.2	133
18	<i>Cryptococcus gattii</i>Dispersal Mechanisms, British Columbia, Canada. Emerging Infectious Diseases, 2007, 13, 51-57.	4.3	132

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19	Iron acquisition in fungal pathogens of humans. Metallomics, 2017, 9, 215-227.	2.4	128
20	HapX Positively and Negatively Regulates the Transcriptional Response to Iron Deprivation in Cryptococcus neoformans. PLoS Pathogens, 2010, 6, e1001209.	4.7	127
21	The mating-type and pathogenicity locus of the fungus <i>Ustilago hordei</i> spans a 500-kb region. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 15026-15031.	7.1	121
22	Comparative Gene Genealogies Indicate that Two Clonal Lineages of Cryptococcus gattii in British Columbia ResembleStrains from Other Geographical Areas. Eukaryotic Cell, 2005, 4, 1629-1638.	3.4	115
23	Role of Ferroxidases in Iron Uptake and Virulence of <i>Cryptococcus neoformans</i>. Eukaryotic Cell, 2009, 8, 1511-1520.	3.4	115
24	<i>ras2</i> Controls Morphogenesis, Pheromone Response, and Pathogenicity in the Fungal Pathogen <i>Ustilago maydis</i>. Eukaryotic Cell, 2002, 1, 954-966.	3.4	105
25	Comparison of AFLP fingerprints and ITS sequences as phylogenetic markers in Ustilaginomycetes. Mycologia, 2000, 92, 510-521.	1.9	104
26	<i>Cryptococcus gattii</i>Isolates from the British Columbia Cryptococcosis Outbreak Induce Less Protective Inflammation in a Murine Model of Infection than<i>Cryptococcus neoformans</i>. Infection and Immunity, 2009, 77, 4284-4294.	2.2	100
27	Lipid-induced filamentous growth in Ustilago maydis. Molecular Microbiology, 2004, 52, 823-835.	2.5	99
28	The emergence of Cryptococcus gattii in British Columbia and the Pacific Northwest. Current Infectious Disease Reports, 2008, 10, 58-65.	3.0	98
29	Adaptation of Cryptococcus neoformans to Mammalian Hosts: Integrated Regulation of Metabolism and Virulence. Eukaryotic Cell, 2012, 11, 109-118.	3.4	97
30	The Mannoprotein Cig1 Supports Iron Acquisition From Heme and Virulence in the Pathogenic Fungus Cryptococcus neoformans. Journal of Infectious Diseases, 2013, 207, 1339-1347.	4.0	96
31	Virulence and cAMP in smuts, blasts and blights. Trends in Plant Science, 1997, 2, 193-199.	8.8	95
32	Iron and fungal pathogenesis: a case study with Cryptococcus neoformans. Cellular Microbiology, 2008, 10, 277-284.	2.1	94
33	Transcriptional Regulation by Protein Kinase A in Cryptococcus neoformans. PLoS Pathogens, 2007, 3, e42.	4.7	92
34	Iron-regulated transcription and capsule formation in the fungal pathogen Cryptococcus neoformans. Molecular Microbiology, 2004, 55, 1452-1472.	2.5	90
35	The iron- and cAMP-regulated gene SIT1 influences ferrioxamine B utilization, melanization and cell wall structure in Cryptococcus neoformans. Microbiology (United Kingdom), 2007, 153, 29-41.	1.8	89
36	Cryptococcus neoformans Requires a Functional Glycolytic Pathway for Disease but Not Persistence in the Host. MBio, 2011, 2, e00103-11.	4.1	89

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37	Temperature-Regulated Transcription in the Pathogenic Fungus Cryptococcus neoformans. Genome Research, 2002, 12, 1386-1400.	5.5	84
38	Comparison of AFLP Fingerprints and ITS Sequences as Phylogenetic Markers in Ustilaginomycetes. Mycologia, 2000, 92, 510.	1.9	83
39	Regulation of the fungal secretome. Current Genetics, 2016, 62, 533-545.	1.7	83
40	Highly Recombinant VGII Cryptococcus gattii Population Develops Clonal Outbreak Clusters through both Sexual Macroevolution and Asexual Microevolution. MBio, 2014, 5, e01494-14.	4.1	81
41	Role of Ferric Reductases in Iron Acquisition and Virulence in the Fungal Pathogen Cryptococcus neoformans. Infection and Immunity, 2014, 82, 839-850.	2.2	74
42	A Decade of Experience: Cryptococcus gattii in British Columbia. Mycopathologia, 2012, 173, 311-319.	3.1	73
43	Chloroplasts and Plant Immunity: Where Are the Fungal Effectors?. Pathogens, 2020, 9, 19.	2.8	70
44	Cryptococcus neoformans Requires the ESCRT Protein Vps23 for Iron Acquisition from Heme, for Capsule Formation, and for Virulence. Infection and Immunity, 2013, 81, 292-302.	2.2	65
45	Variation in chromosome copy number influences the virulence of Cryptococcus neoformans and occurs in isolates from AIDS patients. BMC Genomics, 2011, 12, 526.	2.8	62
46	Role of an Expanded Inositol Transporter Repertoire in Cryptococcus neoformans Sexual Reproduction and Virulence. MBio, 2010, 1, .	4.1	61
47	Role of the Apt1 Protein in Polysaccharide Secretion by Cryptococcus neoformans. Eukaryotic Cell, 2014, 13, 715-726.	3.4	61
48	Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. Fungal Genetics and Biology, 2006, 43, 655-666.	2.1	59
49	An encapsulation of iron homeostasis and virulence in Cryptococcus neoformans. Trends in Microbiology, 2013, 21, 457-465.	7.7	59
50	Comparative hybridization reveals extensive genome variation in the AIDS-associated pathogen Cryptococcus neoformans. Genome Biology, 2008, 9, R41.	9.6	58
51	Disarming Fungal Pathogens: <i>Bacillus safensis</i> Inhibits Virulence Factor Production and Biofilm Formation by <i>Cryptococcus neoformans</i> and <i>Candida albicans</i>. MBio, 2017, 8, .	4.1	57
52	The cAMP/Protein Kinase A Pathway Regulates Virulence and Adaptation to Host Conditions in Cryptococcus neoformans. Frontiers in Cellular and Infection Microbiology, 2019, 9, 212.	3.9	57
53	Role of Homoserine Transacetylase as a New Target for Antifungal Agents. Antimicrobial Agents and Chemotherapy, 2007, 51, 1731-1736.	3.2	55
54	An Ustilago maydis Septin Is Required for Filamentous Growth in Culture and for Full Symptom Development on Maize. Eukaryotic Cell, 2005, 4, 2044-2056.	3.4	53

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55	Peroxisomal and Mitochondrial Î²-Oxidation Pathways Influence the Virulence of the Pathogenic Fungus Cryptococcus neoformans. Eukaryotic Cell, 2012, 11, 1042-1054.	3.4	53
56	The hgl1 gene is required for dimorphism and teliospore formation in the fungal pathogen Ustilago maydis. Molecular Microbiology, 2001, 41, 337-348.	2.5	52
57	Defects in Phosphate Acquisition and Storage Influence Virulence of Cryptococcus neoformans. Infection and Immunity, 2014, 82, 2697-2712.	2.2	52
58	Three selectable markers for transformation of Ustilago maydis. Gene, 1994, 142, 225-230.	2.2	49
59	Regulated expression of cyclic AMPâ€dependent protein kinase A reveals an influence on cell size and the secretion of virulence factors in <i>Cryptococcus neoformans</i>. Molecular Microbiology, 2012, 85, 700-715.	2.5	49
60	A defect in iron uptake enhances the susceptibility of Cryptococcus neoformans to azole antifungal drugs. Fungal Genetics and Biology, 2012, 49, 955-966.	2.1	48
61	The cAMP/protein kinase A signaling pathway in pathogenic basidiomycete fungi: Connections with iron homeostasis. Journal of Microbiology, 2015, 53, 579-587.	2.8	48
62	The Monothiol Glutaredoxin Grx4 Regulates Iron Homeostasis and Virulence in Cryptococcus neoformans. MBio, 2018, 9, .	4.1	48
63	Secretome profiling of Cryptococcus neoformans reveals regulation of a subset of virulence-associated proteins and potential biomarkers by protein kinase A. BMC Microbiology, 2015, 15, 206.	3.3	47
64	The endosomal sorting complex required for transport machinery influences haem uptake and capsule elaboration in <scp><i>C</i></scp><i>ryptococcus neoformans</i>. Molecular Microbiology, 2015, 96, 973-992.	2.5	45
65	The Pheromone Cell Signaling Components of the Ustilago a Mating-Type Loci Determine Intercompatibility Between Species. Genetics, 1996, 143, 1601-1613.	2.9	44
66	The cAMP/Protein Kinase A Pathway and Virulence in<i>Cryptococcus neoformans</i>. Mycobiology, 2011, 39, 143-150.	1.7	42
67	Discovery of a Novel Antifungal Agent in the Pathogen Box. MSphere, 2017, 2, .	2.9	42
68	Heterozygosity at the b mating-type locus attenuates fusion in Ustilago maydis. Current Genetics, 1995, 27, 451-459.	1.7	39
69	Defects in Mitochondrial and Peroxisomal Î²-Oxidation Influence Virulence in the Maize Pathogen Ustilago maydis. Eukaryotic Cell, 2012, 11, 1055-1066.	3.4	39
70	Physical Maps for Genome Analysis of Serotype A and D Strains of the Fungal Pathogen Cryptococcus neoformans. Genome Research, 2002, 12, 1445-1453.	5.5	38
71	The Multifunctional Î²-Oxidation Enzyme Is Required for Full Symptom Development by the Biotrophic Maize Pathogen Ustilago maydis. Eukaryotic Cell, 2006, 5, 2047-2061.	3.4	38
72	The ZIP family zinc transporters support the virulence of<i>Cryptococcus neoformans</i>. Medical Mycology, 2016, 54, 605-615.	0.7	38

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73	Purification and characterization of phenylalanine ammonia-lyase from Ustilago maydis. Phytochemistry, 1996, 43, 351-357.	2.9	37
74	A Putative P-Type ATPase, Apt1, Is Involved in Stress Tolerance and Virulence in Cryptococcus neoformans. Eukaryotic Cell, 2010, 9, 74-83.	3.4	36
75	Maize susceptibility to <i>Ustilago maydis</i> is influenced by genetic and chemical perturbation of carbohydrate allocation. Molecular Plant Pathology, 2017, 18, 1222-1237.	4.2	35
76	The vtc4 Gene Influences Polyphosphate Storage, Morphogenesis, and Virulence in the Maize Pathogen Ustilago maydis. Eukaryotic Cell, 2006, 5, 1399-1409.	3.4	33
77	The cAMP Signal Transduction Pathway Mediates Resistance to Dicarboximide and Aromatic Hydrocarbon Fungicides in Ustilago maydis. Fungal Genetics and Biology, 2001, 32, 183-193.	2.1	32
78	Leu1 plays a role in iron metabolism and is required for virulence in Cryptococcus neoformans. Fungal Genetics and Biology, 2015, 75, 11-19.	2.1	32
79	Beyond the Big Three: Systematic Analysis of Virulence Factors in Cryptococcus neoformans. Cell Host and Microbe, 2008, 4, 308-310.	11.0	31
80	A defect in <scp>ATP</scp>â€citrate lyase links acetylâ€<scp>CoA</scp> production, virulence factor elaboration and virulence in <i><scp>C</scp>ryptococcus neoformans</i>. Molecular Microbiology, 2012, 86, 1404-1423.	2.5	29
81	The Zinc Finger Protein Mig1 Regulates Mitochondrial Function and Azole Drug Susceptibility in the Pathogenic Fungus Cryptococcus neoformans. MSphere, 2016, 1, .	2.9	28
82	The mitochondrial ABC transporter Atm1 plays a role in iron metabolism and virulence in the human fungal pathogen Cryptococcus neoformans. Medical Mycology, 2018, 56, 458-468.	0.7	27
83	Serial Analysis of Gene Expression Reveals Conserved Links between Protein Kinase A, Ribosome Biogenesis, and Phosphate Metabolism in Ustilago maydis. Eukaryotic Cell, 2005, 4, 2029-2043.	3.4	25
84	ATG Genes Influence the Virulence of Cryptococcus neoformans through Contributions beyond Core Autophagy Functions. Infection and Immunity, 2018, 86, .	2.2	25
85	Role of clathrin-mediated endocytosis in the use of heme and hemoglobin by the fungal pathogen <i>Cryptococcus neoformans</i>. Cellular Microbiology, 2019, 21, e12961.	2.1	24
86	The Sec1/Munc18 (SM) protein Vps45 is involved in iron uptake, mitochondrial function and virulence in the pathogenic fungus Cryptococcus neoformans. PLoS Pathogens, 2018, 14, e1007220.	4.7	22
87	Gene disruption in Cryptococcus neoformans and Cryptococcus gattii by in vitro transposition. Current Genetics, 2006, 49, 341-350.	1.7	21
88	The Iron-Responsive, GATA-Type Transcription Factor Cir1 Influences Mating in Cryptococcus neoformans. Molecules and Cells, 2011, 31, 73-78.	2.6	21
89	A P4-ATPase subunit of the Cdc50 family plays a role in iron acquisition and virulence in<i>Cryptococcus neoformans</i>. Cellular Microbiology, 2017, 19, e12718.	2.1	21
90	The putative flippase Apt1 is required for intracellular membrane architecture and biosynthesis of polysaccharide and lipids in Cryptococcus neoformans. Biochimica Et Biophysica Acta - Molecular Cell Research, 2018, 1865, 532-541.	4.1	21

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91	Self-Fertility: The Genetics of Sex in Lonely Fungi. Current Biology, 2007, 17, R843-R845.	3.9	20
92	The phosphate language of fungi. Trends in Microbiology, 2022, 30, 338-349.	7.7	20
93	Verticillium longisporum Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. Frontiers in Microbiology, 2020, 11, 1876.	3.5	18
94	Iron influences the abundance of the iron regulatory protein Cir1 in the fungal pathogen<i>Cryptococcus neoformans</i>. FEBS Letters, 2011, 585, 3342-3347.	2.8	17
95	Acetate provokes mitochondrial stress and cell death in <i>Ustilago maydis</i>. Molecular Microbiology, 2018, 107, 488-507.	2.5	15
96	The Novel J-Domain Protein Mrj1 Is Required for Mitochondrial Respiration and Virulence in Cryptococcus neoformans. MBio, 2020, 11, .	4.1	15
97	Respiring to infect: Emerging links between mitochondria, the electron transport chain, and fungal pathogenesis. PLoS Pathogens, 2021, 17, e1009661.	4.7	15
98	Altered Immune Response Differentially Enhances Susceptibility to Cryptococcus neoformans and Cryptococcus gattii Infection in Mice Expressing the HIV-1 Transgene. Infection and Immunity, 2013, 81, 1100-1113.	2.2	14
99	Phosphorus-rich structures and capsular architecture in <i>Cryptococcus neoformans</i>. Future Microbiology, 2017, 12, 227-238.	2.0	14
100	Chloroplastâ€associated metabolic functions influence the susceptibility of maize to <i>Ustilago maydis</i>. Molecular Plant Pathology, 2017, 18, 1210-1221.	4.2	14
101	Connecting iron regulation and mitochondrial function in Cryptococcus neoformans. Current Opinion in Microbiology, 2019, 52, 7-13.	5.1	14
102	The Spectrum of Interactions between Cryptococcus neoformans and Bacteria. Journal of Fungi (Basel, Switzerland), 2019, 5, 31.	3.5	14
103	Vacuolar zinc transporter Zrc1 is required for detoxification of excess intracellular zinc in the human fungal pathogen Cryptococcus neoformans. Journal of Microbiology, 2018, 56, 65-71.	2.8	13
104	A Transcriptional Regulatory Map of Iron Homeostasis Reveals a New Control Circuit for Capsule Formation in <i>Cryptococcus neoformans</i>. Genetics, 2020, 215, 1171-1189.	2.9	13
105	Chaperone Networks in Fungal Pathogens of Humans. Journal of Fungi (Basel, Switzerland), 2021, 7, 209.	3.5	13
106	Cryptococcus neoformans. Trends in Microbiology, 2020, 28, 163-164.	7.7	12
107	Networks of fibers and factors: regulation of capsule formation in Cryptococcus neoformans. F1000Research, 2016, 5, 1786.	1.6	11
108	A chemical genetic screen reveals a role for proteostasis in capsule and biofilm formation by Cryptococcus neoformans. Microbial Cell, 2018, 5, 495-510.	3.2	11

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109	Cloning and disruption of a phenylalanine ammonia-lyase gene from Ustilago maydis. Current Genetics, 2001, 40, 40-48.	1.7	10
110	The lysine biosynthetic enzyme Lys4 influences iron metabolism, mitochondrial function and virulence in Cryptococcus neoformans. Biochemical and Biophysical Research Communications, 2016, 477, 706-711.	2.1	10
111	Unfolded Protein Response and Scaffold Independent Pheromone MAP Kinase Signaling Control Verticillium dahliae Growth, Development, and Plant Pathogenesis. Journal of Fungi (Basel,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	3.5	10
112	Mating in the Smut Fungi: From a to b to the Downstream Cascades. , 0, , 377-387.		10
113	Transcripts and tumors: regulatory and metabolic programming during biotrophic phytopathogenesis. F1000Research, 2018, 7, 1812.	1.6	8
114	A Cytoplasmic Heme Sensor Illuminates the Impacts of Mitochondrial and Vacuolar Functions and Oxidative Stress on Heme-Iron Homeostasis in Cryptococcus neoformans. MBio, 2020, 11, .	4.1	7
115	Dnj1 Promotes Virulence in Cryptococcus neoformans by Maintaining Robust Endoplasmic Reticulum Homeostasis Under Temperature Stress. Frontiers in Microbiology, 2021, 12, 727039.	3.5	7
116	Castles and cuitlacoche: the first international Ustilago conference. Fungal Genetics and Biology, 2003, 38, 265-271.	2.1	6
117	Serial Analysis of Gene Expression in Eukaryotic Pathogens. Infectious Disorders - Drug Targets, 2006, 6, 281-297.	0.8	6
118	Pathogenic Yeasts Deploy Cell Surface Receptors to Acquire Iron in Vertebrate Hosts. PLoS Pathogens, 2013, 9, e1003498.	4.7	6
119	The putative phospholipase Lip2 counteracts oxidative damage and influences the virulence of <i>Ustilago maydis</i>. Molecular Plant Pathology, 2017, 18, 210-221.	4.2	6
120	Fungal Glycolipid Hydrolase Inhibitors and Their Effect on <i>Cryptococcus neoformans</i>. ChemBioChem, 2017, 18, 284-290.	2.6	6
121	Coordinated regulation of iron metabolism in Cryptococcus neoformans by GATA and CCAAT transcription factors: connections with virulence. Current Genetics, 2021, 67, 583-593.	1.7	6
122	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid Verticillium longisporum. Molecular Plant Pathology, 2021, 22, 939-953.	4.2	6
123	Breaking the bad: Bacillus blocks fungal virulence factors. Microbial Cell, 2017, 4, 384-386.	3.2	6
124	Triggers and targets of cAMP signalling. Trends in Microbiology, 2000, 8, 302.	7.7	5
125	Induction of phenylalanine ammonia-lyase activity by tryptophan in Ustilago maydis. Phytochemistry, 2001, 58, 849-857.	2.9	5
126	Iron in eukaryotic microbes: regulation, trafficking and theft. Current Opinion in Microbiology, 2013, 16, 659-661.	5.1	5

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127	The monothiol glutaredoxin Grx4 influences thermotolerance, cell wall integrity, and Mpk1 signaling in Cryptococcus neoformans. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	5
128	History of the Mating Types in<i>Ustilago maydis</i>. , 0, , 349-375.		5
129	Organic acids and glucose prime late-stage fungal biotrophy in maize. Science, 2022, 376, 1187-1191.	12.6	5
130	Control of filamentous growth by mating and cyclic-AMP inUstilago. Canadian Journal of Botany, 1995, 73, 258-265.	1.1	4
131	Hostâ€"microbe interactions: the response of fungal and oomycete pathogens to the host environment. Current Opinion in Microbiology, 2007, 10, 303-306.	5.1	4
132	The Emergence of Cryptococcus gattii Infections on Vancouver Island and Expansion in the Pacific Northwest. , 0, , 313-325.		3
133	Vam6/Vps39/ <scp>TRAP1</scp> â€domain proteins influence vacuolar morphology, iron acquisition and virulence in <i>Cryptococcus neoformans</i>. Cellular Microbiology, 2021, 23, e13400.	2.1	3
134	Essential Metals in Cryptococcus neoformans: Acquisition and Regulation. Current Fungal Infection Reports, 2014, 8, 153-162.	2.6	2
135	Oxidative Stress Causes Vacuolar Fragmentation in the Human Fungal Pathogen Cryptococcus neoformans. Journal of Fungi (Basel, Switzerland), 2021, 7, 523.	3.5	2
136	Bipolar and Tetrapolar Mating Systems in the Ustilaginales. , 0, , 389-404.		2
137	The Cryptococcus Genomes: Tools for Comparative Genomics and Expression Analysis. , 0, , 113-126.		2
138	Involvement of Mrs3/4 in Mitochondrial Iron Transport and Metabolism in Cryptococcus neoformans. Journal of Microbiology and Biotechnology, 2020, 30, 1142-1148.	2.1	2
139	A J Domain Protein Functions as a Histone Chaperone to Maintain Genome Integrity and the Response to DNA Damage in a Human Fungal Pathogen. MBio, 2021, 12, e0327321.	4.1	2
140	Conservation of the b Mating-Type Gene Complex among Bipolar and Tetrapolar Smut Fungi. Plant Cell, 1993, 5, 123.	6.6	1
141	Growth and development: Signals and their transduction. Current Opinion in Microbiology, 2000, 3, 549-552.	5.1	1
142	Differentiation of sapstain fungi by restriction fragment length polymorphism patterns in nuclear small subunit ribosomal DNA. FEMS Microbiology Letters, 1999, 177, 151-157.	1.8	1
143	Sex in Natural Populations of Cryptococcus gattii. , 0, , 477-488.		1
144	Response from Kronstad. Trends in Microbiology, 2000, 8, 303.	7.7	0

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145	Cryptococcus neoformans: Budding Yeast and Dimorphic Filamentous Fungus. , 2014, , 717-735.		0
146	Origin, Evolution, and Extinction of Asexual Fungi: Experimental Tests Using Cryptococcus neoformans. , 0, , 459-475.		0