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	The phosphate language of fungi. Trends in Microbiology, 2022, 30, 338-349.	7.7	20
2	Organic acids and glucose prime late-stage fungal biotrophy in maize. Science, 2022, 376, 1187-1191.	12.6	5
3	Chaperone Networks in Fungal Pathogens of Humans. Journal of Fungi (Basel, Switzerland), 2021, 7, 209.	3.5	13
4	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
5	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 /Overlook 10 Tf 5	3.5	10
6	A 20â€kb lineageâ€specific genomic region tames virulence in pathogenic amphidiploid Verticillium longisporum. Molecular Plant Pathology, 2021, 22, 939-953.	4.2	6
7	Oxidative Stress Causes Vacuolar Fragmentation in the Human Fungal Pathogen Cryptococcus neoformans. Journal of Fungi (Basel, Switzerland), 2021, 7, 523.	3.5	2
8	Respiring to infect: Emerging links between mitochondria, the electron transport chain, and fungal pathogenesis. PLoS Pathogens, 2021, 17, e1009661.	4.7	15
9	The monothiol glutaredoxin Grx4 influences thermotolerance, cell wall integrity, and Mpk1 signaling in Cryptococcus neoformans. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	5
10	Dnj1 Promotes Virulence in Cryptococcus neoformans by Maintaining Robust Endoplasmic Reticulum Homeostasis Under Temperature Stress. Frontiers in Microbiology, 2021, 12, 727039.	3.5	7
11	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
12	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
13	Cryptococcus neoformans. Trends in Microbiology, 2020, 28, 163-164.	7.7	12
14	Chloroplasts and Plant Immunity: Where Are the Fungal Effectors?. Pathogens, 2020, 9, 19.	2.8	70
15	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
16	Verticillium longisporum Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. Frontiers in Microbiology, 2020, 11, 1876.	3.5	18
17	Threats Posed by the Fungal Kingdom to Humans, Wildlife, and Agriculture. MBio, 2020, 11, .	4.1	275
18	The Novel J-Domain Protein Mrj1 Is Required for Mitochondrial Respiration and Virulence in Cryptococcus neoformans. MBio, 2020, 11, .	4.1	15

#	Article	IF	Citations
19	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
20	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
21	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
22	Connecting iron regulation and mitochondrial function in Cryptococcus neoformans. Current Opinion in Microbiology, 2019, 52, 7-13.	5.1	14
23	The Spectrum of Interactions between Cryptococcus neoformans and Bacteria. Journal of Fungi (Basel, Switzerland), 2019, 5, 31.	3.5	14
24	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
25	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
26	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
27	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
28	Acetate provokes mitochondrial stress and cell death in <i>Ustilago maydis</i>. Molecular Microbiology, 2018, 107, 488-507.	2.5	15
29	The Monothiol Glutaredoxin Grx4 Regulates Iron Homeostasis and Virulence in Cryptococcus neoformans. MBio, 2018, 9, .	4.1	48
30	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
31	ATG Genes Influence the Virulence of Cryptococcus neoformans through Contributions beyond Core Autophagy Functions. Infection and Immunity, 2018, 86, .	2.2	25
32	Transcripts and tumors: regulatory and metabolic programming during biotrophic phytopathogenesis. F1000Research, 2018, 7, 1812.	1.6	8
33	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
34	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
35	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
36	Phosphorus-rich structures and capsular architecture in <i>Cryptococcus neoformans</i>. Future Microbiology, 2017, 12, 227-238.	2.0	14

#	Article	IF	Citations
37	Iron acquisition in fungal pathogens of humans. Metallomics, 2017, 9, 215-227.	2.4	128
38	Discovery of a Novel Antifungal Agent in the Pathogen Box. MSphere, 2017, 2, .	2.9	42
39	Fungal Glycolipid Hydrolase Inhibitors and Their Effect on <i>Cryptococcus neoformans</i>. ChemBioChem, 2017, 18, 284-290.	2.6	6
40	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
41	Chloroplastâ€associated metabolic functions influence the susceptibility of maize to <i>Ustilago maydis</i>. Molecular Plant Pathology, 2017, 18, 1210-1221.	4.2	14
42	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
43	Breaking the bad: Bacillus blocks fungal virulence factors. Microbial Cell, 2017, 4, 384-386.	3.2	6
44	The ZIP family zinc transporters support the virulence of<i>Cryptococcus neoformans</i>. Medical Mycology, 2016, 54, 605-615.	0.7	38
45	The Zinc Finger Protein Mig1 Regulates Mitochondrial Function and Azole Drug Susceptibility in the Pathogenic Fungus Cryptococcus neoformans. MSphere, 2016, 1, .	2.9	28
46	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
47	Regulation of the fungal secretome. Current Genetics, 2016, 62, 533-545.	1.7	83
48	Networks of fibers and factors: regulation of capsule formation in Cryptococcus neoformans. F1000Research, 2016, 5, 1786.	1.6	11
49	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
50	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
51	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
52	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
53	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
54	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

#	Article	IF	Citations
55	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
56	Defects in Phosphate Acquisition and Storage Influence Virulence of Cryptococcus neoformans. Infection and Immunity, 2014, 82, 2697-2712.	2.2	52
57	Role of the Apt1 Protein in Polysaccharide Secretion by Cryptococcus neoformans. Eukaryotic Cell, 2014, 13, 715-726.	3.4	61
58	Essential Metals in Cryptococcus neoformans: Acquisition and Regulation. Current Fungal Infection Reports, 2014, 8, 153-162.	2.6	2
59	Cryptococcus neoformans: Budding Yeast and Dimorphic Filamentous Fungus. , 2014, , 717-735.		0
60	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
61	Iron in eukaryotic microbes: regulation, trafficking and theft. Current Opinion in Microbiology, 2013, 16, 659-661.	5.1	5
62	An encapsulation of iron homeostasis and virulence in Cryptococcus neoformans. Trends in Microbiology, 2013, 21, 457-465.	7.7	59
63	Pathogenic Yeasts Deploy Cell Surface Receptors to Acquire Iron in Vertebrate Hosts. PLoS Pathogens, 2013, 9, e1003498.	4.7	6
64	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
65	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
66	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
67	Peroxisomal and Mitochondrial Î²-Oxidation Pathways Influence the Virulence of the Pathogenic Fungus Cryptococcus neoformans. Eukaryotic Cell, 2012, 11, 1042-1054.	3.4	53
68	Defects in Mitochondrial and Peroxisomal Î²-Oxidation Influence Virulence in the Maize Pathogen Ustilago maydis. Eukaryotic Cell, 2012, 11, 1055-1066.	3.4	39
69	Adaptation of Cryptococcus neoformans to Mammalian Hosts: Integrated Regulation of Metabolism and Virulence. Eukaryotic Cell, 2012, 11, 109-118.	3.4	97
70	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
71	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
72	A Decade of Experience: Cryptococcus gattii in British Columbia. Mycopathologia, 2012, 173, 311-319.	3.1	73

#	Article	IF	Citations
73	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
74	Expanding fungal pathogenesis: Cryptococcus breaks out of the opportunistic box. Nature Reviews Microbiology, 2011, 9, 193-203.	28.6	265
75	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
76	The Iron-Responsive, GATA-Type Transcription Factor Cir1 Influences Mating in Cryptococcus neoformans. Molecules and Cells, 2011, 31, 73-78.	2.6	21
77	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
78	Cryptococcus neoformans Requires a Functional Glycolytic Pathway for Disease but Not Persistence in the Host. MBio, 2011, 2, e00103-11.	4.1	89
79	The cAMP/Protein Kinase A Pathway and Virulence in<i>Cryptococcus neoformans</i>. Mycobiology, 2011, 39, 143-150.	1.7	42
80	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
81	HapX Positively and Negatively Regulates the Transcriptional Response to Iron Deprivation in Cryptococcus neoformans. PLoS Pathogens, 2010, 6, e1001209.	4.7	127
82	Role of an Expanded Inositol Transporter Repertoire in Cryptococcus neoformans Sexual Reproduction and Virulence. MBio, 2010, 1, .	4.1	61
83	Role of Ferroxidases in Iron Uptake and Virulence of <i>Cryptococcus neoformans</i>. Eukaryotic Cell, 2009, 8, 1511-1520.	3.4	115
84	<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
85	Iron and fungal pathogenesis: a case study with Cryptococcus neoformans. Cellular Microbiology, 2008, 10, 277-284.	2.1	94
86	The emergence of Cryptococcus gattii in British Columbia and the Pacific Northwest. Current Infectious Disease Reports, 2008, 10, 58-65.	3.0	98
87	Metabolic adaptation in <i>Cryptococcus neoformans</i> during early murine pulmonary infection. Molecular Microbiology, 2008, 69, 1456-1475.	2.5	147
88	Comparative hybridization reveals extensive genome variation in the AIDS-associated pathogen Cryptococcus neoformans. Genome Biology, 2008, 9, R41.	9.6	58
89	Beyond the Big Three: Systematic Analysis of Virulence Factors in Cryptococcus neoformans. Cell Host and Microbe, 2008, 4, 308-310.	11.0	31
90	Iron Source Preference and Regulation of Iron Uptake in Cryptococcus neoformans. PLoS Pathogens, 2008, 4, e45.	4.7	139

#	Article	IF	Citations
91	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
92	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
93	Transcriptional Regulation by Protein Kinase A in Cryptococcus neoformans. PLoS Pathogens, 2007, 3, e42.	4.7	92
94	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
95	Role of Homoserine Transacetylase as a New Target for Antifungal Agents. Antimicrobial Agents and Chemotherapy, 2007, 51, 1731-1736.	3.2	55
96	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
97	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
98	<i>Cryptococcus gattii</i>Dispersal Mechanisms, British Columbia, Canada. Emerging Infectious Diseases, 2007, 13, 51-57.	4.3	132
99	Self-Fertility: The Genetics of Sex in Lonely Fungi. Current Biology, 2007, 17, R843-R845.	3.9	20
100	Mating factor linkage and genome evolution in basidiomycetous pathogens of cereals. Fungal Genetics and Biology, 2006, 43, 655-666.	2.1	59
101	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	27.8	1,113
102	Gene disruption in Cryptococcus neoformans and Cryptococcus gattii by in vitro transposition. Current Genetics, 2006, 49, 341-350.	1.7	21
103	Serial Analysis of Gene Expression in Eukaryotic Pathogens. Infectious Disorders - Drug Targets, 2006, 6, 281-297.	0.8	6
104	Iron Regulation of the Major Virulence Factors in the AIDS-Associated Pathogen Cryptococcus neoformans. PLoS Biology, 2006, 4, e410.	5.6	192
105	The vtc4 Gene Influences Polyphosphate Storage, Morphogenesis, and Virulence in the Maize Pathogen Ustilago maydis. Eukaryotic Cell, 2006, 5, 1399-1409.	3.4	33
106	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
107	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
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i>. Science, 2005, 307, 1321-1324.	12.6	664
111	Lipid-induced filamentous growth in Ustilago maydis. Molecular Microbiology, 2004, 52, 823-835.	2.5	99
112	Iron-regulated transcription and capsule formation in the fungal pathogen Cryptococcus neoformans. Molecular Microbiology, 2004, 55, 1452-1472.	2.5	90
113	OFSMUTS, BLASTS, MILDEWS,ANDBLIGHTS: cAMP Signaling in Phytopathogenic Fungi. Annual Review of Phytopathology, 2003, 41, 399-427.	7.8	171
114	Castles and cuitlacoche: the first international Ustilago conference. Fungal Genetics and Biology, 2003, 38, 265-271.	2.1	6
115	<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
116	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
117	Temperature-Regulated Transcription in the Pathogenic Fungus Cryptococcus neoformans. Genome Research, 2002, 12, 1386-1400.	5.5	84
118	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
119	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
120	Cloning and disruption of a phenylalanine ammonia-lyase gene from Ustilago maydis. Current Genetics, 2001, 40, 40-48.	1.7	10
121	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
122	Induction of phenylalanine ammonia-lyase activity by tryptophan in Ustilago maydis. Phytochemistry, 2001, 58, 849-857.	2.9	5
123	Comparison of AFLP fingerprints and ITS sequences as phylogenetic markers in Ustilaginomycetes. Mycologia, 2000, 92, 510-521.	1.9	104
124	Comparison of AFLP Fingerprints and ITS Sequences as Phylogenetic Markers in Ustilaginomycetes. Mycologia, 2000, 92, 510.	1.9	83
125	Growth and development: Signals and their transduction. Current Opinion in Microbiology, 2000, 3, 549-552.	5.1	1
126	Triggers and targets of cAMP signalling. Trends in Microbiology, 2000, 8, 302.	7.7	5

#	Article	IF	Citations
127	Response from Kronstad. Trends in Microbiology, 2000, 8, 303.	7.7	0
128	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
129	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
130	Virulence and cAMP in smuts, blasts and blights. Trends in Plant Science, 1997, 2, 193-199.	8.8	95
131	Purification and characterization of phenylalanine ammonia-lyase from Ustilago maydis. Phytochemistry, 1996, 43, 351-357.	2.9	37
132	The Pheromone Cell Signaling Components of the Ustilago a Mating-Type Loci Determine Intercompatibility Between Species. Genetics, 1996, 143, 1601-1613.	2.9	44
133	Heterozygosity at the b mating-type locus attenuates fusion in Ustilago maydis. Current Genetics, 1995, 27, 451-459.	1.7	39
134	Control of filamentous growth by mating and cyclic-AMP inUstilago. Canadian Journal of Botany, 1995, 73, 258-265.	1.1	4
135	Three selectable markers for transformation of Ustilago maydis. Gene, 1994, 142, 225-230.	2.2	49
136	Conservation of the b Mating-Type Gene Complex among Bipolar and Tetrapolar Smut Fungi. Plant Cell, 1993, 5, 123.	6.6	1
137	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
138	A yeast operator overlaps an upstream activation site. Cell, 1987, 50, 369-377.	28.9	216
139	Three classes of homologous Bacillus thuringiensis crystal-protein genes. Gene, 1986, 43, 29-40.	2.2	133
140	History of the Mating Types in<i>Ustilago maydis</i>. , 0, , 349-375.		5
141	Mating in the Smut Fungi: From a to b to the Downstream Cascades. , 0, , 377-387.		10
142	Bipolar and Tetrapolar Mating Systems in the Ustilaginales. , 0, , 389-404.		2
143	The Emergence of Cryptococcus gattii Infections on Vancouver Island and Expansion in the Pacific Northwest. , 0, , 313-325.		3
144	The Cryptococcus Genomes: Tools for Comparative Genomics and Expression Analysis. , 0, , 113-126.		2

#	Article	IF	Citations
145	Origin, Evolution, and Extinction of Asexual Fungi: Experimental Tests Using Cryptococcus neoformans. , 0, , 459-475.		0
146	Sex in Natural Populations of Cryptococcus gattii. , 0, , 477-488.		1