

Hiten D Madhani

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.

97
papers

9,454
citations

43
h-index

97
g-index

133
ext. papers

10,689
ext. citations

20.8
avg, IF

6.26
L-index

#	Paper	IF	Citations
97	Short homology-directed repair using optimized Cas9 in the pathogen <i>Cryptococcus neoformans</i> enables rapid gene deletion and tagging. <i>Genetics</i> , 2021 ,	4	1
96	Re-emerging Aspartic Protease Targets: Examining Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 6706-6719	8.3	4
95	Unbelievable but True: Epigenetics and Chromatin in Fungi. <i>Trends in Genetics</i> , 2021 , 37, 12-20	8.5	5
94	Coupling of spliceosome complexity to intron diversity. <i>Current Biology</i> , 2021 , 31, 4898-4910.e4	6.3	2
93	Cholesterol in quarantine. <i>Nature Immunology</i> , 2020 , 21, 716-717	19.1	5
92	Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. <i>Nucleic Acids Research</i> , 2020 , 48, 2312-2331	20.1	15
91	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. <i>Cell</i> , 2020 , 180, 263-277.e20	56.2	46
90	ATP Hydrolysis by the SNF2 Domain of Dnmt5 Is Coupled to Both Specific Recognition and Modification of Hemimethylated DNA. <i>Molecular Cell</i> , 2020 , 79, 127-139.e4	17.6	3
89	Coordinate genomic association of transcription factors controlled by an imported quorum sensing peptide in <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2020 , 16, e1008744	6	4
88	A natural histone H2A variant lacking the Bub1 phosphorylation site and regulated depletion of centromeric histone CENP-A foster evolvability in <i>Candida albicans</i> . <i>PLoS Biology</i> , 2019 , 17, e3000331	9.7	10
87	A Non-Dicer RNase III and Four Other Novel Factors Required for RNAi-Mediated Transposon Suppression in the Human Pathogenic Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2235-2244	3.2	11
86	Genome-wide analysis of the regulation of Cu metabolism in <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2018 , 108, 473-494	4.1	19
85	Total RNA Isolation and Quantification of Specific RNAs in Fission Yeast. <i>Methods in Molecular Biology</i> , 2018 , 1721, 63-72	1.4	8
84	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. <i>Cell</i> , 2018 , 173, 1014-1030.e17	56.2	27
83	Ten principles of heterochromatin formation and function. <i>Nature Reviews Molecular Cell Biology</i> , 2018 , 19, 229-244	48.7	286
82	Extending chemical perturbations of the ubiquitin fitness landscape in a classroom setting reveals new constraints on sequence tolerance. <i>Biology Open</i> , 2018 , 7,	2.2	11
81	Real-Time Genetic Compensation Defines the Dynamic Demands of Feedback Control. <i>Cell</i> , 2018 , 175, 877-886.e10	56.2	34

80	Polymerase pausing induced by sequence-specific RNA-binding protein drives heterochromatin assembly. <i>Genes and Development</i> , 2018 , 32, 953-964	12.6	21
79	Phospho-site mutants of the RNA Polymerase II C-terminal domain alter subtelomeric gene expression and chromatin modification state in fission yeast. <i>Nucleic Acids Research</i> , 2016 , 44, 9180-9189 ^{20.1}	7	
78	Integrated Activity and Genetic Profiling of Secreted Peptidases in <i>Cryptococcus neoformans</i> Reveals an Aspartyl Peptidase Required for Low pH Survival and Virulence. <i>PLoS Pathogens</i> , 2016 , 12, e1006051	7.6	19
77	Sensitive and Quantitative Three-Color Protein Imaging in Fission Yeast Using Spectrally Diverse, Recoded Fluorescent Proteins with Experimentally-Characterized In Vivo Maturation Kinetics. <i>PLoS ONE</i> , 2016 , 11, e0159292	3.7	7
76	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016 , 19, 849-64	23.4	59
75	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015 , 6, 7121	17.4	56
74	Noncanonical signal recognition particle RNAs in a major eukaryotic phylum revealed by purification of SRP from the human pathogen <i>Cryptococcus neoformans</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 9017-27	20.1	4
73	Intrinsic Toxicity of Unchecked Heterochromatin Spread Is Suppressed by Redundant Chromatin Boundary Functions in <i>Schizosaccharomyces pombe</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1453-61	3.2	9
72	Product binding enforces the genomic specificity of a yeast polycomb repressive complex. <i>Cell</i> , 2015 , 160, 204-18	56.2	96
71	Functional profiling of human fungal pathogen genomes. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2014 , 5, a019596	5.4	6
70	Recognizing the enemy within: licensing RNA-guided genome defense. <i>Trends in Biochemical Sciences</i> , 2014 , 39, 25-34	10.3	24
69	Estrogen receptor antagonists are anti-cryptococcal agents that directly bind EF hand proteins and synergize with fluconazole in vivo. <i>MBio</i> , 2014 , 5, e00765-13	7.8	72
68	Unraveling the biology of a fungal meningitis pathogen using chemical genetics. <i>Cell</i> , 2014 , 159, 1168-1187	38.2	46
67	Division of labor between the chromodomains of HP1 and Suv39 methylase enables coordination of heterochromatin spread. <i>Molecular Cell</i> , 2013 , 51, 80-91	17.6	92
66	The frustrated gene: origins of eukaryotic gene expression. <i>Cell</i> , 2013 , 155, 744-9	56.2	30
65	snRNA catalyzes in the spliceosome's ancient core. <i>Cell</i> , 2013 , 155, 1213-5	56.2	4
64	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013 , 496, 377-81	50.4	107
63	Stalled spliceosomes are a signal for RNAi-mediated genome defense. <i>Cell</i> , 2013 , 152, 957-68	56.2	124

62	The spliceosome as a transposon sensor. <i>RNA Biology</i> , 2013 , 10, 1653-60	4.8	10
61	A conserved ncRNA-binding protein recruits silencing factors to heterochromatin through an RNAi-independent mechanism. <i>Genes and Development</i> , 2013 , 27, 1851-6	12.6	37
60	Timing of transcriptional quiescence during gametogenesis is controlled by global histone H3K4 demethylation. <i>Developmental Cell</i> , 2012 , 23, 1059-71	10.2	23
59	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. <i>EMBO Reports</i> , 2012 , 13, 619-30	6.5	38
58	Approaching the functional annotation of fungal virulence factors using cross-species genetic interaction profiling. <i>PLoS Genetics</i> , 2012 , 8, e1003168	6	9
57	Ers1 links HP1 to RNAi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 11258-63	11.5	19
56	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. <i>EMBO Reports</i> , 2012 , 13, 1152-1152	6.5	78
55	Quorum sensing in fungi: Q&A. <i>PLoS Pathogens</i> , 2011 , 7, e1002301	7.6	18
54	The Cul4-Ddb1(Cdt) ubiquitin ligase inhibits invasion of a boundary-associated antisilencing factor into heterochromatin. <i>Cell</i> , 2011 , 144, 41-54	56.2	71
53	A major role for capsule-independent phagocytosis-inhibitory mechanisms in mammalian infection by <i>Cryptococcus neoformans</i> . <i>Cell Host and Microbe</i> , 2011 , 9, 243-251	23.4	62
52	Can a systems perspective help us appreciate the biological meaning of small effects?. <i>Developmental Cell</i> , 2011 , 21, 11-3	10.2	1
51	Chromodomain-mediated oligomerization of HP1 suggests a nucleosome-bridging mechanism for heterochromatin assembly. <i>Molecular Cell</i> , 2011 , 41, 67-81	17.6	214
50	Spt6 is required for heterochromatic silencing in the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 2011 , 31, 4193-204	4.8	29
49	Site-specific acetylation mark on an essential chromatin-remodeling complex promotes resistance to replication stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10620-5	11.5	16
48	Coordinate control of gene expression noise and interchromosomal interactions in a MAP kinase pathway. <i>Nature Cell Biology</i> , 2010 , 12, 954-62	23.4	49
47	Combinatorial, site-specific requirement for heterochromatic silencing factors in the elimination of nucleosome-free regions. <i>Genes and Development</i> , 2010 , 24, 1758-71	12.6	43
46	Multisite phosphorylation of the <i>Saccharomyces cerevisiae</i> filamentous growth regulator Tec1 is required for its recognition by the E3 ubiquitin ligase adaptor Cdc4 and its subsequent destruction in vivo. <i>Eukaryotic Cell</i> , 2010 , 9, 31-6		14
45	Applying genetics and molecular biology to the study of the human pathogen <i>Cryptococcus neoformans</i> . <i>Methods in Enzymology</i> , 2010 , 470, 797-831	1.7	37

44	Ctr2 links copper homeostasis to polysaccharide capsule formation and phagocytosis inhibition in the human fungal pathogen <i>Cryptococcus neoformans</i> . <i>PLoS ONE</i> , 2010 , 5, e12503	3.7	45
43	Hog1 mitogen-activated protein kinase (MAPK) interrupts signal transduction between the Kss1 MAPK and the Tec1 transcription factor to maintain pathway specificity. <i>Eukaryotic Cell</i> , 2009 , 8, 606-16		39
42	Nonredundant requirement for multiple histone modifications for the early anaphase release of the mitotic exit regulator Cdc14 from nucleolar chromatin. <i>PLoS Genetics</i> , 2009 , 5, e1000588	6	16
41	Mechanisms that specify promoter nucleosome location and identity. <i>Cell</i> , 2009 , 137, 445-58	56.2	311
40	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008 , 5, 711-8	21.6	376
39	Histone Variant H2A.Z Marks the 5' Ends of Both Active and Inactive Genes in Euchromatin. <i>Cell</i> , 2008 , 134, 188	56.2	2
38	Systematic genetic analysis of virulence in the human fungal pathogen <i>Cryptococcus neoformans</i> . <i>Cell</i> , 2008 , 135, 174-88	56.2	313
37	Ers1, a rapidly diverging protein essential for RNA interference-dependent heterochromatic silencing in <i>Schizosaccharomyces pombe</i> . <i>Journal of Biological Chemistry</i> , 2008 , 283, 25770-3	5.4	15
36	Genomewide screen for negative regulators of sirtuin activity in <i>Saccharomyces cerevisiae</i> reveals 40 loci and links to metabolism. <i>Genetics</i> , 2008 , 179, 1933-44	4	15
35	Epigenomics: a roadmap, but to where?. <i>Science</i> , 2008 , 322, 43-4	33.3	25
34	Optimizing TiO ₂ -based phosphopeptide enrichment for automated multidimensional liquid chromatography coupled to tandem mass spectrometry. <i>Analytical Chemistry</i> , 2007 , 79, 4666-73	7.8	121
33	Exploration of whole-genome responses of the human AIDS-associated yeast pathogen <i>Cryptococcus neoformans</i> var <i>grubii</i> : nitric oxide stress and body temperature. <i>Current Genetics</i> , 2007 , 52, 137-48	2.9	44
32	Histone H3 lysine 36 methylation antagonizes silencing in <i>Saccharomyces cerevisiae</i> independently of the Rpd3S histone deacetylase complex. <i>Genetics</i> , 2007 , 175, 585-93	4	42
31	Genome-wide, as opposed to local, antisilencing is mediated redundantly by the euchromatic factors Set1 and H2A.Z. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 16609-14	11.5	100
30	A link between virulence and homeostatic responses to hypoxia during infection by the human fungal pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Pathogens</i> , 2007 , 3, e22	7.6	145
29	Parallel beta-helix proteins required for accurate capsule polysaccharide synthesis and virulence in the yeast <i>Cryptococcus neoformans</i> . <i>Eukaryotic Cell</i> , 2007 , 6, 630-40		19
28	Control of MAPK signaling specificity by a conserved residue in the MEK-binding domain of the yeast scaffold protein Ste5. <i>Current Genetics</i> , 2006 , 49, 351-63	2.9	14
27	Patterning chromatin: form and function for H2A.Z variant nucleosomes. <i>Current Opinion in Genetics and Development</i> , 2006 , 16, 119-24	4.9	89

26	Functional analysis of protein kinase networks in living cells: beyond "knock-outs" and "knock-downs". <i>Methods</i> , 2006 , 40, 251-4	4.6	7
25	Selective kinase inhibition by exploiting differential pathway sensitivity. <i>Chemistry and Biology</i> , 2006 , 13, 399-407		19
24	H2A.Z marks the 5' ends of both active and inactive genes in euchromatin. <i>FASEB Journal</i> , 2006 , 20, A466.9		
23	Histone variant H2A.Z marks the 5' ends of both active and inactive genes in euchromatin. <i>Cell</i> , 2005 , 123, 233-48	56.2	527
22	Chemical genomic profiling to identify intracellular targets of a multiplex kinase inhibitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 3587-92	11.5	50
21	Principles of MAP kinase signaling specificity in <i>Saccharomyces cerevisiae</i> . <i>Annual Review of Genetics</i> , 2004 , 38, 725-48	14.5	208
20	Pheromone-dependent destruction of the Tec1 transcription factor is required for MAP kinase signaling specificity in yeast. <i>Cell</i> , 2004 , 119, 991-1000	56.2	113
19	A protein complex containing the conserved Swi2/Snf2-related ATPase Swr1p deposits histone variant H2A.Z into euchromatin. <i>PLoS Biology</i> , 2004 , 2, E131	9.7	453
18	Conserved histone variant H2A.Z protects euchromatin from the ectopic spread of silent heterochromatin. <i>Cell</i> , 2003 , 112, 725-36	56.2	501
17	A conserved RING finger protein required for histone H2B monoubiquitination and cell size control. <i>Molecular Cell</i> , 2003 , 11, 261-6	17.6	341
16	Unconventional Rac-GEF activity is mediated through the Dock180-ELMO complex. <i>Nature Cell Biology</i> , 2002 , 4, 574-82	23.4	476
15	Accounting for specificity in receptor tyrosine kinase signaling. <i>Cell</i> , 2001 , 106, 9-11	56.2	31
14	Interplay of intrinsic and extrinsic signals in yeast differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 13461-3	11.5	19
13	Effectors of a developmental mitogen-activated protein kinase cascade revealed by expression signatures of signaling mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 12530-5	11.5	167
12	The riddle of MAP kinase signaling specificity. <i>Trends in Genetics</i> , 1998 , 14, 151-5	8.5	256
11	The control of filamentous differentiation and virulence in fungi. <i>Trends in Cell Biology</i> , 1998 , 8, 348-53	18.3	238
10	Combinatorial control required for the specificity of yeast MAPK signaling. <i>Science</i> , 1997 , 275, 1314-7	33.3	343
9	MAP kinases with distinct inhibitory functions impart signaling specificity during yeast differentiation. <i>Cell</i> , 1997 , 91, 673-84	56.2	385

8	Dynamic RNA-RNA interactions in the spliceosome. <i>Annual Review of Genetics</i> , 1994 , 28, 1-26	14.5	330
7	A novel base-pairing interaction between U2 and U6 snRNAs suggests a mechanism for the catalytic activation of the spliceosome. <i>Cell</i> , 1992 , 71, 803-17	56.2	395
6	Signals for ribosomal frameshifting in the Rous sarcoma virus gag-pol region. <i>Cell</i> , 1988 , 55, 447-58	56.2	546
5	Differential DNA repair in transcriptionally active and inactive proto-oncogenes: c-abl and c-mos. <i>Cell</i> , 1986 , 45, 417-23	56.2	190
4	Evolutionary persistence of DNA methylation for millions of years after ancient loss of a de novo methyltransferase		
3	Real time genetic compensation operationally defines the dynamic demands of feedback control		1
2	A non-Dicer RNase III and four other novel factors required for RNAi-mediated transposon suppression in the human pathogenic yeast <i>C. neoformans</i>		1
1	Start codon context controls translation initiation in the fungal kingdom		1