

# Hiten D Madhani

## List of Publications by Year in descending order

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96  
papers

11,363  
citations

57631

44  
h-index

38300

95  
g-index

133  
all docs

133  
docs citations

133  
times ranked

10724  
citing authors

#	ARTICLE	IF	CITATIONS
1	Signals for ribosomal frameshifting in the rous sarcoma virus gag-pol region. <i>Cell</i> , 1988, 55, 447-458.	13.5	647
2	Histone Variant H2A.Z Marks the 5' Ends of Both Active and Inactive Genes in Euchromatin. <i>Cell</i> , 2005, 123, 233-248.	13.5	601
3	Conserved Histone Variant H2A.Z Protects Euchromatin from the Ectopic Spread of Silent Heterochromatin. <i>Cell</i> , 2003, 112, 725-736.	13.5	553
4	Ten principles of heterochromatin formation and function. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 229-244.	16.1	523
5	Unconventional Rac-GEF activity is mediated through the Dock180-ELMO complex. <i>Nature Cell Biology</i> , 2002, 4, 574-582.	4.6	522
6	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.	2.6	512
7	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. <i>Nature Methods</i> , 2008, 5, 711-718.	9.0	473
8	MAP Kinases with Distinct Inhibitory Functions Impart Signaling Specificity during Yeast Differentiation. <i>Cell</i> , 1997, 91, 673-684.	13.5	438
9	Systematic Genetic Analysis of Virulence in the Human Fungal Pathogen <i>Cryptococcus neoformans</i> . <i>Cell</i> , 2008, 135, 174-188.	13.5	418
10	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, 803-817.	13.5	414
11	A Conserved RING Finger Protein Required for Histone H2B Monoubiquitination and Cell Size Control. <i>Molecular Cell</i> , 2003, 11, 261-266.	4.5	413
12	Combinatorial Control Required for the Specificity of Yeast MAPK Signaling. <i>Science</i> , 1997, 275, 1314-1317.	6.0	399
13	Mechanisms that Specify Promoter Nucleosome Location and Identity. <i>Cell</i> , 2009, 137, 445-458.	13.5	376
14	Dynamic RNA-RNA Interactions in the Spliceosome. <i>Annual Review of Genetics</i> , 1994, 28, 1-26.	3.2	359
15	The riddle of MAP kinase signaling specificity. <i>Trends in Genetics</i> , 1998, 14, 151-155.	2.9	292
16	The control of filamentous differentiation and virulence in fungi. <i>Trends in Cell Biology</i> , 1998, 8, 348-353.	3.6	269
17	Chromodomain-Mediated Oligomerization of HP1 Suggests a Nucleosome-Bridging Mechanism for Heterochromatin Assembly. <i>Molecular Cell</i> , 2011, 41, 67-81.	4.5	262
18	Principles of MAP Kinase Signaling Specificity in <i>Saccharomyces cerevisiae</i> . <i>Annual Review of Genetics</i> , 2004, 38, 725-748.	3.2	222

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19	Differential DNA repair in transcriptionally active and inactive proto-oncogenes: c-abl and c-mos. <i>Cell</i> , 1986, 45, 417-423.	13.5	198
20	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, 12530-12535.	3.3	181
21	Stalled Spliceosomes Are a Signal for RNAi-Mediated Genome Defense. <i>Cell</i> , 2013, 152, 957-968.	13.5	173
22	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.	2.1	159
23	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. <i>Nature</i> , 2013, 496, 377-381.	13.7	141
24	Pheromone-Dependent Destruction of the Tec1 Transcription Factor Is Required for MAP Kinase Signaling Specificity in Yeast. <i>Cell</i> , 2004, 119, 991-1000.	13.5	138
25	Optimizing TiO <sub>2</sub> -Based Phosphopeptide Enrichment for Automated Multidimensional Liquid Chromatography Coupled to Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2007, 79, 4666-4673.	3.2	132
26	Division of Labor between the Chromodomains of HP1 and Suv39 Methylase Enables Coordination of Heterochromatin Spread. <i>Molecular Cell</i> , 2013, 51, 80-91.	4.5	125
27	Product Binding Enforces the Genomic Specificity of a Yeast Polycomb Repressive Complex. <i>Cell</i> , 2015, 160, 204-218.	13.5	124
28	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, 16609-16614.	3.3	112
29	Patterning chromatin: form and function for H2A.Z variant nucleosomes. <i>Current Opinion in Genetics and Development</i> , 2006, 16, 119-124.	1.5	95
30	The Cul4-Ddb1Cdt2 Ubiquitin Ligase Inhibits Invasion of a Boundary-Associated Antisilencing Factor into Heterochromatin. <i>Cell</i> , 2011, 144, 41-54.	13.5	93
31	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. <i>Cell Host and Microbe</i> , 2016, 19, 849-864.	5.1	93
32	Estrogen Receptor Antagonists Are Anti-Cryptococcal Agents That Directly Bind EF Hand Proteins and Synergize with Fluconazole <i>In Vivo</i> . <i>MBio</i> , 2014, 5, e00765-13.	1.8	91
33	Contrasting host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. <i>Nature Communications</i> , 2015, 6, 7121.	5.8	90
34	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.	13.5	87
35	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.	5.1	77
36	Unraveling the Biology of a Fungal Meningitis Pathogen Using Chemical Genetics. <i>Cell</i> , 2014, 159, 1168-1187.	13.5	67

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37	Real-Time Genetic Compensation Defines the Dynamic Demands of Feedback Control. <i>Cell</i> , 2018, 175, 877-886.e10.	13.5	67
38	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.	0.4	61
39	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, 3587-3592.	3.3	59
40	Coordinate control of gene expression noise and interchromosomal interactions in a MAP kinase pathway. <i>Nature Cell Biology</i> , 2010, 12, 954-962.	4.6	59
41	Combinatorial, site-specific requirement for heterochromatic silencing factors in the elimination of nucleosome-free regions. <i>Genes and Development</i> , 2010, 24, 1758-1771.	2.7	52
42	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.	1.1	50
43	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, 137-148.	0.8	47
44	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, 606-616.	3.4	47
45	A conserved ncRNA-binding protein recruits silencing factors to heterochromatin through an RNAi-independent mechanism. <i>Genes and Development</i> , 2013, 27, 1851-1856.	2.7	46
46	The Frustrated Gene: Origins of Eukaryotic Gene Expression. <i>Cell</i> , 2013, 155, 744-749.	13.5	45
47	Histone H3 Lysine 36 Methylation Antagonizes Silencing in <i>Saccharomyces cerevisiae</i> Independently of the Rpd3S Histone Deacetylase Complex. <i>Genetics</i> , 2007, 175, 585-593.	1.2	44
48	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. <i>EMBO Reports</i> , 2012, 13, 619-630.	2.0	43
49	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. <i>Cell</i> , 2018, 173, 1014-1030.e17.	13.5	39
50	Spt6 Is Required for Heterochromatic Silencing in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4193-4204.	1.1	37
51	Accounting for Specificity in Receptor Tyrosine Kinase Signaling. <i>Cell</i> , 2001, 106, 9-11.	13.5	36
52	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.	2.1	36
53	Genome-wide analysis of the regulation of Cu metabolism in <i>Cryptococcus neoformans</i> . <i>Molecular Microbiology</i> , 2018, 108, 473-494.	1.2	34
54	Polymerase pausing induced by sequence-specific RNA-binding protein drives heterochromatin assembly. <i>Genes and Development</i> , 2018, 32, 953-964.	2.7	33

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55	Epigenomics: A Roadmap, But to Where?. <i>Science</i> , 2008, 322, 43-44.	6.0	32
56	Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. <i>Nucleic Acids Research</i> , 2020, 48, 2312-2331.	6.5	30
57	Timing of Transcriptional Quiescence during Gametogenesis Is Controlled by Global Histone H3K4 Demethylation. <i>Developmental Cell</i> , 2012, 23, 1059-1071.	3.1	29
58	Ers1 links HP1 to RNAi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11258-11263.	3.3	27
59	Recognizing the enemy within: licensing RNA-guided genome defense. <i>Trends in Biochemical Sciences</i> , 2014, 39, 25-34.	3.7	26
60	Short homology-directed repair using optimized Cas9 in the pathogen <i>Cryptococcus neoformans</i> enables rapid gene deletion and tagging. <i>Genetics</i> , 2022, 220, .	1.2	26
61	Selective Kinase Inhibition by Exploiting Differential Pathway Sensitivity. <i>Chemistry and Biology</i> , 2006, 13, 399-407.	6.2	25
62	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, 13461-13463.	3.3	24
63	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, 630-640.	3.4	23
64	Coupling of spliceosome complexity to intron diversity. <i>Current Biology</i> , 2021, 31, 4898-4910.e4.	1.8	22
65	Quorum Sensing in Fungi: Q&A. <i>PLoS Pathogens</i> , 2011, 7, e1002301.	2.1	21
66	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, 10620-10625.	3.3	20
67	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, 351-363.	0.8	18
68	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, 25770-25773.	1.6	18
69	A Non-Dicer RNase III and Four Other Novel Factors Required for RNAi-Mediated Transposon Suppression in the Human Pathogenic Yeast <i>Cryptococcus neoformans</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2235-2244.	0.8	18
70	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, 1933-1944.	1.2	17
71	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.	1.5	17
72	Total RNA Isolation and Quantification of Specific RNAs in Fission Yeast. <i>Methods in Molecular Biology</i> , 2018, 1721, 63-72.	0.4	17

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73	Extending chemical perturbations of the ubiquitin fitness landscape in a classroom setting reveals new constraints on sequence tolerance. <i>Biology Open</i> , 2018, 7, .	0.6	17
74	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.	1.1	16
75	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.	2.6	16
76	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, 31-36.	3.4	15
77	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.	4.5	15
78	Re-emerging Aspartic Protease Targets: Examining <i>Cryptococcus neoformans</i> Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 6706-6719.	2.9	14
79	The spliceosome as a transposon sensor. <i>RNA Biology</i> , 2013, 10, 1653-1660.	1.5	13
80	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, 1453-1461.	0.8	13
81	Unbelievable but True: Epigenetics and Chromatin in Fungi. <i>Trends in Genetics</i> , 2021, 37, 12-20.	2.9	13
82	Structural insights into DNMT5-mediated ATP-dependent high-fidelity epigenome maintenance. <i>Molecular Cell</i> , 2022, 82, 1186-1198.e6.	4.5	11
83	Approaching the Functional Annotation of Fungal Virulence Factors Using Cross-Species Genetic Interaction Profiling. <i>PLoS Genetics</i> , 2012, 8, e1003168.	1.5	10
84	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.	1.5	10
85	snRNA Catalysts in the Spliceosome's Ancient Core. <i>Cell</i> , 2013, 155, 1213-1215.	13.5	9
86	Functional Profiling of Human Fungal Pathogen Genomes. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a019596-a019596.	2.9	9
87	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, gkw603.	6.5	9
88	Model organism databases are in jeopardy. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	9
89	Functional analysis of protein kinase networks in living cells: Beyond "knock-outs" and "knock-downs". <i>Methods</i> , 2006, 40, 251-254.	1.9	7
90	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, 9017-9027.	6.5	7

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91	Cholesterol in quarantine. <i>Nature Immunology</i> , 2020, 21, 716-717.	7.0	7
92	Histone Variant H2A.Z Marks the 5' Ends of Both Active and Inactive Genes in Euchromatin. <i>Cell</i> , 2008, 134, 188.	13.5	2
93	Can a Systems Perspective Help Us Appreciate the Biological Meaning of Small Effects?. <i>Developmental Cell</i> , 2011, 21, 11-13.	3.1	2
94	“Pearls” A New Type of Open-Access Educational Resource. <i>PLoS Pathogens</i> , 2009, 5, e1000499.	2.1	1
95	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. <i>EMBO Reports</i> , 2012, 13, 1152-1152.	2.0	0
96	H2A.Z marks the 5' ends of both active and inactive genes in euchromatin. <i>FASEB Journal</i> , 2006, 20, A466.	0.2	0