List of Publications by Year in descending order

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		57758	38395
96	11,363	44	95
papers	citations	h-index	g-index
133	133	133	10724
all docs	docs citations	times ranked	citing authors

ΗΙΤΕΝ Ο ΜΑΠΗΛΝΙ

#	Article	IF	CITATIONS
1	Signals for ribosomal frameshifting in the rous sarcoma virus gag-pol region. Cell, 1988, 55, 447-458.	28.9	647
2	Histone Variant H2A.Z Marks the 5′ Ends of Both Active and Inactive Genes in Euchromatin. Cell, 2005, 123, 233-248.	28.9	601
3	Conserved Histone Variant H2A.Z Protects Euchromatin from the Ectopic Spread of Silent Heterochromatin. Cell, 2003, 112, 725-736.	28.9	553
4	Ten principles of heterochromatin formation and function. Nature Reviews Molecular Cell Biology, 2018, 19, 229-244.	37.0	523
5	Unconventional Rac-GEF activity is mediated through the Dock180–ELMO complex. Nature Cell Biology, 2002, 4, 574-582.	10.3	522
6	A Protein Complex Containing the Conserved Swi2/Snf2-Related ATPase Swr1p Deposits Histone Variant H2A.Z into Euchromatin. PLoS Biology, 2004, 2, e131.	5.6	512
7	A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. Nature Methods, 2008, 5, 711-718.	19.0	473
8	MAP Kinases with Distinct Inhibitory Functions Impart Signaling Specificity during Yeast Differentiation. Cell, 1997, 91, 673-684.	28.9	438
9	Systematic Genetic Analysis of Virulence in the Human Fungal Pathogen Cryptococcus neoformans. Cell, 2008, 135, 174-188.	28.9	418
10	A novel base-pairing interaction between U2 and U6 snRNAs suggests a mechanism for the catalytic activation of the spliceosome. Cell, 1992, 71, 803-817.	28.9	414
11	A Conserved RING Finger Protein Required for Histone H2B Monoubiquitination and Cell Size Control. Molecular Cell, 2003, 11, 261-266.	9.7	413
12	Combinatorial Control Required for the Specificity of Yeast MAPK Signaling. Science, 1997, 275, 1314-1317.	12.6	399
13	Mechanisms that Specify Promoter Nucleosome Location and Identity. Cell, 2009, 137, 445-458.	28.9	376
14	Dynamic RNA-RNA Interactions in the Spliceosome. Annual Review of Genetics, 1994, 28, 1-26.	7.6	359
15	The riddle of MAP kinase signaling specificity. Trends in Genetics, 1998, 14, 151-155.	6.7	292
16	The control of filamentous differentiation and virulence in fungi. Trends in Cell Biology, 1998, 8, 348-353.	7.9	269
17	Chromodomain-Mediated Oligomerization of HP1 Suggests a Nucleosome-Bridging Mechanism for Heterochromatin Assembly. Molecular Cell, 2011, 41, 67-81.	9.7	262
18	Principles of MAP Kinase Signaling Specificity inSaccharomyces cerevisiae. Annual Review of Genetics, 2004, 38, 725-748.	7.6	222

#	Article	IF	CITATIONS
19	Differential DNA repair in transcriptionally active and inactive proto-oncogenes: c-abl and c-mos. Cell, 1986, 45, 417-423.	28.9	198
20	Effectors of a developmental mitogen-activated protein kinase cascade revealed by expression signatures of signaling mutants. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 12530-12535.	7.1	181
21	Stalled Spliceosomes Are a Signal for RNAi-Mediated Genome Defense. Cell, 2013, 152, 957-968.	28.9	173
22	A Link between Virulence and Homeostatic Responses to Hypoxia during Infection by the Human Fungal Pathogen Cryptococcus neoformans. PLoS Pathogens, 2007, 3, e22.	4.7	159
23	A conformational switch in HP1 releases auto-inhibition to drive heterochromatin assembly. Nature, 2013, 496, 377-381.	27.8	141
24	Pheromone-Dependent Destruction of the Tec1 Transcription Factor Is Required for MAP Kinase Signaling Specificity in Yeast. Cell, 2004, 119, 991-1000.	28.9	138
25	Optimizing TiO2-Based Phosphopeptide Enrichment for Automated Multidimensional Liquid Chromatography Coupled to Tandem Mass Spectrometry. Analytical Chemistry, 2007, 79, 4666-4673.	6.5	132
26	Division of Labor between the Chromodomains of HP1 and Suv39 Methylase Enables Coordination of Heterochromatin Spread. Molecular Cell, 2013, 51, 80-91.	9.7	125
27	Product Binding Enforces the Genomic Specificity of a Yeast Polycomb Repressive Complex. Cell, 2015, 160, 204-218.	28.9	124
28	Genome-wide, as opposed to local, antisilencing is mediated redundantly by the euchromatic factors Set1 and H2A.Z. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16609-16614.	7.1	112
29	Patterning chromatin: form and function for H2A.Z variant nucleosomes. Current Opinion in Genetics and Development, 2006, 16, 119-124.	3.3	95
30	The Cul4-Ddb1Cdt2 Ubiquitin Ligase Inhibits Invasion of a Boundary-Associated Antisilencing Factor into Heterochromatin. Cell, 2011, 144, 41-54.	28.9	93
31	Intracellular Action of a Secreted Peptide Required for Fungal Virulence. Cell Host and Microbe, 2016, 19, 849-864.	11.0	93
32	Estrogen Receptor Antagonists Are Anti-Cryptococcal Agents That Directly Bind EF Hand Proteins and Synergize with Fluconazole <i>In Vivo</i> . MBio, 2014, 5, e00765-13.	4.1	91
33	Contrasting host–pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes. Nature Communications, 2015, 6, 7121.	12.8	90
34	Evolutionary Persistence of DNA Methylation for Millions of Years after Ancient Loss of a De Novo Methyltransferase. Cell, 2020, 180, 263-277.e20.	28.9	87
35	A Major Role for Capsule-Independent Phagocytosis-Inhibitory Mechanisms in Mammalian Infection by Cryptococcus neoformans. Cell Host and Microbe, 2011, 9, 243-251.	11.0	77
36	Unraveling the Biology of a Fungal Meningitis Pathogen Using Chemical Genetics. Cell, 2014, 159, 1168-1187.	28.9	67

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37	Real-Time Genetic Compensation Defines the Dynamic Demands of Feedback Control. Cell, 2018, 175, 877-886.e10.	28.9	67
38	Applying Genetics and Molecular Biology to the Study of the Human Pathogen Cryptococcus neoformans. Methods in Enzymology, 2010, 470, 797-831.	1.0	61
39	Chemical genomic profiling to identify intracellular targets of a multiplex kinase inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3587-3592.	7.1	59
40	Coordinate control of gene expression noise and interchromosomal interactions in a MAP kinase pathway. Nature Cell Biology, 2010, 12, 954-962.	10.3	59
41	Combinatorial, site-specific requirement for heterochromatic silencing factors in the elimination of nucleosome-free regions. Genes and Development, 2010, 24, 1758-1771.	5.9	52
42	Ctr2 Links Copper Homeostasis to Polysaccharide Capsule Formation and Phagocytosis Inhibition in the Human Fungal Pathogen Cryptococcus neoformans. PLoS ONE, 2010, 5, e12503.	2.5	50
43	Exploration of whole-genome responses of the human AIDS-associated yeast pathogen Cryptococcus neoformans var grubii: nitric oxide stress and body temperature. Current Genetics, 2007, 52, 137-148.	1.7	47
44	Hog1 Mitogen-Activated Protein Kinase (MAPK) Interrupts Signal Transduction between the Kss1 MAPK and the Tec1 Transcription Factor To Maintain Pathway Specificity. Eukaryotic Cell, 2009, 8, 606-616.	3.4	47
45	A conserved ncRNA-binding protein recruits silencing factors to heterochromatin through an RNAi-independent mechanism. Genes and Development, 2013, 27, 1851-1856.	5.9	46
46	The Frustrated Gene: Origins of Eukaryotic Gene Expression. Cell, 2013, 155, 744-749.	28.9	45
47	Histone H3 Lysine 36 Methylation Antagonizes Silencing in Saccharomyces cerevisiae Independently of the Rpd3S Histone Deacetylase Complex. Genetics, 2007, 175, 585-593.	2.9	44
48	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. EMBO Reports, 2012, 13, 619-630.	4.5	43
49	Spliceosome Profiling Visualizes Operations of a Dynamic RNP at Nucleotide Resolution. Cell, 2018, 173, 1014-1030.e17.	28.9	39
50	Spt6 Is Required for Heterochromatic Silencing in the Fission Yeast Schizosaccharomyces pombe. Molecular and Cellular Biology, 2011, 31, 4193-4204.	2.3	37
51	Accounting for Specificity in Receptor Tyrosine Kinase Signaling. Cell, 2001, 106, 9-11.	28.9	36
52	Integrated Activity and Genetic Profiling of Secreted Peptidases in Cryptococcus neoformans Reveals an Aspartyl Peptidase Required for Low pH Survival and Virulence. PLoS Pathogens, 2016, 12, e1006051.	4.7	36
53	Genomeâ€wide analysis of the regulation of Cu metabolism in <i>Cryptococcus neoformans</i> . Molecular Microbiology, 2018, 108, 473-494.	2.5	34
54	Polymerase pausing induced by sequence-specific RNA-binding protein drives heterochromatin assembly. Genes and Development, 2018, 32, 953-964.	5.9	33

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55	Epigenomics: A Roadmap, But to Where?. Science, 2008, 322, 43-44.	12.6	32
56	Quantitative global studies reveal differential translational control by start codon context across the fungal kingdom. Nucleic Acids Research, 2020, 48, 2312-2331.	14.5	30
57	Timing of Transcriptional Quiescence during Gametogenesis Is Controlled by Global Histone H3K4 Demethylation. Developmental Cell, 2012, 23, 1059-1071.	7.0	29
58	Ers1 links HP1 to RNAi. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11258-11263.	7.1	27
59	Recognizing the enemy within: licensing RNA-guided genome defense. Trends in Biochemical Sciences, 2014, 39, 25-34.	7.5	26
60	Short homology-directed repair using optimized Cas9 in the pathogen <i>Cryptococcus neoformans</i> enables rapid gene deletion and tagging. Genetics, 2022, 220, .	2.9	26
61	Selective Kinase Inhibition by Exploiting Differential Pathway Sensitivity. Chemistry and Biology, 2006, 13, 399-407.	6.0	25
62	Interplay of intrinsic and extrinsic signals in yeast differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13461-13463.	7.1	24
63	Parallel β-Helix Proteins Required for Accurate Capsule Polysaccharide Synthesis and Virulence in the Yeast Cryptococcus neoformans. Eukaryotic Cell, 2007, 6, 630-640.	3.4	23
64	Coupling of spliceosome complexity to intron diversity. Current Biology, 2021, 31, 4898-4910.e4.	3.9	22
65	Quorum Sensing in Fungi: Q&A. PLoS Pathogens, 2011, 7, e1002301.	4.7	21
66	Site-specific acetylation mark on an essential chromatin-remodeling complex promotes resistance to replication stress. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10620-10625.	7.1	20
67	Control of MAPK signaling specificity by a conserved residue in the MEK-binding domain of the yeast scaffold protein Ste5. Current Genetics, 2006, 49, 351-363.	1.7	18
68	Ers1, a Rapidly Diverging Protein Essential for RNA Interference-dependent Heterochromatic Silencing in Schizosaccharomyces pombe. Journal of Biological Chemistry, 2008, 283, 25770-25773.	3.4	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> . G3: Genes, Genomes, Genetics, 2019, 9, 2235-2244.	1.8	18
70	Genomewide Screen for Negative Regulators of Sirtuin Activity in <i>Saccharomyces cerevisiae</i> Reveals 40 Loci and Links to Metabolism. Genetics, 2008, 179, 1933-1944.	2.9	17
71	Nonredundant Requirement for Multiple Histone Modifications for the Early Anaphase Release of the Mitotic Exit Regulator Cdc14 from Nucleolar Chromatin. PLoS Genetics, 2009, 5, e1000588.	3.5	17
72	Total RNA Isolation and Quantification of Specific RNAs in Fission Yeast. Methods in Molecular Biology, 2018, 1721, 63-72.	0.9	17

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73	Extending chemical perturbations of the ubiquitin fitness landscape in a classroom setting reveals new constraints on sequence tolerance. Biology Open, 2018, 7, .	1.2	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. PLoS ONE, 2016, 11, e0159292.	2.5	16
75	A natural histone H2A variant lacking the Bub1 phosphorylation site and regulated depletion of centromeric histone CENP-A foster evolvability in Candida albicans. PLoS Biology, 2019, 17, e3000331.	5.6	16
76	Multisite Phosphorylation of the Saccharomyces cerevisiae Filamentous Growth Regulator Tec1 Is Required for its Recognition by the E3 Ubiquitin Ligase Adaptor Cdc4 and Its Subsequent Destruction In Vivo. Eukaryotic Cell, 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. Molecular Cell, 2020, 79, 127-139.e4.	9.7	15
78	Re-emerging Aspartic Protease Targets: Examining <i>Cryptococcus neoformans</i> Major Aspartyl Peptidase 1 as a Target for Antifungal Drug Discovery. Journal of Medicinal Chemistry, 2021, 64, 6706-6719.	6.4	14
79	The spliceosome as a transposon sensor. RNA Biology, 2013, 10, 1653-1660.	3.1	13
80	Intrinsic Toxicity of Unchecked Heterochromatin Spread Is Suppressed by Redundant Chromatin Boundary Functions in <i>Schizosacchromyces pombe</i> . G3: Genes, Genomes, Genetics, 2015, 5, 1453-1461.	1.8	13
81	Unbelievable but True: Epigenetics and Chromatin in Fungi. Trends in Genetics, 2021, 37, 12-20.	6.7	13
82	Structural insights into DNMT5-mediated ATP-dependent high-fidelity epigenome maintenance. Molecular Cell, 2022, 82, 1186-1198.e6.	9.7	11
83	Approaching the Functional Annotation of Fungal Virulence Factors Using Cross-Species Genetic Interaction Profiling. PLoS Genetics, 2012, 8, e1003168.	3.5	10
84	Coordinate genomic association of transcription factors controlled by an imported quorum sensing peptide in Cryptococcus neoformans. PLoS Genetics, 2020, 16, e1008744.	3.5	10
85	snRNA Catalysts in the Spliceosome's Ancient Core. Cell, 2013, 155, 1213-1215.	28.9	9
86	Functional Profiling of Human Fungal Pathogen Genomes. Cold Spring Harbor Perspectives in Medicine, 2015, 5, a019596-a019596.	6.2	9
87	Phospho-site mutants of the RNA Polymerase II C-terminal domain alter subtelomeric gene expression and chromatin modification state in fission yeast. Nucleic Acids Research, 2016, 44, gkw603.	14.5	9
88	Model organism databases are in jeopardy. Development (Cambridge), 2021, 148, .	2.5	9
89	Functional analysis of protein kinase networks in living cells: Beyond "knock-outs―and "knock-downs― Methods, 2006, 40, 251-254.	3.8	7
90	Noncanoncial signal recognition particle RNAs in a major eukaryotic phylum revealed by purification of SRP from the human pathogenCryptococcus neoformans. Nucleic Acids Research, 2015, 43, 9017-9027.	14.5	7

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91	Cholesterol in quarantine. Nature Immunology, 2020, 21, 716-717.	14.5	7
92	Histone Variant H2A.Z Marks the 5′ Ends of Both Active and Inactive Genes in Euchromatin. Cell, 2008, 134, 188.	28.9	2
93	Can a Systems Perspective Help Us Appreciate the Biological Meaning of Small Effects?. Developmental Cell, 2011, 21, 11-13.	7.0	2
94	"Pearlsâ€: A New Type of Open-Access Educational Resource. PLoS Pathogens, 2009, 5, e1000499.	4.7	1
95	Shaping the landscape: mechanistic consequences of ubiquitin modification of chromatin. EMBO Reports, 2012, 13, 1152-1152.	4.5	0
96	H2A.Z marks the 5′ ends of both active and inactive genes in euchromatin. FASEB Journal, 2006, 20, A466.	0.5	0