

Denes Hnisz

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

15,234
citations

236912

25
h-index

414395

32
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37
all docs

37
docs citations

37
times ranked

21116
citing authors

#	ARTICLE	IF	CITATIONS
1	Master Transcription Factors and Mediator Establish Super-Enhancers at Key Cell Identity Genes. <i>Cell</i> , 2013, 153, 307-319.	28.9	3,202
2	Super-Enhancers in the Control of Cell Identity and Disease. <i>Cell</i> , 2013, 155, 934-947.	28.9	2,916
3	Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018, 361, .	12.6	1,687
4	A Phase Separation Model for Transcriptional Control. <i>Cell</i> , 2017, 169, 13-23.	28.9	1,341
5	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016, 351, 1454-1458.	12.6	880
6	Transcriptional Addiction in Cancer. <i>Cell</i> , 2017, 168, 629-643.	28.9	843
7	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	28.9	793
8	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017, 171, 1573-1588.e28.	28.9	749
9	Convergence of Developmental and Oncogenic Signaling Pathways at Transcriptional Super-Enhancers. <i>Molecular Cell</i> , 2015, 58, 362-370.	9.7	382
10	Insulated Neighborhoods: Structural and Functional Units of Mammalian Gene Control. <i>Cell</i> , 2016, 167, 1188-1200.	28.9	373
11	3D Chromosome Regulatory Landscape of Human Pluripotent Cells. <i>Cell Stem Cell</i> , 2016, 18, 262-275.	11.1	369
12	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018, 172, 979-992.e6.	28.9	351
13	Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016, 48, 1253-1259.	21.4	265
14	Transcriptional Dysregulation of MYC Reveals Common Enhancer-Docking Mechanism. <i>Cell Reports</i> , 2018, 23, 349-360.	6.4	144
15	Unblending of Transcriptional Condensates in Human Repeat Expansion Disease. <i>Cell</i> , 2020, 181, 1062-1079.e30.	28.9	115
16	The Set3/Hos2 Histone Deacetylase Complex Attenuates cAMP/PKA Signaling to Regulate Morphogenesis and Virulence of <i>Candida albicans</i> . <i>PLoS Pathogens</i> , 2010, 6, e1000889.	4.7	99
17	Transcriptional loops meet chromatin: a dual-layer network controls white-opaque switching in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2009, 74, 1-15.	2.5	91
18	Integration of multiomics data with graph convolutional networks to identify new cancer genes and their associated molecular mechanisms. <i>Nature Machine Intelligence</i> , 2021, 3, 513-526.	16.0	91

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19	A Histone Deacetylase Adjusts Transcription Kinetics at Coding Sequences during <i>Candida albicans</i> Morphogenesis. <i>PLoS Genetics</i> , 2012, 8, e1003118.	3.5	88
20	Selective Mediator dependence of cell-type-specifying transcription. <i>Nature Genetics</i> , 2020, 52, 719-727.	21.4	84
21	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385.	12.8	76
22	A Histone Deacetylase Complex Mediates Biofilm Dispersal and Drug Resistance in <i>Candida albicans</i> . <i>MBio</i> , 2014, 5, e01201-14.	4.1	70
23	TNF α shedding and epidermal inflammation are controlled by Jun proteins. <i>Genes and Development</i> , 2009, 23, 2663-2674.	5.9	64
24	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10.	16.8	49
25	The histone acetyltransferase <i>Hat1</i> facilitates DNA damage repair and morphogenesis in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2012, 86, 1197-1214.	2.5	42
26	Regulation and Dysregulation of Chromosome Structure in Cancer. <i>Annual Review of Cancer Biology</i> , 2018, 2, 21-40.	4.5	26
27	Graph Convolutional Networks Improve the Prediction of Cancer Driver Genes. <i>Lecture Notes in Computer Science</i> , 2019, , 658-668.	1.3	17
28	Targeting chromatin in fungal pathogens as a novel therapeutic strategy: histone modification gets infectious. <i>Epigenomics</i> , 2011, 3, 129-132.	2.1	10
29	New Insights into Genome Structure: Genes of a Feather Stick Together. <i>Molecular Cell</i> , 2017, 67, 730-731.	9.7	9
30	Morphological and Molecular Genetic Analysis of Epigenetic Switching of the Human Fungal Pathogen <i>Candida albicans</i> . <i>Methods in Molecular Biology</i> , 2011, 734, 303-315.	0.9	5
31	STAG2 Mutations Alter Cohesin Ring Function and Provide Therapeutic Vulnerabilities in Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 940-940.	1.4	1
32	Abstract PR14: Nucleation of transcriptional super-enhancers at tumor oncogenes. , 2015, , .		0
33	Abstract PR06: Nucleation of transcriptional super-enhancers at tumor oncogenes. , 2015, , .		0
34	Abstract 2004: Nucleation of transcriptional super-enhancers at tumor oncogenes by small insertions. , 2016, , .		0
35	Abstract 971: Three-dimensional gene regulatory landscapes in normal and cancer cells. , 2018, , .		0