

Brian J Abraham

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

19,161
citations

66234

42
h-index

114278

63
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68
all docs

68
docs citations

68
times ranked

25386
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.	13.5	3,202
2	Super-Enhancers in the Control of Cell Identity and Disease. <i>Cell</i> , 2013, 155, 934-947.	13.5	2,916
3	Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018, 361, .	6.0	1,687
4	Transcription Factors Activate Genes through the Phase-Separation Capacity of Their Activation Domains. <i>Cell</i> , 2018, 175, 1842-1855.e16.	13.5	1,195
5	Control of Cell Identity Genes Occurs in Insulated Neighborhoods in Mammalian Chromosomes. <i>Cell</i> , 2014, 159, 374-387.	13.5	793
6	YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017, 171, 1573-1588.e28.	13.5	749
7	Targeting transcription regulation in cancer with a covalent CDK7 inhibitor. <i>Nature</i> , 2014, 511, 616-620.	13.7	698
8	An oncogenic super-enhancer formed through somatic mutation of a noncoding intergenic element. <i>Science</i> , 2014, 346, 1373-1377.	6.0	665
9	CDK7 Inhibition Suppresses Super-Enhancer-Linked Oncogenic Transcription in MYCN-Driven Cancer. <i>Cell</i> , 2014, 159, 1126-1139.	13.5	498
10	Parkinson-associated risk variant in distal enhancer of α -synuclein modulates target gene expression. <i>Nature</i> , 2016, 533, 95-99.	13.7	466
11	PolII phosphorylation regulates a switch between transcriptional and splicing condensates. <i>Nature</i> , 2019, 572, 543-548.	13.7	457
12	Transcription factor trapping by RNA in gene regulatory elements. <i>Science</i> , 2015, 350, 978-981.	6.0	389
13	Convergence of Developmental and Oncogenic Signaling Pathways at Transcriptional Super-Enhancers. <i>Molecular Cell</i> , 2015, 58, 362-370.	4.5	382
14	Targeting Transcriptional Addictions in Small Cell Lung Cancer with a Covalent CDK7 Inhibitor. <i>Cancer Cell</i> , 2014, 26, 909-922.	7.7	376
15	CDK7-Dependent Transcriptional Addiction in Triple-Negative Breast Cancer. <i>Cell</i> , 2015, 163, 174-186.	13.5	346
16	Genome-wide Analyses of Transcription Factor GATA3-Mediated Gene Regulation in Distinct T Cell Types. <i>Immunity</i> , 2011, 35, 299-311.	6.6	293
17	Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016, 48, 1253-1259.	9.4	265
18	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. <i>Nature</i> , 2015, 528, 418-421.	13.7	263

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19	Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016, 12, 876-884.	3.9	249
20	The long noncoding RNA <i>Wisper</i> controls cardiac fibrosis and remodeling. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	232
21	Models of human core transcriptional regulatory circuitries. <i>Genome Research</i> , 2016, 26, 385-396.	2.4	223
22	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	9.4	199
23	Mediator Condensates Localize Signaling Factors to Key Cell Identity Genes. <i>Molecular Cell</i> , 2019, 76, 753-766.e6.	4.5	188
24	<i>MYC</i> Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018, 8, 320-335.	7.7	172
25	A CD47-associated super-enhancer links pro-inflammatory signalling to CD47 upregulation in breast cancer. <i>Nature Communications</i> , 2017, 8, 14802.	5.8	168
26	Integrated genomic analyses of de novo pathways underlying atypical meningiomas. <i>Nature Communications</i> , 2017, 8, 14433.	5.8	156
27	The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. <i>Cell Stem Cell</i> , 2014, 15, 295-309.	5.2	137
28	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. <i>Genome Biology</i> , 2013, 14, R121.	13.9	123
29	Chromatin proteomic profiling reveals novel proteins associated with histone-marked genomic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3841-3846.	3.3	123
30	Cross-Cohort Analysis Identifies a TEAD4-MYC Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. <i>Cancer Discovery</i> , 2018, 8, 582-599.	7.7	119
31	EWS/FLI Confers Tumor Cell Synthetic Lethality to CDK12 Inhibition in Ewing Sarcoma. <i>Cancer Cell</i> , 2018, 33, 202-216.e6.	7.7	116
32	Multiple Structural Maintenance of Chromosome Complexes at Transcriptional Regulatory Elements. <i>Stem Cell Reports</i> , 2013, 1, 371-378.	2.3	113
33	Suppression of Adaptive Responses to Targeted Cancer Therapy by Transcriptional Repression. <i>Cancer Discovery</i> , 2018, 8, 59-73.	7.7	96
34	Novel Mechanism of Positive versus Negative Regulation by Thyroid Hormone Receptor $\beta 1$ (TR $\beta 1$) Identified by Genome-wide Profiling of Binding Sites in Mouse Liver. <i>Journal of Biological Chemistry</i> , 2014, 289, 1313-1328.	1.6	92
35	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385.	5.8	76
36	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. <i>Molecular Cell</i> , 2020, 78, 459-476.e13.	4.5	76

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37	Activation of the p53 Transcriptional Program Sensitizes Cancer Cells to Cdk7 Inhibitors. <i>Cell Reports</i> , 2017, 21, 467-481.	2.9	65
38	EP300 Selectively Controls the Enhancer Landscape of <i>MYCN</i> -Amplified Neuroblastoma. <i>Cancer Discovery</i> , 2022, 12, 730-751.	7.7	64
39	Activation of the LMO2 oncogene through a somatically acquired neomorphic promoter in T-cell acute lymphoblastic leukemia. <i>Blood</i> , 2017, 129, 3221-3226.	0.6	61
40	ASCL1 is a MYCN- and LMO1-dependent member of the adrenergic neuroblastoma core regulatory circuitry. <i>Nature Communications</i> , 2019, 10, 5622.	5.8	56
41	APOBEC signature mutation generates an oncogenic enhancer that drives LMO1 expression in T-ALL. <i>Leukemia</i> , 2017, 31, 2057-2064.	3.3	54
42	TOX Regulates Growth, DNA Repair, and Genomic Instability in T-cell Acute Lymphoblastic Leukemia. <i>Cancer Discovery</i> , 2017, 7, 1336-1353.	7.7	48
43	ARID1A loss in neuroblastoma promotes the adrenergic-to-mesenchymal transition by regulating enhancer-mediated gene expression. <i>Science Advances</i> , 2020, 6, eaaz3440.	4.7	47
44	High MITF Expression Is Associated with Super-Enhancers and Suppressed by CDK7 Inhibition in Melanoma. <i>Journal of Investigative Dermatology</i> , 2018, 138, 1582-1590.	0.3	46
45	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. <i>American Journal of Human Genetics</i> , 2017, 100, 51-63.	2.6	45
46	Dynamic regulation of epigenomic landscapes during hematopoiesis. <i>BMC Genomics</i> , 2013, 14, 193.	1.2	41
47	RNA helicase DDX21 mediates nucleotide stress responses in neural crest and melanoma cells. <i>Nature Cell Biology</i> , 2020, 22, 372-379.	4.6	37
48	O-GlcNAcase Is an RNA Polymerase II Elongation Factor Coupled to Pausing Factors SPT5 and TIF1 ² . <i>Journal of Biological Chemistry</i> , 2016, 291, 22703-22713.	1.6	35
49	LIN28B regulates transcription and potentiates MYCN-induced neuroblastoma through binding to ZNF143 at target gene promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16516-16526.	3.3	31
50	Predicting master transcription factors from pan-cancer expression data. <i>Science Advances</i> , 2021, 7, eabf6123.	4.7	30
51	Cell-specific transcriptional control of mitochondrial metabolism by TIF1 ³ drives erythropoiesis. <i>Science</i> , 2021, 372, 716-721.	6.0	25
52	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	9.4	24
53	JDP2: An oncogenic bZIP transcription factor in T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2018, 215, 1929-1945.	4.2	22
54	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. <i>Science Advances</i> , 2021, 7, eabe0834.	4.7	22

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55	Super-enhancer-based identification of a BATF3/IL-2R α module reveals vulnerabilities in anaplastic large cell lymphoma. <i>Nature Communications</i> , 2021, 12, 5577.	5.8	21
56	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23626-23635.	3.3	18
57	MEIS2 Is an Adrenergic Core Regulatory Transcription Factor Involved in Early Initiation of TH-MYCN-Driven Neuroblastoma Formation. <i>Cancers</i> , 2021, 13, 4783.	1.7	12
58	Intrinsic transcriptional heterogeneity in neuroblastoma guides mechanistic and therapeutic insights. <i>Cell Reports Medicine</i> , 2022, 3, 100632.	3.3	12
59	Synergistic Anti-Tumor Effect of Combining Selective CDK7 and BRD4 Inhibition in Neuroblastoma. <i>Frontiers in Oncology</i> , 2021, 11, 773186.	1.3	11
60	BRD2 interconnects with BRD3 to facilitate Pol II transcription initiation and elongation to prime promoters for cell differentiation. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	9
61	The nuclear receptor THRB facilitates differentiation of human PSCs into more mature hepatocytes. <i>Cell Stem Cell</i> , 2022, 29, 795-809.e11.	5.2	5
62	SEaseq: a portable and cloud-based chromatin occupancy analysis suite. <i>BMC Bioinformatics</i> , 2022, 23, 77.	1.2	3
63	Abstract 2441: CDK12/13 inhibition cooperates with the Ewing sarcoma oncoprotein EWS/FLI to attenuate homologous recombination repair in Ewing sarcoma cells. , 2016, , .		1