

Arthur I Skoultchi

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/46399/publications.pdf>

Version: 2024-02-01

49
papers

5,127
citations

236833

25
h-index

265120

42
g-index

50
all docs

50
docs citations

50
times ranked

7934
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	13.7	155
2	H1 histones control the epigenetic landscape by local chromatin compaction. <i>Nature</i> , 2021, 589, 293-298.	13.7	101
3	The chromatin remodeler Snf2h is essential for oocyte meiotic cell cycle progression. <i>Genes and Development</i> , 2020, 34, 166-178.	2.7	21
4	Single-molecule imaging of transcription dynamics in somatic stem cells. <i>Nature</i> , 2020, 583, 431-436.	13.7	61
5	H1 linker histones silence repetitive elements by promoting both histone H3K9 methylation and chromatin compaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14251-14258.	3.3	57
6	Linker histone H1.2 and H1.4 affect the neutrophil lineage determination. <i>ELife</i> , 2020, 9, .	2.8	12
7	Runx1 promotes murine erythroid progenitor proliferation and inhibits differentiation by preventing Pu.1 downregulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17841-17847.	3.3	18
8	ISWI ATPase Smarca5 Regulates Differentiation of Thymocytes Undergoing \hat{I}^2 -Selection. <i>Journal of Immunology</i> , 2019, 202, 3434-3446.	0.4	10
9	Bidirectional Analysis of Cryba4-Crybb1 Nascent Transcription and Nuclear Accumulation of Crybb3 mRNAs in Lens Fibers. , 2019, 60, 234.		11
10	Histone 1 Mutations Drive Lymphomagenesis By Inducing Primitive Stem Cell Functions and Epigenetic Instructions through Profound 3D Re-Organization of the B-Cell Genome. <i>Blood</i> , 2019, 134, 23-23.	0.6	6
11	Emerging roles of linker histones in regulating chromatin structure and function. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 192-206.	16.1	336
12	The ISWI ATPase Smarca5 (Snf2h) Is Required for Proliferation and Differentiation of Hematopoietic Stem and Progenitor Cells. <i>Stem Cells</i> , 2017, 35, 1614-1623.	1.4	37
13	Regulatory functions and chromatin loading dynamics of linker histone H1 during endoreplication in <i>Drosophila</i> . <i>Genes and Development</i> , 2017, 31, 603-616.	2.7	30
14	Independent Biological and Biochemical Functions for Individual Structural Domains of Drosophila Linker Histone H1. <i>Journal of Biological Chemistry</i> , 2016, 291, 15143-15155.	1.6	11
15	BEN domain protein Elba2 can functionally substitute for linker histone H1 in Drosophila in vivo. <i>Scientific Reports</i> , 2016, 6, 34354.	1.6	4
16	Chromatin remodeling enzyme Snf2h regulates embryonic lens differentiation and denucleation. <i>Development (Cambridge)</i> , 2016, 143, 1937-1947.	1.2	41
17	Local compartment changes and regulatory landscape alterations in histone H1-depleted cells. <i>Genome Biology</i> , 2015, 16, 289.	3.8	56
18	Proteomic Characterization of the Nucleolar Linker Histone H1 Interaction Network. <i>Journal of Molecular Biology</i> , 2015, 427, 2056-2071.	2.0	42

#	ARTICLE	IF	CITATIONS
19	A Genetic Screen and Transcript Profiling Reveal a Shared Regulatory Program for Drosophila Linker Histone H1 and Chromatin Remodeler CHD1. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 677-687.	0.8	4
20	The Role of H1 Linker Histone Subtypes in Preserving the Fidelity of Elaboration of Mesendodermal and Neuroectodermal Lineages during Embryonic Development. <i>PLoS ONE</i> , 2014, 9, e96858.	1.1	6
21	Snf2h-mediated chromatin organization and histone H1 dynamics govern cerebellar morphogenesis and neural maturation. <i>Nature Communications</i> , 2014, 5, 4181.	5.8	71
22	Drosophila linker histone H1 coordinates STAT-dependent organization of heterochromatin and suppresses tumorigenesis caused by hyperactive JAK-STAT signaling. <i>Epigenetics and Chromatin</i> , 2014, 7, 16.	1.8	22
23	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
24	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. <i>Science</i> , 2014, 346, 1007-1012.	6.0	244
25	H1 linker histone promotes epigenetic silencing by regulating both DNA methylation and histone H3 methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 1708-1713.	3.3	99
26	<i>Drosophila</i> H1 Regulates the Genetic Activity of Heterochromatin by Recruitment of Su(var)3-9. <i>Science</i> , 2013, 340, 78-81.	6.0	93
27	The <i>Rhox</i> Homeobox Gene Cluster Is Imprinted and Selectively Targeted for Regulation by Histone H1 and DNA Methylation. <i>Molecular and Cellular Biology</i> , 2011, 31, 1275-1287.	1.1	38
28	Smarca5 Regulates Ctfc Recruitment to Chromatin, Including to Regulatory Loci Involved In Control of Globin Gene Expression In Erythroleukemia. <i>Blood</i> , 2010, 116, 5159-5159.	0.6	0
29	ISWI Chromatin Remodeling ATPase Smarca5 (Snf2h) Is Required for Murine Erythroid Development and Globin Gene Regulation. <i>Blood</i> , 2010, 116, 2062-2062.	0.6	0
30	MicroRNA Mir-155 and Myb Proto-Oncogene Family Members Cooperate in Pathogenesis of Chronic Lymphocytic Leukemia.. <i>Blood</i> , 2009, 114, 58-58.	0.6	3
31	PU.1 Relieves Its GATA-1-Mediated Repression near Cebpa and Cbfb During Transdifferentiation of Murine Erythroleukemia - Tool of Inducing Leukemic Blasts to Differentiate.. <i>Blood</i> , 2009, 114, 547-547.	0.6	5
32	Gata1 Regulates Erythroid Transcription by Cooperating with Chromatin Remodeling Protein Snf2h. <i>Blood</i> , 2008, 112, 4759-4759.	0.6	0
33	Mutual Regulatory Loop between miR-155 and PU.1 Is a Candidate Pathogenesis Factor in CLL.. <i>Blood</i> , 2007, 110, 1130-1130.	0.6	1
34	ISWI ATPase Snf2h Is Required for Both Heterochromatin and Euchromatin Structure in ES Cells.. <i>Blood</i> , 2007, 110, 4062-4062.	0.6	0
35	PU.1 Dose-Dependently Induces Granulocyte or Macrophage Commitment by Targeting Lineage Restricted Genes and by Regulating Transcription Factors Egr2, Nab2, Cebpa and Gfi1.. <i>Blood</i> , 2007, 110, 661-661.	0.6	2
36	Fog1 and Cebpa Are DNA Targets of GATA-1/PU.1 Antagonism during Leukemia Differentiation.. <i>Blood</i> , 2007, 110, 4121-4121.	0.6	0

#	ARTICLE	IF	CITATIONS
37	Role of linker histone in chromatin structure and function: H1 stoichiometry and nucleosome repeat length. <i>Chromosome Research</i> , 2006, 14, 17-25.	1.0	396
38	Histone H1 Depletion in Mammals Alters Global Chromatin Structure but Causes Specific Changes in Gene Regulation. <i>Cell</i> , 2005, 123, 1199-1212.	13.5	493
39	Reductions in Linker Histone Levels Are Tolerated in Developing Spermatocytes but Cause Changes in Specific Gene Expression. <i>Journal of Biological Chemistry</i> , 2004, 279, 23525-23535.	1.6	48
40	PU.1 and pRb Bind GATA-1 on DNA and Recruit a Histone H3K9 Methyl Transferase-Containing Complex to Repress the Erythroid Transcription Program.. <i>Blood</i> , 2004, 104, 1614-1614.	0.6	0
41	H1 Linker Histones Are Essential for Mouse Development and Affect Nucleosome Spacing In Vivo. <i>Molecular and Cellular Biology</i> , 2003, 23, 4559-4572.	1.1	283
42	Individual Somatic H1 Subtypes Are Dispensable for Mouse Development Even in Mice Lacking the H1 0 Replacement Subtype. <i>Molecular and Cellular Biology</i> , 2001, 21, 7933-7943.	1.1	167
43	Manipulating the onset of cell cycle withdrawal in differentiated erythroid cells with cyclin-dependent kinases and inhibitors. <i>Blood</i> , 2000, 96, 2755-2764.	0.6	46
44	Manipulating the onset of cell cycle withdrawal in differentiated erythroid cells with cyclin-dependent kinases and inhibitors. <i>Blood</i> , 2000, 96, 2755-2764.	0.6	13
45	Goosecoid-like (GSCL), a candidate gene for velocardiofacial syndrome, is not essential for normal mouse development. <i>Human Molecular Genetics</i> , 1998, 7, 1841-1849.	1.4	24
46	Deregulated expression of the PU.1 transcription factor blocks murine erythroleukemia cell terminal differentiation. <i>Oncogene</i> , 1997, 14, 123-131.	2.6	91
47	Expression of c-myc changes during differentiation of mouse erythroleukaemia cells. <i>Nature</i> , 1984, 310, 592-594.	13.7	389
48	Inducibility of transferrin receptors on friend erythroleukemic cells. <i>Science</i> , 1977, 197, 559-561.	6.0	97
49	Somatic cell hybrids between Friend erythroleukemia cells and mouse hepatoma cells. <i>Somatic Cell Genetics</i> , 1977, 3, 157-172.	2.7	39