Colin Logie

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/6479519/colin-logie-publications-by-year.pdf
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67 papers	8,185 citations	34 h-index	72 g-index
72 ext. papers	11,659 ext. citations	10 avg, IF	7.55 L-index

#	Paper	IF	Citations
67	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194766	6	3
66	A GO catalogue of human DNA-binding transcription factors. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194765	6	0
65	The gene regulation knowledge commons: the action area of GREEKC. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1865, 194768	6	1
64	The Gene Ontology resource: enriching a GOld mine. *Nucleic Acids Research*, **2021**, 49, D325-D334	20.1	494
63	Fibronectin-functionalization of 3D collagen networks supports immune tolerance and inflammation suppression in human monocyte-derived macrophages. *Biomaterials*, **2021**, 268, 120498	15.6	7
62	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194749	6	2
61	Sequence Ontology terminology for gene regulation. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194745	6	3
60	Gene Ontology representation for transcription factor functions. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2021**, 1864, 194752	6	2
59	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. *IScience*, **2021**, 24, 103444	6.1	0
58	Spatial patterns of CTCF sites define the anatomy of TADs and their boundaries. *Genome Biology*, **2020**, 21, 197	18.3	17
57	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. *FASEB Journal*, **2019**, 33, 10104-10115	0.9	6
56	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. *Nature Cell Biology*, **2019**, 21, 568-578	23.4	33
55	Underreported and unknown student harassment at the Faculty of Science. *PLoS ONE*, **2019**, 14, e0215067	3.7	2
54	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. *Scientific Reports*, **2019**, 9, 2772	4.9	16
53	The Gene Ontology Resource: 20 years and still GOing strong. *Nucleic Acids Research*, **2019**, 47, D330-D338	20.1	1962
52	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions DC-SCRIPT and Dual-Specificity Phosphatase 4. *Frontiers in Immunology*, **2018**, 9, 1420	8.4	13
51	Combined HAT/EZH2 modulation leads to cancer-selective cell death. *Oncotarget*, **2018**, 9, 25630-25646	3.3	5

50	HDAC11 is a regulator of diverse immune functions. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2018**, 1861, 54-59	6	46
49	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. *Oncotarget*, **2018**, 9, 25647-25660	3.3	11
48	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. *Cell Reports*, **2018**, 25, 3490-3503.e4	10.6	25
47	Cellular reprogramming for clinical cartilage repair. *Cell Biology and Toxicology*, **2017**, 33, 329-349	7.4	19
46	We Can Still Be Friends: IFN-Breaks Up Macrophage Enhancers. *Immunity*, **2017**, 47, 209-211	32.3	0
45	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. *Cell Metabolism*, **2016**, 24, 807-819	24.6	398
44	Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. *Cell*, **2016**, 167, 1354-1368.e14	56.2	283
43	Epigenetic memory: A macrophage perspective. *Seminars in Immunology*, **2016**, 28, 359-67	10.7	23
42	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. *Genome Biology*, **2015**, 16, 264	18.3	38
41	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. *Science*, **2014**, 345, 1251086	33.3	870
40	mTOR- and HIF-1mediated aerobic glycolysis as metabolic basis for trained immunity. *Science*, **2014**, 345, 1250684	33.3	1020
39	Chromatin accessibility, p300, and histone acetylation define PML-RARand AML1-ETO binding sites in acute myeloid leukemia. *Blood*, **2012**, 120, 3058-68	2.2	51
38	Candida albicans infection affords protection against reinfection via functional reprogramming of monocytes. *Cell Host and Microbe*, **2012**, 12, 223-32	23.4	654
37	SS18 together with animal-specific factors defines human BAF-type SWI/SNF complexes. *PLoS ONE*, **2012**, 7, e33834	3.7	81
36	Sequence-based prediction of single nucleosome positioning and genome-wide nucleosome occupancy. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E2514-22	11.5	51
35	The human histone H3 complement anno 2011. *Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms*, **2011**, 1809, 577-86	6	22
34	Genome-wide functions of PML-RARin acute promyelocytic leukaemia. *British Journal of Cancer*, **2011**, 104, 554-8	8.7	42
33	Death receptor pathway activation and increase of ROS production by the triple epigenetic inhibitor UVI5008. *Molecular Cancer Therapeutics*, **2011**, 10, 2394-404	6.1	46

32	The decade of the epigenomes?. *Genes and Cancer*, **2011**, 2, 680-7	2.9	14
31	Histone H3 serine 57 and lysine 56 interplay in transcription elongation and recovery from S-phase stress. *PLoS ONE*, **2010**, 5, e10851	3.7	14
30	Multiple aspects of ATP-dependent nucleosome translocation by RSC and Mi-2 are directed by the underlying DNA sequence. *PLoS ONE*, **2009**, 4, e6345	3.7	34
29	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. *EMBO Journal*, **2009**, 28, 326-36	13	89
28	Single-molecule force spectroscopy reveals a highly compliant helical folding for the 30-nm chromatin fiber. *Nature Structural and Molecular Biology*, **2009**, 16, 534-40	17.6	194
27	Identification of potentially hazardous human gene products in GMO risk assessment. *Environmental Biosafety Research*, **2008**, 7, 1-9		11
26	dCHD3, a novel ATP-dependent chromatin remodeler associated with sites of active transcription. *Molecular and Cellular Biology*, **2008**, 28, 2745-57	4.8	44
25	Genetic identification of a network of factors that functionally interact with the nucleosome remodeling ATPase ISWI. *PLoS Genetics*, **2008**, 4, e1000089	6	27
24	The ins and outs of ATP-dependent chromatin remodeling in budding yeast: biophysical and proteomic perspectives. *Biochimica Et Biophysica Acta Gene Regulatory Mechanisms*, **2007**, 1769, 153-71		34
23	Single-pair FRET microscopy reveals mononucleosome dynamics. *Journal of Fluorescence*, **2007**, 17, 785-95	2.4	95
22	The new frontier in cancer research: deciphering cancer epigenetics. *International Journal of Biochemistry and Cell Biology*, **2007**, 39, 1450-61	5.6	15
21	Reverse genetic analysis of the yeast RSC chromatin remodeler reveals a role for RSC3 and SNF5 homolog 1 in ploidy maintenance. *PLoS Genetics*, **2007**, 3, e92	6	36
20	Histone H3 lysine 56 acetylation: a new twist in the chromosome cycle. *Cell Cycle*, **2006**, 5, 2602-8	4.7	44
19	A feed-forward repression mechanism anchors the Sin3/histone deacetylase and N-CoR/SMRT corepressors on chromatin. *Molecular and Cellular Biology*, **2006**, 26, 5226-36	4.8	25
18	Characterization of lysine 56 of histone H3 as an acetylation site in Saccharomyces cerevisiae. *Journal of Biological Chemistry*, **2005**, 280, 25949-52	5.4	97
17	In vitro targeting reveals intrinsic histone tail specificity of the Sin3/histone deacetylase and N-CoR/SMRT corepressor complexes. *Molecular and Cellular Biology*, **2004**, 24, 2364-72	4.8	39
16	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. *Nature Structural Biology*, **2002**, 9, 263-7		148
15	The interactions of yeast SWI/SNF and RSC with the nucleosome before and after chromatin remodeling. *Journal of Biological Chemistry*, **2001**, 276, 12636-44	5.4	47

14	Recruitment of chromatin remodeling machines. *Journal of Cellular Biochemistry*, **2000**, 78, 179-85	4.7	65
13	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. *Journal of Biological Chemistry*, **2000**, 275, 18864-70	5.4	87
12	SWI-SNF-mediated nucleosome remodeling: role of histone octamer mobility in the persistence of the remodeled state. *Molecular and Cellular Biology*, **2000**, 20, 3058-68	4.8	93
11	The core histone N-terminal domains are required for multiple rounds of catalytic chromatin remodeling by the SWI/SNF and RSC complexes. *Biochemistry*, **1999**, 38, 2514-22	3.2	71
10	Purification and biochemical properties of yeast SWI/SNF complex. *Methods in Enzymology*, **1999**, 304, 726-41	1.7	49
9	Recruitment of the SWI/SNF chromatin remodeling complex by transcriptional activators. *Genes and Development*, **1999**, 13, 2369-74	12.6	188
8	Positive and negative discrimination of estrogen receptor agonists and antagonists using site-specific DNA recombinase fusion proteins. *Molecular Endocrinology*, **1998**, 12, 1120-32		12
7	FLP recombinase/estrogen receptor fusion proteins require the receptor D domain for responsiveness to antagonists, but not agonists. *Molecular Endocrinology*, **1997**, 11, 950-61		19
6	Catalytic activity of the yeast SWI/SNF complex on reconstituted nucleosome arrays. *EMBO Journal*, **1997**, 16, 6772-82	13	158
5	Excision of Ets by an inducible site-specific recombinase causes differentiation of Myb-Ets-transformed hematopoietic progenitors. *Current Biology*, **1996**, 6, 866-72	6.3	15
4	Ligand-regulated site-specific recombination. *Proceedings of the National Academy of Sciences of the United States of America*, **1995**, 92, 5940-4	11.5	162
3	FLP Recombinase/Estrogen Receptor Fusion Proteins Require the Receptor D Domain for Responsiveness to Antagonists, but not Agonists		7
2	A GO catalogue of human DNA-binding transcription factors		4
1	The CTCF Anatomy of Topologically Associating Domains		1