

Colin Logie

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

13,711
citations

109321

35
h-index

102487

66
g-index

73
all docs

73
docs citations

73
times ranked

21969
citing authors

#	ARTICLE	IF	CITATIONS
1	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
2	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
3	mTOR- and HIF-1 α -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , 2014, 345, 1250684.	12.6	1,517
4	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. <i>Science</i> , 2014, 345, 1251086.	12.6	1,338
5	<i>Candida albicans</i> Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. <i>Cell Host and Microbe</i> , 2012, 12, 223-232.	11.0	926
6	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. <i>Cell Metabolism</i> , 2016, 24, 807-819.	16.2	584
7	β -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	28.9	467
8	Single-molecule force spectroscopy reveals a highly compliant helical folding for the 30-nm chromatin fiber. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 534-540.	8.2	230
9	Recruitment of the SWI/SNF chromatin remodeling complex by transcriptional activators. <i>Genes and Development</i> , 1999, 13, 2369-2374.	5.9	204
10	Ligand-regulated site-specific recombination.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 5940-5944.	7.1	173
11	Catalytic activity of the yeast SWI/SNF complex on reconstituted nucleosome arrays. <i>EMBO Journal</i> , 1997, 16, 6772-6782.	7.8	169
12	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , 2002, 9, 263-267.	9.7	160
13	Characterization of Lysine 56 of Histone H3 as an Acetylation Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25949-25952.	3.4	105
14	Single-Pair FRET Microscopy Reveals Mononucleosome Dynamics. <i>Journal of Fluorescence</i> , 2007, 17, 785-795.	2.5	105
15	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. <i>EMBO Journal</i> , 2009, 28, 326-336.	7.8	104
16	SS18 Together with Animal-Specific Factors Defines Human BAF-Type SWI/SNF Complexes. <i>PLoS ONE</i> , 2012, 7, e33834.	2.5	102
17	Functional Delineation of Three Groups of the ATP-dependent Family of Chromatin Remodeling Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 18864-18870.	3.4	95
18	SWI-SNF-Mediated Nucleosome Remodeling: Role of Histone Octamer Mobility in the Persistence of the Remodeled State. <i>Molecular and Cellular Biology</i> , 2000, 20, 3058-3068.	2.3	94

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19	The Core Histone N-Terminal Domains Are Required for Multiple Rounds of Catalytic Chromatin Remodeling by the SWI/SNF and RSC Complexes. <i>Biochemistry</i> , 1999, 38, 2514-2522.	2.5	73
20	Recruitment of chromatin remodeling machines. , 2000, 78, 179-185.		72
21	Sequence-based prediction of single nucleosome positioning and genome-wide nucleosome occupancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2514-22.	7.1	70
22	HDAC11 is a regulator of diverse immune functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2018, 1861, 54-59.	1.9	70
23	Chromatin accessibility, p300, and histone acetylation define PML-RAR \pm and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	1.4	60
24	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. <i>Nature Cell Biology</i> , 2019, 21, 568-578.	10.3	55
25	Purification and biochemical properties of yeast SWI/SNF complex. <i>Methods in Enzymology</i> , 1999, 304, 726-741.	1.0	54
26	Genome-wide functions of PML-RAR \pm in acute promyelocytic leukaemia. <i>British Journal of Cancer</i> , 2011, 104, 554-558.	6.4	54
27	The Interactions of Yeast SWI/SNF and RSC with the Nucleosome before and after Chromatin Remodeling. <i>Journal of Biological Chemistry</i> , 2001, 276, 12636-12644.	3.4	49
28	Death Receptor Pathway Activation and Increase of ROS Production by the Triple Epigenetic Inhibitor UVI5008. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 2394-2404.	4.1	49
29	Epigenetic memory: A macrophage perspective. <i>Seminars in Immunology</i> , 2016, 28, 359-367.	5.6	49
30	dCHD3, a Novel ATP-Dependent Chromatin Remodeler Associated with Sites of Active Transcription. <i>Molecular and Cellular Biology</i> , 2008, 28, 2745-2757.	2.3	48
31	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	8.8	48
32	Histone H3 Lysine 56 Acetylation: A New Twist in the Chromosome Cycle. <i>Cell Cycle</i> , 2006, 5, 2602-2608.	2.6	45
33	Spatial patterns of CTCF sites define the anatomy of TADs and their boundaries. <i>Genome Biology</i> , 2020, 21, 197.	8.8	45
34	In Vitro Targeting Reveals Intrinsic Histone Tail Specificity of the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressor Complexes. <i>Molecular and Cellular Biology</i> , 2004, 24, 2364-2372.	2.3	43
35	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. <i>Cell Reports</i> , 2018, 25, 3490-3503.e4.	6.4	41
36	Multiple Aspects of ATP-Dependent Nucleosome Translocation by RSC and Mi-2 Are Directed by the Underlying DNA Sequence. <i>PLoS ONE</i> , 2009, 4, e6345.	2.5	40

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37	Reverse Genetic Analysis of the Yeast RSC Chromatin Remodeler Reveals a Role for RSC3 and SNF5 Homolog 1 in Ploidy Maintenance. <i>PLoS Genetics</i> , 2007, 3, e92.	3.5	39
38	The ins and outs of ATP-dependent chromatin remodeling in budding yeast: Biophysical and proteomic perspectives. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2007, 1769, 153-171.	2.4	38
39	Genetic Identification of a Network of Factors that Functionally Interact with the Nucleosome Remodeling ATPase ISWI. <i>PLoS Genetics</i> , 2008, 4, e1000089.	3.5	28
40	The human histone H3 complement anno 2011. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2011, 1809, 577-586.	1.9	28
41	Cellular reprogramming for clinical cartilage repair. <i>Cell Biology and Toxicology</i> , 2017, 33, 329-349.	5.3	27
42	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. <i>Scientific Reports</i> , 2019, 9, 2772.	3.3	27
43	A Feed-Forward Repression Mechanism Anchors the Sin3/Histone Deacetylase and N-CoR/SMRT Corepressors on Chromatin. <i>Molecular and Cellular Biology</i> , 2006, 26, 5226-5236.	2.3	26
44	FLP Recombinase/Estrogen Receptor Fusion Proteins Require the Receptor D Domain for Responsiveness to Antagonists, but not Agonists. <i>Molecular Endocrinology</i> , 1997, 11, 950-961.	3.7	20
45	Excision of Ets by an inducible site-specific recombinase causes differentiation of Myb ⁺ Ets-transformed hematopoietic progenitors. <i>Current Biology</i> , 1996, 6, 866-872.	3.9	17
46	The new frontier in cancer research: Deciphering cancer epigenetics. <i>International Journal of Biochemistry and Cell Biology</i> , 2007, 39, 1450-1461.	2.8	17
47	Histone H3 Serine 57 and Lysine 56 Interplay in Transcription Elongation and Recovery from S-Phase Stress. <i>PLoS ONE</i> , 2010, 5, e10851.	2.5	17
48	Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194752.	1.9	17
49	The Decade of the Epigenomes?. <i>Genes and Cancer</i> , 2011, 2, 680-687.	1.9	16
50	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions via DC-SCRIPT and Dual-Specificity Phosphatase 4. <i>Frontiers in Immunology</i> , 2018, 9, 1420.	4.8	16
51	Fibronectin-functionalization of 3D collagen networks supports immune tolerance and inflammation suppression in human monocyte-derived macrophages. <i>Biomaterials</i> , 2021, 268, 120498.	11.4	16
52	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194765.	1.9	15
53	Identification of potentially hazardous human gene products in GMO risk assessment. <i>Environmental Biosafety Research</i> , 2008, 7, 1-9.	1.1	14
54	Positive and Negative Discrimination of Estrogen Receptor Agonists and Antagonists Using Site-Specific DNA Recombinase Fusion Proteins. <i>Molecular Endocrinology</i> , 1998, 12, 1120-1132.	3.7	13

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55	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	1.8	13
56	Underreported and unknown student harassment at the Faculty of Science. <i>PLoS ONE</i> , 2019, 14, e0215067.	2.5	10
57	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. <i>IScience</i> , 2021, 24, 103444.	4.1	10
58	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. <i>FASEB Journal</i> , 2019, 33, 10104-10115.	0.5	9
59	FLP Recombinase/Estrogen Receptor Fusion Proteins Require the Receptor D Domain for Responsiveness to Antagonists, but not Agonists. <i>Molecular Endocrinology</i> , 1997, 11, 950-961.	3.7	8
60	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194749.	1.9	6
61	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194766.	1.9	6
62	Sequence Ontology terminology for gene regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2021, 1864, 194745.	1.9	5
63	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , 2018, 9, 25630-25646.	1.8	5
64	Positive and Negative Discrimination of Estrogen Receptor Agonists and Antagonists Using Site-Specific DNA Recombinase Fusion Proteins. <i>Molecular Endocrinology</i> , 1998, 12, 1120-1132.	3.7	3
65	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	1.9	3
66	Regulation of nuclear receptors by agonists and antagonists. <i>Current Opinion in Endocrinology, Diabetes and Obesity</i> , 1996, 3, 397-402.	0.6	2
67	We Can Still Be Friends: IFN- β Breaks Up Macrophage Enhancers. <i>Immunity</i> , 2017, 47, 209-211.	14.3	2
68	Twenty-First Century Glucocorticoid Receptor Molecular Biology. , 2018, , .		0
69	Synthetic Point Mutagenesis. , 0, , .		0