

# Colin Logie

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D330-D338.	38.1	1962
66	mTOR- and HIF-1 $\beta$ -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , <b>2014</b> , 345, 1250684	33.3	1020
65	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. <i>Science</i> , <b>2014</b> , 345, 1251086	33.3	870
64	<i>Candida albicans</i> infection affords protection against reinfection via functional reprogramming of monocytes. <i>Cell Host and Microbe</i> , <b>2012</b> , 12, 223-32	23.4	654
63	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D325-D334	20.1	494
62	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. <i>Cell Metabolism</i> , <b>2016</b> , 24, 807-819	24.6	398
61	$\beta$ -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , <b>2016</b> , 167, 1354-1368.	36.2	1423
60	Single-molecule force spectroscopy reveals a highly compliant helical folding for the 30-nm chromatin fiber. <i>Nature Structural and Molecular Biology</i> , <b>2009</b> , 16, 534-40	17.6	194
59	Recruitment of the SWI/SNF chromatin remodeling complex by transcriptional activators. <i>Genes and Development</i> , <b>1999</b> , 13, 2369-74	12.6	188
58	Ligand-regulated site-specific recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1995</b> , 92, 5940-4	11.5	162
57	Catalytic activity of the yeast SWI/SNF complex on reconstituted nucleosome arrays. <i>EMBO Journal</i> , <b>1997</b> , 16, 6772-82	13	158
56	Phosphorylation of linker histones regulates ATP-dependent chromatin remodeling enzymes. <i>Nature Structural Biology</i> , <b>2002</b> , 9, 263-7		148
55	Characterization of lysine 56 of histone H3 as an acetylation site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 25949-52	5.4	97
54	Single-pair FRET microscopy reveals mononucleosome dynamics. <i>Journal of Fluorescence</i> , <b>2007</b> , 17, 785-95	25.4	95
53	SWI-SNF-mediated nucleosome remodeling: role of histone octamer mobility in the persistence of the remodeled state. <i>Molecular and Cellular Biology</i> , <b>2000</b> , 20, 3058-68	4.8	93
52	Recruitment of a chromatin remodelling complex by the Hog1 MAP kinase to stress genes. <i>EMBO Journal</i> , <b>2009</b> , 28, 326-36	13	89
51	Functional delineation of three groups of the ATP-dependent family of chromatin remodeling enzymes. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 18864-70	5.4	87

50	SS18 together with animal-specific factors defines human BAF-type SWI/SNF complexes. <i>PLoS ONE</i> , <b>2012</b> , 7, e33834	3.7	81
49	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> , <b>1999</b> , 38, 2514-22	3.2	71
48	Recruitment of chromatin remodeling machines. <i>Journal of Cellular Biochemistry</i> , <b>2000</b> , 78, 179-85	4.7	65
47	Chromatin accessibility, p300, and histone acetylation define PML-RAR and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , <b>2012</b> , 120, 3058-68	2.2	51
46	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> , <b>2012</b> , 109, E2514-22	11.5	51
45	Purification and biochemical properties of yeast SWI/SNF complex. <i>Methods in Enzymology</i> , <b>1999</b> , 304, 726-41	1.7	49
44	The interactions of yeast SWI/SNF and RSC with the nucleosome before and after chromatin remodeling. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 12636-44	5.4	47
43	Death receptor pathway activation and increase of ROS production by the triple epigenetic inhibitor UVI5008. <i>Molecular Cancer Therapeutics</i> , <b>2011</b> , 10, 2394-404	6.1	46
42	HDAC11 is a regulator of diverse immune functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2018</b> , 1861, 54-59	6	46
41	dCHD3, a novel ATP-dependent chromatin remodeler associated with sites of active transcription. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 2745-57	4.8	44
40	Histone H3 lysine 56 acetylation: a new twist in the chromosome cycle. <i>Cell Cycle</i> , <b>2006</b> , 5, 2602-8	4.7	44
39	Genome-wide functions of PML-RAR in acute promyelocytic leukaemia. <i>British Journal of Cancer</i> , <b>2011</b> , 104, 554-8	8.7	42
38	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> , <b>2004</b> , 24, 2364-72	4.8	39
37	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , <b>2015</b> , 16, 264	18.3	38
36	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> , <b>2007</b> , 3, e92	6	36
35	Multiple aspects of ATP-dependent nucleosome translocation by RSC and Mi-2 are directed by the underlying DNA sequence. <i>PLoS ONE</i> , <b>2009</b> , 4, e6345	3.7	34
34	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> , <b>2007</b> , 1769, 153-71		34
33	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. <i>Nature Cell Biology</i> , <b>2019</b> , 21, 568-578	23.4	33

32	Genetic identification of a network of factors that functionally interact with the nucleosome remodeling ATPase ISWI. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000089	6	27
31	A feed-forward repression mechanism anchors the Sin3/histone deacetylase and N-CoR/SMRT corepressors on chromatin. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 5226-36	4.8	25
30	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. <i>Cell Reports</i> , <b>2018</b> , 25, 3490-3503.e4	10.6	25
29	Epigenetic memory: A macrophage perspective. <i>Seminars in Immunology</i> , <b>2016</b> , 28, 359-67	10.7	23
28	The human histone H3 complement anno 2011. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2011</b> , 1809, 577-86	6	22
27	Cellular reprogramming for clinical cartilage repair. <i>Cell Biology and Toxicology</i> , <b>2017</b> , 33, 329-349	7.4	19
26	FLP recombinase/estrogen receptor fusion proteins require the receptor D domain for responsiveness to antagonists, but not agonists. <i>Molecular Endocrinology</i> , <b>1997</b> , 11, 950-61		19
25	Spatial patterns of CTCF sites define the anatomy of TADs and their boundaries. <i>Genome Biology</i> , <b>2020</b> , 21, 197	18.3	17
24	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. <i>Scientific Reports</i> , <b>2019</b> , 9, 2772	4.9	16
23	The new frontier in cancer research: deciphering cancer epigenetics. <i>International Journal of Biochemistry and Cell Biology</i> , <b>2007</b> , 39, 1450-61	5.6	15
22	Excision of Ets by an inducible site-specific recombinase causes differentiation of Myb-Ets-transformed hematopoietic progenitors. <i>Current Biology</i> , <b>1996</b> , 6, 866-72	6.3	15
21	Histone H3 serine 57 and lysine 56 interplay in transcription elongation and recovery from S-phase stress. <i>PLoS ONE</i> , <b>2010</b> , 5, e10851	3.7	14
20	The decade of the epigenomes?. <i>Genes and Cancer</i> , <b>2011</b> , 2, 680-7	2.9	14
19	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions DC-SCRIPT and Dual-Specificity Phosphatase 4. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 1420	8.4	13
18	Positive and negative discrimination of estrogen receptor agonists and antagonists using site-specific DNA recombinase fusion proteins. <i>Molecular Endocrinology</i> , <b>1998</b> , 12, 1120-32		12
17	Identification of potentially hazardous human gene products in GMO risk assessment. <i>Environmental Biosafety Research</i> , <b>2008</b> , 7, 1-9		11
16	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , <b>2018</b> , 9, 25647-25660	3.3	11
15	FLP Recombinase/Estrogen Receptor Fusion Proteins Require the Receptor D Domain for Responsiveness to Antagonists, but not Agonists		7

14	Fibronectin-functionalization of 3D collagen networks supports immune tolerance and inflammation suppression in human monocyte-derived macrophages. <i>Biomaterials</i> , <b>2021</b> , 268, 120498	15.6	7
13	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. <i>FASEB Journal</i> , <b>2019</b> , 33, 10104-10115	0.9	6
12	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , <b>2018</b> , 9, 25630-25646	3.3	5
11	A GO catalogue of human DNA-binding transcription factors		4
10	Formalization of gene regulation knowledge using ontologies and gene ontology causal activity models. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194766	6	3
9	Sequence Ontology terminology for gene regulation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194745	6	3
8	Underreported and unknown student harassment at the Faculty of Science. <i>PLoS ONE</i> , <b>2019</b> , 14, e0215067	7	2
7	Integration of transcription coregulator complexes with sequence-specific DNA-binding factor interactomes. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194749	6	2
6	Gene Ontology representation for transcription factor functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194752	6	2
5	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1865, 194768	6	1
4	The CTCF Anatomy of Topologically Associating Domains		1
3	We Can Still Be Friends: IFN- $\beta$ Breaks Up Macrophage Enhancers. <i>Immunity</i> , <b>2017</b> , 47, 209-211	32.3	0
2	A GO catalogue of human DNA-binding transcription factors. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2021</b> , 1864, 194765	6	0
1	Retinoic acid signaling drives differentiation toward the absorptive lineage in colorectal cancer. <i>Science</i> , <b>2021</b> , 24, 103444	6.1	0