

# Peter N Cockerill

## List of Publications by Year in descending order

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73  
papers

4,219  
citations

136950

32  
h-index

118850

62  
g-index

74  
all docs

74  
docs citations

74  
times ranked

5212  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Basis of Hematological Disease Caused by Inherited or Acquired RUNX1 Mutations. <i>Experimental Hematology</i> , 2022, 111, 1-12.	0.4	7
2	Epigenetic regulator genes direct lineage switching in MLL/AF4 leukemia. <i>Blood</i> , 2022, 140, 1875-1890.	1.4	26
3	Isoform-specific and signaling-dependent propagation of acute myeloid leukemia by Wilms tumor 1. <i>Cell Reports</i> , 2021, 35, 109010.	6.4	12
4	Stable Epigenetic Programming of Effector and Central Memory CD4 T Cells Occurs Within 7 Days of Antigen Exposure In Vivo. <i>Frontiers in Immunology</i> , 2021, 12, 642807.	4.8	4
5	Unravelling the apoptotic machinery in CMML. <i>Blood</i> , 2021, 137, 3321-3322.	1.4	0
6	RUNX1/ETO and mutant KIT both contribute to programming the transcriptional and chromatin landscape in t(8;21) acute myeloid leukemia. <i>Experimental Hematology</i> , 2020, 92, 62-74.	0.4	2
7	Chromatin Priming Renders T Cell Tolerance-Associated Genes Sensitive to Activation below the Signaling Threshold for Immune Response Genes. <i>Cell Reports</i> , 2020, 31, 107748.	6.4	21
8	IL2/IL7 inducible factors pioneer the path to T cell differentiation in advance of lineage-defining factors. <i>EMBO Journal</i> , 2020, 39, e105220.	7.8	26
9	Rewiring of the Transcription Factor Network in Acute Myeloid Leukemia. <i>Cancer Informatics</i> , 2019, 18, 117693511985986.	1.9	7
10	RUNX1-ETO Depletion in t(8;21) AML Leads to C/EBP $\beta$ - and AP-1-Mediated Alterations in Enhancer-Promoter Interaction. <i>Cell Reports</i> , 2019, 28, 3022-3031.e7.	6.4	25
11	Subtype-specific regulatory network rewiring in acute myeloid leukemia. <i>Nature Genetics</i> , 2019, 51, 151-162.	21.4	140
12	Global long terminal repeat activation participates in establishing the unique gene expression programme of classical Hodgkin lymphoma. <i>Leukemia</i> , 2019, 33, 1463-1474.	7.2	19
13	The Oncogenic Transcription Factor RUNX1/ETO Corrupts Cell Cycle Regulation to Drive Leukemic Transformation. <i>Cancer Cell</i> , 2018, 34, 626-642.e8.	16.8	81
14	Prospective Isolation and Characterization of Genetically and Functionally Distinct AML Subclones. <i>Cancer Cell</i> , 2018, 34, 674-689.e8.	16.8	71
15	C/EBP $\beta$ overrides epigenetic reprogramming by oncogenic transcription factors in acute myeloid leukemia. <i>Blood Advances</i> , 2018, 2, 271-284.	5.2	14
16	Chromatin priming of genes in development: Concepts, mechanisms and consequences. <i>Experimental Hematology</i> , 2017, 49, 1-8.	0.4	41
17	RUNX1-ETO and RUNX1-EVI1 Differentially Reprogram the Chromatin Landscape in t(8;21) and t(3;21) AML. <i>Cell Reports</i> , 2017, 19, 1654-1668.	6.4	46
18	Chromatin priming elements establish immunological memory in T cells without activating transcription. <i>BioEssays</i> , 2017, 39, 1600184.	2.5	25

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19	Integration of Kinase and Calcium Signaling at the Level of Chromatin Underlies Inducible Gene Activation in T Cells. <i>Journal of Immunology</i> , 2017, 199, 2652-2667.	0.8	51
20	Prognostic significance of high GFI1 expression in AML of normal karyotype and its association with a FLT3-ITD signature. <i>Scientific Reports</i> , 2017, 7, 11148.	3.3	16
21	T Cell Receptor and Cytokine Signaling Can Function at Different Stages to Establish and Maintain Transcriptional Memory and Enable T Helper Cell Differentiation. <i>Frontiers in Immunology</i> , 2017, 8, 204.	4.8	25
22	Cooperative binding of AP-1 and TEAD4 modulates the balance between vascular smooth muscle and hemogenic cell fate. <i>Development (Cambridge)</i> , 2016, 143, 4324-4340.	2.5	43
23	Inducible chromatin priming is associated with the establishment of immunological memory in T cells. <i>EMBO Journal</i> , 2016, 35, 515-535.	7.8	92
24	Receptor Signaling Directs Global Recruitment of Pre-existing Transcription Factors to Inducible Elements. <i>Yale Journal of Biology and Medicine</i> , 2016, 89, 591-596.	0.2	4
25	Chromatin Structure Profiling Identifies Crucial Regulators of Tumor Maintenance. <i>Trends in Cancer</i> , 2015, 1, 157-160.	7.4	11
26	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. <i>BMC Genomics</i> , 2015, 16, 1000.	2.8	49
27	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. <i>Cell Reports</i> , 2015, 12, 821-836.	6.4	63
28	Aberrant Transcriptional Programming in Blood Cancers. , 2015, , 467-484.		0
29	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. <i>Cell Reports</i> , 2014, 8, 1974-1988.	6.4	106
30	Mapping of transcription factor motifs in active chromatin identifies IRF5 as key regulator in classical Hodgkin lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4513-22.	7.1	53
31	The Epigenetic Regulatory Machinery. <i>Epigenetics and Human Health</i> , 2014, , 1-11.	0.2	0
32	Prior epigenetic priming of cytokine genes in naive T cells is required for their subsequent activation by inducible enhancers. <i>Epigenetics and Chromatin</i> , 2013, 6, .	3.9	0
33	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. <i>Nucleic Acids Research</i> , 2013, 41, e201-e201.	14.5	196
34	The Inducible Tissue-Specific Expression of the Human IL-3/GM-CSF Locus Is Controlled by a Complex Array of Developmentally Regulated Enhancers. <i>Journal of Immunology</i> , 2012, 189, 4459-4469.	0.8	9
35	Induction of differentiation and apoptosis in leukaemic cell lines by the novel benzamide family histone deacetylase 2 and 3 inhibitor MI-192. <i>Leukemia Research</i> , 2012, 36, 1304-1310.	0.8	42
36	Structure and function of active chromatin and DNase I hypersensitive sites. <i>FEBS Journal</i> , 2011, 278, 2182-2210.	4.7	110

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37	Chromatin Mechanisms Regulating Gene Expression in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2011, 711, 12-25.	1.6	20
38	Transcriptional and epigenetic regulation of the GM-CSF promoter by RUNX1. <i>Leukemia Research</i> , 2010, 34, 1203-1213.	0.8	17
39	Transcription-dependent silencing of inducible convergent transgenes in transgenic mice. <i>Epigenetics and Chromatin</i> , 2010, 3, 3.	3.9	27
40	Derepression of an endogenous long terminal repeat activates the CSF1R proto-oncogene in human lymphoma. <i>Nature Medicine</i> , 2010, 16, 571-579.	30.7	317
41	Runx1 binds as a dimeric complex to overlapping Runx1 sites within a palindromic element in the human GM-CSF enhancer. <i>Nucleic Acids Research</i> , 2010, 38, 6124-6134.	14.5	35
42	The Human IL-3/Granulocyte-Macrophage Colony-Stimulating Factor Locus Is Epigenetically Silent in Immature Thymocytes and Is Progressively Activated during T Cell Development. <i>Journal of Immunology</i> , 2010, 184, 3043-3054.	0.8	28
43	A Conserved Insulator That Recruits CTCF and Cohesin Exists between the Closely Related but Divergently Regulated Interleukin-3 and Granulocyte-Macrophage Colony-Stimulating Factor Genes. <i>Molecular and Cellular Biology</i> , 2009, 29, 1682-1693.	2.3	28
44	The LPS-Induced Transcriptional Upregulation of the Chicken Lysozyme Locus Involves CTCF Eviction and Noncoding RNA Transcription. <i>Molecular Cell</i> , 2008, 32, 129-139.	9.7	129
45	NFAT Is Well Placed to Direct Both Enhancer Looping and Domain-Wide Models of Enhancer Function. <i>Science Signaling</i> , 2008, 1, pe15.	3.6	13
46	The <i>Pu.1</i> Locus Is Differentially Regulated at the Level of Chromatin Structure and Noncoding Transcription by Alternate Mechanisms at Distinct Developmental Stages of Hematopoiesis. <i>Molecular and Cellular Biology</i> , 2007, 27, 7425-7438.	2.3	56
47	A Modular Enhancer Is Differentially Regulated by GATA and NFAT Elements That Direct Different Tissue-Specific Patterns of Nucleosome Positioning and Inducible Chromatin Remodeling. <i>Molecular and Cellular Biology</i> , 2007, 27, 2870-2885.	2.3	47
48	In Vivo Genomic Footprinting Using LM-PCR Methods. , 2006, 325, 285-314.		20
49	Role of a 5' enhancer in the transcriptional regulation of the human endothelial cell protein C receptor gene. <i>Blood</i> , 2006, 108, 1251-1259.	1.4	21
50	Transcriptional Regulation of Human CD5: Important Role of Ets Transcription Factors in CD5 Expression in T Cells. <i>Journal of Immunology</i> , 2004, 172, 7519-7529.	0.8	22
51	Granulocyte-Macrophage Colony-Stimulating Factor Enhancer Activation Requires Cooperation between NFAT and AP-1 Elements and Is Associated with Extensive Nucleosome Reorganization. <i>Molecular and Cellular Biology</i> , 2004, 24, 7914-7930.	2.3	72
52	Mechanisms of Transcriptional Regulation of the Human IL-3/GM-CSF Locus by Inducible Tissue-Specific Promoters and Enhancers. <i>Critical Reviews in Immunology</i> , 2004, 24, 24.	0.5	24
53	Regulation of the human endothelial cell protein C receptor gene promoter by multiple Sp1 binding sites. <i>Blood</i> , 2003, 101, 4393-4401.	1.4	12
54	The Human IL-3 Locus Is Regulated Cooperatively by Two NFAT-Dependent Enhancers That Have Distinct Tissue-Specific Activities. <i>Journal of Immunology</i> , 2002, 169, 1876-1886.	0.8	41

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55	Identification of DNaseI Hypersensitive Sites Within Nuclei. , 2000, 130, 29-46.		35
56	Generation of an Improved Luciferase Reporter Gene Plasmid That Employs a Novel Mechanism for High-Copy Replication. Plasmid, 2000, 44, 173-182.	1.4	56
57	Reconstitution of T Cell-Specific Transcription Directed by Composite NFAT/Oct Elements. Journal of Immunology, 2000, 165, 5646-5655.	0.8	37
58	Nuclear factor of activated T cells contributes to the function of the CD28 response region of the granulocyte macrophage-colony stimulating factor promoter. International Immunology, 1999, 11, 1945-1956.	4.0	27
59	A T Cell-Specific Enhancer in the Interleukin-3 Locus Is Activated Cooperatively by Oct and NFAT Elements within a DNase I-Hypersensitive Site. Immunity, 1997, 6, 175-185.	14.3	77
60	Cytokines and allergy. Journal of Allergy and Clinical Immunology, 1994, 94, 1289-1293.	2.9	14
61	Isolation and characterization of the promoter region of the human intercellular adhesion molecule-1 gene. International Immunology, 1991, 3, 83-93.	4.0	43
62	Nuclear matrix attachment occurs in several regions of the IgH locus. Nucleic Acids Research, 1990, 18, 2643-2648.	14.5	71
63	Protein:DNA interactions at chromosomal loop attachment sites. Genome, 1989, 31, 503-509.	2.0	69
64	Two methods that facilitate autoradiography of small <sup>32</sup> P-labeled DNA fragments following electrophoresis in agarose gels. Analytical Biochemistry, 1988, 168, 451-454.	2.4	3
65	Chromosomal loop anchorage sites appear to be evolutionarily conserved. FEBS Letters, 1986, 204, 5-7.	2.8	111
66	Chromosomal loop anchorage of the kappa immunoglobulin gene occurs next to the enhancer in a region containing topoisomerase II sites. Cell, 1986, 44, 273-282.	28.9	948
67	Fractionation by high-performance liquid chromatography of the low-molecular-mass high-mobility-group (HMG) chromosomal proteins present in proliferating rat cells and an investigation of the HMG proteins present in virus transformed cells. FEBS Journal, 1985, 149, 47-51.	0.2	52
68	Comparison of the structures of the chromosomal high mobility group proteins HMG1 and HMG2 prepared under conditions of neutral and acidic pH. BBA - Proteins and Proteomics, 1983, 745, 70-81.	2.1	21
69	Demonstration of an S1-nuclease sensitive site near the human $\beta$ -globin gene, and its protection by HMG 1 and 2. Biochemical and Biophysical Research Communications, 1983, 112, 547-554.	2.1	25
70	The nuclease sensitivity of active genes. Nucleic Acids Research, 1983, 11, 753-772.	14.5	61
71	Biochemical and histological changes in pulmonary fibrosis induced in rabbits with intratracheal bleomycin. European Journal of Clinical Investigation, 1981, 11, 441-448.	3.4	61
72	A simplified method for quantitation of the relative amounts of type I and type III collagen in small tissue samples. Analytical Biochemistry, 1981, 113, 301-312.	2.4	142

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73	RUNX1-ETO Orchestrates Dynamic Enhancer Promoter Communication in T(8;21) Acute Myeloid Leukaemia. SSRN Electronic Journal, 0, , .	0.4	0