

Jim R Hughes

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

6,676
citations

71061

41
h-index

85498

71
g-index

97
all docs

97
docs citations

97
times ranked

9171
citing authors

#	ARTICLE	IF	CITATIONS
1	Making connections: enhancers in cellular differentiation. Trends in Genetics, 2022, 38, 395-408.	2.9	6
2	Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. Nature Protocols, 2022, 17, 445-475.	5.5	24
3	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. Nature Communications, 2022, 13, 773.	5.8	10
4	Natural and Experimental Rewiring of Gene Regulatory Regions. Annual Review of Genomics and Human Genetics, 2022, 23, .	2.5	1
5	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	5.8	20
6	Chromatin interaction maps identify Wnt responsive cis-regulatory elements coordinating Paupar-Pax6 expression in neuronal cells. PLoS Genetics, 2022, 18, e1010230.	1.5	6
7	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	1.5	9
8	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. Nature Communications, 2021, 12, 531.	5.8	32
9	Fra-1 regulates its target genes via binding to remote enhancers without exerting major control on chromatin architecture in triple negative breast cancers. Nucleic Acids Research, 2021, 49, 2488-2508.	6.5	15
10	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7.	4.5	27
11	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. Communications Biology, 2021, 4, 623.	2.0	4
12	Defining genome architecture at base-pair resolution. Nature, 2021, 595, 125-129.	13.7	107
13	A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. Nature Communications, 2021, 12, 3806.	5.8	18
14	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	5.8	19
15	Recapitulation of erythropoiesis in congenital dyserythropoietic anemia type I (CDA-I) identifies defects in differentiation and nucleolar abnormalities. Haematologica, 2021, 106, 2960-2970.	1.7	10
16	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
17	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38.	1.5	8
18	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. Cell Stem Cell, 2020, 27, 765-783.e14.	5.2	101

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19	DeepC: predicting 3D genome folding using megabase-scale transfer learning. <i>Nature Methods</i> , 2020, 17, 1118-1124.	9.0	109
20	Dynamics of the 4D genome during in vivo lineage specification and differentiation. <i>Nature Communications</i> , 2020, 11, 2722.	5.8	79
21	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , 2020, 30, 472-484.	2.4	38
22	A Dynamic Folded Hairpin Conformation Is Associated with $\hat{\pm}$ -Globin Activation in Erythroid Cells. <i>Cell Reports</i> , 2020, 30, 2125-2135.e5.	2.9	38
23	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. <i>Molecular Cell</i> , 2020, 78, 960-974.e11.	4.5	83
24	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. <i>Nature Communications</i> , 2019, 10, 2803.	5.8	99
25	Reconstruction of the Global Neural Crest Gene Regulatory Network In Vivo. <i>Developmental Cell</i> , 2019, 51, 255-276.e7.	3.1	108
26	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. <i>Nature Genetics</i> , 2019, 51, 1024-1034.	9.4	60
27	Nrf2 controls iron homeostasis in haemochromatosis and thalassaemia via Bmp6 and hepcidin. <i>Nature Metabolism</i> , 2019, 1, 519-531.	5.1	88
28	A revised model for promoter competition based on multi-way chromatin interactions at the $\hat{\pm}$ -globin locus. <i>Nature Communications</i> , 2019, 10, 5412.	5.8	60
29	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. <i>Nature Communications</i> , 2018, 9, 100.	5.8	38
30	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. <i>Methods and Protocols</i> , 2018, 1, 29.	0.9	6
31	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. <i>Nature Communications</i> , 2018, 9, 3849.	5.8	62
32	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. <i>Nature Genetics</i> , 2018, 50, 1744-1751.	9.4	150
33	MLL-AF4 binds directly to a BCL-2 specific enhancer and modulates H3K27 $\hat{\Delta}$ Acetylation. <i>Experimental Hematology</i> , 2017, 47, 64-75.	0.2	25
34	How best to identify chromosomal interactions: a comparison of approaches. <i>Nature Methods</i> , 2017, 14, 125-134.	9.0	124
35	Functional characterisation of cis-regulatory elements governing dynamic <i>Eomes</i> expression in the early mouse embryo. <i>Development (Cambridge)</i> , 2017, 144, 1249-1260.	1.2	32
36	DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7526-E7535.	3.3	125

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37	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. <i>Genes and Development</i> , 2017, 31, 1704-1713.	2.7	113
38	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. <i>Genome Research</i> , 2017, 27, 1730-1742.	2.4	33
39	<i>VHL</i> Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. <i>Cancer Discovery</i> , 2017, 7, 1284-1305.	7.7	111
40	Hepcidin is regulated by promoter-associated histone acetylation and HDAC3. <i>Nature Communications</i> , 2017, 8, 403.	5.8	45
41	Editing an β -globin enhancer in primary human hematopoietic stem cells as a treatment for β^0 -thalassemia. <i>Nature Communications</i> , 2017, 8, 424.	5.8	85
42	Tissue-specific CTCF-cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. <i>Nature Cell Biology</i> , 2017, 19, 952-961.	4.6	179
43	Between form and function: the complexity of genome folding. <i>Human Molecular Genetics</i> , 2017, 26, R208-R215.	1.4	20
44	Robust detection of chromosomal interactions from small numbers of cells using low-input Capture-C. <i>Nucleic Acids Research</i> , 2017, 45, e184-e184.	6.5	27
45	Low-input Capture-C: A Chromosome Conformation Capture Assay to Analyze Chromatin Architecture in Small Numbers of Cells. <i>Bio-protocol</i> , 2017, 7, .	0.2	15
46	Comparison of Fetal and Adult Erythroid Chromosomal Architectures Identifies a Novel Fetal Hemoglobin Regulatory Region. <i>Blood</i> , 2017, 130, 774-774.	0.6	0
47	Genetic dissection of the β -globin super-enhancer in vivo. <i>Nature Genetics</i> , 2016, 48, 895-903.	9.4	308
48	Capture-C reveals preformed chromatin interactions between HIF binding sites and distant promoters. <i>EMBO Reports</i> , 2016, 17, 1410-1421.	2.0	63
49	Unlinking an lncRNA from Its Associated cis Element. <i>Molecular Cell</i> , 2016, 62, 104-110.	4.5	216
50	A genome-editing strategy to treat β^0 -hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. <i>Nature Medicine</i> , 2016, 22, 987-990.	15.2	279
51	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. <i>Nature Communications</i> , 2016, 7, 12983.	5.8	123
52	Predicting the three-dimensional folding of cis-regulatory regions in mammalian genomes using bioinformatic data and polymer models. <i>Genome Biology</i> , 2016, 17, 59.	3.8	97
53	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. <i>Nature Methods</i> , 2016, 13, 74-80.	9.0	225
54	ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. <i>Cell Reports</i> , 2015, 11, 405-418.	2.9	152

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55	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. <i>Nature Genetics</i> , 2014, 46, 205-212.	9.4	417
56	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. <i>Genome Biology</i> , 2013, 14, R131.	13.9	183
57	Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. <i>Human Mutation</i> , 2013, 34, 1140-1148.	1.1	10
58	Causes and Consequences of Chromatin Variation between Inbred Mice. <i>PLoS Genetics</i> , 2013, 9, e1003570.	1.5	18
59	MIG: Multi-Image Genome viewer. <i>Bioinformatics</i> , 2013, 29, 2477-2478.	1.8	15
60	High-resolution analysis of cis-acting regulatory networks at the β -globin locus. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120361.	1.8	12
61	Intragenic Enhancers Act as Alternative Promoters. <i>Molecular Cell</i> , 2012, 45, 447-458.	4.5	237
62	Nprl3 is required for normal development of the cardiovascular system. <i>Mammalian Genome</i> , 2012, 23, 404-415.	1.0	38
63	Genome-wide identification of TAL1's functional targets: Insights into its mechanisms of action in primary erythroid cells. <i>Genome Research</i> , 2010, 20, 1064-1083.	2.4	154
64	Adventitious changes in long-range gene expression caused by polymorphic structural variation and promoter competition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21771-21776.	3.3	77
65	Alternative Runx1 promoter usage in mouse developmental hematopoiesis. <i>Blood Cells, Molecules, and Diseases</i> , 2009, 43, 35-42.	0.6	52
66	Manipulating the Mouse Genome to Engineer Precise Functional Syntenic Replacements with Human Sequence. <i>Cell</i> , 2007, 128, 197-209.	13.5	150
67	Tissue-specific histone modification and transcription factor binding in β globin gene expression. <i>Blood</i> , 2007, 110, 4503-4510.	0.6	69
68	A Regulatory SNP Causes a Human Genetic Disease by Creating a New Transcriptional Promoter. <i>Science</i> , 2006, 312, 1215-1217.	6.0	254
69	Annotation of cis-regulatory elements by identification, subclassification, and functional assessment of multispecies conserved sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9830-9835.	3.3	133
70	Globin gene activation during haemopoiesis is driven by protein complexes nucleated by GATA-1 and GATA-2. <i>EMBO Journal</i> , 2004, 23, 2841-2852.	3.5	193
71	Comparative analysis of the polycystic kidney disease 1 (PKD1) gene reveals an integral membrane glycoprotein with multiple evolutionary conserved domains. <i>Human Molecular Genetics</i> , 1997, 6, 1483-1489.	1.4	141
72	Deletion of the TSC2 and PKD1 genes associated with severe infantile polycystic kidney disease is a contiguous gene syndrome. <i>Nature Genetics</i> , 1994, 8, 328-332.	9.4	466

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73	Tri-C. Protocol Exchange, 0, , .	0.3	3