Jim R Hughes

List of Publications by Year
in descending order

73 papers	6,676 citations	70961 41 h-index	85405 71 g-index
97 all docs	97 docs citations	97 times ranked	9171 citing authors

#	Article	IF	Citations
1	Deletion of the TSC2 and PKD1 genes associated with severe infantile polycystic kidney disease â€" a contiguous gene syndrome. Nature Genetics, 1994, 8, 328-332.	9.4	466
2	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. Nature Genetics, 2014, 46, 205-212.	9.4	417
3	Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903.	9.4	308
4	A genome-editing strategy to treat Î²-hemoglobinopathies that recapitulates a mutation associated with a benign genetic condition. Nature Medicine, 2016, 22, 987-990.	15.2	279
5	A Regulatory SNP Causes a Human Genetic Disease by Creating a New Transcriptional Promoter. Science, 2006, 312, 1215-1217.	6.0	254
6	Intragenic Enhancers Act as Alternative Promoters. Molecular Cell, 2012, 45, 447-458.	4.5	237
7	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	9.0	225
8	Unlinking an lncRNA from Its Associated cis Element. Molecular Cell, 2016, 62, 104-110.	4.5	216
9	Globin gene activation during haemopoiesis is driven by protein complexes nucleated by GATA-1 and GATA-2. EMBO Journal, 2004, 23, 2841-2852.	3.5	193
10	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. Genome Biology, 2013, 14, R131.	13.9	183
11	Tissue-specific CTCFâ€"cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. Nature Cell Biology, 2017, 19, 952-961.	4.6	179
12	Genome-wide identification of TAL1's functional targets: Insights into its mechanisms of action in primary erythroid cells. Genome Research, 2010, 20, 1064-1083.	2.4	154
13	ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. Cell Reports, 2015, 11, 405-418.	2.9	152
14	Manipulating the Mouse Genome to Engineer Precise Functional Syntenic ReplacementsÂwith Human Sequence. Cell, 2007, 128, 197-209.	13.5	150
15	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. Nature Genetics, 2018, 50, 1744-1751.	9.4	150
16	Comparative analysis of the polycystic kidney disease 1 (PKD1) gene reveals an integral membrane glycoprotein with multiple evolutionary conserved domains. Human Molecular Genetics, 1997, 6, 1483-1489.	1.4	141
17	Annotation of cis-regulatory elements by identification, subclassification, and functional assessment of multispecies conserved sequences. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9830-9835.	3.3	133
18	DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7526-E7535.	3.3	125

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19	How best to identify chromosomal interactions: a comparison of approaches. Nature Methods, 2017, 14, 125-134.	9.0	124
20	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	5.8	123
21	Comparative analysis of three-dimensional chromosomal architecture identifies a novel fetal hemoglobin regulatory element. Genes and Development, 2017, 31, 1704-1713.	2.7	113
22	<i>VHL</i> Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2017, 7, 1284-1305.	7.7	111
23	DeepC: predicting 3D genome folding using megabase-scale transfer learning. Nature Methods, 2020, 17, 1118-1124.	9.0	109
24	Reconstruction of the Global Neural Crest Gene Regulatory Network InÂVivo. Developmental Cell, 2019, 51, 255-276.e7.	3.1	108
25	Defining genome architecture at base-pair resolution. Nature, 2021, 595, 125-129.	13.7	107
26	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
27	DOT1L inhibition reveals a distinct subset of enhancers dependent on H3K79 methylation. Nature Communications, 2019, 10, 2803.	5.8	99
28	Predicting the three-dimensional folding of cis-regulatory regions in mammalian genomes using bioinformatic data and polymer models. Genome Biology, 2016, 17, 59.	3.8	97
29	Identification of LZTFL1 as a candidate effector gene at a COVID-19 risk locus. Nature Genetics, 2021, 53, 1606-1615.	9.4	93
30	Nrf2 controls iron homoeostasis in haemochromatosis and thalassaemia via Bmp6 and hepcidin. Nature Metabolism, 2019, 1, 519-531.	5.1	88
31	Editing an Î±-globin enhancer in primary human hematopoietic stem cells as a treatment for Î²-thalassemia. Nature Communications, 2017, 8, 424.	5.8	85
32	Absolute Quantification of Transcription Factors Reveals Principles of Gene Regulation in Erythropoiesis. Molecular Cell, 2020, 78, 960-974.e11.	4.5	83
33	Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722.	5.8	79
34	Adventitious changes in long-range gene expression caused by polymorphic structural variation and promoter competition. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21771-21776.	3.3	77
35	Tissue-specific histone modification and transcription factor binding in Î± globin gene expression. Blood, 2007, 110, 4503-4510.	0.6	69
36	Captureâ€C reveals preformed chromatin interactions between <scp>HIF</scp> â€binding sites and distant promoters. EMBO Reports, 2016, 17, 1410-1421.	2.0	63

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37	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. Nature Communications, 2018, 9, 3849.	5.8	62
38	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. Nature Genetics, 2019, 51, 1024-1034.	9.4	60
39	A revised model for promoter competition based on multi-way chromatin interactions at the Î±-globin locus. Nature Communications, 2019, 10, 5412.	5.8	60
40	Alternative Runx1 promoter usage in mouse developmental hematopoiesis. Blood Cells, Molecules, and Diseases, 2009, 43, 35-42.	0.6	52
41	Hepcidin is regulated by promoter-associated histone acetylation and HDAC3. Nature Communications, 2017, 8, 403.	5.8	45
42	Nprl3 is required for normal development of the cardiovascular system. Mammalian Genome, 2012, 23, 404-415.	1.0	38
43	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. Nature Communications, 2018, 9, 100.	5.8	38
44	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	2.4	38
45	A Dynamic Folded Hairpin Conformation Is Associated with Î±-Globin Activation in Erythroid Cells. Cell Reports, 2020, 30, 2125-2135.e5.	2.9	38
46	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. Genome Research, 2017, 27, 1730-1742.	2.4	33
47	Functional characterisation of cis-regulatory elements governing dynamic *Eomes* expression in the early mouse embryo. Development (Cambridge), 2017, 144, 1249-1260.	1.2	32
48	High-resolution targeted 3C interrogation of cis-regulatory element organization at genome-wide scale. Nature Communications, 2021, 12, 531.	5.8	32
49	Robust detection of chromosomal interactions from small numbers of cells using low-input Capture-C. Nucleic Acids Research, 2017, 45, e184-e184.	6.5	27
50	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7.	4.5	27
51	MLL-AF4 binds directly to a BCL-2 specific enhancer and modulates H3K27Âacetylation. Experimental Hematology, 2017, 47, 64-75.	0.2	25
52	Capture-C: a modular and flexible approach for high-resolution chromosome conformation capture. Nature Protocols, 2022, 17, 445-475.	5.5	24
53	Between form and function: the complexity of genome folding. Human Molecular Genetics, 2017, 26, R208-R215.	1.4	20
54	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	5.8	20

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55	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	5.8	19
56	Causes and Consequences of Chromatin Variation between Inbred Mice. PLoS Genetics, 2013, 9, e1003570.	1.5	18
57	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
58	MIG: Multi-Image Genome viewer. Bioinformatics, 2013, 29, 2477-2478.	1.8	15
59	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
60	Low-input Capture-C: A Chromosome Conformation Capture Assay to Analyze Chromatin Architecture in Small Numbers of Cells. Bio-protocol, 2017, 7, .	0.2	15
61	High-resolution analysis of <i>cis</i> -acting regulatory networks at the α-globin locus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120361.	1.8	12
62	Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. Human Mutation, 2013, 34, 1140-1148.	1.1	10
63	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
64	Dynamic Runx1 chromatin boundaries affect gene expression in hematopoietic development. Nature Communications, 2022, 13, 773.	5.8	10
65	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	1.5	9
66	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
67	High-Throughput Genotyping of CRISPR/Cas Edited Cells in 96-Well Plates. Methods and Protocols, 2018, 1, 29.	0.9	6
68	Making connections: enhancers in cellular differentiation. Trends in Genetics, 2022, 38, 395-408.	2.9	6
69	Chromatin interaction maps identify Wnt responsive cis-regulatory elements coordinating Paupar-Pax6 expression in neuronal cells. PLoS Genetics, 2022, 18, e1010230.	1.5	6
70	Multi Locus View: an extensible web-based tool for the analysis of genomic data.. Communications Biology, 2021, 4, 623.	2.0	4
71	Tri-C. Protocol Exchange, 0, , .	0.3	3
72	Natural and Experimental Rewiring of Gene Regulatory Regions. Annual Review of Genomics and Human Genetics, 2022, 23, .	2.5	1

#	ARTICLE	IF	CITATIONS
73	Comparison of Fetal and Adult Erythroid Chromosomal Architectures Identifies a Novel Fetal Hemoglobin Regulatory Region. Blood, 2017, 130, 774-774.	0.6	0