

David Garrick

List of Publications by Year in descending order

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43
papers

5,436
citations

236925

25
h-index

377865

34
g-index

46
all docs

46
docs citations

46
times ranked

7180
citing authors

#	ARTICLE	IF	CITATIONS
1	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. <i>Cell</i> , 2010, 140, 678-691.	28.9	1,069
2	Repeat-induced gene silencing in mammals. <i>Nature Genetics</i> , 1998, 18, 56-59.	21.4	804
3	Transcription of antisense RNA leading to gene silencing and methylation as a novel cause of human genetic disease. <i>Nature Genetics</i> , 2003, 34, 157-165.	21.4	505
4	Mutations in ATRX, encoding a SWI/SNF-like protein, cause diverse changes in the pattern of DNA methylation. <i>Nature Genetics</i> , 2000, 24, 368-371.	21.4	476
5	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. <i>Cell</i> , 2010, 143, 367-378.	28.9	365
6	Intragenic Enhancers Act as Alternative Promoters. <i>Molecular Cell</i> , 2012, 45, 447-458.	9.7	237
7	Combinatorial readout of histone H3 modifications specifies localization of ATRX to heterochromatin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 777-782.	8.2	187
8	An interspecies analysis reveals a key role for unmethylated CpG dinucleotides in vertebrate Polycomb complex recruitment. <i>EMBO Journal</i> , 2012, 31, 317-329.	7.8	173
9	The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. <i>Journal of Clinical Investigation</i> , 2005, 115, 258-267.	8.2	169
10	Position-dependent variegation of globin transgene expression in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 5371-5375.	7.1	164
11	Loss of Atrx Affects Trophoblast Development and the Pattern of X-Inactivation in Extraembryonic Tissues. <i>PLoS Genetics</i> , 2006, 2, e58.	3.5	140
12	Identification of acquired somatic mutations in the gene encoding chromatin-remodeling factor ATRX in the α -thalassemia myelodysplasia syndrome (ATMDS). <i>Nature Genetics</i> , 2003, 34, 446-449.	21.4	132
13	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.	7.1	125
14	The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. <i>Journal of Clinical Investigation</i> , 2005, 115, 258-267.	8.2	119
15	Age-Associated Decrease of the Histone Methyltransferase SUV39H1 in HSC Perturbs Heterochromatin and B Lymphoid Differentiation. <i>Stem Cell Reports</i> , 2016, 6, 970-984.	4.8	88
16	Age-dependent silencing of globin transgenes in the mouse. <i>Nucleic Acids Research</i> , 1996, 24, 1465-1471.	14.5	84
17	Polycomb eviction as a new distant enhancer function. <i>Genes and Development</i> , 2011, 25, 1583-1588.	5.9	78
18	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.	7.1	77

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19	Generation of bivalent chromatin domains during cell fate decisions. <i>Epigenetics and Chromatin</i> , 2011, 4, 9.	3.9	54
20	A conserved truncated isoform of the ATR-X syndrome protein lacking the SWI/SNF-homology domain. <i>Gene</i> , 2004, 326, 23-34.	2.2	53
21	Variegated Expression of a Globin Transgene Correlates with Chromatin Accessibility But Not Methylation Status. <i>Nucleic Acids Research</i> , 1996, 24, 4902-4909.	14.5	52
22	The role of the polycomb complex in silencing $\hat{\pm}$ -globin gene expression in nonerythroid cells. <i>Blood</i> , 2008, 112, 3889-3899.	1.4	51
23	Understanding $\hat{\pm}$ -Globin Gene Regulation: Aiming to Improve the Management of Thalassemia. <i>Annals of the New York Academy of Sciences</i> , 2005, 1054, 92-102.	3.8	47
24	Defining the Cause of Skewed X-Chromosome Inactivation in X-Linked Mental Retardation by Use of a Mouse Model. <i>American Journal of Human Genetics</i> , 2007, 80, 1138-1149.	6.2	32
25	Epigenetic Effects on Transgene Expression. , 2001, 158, 351-368.		31
26	A large deletion in the human $\hat{\pm}$ -globin cluster caused by a replication error is associated with an unexpectedly mild phenotype. <i>Human Molecular Genetics</i> , 2008, 17, 3084-3093.	2.9	26
27	The long non-coding RNA CRNDE regulates growth of multiple myeloma cells via an effect on IL6 signalling. <i>Leukemia</i> , 2021, 35, 1710-1721.	7.2	26
28	CpG binding protein (CFP1) occupies open chromatin regions of active genes, including enhancers and non-CpG islands. <i>Epigenetics and Chromatin</i> , 2018, 11, 59.	3.9	19
29	Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. <i>Human Mutation</i> , 2013, 34, 1140-1148.	2.5	10
30	Identification of the transcription factor MAZ as a regulator of erythropoiesis. <i>Blood Advances</i> , 2021, 5, 3002-3015.	5.2	8
31	CAR $\hat{\pm}$ cells derived from multiple myeloma patients at diagnosis have improved cytotoxic functions compared to those produced at relapse or following daratumumab treatment. <i>EJHaem</i> , 2022, 3, 970-974.	1.0	8
32	Epigenetic mechanisms. , 0, , 62-74.		7
33	How transcriptional and epigenetic programmes are played out on an individual mammalian gene cluster during lineage commitment and differentiation. <i>Biochemical Society Symposia</i> , 2006, 73, 11-22.	2.7	7
34	Switching genes on and off in haemopoiesis. <i>Biochemical Society Transactions</i> , 2008, 36, 613-618.	3.4	6
35	Aging of Human Haematopoietic Stem Cells. , 2015, , 127-147.		2
36	Hematopoietic Stem Cell Aging and Malignant Hemopathies. , 2018, , 1-13.		2

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37	CTCF, cohesin and higher-order chromatin structure. Epigenomics, 2009, 1, 232.	2.1	1
38	Research Highlights. Epigenomics, 2009, 1, 231-234.	2.1	0
39	Noncoding RNA and Epigenetic Change in Hematopoietic Stem Cell Aging. , 2018, , 1-29.		0
40	Noncoding RNA and Epigenetic Change in Hematopoietic Stem Cell Aging. , 2019, , 1011-1038.		0
41	Hematopoietic Stem Cell Aging and Malignant Hemopathies. , 2020, , 169-181.		0
42	The regulatory interplay of CpG islands and nucleosome remodeling at mammalian primary response genes. Epigenomics, 2009, 1, 233.	2.1	0
43	XNP/ATRX at sites of nucleosome replacement. Epigenomics, 2009, 1, 233-4.	2.1	0