## David Garrick

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1159750/publications.pdf

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43 papers 5,436 citations

236925 25 h-index 34 g-index

46 all docs

46 docs citations

46 times ranked 7180 citing authors

#	Article	IF	CITATIONS
1	CARâ€T cells derived from multiple myeloma patients at diagnosis have improved cytotoxic functions compared to those produced at relapse or following daratumumab treatment. EJHaem, 2022, 3, 970-974.	1.0	8
2	The long non-coding RNA CRNDE regulates growth of multiple myeloma cells via an effect on IL6 signalling. Leukemia, 2021, 35, 1710-1721.	7.2	26
3	Identification of the transcription factor MAZ as a regulator of erythropoiesis. Blood Advances, 2021, 5, 3002-3015.	5.2	8
4	Hematopoietic Stem Cell Aging and Malignant Hemopathies. , 2020, , 169-181.		0
5	Noncoding RNA and Epigenetic Change in Hematopoietic Stem Cell Aging. , 2019, , 1011-1038.		O
6	CpG binding protein (CFP1) occupies open chromatin regions of active genes, including enhancers and non-CpG islands. Epigenetics and Chromatin, $2018$ , $11$ , $59$ .	3.9	19
7	Hematopoietic Stem Cell Aging and Malignant Hemopathies. , 2018, , 1-13.		2
8	Noncoding RNA and Epigenetic Change in Hematopoietic Stem Cell Aging. , 2018, , 1-29.		0
9	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.	7.1	125
10	Age-Associated Decrease of the Histone Methyltransferase SUV39H1 in HSC Perturbs Heterochromatin and B Lymphoid Differentiation. Stem Cell Reports, 2016, 6, 970-984.	4.8	88
11	Aging of Human Haematopoietic Stem Cells. , 2015, , 127-147.		2
12	Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. Human Mutation, $2013$ , $34$ , $1140$ - $1148$ .	2.5	10
13	An interspecies analysis reveals a key role for unmethylated CpG dinucleotides in vertebrate Polycomb complex recruitment. EMBO Journal, 2012, 31, 317-329.	7.8	173
14	Intragenic Enhancers Act as Alternative Promoters. Molecular Cell, 2012, 45, 447-458.	9.7	237
15	Combinatorial readout of histone H3 modifications specifies localization of ATRX to heterochromatin. Nature Structural and Molecular Biology, 2011, 18, 777-782.	8.2	187
16	Polycomb eviction as a new distant enhancer function. Genes and Development, 2011, 25, 1583-1588.	5.9	78
17	Generation of bivalent chromatin domains during cell fate decisions. Epigenetics and Chromatin, 2011, 4, 9.	3.9	54
18	Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691.	28.9	1,069

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19	ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. Cell, 2010, 143, 367-378.	28.9	365
20	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.	7.1	77
21	Research Highlights. Epigenomics, 2009, 1, 231-234.	2.1	O
22	CTCF, cohesin and higher-order chromatin structure. Epigenomics, 2009, 1, 232.	2.1	1
23	The regulatory interplay of CpG islands and nucleosome remodeling at mammalian primary response genes. Epigenomics, 2009, 1, 233.	2.1	0
24	XNP/ATRX at sites of nucleosome replacement. Epigenomics, 2009, 1, 233-4.	2.1	0
25	A large deletion in the human Â-globin cluster caused by a replication error is associated with an unexpectedly mild phenotype. Human Molecular Genetics, 2008, 17, 3084-3093.	2.9	26
26	Switching genes on and off in haemopoiesis. Biochemical Society Transactions, 2008, 36, 613-618.	3.4	6
27	The role of the polycomb complex in silencing $\hat{l}_{\pm}$ -globin gene expression in nonerythroid cells. Blood, 2008, 112, 3889-3899.	1.4	51
28	Defining the Cause of Skewed X-Chromosome Inactivation in X-Linked Mental Retardation by Use of a Mouse Model. American Journal of Human Genetics, 2007, 80, 1138-1149.	6.2	32
29	Loss of Atrx Affects Trophoblast Development and the Pattern of X-Inactivation in Extraembryonic Tissues. PLoS Genetics, 2006, 2, e58.	3.5	140
30	How transcriptional and epigenetic programmes are played out on an individual mammalian gene cluster during lineage commitment and differentiation. Biochemical Society Symposia, 2006, 73, 11-22.	2.7	7
31	Understanding $\hat{I}_{\pm}$ -Globin Gene Regulation: Aiming to Improve the Management of Thalassemia. Annals of the New York Academy of Sciences, 2005, 1054, 92-102.	3.8	47
32	The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. Journal of Clinical Investigation, 2005, 115, 258-267.	8.2	169
33	The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. Journal of Clinical Investigation, 2005, 115, 258-267.	8.2	119
34	A conserved truncated isoform of the ATR-X syndrome protein lacking the SWI/SNF-homology domain. Gene, 2004, 326, 23-34.	2.2	53
35	Transcription of antisense RNA leading to gene silencing and methylation as a novel cause of human genetic disease. Nature Genetics, 2003, 34, 157-165.	21.4	505
36	Identification of acquired somatic mutations in the gene encoding chromatin-remodeling factor ATRX in the α-thalassemia myelodysplasia syndrome (ATMDS). Nature Genetics, 2003, 34, 446-449.	21.4	132

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37	Epigenetic Effects on Transgene Expression. , 2001, 158, 351-368.		31
38	Mutations in ATRX, encoding a SWI/SNF-like protein, cause diverse changes in the pattern of DNA methylation. Nature Genetics, 2000, 24, 368-371.	21.4	476
39	Repeat-induced gene silencing in mammals. Nature Genetics, 1998, 18, 56-59.	21.4	804
40	Age-dependent silencing of globin transgenes in the mouse. Nucleic Acids Research, 1996, 24, 1465-1471.	14.5	84
41	Variegated Expression of a Globin Transgene Correlates with Chromatin Accessibility But Not Methylation Status. Nucleic Acids Research, 1996, 24, 4902-4909.	14.5	52
42	Position-dependent variegation of globin transgene expression in mice Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5371-5375.	7.1	164
43	Epigenetic mechanisms. , 0, , 62-74.		7