David Vetrie

List of Publications by Year
in descending order

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37	11,051	172457	330143
papers	citations	29 h-index	37 g-index

38	38	38	16932
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	Requirement of bic/microRNA-155 for Normal Immune Function. Science, 2007, 316, 608-611.	12.6	1,786
3	The gene involved in X-linked agammaglobulinaemia is a member of the src family of protein-tyrosine kinases. Nature, 1993, 361, 226-233.	27.8	1,400
4	DNA microarrays for comparative genomic hybridization based on DOPâ€PCR amplification of BAC and PAC clones. Genes Chromosomes and Cancer, 2003, 36, 361-374.	2.8	439
5	The landscape of histone modifications across 1% of the human genome in five human cell lines. Genome Research, 2007, 17, 691-707.	5.5	353
6	A novel Xâ€“linked gene, DDP, shows mutations in families with deafness (DFNâ€“1), dystonia, mental deficiency and blindness. Nature Genetics, 1996, 14, 177-180.	21.4	256
7	The chronic myeloid leukemia stem cell: stemming the tide of persistence. Blood, 2017, 129, 1595-1606.	1.4	240
8	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. Nature, 2016, 534, 341-346.	27.8	204
9	The leukaemia stem cell: similarities, differences and clinical prospects in CML and AML. Nature Reviews Cancer, 2020, 20, 158-173.	28.4	181
10	Structural instability of human tandemly repeated DNA sequences cloned in yeast artificial chromosome vectors. Nucleic Acids Research, 1990, 18, 1421-1428.	14.5	140
11	Exon Array CGH: Detection of Copy-Number Changes at the Resolution of Individual Exons in the Human Genome. American Journal of Human Genetics, 2005, 76, 750-762.	6.2	132
12	Epigenetic Reprogramming Sensitizes CML Stem Cells to Combined EZH2 and Tyrosine Kinase Inhibition. Cancer Discovery, 2016, 6, 1248-1257.	9.4	120
13	Pelizaeus-Merzbacher Disease: Identification of Xq22 Proteolipid-Protein Duplications and Characterization of Breakpoints by Interphase FISH. American Journal of Human Genetics, 1998, 63, 207-217.	6.2	108
14	Expression profiling of the Leishmania life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. Molecular and Biochemical Parasitology, 2004, 136, 87-100.	1.1	76
15	Gene expression profiling in the myelodysplastic syndromes using cDNA microarray technology. British Journal of Haematology, 2004, 125, 576-583.	2.5	75
16	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. Genome Research, 2009, 19, 994-1005.	5.5	73
17	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. Human Molecular Genetics, 2005, 14, 3435-3447.	2.9	71
18	Complex Exon-Intron Marking by Histone Modifications Is Not Determined Solely by Nucleosome Distribution. PLoS ONE, 2010, 5, e12339.	2.5	64

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19	Identification of Btk mutations in 20 unrelated patients with X-linked agammaglobulinaemia (XLA). Human Molecular Genetics, 1995, 4, 693-700.	2.9	59
20	CML cells actively evade host immune surveillance through cytokine-mediated downregulation of MHC-II expression. Blood, 2017, 129, 199-208.	1.4	58
21	Detection of mutations in COL4A5 in patients with Alport Syndrome. Human Mutation, 1999, 13, 124-132.	2.5	57
22	Epigenetic dysregulation in chronic myeloid leukaemia: A myriad of mechanisms and therapeutic options. Seminars in Cancer Biology, 2018, 51, 180-197.	9.6	53
23	From genomes to vaccines:Leishmaniaas a model. Philosophical Transactions of the Royal Society B: Biological Sciences, 2002, 357, 5-11.	4.0	49
24	Autosomal-Dominant Microtia Linked to Five Tandem Copies of a Copy-Number-Variable Region at Chromosome 4p16. American Journal of Human Genetics, 2008, 82, 181-187.	6.2	42
25	Gene expression profiling in polycythemia vera using cDNA microarray technology. Cancer Research, 2003, 63, 3940-4.	0.9	42
26	Isolation of Cosmid and cDNA Clones in the Region Surrounding the BTK Gene at Xq21.3-q22. Genomics, 1994, 21, 517-524.	2.9	41
27	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. Genome Research, 2006, 16, 1310-1319.	5.5	34
28	A 6.5-Mb Yeast Artificial Chromosome Contig Incorporating 33 DNA Markers on the Human X Chromosome at Xq22. Genomics, 1994, 19, 42-47.	2.9	30
29	Identification of genetic aberrations on chromosome 22 outside theNF2locus in schwannomatosis and neurofibromatosis type 2. Human Mutation, 2005, 26, 540-549.	2.5	29
30	ULK1 inhibition promotes oxidative stressâ€“induced differentiation and sensitizes leukemic stem cells to targeted therapy. Science Translational Medicine, 2021, 13, eabd5016.	12.4	26
31	Construction of a 5.2-Megabase Physical Map of the Human X Chromosome at Xq22 Using Pulsed-Field Gel Electrophoresis and Yeast Artificial Chromosomes. Genomics, 1993, 15, 631-642.	2.9	25
32	Applications of genomic microarrays to explore human chromosome structure and function. Human Molecular Genetics, 2004, 13, R297-R302.	2.9	19
33	A Complete YAC Contig and Cosmid Interval Map Covering the Entirety of Human Xq21.33 to Xq22.3 from DXS3 to DXS287. Genomics, 1997, 43, 171-182.	2.9	17
34	Epigenetic Reprogramming and Emerging Epigenetic Therapies in CML. Frontiers in Cell and Developmental Biology, 2019, 7, 136.	3.7	16
35	Genomic Approaches Uncover Increasing Complexities in the Regulatory Landscape at the Human SCL (TAL1) Locus. PLoS ONE, 2010, 5, e9059.	2.5	15
36	Identification of deletions in thebtk gene allows unambiguous assessment of carrier status in families with X-linked agammaglobulinaemia. Human Genetics, 1994, 94, 77-79.	3.8	8

#	Article	IF	Citations
37	Repositioned to kill stem cells. Nature, 2015, 525, 328-329.	27.8	4