

David Vetrie

List of Publications by Year in descending order

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37
papers

11,051
citations

172457

29
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330143

37
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38
docs citations

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times ranked

16932
citing authors

#	ARTICLE	IF	CITATIONS
1	ULK1 inhibition promotes oxidative stressâ€“induced differentiation and sensitizes leukemic stem cells to targeted therapy. <i>Science Translational Medicine</i> , 2021, 13, eabd5016.	12.4	26
2	The leukaemia stem cell: similarities, differences and clinical prospects in CML and AML. <i>Nature Reviews Cancer</i> , 2020, 20, 158-173.	28.4	181
3	Epigenetic Reprogramming and Emerging Epigenetic Therapies in CML. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 136.	3.7	16
4	Epigenetic dysregulation in chronic myeloid leukaemia: A myriad of mechanisms and therapeutic options. <i>Seminars in Cancer Biology</i> , 2018, 51, 180-197.	9.6	53
5	The chronic myeloid leukemia stem cell: stemming the tide of persistence. <i>Blood</i> , 2017, 129, 1595-1606.	1.4	240
6	CML cells actively evade host immune surveillance through cytokine-mediated downregulation of MHC-II expression. <i>Blood</i> , 2017, 129, 199-208.	1.4	58
7	Epigenetic Reprogramming Sensitizes CML Stem Cells to Combined EZH2 and Tyrosine Kinase Inhibition. <i>Cancer Discovery</i> , 2016, 6, 1248-1257.	9.4	120
8	Dual targeting of p53 and c-MYC selectively eliminates leukaemic stem cells. <i>Nature</i> , 2016, 534, 341-346.	27.8	204
9	Repositioned to kill stem cells. <i>Nature</i> , 2015, 525, 328-329.	27.8	4
10	Complex Exon-Intron Marking by Histone Modifications Is Not Determined Solely by Nucleosome Distribution. <i>PLoS ONE</i> , 2010, 5, e12339.	2.5	64
11	Genomic Approaches Uncover Increasing Complexities in the Regulatory Landscape at the Human SCL (TAL1) Locus. <i>PLoS ONE</i> , 2010, 5, e9059.	2.5	15
12	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. <i>Genome Research</i> , 2009, 19, 994-1005.	5.5	73
13	Autosomal-Dominant Microtia Linked to Five Tandem Copies of a Copy-Number-Variable Region at Chromosome 4p16. <i>American Journal of Human Genetics</i> , 2008, 82, 181-187.	6.2	42
14	The landscape of histone modifications across 1% of the human genome in five human cell lines. <i>Genome Research</i> , 2007, 17, 691-707.	5.5	353
15	Requirement of <i>bic/microRNA-155</i> for Normal Immune Function. <i>Science</i> , 2007, 316, 608-611.	12.6	1,786
16	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
17	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. <i>Genome Research</i> , 2006, 16, 1310-1319.	5.5	34
18	Identification of genetic aberrations on chromosome 22 outside theNF2locus in schwannomatosis and neurofibromatosis type 2. <i>Human Mutation</i> , 2005, 26, 540-549.	2.5	29

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19	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. <i>Human Molecular Genetics</i> , 2005, 14, 3435-3447.	2.9	71
20	Exon Array CGH: Detection of Copy-Number Changes at the Resolution of Individual Exons in the Human Genome. <i>American Journal of Human Genetics</i> , 2005, 76, 750-762.	6.2	132
21	Applications of genomic microarrays to explore human chromosome structure and function. <i>Human Molecular Genetics</i> , 2004, 13, R297-R302.	2.9	19
22	Gene expression profiling in the myelodysplastic syndromes using cDNA microarray technology. <i>British Journal of Haematology</i> , 2004, 125, 576-583.	2.5	75
23	Expression profiling of the <i>Leishmania</i> life cycle: cDNA arrays identify developmentally regulated genes present but not annotated in the genome. <i>Molecular and Biochemical Parasitology</i> , 2004, 136, 87-100.	1.1	76
24	DNA microarrays for comparative genomic hybridization based on DOP-PCR amplification of BAC and PAC clones. <i>Genes Chromosomes and Cancer</i> , 2003, 36, 361-374.	2.8	439
25	Gene expression profiling in polycythemia vera using cDNA microarray technology. <i>Cancer Research</i> , 2003, 63, 3940-4.	0.9	42
26	From genomes to vaccines: <i>Leishmania</i> as a model. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2002, 357, 5-11.	4.0	49
27	Detection of mutations in COL4A5 in patients with Alport Syndrome. <i>Human Mutation</i> , 1999, 13, 124-132.	2.5	57
28	Pelizaeus-Merzbacher Disease: Identification of Xq22 Proteolipid-Protein Duplications and Characterization of Breakpoints by Interphase FISH. <i>American Journal of Human Genetics</i> , 1998, 63, 207-217.	6.2	108
29	A Complete YAC Contig and Cosmid Interval Map Covering the Entirety of Human Xq21.33 to Xq22.3 from DXS3 to DXS287. <i>Genomics</i> , 1997, 43, 171-182.	2.9	17
30	A novel X-linked gene, DDP, shows mutations in families with deafness (DFN1), dystonia, mental deficiency and blindness. <i>Nature Genetics</i> , 1996, 14, 177-180.	21.4	256
31	Identification of Btk mutations in 20 unrelated patients with X-linked agammaglobulinaemia (XLA). <i>Human Molecular Genetics</i> , 1995, 4, 693-700.	2.9	59
32	Identification of deletions in the btk gene allows unambiguous assessment of carrier status in families with X-linked agammaglobulinaemia. <i>Human Genetics</i> , 1994, 94, 77-79.	3.8	8
33	A 6.5-Mb Yeast Artificial Chromosome Contig Incorporating 33 DNA Markers on the Human X Chromosome at Xq22. <i>Genomics</i> , 1994, 19, 42-47.	2.9	30
34	Isolation of Cosmid and cDNA Clones in the Region Surrounding the BTK Gene at Xq21.3-q22. <i>Genomics</i> , 1994, 21, 517-524.	2.9	41
35	The gene involved in X-linked agammaglobulinaemia is a member of the src family of protein-tyrosine kinases. <i>Nature</i> , 1993, 361, 226-233.	27.8	1,400
36	Construction of a 5.2-Megabase Physical Map of the Human X Chromosome at Xq22 Using Pulsed-Field Gel Electrophoresis and Yeast Artificial Chromosomes. <i>Genomics</i> , 1993, 15, 631-642.	2.9	25

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37	Structural instability of human tandemly repeated DNA sequences cloned in yeast artificial chromosome vectors. <i>Nucleic Acids Research</i> , 1990, 18, 1421-1428.	14.5	140