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List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

16,264
citations

71061

41
h-index

48277

88
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103
all docs

103
docs citations

103
times ranked

25180
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiomic Characterization of High-Grade Serous Ovarian Carcinoma Enables High-Resolution Patient Stratification. <i>Clinical Cancer Research</i> , 2022, 28, 3546-3556.	3.2	5
2	Functional brain defects in a mouse model of a chromosomal t(1;11) translocation that disrupts DISC1 and confers increased risk of psychiatric illness. <i>Translational Psychiatry</i> , 2021, 11, 135.	2.4	3
3	Structural Variants at the <i>BRCA1/2</i> Loci are a Common Source of Homologous Repair Deficiency in High-grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2021, 27, 3201-3214.	3.2	27
4	Integrated molecular characterisation of endometrioid ovarian carcinoma identifies opportunities for stratification. <i>Npj Precision Oncology</i> , 2021, 5, 47.	2.3	10
5	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. <i>Genome Research</i> , 2021, 31, 1994-2007.	2.4	4
6	ISGylation drives basal breast tumour progression by promoting EGFR recycling and Akt signalling. <i>Oncogene</i> , 2021, 40, 6235-6247.	2.6	16
7	Gene Co-Expression Network Analysis Identifies Vitamin D-Associated Gene Modules in Adult Normal Rectal Epithelium Following Supplementation. <i>Frontiers in Genetics</i> , 2021, 12, 783970.	1.1	3
8	Molecular stratification of endometrioid ovarian carcinoma predicts clinical outcome. <i>Nature Communications</i> , 2020, 11, 4995.	5.8	70
9	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
10	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020, 583, 265-270.	13.7	36
11	An actionable <i>KCNH2</i> Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. <i>Scientific Reports</i> , 2019, 9, 10964.	1.6	17
12	Clinical and molecular characterization of ovarian carcinoma displaying isolated lymph node relapse. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 221, 245.e1-245.e15.	0.7	22
13	Zebrafish <i>MITF</i> -Low Melanoma Subtype Models Reveal Transcriptional Subclusters and <i>MITF</i> -Independent Residual Disease. <i>Cancer Research</i> , 2019, 79, 5769-5784.	0.4	36
14	Modeling double strand break susceptibility to interrogate structural variation in cancer. <i>Genome Biology</i> , 2019, 20, 28.	3.8	11
15	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. <i>PLoS Genetics</i> , 2019, 15, e1008480.	1.5	17
16	Abstract 749: Multi-layer molecular characterization of high grade serous ovarian carcinomas. <i>Cancer Research</i> , 2019, 79, 749-749.	0.4	1
17	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018, 8, 180011.	1.5	13
18	<i>DISC1</i> regulates N-methyl-D-aspartate receptor dynamics: abnormalities induced by a <i>Disc1</i> mutation modelling a translocation linked to major mental illness. <i>Translational Psychiatry</i> , 2018, 8, 184.	2.4	21

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19	Chromatin loop anchors are associated with genome instability in cancer and recombination hotspots in the germline. <i>Genome Biology</i> , 2018, 19, 101.	3.8	43
20	Enhanced response rate to pegylated liposomal doxorubicin in high grade serous ovarian carcinomas harbouring BRCA1 and BRCA2 aberrations. <i>BMC Cancer</i> , 2018, 18, 16.	1.1	13
21	Breaking point: the genesis and impact of structural variation in tumours. <i>F1000Research</i> , 2018, 7, 1814.	0.8	7
22	The circadian dynamics of small nucleolar RNA in the mouse liver. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170034.	1.5	13
23	Crossing Borders. , 2017, , 45-67.		0
24	When TADs go bad: chromatin structure and nuclear organisation in human disease. <i>F1000Research</i> , 2017, 6, 314.	0.8	52
25	Mutational Biases Drive Elevated Rates of Substitution at Regulatory Sites across Cancer Types. <i>PLoS Genetics</i> , 2016, 12, e1006207.	1.5	75
26	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. <i>Molecular Systems Biology</i> , 2015, 11, 852.	3.2	305
27	Integrative modeling reveals the principles of multi-scale chromatin boundary formation in human nuclear organization. <i>Genome Biology</i> , 2015, 16, 110.	3.8	33
28	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. <i>Human Molecular Genetics</i> , 2015, 24, 5464-5474.	1.4	27
29	Transcriptional Dynamics Reveal Critical Roles for Non-coding RNAs in the Immediate-Early Response. <i>PLoS Computational Biology</i> , 2015, 11, e1004217.	1.5	22
30	Abundant local interactions in the 4p16.1 region suggest functional mechanisms underlying SLC2A9 associations with human serum uric acid. <i>Human Molecular Genetics</i> , 2014, 23, 5061-5068.	1.4	29
31	Sequence-Level Mechanisms of Human Epigenome Evolution. <i>Genome Biology and Evolution</i> , 2014, 6, 1758-1771.	1.1	17
32	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
33	The genomic signature of trait-associated variants. <i>BMC Genomics</i> , 2013, 14, 108.	1.2	45
34	Divergence of Mammalian Higher Order Chromatin Structure Is Associated with Developmental Loci. <i>PLoS Computational Biology</i> , 2013, 9, e1003017.	1.5	36
35	Side Effects: Substantial Non-Neutral Evolution Flanking Regulatory Sites. <i>PLoS Genetics</i> , 2013, 9, e1003528.	1.5	1
36	Corrigendum of 'High throughput analysis of epistasis in genome-wide association studies with BiForce'. <i>Bioinformatics</i> , 2013, 29, 2667-2668.	1.8	0

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37	Lsh regulates LTR retrotransposon repression independently of Dnmt3b function. <i>Genome Biology</i> , 2013, 14, R146.	13.9	54
38	Properties of Local Interactions and Their Potential Value in Complementing Genome-Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e71203.	1.1	15
39	High-throughput analysis of epistasis in genome-wide association studies with BiForce. <i>Bioinformatics</i> , 2012, 28, 1957-1964.	1.8	49
40	BiForce Toolbox: powerful high-throughput computational analysis of gene-gene interactions in genome-wide association studies. <i>Nucleic Acids Research</i> , 2012, 40, W628-W632.	6.5	25
41	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012, 44, 770-776.	9.4	210
42	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. <i>Epigenetics and Chromatin</i> , 2012, 5, 6.	1.8	20
43	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E944-53.	3.3	332
44	Genome-wide methylation profiling in Crohn's disease identifies altered epigenetic regulation of key host defense mechanisms including the Th17 pathway. <i>Inflammatory Bowel Diseases</i> , 2012, 18, 889-899.	0.9	152
45	The retroviral proteinase active site and the N-terminus of Ddi1 are required for repression of protein secretion. <i>FEBS Letters</i> , 2011, 585, 139-142.	1.3	26
46	Human Î²-defensin 3 affects the activity of pro-inflammatory pathways associated with MyD88 and TRIF. <i>European Journal of Immunology</i> , 2011, 41, 3291-3300.	1.6	122
47	Widespread signatures of recent selection linked to nucleosome positioning in the human lineage. <i>Genome Research</i> , 2011, 21, 1777-1787.	2.4	65
48	A High-Resolution Anatomical Atlas of the Transcriptome in the Mouse Embryo. <i>PLoS Biology</i> , 2011, 9, e1000582.	2.6	552
49	Thioredoxin Txnl1/TRP32 Is a Redox-active Cofactor of the 26 S Proteasome. <i>Journal of Biological Chemistry</i> , 2009, 284, 15246-15254.	1.6	68
50	The Structure of Change. <i>Science</i> , 2009, 323, 347-348.	6.0	7
51	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
52	New ATPase regulators p97 goes to the PUB. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 2380-2388.	1.2	67
53	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. <i>Nature Genetics</i> , 2008, 40, 631-637.	9.4	542
54	Rapidly evolving human promoter regions. <i>Nature Genetics</i> , 2008, 40, 1262-1263.	9.4	18

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55	Posttranscriptional Regulation of miRNAs Harboring Conserved Terminal Loops. <i>Molecular Cell</i> , 2008, 32, 383-393.	4.5	316
56	Ubx1 is a novel co-factor of the human p97 ATPase. <i>International Journal of Biochemistry and Cell Biology</i> , 2008, 40, 2927-2942.	1.2	42
57	Chromatin structure and evolution in the human genome. <i>BMC Evolutionary Biology</i> , 2007, 7, 72.	3.2	80
58	Characterisation of the nascent polypeptide-associated complex in fission yeast. <i>Molecular Biology Reports</i> , 2007, 34, 275-281.	1.0	16
59	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	9.4	1,201
60	Mutations in genes encoding ribonuclease H2 subunits cause Aicardi-Goutières syndrome and mimic congenital viral brain infection. <i>Nature Genetics</i> , 2006, 38, 910-916.	9.4	592
61	The changing of the guard: Molecular diversity and rapid evolution of β -defensins. <i>Molecular Diversity</i> , 2006, 10, 575-584.	2.1	75
62	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. <i>Nucleic Acids Research</i> , 2006, 34, 3067-3081.	6.5	134
63	Disruption of <i>Ledgf/Prp1</i> Results in Perinatal Mortality and Homeotic Skeletal Transformations. <i>Molecular and Cellular Biology</i> , 2006, 26, 7201-7210.	1.1	96
64	Heterotachy in Mammalian Promoter Evolution. <i>PLoS Genetics</i> , 2006, 2, e30.	1.5	102
65	Mouse MAELSTROM: the link between meiotic silencing of unsynapsed chromatin and microRNA pathway?. <i>Human Molecular Genetics</i> , 2006, 15, 2324-2334.	1.4	131
66	The complexity of selection at the major primate beta-defensin locus. <i>BMC Evolutionary Biology</i> , 2005, 5, 32.	3.2	38
67	<i>Dazl</i> binds in vivo to specific transcripts and can regulate the pre-meiotic translation of <i>Mvh</i> in germ cells. <i>Human Molecular Genetics</i> , 2005, 14, 3899-3909.	1.4	158
68	Two novel proteins recruited by synaptonemal complex protein 1 (SYCP1) are at the centre of meiosis. <i>Journal of Cell Science</i> , 2005, 118, 2755-2762.	1.2	190
69	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	6.0	3,227
70	Deep genomics in shallow times: the finished sequence of human chromosomes 13 and 19. <i>European Journal of Human Genetics</i> , 2004, 12, 875-876.	1.4	6
71	UBA domain containing proteins in fission yeast. <i>International Journal of Biochemistry and Cell Biology</i> , 2003, 35, 629-636.	1.2	30
72	POCUS: mining genomic sequence annotation to predict disease genes. <i>Genome Biology</i> , 2003, 4, R75.	13.9	199

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73	Duplication and selection in the evolution of primate beta-defensin genes. <i>Genome Biology</i> , 2003, 4, R31.	13.9	134
74	The Comparative Proteomics of Ubiquitination in Mouse. <i>Genome Research</i> , 2003, 13, 1389-1394.	2.4	122
75	Signal Sequence Conservation and Mature Peptide Divergence Within Subgroups of the Murine beta-Defensin Gene Family. <i>Molecular Biology and Evolution</i> , 2003, 20, 460-470.	3.5	81
76	SNP genotyping on pooled DNAs: comparison of genotyping technologies and a semi automated method for data storage and analysis. <i>Nucleic Acids Research</i> , 2002, 30, 74e-74.	6.5	114
77	Computational Comparison of Human Genomic Sequence Assemblies for a Region of Chromosome 4. <i>Genome Research</i> , 2002, 12, 424-429.	2.4	12
78	Sushi gets serious: the draft genome sequence of the pufferfish <i>Fugu rubripes</i> . <i>Genome Biology</i> , 2002, 3, reviews1025.1.	13.9	1
79	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	13.7	1,548
80	A 6.9-Mb High-Resolution BAC/PAC Contig of Human 4p15.3â€“p16.1, a Candidate Region for Bipolar Affective Disorder. <i>Genomics</i> , 2001, 71, 315-323.	1.3	12
81	Identification of Genes from a Schizophrenia-Linked Translocation Breakpoint Region. <i>Genomics</i> , 2001, 73, 123-126.	1.3	21
82	Identification of polymorphisms within Disrupted in Schizophrenia 1 and Disrupted in Schizophrenia 2, and an investigation of their association with schizophrenia and bipolar affective disorder. <i>Psychiatric Genetics</i> , 2001, 11, 71-78.	0.6	116
83	Proteins containing the UBA domain are able to bind to multi-ubiquitin chains. <i>Nature Cell Biology</i> , 2001, 3, 939-943.	4.6	375
84	Physical mapping: integrating computational and molecular genetic data. <i>Annals of Human Genetics</i> , 2001, 65, 221-228.	0.3	2
85	Comparing Human Genome Mapping Data. <i>Science</i> , 2001, 293, 2394b-2395.	6.0	1
86	Disruption of two novel genes by a translocation co-segregating with schizophrenia. <i>Human Molecular Genetics</i> , 2000, 9, 1415-1423.	1.4	1,135
87	Chromosomal Location and Genomic Structure of the Human Translin-Associated Factor X Gene (TRAX; TSNA) Revealed by Intergenic Splicing to DISC1, a Gene Disrupted by a Translocation Segregating with Schizophrenia. <i>Genomics</i> , 2000, 67, 69-77.	1.3	106
88	Gene Duplication and Gene Conversion in the <i>Caenorhabditis elegans</i> Genome. <i>Journal of Molecular Evolution</i> , 1999, 48, 555-564.	0.8	127
89	Assembling a View of the Human Genome. , 0, , 93-117.		2
90	Assembling a View of the Human Genome. , 0, , 59-84.		0