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List of Publications by Year
in descending order

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168 papers	70,169 citations	6613 79 h-index	5394 164 g-index
202 all docs	202 docs citations	202 times ranked	90977 citing authors

#	Article	IF	Citations
1	Somatic structural variant formation is guided by and influences genome architecture. Genome Research, 2022, 32, 643-655.	5.5	12
2	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
3	Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. Nature Genetics, 2022, 54, 518-525.	21.4	92
4	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
5	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52
6	Pediatric T-ALL type-1 and type-2 relapses develop along distinct pathways of clonal evolution. Leukemia, 2022, 36, 1759-1768.	7.2	4
7	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. European Urology, 2022, 82, 201-211.	1.9	2
8	Structural Variation in Cancer: Role, Prevalence, and Mechanisms. Annual Review of Genomics and Human Genetics, 2022, 23, 123-152.	6.2	23
9	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
10	Versatile workflow for cell typeâ€“resolved transcriptional and epigenetic profiles from cryopreserved human lung. JCI Insight, 2021, 6, .	5.0	8
11	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	4.1	9
12	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
13	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	6.2	72
14	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
15	The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. Faculty Reviews, 2021, 10, 63.	3.9	1
16	Systems approaches identify the consequences of monosomy in somatic human cells. Nature Communications, 2021, 12, 5576.	12.8	29
17	The Porto European Cancer Research Summit 2021. Molecular Oncology, 2021, 15, 2507-2543.	4.6	7
18	TP53 and KRAS Variants at Initial Diagnosis Identify an Ultra-High Risk Group of Pediatric T-Lymphoblastic Leukemia (T-ALL). Blood, 2021, 138, 1315-1315.	1.4	0

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19	Chromothripsis followed by circular recombination drives oncogene amplification in human cancer. Nature Genetics, 2021, 53, 1673-1685.	21.4	61
20	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. Bioinformatics, 2020, 36, 1267-1269.	4.1	29
21	Germline GPR161 Mutations Predispose to Pediatric Medulloblastoma. Journal of Clinical Oncology, 2020, 38, 43-50.	1.6	50
22	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
23	TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. GigaScience, 2020, 9, .	6.4	15
24	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	6.9	13
25	A scalable CRISPR/Cas9-based fluorescent reporter assay to study DNA double-strand break repair choice. Nature Communications, 2020, 11, 4077.	12.8	33
26	Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. Genome Research, 2020, 30, 1680-1693.	5.5	16
27	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	12.6	105
28	Effects of the COVID-19 pandemic on life scientists. Genome Biology, 2020, 21, 113.	8.8	90
29	Targeted Perturb-seq enables genome-scale genetic screens in single cells. Nature Methods, 2020, 17, 629-635.	19.0	139
30	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
31	Acquisition of chromosome instability is a mechanism to evade oncogene addiction. EMBO Molecular Medicine, 2020, 12, e10941.	6.9	45
32	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	27.8	94
33	Genomics: data sharing needs an international code of conduct. Nature, 2020, 578, 31-33.	27.8	31
34	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
35	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
36	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280

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37	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
38	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
39	Genome-wide Screens Implicate Loss of Cullin Ring Ligase 3 in Persistent Proliferation and Genome Instability in TP53-Deficient Cells. Cell Reports, 2020, 31, 107465.	6.4	24
40	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	17.5	11
41	Genomic data sharing in Europe is stumblingâ€"Could a code of conduct prevent its fall?. EMBO Molecular Medicine, 2020, 12, e11421.	6.9	22
42	Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. Nature Genetics, 2019, 51, 1272-1282.	21.4	272
43	Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. European Journal of Human Genetics, 2019, 27, 631-636.	2.8	4
44	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
45	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. Nature Cell Biology, 2019, 21, 1248-1260.	10.3	61
46	InTAD: chromosome conformation guided analysis of enhancer target genes. BMC Bioinformatics, 2019, 20, 60.	2.6	14
47	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
48	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
49	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	27.8	94
50	Comprehensive Analysis of Chromatin States in Atypical Teratoid/Rhabdoid Tumor Identifies Diverging Roles for SWI/SNF and Polycomb in Gene Regulation. Cancer Cell, 2019, 35, 95-110.e8.	16.8	65
51	Alfred: interactive multi-sample BAM alignment statistics, feature counting and feature annotation for long- and short-read sequencing. Bioinformatics, 2019, 35, 2489-2491.	4.1	61
52	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
53	Genomic structural variations lead to dysregulation of important coding and nonâ€coding RNA species in dilated cardiomyopathy. EMBO Molecular Medicine, 2018, 10, 107-120.	6.9	43
54	Chromatin modifiers Mdm2 and RNF2 prevent RNA:DNA hybrids that impair DNA replication. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11311-E11320.	7.1	44

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55	<scp>PDX</scp> models recapitulate the genetic and epigenetic landscape of pediatric Tâ€cell leukemia. EMBO Molecular Medicine, 2018, 10, .	6.9	38
56	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
57	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. Lancet Oncology, The, 2018, 19, 768-784.	10.7	151
58	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24
59	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
60	Pan-cancer analysis distinguishes transcriptional changes of aneuploidy from proliferation. Genome Research, 2017, 27, 501-511.	5.5	52
61	Systematic Identification of Determinants for Single-Strand Annealing-Mediated Deletion Formation in Saccharomyces cerevisiae. G3: Genes, Genomes, Genetics, 2017, 7, 3269-3279.	1.8	1
62	Mitochondrial mutations drive prostate cancer aggression. Nature Communications, 2017, 8, 656.	12.8	100
63	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
64	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
65	Computing patient data in the cloud: practical and legal considerations for genetics and genomics research in Europe and internationally. Genome Medicine, 2017, 9, 58.	8.2	21
66	Genomes of early onset prostate cancer. Current Opinion in Urology, 2017, 27, 481-487.	1.8	9
67	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	21.4	326
68	Deletion lengthening at chromosomes 6q and 16q targets multiple tumor suppressor genes and is associated with an increasingly poor prognosis in prostate cancer. Oncotarget, 2017, 8, 108923-108935.	1.8	26
69	Using large-scale genome variation cohorts to decipher the molecular mechanism of cancer. Comptes Rendus - Biologies, 2016, 339, 308-313.	0.2	5
70	Identification of ZCCHC8 as fusion partner of ROS1 in a case of congenital glioblastoma multiforme with a t(6;12)(q21;q24.3). Genes Chromosomes and Cancer, 2016, 55, 677-687.	2.8	33
71	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	3.5	43
72	Negative Selection and Chromosome Instability Induced by Mad2 Overexpression Delay Breast Cancer but Facilitate Oncogene-Independent Outgrowth. Cell Reports, 2016, 15, 2679-2691.	6.4	65

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73	Genetic code expansion for multiprotein complex engineering. Nature Methods, 2016, 13, 997-1000.	19.0	63
74	Heterogeneity of ERG expression in prostate cancer: a large section mapping study of entire prostatectomy specimens from 125 patients. BMC Cancer, 2016, 16, 641.	2.6	24
75	Next-generation sequencing-based detection of germline L1-mediated transductions. BMC Genomics, 2016, 17, 342.	2.8	7
76	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
77	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
78	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. Current Biology, 2016, 26, 38-51.	3.9	212
79	Immortalization capacity of HPV types is inversely related to chromosomal instability. Oncotarget, 2016, 7, 37608-37621.	1.8	25
80	A cellâ€based model system links chromothripsis with hyperploidy. Molecular Systems Biology, 2015, 11, 828.	7.2	118
81	Data analysis: Create a cloud commons. Nature, 2015, 523, 149-151.	27.8	89
82	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	12.8	77
83	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. Nature Communications, 2015, 6, 8940.	12.8	242
84	Prevalence of chromosomal rearrangements involving non-ETS genes in prostate cancer. International Journal of Oncology, 2015, 46, 1637-1642.	3.3	13
85	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
86	Genomics and drug profiling of fatal TCF3-HLFâ˜positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. Nature Genetics, 2015, 47, 1020-1029.	21.4	190
87	Comprehensive genomic profiles of small cell lung cancer. Nature, 2015, 524, 47-53.	27.8	1,634
88	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	19.0	465
89	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
90	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994

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91	The Aging Prostate Is Never â€œNormalâ€• Implications from the Genomic Characterization of Multifocal Prostate Cancers. European Urology, 2015, 68, 348-350.	1.9	5
92	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. Haematologica, 2015, 100, 1442-1450.	3.5	65
93	BAZ2A (TIP5) is involved in epigenetic alterations in prostate cancer and its overexpression predicts disease recurrence. Nature Genetics, 2015, 47, 22-30.	21.4	141
94	Gene Panel Sequencing of Primary and Relapsed Pediatric T-ALL Shows That Relapse-Specific Mutations Are Diverse and Mostly Non-Recurrent. Blood, 2015, 126, 1428-1428.	1.4	0
95	Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
96	Clinical significance of different types ofp53gene alteration in surgically treated prostate cancer. International Journal of Cancer, 2014, 135, 1369-1380.	5.1	95
97	A common microdeletion affecting a hippocampusâ€•and amygdalaâ€•specific isoform of tryptophan hydroxylase 2 is not associated with affective disorders. Bipolar Disorders, 2014, 16, 764-768.	1.9	2
98	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
99	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
100	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74
101	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. European Urology, 2014, 66, 978-981.	1.9	54
102	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	6.4	219
103	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
104	Targeted Deep Sequencing of Genetic Alterations Identified By Whole Exome Sequencing Reveals Clonal Evolution in Pediatric T-Lymphoblastic Leukemia. Blood, 2014, 124, 491-491.	1.4	0
105	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674
106	Primate genome architecture influences structural variation mechanisms and functional consequences. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15764-15769.	7.1	80
107	Genome assembly and haplotyping with Hi-C. Nature Biotechnology, 2013, 31, 1099-1101.	17.5	53
108	Whole-exome sequencing links caspase recruitment domainÂ11 (CARD11) inactivation to severe combined immunodeficiency. Journal of Allergy and Clinical Immunology, 2013, 131, 1376-1383.e3.	2.9	127

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109	Phenotypic impact of genomic structural variation: insights from and for human disease. Nature Reviews Genetics, 2013, 14, 125-138.	16.3	502
110	Identification of a Ninein (NIN) mutation in a family with spondyloepimetaphyseal dysplasia with joint laxity (leptodactylic type)-like phenotype. Matrix Biology, 2013, 32, 387-392.	3.6	15
111	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
112	Criteria for Inference of Chromothripsis in Cancer Genomes. Cell, 2013, 152, 1226-1236.	28.9	457
113	Genomic deletion of MAP3K7 at 6q12-22 is associated with early PSA recurrence in prostate cancer and absence of TMPRSS2:ERG fusions. Modern Pathology, 2013, 26, 975-983.	5.5	127
114	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	1.8	355
115	Impact of genomic structural variation in Drosophila melanogaster based on population-scale sequencing. Genome Research, 2013, 23, 568-579.	5.5	72
116	Whole Exome Sequencing Identifies Novel Lyst-Missense Mutations In Incomplete Childhood Chediak-Higashi-Syndrome Presenting As Hemphagocytic Lymphohistiocytosis (HLH). Blood, 2013, 122, 3479-3479.	1.4	0
117	Whole Exome Sequencing In Relapsed Pediatric T-ALL: Progression Into Relapse Is Characterized By An Increased Number Of Somatic Mutations and a Conservation Of Mutations In Leukemogenic Driver Genes. Blood, 2013, 122, 228-228.	1.4	0
118	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
119	DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinformatics, 2012, 28, i333-i339.	4.1	1,785
120	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
121	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
122	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. Blood, 2012, 120, 4783-4794.	1.4	179
123	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	21.4	389
124	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
125	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.6	1
126	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765

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127	A 15q24 microdeletion in transient myeloproliferative disease (<scp>TMD</scp>) and acute megakaryoblastic leukaemia (<scp>AMKL</scp>) implicates <scp>PML</scp> and <scp>SUMO</scp>3 in the leukaemogenesis of <scp>TMD</scp>/<scp>AMKL</scp>. British Journal of Haematology, 2012, 157, 180-187.	2.5	9
128	Whole-Exome Sequencing Links CARD11 Inactivation with SCID. Blood, 2012, 120, 258-258.	1.4	0
129	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
130	Challenges in studying genomic structural variant formation mechanisms: The shortâ€read dilemma and beyond. BioEssays, 2011, 33, 840-850.	2.5	34
131	Relating CNVs to transcriptome data at fine resolution: Assessment of the effect of variant size, type, and overlap with functional regions. Genome Research, 2011, 21, 2004-2013.	5.5	109
132	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
133	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
134	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
135	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nature Biotechnology, 2010, 28, 47-55.	17.5	158
136	The Baker's Yeast Diploid Genome Is Remarkably Stable in Vegetative Growth and Meiosis. PLoS Genetics, 2010, 6, e1001109.	3.5	89
137	Systematic Inference of Copy-Number Genotypes from Personal Genome Sequencing Data Reveals Extensive Olfactory Receptor Gene Content Diversity. PLoS Computational Biology, 2010, 6, e1000988.	3.2	56
138	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	12.6	521
139	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. Genome Research, 2009, 19, 106-117.	5.5	33
140	Quantifying environmental adaptation of metabolic pathways in metagenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1374-1379.	7.1	177
141	Distinct genomic aberrations associated with ERG rearranged prostate cancer. Genes Chromosomes and Cancer, 2009, 48, 366-380.	2.8	86
142	The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12031-12036.	7.1	342
143	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. Genome Biology, 2009, 10, R23.	9.6	223
144	The current excitement about copy-number variation: how it relates to gene duplications and protein families. Current Opinion in Structural Biology, 2008, 18, 366-374.	5.7	92

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145	Analysis of copy number variation in the rhesus macaque genome identifies candidate loci for evolutionary and human disease studies. Human Molecular Genetics, 2008, 17, 1127-1136.	2.9	101
146	Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. Genome Research, 2008, 18, 1865-1874.	5.5	126
147	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. PLoS Genetics, 2008, 4, e1000249.	3.5	99
148	Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10110-10115.	7.1	78
149	The DART classification of unannotated transcription within the ENCODE regions: Associating transcription with known and novel loci. Genome Research, 2007, 17, 732-745.	5.5	25
150	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
151	Positive selection at the protein network periphery: Evaluation in terms of structural constraints and cellular context. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20274-20279.	7.1	132
152	Use of pathway analysis and genome context methods for functional genomics of Mycoplasma pneumoniae nucleotide metabolism. Gene, 2007, 396, 215-225.	2.2	13
153	Prediction of effective genome size in metagenomic samples. Genome Biology, 2007, 8, R10.	9.6	281
154	What is a gene, post-ENCODE? History and updated definition. Genome Research, 2007, 17, 669-681.	5.5	530
155	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. PLoS ONE, 2007, 2, e294.	2.5	82
156	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
157	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. Science, 2007, 318, 420-426.	12.6	1,003
158	Similar gene expression profiles do not imply similar tissue functions. Trends in Genetics, 2006, 22, 132-138.	6.7	59
159	A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and chIP-chip experiments: systematically incorporating validated biological knowledge. Bioinformatics, 2006, 22, 3016-3024.	4.1	32
160	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4534-4539.	7.1	125
161	Systematic Association of Genes to Phenotypes by Genome and Literature Mining. PLoS Biology, 2005, 3, e134.	5.6	138
162	The Helmholtz Network for Bioinformatics: an integrative web portal for bioinformatics resources. Bioinformatics, 2004, 20, 268-270.	4.1	7

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163	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. Nature Biotechnology, 2004, 22, 911-917.	17.5	166
164	Transgene Methylation in Mice Reflects Copy Number But Not Expression Level. Molecular Biotechnology, 2004, 26, 215-220.	2.4	5
165	Systematic discovery of analogous enzymes in thiamin biosynthesis. Nature Biotechnology, 2003, 21, 790-795.	17.5	121
166	SHOT: a web server for the construction of genome phylogenies. Trends in Genetics, 2002, 18, 158-162.	6.7	193
167	Combining frequency and positional information to predict transcription factor binding sites. Bioinformatics, 2001, 17, 1019-1026.	4.1	42
168	Extracting information from cDNA arrays. Chaos, 2001, 11, 98.	2.5	23