Jan O Korbel

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3735433/publications.pdf

Version: 2024-02-01

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	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
4	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
5	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
6	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
7	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
8	DELLY: structural variant discovery by integrated paired-end and split-read analysis. Bioinformatics, 2012, 28, i333-i339.	4.1	1,785
9	Comprehensive genomic profiles of small cell lung cancer. Nature, 2015, 524, 47-53.	27.8	1,634
10	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
11	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. Science, 2007, 318, 420-426.	12.6	1,003
12	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
13	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
14	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	27.8	765
15	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
16	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	28.9	743
17	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	8.8	742
18	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	21.4	674

#	Article	IF	Citations
19	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
20	Genome Sequencing of SHH Medulloblastoma Predicts Genotype-Related Response to Smoothened Inhibition. Cancer Cell, 2014, 25, 393-405.	16.8	627
21	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	30.7	604
22	Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
23	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
24	What is a gene, post-ENCODE? History and updated definition. Genome Research, 2007, 17, 669-681.	5.5	530
25	Variation in Transcription Factor Binding Among Humans. Science, 2010, 328, 232-235.	12.6	521
26	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	27.8	521
27	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
28	Phenotypic impact of genomic structural variation: insights from and for human disease. Nature Reviews Genetics, 2013, 14, 125-138.	16.3	502
29	Assembly and diploid architecture of an individual human genome via single-molecule technologies. Nature Methods, 2015, 12, 780-786.	19.0	465
30	Criteria for Inference of Chromothripsis in Cancer Genomes. Cell, 2013, 152, 1226-1236.	28.9	457
31	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
32	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
33	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
34	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
35	The Genomic and Transcriptomic Landscape of a HeLa Cell Line. G3: Genes, Genomes, Genetics, 2013, 3, 1213-1224.	1.8	355
36	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

#	Article	IF	Citations
37	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	21.4	326
38	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
39	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	16.8	292
40	Prediction of effective genome size in metagenomic samples. Genome Biology, 2007, 8, R10.	9.6	281
41	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	27.8	280
42	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
43	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
44	Highly rearranged chromosomes reveal uncoupling between genome topology and gene expression. Nature Genetics, 2019, 51, 1272-1282.	21.4	272
45	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
46	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. Nature Communications, 2015, 6, 8940.	12.8	242
47	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
48	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	6.4	219
49	Shadow Enhancers Are Pervasive Features of Developmental Regulatory Networks. Current Biology, 2016, 26, 38-51.	3.9	212
50	SHOT: a web server for the construction of genome phylogenies. Trends in Genetics, 2002, 18, 158-162.	6.7	193
51	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
52	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	16.8	190
53	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. Blood, 2012, 120, 4783-4794.	1.4	179
54	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

#	Article	IF	Citations
55	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. Nature Biotechnology, 2004, 22, 911-917.	17.5	166
56	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. Nature Biotechnology, 2010, 28, 47-55.	17.5	158
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	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
59	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
60	Targeted Perturb-seq enables genome-scale genetic screens in single cells. Nature Methods, 2020, 17, 629-635.	19.0	139
61	Systematic Association of Genes to Phenotypes by Genome and Literature Mining. PLoS Biology, 2005, 3, e134.	5.6	138
62	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
63	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
64	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
65	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
66	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
67	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
68	Systematic discovery of analogous enzymes in thiamin biosynthesis. Nature Biotechnology, 2003, 21, 790-795.	17.5	121
69	A cellâ€based model system links chromothripsis with hyperploidy. Molecular Systems Biology, 2015, 11, 828.	7.2	118
70	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
71	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	12.6	105
72	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

#	Article	IF	Citations
73	Mitochondrial mutations drive prostate cancer aggression. Nature Communications, 2017, 8, 656.	12.8	100
74	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. PLoS Genetics, 2008, 4, e1000249.	3.5	99
75	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	12.8	99
76	Clinical significance of different types ofp53gene alteration in surgically treated prostate cancer. International Journal of Cancer, 2014, 135, 1369-1380.	5.1	95
77	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	27.8	94
78	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	27.8	94
79	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
80	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
81	Effects of the COVID-19 pandemic on life scientists. Genome Biology, 2020, 21, 113.	8.8	90
82	The Baker's Yeast Diploid Genome Is Remarkably Stable in Vegetative Growth and Meiosis. PLoS Genetics, 2010, 6, e1001109.	3.5	89
83	Data analysis: Create a cloud commons. Nature, 2015, 523, 149-151.	27.8	89
84	Distinct genomic aberrations associated with ERG rearranged prostate cancer. Genes Chromosomes and Cancer, 2009, 48, 366-380.	2.8	86
85	Dense and accurate whole-chromosome haplotyping of individual genomes. Nature Communications, 2017, 8, 1293.	12.8	83
86	Global Identification and Characterization of Transcriptionally Active Regions in the Rice Genome. PLoS ONE, 2007, 2, e294.	2.5	82
87	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
88	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
89	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	12.8	77
90	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	17.5	74

#	Article	IF	Citations
91	Impact of genomic structural variation in Drosophila melanogaster based on population-scale sequencing. Genome Research, 2013, 23, 568-579.	5.5	72
92	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
93	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
94	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
95	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
96	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
97	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
98	Genetic code expansion for multiprotein complex engineering. Nature Methods, 2016, 13, 997-1000.	19.0	63
99	The NSL complex maintains nuclear architecture stability via lamin A/C acetylation. Nature Cell Biology, 2019, 21, 1248-1260.	10.3	61
100	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
101	Chromothripsis followed by circular recombination drives oncogene amplification in human cancer. Nature Genetics, 2021, 53, 1673-1685.	21.4	61
102	Similar gene expression profiles do not imply similar tissue functions. Trends in Genetics, 2006, 22, 132-138.	6.7	59
103	Single-cell analysis of structural variations and complex rearrangements with tri-channel processing. Nature Biotechnology, 2020, 38, 343-354.	17.5	59
104	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
105	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. European Urology, 2014, 66, 978-981.	1.9	54
106	Genome assembly and haplotyping with Hi-C. Nature Biotechnology, 2013, 31, 1099-1101.	17.5	53
107	Pan-cancer analysis distinguishes transcriptional changes of aneuploidy from proliferation. Genome Research, 2017, 27, 501-511.	5.5	52
108	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	12.8	52

#	Article	IF	Citations
109	Germline GPR161 Mutations Predispose to Pediatric Medulloblastoma. Journal of Clinical Oncology, 2020, 38, 43-50.	1.6	50
110	Acquisition of chromosome instability is a mechanism to evade oncogene addiction. EMBO Molecular Medicine, 2020, 12, e10941.	6.9	45
111	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
112	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
113	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
114	Combining frequency and positional information to predict transcription factor binding sites. Bioinformatics, 2001, 17, 1019-1026.	4.1	42
115	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
116	<scp>PDX</scp> models recapitulate the genetic and epigenetic landscape of pediatric Tâ€cell leukemia. EMBO Molecular Medicine, 2018, 10, .	6.9	38
117	Challenges in studying genomic structural variant formation mechanisms: The shortâ€read dilemma and beyond. BioEssays, 2011, 33, 840-850.	2.5	34
118	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	7.2	34
119	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. Genome Research, 2009, 19, 106-117.	5.5	33
120	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
121	A scalable CRISPR/Cas9-based fluorescent reporter assay to study DNA double-strand break repair choice. Nature Communications, 2020, 11, 4077.	12.8	33
122	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
123	Familial long-read sequencing increases yield of de novo mutations. American Journal of Human Genetics, 2022, 109, 631-646.	6.2	32
124	Genomics: data sharing needs an international code of conduct. Nature, 2020, 578, 31-33.	27.8	31
125	VISOR: a versatile haplotype-aware structural variant simulator for short- and long-read sequencing. Bioinformatics, 2020, 36, 1267-1269.	4.1	29
126	Systems approaches identify the consequences of monosomy in somatic human cells. Nature Communications, 2021, 12, 5576.	12.8	29

#	Article	IF	Citations
127	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
128	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
129	Immortalization capacity of HPV types is inversely related to chromosomal instability. Oncotarget, 2016, 7, 37608-37621.	1.8	25
130	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
131	Strand-seq enables reliable separation of long reads by chromosome via expectation maximization. Bioinformatics, 2018, 34, i115-i123.	4.1	24
132	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
133	Extracting information from cDNA arrays. Chaos, 2001, 11, 98.	2.5	23
134	Structural Variation in Cancer: Role, Prevalence, and Mechanisms. Annual Review of Genomics and Human Genetics, 2022, 23, 123-152.	6.2	23
135	Genomic data sharing in Europe is stumblingâ€"Could a code of conduct prevent its fall?. EMBO Molecular Medicine, 2020, 12, e11421.	6.9	22
136	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
137	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
138	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
139	TRiCoLOR: tandem repeat profiling using whole-genome long-read sequencing data. GigaScience, 2020, 9, .	6.4	15
140	InTAD: chromosome conformation guided analysis of enhancer target genes. BMC Bioinformatics, 2019, 20, 60.	2.6	14
141	Use of pathway analysis and genome context methods for functional genomics of Mycoplasma pneumoniae nucleotide metabolism. Gene, 2007, 396, 215-225.	2.2	13
142	Prevalence of chromosomal rearrangements involving non-ETS genes in prostate cancer. International Journal of Oncology, 2015, 46, 1637-1642.	3.3	13
143	Chromatin accessibility landscape of pediatric Tâ€lymphoblastic leukemia and human Tâ€cell precursors. EMBO Molecular Medicine, 2020, 12, e12104.	6.9	13
144	Somatic structural variant formation is guided by and influences genome architecture. Genome Research, 2022, 32, 643-655.	5.5	12

#	Article	IF	Citations
145	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	17.5	11
146	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
147	Genomes of early onset prostate cancer. Current Opinion in Urology, 2017, 27, 481-487.	1.8	9
148	ASHLEYS: automated quality control for single-cell Strand-seq data. Bioinformatics, 2021, 37, 3356-3357.	4.1	9
149	Versatile workflow for cell typeâ€"resolved transcriptional and epigenetic profiles from cryopreserved human lung. JCI Insight, 2021, 6, .	5.0	8
150	The Helmholtz Network for Bioinformatics: an integrative web portal for bioinformatics resources. Bioinformatics, 2004, 20, 268-270.	4.1	7
151	Next-generation sequencing-based detection of germline L1-mediated transductions. BMC Genomics, 2016, 17, 342.	2.8	7
152	The Porto European Cancer Research Summit 2021. Molecular Oncology, 2021, 15, 2507-2543.	4.6	7
153	Transgene Methylation in Mice Reflects Copy Number But Not Expression Level. Molecular Biotechnology, 2004, 26, 215-220.	2.4	5
154	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
155	Using large-scale genome variation cohorts to decipher the molecular mechanism of cancer. Comptes Rendus - Biologies, 2016, 339, 308-313.	0.2	5
156	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
157	Pediatric T-ALL type-1 and type-2 relapses develop along distinct pathways of clonal evolution. Leukemia, 2022, 36, 1759-1768.	7.2	4
158	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
159	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
160	ICGC PedBrain - dissecting the genomic complexity underlying medulloblastoma using whole-genome sequencing. BMC Proceedings, 2012, 6, .	1.6	1
161	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
162	The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. Faculty Reviews, 2021, 10, 63.	3.9	1

#	Article	IF	Citations
163	Whole-Exome Sequencing Links CARD11 Inactivation with SCID. Blood, 2012, 120, 258-258.	1.4	0
164	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
165	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
166	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
167	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
168	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