Jinghui Zhang

List of Publications by Year
in descending order

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229 papers	30,487 citations	10389 72 h-index	5120 166 g-index
243 all docs	243 docs citations	243 times ranked	31542 citing authors

#	Article	IF	Citations
1	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
2	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. Nature Genetics, 2012, 44, 251-253.	21.4	1,402
3	Deletion ofIKZF1and Prognosis in Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2009, 360, 470-480.	27.0	1,260
4	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	27.0	1,161
5	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
6	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
7	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
8	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
9	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742
10	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
11	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	21.4	693
12	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
13	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
14	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
15	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
16	Rearrangement of CRLF2 in B-progenitorâ€“ and Down syndromeâ€“associated acute lymphoblastic leukemia. Nature Genetics, 2009, 41, 1243-1246.	21.4	559
17	C11orf95â€“RELA fusions drive oncogenic NF-Î²B signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
18	CREBBP mutations in relapsed acute lymphoblastic leukaemia. Nature, 2011, 471, 235-239.	27.8	542

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19	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. Nature Medicine, 2018, 24, 103-112.	30.7	525
20	JAK mutations in high-risk childhood acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9414-9418.	7.1	516
21	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
22	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
23	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	9.4	418
24	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
25	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. Nature Genetics, 2019, 51, 296-307.	21.4	384
26	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. JAMA - Journal of the American Medical Association, 2012, 307, 1062.	7.4	379
27	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
28	High Frequency and Poor Outcome of Philadelphia Chromosomeâ€“Like Acute Lymphoblastic Leukemia in Adults. Journal of Clinical Oncology, 2017, 35, 394-401.	1.6	326
29	The Pediatric Cancer Genome Project. Nature Genetics, 2012, 44, 619-622.	21.4	315
30	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathologica, 2016, 131, 833-845.	7.7	288
31	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	12.8	281
32	Exploring genomic alteration in pediatric cancer using ProteinPaint. Nature Genetics, 2016, 48, 4-6.	21.4	275
33	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	21.4	270
34	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
35	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. Blood, 2011, 118, 3080-3087.	1.4	255
36	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252

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37	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. EBioMedicine, 2016, 8, 173-183.	6.1	241
38	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1386-1391.	21.4	238
39	Targetable kinase gene fusions in high-risk B-ALL: a study from the Childrenâ€™s Oncology Group. Blood, 2017, 129, 3352-3361.	1.4	236
40	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
41	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
42	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	27.8	223
43	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222
44	Caspase-8 mediates caspase-1 processing and innate immune defense in response to bacterial blockade of NF-Î°B and MAPK signaling. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7385-7390.	7.1	215
45	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
46	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. Cancer Cell, 2012, 22, 683-697.	16.8	213
47	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
48	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	8.8	196
49	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. Cancer Cell, 2019, 35, 140-155.e7.	16.8	194
50	Novel Oncogenic PDGFRA Mutations in Pediatric High-Grade Gliomas. Cancer Research, 2013, 73, 6219-6229.	0.9	189
51	Genomic analysis reveals few genetic alterations in pediatric acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12944-12949.	7.1	172
52	MYC Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. Cancer Discovery, 2018, 8, 320-335.	9.4	172
53	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
54	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166

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55	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. Lancet Oncology, The, 2015, 16, 1659-1666.	10.7	161
56	Pediatric nonâ€“Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. Nature Genetics, 2017, 49, 451-456.	21.4	152
57	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
58	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	12.8	142
59	Negative feedbackâ€“defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. Nature Medicine, 2015, 21, 563-571.	30.7	141
60	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. PLoS Genetics, 2015, 11, e1005262.	3.5	128
61	Cancer-associated DDX3X mutations drive stress granule assembly and impair global translation. Scientific Reports, 2016, 6, 25996.	3.3	121
62	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. Cancer Cell, 2016, 29, 186-200.	16.8	118
63	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
64	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
65	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
66	Bambino: a variant detector and alignment viewer for next-generation sequencing data in the SAM/BAM format. Bioinformatics, 2011, 27, 865-866.	4.1	103
67	Premature Physiologic Aging as a Paradigm for Understanding Increased Risk of Adverse Health Across the Lifespan of Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2206-2215.	1.6	99
68	Genomic and outcome analyses of Ph-like ALL in NCI standard-risk patients: a report from the Childrenâ€™s Oncology Group. Blood, 2018, 132, 815-824.	1.4	97
69	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	5.0	93
70	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. Nature Communications, 2015, 6, 6553.	12.8	90
71	MAPK signaling cascades mediate distinct glucocorticoid resistance mechanisms in pediatric leukemia. Blood, 2015, 126, 2202-2212.	1.4	88
72	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	9.4	88

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73	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	12.8	87
74	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. Acta Neuropathologica, 2019, 137, 637-655.	7.7	85
75	Enhancer Hijacking Drives Oncogenic BCL11B Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	9.4	83
76	The neoepitope landscape in pediatric cancers. Genome Medicine, 2017, 9, 78.	8.2	77
77	Outcome of children with hypodiploid ALL treated with risk-directed therapy based on MRD levels. Blood, 2015, 126, 2896-2899.	1.4	76
78	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. Journal of Proteome Research, 2016, 15, 2309-2320.	3.7	76
79	Small genomic insertions form enhancers that misregulate oncogenes. Nature Communications, 2017, 8, 14385.	12.8	76
80	Cross-Species Genomics Identifies TAF12, NFYC, and RAD54L as Choroid Plexus Carcinoma Oncogenes. Cancer Cell, 2015, 27, 712-727.	16.8	74
81	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. Genome Biology, 2020, 21, 126.	8.8	74
82	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	1.4	72
83	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. Nature Communications, 2015, 6, 7553.	12.8	72
84	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. Cancer Discovery, 2020, 10, 568-587.	9.4	72
85	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. Nature Cancer, 2021, 2, 284-299.	13.2	70
86	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. International Journal of Epidemiology, 2021, 50, 39-49.	1.9	70
87	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	19.0	68
88	Pediatric patients with acute lymphoblastic leukemia generate abundant and functional neoantigen-specific CD8 ⁺ T cell responses. Science Translational Medicine, 2019, 11, .	12.4	66
89	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66
90	Development and Validation Of a Highly Sensitive and Specific Gene Expression Classifier To Prospectively Screen and Identify B-Precursor Acute Lymphoblastic Leukemia (ALL) Patients With a Philadelphia Chromosome-Like (â€œPh-likeâ€•or â€œBCR-ABL1-Likeâ€) Signature For Therapeutic Targeting and Clinical Intervention. Blood, 2013, 122, 826-826.	1.4	65

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91	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	7.7	63
92	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. Modern Pathology, 2016, 29, 359-369.	5.5	61
93	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. Nature Medicine, 2019, 25, 597-602.	30.7	61
94	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56
95	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. Nature Genetics, 2020, 52, 811-818.	21.4	47
96	Inhibition of SF3B1 by molecules targeting the spliceosome results in massive aberrant exon skipping. Rna, 2018, 24, 1056-1066.	3.5	42
97	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
98	Therapeutic and prognostic insights from the analysis of cancer mutational signatures. Trends in Genetics, 2022, 38, 194-208.	6.7	39
99	Integrated Genomic Analysis Identifies UBTF Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. Blood Cancer Discovery, 2022, 3, 194-207.	5.0	38
100	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISHÂand IHC in Lung Adenocarcinoma. Journal of Thoracic Oncology, 2016, 11, 1891-1900.	1.1	37
101	XAF1 as a modifier of p53 function and cancer susceptibility. Science Advances, 2020, 6, eaba3231.	10.3	37
102	Molecular basis of ETV6-mediated predisposition to childhood acute lymphoblastic leukemia. Blood, 2021, 137, 364-373.	1.4	37
103	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 597-605.	6.3	37
104	Pathogenic Germline Mutations in DNA Repair Genes in Combination With Cancer Treatment Exposures and Risk of Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2020, 38, 2728-2740.	1.6	34
105	Shortened Leukocyte Telomere Length Associates with an Increased Prevalence of Chronic Health Conditions among Survivors of Childhood Cancer: A Report from the St. Jude Lifetime Cohort. Clinical Cancer Research, 2020, 26, 2362-2371.	7.0	34
106	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (PRKCA) Fusion. JAMA Dermatology, 2016, 152, 318.	4.1	33
107	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. Genome Biology, 2012, 13, R113.	9.6	31
108	Subsequent Breast Cancer in Female Childhood Cancer Survivors in the St Jude Lifetime Cohort Study (SJLIFE). Journal of Clinical Oncology, 2019, 37, 1647-1656.	1.6	31

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109	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31
110	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. Nature Communications, 2021, 12, 5531.	12.8	31
111	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. Genome Research, 2019, 29, 1555-1565.	5.5	28
112	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
113	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. Leukemia, 2020, 34, 2025-2037.	7.2	27
114	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. Nature Communications, 2021, 12, 4089.	12.8	27
115	Enrichment of heterozygous germline RECQL4 loss-of-function variants in pediatric osteosarcoma. Journal of Physical Education and Sports Management, 2019, 5, a004218.	1.2	26
116	ChIPseqSpikeInFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. Bioinformatics, 2020, 36, 1270-1272.	4.1	25
117	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. Cancer Research, 2021, 81, 2556-2565.	0.9	24
118	Chemotherapy and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. Nature Cancer, 2021, 2, 819-834.	13.2	24
119	Antitumor Effects of CAR T Cells Redirected to the EDB Splice Variant of Fibronectin. Cancer Immunology Research, 2021, 9, 279-290.	3.4	24
120	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. Science Advances, 2021, 7, eabe0834.	10.3	22
121	Wholeâ€“Genome Sequencing of Childhood Cancer Survivors Treated with Cranial Radiation Therapy Identifies 5p15.33 Locus for Stroke: A Report from the St. Jude Lifetime Cohort Study. Clinical Cancer Research, 2019, 25, 6700-6708.	7.0	21
122	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. Blood Cancer Discovery, 2021, 2, 586-599.	5.0	21
123	PTEN Signaling in the Postnatal Perivascular Progenitor Niche Drives Medulloblastoma Formation. Cancer Research, 2017, 77, 123-133.	0.9	20
124	Pathologic Characteristics of Spitz Melanoma With MAP3K8 Fusion or Truncation in a Pediatric Cohort. American Journal of Surgical Pathology, 2019, 43, 1631-1637.	3.7	20
125	The NSD2 p.E1099K Mutation Is Enriched at Relapse and Confers Drug Resistance in a Cell Contextâ€“Dependent Manner in Pediatric Acute Lymphoblastic Leukemia. Molecular Cancer Research, 2020, 18, 1153-1165.	3.4	20
126	Enhancer retargeting of CDX2 and UBTF::ATXN7L3 define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. Blood, 2022, 139, 3519-3531.	1.4	20

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127	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. Journal of the National Cancer Institute, 2018, 110, 895-904.	6.3	19
128	Association of Germline BRCA2 Mutations With the Risk of Pediatric or Adolescent Nonâ€“Hodgkin Lymphoma. JAMA Oncology, 2019, 5, 1362.	7.1	19
129	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). Clinical Cancer Research, 2018, 24, 6230-6235.	7.0	18
130	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies HTR2A forÂSubsequent Basal Cell Carcinoma. Journal of Investigative Dermatology, 2019, 139, 2042-2045.e8.	0.7	18
131	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. Cancer Cell, 2021, 39, 83-95.e4.	16.8	18
132	A genomic random interval model for statistical analysis of genomic lesion data. Bioinformatics, 2013, 29, 2088-2095.	4.1	17
133	Persistent variations of blood DNA methylation associated with treatment exposures and risk for cardiometabolic outcomes in long-term survivors of childhood cancer in the St. Jude Lifetime Cohort. Genome Medicine, 2021, 13, 53.	8.2	16
134	Identification of compound heterozygous variants in OPTN in an ALS-FTD patient from the CReATe consortium: a case report. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2018, 19, 469-471.	1.7	15
135	Clear cell sarcoma of kidney involving a horseshoe kidney and harboring EGFR internal tandem duplication. Pediatric Blood and Cancer, 2017, 64, e26602.	1.5	14
136	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. Nature Communications, 2019, 10, 2789.	12.8	14
137	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. Acta Neuropathologica, 2020, 140, 963-965.	7.7	14
138	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. Blood, 2018, 132, 565-565.	1.4	14
139	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. Scientific Reports, 2014, 4, 7455.	3.3	13
140	Estimated number of adult survivors of childhood cancer in United States with cancerâ€predisposing germline variants. Pediatric Blood and Cancer, 2020, 67, e28047.	1.5	13
141	Contribution of Polygenic Risk to Hypertension Among Long-Term Survivors of Childhood Cancer. JACC: CardioOncology, 2021, 3, 76-84.	4.0	13
142	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. Bioinformatics, 2020, 36, 1382-1390.	4.1	12
143	Generalizability of â€œGWAS Hitsâ€•in Clinical Populations: Lessons from Childhood Cancer Survivors. American Journal of Human Genetics, 2020, 107, 636-653.	6.2	12
144	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. Genome Medicine, 2022, 14, 32.	8.2	12

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145	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. Journal of the National Cancer Institute, 2020, 112, 756-764.	6.3	11
146	A Novel Locus Predicts Spermatogenic Recovery among Childhood Cancer Survivors Exposed to Alkylating Agents. Cancer Research, 2020, 80, 3755-3764.	0.9	11
147	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 2096-2104.	2.5	11
148	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. Bioinformatics, 2014, 30, 1400-1408.	4.1	10
149	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). Scientific Reports, 2021, 11, 5154.	3.3	10
150	indelPost: harmonizing ambiguities in simple and complex indel alignments. Bioinformatics, 2022, 38, 549-551.	4.1	10
151	Exome sequencing analysis of murine medulloblastoma models identifies WDR11 as a potential tumor suppressor in Group 3 tumors. Oncotarget, 2017, 8, 64685-64697.	1.8	10
152	CPX-351 induces remission in newly diagnosed pediatric secondary myeloid malignancies. Blood Advances, 2022, 6, 521-527.	5.2	10
153	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	1.4	9
154	Genomic Characterization and Experimental Modeling Of BCR-ABL1-Like Acute Lymphoblastic Leukemia. Blood, 2013, 122, 232-232.	1.4	8
155	Integrated Genomic and Mutational Profiling Of Adolescent and Young Adult ALL Identifies a High Frequency Of BCR-ABL1-Like ALL with Very Poor Outcome. Blood, 2013, 122, 825-825.	1.4	8
156	The Genomic Contributions of Avian H1N1 Influenza A Viruses to the Evolution of Mammalian Strains. PLoS ONE, 2015, 10, e0133795.	2.5	7
157	The Association of Mitochondrial Copy Number With Sarcopenia in Adult Survivors of Childhood Cancer. Journal of the National Cancer Institute, 2021, 113, 1570-1580.	6.3	7
158	Lack of Somatic Sequence Mutations In Protein Tyrosine Kinase Genes Other Than the JAK Kinase Family In High Risk B-Precursor Childhood Acute Lymphoblastic Leukemia (ALL): A Report From the Children's Oncology Group (COG) High-Risk (HR) ALL TARGET Project. Blood, 2010, 116, 2752-2752.	1.4	7
159	Transcriptome Sequence Analysis of Pediatric Acute Megakaryoblastic Leukemia Identifies An Inv(16)(p13.3;q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein As a Recurrent Lesion in 39% of Non-Infant Cases: A Report From the St. Jude Children's Research Hospital â€“ Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 757-757.	1.4	7
160	Resistant T-Cell Acute Lymphoblastic Leukemias That Emerge after In Vivo Treatment with Dexamethasone Frequently Down-Regulate Glucocorticoid Receptor Protein Expression. Blood, 2016, 128, 753-753.	1.4	7
161	The landscape of coding RNA editing events in pediatric cancer. BMC Cancer, 2021, 21, 1233.	2.6	7
162	FPGS relapse-specific mutations in relapsed childhood acute lymphoblastic leukemia. Scientific Reports, 2020, 10, 12074.	3.3	6

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163	Abstract IA-18: Big pediatric cancer genomic data: Discovery, precision medicine, and data sharing. , 2021, , .		6
164	Whole Genome Sequence Analysis of 22 MLL Rearranged Infant Acute Lymphoblastic Leukemias Reveals Remarkably Few Somatic Mutations: A Report From the St Jude Childrenâ€˜s Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 69-69.	1.4	6
165	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. PLoS Genetics, 2019, 15, e1008168.	3.5	5
166	Data-driven approaches to advance research and clinical care for pediatric cancer. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188571.	7.4	5
167	High Frequency and Poor Outcome of Ph-like Acute Lymphoblastic Leukemia in Adults. Blood, 2015, 126, 2618-2618.	1.4	5
168	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. Blood, 2019, 134, 649-649.	1.4	5
169	Phase I study using crenolanib to target PDGFR kinase in children and young adults with newly diagnosed DIPG or recurrent high-grade glioma, including DIPG. Neuro-Oncology Advances, 2021, 3, vdab179.	0.7	5
170	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	2.7	5
171	VCF2CNA: A tool for efficiently detecting copy-number alterations in VCF genotype data and tumor purity. Scientific Reports, 2019, 9, 10357.	3.3	4
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