

# Jinghui Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

229  
papers

30,487  
citations

10351

72  
h-index

5101

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. <i>Nature</i> , 2012, 481, 157-163.	13.7	1,430
2	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. <i>Nature Genetics</i> , 2012, 44, 251-253.	9.4	1,402
3	Deletion of <i>IKZF1</i> and Prognosis in Acute Lymphoblastic Leukemia. <i>New England Journal of Medicine</i> , 2009, 360, 470-480.	13.9	1,260
4	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. <i>New England Journal of Medicine</i> , 2014, 371, 1005-1015.	13.9	1,161
5	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	13.7	1,068
6	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015, 373, 2336-2346.	13.9	949
7	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. <i>Nature Genetics</i> , 2014, 46, 444-450.	9.4	871
8	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
9	Novel mutations target distinct subgroups of medulloblastoma. <i>Nature</i> , 2012, 488, 43-48.	13.7	742
10	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. <i>Nature Genetics</i> , 2013, 45, 602-612.	9.4	704
11	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2017, 49, 1211-1218.	9.4	693
12	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. <i>Nature</i> , 2018, 555, 371-376.	13.7	649
13	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 153-166.	7.7	621
14	The genomic landscape of hypodiploid acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 242-252.	9.4	588
15	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. <i>Cell Reports</i> , 2014, 7, 104-112.	2.9	583
16	Rearrangement of <i>CRLF2</i> in B-progenitor- and Down syndrome-associated acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2009, 41, 1243-1246.	9.4	559
17	<i>C11orf95</i> - <i>RELA</i> fusions drive oncogenic NF- $\kappa$ B signalling in ependymoma. <i>Nature</i> , 2014, 506, 451-455.	13.7	559
18	CREBBP mutations in relapsed acute lymphoblastic leukaemia. <i>Nature</i> , 2011, 471, 235-239.	13.7	542

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19	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018, 24, 103-112.	15.2	525
20	JAK mutations in high-risk childhood acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9414-9418.	3.3	516
21	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654.	9.0	451
22	A novel retinoblastoma therapy from genomic and epigenetic analyses. <i>Nature</i> , 2012, 481, 329-334.	13.7	442
23	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of <i>STAG2</i> and <i>TP53</i> Mutations. <i>Cancer Discovery</i> , 2014, 4, 1342-1353.	7.7	418
24	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. <i>Nature Genetics</i> , 2015, 47, 330-337.	9.4	405
25	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2019, 51, 296-307.	9.4	384
26	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. <i>JAMA - Journal of the American Medical Association</i> , 2012, 307, 1062.	3.8	379
27	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. <i>Nature Communications</i> , 2014, 5, 3630.	5.8	342
28	High Frequency and Poor Outcome of Philadelphia Chromosome-“Like Acute Lymphoblastic Leukemia in Adults. <i>Journal of Clinical Oncology</i> , 2017, 35, 394-401.	0.8	326
29	The Pediatric Cancer Genome Project. <i>Nature Genetics</i> , 2012, 44, 619-622.	9.4	315
30	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016, 131, 833-845.	3.9	288
31	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2015, 6, 6604.	5.8	281
32	Exploring genomic alteration in pediatric cancer using ProteinPaint. <i>Nature Genetics</i> , 2016, 48, 4-6.	9.4	275
33	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1226-1231.	9.4	270
34	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	5.1	268
35	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. <i>Blood</i> , 2011, 118, 3080-3087.	0.6	255
36	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. <i>Cancer Cell</i> , 2013, 24, 710-724.	7.7	252

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37	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. <i>EBioMedicine</i> , 2016, 8, 173-183.	2.7	241
38	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1386-1391.	9.4	238
39	Targetable kinase gene fusions in high-risk B-ALL: a study from the Children's Oncology Group. <i>Blood</i> , 2017, 129, 3352-3361.	0.6	236
40	The genetic basis and cell of origin of mixed phenotype acute leukaemia. <i>Nature</i> , 2018, 562, 373-379.	13.7	236
41	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	9.4	231
42	Orthotopic patient-derived xenografts of paediatric solid tumours. <i>Nature</i> , 2017, 549, 96-100.	13.7	223
43	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. <i>Neuron</i> , 2017, 94, 550-568.e10.	3.8	222
44	Caspase-8 mediates caspase-1 processing and innate immune defense in response to bacterial blockade of NF- $\kappa$ B and MAPK signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7385-7390.	3.3	215
45	The genomic landscape of core-binding factor acute myeloid leukemias. <i>Nature Genetics</i> , 2016, 48, 1551-1556.	9.4	215
46	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 683-697.	7.7	213
47	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. <i>Acta Neuropathologica</i> , 2018, 136, 211-226.	3.9	199
48	Analysis of error profiles in deep next-generation sequencing data. <i>Genome Biology</i> , 2019, 20, 50.	3.8	196
49	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. <i>Cancer Cell</i> , 2019, 35, 140-155.e7.	7.7	194
50	Novel Oncogenic <i>PDGFRA</i> Mutations in Pediatric High-Grade Gliomas. <i>Cancer Research</i> , 2013, 73, 6219-6229.	0.4	189
51	Genomic analysis reveals few genetic alterations in pediatric acute myeloid leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12944-12949.	3.3	172
52	<i>MYC</i> Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018, 8, 320-335.	7.7	172
53	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. <i>Blood</i> , 2020, 135, 41-55.	0.6	171
54	Genomic landscape of paediatric adrenocortical tumours. <i>Nature Communications</i> , 2015, 6, 6302.	5.8	166

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55	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. <i>Lancet Oncology</i> , 2015, 16, 1659-1666.	5.1	161
56	Pediatric non-Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. <i>Nature Genetics</i> , 2017, 49, 451-456.	9.4	152
57	The Genomic Landscape of Childhood and Adolescent Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 816-823.	0.3	148
58	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. <i>Nature Communications</i> , 2018, 9, 3962.	5.8	142
59	Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. <i>Nature Medicine</i> , 2015, 21, 563-571.	15.2	141
60	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. <i>PLoS Genetics</i> , 2015, 11, e1005262.	1.5	128
61	Cancer-associated DDX3X mutations drive stress granule assembly and impair global translation. <i>Scientific Reports</i> , 2016, 6, 25996.	1.6	121
62	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2016, 29, 186-200.	7.7	118
63	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. <i>Cancer Discovery</i> , 2021, 11, 1082-1099.	7.7	109
64	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. <i>Cancer Cell</i> , 2018, 34, 411-426.e19.	7.7	106
65	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2078-2087.	0.8	105
66	Bambino: a variant detector and alignment viewer for next-generation sequencing data in the SAM/BAM format. <i>Bioinformatics</i> , 2011, 27, 865-866.	1.8	103
67	Premature Physiologic Aging as a Paradigm for Understanding Increased Risk of Adverse Health Across the Lifespan of Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2206-2215.	0.8	99
68	Genomic and outcome analyses of Ph-like ALL in NCI standard-risk patients: a report from the Children's Oncology Group. <i>Blood</i> , 2018, 132, 815-824.	0.6	97
69	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. <i>Blood Cancer Discovery</i> , 2020, 1, 96-111.	2.6	93
70	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. <i>Nature Communications</i> , 2015, 6, 6553.	5.8	90
71	MAPK signaling cascades mediate distinct glucocorticoid resistance mechanisms in pediatric leukemia. <i>Blood</i> , 2015, 126, 2202-2212.	0.6	88
72	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. <i>Cancer Discovery</i> , 2021, 11, 3008-3027.	7.7	88

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73	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. <i>Nature Communications</i> , 2020, 11, 5183.	5.8	87
74	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. <i>Acta Neuropathologica</i> , 2019, 137, 637-655.	3.9	85
75	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867.	7.7	83
76	The neoepitope landscape in pediatric cancers. <i>Genome Medicine</i> , 2017, 9, 78.	3.6	77
77	Outcome of children with hypodiploid ALL treated with risk-directed therapy based on MRD levels. <i>Blood</i> , 2015, 126, 2896-2899.	0.6	76
78	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 2309-2320.	1.8	76
79	Small genomic insertions form enhancers that misregulate oncogenes. <i>Nature Communications</i> , 2017, 8, 14385.	5.8	76
80	Cross-Species Genomics Identifies TAF12, NFYC, and RAD54L as Choroid Plexus Carcinoma Oncogenes. <i>Cancer Cell</i> , 2015, 27, 712-727.	7.7	74
81	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. <i>Genome Biology</i> , 2020, 21, 126.	3.8	74
82	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. <i>Blood</i> , 2015, 125, 3609-3617.	0.6	72
83	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. <i>Nature Communications</i> , 2015, 6, 7553.	5.8	72
84	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. <i>Cancer Discovery</i> , 2020, 10, 568-587.	7.7	72
85	Network-based systems pharmacology reveals heterogeneity in LCK and BCL2 signaling and therapeutic sensitivity of T-cell acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 284-299.	5.7	70
86	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. <i>International Journal of Epidemiology</i> , 2021, 50, 39-49.	0.9	70
87	CONSORTING: integrating copy-number analysis with structural-variation detection. <i>Nature Methods</i> , 2015, 12, 527-530.	9.0	68
88	Pediatric patients with acute lymphoblastic leukemia generate abundant and functional neoantigen-specific CD8 <sup>+</sup> T cell responses. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	66
89	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. <i>Nature Communications</i> , 2020, 11, 913.	5.8	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 (Ph-like) or BCR-ABL1-Like Signature For Therapeutic Targeting and Clinical Intervention. <i>Blood</i> , 2013, 122, 826-826.	0.6	65

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91	Structure and evolution of double minutes in diagnosis and relapse brain tumors. <i>Acta Neuropathologica</i> , 2019, 137, 123-137.	3.9	63
92	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. <i>Modern Pathology</i> , 2016, 29, 359-369.	2.9	61
93	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. <i>Nature Medicine</i> , 2019, 25, 597-602.	15.2	61
94	Germline Lysine-Specific Demethylase 1 ( <i>LSD1/KDM1A</i> ) Mutations Confer Susceptibility to Multiple Myeloma. <i>Cancer Research</i> , 2018, 78, 2747-2759.	0.4	56
95	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. <i>Nature Genetics</i> , 2020, 52, 811-818.	9.4	47
96	Inhibition of SF3B1 by molecules targeting the spliceosome results in massive aberrant exon skipping. <i>Rna</i> , 2018, 24, 1056-1066.	1.6	42
97	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. <i>Molecular Cancer Research</i> , 2019, 17, 895-906.	1.5	40
98	Therapeutic and prognostic insights from the analysis of cancer mutational signatures. <i>Trends in Genetics</i> , 2022, 38, 194-208.	2.9	39
99	Integrated Genomic Analysis Identifies <i>UBTF</i> Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 194-207.	2.6	38
100	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISH and IHC in Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016, 11, 1891-1900.	0.5	37
101	XAF1 as a modifier of p53 function and cancer susceptibility. <i>Science Advances</i> , 2020, 6, eaba3231.	4.7	37
102	Molecular basis of <i>ETV6</i> -mediated predisposition to childhood acute lymphoblastic leukemia. <i>Blood</i> , 2021, 137, 364-373.	0.6	37
103	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 597-605.	3.0	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. <i>Journal of Clinical Oncology</i> , 2020, 38, 2728-2740.	0.8	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. <i>Clinical Cancer Research</i> , 2020, 26, 2362-2371.	3.2	34
106	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha ( <i>PRKCA</i> ) Fusion. <i>JAMA Dermatology</i> , 2016, 152, 318.	2.0	33
107	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. <i>Genome Biology</i> , 2012, 13, R113.	13.9	31
108	Subsequent Breast Cancer in Female Childhood Cancer Survivors in the St Jude Lifetime Cohort Study (SJLIFE). <i>Journal of Clinical Oncology</i> , 2019, 37, 1647-1656.	0.8	31

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109	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. <i>Nature Communications</i> , 2021, 12, 985.	5.8	31
110	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. <i>Nature Communications</i> , 2021, 12, 5531.	5.8	31
111	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. <i>Genome Research</i> , 2019, 29, 1555-1565.	2.4	28
112	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. <i>Nature Communications</i> , 2019, 10, 5806.	5.8	27
113	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2020, 34, 2025-2037.	3.3	27
114	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. <i>Nature Communications</i> , 2021, 12, 4089.	5.8	27
115	Enrichment of heterozygous germline <i>RECQL4</i> loss-of-function variants in pediatric osteosarcoma. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004218.	0.5	26
116	ChIPseqSpikelnFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. <i>Bioinformatics</i> , 2020, 36, 1270-1272.	1.8	25
117	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. <i>Cancer Research</i> , 2021, 81, 2556-2565.	0.4	24
118	Chemotherapy and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. <i>Nature Cancer</i> , 2021, 2, 819-834.	5.7	24
119	Antitumor Effects of CAR T Cells Redirected to the EDB Splice Variant of Fibronectin. <i>Cancer Immunology Research</i> , 2021, 9, 279-290.	1.6	24
120	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. <i>Science Advances</i> , 2021, 7, eabe0834.	4.7	22
121	Whole-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. <i>Clinical Cancer Research</i> , 2019, 25, 6700-6708.	3.2	21
122	Integrative Genomic Analysis of Pediatric Myeloid-Related Acute Leukemias Identifies Novel Subtypes and Prognostic Indicators. <i>Blood Cancer Discovery</i> , 2021, 2, 586-599.	2.6	21
123	PTEN Signaling in the Postnatal Perivascular Progenitor Niche Drives Medulloblastoma Formation. <i>Cancer Research</i> , 2017, 77, 123-133.	0.4	20
124	Pathologic Characteristics of Spitz Melanoma With MAP3K8 Fusion or Truncation in a Pediatric Cohort. <i>American Journal of Surgical Pathology</i> , 2019, 43, 1631-1637.	2.1	20
125	The NSD2 p.E1099K Mutation Is Enriched at Relapse and Confers Drug Resistance in a Cell Context-Dependent Manner in Pediatric Acute Lymphoblastic Leukemia. <i>Molecular Cancer Research</i> , 2020, 18, 1153-1165.	1.5	20
126	Enhancer retargeting of <i>CDX2</i> and <i>UBTF::ATXN7L3</i> define a subtype of high-risk B-progenitor acute lymphoblastic leukemia. <i>Blood</i> , 2022, 139, 3519-3531.	0.6	20



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127	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. <i>Journal of the National Cancer Institute</i> , 2018, 110, 895-904.	3.0	19
128	Association of Germline <i>BRCA2</i> Mutations With the Risk of Pediatric or Adolescent Non-Hodgkin Lymphoma. <i>JAMA Oncology</i> , 2019, 5, 1362.	3.4	19
129	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). <i>Clinical Cancer Research</i> , 2018, 24, 6230-6235.	3.2	18
130	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies <i>HTR2A</i> for Subsequent Basal Cell Carcinoma. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2042-2045.e8.	0.3	18
131	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. <i>Cancer Cell</i> , 2021, 39, 83-95.e4.	7.7	18
132	A genomic random interval model for statistical analysis of genomic lesion data. <i>Bioinformatics</i> , 2013, 29, 2088-2095.	1.8	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. <i>Genome Medicine</i> , 2021, 13, 53.	3.6	16
134	Identification of compound heterozygous variants in <i>OPTN</i> in an ALS-FTD patient from the CReATe consortium: a case report. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2018, 19, 469-471.	1.1	15
135	Clear cell sarcoma of kidney involving a horseshoe kidney and harboring <i>EGFR</i> internal tandem duplication. <i>Pediatric Blood and Cancer</i> , 2017, 64, e26602.	0.8	14
136	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. <i>Nature Communications</i> , 2019, 10, 2789.	5.8	14
137	Infratentorial <i>C11orf95</i> -fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial <i>RELA</i> -fused ependymoma. <i>Acta Neuropathologica</i> , 2020, 140, 963-965.	3.9	14
138	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. <i>Blood</i> , 2018, 132, 565-565.	0.6	14
139	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. <i>Scientific Reports</i> , 2014, 4, 7455.	1.6	13
140	Estimated number of adult survivors of childhood cancer in United States with cancer-predisposing germline variants. <i>Pediatric Blood and Cancer</i> , 2020, 67, e28047.	0.8	13
141	Contribution of Polygenic Risk to Hypertension Among Long-Term Survivors of Childhood Cancer. <i>JACC: CardioOncology</i> , 2021, 3, 76-84.	1.7	13
142	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. <i>Bioinformatics</i> , 2020, 36, 1382-1390.	1.8	12
143	Generalizability of GWAS Hits in Clinical Populations: Lessons from Childhood Cancer Survivors. <i>American Journal of Human Genetics</i> , 2020, 107, 636-653.	2.6	12
144	Genome-wide association studies identify novel genetic loci for epigenetic age acceleration among survivors of childhood cancer. <i>Genome Medicine</i> , 2022, 14, 32.	3.6	12

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145	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. <i>Journal of the National Cancer Institute</i> , 2020, 112, 756-764.	3.0	11
146	A Novel Locus Predicts Spermatogenic Recovery among Childhood Cancer Survivors Exposed to Alkylating Agents. <i>Cancer Research</i> , 2020, 80, 3755-3764.	0.4	11
147	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 2096-2104.	1.1	11
148	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. <i>Bioinformatics</i> , 2014, 30, 1400-1408.	1.8	10
149	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). <i>Scientific Reports</i> , 2021, 11, 5154.	1.6	10
150	indelPost: harmonizing ambiguities in simple and complex indel alignments. <i>Bioinformatics</i> , 2022, 38, 549-551.	1.8	10
151	Exome sequencing analysis of murine medulloblastoma models identifies WDR11 as a potential tumor suppressor in Group 3 tumors. <i>Oncotarget</i> , 2017, 8, 64685-64697.	0.8	10
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