Jinghui Zhang

List of Publications by Citations

215 papers	21,361 citations	67 h-index	145 g-index
243 ext. papers	26,715 ext. citations	13.4 avg, IF	5.67 L-index

#	Paper	IF	Citations
215	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. *Nature*, **2012**, 481, 157-63	50.4	1163
214	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. *Nature Genetics*, **2012**, 44, 251-3	36.3	1081
213	Deletion of IKZF1 and prognosis in acute lymphoblastic leukemia. *New England Journal of Medicine*, **2009**, 360, 470-80	59.2	1030
212	Targetable kinase-activating lesions in Ph-like acute lymphoblastic leukemia. *New England Journal of Medicine*, **2014**, 371, 1005-15	59.2	885
211	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. *Nature Genetics*, **2014**, 46, 444-450	36.3	659
210	Germline Mutations in Predisposition Genes in Pediatric Cancer. *New England Journal of Medicine*, **2015**, 373, 2336-2346	59.2	641
209	The landscape of genomic alterations across childhood cancers. *Nature*, **2018**, 555, 321-327	50.4	603
208	Novel mutations target distinct subgroups of medulloblastoma. *Nature*, **2012**, 488, 43-8	50.4	590
207	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. *Nature Genetics*, **2013**, 45, 602-12	36.3	562
206	Genetic alterations activating kinase and cytokine receptor signaling in high-risk acute lymphoblastic leukemia. *Cancer Cell*, **2012**, 22, 153-66	24.3	515
205	The genomic landscape of hypodiploid acute lymphoblastic leukemia. *Nature Genetics*, **2013**, 45, 242-52	36.3	474
204	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
203	CREBBP mutations in relapsed acute lymphoblastic leukaemia. *Nature*, **2011**, 471, 235-9	50.4	468
202	Rearrangement of CRLF2 in B-progenitor- and Down syndrome-associated acute lymphoblastic leukemia. *Nature Genetics*, **2009**, 41, 1243-6	36.3	465
201	C11orf95-RELA fusions drive oncogenic NF-Ƀ signalling in ependymoma. *Nature*, **2014**, 506, 451-5	50.4	459
200	JAK mutations in high-risk childhood acute lymphoblastic leukemia. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 9414-8	11.5	446
199	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. *Nature Genetics*, **2017**, 49, 1211-1218	36.3	430

198	Recurrent somatic structural variations contribute to tumorigenesis in pediatric osteosarcoma. *Cell Reports*, **2014**, 7, 104-12	10.6	423
197	CREST maps somatic structural variation in cancer genomes with base-pair resolution. *Nature Methods*, **2011**, 8, 652-4	21.6	396
196	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. *Nature*, **2018**, 555, 371-376	50.4	380
195	A novel retinoblastoma therapy from genomic and epigenetic analyses. *Nature*, **2012**, 481, 329-34	50.4	364
194	Genomic landscape of Ewing sarcoma defines an aggressive subtype with co-association of STAG2 and TP53 mutations. *Cancer Discovery*, **2014**, 4, 1342-53	24.4	310
193	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. *Nature Genetics*, **2015**, 47, 330-7	36.3	303
192	Association of age at diagnosis and genetic mutations in patients with neuroblastoma. *JAMA - Journal of the American Medical Association*, **2012**, 307, 1062-71	27.4	289
191	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. *Nature Medicine*, **2018**, 24, 103-112	50.5	272
190	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. *Nature Communications*, **2014**, 5, 3630	17.4	263
189	The Pediatric Cancer Genome Project. *Nature Genetics*, **2012**, 44, 619-22	36.3	239
188	High Frequency and Poor Outcome of Philadelphia Chromosome-Like Acute Lymphoblastic Leukemia in Adults. *Journal of Clinical Oncology*, **2017**, 35, 394-401	2.2	227
187	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. *Blood*, **2011**, 118, 3080-7	2.2	218
186	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. *Nature Communications*, **2015**, 6, 6604	17.4	215
185	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, 833-45	14.3	209
184	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. *Nature Genetics*, **2013**, 45, 1226-1231	36.3	205
183	Global chromatin profiling reveals NSD2 mutations in pediatric acute lymphoblastic leukemia. *Nature Genetics*, **2013**, 45, 1386-91	36.3	192
182	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. *Nature Genetics*, **2019**, 51, 296-307	36.3	189
181	Targeting oxidative stress in embryonal rhabdomyosarcoma. *Cancer Cell*, **2013**, 24, 710-24	24.3	182

180	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. *EBioMedicine*, **2016**, 8, 173-183	8.8	169
179	Targetable kinase gene fusions in high-risk B-ALL: a study from the Children's Oncology Group. *Blood*, **2017**, 129, 3352-3361	2.2	168
178	Exploring genomic alteration in pediatric cancer using ProteinPaint. *Nature Genetics*, **2016**, 48, 4-6	36.3	163
177	Caspase-8 mediates caspase-1 processing and innate immune defense in response to bacterial blockade of NF-B and MAPK signaling. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 7385-90	11.5	162
176	An Inv(16)(p13.3q24.3)-encoded CBFA2T3-GLIS2 fusion protein defines an aggressive subtype of pediatric acute megakaryoblastic leukemia. *Cancer Cell*, **2012**, 22, 683-97	24.3	161
175	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	21.7	159
174	Novel oncogenic PDGFRA mutations in pediatric high-grade gliomas. *Cancer Research*, **2013**, 73, 6219-29	10.1	148
173	The genomic landscape of core-binding factor acute myeloid leukemias. *Nature Genetics*, **2016**, 48, 1551-1556	36.3	147
172	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. *Nature Genetics*, **2016**, 48, 1481-1489	36.3	145
171	Orthotopic patient-derived xenografts of paediatric solid tumours. *Nature*, **2017**, 549, 96-100	50.4	144
170	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, 12944-9	11.5	143
169	The genetic basis and cell of origin of mixed phenotype acute leukaemia. *Nature*, **2018**, 562, 373-379	50.4	140
168	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. *Neuron*, **2017**, 94, 550-568.e10	13.9	133
167	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. *Lancet Oncology, The*, **2015**, 16, 1659-66	21.7	123
166	The genomic landscape of childhood and adolescent melanoma. *Journal of Investigative Dermatology*, **2015**, 135, 816-823	4.3	121
165	Genomic landscape of paediatric adrenocortical tumours. *Nature Communications*, **2015**, 6, 6302	17.4	116
164	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. *Acta Neuropathologica*, **2018**, 136, 211-226	14.3	111
163	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. *Cancer Cell*, **2019**, 35, 140-155.e7	24.3	109

162	Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. *Nature Medicine*, **2015**, 21, 563-71	50.5	106
161	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. *PLoS Genetics*, **2015**, 11, e1005262	6	99
160	Analysis of error profiles in deep next-generation sequencing data. *Genome Biology*, **2019**, 20, 50	18.3	98
159	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	24.4	98
158	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. *Cancer Cell*, **2016**, 29, 186-200	24.3	92
157	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. *Nature Communications*, **2018**, 9, 3962	17.4	88
156	Pediatric non-Down syndrome acute megakaryoblastic leukemia is characterized by distinct genomic subsets with varying outcomes. *Nature Genetics*, **2017**, 49, 451-456	36.3	84
155	Bambino: a variant detector and alignment viewer for next-generation sequencing data in the SAM/BAM format. *Bioinformatics*, **2011**, 27, 865-6	7.2	82
154	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. *Blood*, **2020**, 135, 41-55	2.2	81
153	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. *Neuro-Oncology*, **2014**, 16, iii16-iii16	1	78
152	MAPK signaling cascades mediate distinct glucocorticoid resistance mechanisms in pediatric leukemia. *Blood*, **2015**, 126, 2202-12	2.2	75
151	Cancer-associated DDX3X mutations drive stress granule assembly and impair global translation. *Scientific Reports*, **2016**, 6, 25996	4.9	75
150	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. *Nature Communications*, **2015**, 6, 6553	17.4	70
149	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. *Cancer Cell*, **2018**, 34, 411-426.e19	24.3	67
148	Outcome of children with hypodiploid ALL treated with risk-directed therapy based on MRD levels. *Blood*, **2015**, 126, 2896-9	2.2	62
147	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. *Journal of Clinical Oncology*, **2018**, 36, 2078-2087	2.2	60
146	Genomic and outcome analyses of Ph-like ALL in NCI standard-risk patients: a report from the Children's Oncology Group. *Blood*, **2018**, 132, 815-824	2.2	58
145	CONSERTING: integrating copy-number analysis with structural-variation detection. *Nature Methods*, **2015**, 12, 527-30	21.6	56

144	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. *Blood*, **2015**, 125, 3609-17	2.2	56
143	Cross-Species Genomics Identifies TAF12, NFYC, and RAD54L as Choroid Plexus Carcinoma Oncogenes. *Cancer Cell*, **2015**, 27, 712-27	24.3	55
142	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. *Journal of Proteome Research*, **2016**, 15, 2309-20	5.6	52
141	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. *Nature Communications*, **2015**, 6, 7553	17.4	51
140	The neoepitope landscape in pediatric cancers. *Genome Medicine*, **2017**, 9, 78	14.4	51
139	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	2.2	51
138	Small genomic insertions form enhancers that misregulate oncogenes. *Nature Communications*, **2017**, 8, 14385	17.4	46
137	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. *Blood*, **2013**, 122, 826-826	2.2	45
136	Mutational landscape and patterns of clonal evolution in relapsed pediatric acute lymphoblastic leukemia. *Blood Cancer Discovery*, **2020**, 1, 96-111	7	44
135	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. *Modern Pathology*, **2016**, 29, 359-69	9.8	44
134	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. *Acta Neuropathologica*, **2019**, 137, 637-655	14.3	43
133	Pediatric patients with acute lymphoblastic leukemia generate abundant and functional neoantigen-specific CD8 T cell responses. *Science Translational Medicine*, **2019**, 11,	17.5	43
132	Relapse-Fated Latent Diagnosis Subclones in Acute B Lineage Leukemia Are Drug Tolerant and Possess Distinct Metabolic Programs. *Cancer Discovery*, **2020**, 10, 568-587	24.4	37
131	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. *Nature Medicine*, **2019**, 25, 597-602	50.5	36
130	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. *Genome Biology*, **2020**, 21, 126	18.3	36
129	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. *Nature Communications*, **2020**, 11, 913	17.4	32
128	Germline Lysine-Specific Demethylase 1 () Mutations Confer Susceptibility to Multiple Myeloma. *Cancer Research*, **2018**, 78, 2747-2759	10.1	32
127	Structure and evolution of double minutes in diagnosis and relapse brain tumors. *Acta Neuropathologica*, **2019**, 137, 123-137	14.3	32

126	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. *Cancer Discovery*, **2021**, 11, 1082-1099	24.4	32
125	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. *Nature Communications*, **2020**, 11, 5183	17.4	31
124	Custom Gene Capture and Next-Generation Sequencing to Resolve Discordant ALK Status by FISH and IHC in Lung Adenocarcinoma. *Journal of Thoracic Oncology*, **2016**, 11, 1891-1900	8.9	30
123	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. *Genome Biology*, **2012**, 13, R113	18.3	28
122	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. *Nature Genetics*, **2020**, 52, 811-818	36.3	26
121	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. *Molecular Cancer Research*, **2019**, 17, 895-906	6.6	25
120	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (PRKCA) Fusion. *JAMA Dermatology*, **2016**, 152, 318-22	5.1	24
119	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. *Cancer Discovery*, **2021**,	24.4	21
118	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	15.4	19
117	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	12.9	18
116	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. *International Journal of Epidemiology*, **2021**, 50, 39-49	7.8	18
115	Inhibition of SF3B1 by molecules targeting the spliceosome results in massive aberrant exon skipping. *Rna*, **2018**, 24, 1056-1066	5.8	18
114	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. *Leukemia*, **2020**, 34, 2025-2037	10.7	17
113	Pediatric Cancer Variant Pathogenicity Information Exchange (PeCanPIE): a cloud-based platform for curating and classifying germline variants. *Genome Research*, **2019**, 29, 1555-1565	9.7	16
112	XAF1 as a modifier of p53 function and cancer susceptibility. *Science Advances*, **2020**, 6, eaba3231	14.3	14
111	PTEN Signaling in the Postnatal Perivascular Progenitor Niche Drives Medulloblastoma Formation. *Cancer Research*, **2017**, 77, 123-133	10.1	14
110	Subsequent Breast Cancer in Female Childhood Cancer Survivors in the St Jude Lifetime Cohort Study (SJLIFE). *Journal of Clinical Oncology*, **2019**, 37, 1647-1656	2.2	13
109	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	9.7	13

108	A genomic random interval model for statistical analysis of genomic lesion data. *Bioinformatics*, **2013**, 29, 2088-95	7.2	13
107	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	3.6	12
106	Enrichment of heterozygous germline loss-of-function variants in pediatric osteosarcoma. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	12
105	Enhancer Hijacking Drives Oncogenic Expression in Lineage-Ambiguous Stem Cell Leukemia. *Cancer Discovery*, **2021**, 11, 2846-2867	24.4	12
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	2.2	11
103	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. *Scientific Reports*, **2014**, 4, 7455	4.9	11
102	ChIPseqSpikeInFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. *Bioinformatics*, **2020**, 36, 1270-1272	7.2	11
101	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	12.9	11
100	Association of Germline BRCA2 Mutations With the Risk of Pediatric or Adolescent Non-Hodgkin Lymphoma. *JAMA Oncology*, **2019**, 5, 1362-1364	13.4	10
99	Antitumor Effects of CAR T Cells Redirected to the EDB Splice Variant of Fibronectin. *Cancer Immunology Research*, **2021**, 9, 279-290	12.5	10
98	Clear cell sarcoma of kidney involving a horseshoe kidney and harboring EGFR internal tandem duplication. *Pediatric Blood and Cancer*, **2017**, 64, e26602	3	9
97	Genome-Wide Association Study in Irradiated Childhood Cancer Survivors Identifies HTR2A for Subsequent Basal Cell Carcinoma. *Journal of Investigative Dermatology*, **2019**, 139, 2042-2045.e8	4.3	9
96	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. *Nature Communications*, **2021**, 12, 985	17.4	9
95	Long-read sequencing unveils IGH-DUX4 translocation into the silenced IGH allele in B-cell acute lymphoblastic leukemia. *Nature Communications*, **2019**, 10, 2789	17.4	8
94	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. *Bioinformatics*, **2014**, 30, 1400-8	7.2	8
93	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. *Acta Neuropathologica*, **2020**, 140, 963-965	14.3	8
92	Pathologic Characteristics of Spitz Melanoma With MAP3K8 Fusion or Truncation in a Pediatric Cohort. *American Journal of Surgical Pathology*, **2019**, 43, 1631-1637	6.7	8
91	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. *Cancer Research*, **2021**, 81, 2556-2565	10.1	8

90	Therapeutic and prognostic insights from the analysis of cancer mutational signatures. *Trends in Genetics*, **2021**,	8.5	8
89	Generalizability of "GWAS Hits" in Clinical Populations: Lessons from Childhood Cancer Survivors. *American Journal of Human Genetics*, **2020**, 107, 636-653	11	7
88	The Genomic Contributions of Avian H1N1 Influenza A Viruses to the Evolution of Mammalian Strains. *PLoS ONE*, **2015**, 10, e0133795	3.7	7
87	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	2.2	7
86	Estimated number of adult survivors of childhood cancer in United States with cancer-predisposing germline variants. *Pediatric Blood and Cancer*, **2020**, 67, e28047	3	7
85	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. *Nature Communications*, **2019**, 10, 5806	17.4	7
84	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. *Bioinformatics*, **2020**, 36, 1382-1390	7.9	7
83	Molecular basis of ETV6-mediated predisposition to childhood acute lymphoblastic leukemia. *Blood*, **2021**, 137, 364-373	2.2	7
82	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. *Cancer Cell*, **2021**, 39, 83-95.e4	24.5	7
81	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. *Nature Communications*, **2021**, 12, 5531	17.4	7
80	Genomic Characterization and Experimental Modeling Of BCR-ABL1-Like Acute Lymphoblastic Leukemia. *Blood*, **2013**, 122, 232-232	2.2	6
79	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. *Clinical Cancer Research*, **2019**, 25, 6700-6708	12.9	6
78	Integrative network analysis reveals USP7 haploinsufficiency inhibits E-protein activity in pediatric T-lineage acute lymphoblastic leukemia (T-ALL). *Scientific Reports*, **2021**, 11, 5154	4.9	5
77	Epigenetic Age Acceleration and Chronic Health Conditions Among Adult Survivors of Childhood Cancer. *Journal of the National Cancer Institute*, **2021**, 113, 597-605	9.7	5
76	Chemotherapy and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse.. *Nature Cancer*, **2021**, 2, 819-834	15.4	5
75	The NSD2 p.E1099K Mutation Is Enriched at Relapse and Confers Drug Resistance in a Cell Context-Dependent Manner in Pediatric Acute Lymphoblastic Leukemia. *Molecular Cancer Research*, **2020**, 18, 1153-1165	6.6	4
74	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	2.2	4
73	High Frequency and Poor Outcome of Ph-like Acute Lymphoblastic Leukemia in Adults. *Blood*, **2015**, 126, 2618-2618	2.2	4

72	Exome sequencing analysis of murine medulloblastoma models identifies WDR11 as a potential tumor suppressor in Group 3 tumors. *Oncotarget*, **2017**, 8, 64685-64697	3.3	4
71	Contribution of Polygenic Risk to Hypertension Among Long-Term Survivors of Childhood Cancer. *JACC: CardioOncology*, **2021**, 3, 76-84	3.8	4
70	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. *Journal of the National Cancer Institute*, **2020**, 112, 756-764	9.7	4
69	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. *PLoS Genetics*, **2019**, 15, e1008168	6	3
68	A Novel Locus Predicts Spermatogenic Recovery among Childhood Cancer Survivors Exposed to Alkylating Agents. *Cancer Research*, **2020**, 80, 3755-3764	10.1	3
67	VCF2CNA: A tool for efficiently detecting copy-number alterations in VCF genotype data and tumor purity. *Scientific Reports*, **2019**, 9, 10357	4.9	3
66	Genome-Wide Analysis of Genetic Alterations In Hypodiploid Acute Lymphoblastic Leukemia Identifies a High Frequency of Mutations Targeting the IKAROS Gene Family and Ras Signaling. *Blood*, **2010**, 116, 411-411	2.2	3
65	Whole Genome Sequence Analysis of 22 MLL Rearranged Infant Acute Lymphoblastic Leukemias Reveals Remarkably Few Somatic Mutations: A Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. *Blood*, **2011**, 118, 69-69	2.2	3
64	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. *Blood*, **2013**, 122, 824-824	2.2	3
63	The Genomic Landscape of Childhood T-Lineage Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 691-691	2.1	3
62	CPX-351 Induces Remission in Newly Diagnosed Pediatric Secondary Myeloid Malignancies. *Blood Advances*, **2021**,	7.8	3
61	XenoCP: Cloud-based BAM cleansing tool for RNA and DNA from Xenograft		3
60	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	14.4	3
59	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. *Nature Communications*, **2021**, 12, 4089	17.4	3
58	Polygenic Risk Score Improves Risk Stratification and Prediction of Subsequent Thyroid Cancer after Childhood Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 2096-2104	4	3
57	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	0.9	2
56	Data Access and Interactive Visualization of Whole Genome Sequence of Sickle Cell Patients within the St. Jude Cloud. *Blood*, **2018**, 132, 723-723	2.2	2
55	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. *Blood*, **2018**, 132, 3641-3641	2.2	2

54	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	2.2	2
53	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. *Science Advances*, **2021**, 7, eabe0834	14.3	2
52	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. *Blood*, **2019**, 134, 649-649	2.2	2
51	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	2.2	2
50	FPGS relapse-specific mutations in relapsed childhood acute lymphoblastic leukemia. *Scientific Reports*, **2020**, 10, 12074	4.9	2
49	Comprehensive Genomic Profiling of Pediatric Therapy-Related Myeloid Neoplasms Identifies Mecom Dysregulation to be Associated with Poor Outcome. *Blood*, **2019**, 134, 1394-1394	2.2	1
48	A BCR-ABL1-Like Gene Expression Profile Confers a Poor Prognosis In Patients with High-Risk Acute Lymphoblastic Leukemia (HR-ALL): A Report From Children's Oncology Group (COG) AALL0232. *Blood*, **2011**, 118, 743-743	2.2	1
47	De Novo Purine Biosynthesis in Drug Resistance and Tumor Relapse of Childhood ALL. *Blood*, **2015**, 126, 2627-2627	2.2	1
46	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. *Blood*, **2015**, 126, 693-693	2.2	1
45	Mixed Lineage Leukemia Rearrangements (MLL-R) Are Determinants of High Risk Disease in Homeobox A (HOXA)-deregulated T-Lineage Acute Lymphoblastic Leukemia: A Children's Oncology Group Study. *Blood*, **2015**, 126, 694-694	2.2	1
44	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. *Blood*, **2018**, 132, 565-565	2.2	1
43	St. Jude Cloud Pediatric Cancer Genomic Data Sharing Ecosystem		1
42	Patient-Derived Orthotopic Xenografts and Cell Lines from Pediatric High-Grade Glioma Recapitulate the Heterogeneity of Histopathology, Molecular Signatures, and Drug Response		1
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