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	indelPost: harmonizing ambiguities in simple and complex indel alignments. Bioinformatics, 2022, 38, 549-551.	4.1	10
2	Therapeutic and prognostic insights from the analysis of cancer mutational signatures. Trends in Genetics, 2022, 38, 194-208.	6.7	39
3	CPX-351 induces remission in newly diagnosed pediatric secondary myeloid malignancies. Blood Advances, 2022, 6, 521-527.	5.2	10
4	Blood DNA methylation signatures are associated with social determinants of health among survivors of childhood cancer. Epigenetics, 2022, , 1-15.	2.7	5
5	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
6	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
7	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
8	Somatic LINE-1 promoter acquisition drives oncogenic FOXR2 activation in pediatric brain tumor. Acta Neuropathologica, 2022, 143, 605-607.	7.7	4
9	Convergent evolution and multi-wave clonal invasion in H3 K27-altered diffuse midline gliomas treated with a PDGFR inhibitor. Acta Neuropathologica Communications, 2022, 10, .	5.2	3
10	A community approach to the cancer-variant-interpretation bottleneck. Nature Cancer, 2022, 3, 522-525.	13.2	3
11	Contribution of Genome-Wide Polygenic Score to Risk of Coronary Artery Disease in Childhood Cancer Survivors. JACC: CardioOncology, 2022, 4, 258-267.	4.0	3
12	A Novel Locus on 6p21.2 for Cancer Treatmentâ€“Induced Cardiac Dysfunction Among Childhood Cancer Survivors. Journal of the National Cancer Institute, 2022, 114, 1109-1116.	6.3	4
13	Molecular basis of ETV6-mediated predisposition to childhood acute lymphoblastic leukemia. Blood, 2021, 137, 364-373.	1.4	37
14	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
15	Genetic Variants Associated with Therapy-Related Cardiomyopathy among Childhood Cancer Survivors of African Ancestry. Cancer Research, 2021, 81, 2556-2565.	0.9	24
16	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
17	Exploration of Coding and Non-coding Variants in Cancer Using GenomePaint. Cancer Cell, 2021, 39, 83-95.e4.	16.8	18
18	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31

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19	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
20	Contribution of Polygenic Risk to Hypertension Among Long-Term Survivors of Childhood Cancer. JACC: CardioOncology, 2021, 3, 76-84.	4.0	13
21	Abstract IA-18: Big pediatric cancer genomic data: Discovery, precision medicine, and data sharing. , 2021, , .		6
22	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
23	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
24	Targeted gene expression classifier identifies pediatric T-cell acute lymphoblastic leukemia (T-ALL) patients at high risk for end induction minimal residual disease positivity.. Journal of Clinical Oncology, 2021, 39, 10002-10002.	1.6	0
25	Enhancer Hijacking Drives Oncogenic BCL11B Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	9.4	83
26	Abstract 2289: Empowering point-and-click genomic analysis with large pediatric genomic reference data on St. Jude Cloud. , 2021, , .		0
27	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
28	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. Nature Communications, 2021, 12, 4089.	12.8	27
29	Abstract 3028: Integrative genomics reveals lncRNAs associated with pediatric cancer. , 2021, , .		1
30	Abstract 1543: Mining cancer-specific isoforms as CAR T-cell therapy targets for pediatric solid and brain tumors. , 2021, , .		1
31	Abstract 685: A social epigenomic investigation of racial disparity in pulmonary impairment among aging survivors of childhood cancer. , 2021, , .		0
32	Abstract 633: Thiopurines and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. , 2021, , .		0
33	Abstract 904: Epigenome-wide association study of dyslipidemia in survivors of childhood cancer: A report from the St. Jude lifetime cohort. , 2021, , .		0
34	Abstract 642: Genomes for Kids: Comprehensive DNA and RNA sequencing defining the scope of actionable mutations in pediatric cancer. , 2021, , .		0
35	Chemotherapy and mismatch repair deficiency cooperate to fuel TP53 mutagenesis and ALL relapse. Nature Cancer, 2021, 2, 819-834.	13.2	24
36	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

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37	Cancer Informatics for Cancer Centers: Scientific Drivers for Informatics, Data Science, and Care in Pediatric, Adolescent, and Young Adult Cancer. JCO Clinical Cancer Informatics, 2021, 5, 881-896.	2.1	3
38	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
39	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
40	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. Nature Communications, 2021, 12, 5531.	12.8	31
41	In a multi-institutional cohort of myeloid sarcomas, NFE2 mutation prevalence is lower than previously reported. Blood Advances, 2021, 5, 5057-5059.	5.2	2
42	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
43	Cohort Profile: The St. Jude Lifetime Cohort Study (SJLIFE) for paediatric cancer survivors. International Journal of Epidemiology, 2021, 50, 39-49.	1.9	70
44	Antitumor Effects of CAR T Cells Redirected to the EDB Splice Variant of Fibronectin. Cancer Immunology Research, 2021, 9, 279-290.	3.4	24
45	Retinoic acid rewires the adrenergic core regulatory circuitry of childhood neuroblastoma. Science Advances, 2021, 7, eabe0834.	10.3	22
46	A systematic analysis of genetic interactions and their underlying biology in childhood cancer. Communications Biology, 2021, 4, 1139.	4.4	2
47	Liposome-Encapsulated Cytarabine and Daunorubicin (CPX-351) Induces Remission in Newly Diagnosed Pediatric Secondary Myeloid Malignancies. Blood, 2021, 138, 4415-4415.	1.4	0
48	The landscape of coding RNA editing events in pediatric cancer. BMC Cancer, 2021, 21, 1233.	2.6	7
49	The Molecular Landscape of KMT2A-Rearranged Leukemia from Infancy to Adulthood Reveals Age and Leukemia-Specific Mutational Patterns. Blood, 2021, 138, 3479-3479.	1.4	0
50	Integrated Genomic Analysis Identifies UBTF Tandem Duplications As a Subtype-Defining Lesion in Pediatric Acute Myeloid Leukemia. Blood, 2021, 138, LBA-4-LBA-4.	1.4	0
51	Unifying heterogeneous expression data to predict targets for CAR-T cell therapy. OncoImmunology, 2021, 10, 2000109.	4.6	1
52	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
53	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
54	RNAIndel: discovering somatic coding indels from tumor RNA-Seq data. Bioinformatics, 2020, 36, 1382-1390.	4.1	12

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55	ChIPseqSpikeInFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. Bioinformatics, 2020, 36, 1270-1272.	4.1	25
56	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
57	Pan-neuroblastoma analysis reveals age- and signature-associated driver alterations. Nature Communications, 2020, 11, 5183.	12.8	87
58	FPGS relapse-specific mutations in relapsed childhood acute lymphoblastic leukemia. Scientific Reports, 2020, 10, 12074.	3.3	6
59	Therapy-induced mutagenesis in relapsed ALL is supported by mutational signature analysis. Blood, 2020, 136, 2235-2237.	1.4	1
60	Infratentorial C11orf95-fused gliomas share histologic, immunophenotypic, and molecular characteristics of supratentorial RELA-fused ependymoma. Acta Neuropathologica, 2020, 140, 963-965.	7.7	14
61	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
62	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
63	CICERO: a versatile method for detecting complex and diverse driver fusions using cancer RNA sequencing data. Genome Biology, 2020, 21, 126.	8.8	74
64	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
65	A Novel Locus Predicts Spermatogenic Recovery among Childhood Cancer Survivors Exposed to Alkylating Agents. Cancer Research, 2020, 80, 3755-3764.	0.9	11
66	XAF1 as a modifier of p53 function and cancer susceptibility. Science Advances, 2020, 6, eaba3231.	10.3	37
67	Discovery of regulatory noncoding variants in individual cancer genomes by using cis-X. Nature Genetics, 2020, 52, 811-818.	21.4	47
68	MYCN amplification and ATRX mutations are incompatible in neuroblastoma. Nature Communications, 2020, 11, 913.	12.8	66
69	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. Leukemia, 2020, 34, 2025-2037.	7.2	27
70	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
71	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	5.0	93
72	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

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73	Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. Blood, 2020, 135, 41-55.	1.4	171
74	Cardiomyopathy risk among childhood cancer survivors of African ancestry and its molecular mechanisms.. Journal of Clinical Oncology, 2020, 38, 10514-10514.	1.6	3
75	Creating a Variant Database for the American Society of Hematalogy By Consensus Variant Classification of Common Genes Associated with Hematologic Malignancies. Blood, 2020, 136, 4-5.	1.4	2
76	Genome and Transcriptome Profiling of Monosomy 7 AML Defines Novel Risk and Therapeutic Cohorts. Blood, 2020, 136, 20-21.	1.4	1
77	Association of Germline BRCA2 Mutations With the Risk of Pediatric or Adolescent Nonâ€“Hodgkin Lymphoma. JAMA Oncology, 2019, 5, 1362.	7.1	19
78	VCF2CNA: A tool for efficiently detecting copy-number alterations in VCF genotype data and tumor purity. Scientific Reports, 2019, 9, 10357.	3.3	4
79	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
80	Pediatric patients with acute lymphoblastic leukemia generate abundant and functional neoantigen-specific CD8 ⁺ T cell responses. Science Translational Medicine, 2019, 11, .	12.4	66
81	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
82	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
83	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
84	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
85	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. PLoS Genetics, 2019, 15, e1008168.	3.5	5
86	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
87	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
88	Analysis of error profiles in deep next-generation sequencing data. Genome Biology, 2019, 20, 50.	8.8	196
89	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
90	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

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91	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
92	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
93	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
94	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. Nature Genetics, 2019, 51, 296-307.	21.4	384
95	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	7.7	63
96	Abstract 3538: Analysis of error profiles in deep next-generation sequencing data. Cancer Research, 2019, 79, 3538-3538.	0.9	2
97	Integrative Analysis of Pediatric Acute Leukemia Identifies Immature Subtypes That Span a T Lineage and Myeloid Continuum with Distinct Prognoses. Blood, 2019, 134, 918-918.	1.4	1
98	Comprehensive Genomic Profiling of Pediatric Therapy-Related Myeloid Neoplasms Identifies Mecom Dysregulation to be Associated with Poor Outcome. Blood, 2019, 134, 1394-1394.	1.4	2
99	Genome-wide association study using whole-genome sequencing to identify a novel locus associated with cardiomyopathy risk in adult survivors of childhood cancer: Utility of a two-stage analytic approach.. Journal of Clinical Oncology, 2019, 37, 1516-1516.	1.6	0
100	Real-time sharing of comprehensive clinical genomics sequencing data in St. Jude Cloud.. Journal of Clinical Oncology, 2019, 37, 10019-10019.	1.6	0
101	Polygenic risk of subsequent thyroid cancer after childhood cancer: A report from St. Jude lifetime cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2019, 37, 10060-10060.	1.6	0
102	Gene expression signature associated with in vitro dexamethasone resistance and post-induction minimal residual disease in pediatric T-cell acute lymphoblastic leukemia.. Journal of Clinical Oncology, 2019, 37, 10033-10033.	1.6	0
103	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. Blood, 2019, 134, 649-649.	1.4	5
104	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
105	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
106	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
107	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
108	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56

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109	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
110	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
111	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
112	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
113	Clinical cancer genomic profiling by three-platform sequencing of whole genome, whole exome and transcriptome. Nature Communications, 2018, 9, 3962.	12.8	142
114	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
115	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
116	Inhibition of SF3B1 by molecules targeting the spliceosome results in massive aberrant exon skipping. Rna, 2018, 24, 1056-1066.	3.5	42
117	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
118	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
119	Identification of Therapeutic Targets in Rhabdomyosarcoma through Integrated Genomic, Epigenomic, and Proteomic Analyses. Cancer Cell, 2018, 34, 411-426.e19.	16.8	106
120	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
121	Data Access and Interactive Visualization of Whole Genome Sequence of Sickle Cell Patients within the St. Jude Cloud. Blood, 2018, 132, 723-723.	1.4	2
122	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	1.4	3
123	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. Blood, 2018, 132, 565-565.	1.4	14
124	Mutational Landscape and Temporal Evolution during Treatment of Relapsed Acute Lymphoblastic Leukemia. Blood, 2018, 132, 917-917.	1.4	0
125	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
126	Small genomic insertions form enhancers that misregulate oncogenes. Nature Communications, 2017, 8, 14385.	12.8	76

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127	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
128	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
129	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222
130	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
131	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	27.8	223
132	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
133	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	21.4	693
134	PTEN Signaling in the Postnatal Perivascular Progenitor Niche Drives Medulloblastoma Formation. Cancer Research, 2017, 77, 123-133.	0.9	20
135	The neoepitope landscape in pediatric cancers. Genome Medicine, 2017, 9, 78.	8.2	77
136	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
137	A high-risk genetic profile for premature menopause (PM) in childhood cancer survivors (CCS) exposed to gonadotoxic therapy: A report from the St. Jude Lifetime Cohort (SJLIFE) and Childhood Cancer Survivor Study (CCSS).. Journal of Clinical Oncology, 2017, 35, 10502-10502.	1.6	1
138	Cancer-associated DDX3X mutations drive stress granule assembly and impair global translation. Scientific Reports, 2016, 6, 25996.	3.3	121
139	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
140	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. EBioMedicine, 2016, 8, 173-183.	6.1	241
141	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
142	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
143	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
144	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

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145	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
146	Truncating Erythropoietin Receptor Rearrangements in Acute Lymphoblastic Leukemia. Cancer Cell, 2016, 29, 186-200.	16.8	118
147	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (PRKCA) Fusion. JAMA Dermatology, 2016, 152, 318.	4.1	33
148	Exploring genomic alteration in pediatric cancer using ProteinPaint. Nature Genetics, 2016, 48, 4-6.	21.4	275
149	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
150	Prevalence of RNA Editing Events Affecting Coding Regions in Pediatric Leukemia. Blood, 2016, 128, 3928-3928.	1.4	0
151	Outcome of children with hypodiploid ALL treated with risk-directed therapy based on MRD levels. Blood, 2015, 126, 2896-2899.	1.4	76
152	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	1.4	72
153	MAPK signaling cascades mediate distinct glucocorticoid resistance mechanisms in pediatric leukemia. Blood, 2015, 126, 2202-2212.	1.4	88
154	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. PLoS Genetics, 2015, 11, e1005262.	3.5	128
155	The Genomic Contributions of Avian H1N1 Influenza A Viruses to the Evolution of Mammalian Strains. PLoS ONE, 2015, 10, e0133795.	2.5	7
156	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
157	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
158	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
159	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. Nature Communications, 2015, 6, 7553.	12.8	72
160	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. Nature Communications, 2015, 6, 6553.	12.8	90
161	Cross-Species Genomics Identifies TAF12, NFYC, and RAD54L as Choroid Plexus Carcinoma Oncogenes. Cancer Cell, 2015, 27, 712-727.	16.8	74
162	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	12.8	281

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163	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
164	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	19.0	68
165	Negative feedbackâ€“defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. Nature Medicine, 2015, 21, 563-571.	30.7	141
166	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
167	High Frequency and Poor Outcome of Ph-like Acute Lymphoblastic Leukemia in Adults. Blood, 2015, 126, 2618-2618.	1.4	5
168	De Novo Purine Biosynthesis in Drug Resistance and Tumor Relapse of Childhood ALL. Blood, 2015, 126, 2627-2627.	1.4	2
169	The Genomic Landscape of Childhood T-Lineage Acute Lymphoblastic Leukemia. Blood, 2015, 126, 691-691.	1.4	4
170	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	1.4	1
171	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.	1.4	2
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