Stanley B Pounds

List of Publications by Year
in descending order

218 papers	18,890 citations	23567 58 h-index	12946 131 g-index
222 all docs	222 docs citations	222 times ranked	23838 citing authors

#	Article	IF	Citations
1	Genome-wide analysis of genetic alterations in acute lymphoblastic leukaemia. Nature, 2007, 446, 758-764.	27.8	1,602
2	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
3	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
4	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742
5	Subtypes of medulloblastoma have distinct developmental origins. Nature, 2010, 468, 1095-1099.	27.8	710
6	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	21.4	693
7	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
8	NKAML: A Pilot Study to Determine the Safety and Feasibility of Haploidentical Natural Killer Cell Transplantation in Childhood Acute Myeloid Leukemia. Journal of Clinical Oncology, 2010, 28, 955-959.	1.6	563
9	Minimal residual disease-directed therapy for childhood acute myeloid leukaemia: results of the AML02 multicentre trial. Lancet Oncology, The, 2010, 11, 543-552.	10.7	514
10	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
11	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
12	Gene expression profiling of pediatric acute myelogenous leukemia. Blood, 2004, 104, 3679-3687.	1.4	404
13	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. Nature Genetics, 2019, 51, 296-307.	21.4	384
14	Estimating the occurrence of false positives and false negatives in microarray studies by approximating and partitioning the empirical distribution of p-values. Bioinformatics, 2003, 19, 1236-1242.	4.1	376
15	High Frequency and Poor Outcome of Philadelphia Chromosome–Like Acute Lymphoblastic Leukemia in Adults. Journal of Clinical Oncology, 2017, 35, 394-401.	1.6	326
16	Cross-species genomics matches driver mutations and cell compartments to model ependymoma. Nature, 2010, 466, 632-636.	27.8	324
17	Comparison of Droplet Digital PCR to Real-Time PCR for Quantitative Detection of Cytomegalovirus. Journal of Clinical Microbiology, 2013, 51, 540-546.	3.9	280
18	A Mouse Model of the Most Aggressive Subgroup of Human Medulloblastoma. Cancer Cell, 2012, 21, 168-180.	16.8	250

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19	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
20	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
21	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
22	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
23	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
24	Genome-wide Interrogation of Germline Genetic Variation Associated With Treatment Response in Childhood Acute Lymphoblastic Leukemia. JAMA - Journal of the American Medical Association, 2009, 301, 393.	7.4	193
25	Comparative Analysis of Different Approaches to Measure Treatment Response in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2012, 30, 3625-3632.	1.6	188
26	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. Blood, 2012, 120, 4783-4794.	1.4	179
27	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
28	Higher‐order oligomerization promotes localization of <scp>SPOP</scp> to liquid nuclear speckles. EMBO Journal, 2016, 35, 1254-1275.	7.8	172
29	Robust estimation of the false discovery rate. Bioinformatics, 2006, 22, 1979-1987.	4.1	170
30	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
31	Acute mixed lineage leukemia in children: the experience of St Jude Children's Research Hospital. Blood, 2009, 113, 5083-5089.	1.4	159
32	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
33	Gene Expression Profiling of Childhood Adrenocortical Tumors. Cancer Research, 2007, 67, 600-608.	0.9	146
34	Phase I Pharmacokinetic and Pharmacodynamic Study of the Multikinase Inhibitor Sorafenib in Combination With Clofarabine and Cytarabine in Pediatric Relapsed/Refractory Leukemia. Journal of Clinical Oncology, 2011, 29, 3293-3300.	1.6	142
35	Improving false discovery rate estimation. Bioinformatics, 2004, 20, 1737-1745.	4.1	138
36	Multi-organ Mapping of Cancer Risk. Cell, 2016, 166, 1132-1146.e7.	28.9	128

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37	Multicenter Comparison of Different Real-Time PCR Assays for Quantitative Detection of Epstein-Barr Virus. Journal of Clinical Microbiology, 2008, 46, 157-163.	3.9	123
38	Clinical significance of residual disease during treatment in childhood acute myeloid leukaemia. British Journal of Haematology, 2003, 123, 243-252.	2.5	122
39	Gut Microbiome Composition Predicts Infection Risk During Chemotherapy in Children With Acute Lymphoblastic Leukemia. Clinical Infectious Diseases, 2018, 67, 541-548.	5.8	122
40	RB1 gene inactivation by chromothripsis in human retinoblastoma. Oncotarget, 2014, 5, 438-450.	1.8	104
41	Genomic subtyping and therapeutic targeting of acute erythroleukemia. Nature Genetics, 2019, 51, 694-704.	21.4	97
42	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	5.0	93
43	Venetoclax in combination with cytarabine with or without idarubicin in children with relapsed or refractory acute myeloid leukaemia: a phase 1, dose-escalation study. Lancet Oncology, The, 2020, 21, 551-560.	10.7	92
44	TERT promoter mutations and prognosis in solitary fibrous tumor. Modern Pathology, 2016, 29, 1511-1522.	5.5	88
45	Premedication with acetaminophen or diphenhydramine for transfusion with leucoreduced blood products in children. British Journal of Haematology, 2005, 130, 781-787.	2.5	87
46	Prophylactic antibiotics reduce morbidity due to septicemia during intensive treatment for pediatric acute myeloid leukemia. Cancer, 2008, 113, 376-382.	4.1	87
47	Prognostic factors and outcome of recurrence in childhood acute myeloid leukemia. Cancer, 2007, 109, 157-163.	4.1	85
48	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
49	Clinical and biologic features and treatment outcome of children with newly diagnosed acute myeloid leukemia and hyperleukocytosis. Cancer, 2008, 113, 522-529.	4.1	83
50	A therapeutic trial of decitabine and vorinostat in combination with chemotherapy for relapsed/refractory acute lymphoblastic leukemia. American Journal of Hematology, 2014, 89, 889-895.	4.1	82
51	IDH1 and IDH2 mutations in pediatric acute leukemia. Leukemia, 2011, 25, 1570-1577.	7.2	80
52	Estimation and control of multiple testing error rates for microarray studies. Briefings in Bioinformatics, 2006, 7, 25-36.	6.5	76
53	Pharmacogenetics of Deoxycytidine Kinase: Identification and Characterization of Novel Genetic Variants. Journal of Pharmacology and Experimental Therapeutics, 2007, 323, 935-945.	2.5	76
54	Commutability of the First World Health Organization International Standard for Human Cytomegalovirus. Journal of Clinical Microbiology, 2015, 53, 3325-3333.	3.9	76

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55	A phase II clinical trial of adoptive transfer of haploidentical natural killer cells for consolidation therapy of pediatric acute myeloid leukemia. , 2019, 7, 81.		74
56	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
57	Galactomannan Antigenemia in Pediatric Oncology Patients With Invasive Aspergillosis. Pediatric Infectious Disease Journal, 2008, 27, 815-819.	2.0	69
58	Classification analysis of the transcriptosome of nonlesional cultured dermal fibroblasts from systemic sclerosis patients with early disease. Arthritis and Rheumatism, 2005, 52, 865-876.	6.7	68
59	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	19.0	68
60	Analysis of MDM2 and MDM4 Single Nucleotide Polymorphisms, mRNA Splicing and Protein Expression in Retinoblastoma. PLoS ONE, 2012, 7, e42739.	2.5	68
61	Phase Separation Mediates NUP98 Fusion Oncoprotein Leukemic Transformation. Cancer Discovery, 2022, 12, 1152-1169.	9.4	68
62	High-resolution genomic profiling of adult and pediatric core-binding factor acute myeloid leukemia reveals new recurrent genomic alterations. Blood, 2012, 119, e67-e75.	1.4	66
63	Molecular classification improves risk assessment in adult <i>BCR-ABL1–</i>negative B-ALL. Blood, 2021, 138, 948-958.	1.4	59
64	Sample size determination for the false discovery rate. Bioinformatics, 2005, 21, 4263-4271.	4.1	58
65	Clinical Significance of CD33 Nonsynonymous Single-Nucleotide Polymorphisms in Pediatric Patients with Acute Myeloid Leukemia Treated with Gemtuzumab-Ozogamicin–Containing Chemotherapy. Clinical Cancer Research, 2013, 19, 1620-1627.	7.0	58
66	Effect of body mass index on the outcome of children with acute myeloid leukemia. Cancer, 2012, 118, 5989-5996.	4.1	56
67	A six-gene leukemic stem cell score identifies high risk pediatric acute myeloid leukemia. Leukemia, 2020, 34, 735-745.	7.2	56
68	Reference alignment of SNP microarray signals for copy number analysis of tumors. Bioinformatics, 2009, 25, 315-321.	4.1	55
69	Successive clinical trials for childhood acute myeloid leukemia at St Jude Children's Research Hospital, from 1980 to 2000. Leukemia, 2005, 19, 2125-2129.	7.2	53
70	Combination of cladribine and cytarabine is effective for childhood acute myeloid leukemia: results of the St Jude AML97 trial. Leukemia, 2009, 23, 1410-1416.	7.2	53
71	Feasibility, efficacy, and adverse effects of outpatient antibacterial prophylaxis in children with acute myeloid leukemia. Cancer, 2014, 120, 1985-1992.	4.1	53
72	Impact of age on outcome of pediatric acute myeloid leukemia. Cancer, 2006, 106, 2495-2502.	4.1	52

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73	Genetic Variants in Cytosolic 5â€²-Nucleotidase II Are Associated with Its Expression and Cytarabine Sensitivity in HapMap Cell Lines and in Patients with Acute Myeloid Leukemia. Journal of Pharmacology and Experimental Therapeutics, 2011, 339, 9-23.	2.5	50
74	Activity of the Multikinase Inhibitor Sorafenib in Combination With Cytarabine in Acute Myeloid Leukemia. Journal of the National Cancer Institute, 2011, 103, 893-905.	6.3	50
75	Bacterial Factors Required for Transmission of Streptococcus pneumoniae in Mammalian Hosts. Cell Host and Microbe, 2019, 25, 884-891.e6.	11.0	48
76	Effect of race on outcome of white and black children with acute myeloid leukemia: The St. Jude experience. Pediatric Blood and Cancer, 2007, 48, 10-15.	1.5	46
77	N-myc coordinates retinal growth with eye size during mouse development. Genes and Development, 2008, 22, 179-193.	5.9	45
78	Integrative genomic analyses reveal mechanisms of glucocorticoid resistance in acute lymphoblastic leukemia. Nature Cancer, 2020, 1, 329-344.	13.2	44
79	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. Blood, 2013, 121, 4366-4376.	1.4	42
80	Gemtuzumab ozogamicin can reduce minimal residual disease in patients with childhood acute myeloid leukemia. Cancer, 2013, 119, 4036-4043.	4.1	41
81	Prognostic features in acute megakaryoblastic leukemia in children without Down syndrome: a report from the AML02 multicenter trial and the Childrenâ€™s Oncology Group Study POG 9421. Leukemia, 2013, 27, 731-734.	7.2	41
82	OCTN1 Is a High-Affinity Carrier of Nucleoside Analogues. Cancer Research, 2017, 77, 2102-2111.	0.9	41
83	Hypoxia-induced upregulation of BMX kinase mediates therapeutic resistance in acute myeloid leukemia. Journal of Clinical Investigation, 2017, 128, 369-380.	8.2	39
84	Gliomatosis cerebri in children shares molecular characteristics with other pediatric gliomas. Acta Neuropathologica, 2016, 131, 299-307.	7.7	38
85	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
86	Coding polymorphisms in CD33 and response to gemtuzumab ozogamicin in pediatric patients with AML: a pilot study. Leukemia, 2009, 23, 402-404.	7.2	37
87	Cross-species genomic and epigenomic landscape of retinoblastoma. Oncotarget, 2013, 4, 844-859.	1.8	37
88	Comparative Evaluation of Three Commercial Quantitative Cytomegalovirus Standards by Use of Digital and Real-Time PCR. Journal of Clinical Microbiology, 2015, 53, 1500-1505.	3.9	37
89	Rapid Antimicrobial Susceptibility Testing Using Forward Laser Light Scatter Technology. Journal of Clinical Microbiology, 2016, 54, 2701-2706.	3.9	36
90	Severe cardiopulmonary complications consistent with systemic inflammatory response syndrome caused by leukemia cell lysis in childhood acute myelomonocytic or monocytic leukemia. Pediatric Blood and Cancer, 2005, 44, 63-69.	1.5	35

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91	Identification of Clinical Coryneform Bacterial Isolates: Comparison of Biochemical Methods and Sequence Analysis of 16S rRNA and <i>rpoB</i> Genes. Journal of Clinical Microbiology, 2008, 46, 921-927.	3.9	35
92	Statistical Significance Threshold Criteria For Analysis of Microarray Gene Expression Data. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-30.	0.6	34
93	Decreased relapsed rate and treatmentâ€related mortality contribute to improved outcomes for pediatric acute myeloid leukemia in successive clinical trials. Cancer, 2017, 123, 3791-3798.	4.1	34
94	Clofarabine Can Replace Anthracyclines and Etoposide in Remission Induction Therapy for Childhood Acute Myeloid Leukemia: The AML08 Multicenter, Randomized Phase III Trial. Journal of Clinical Oncology, 2019, 37, 2072-2081.	1.6	34
95	False discovery rate paradigms for statistical analyses of microarray gene expression data. Bioinformation, 2007, 1, 436-446.	0.5	34
96	Identification of Clinical and Biologic Correlates Associated With Outcome in Children With Adrenocortical Tumors Without Germline TP53 Mutations: A St Jude Adrenocortical Tumor Registry and Childrenâ€™s Oncology Group Study. Journal of Clinical Oncology, 2017, 35, 3956-3963.	1.6	33
97	Treatment outcome in older patients with childhood acute myeloid leukemia. Cancer, 2012, 118, 6253-6259.	4.1	32
98	Persistent Hyperplastic Primary Vitreous Due to Somatic Mosaic Deletion of theArfTumor Suppressor. , 2007, 48, 491.		31
99	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31
100	Statistical Development and Evaluation of Microarray Gene Expression Data Filters. Journal of Computational Biology, 2005, 12, 482-495.	1.6	29
101	Identification of predictive markers of cytarabine response in AML by integrative analysis of gene-expression profiles with multiple phenotypes. Pharmacogenomics, 2011, 12, 327-339.	1.3	27
102	<i>RRM1</i> and <i>RRM2</i> pharmacogenetics: association with phenotypes in HapMap cell lines and acute myeloid leukemia patients. Pharmacogenomics, 2013, 14, 1449-1466.	1.3	27
103	Inherited variation in OATP1B1 is associated with treatment outcome in acute myeloid leukemia. Clinical Pharmacology and Therapeutics, 2016, 99, 651-660.	4.7	27
104	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
105	Contribution of the <i>TP53</i> R337H mutation to the cancer burden in southern Brazil: Insights from the study of 55 families of children with adrenocortical tumors. Cancer, 2017, 123, 3150-3158.	4.1	26
106	Malignant rhabdoid tumors originating within and outside the central nervous system are clinically and molecularly heterogeneous. Acta Neuropathologica, 2018, 136, 315-326.	7.7	26
107	Bithalamic gliomas may be molecularly distinct from their unilateral highâ€grade counterparts. Brain Pathology, 2018, 28, 112-120.	4.1	26
108	Integrated epigenetic and genetic analysis identifies markers of prognostic significance in pediatric acute myeloid leukemia. Oncotarget, 2018, 9, 26711-26723.	1.8	26

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109	Genome scan implicates adhesion biological pathways in secondary leukemia. Leukemia, 2007, 21, 2128-2136.	7.2	25
110	Comparative Performance of Reagents and Platforms for Quantitation of Cytomegalovirus DNA by Digital PCR. Journal of Clinical Microbiology, 2016, 54, 2602-2608.	3.9	25
111	Combination of cladribine plus topotecan for recurrent or refractory pediatric acute myeloid leukemia. Cancer, 2010, 116, 98-105.	4.1	24
112	Quantitative real-time PCR detection of adenovirus in clinical blood specimens: A comparison of plasma, whole blood and peripheral blood mononuclear cells. Journal of Clinical Virology, 2007, 40, 295-300.	3.1	22
113	Prognostic Significance of Major Histocompatibility Complex Class II Expression in Pediatric Adrenocortical Tumors: A St. Jude and Children's Oncology Group Study. Clinical Cancer Research, 2016, 22, 6247-6255.	7.0	22
114	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
115	Integrated Transcriptomic and Genomic Sequencing Identifies Prognostic Constellations of Driver Mutations in Acute Myeloid Leukemia and Myelodysplastic Syndromes. Blood, 2019, 134, LBA-4-LBA-4.	1.4	20
116	Impact of genetic variation in FKBP5 on clinical response in pediatric acute myeloid leukemia patients: a pilot study. Leukemia, 2011, 25, 1354-1356.	7.2	19
117	A New System Identification Approach to Identify Genetic Variants in Sequencing Studies for a Binary Phenotype. Human Heredity, 2014, 78, 104-116.	0.8	19
118	MicroRNAâ€"mRNA Pairs Associated with Outcome in AML: From In Vitro Cell-Based Studies to AML Patients. Frontiers in Pharmacology, 2015, 6, 324.	3.5	19
119	Pharmacogenomics of intracellular methotrexate polyglutamates in patientsâ€™ leukemia cells in vivo. Journal of Clinical Investigation, 2020, 130, 6600-6615.	8.2	18
120	Comparison of two multiplexed PCR assays for the detection of HSV-1, HSV-2, and VZV with extracted and unextracted cutaneous and mucosal specimens. Journal of Clinical Virology, 2013, 58, 84-88.	3.1	17
121	A genomic random interval model for statistical analysis of genomic lesion data. Bioinformatics, 2013, 29, 2088-2095.	4.1	17
122	ChIP-PaM: an algorithm to identify protein-DNA interaction using ChIP-Seq data. Theoretical Biology and Medical Modelling, 2010, 7, 18.	2.1	16
123	A procedure to statistically evaluate agreement of differential expression for cross-species genomics. Bioinformatics, 2011, 27, 2098-2103.	4.1	16
124	Quantitative Assessment of Commutability for Clinical Viral Load Testing Using a Digital PCR-Based Reference Standard. Journal of Clinical Microbiology, 2016, 54, 1616-1623.	3.9	16
125	DNA Methylationâ€"Based Epigenetic Repression of SLC22A4 Promotes Resistance to Cytarabine in Acute Myeloid Leukemia. Clinical and Translational Science, 2021, 14, 137-142.	3.1	16
126	PROMISE: a tool to identify genomic features with a specific biologically interesting pattern of associations with multiple endpoint variables. Bioinformatics, 2009, 25, 2013-2019.	4.1	15

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127	Comparative Evaluation of Four Real-Time PCR Methods for the Quantitative Detection of Epstein-Barr Virus from Whole Blood Specimens. Journal of Molecular Diagnostics, 2016, 18, 527-534.	2.8	15
128	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	8.8	15
129	An R package that automatically collects and archives details for reproducible computing. BMC Bioinformatics, 2014, 15, 138.	2.6	14
130	Sorafenib Population Pharmacokinetics and Skin Toxicities in Children and Adolescents with Refractory/Relapsed Leukemia or Solid Tumor Malignancies. Clinical Cancer Research, 2019, 25, 7320-7330.	7.0	14
131	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. Blood, 2018, 132, 565-565.	1.4	14
132	Assumption adequacy averaging as a concept for developing more robust methods for differential gene expression analysis. Computational Statistics and Data Analysis, 2009, 53, 1604-1612.	1.2	13
133	Randomized trial of 2 dosages of prophylactic granulocyte–colony–stimulating factor after induction chemotherapy in pediatric acute myeloid leukemia. Cancer, 2011, 117, 1313-1320.	4.1	13
134	Empirical Bayesian Selection of Hypothesis Testing Procedures for Analysis of Sequence Count Expression Data. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.6	12
135	Definition of cure in childhood acute myeloid leukemia. Cancer, 2014, 120, 2490-2496.	4.1	12
136	Uncovering the Genomic Landscape in Newly Diagnosed and Relapsed Pediatric Cytogenetically Normal *FLT* *3–*ITD AML. Clinical and Translational Science, 2019, 12, 641-647.	3.1	12
137	Genome-wide association analysis identifies SNPs predictive of *in vitro* leukemic cell sensitivity to cytarabine in pediatric AML. Oncotarget, 2018, 9, 34859-34875.	1.8	12
138	Integrated analysis of pharmacologic, clinical and SNP microarray data using Projection Onto the Most Interesting Statistical Evidence with Adaptive Permutation Testing. International Journal of Data Mining and Bioinformatics, 2011, 5, 143.	0.1	11
139	Baseline mannose binding lectin levels may not predict infection among children with leukemia. Pediatric Blood and Cancer, 2008, 50, 866-868.	1.5	10
140	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. Bioinformatics, 2014, 30, 1400-1408.	4.1	10
141	SVSI: Fast and Powerful Set–Valued System Identification Approach to Identifying Rare Variants in Sequencing Studies for Ordered Categorical Traits. Annals of Human Genetics, 2015, 79, 294-309.	0.8	9
142	The Common Germline *TP53-R337H* Mutation Is Hypomorphic and Confers Incomplete Penetrance and Late Tumor Onset in a Mouse Model. Cancer Research, 2021, 81, 2442-2456.	0.9	9
143	Statistical analysis of data from retroviral clonal experiments in the developing retina. Brain Research, 2008, 1192, 178-185.	2.2	8
144	Regression analysis of longitudinal data with informative observation times and application to medical cost data. Statistics in Medicine, 2011, 30, 1429-1440.	1.6	8

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145	Cellular Metabolomics Profiles Associated With Drug Chemosensitivity in AML. Frontiers in Oncology, 2021, 11, 678008.	2.8	8
146	Statistical Methods for Overdispersion in mRNA-Seq Count Data. Open Bioinformatics Journal, 2013, 7, 34-40.	1.0	8
147	Clinical significance of *in vivo* cytarabine-induced gene expression signature in AML. Leukemia and Lymphoma, 2016, 57, 909-920.	1.3	7
148	Comprehensive Ara-C SNP score predicts leukemic cell intracellular ara-CTP levels in pediatric acute myeloid leukemia patients. Pharmacogenomics, 2018, 19, 1101-1110.	1.3	7
149	Polygenic Ara-C Response Score Identifies Pediatric Patients With Acute Myeloid Leukemia in Need of Chemotherapy Augmentation. Journal of Clinical Oncology, 2022, 40, 772-783.	1.6	7
150	PAIR: paired allelic log-intensity-ratio-based normalization method for SNP-CGH arrays. Bioinformatics, 2013, 29, 299-307.	4.1	6
151	Comparative evaluation of whole blood versus plasma for quantitative detection of cytomegalovirus using an automated system. Diagnostic Microbiology and Infectious Disease, 2016, 85, 23-25.	1.8	6
152	MicroRNAs Mediated Regulation of Expression of Nucleoside Analog Pathway Genes in Acute Myeloid Leukemia. Genes, 2019, 10, 319.	2.4	6
153	DNA Methylation Profiling Reveals Prognostically Significant Groups in Pediatric Adrenocortical Tumors: A Report From the International Pediatric Adrenocortical Tumor Registry. JCO Precision Oncology, 2019, 3, 1-21.	3.0	6
154	Global Proteomic Profiling of Pediatric AML: A Pilot Study. Cancers, 2021, 13, 3161.	3.7	6
155	The beta-binomial distribution for estimating the number of false rejections in microarray gene expression studies. Computational Statistics and Data Analysis, 2009, 53, 1688-1700.	1.2	5
156	Joint analysis of longitudinal data and recurrent episodes data with application to medical cost analysis. Biometrical Journal, 2013, 55, 5-16.	1.0	5
157	CC-PROMISE effectively integrates two forms of molecular data with multiple biologically related endpoints. BMC Bioinformatics, 2016, 17, 382.	2.6	5
158	Transcriptome profiling of patient derived xenograft models established from pediatric acute myeloid leukemia patients confirm maintenance of FLT3-ITD mutation. Leukemia and Lymphoma, 2017, 58, 247-250.	1.3	5
159	MLF1 is a proapoptotic antagonist of HOP complex-mediated survival. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 719-727.	4.1	5
160	Statistical selection of biological models for genome-wide association analyses. Methods, 2018, 145, 67-75.	3.8	5
161	DNA Methylation Clusters and Their Relation to Cytogenetic Features in Pediatric AML. Cancers, 2020, 12, 3024.	3.7	5
162	Metabolomics Profiling Reveals Markers for Chemosensitivity and Clinical Outcomes in Pediatric AML Patients. Blood, 2018, 132, 1536-1536.	1.4	5

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163	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. Blood, 2019, 134, 649-649.	1.4	5
164	Prognostic significance of myeloperoxidase expression in childhood acute myeloid leukemia. Pediatric Blood and Cancer, 2008, 50, 542-548.	1.5	4
165	An empirical Bayes approach for analysis of diverse periodic trends in time-course gene expression data. Bioinformatics, 2013, 29, 182-188.	4.1	4
166	A Robust and Powerful Set-Valued Approach to Rare Variant Association Analyses of Secondary Traits in Case-Control Sequencing Studies. Genetics, 2017, 205, 1049-1062.	2.9	4
167	Genomic Landscape of Pediatric Mixed Phenotype Acute Leukemia. Blood, 2016, 128, 454-454.	1.4	4
168	Acute Megakaryoblastic Leukemia (AMKL) in Children without Down Syndrome.. Blood, 2009, 114, 482-482.	1.4	3
169	Clinical Activity, Pharmacokinetics, and Pharmacodynamics of Sorafenib In Pediatric Acute Myeloid Leukemia.. Blood, 2010, 116, 1073-1073.	1.4	3
170	Gene Expression Patterns Associated with Cytarabine Pharmacology and Outcome in Pediatric Acute Myeloid Leukemia.. Blood, 2009, 114, 114-114.	1.4	3
171	Changes in body mass index, weight, and height in children with acute myeloid leukemia and the associations with outcome. Blood Advances, 2022, 6, 2824-2834.	5.2	3
172	Preclinical and Pilot Study of Type I FLT3 Tyrosine Kinase Inhibitor, Crenolanib, with Sorafenib in Acute Myeloid Leukemia and *FLT3*-Internal Tandem Duplication. Clinical Cancer Research, 2022, 28, 2536-2546.	7.0	3
173	The Genomic Landscape of Childhood and Adult Acute Erythroid Leukemia. Blood, 2016, 128, 39-39.	1.4	2
174	Abstract PR03: The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. , 2014, , .		2
175	Integrated Genome Wide Association Study (GWAS) Identifies SNPs Associated with Outcome in Pediatric AML. Blood, 2018, 132, 2758-2758.	1.4	2
176	Estimating the Fraction of Clonable Genomic DNA. Bulletin of Mathematical Biology, 2001, 63, 995-1002.	1.9	1
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