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	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
2	Proteomics: a new era in pediatric acute myeloid leukemia research. Haematologica, 2022, , .	3.5	0
3	Phase Separation Mediates NUP98 Fusion Oncoprotein Leukemic Transformation. Cancer Discovery, 2022, 12, 1152-1169.	9.4	68
4	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
5	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
6	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
7	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
8	SequencErr: measuring and suppressing sequencer errors in next-generation sequencing data. Genome Biology, 2021, 22, 37.	8.8	15
9	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
10	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
11	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31
12	Gene-set distance analysis (GSDA): a powerful tool for gene-set association analysis. BMC Bioinformatics, 2021, 22, 207.	2.6	0
13	Molecular classification improves risk assessment in adult BCR-ABL1â€“negative B-ALL. Blood, 2021, 138, 948-958.	1.4	59
14	Global Proteomic Profiling of Pediatric AML: A Pilot Study. Cancers, 2021, 13, 3161.	3.7	6
15	Cellular Metabolomics Profiles Associated With Drug Chemosensitivity in AML. Frontiers in Oncology, 2021, 11, 678008.	2.8	8
16	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
17	Clinical Features and Cytoreduction Therapy in Children with Newly Diagnosed Acute Myeloid Leukemia and Hyperleukocytosis. Blood, 2021, 138, 2295-2295.	1.4	0
18	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

#	Article	IF	Citations
19	A six-gene leukemic stem cell score identifies high risk pediatric acute myeloid leukemia. Leukemia, 2020, 34, 735-745.	7.2	56
20	DNA Methylation Clusters and Their Relation to Cytogenetic Features in Pediatric AML. Cancers, 2020, 12, 3024.	3.7	5
21	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
22	Integrative genomic analyses reveal mechanisms of glucocorticoid resistance in acute lymphoblastic leukemia. Nature Cancer, 2020, 1, 329-344.	13.2	44
23	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	5.0	93
24	Pharmacogenomics of intracellular methotrexate polyglutamates in patientsâ€™ leukemia cells in vivo. Journal of Clinical Investigation, 2020, 130, 6600-6615.	8.2	18
25	The St. Jude STEM Clubs: An Afterschool STEM Club for Upper Elementary School Students in Memphis, TN. Journal of STEM Outreach, 2020, 3, .	0.5	0
26	Uncovering the Genomic Landscape in Newly Diagnosed and Relapsed Pediatric Cytogenetically Normal FLT3â€ITD AML. Clinical and Translational Science, 2019, 12, 641-647.	3.1	12
27	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
28	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
29	Bacterial Factors Required for Transmission of Streptococcus pneumoniae in Mammalian Hosts. Cell Host and Microbe, 2019, 25, 884-891.e6.	11.0	48
30	MicroRNAs Mediated Regulation of Expression of Nucleoside Analog Pathway Genes in Acute Myeloid Leukemia. Genes, 2019, 10, 319.	2.4	6
31	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
32	Genomic subtyping and therapeutic targeting of acute erythroleukemia. Nature Genetics, 2019, 51, 694-704.	21.4	97
33	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
34	Forty-five patient-derived xenografts capture the clinical and biological heterogeneity of Wilms tumor. Nature Communications, 2019, 10, 5806.	12.8	27
35	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
36	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

#	Article	IF	Citations
37	PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia. Nature Genetics, 2019, 51, 296-307.	21.4	384
38	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
39	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
40	OR02-1 DNA Methylation Profiling in Pediatric Adrenocortical Tumors Reveals Distinct Methylation Signatures with Prognostic Significance: A Report from the International Pediatric Adrenocortical Tumor Registry. Journal of the Endocrine Society, 2019, 3, .	0.2	0
41	SAT-LB058 Effect of a Genetic Modifier of Cancer Risk in TP53 Mutation Carriers. Journal of the Endocrine Society, 2019, 3, .	0.2	0
42	Venetoclax in Combination with High-Dose Chemotherapy Is Active and Well-Tolerated in Children with Relapsed or Refractory Acute Myeloid Leukemia. Blood, 2019, 134, 178-178.	1.4	0
43	The Genomic Landscape of Childhood Acute Lymphoblastic Leukemia. Blood, 2019, 134, 649-649.	1.4	5
44	A 5-Gene Ara-C, Daunorubicin and Etoposide (ADE) Drug Response Score As a Prognostic Tool to Predict AML Treatment Outcome. Blood, 2019, 134, 1429-1429.	1.4	1
45	Gut Microbiome Composition Predicts Infection Risk During Chemotherapy in Children With Acute Lymphoblastic Leukemia. Clinical Infectious Diseases, 2018, 67, 541-548.	5.8	122
46	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	27.8	649
47	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
48	Bithalamic gliomas may be molecularly distinct from their unilateral highâ€grade counterparts. Brain Pathology, 2018, 28, 112-120.	4.1	26
49	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
50	POST: A framework for set-based association analysis in high-dimensional data. Methods, 2018, 145, 76-81.	3.8	1
51	Statistical selection of biological models for genome-wide association analyses. Methods, 2018, 145, 67-75.	3.8	5
52	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
53	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
54	Metabolomics Profiling Reveals Markers for Chemosensitivity and Clinical Outcomes in Pediatric AML Patients. Blood, 2018, 132, 1536-1536.	1.4	5

#	Article	IF	Citations
55	Integrated epigenetic and genetic analysis identifies markers of prognostic significance in pediatric acute myeloid leukemia. Oncotarget, 2018, 9, 26711-26723.	1.8	26
56	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
57	Pediatric LSC3 (pLSC3) Score Derived from DNMT3B-CD34-GPR56 As a Prognostic Tool to Predict AML Patient Outcome: Results from Two Independent Pediatric AML Cohorts. Blood, 2018, 132, 290-290.	1.4	1
58	Characterization of Novel Subtypes in B Progenitor Acute Lymphoblastic Leukemia. Blood, 2018, 132, 565-565.	1.4	14
59	Integrated Genome Wide Association Study (GWAS) Identifies SNPs Associated with Outcome in Pediatric AML. Blood, 2018, 132, 2758-2758.	1.4	2
60	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
61	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
62	OCTN1 Is a High-Affinity Carrier of Nucleoside Analogues. Cancer Research, 2017, 77, 2102-2111.	0.9	41
63	MLF1 is a proapoptotic antagonist of HOP complex-mediated survival. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 719-727.	4.1	5
64	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
65	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
66	Contribution of the TP53 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
67	The genomic landscape of pediatric and young adult T-lineage acute lymphoblastic leukemia. Nature Genetics, 2017, 49, 1211-1218.	21.4	693
68	Statistical selection of biological models for genome-wide association analyses. , 2017, , .		0
69	POST: A framework for set-based association analysis in high-dimensional data. , 2017, , .		0
70	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
71	Hypoxia-induced upregulation of BMX kinase mediates therapeutic resistance in acute myeloid leukemia. Journal of Clinical Investigation, 2017, 128, 369-380.	8.2	39
72	Higherâ€order oligomerization promotes localization of <scp>SPOP</scp> to liquid nuclear speckles. EMBO Journal, 2016, 35, 1254-1275.	7.8	172

#	Article	IF	Citations
73	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
74	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
75	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
76	Multi-organ Mapping of Cancer Risk. Cell, 2016, 166, 1132-1146.e7.	28.9	128
77	TERT promoter mutations and prognosis in solitary fibrous tumor. Modern Pathology, 2016, 29, 1511-1522.	5.5	88
78	Rapid Antimicrobial Susceptibility Testing Using Forward Laser Light Scatter Technology. Journal of Clinical Microbiology, 2016, 54, 2701-2706.	3.9	36
79	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
80	CC-PROMISE effectively integrates two forms of molecular data with multiple biologically related endpoints. BMC Bioinformatics, 2016, 17, 382.	2.6	5
81	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
82	Inherited variation in OATP1B1 is associated with treatment outcome in acute myeloid leukemia. Clinical Pharmacology and Therapeutics, 2016, 99, 651-660.	4.7	27
83	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
84	Gliomatosis cerebri in children shares molecular characteristics with other pediatric gliomas. Acta Neuropathologica, 2016, 131, 299-307.	7.7	38
85	Clinical significance ofin vivocytarabine-induced gene expression signature in AML. Leukemia and Lymphoma, 2016, 57, 909-920.	1.3	7
86	The Genomic Landscape of Childhood and Adult Acute Erythroid Leukemia. Blood, 2016, 128, 39-39.	1.4	2
87	Genomic Landscape of Pediatric Mixed Phenotype Acute Leukemia. Blood, 2016, 128, 454-454.	1.4	4
88	Linking Subclonal Genetic Diversity with Functional Heterogeneity Identifies Diagnosis Subclones Destined to Relapse. Blood, 2016, 128, 605-605.	1.4	0
89	Genomic Profiling Identifies Novel Mutations and Fusion Genes in Newly Diagnosed and Relapsed Pediatric FLT3-ITD-Positive AML. Blood, 2016, 128, 2838-2838.	1.4	0
90	MPTH-26MOLECULAR REFINEMENT OF PEDIATRIC POSTERIOR FOSSA EPENDYMOMA. Neuro-Oncology, 2015, 17, v144.1-v144.	1.2	0

#	Article	IF	Citations
91	SVSI: Fast and Powerful Setâ€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
92	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
93	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
94	Genomic landscape of paediatric adrenocortical tumours. Nature Communications, 2015, 6, 6302.	12.8	166
95	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
96	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	19.0	68
97	Commutability of the First World Health Organization International Standard for Human Cytomegalovirus. Journal of Clinical Microbiology, 2015, 53, 3325-3333.	3.9	76
98	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
99	The methylome of pediatric acute myeloid leukemia.. Journal of Clinical Oncology, 2015, 33, 10027-10027.	1.6	1
100	Abstract 5464: Host variation in OATP1B1 is associated with treatment outcome in pediatric AML. , 2015, , .		0
101	Methylation of DNMT3B Strongly Associates with the Methylome, Cytogenetic Risk Groups, and Prognosis of Pediatric Acute Myeloid Leukemia. Blood, 2015, 126, 2434-2434.	1.4	0
102	Identification and Characterization of Novel Fusion Proteins in Pediatric Acute Megakaryoblastic Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S123-S124.	0.4	0
103	Feasibility, efficacy, and adverse effects of outpatient antibacterial prophylaxis in children with acute myeloid leukemia. Cancer, 2014, 120, 1985-1992.	4.1	53
104	Definition of cure in childhood acute myeloid leukemia. Cancer, 2014, 120, 2490-2496.	4.1	12
105	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
106	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. Bioinformatics, 2014, 30, 1400-1408.	4.1	10
107	An R package that automatically collects and archives details for reproducible computing. BMC Bioinformatics, 2014, 15, 138.	2.6	14
108	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871

#	Article	IF	Citations
109	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
110	A Conditional Approach for Regression Analysis of Longitudinal Data with Informative Observation Time and Non-negligible Observation Duration. Communications in Statistics - Theory and Methods, 2014, 43, 4998-5011.	1.0	1
111	RB1 gene inactivation by chromothripsis in human retinoblastoma. Oncotarget, 2014, 5, 438-450.	1.8	104
112	Abstract LB-63: Cell ground state dictates cancer susceptibility across organs. , 2014, , .		0
113	Abstract PR03: The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. , 2014, , .		2
114	High-Throughput, High-Content siRNA/Drug Modifier Screen for Validation of Transcriptional Profiles Predictive of Cytarabine Response in AML. Blood, 2014, 124, 3615-3615.	1.4	0
115	Gemtuzumab ozogamicin can reduce minimal residual disease in patients with childhood acute myeloid leukemia. Cancer, 2013, 119, 4036-4043.	4.1	41
116	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
117	Joint analysis of longitudinal data and recurrent episodes data with application to medical cost analysis. Biometrical Journal, 2013, 55, 5-16.	1.0	5
118	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
119	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
120	A genomic random interval model for statistical analysis of genomic lesion data. Bioinformatics, 2013, 29, 2088-2095.	4.1	17
121	PAIR: paired allelic log-intensity-ratio-based normalization method for SNP-CGH arrays. Bioinformatics, 2013, 29, 299-307.	4.1	6
122	Clinical Significance of CD33 Nonsynonymous Single-Nucleotide Polymorphisms in Pediatric Patients with Acute Myeloid Leukemia Treated with Gemtuzumab-Ozogamicinâ€“Containing Chemotherapy. Clinical Cancer Research, 2013, 19, 1620-1627.	7.0	58
123	RRM1 and RRM2 pharmacogenetics: association with phenotypes in HapMap cell lines and acute myeloid leukemia patients. Pharmacogenomics, 2013, 14, 1449-1466.	1.3	27
124	An empirical Bayes approach for analysis of diverse periodic trends in time-course gene expression data. Bioinformatics, 2013, 29, 182-188.	4.1	4
125	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
126	Cross-species genomic and epigenomic landscape of retinoblastoma. Oncotarget, 2013, 4, 844-859.	1.8	37

#	Article	IF	Citations
127	Statistical Methods for Overdispersion in mRNA-Seq Count Data. Open Bioinformatics Journal, 2013, 7, 34-40.	1.0	8
128	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
129	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
130	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
131	Comparative Analysis of Different Approaches to Measure Treatment Response in Acute Myeloid Leukemia. Journal of Clinical Oncology, 2012, 30, 3625-3632.	1.6	188
132	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. Blood, 2012, 120, 4783-4794.	1.4	179
133	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
134	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
135	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742
136	Effect of body mass index on the outcome of children with acute myeloid leukemia. Cancer, 2012, 118, 5989-5996.	4.1	56
137	Treatment outcome in older patients with childhood acute myeloid leukemia. Cancer, 2012, 118, 6253-6259.	4.1	32
138	A Mouse Model of the Most Aggressive Subgroup of Human Medulloblastoma. Cancer Cell, 2012, 21, 168-180.	16.8	250
139	Analysis of MDM2 and MDM4 Single Nucleotide Polymorphisms, mRNA Splicing and Protein Expression in Retinoblastoma. PLoS ONE, 2012, 7, e42739.	2.5	68
140	Abstract 1434: A mouse model of the most aggressive subgroup of human medulloblastoma. , 2012, , .		0
141	Abstract 2487: CONSERTING: an accurate method for detecting focal and gross somatic copy number alterations in cancer genome by next generation sequencing. , 2012, , .		0
142	Abstract 4867: Identification of an inv(16)-encodedCBFA2T3-GLIS2fusion protein in 34% of non-infant acute megkaryoblastic leukemias: A report from the Pediatric Cancer Genome Project. , 2012, , .		0
143	Abstract LB-228: Association of XRCC1 SNPs with clinical response in AML patients. , 2012, , .		0
144	Cytarabine-Induced Gene Expression Signatures in AML Patients and Its Association with Clinical Outcome.. Blood, 2012, 120, 2470-2470.	1.4	0

#	Article	IF	Citations
145	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
146	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
147	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
148	Randomized trial of 2 dosages of prophylactic granulocyteâ€“colonyâ€stimulating factor after induction chemotherapy in pediatric acute myeloid leukemia. Cancer, 2011, 117, 1313-1320.	4.1	13
149	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
150	IDH1 and IDH2 mutations in pediatric acute leukemia. Leukemia, 2011, 25, 1570-1577.	7.2	80
151	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
152	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
153	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
154	A procedure to statistically evaluate agreement of differential expression for cross-species genomics. Bioinformatics, 2011, 27, 2098-2103.	4.1	16
155	Abstract 3448: Subtypes of medulloblastoma have distinct developmental origins. , 2011, , .		1
156	Discovery of Novel Recurrent Mutations in Childhood Early T-Cell Precursor Acute Lymphoblastic Leukemia by Whole Genome Sequencing - a Report From the St Jude Children's Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 68-68.	1.4	0
157	Combination of cladribine plus topotecan for recurrent or refractory pediatric acute myeloid leukemia. Cancer, 2010, 116, 98-105.	4.1	24
158	ChIP-PaM: an algorithm to identify protein-DNA interaction using ChIP-Seq data. Theoretical Biology and Medical Modelling, 2010, 7, 18.	2.1	16
159	Cross-species genomics matches driver mutations and cell compartments to model ependymoma. Nature, 2010, 466, 632-636.	27.8	324
160	Subtypes of medulloblastoma have distinct developmental origins. Nature, 2010, 468, 1095-1099.	27.8	710
161	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
162	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

#	Article	IF	Citations
163	Clinical Activity, Pharmacokinetics, and Pharmacodynamics of Sorafenib In Pediatric Acute Myeloid Leukemia.. Blood, 2010, 116, 1073-1073.	1.4	3
164	Pathway Based Pharmacogenomics of Cytarabine In Pediatric Acute Myeloid Leukemia. Blood, 2010, 116, 294-294.	1.4	0
165	High-Resolution Genomic Profiling of Adult and Pediatric Core Binding Factor Acute Myeloid Leukemia Reveals New Recurrent Genomic Aberrations. Blood, 2010, 116, 849-849.	1.4	0
166	IDH1 and IDH2 Mutations In Pediatric Acute Myeloid Leukemia. Blood, 2010, 116, 1699-1699.	1.4	0
167	Reference alignment of SNP microarray signals for copy number analysis of tumors. Bioinformatics, 2009, 25, 315-321.	4.1	55
168	Integrated Analysis of Pharmacokinetic, Clinical, and SNP Microarray Data Using Projection onto the Most Interesting Statistical Evidence with Adaptive Permutation Testing. , 2009, , .		1
169	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
170	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
171	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
172	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
173	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
174	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
175	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
176	Acute mixed lineage leukemia in children: the experience of St Jude Children's Research Hospital. Blood, 2009, 113, 5083-5089.	1.4	159
177	Acute Megakaryoblastic Leukemia (AMKL) in Children without Down Syndrome.. Blood, 2009, 114, 482-482.	1.4	3
178	Gene Expression Patterns Associated with Cytarabine Pharmacology and Outcome in Pediatric Acute Myeloid Leukemia.. Blood, 2009, 114, 114-114.	1.4	3
179	Minimal Residual Diseaseâ€“Directed Therapy for Childhood Acute Myeloid Leukemia: Results of the AML02 Multicenter Trial.. Blood, 2009, 114, 16-16.	1.4	0
180	5'Nucleotidase (NT5C2) Genotype Influences Leukemic Blast Concentration of Ara-CTP in Pediatric Patients with Acute Myeloid Leukemia.. Blood, 2009, 114, 593-593.	1.4	0

#	Article	IF	Citations
181	Prognostic significance of myeloperoxidase expression in childhood acute myeloid leukemia. Pediatric Blood and Cancer, 2008, 50, 542-548.	1.5	4
182	Baseline mannose binding lectin levels may not predict infection among children with leukemia. Pediatric Blood and Cancer, 2008, 50, 866-868.	1.5	10
183	Prophylactic antibiotics reduce morbidity due to septicemia during intensive treatment for pediatric acute myeloid leukemia. Cancer, 2008, 113, 376-382.	4.1	87
184	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
185	Robust detection method for differential expression studies. BMC Bioinformatics, 2008, 9, .	2.6	0
186	Statistical analysis of data from retroviral clonal experiments in the developing retina. Brain Research, 2008, 1192, 178-185.	2.2	8
187	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
188	N-myc coordinates retinal growth with eye size during mouse development. Genes and Development, 2008, 22, 179-193.	5.9	45
189	Identification of Clinical Coryneform Bacterial Isolates: Comparison of Biochemical Methods and Sequence Analysis of 16S rRNA and rpoB Genes. Journal of Clinical Microbiology, 2008, 46, 921-927.	3.9	35
190	Galactomannan Antigenemia in Pediatric Oncology Patients With Invasive Aspergillosis. Pediatric Infectious Disease Journal, 2008, 27, 815-819.	2.0	69
191	Gene Expression Profiling of Acute Myeloid Leukemia Shows Therapeutically Meaningful Patterns of Association with Ara-CTP Pharmacokinetics and Pharmacodynamics. Blood, 2008, 112, 215-215.	1.4	0
192	Gene Expression Profiling of Childhood Adrenocortical Tumors. Cancer Research, 2007, 67, 600-608.	0.9	146
193	Pharmacogenetics of Deoxycytidine Kinase: Identification and Characterization of Novel Genetic Variants. Journal of Pharmacology and Experimental Therapeutics, 2007, 323, 935-945.	2.5	76
194	Persistent Hyperplastic Primary Vitreous Due to Somatic Mosaic Deletion of theArfTumor Suppressor. , 2007, 48, 491.		31
195	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
196	Prognostic factors and outcome of recurrence in childhood acute myeloid leukemia. Cancer, 2007, 109, 157-163.	4.1	85
197	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
198	Genome scan implicates adhesion biological pathways in secondary leukemia. Leukemia, 2007, 21, 2128-2136.	7.2	25

#	Article	IF	Citations
199	Genome-wide analysis of genetic alterations in acute lymphoblastic leukaemia. Nature, 2007, 446, 758-764.	27.8	1,602
200	False discovery rate paradigms for statistical analyses of microarray gene expression data. Bioinformation, 2007, 1, 436-446.	0.5	34
201	Filtration-based culture methods improve recovery of fungal pathogens in respiratory specimens. Diagnostic Microbiology and Infectious Disease, 2006, 56, 221-223.	1.8	1
202	Impact of age on outcome of pediatric acute myeloid leukemia. Cancer, 2006, 106, 2495-2502.	4.1	52
203	Robust estimation of the false discovery rate. Bioinformatics, 2006, 22, 1979-1987.	4.1	170
204	Estimation and control of multiple testing error rates for microarray studies. Briefings in Bioinformatics, 2006, 7, 25-36.	6.5	76
205	Genes Regulating B-Cell Development and Differentiation Are Mutated in 40% of Pediatric Acute Lymphoblastic Leukemia.. Blood, 2006, 108, 217-217.	1.4	1
206	Premedication with acetaminophen or diphenhydramine for transfusion with leucoreduced blood products in children. British Journal of Haematology, 2005, 130, 781-787.	2.5	87
207	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
208	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
209	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
210	Sample size determination for the false discovery rate. Bioinformatics, 2005, 21, 4263-4271.	4.1	58
211	Statistical Development and Evaluation of Microarray Gene Expression Data Filters. Journal of Computational Biology, 2005, 12, 482-495.	1.6	29
212	Outcome after Relapse of Childhood Acute Myeloid Leukemia: The St. Jude Experience.. Blood, 2005, 106, 273-273.	1.4	0
213	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
214	Improving false discovery rate estimation. Bioinformatics, 2004, 20, 1737-1745.	4.1	138
215	Gene expression profiling of pediatric acute myelogenous leukemia. Blood, 2004, 104, 3679-3687.	1.4	404
216	Clinical significance of residual disease during treatment in childhood acute myeloid leukaemia. British Journal of Haematology, 2003, 123, 243-252.	2.5	122

#	Article	IF	Citations
217	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
218	Estimating the Fraction of Clonable Genomic DNA. Bulletin of Mathematical Biology, 2001, 63, 995-1002.	1.9	1