

Gang Wu

List of Publications by Year in descending order

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Version: 2024-02-01

160
papers

21,157
citations

27035

58
h-index

11946

139
g-index

171
all docs

171
docs citations

171
times ranked

30989
citing authors

#	ARTICLE	IF	CITATIONS
1	Revealing the Mutational Spectrum in Southern Africans With Amyotrophic Lateral Sclerosis. <i>Neurology: Genetics</i> , 2022, 8, e654.	0.9	10
2	Antigen cross-presentation in young tumor-bearing hosts promotes CD8 ⁺ T cell terminal differentiation. <i>Science Immunology</i> , 2022, 7, eabf6136.	5.6	5
3	Somatic and Germline Variant Calling from Next-Generation Sequencing Data. <i>Advances in Experimental Medicine and Biology</i> , 2022, 1361, 37-54.	0.8	2
4	Integrated Genomic Analysis Identifies <i>UBTF</i> Tandem Duplications as a Recurrent Lesion in Pediatric Acute Myeloid Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 194-207.	2.6	38
5	The molecular characteristics of low-grade and high-grade areas in desmoplastic infantile astrocytoma/ganglioglioma. <i>Neuropathology and Applied Neurobiology</i> , 2022, 48, .	1.8	5
6	Genomic profiling identifies genes and pathways dysregulated by <i>HEY1</i> – <i>NCOA2</i> fusion and shines a light on mesenchymal chondrosarcoma tumorigenesis. <i>Journal of Pathology</i> , 2022, 257, 579-592.	2.1	7
7	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. <i>Blood Cancer Discovery</i> , 2022, 3, 240-263.	2.6	11
8	SARS-CoV-2 antigen exposure history shapes phenotypes and specificity of memory CD8 ⁺ T cells. <i>Nature Immunology</i> , 2022, 23, 781-790.	7.0	116
9	A rare variant analysis framework using public genotype summary counts to prioritize disease-predisposition genes. <i>Nature Communications</i> , 2022, 13, 2592.	5.8	6
10	Acute lymphoblastic leukemia displays a distinct highly methylated genome. <i>Nature Cancer</i> , 2022, 3, 768-782.	5.7	15
11	Targeting KDM4 for treating PAX3-FOXO1-driven alveolar rhabdomyosarcoma. <i>Science Translational Medicine</i> , 2022, 14, .	5.8	16
12	Molecular basis of <i>ETV6</i> -mediated predisposition to childhood acute lymphoblastic leukemia. <i>Blood</i> , 2021, 137, 364-373.	0.6	37
13	Outcome and molecular analysis of young children with choroid plexus carcinoma treated with non-myeloablative therapy: results from the SJYC07 trial. <i>Neuro-Oncology Advances</i> , 2021, 3, vdaa168.	0.4	6
14	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. <i>Nature Communications</i> , 2021, 12, 985.	5.8	31
15	Relevance of Molecular Groups in Children with Newly Diagnosed Atypical Teratoid Rhabdoid Tumor: Results from Prospective St. Jude Multi-institutional Trials. <i>Clinical Cancer Research</i> , 2021, 27, 2879-2889.	3.2	35
16	Molecular classification improves risk assessment in adult <i>BCR-ABL1</i> -negative B-ALL. <i>Blood</i> , 2021, 138, 948-958.	0.6	59
17	Repeats expansions in <i>ATXN2</i> , <i>NOP56</i> , <i>NIPA1</i> and <i>ATXN1</i> are not associated with ALS in Africans. <i>IBRO Neuroscience Reports</i> , 2021, 10, 130-135.	0.7	6
18	Enhancer Hijacking Drives Oncogenic <i>BCL11B</i> Expression in Lineage-Ambiguous Stem Cell Leukemia. <i>Cancer Discovery</i> , 2021, 11, 2846-2867.	7.7	83

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19	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. <i>Nature Communications</i> , 2021, 12, 4089.	5.8	27
20	Retinoblastoma from human stem cell-derived retinal organoids. <i>Nature Communications</i> , 2021, 12, 4535.	5.8	48
21	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. <i>Nature Communications</i> , 2021, 12, 5531.	5.8	31
22	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. <i>Cancer Discovery</i> , 2021, 11, 1082-1099.	7.7	109
23	Machine learning suggests polygenic risk for cognitive dysfunction in amyotrophic lateral sclerosis. <i>EMBO Molecular Medicine</i> , 2021, 13, e12595.	3.3	13
24	Integrated Genomic Analysis Identifies UBTF Tandem Duplications As a Subtype-Defining Lesion in Pediatric Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, LBA-4-LBA-4.	0.6	0
25	Molecular Mechanism of Telomere Length Dynamics and Its Prognostic Value in Pediatric Cancers. <i>Journal of the National Cancer Institute</i> , 2020, 112, 756-764.	3.0	11
26	ChIPseqSpikelnFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. <i>Bioinformatics</i> , 2020, 36, 1270-1272.	1.8	25
27	Estimated number of adult survivors of childhood cancer in United States with cancer-predisposing germline variants. <i>Pediatric Blood and Cancer</i> , 2020, 67, e28047.	0.8	13
28	Dasatinib induces a dramatic response in a child with refractory juvenile xanthogranuloma with a novel MRC1-PDGFRB fusion. <i>Blood Advances</i> , 2020, 4, 2991-2995.	2.5	10
29	A novel algorithm comprehensively characterizes human RH genes using whole-genome sequencing data. <i>Blood Advances</i> , 2020, 4, 4347-4357.	2.5	9
30	Patient-derived orthotopic xenografts of pediatric brain tumors: a St. Jude resource. <i>Acta Neuropathologica</i> , 2020, 140, 209-225.	3.9	45
31	XAF1 as a modifier of p53 function and cancer susceptibility. <i>Science Advances</i> , 2020, 6, eaba3231.	4.7	37
32	Germline Variants in Phosphodiesterase Genes and Genetic Predisposition to Pediatric Adrenocortical Tumors. <i>Cancers</i> , 2020, 12, 506.	1.7	17
33	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. <i>Cancer Research</i> , 2020, 80, 1524-1537.	0.4	10
34	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. <i>Blood Cancer Discovery</i> , 2020, 1, 96-111.	2.6	93
35	A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 861-873.	1.9	28
36	Enhancer Hijacking of BCL11B Defines a Subtype of Lineage Ambiguous Acute Leukemia. <i>Blood</i> , 2020, 136, LBA-3-LBA-3.	0.6	2

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37	Genomic Analysis of Congenital Myeloid Sarcoma Identifies Significant Bone Marrow Involvement in the Absence of Morphologic Blasts. <i>Blood</i> , 2020, 136, 41-41.	0.6	0
38	Stellate ganglion block and cardiac sympathetic denervation in patients with inappropriate sinus tachycardia. <i>Journal of Cardiovascular Electrophysiology</i> , 2019, 30, 2920-2928.	0.8	12
39	Enrichment of heterozygous germline <i>RECQL4</i> loss-of-function variants in pediatric osteosarcoma. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a004218.	0.5	26
40	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. <i>Molecular Cancer Research</i> , 2019, 17, 895-906.	1.5	40
41	Clinical genome sequencing uncovers potentially targetable truncations and fusions of MAP3K8 in spitzoid and other melanomas. <i>Nature Medicine</i> , 2019, 25, 597-602.	15.2	61
42	Children with sickle cell anemia and APOL1 genetic variants develop albuminuria early in life. <i>Haematologica</i> , 2019, 104, e385-e387.	1.7	26
43	Regulation of gene expression by miR-144/451 during mouse erythropoiesis. <i>Blood</i> , 2019, 133, 2518-2528.	0.6	33
44	H3.3 K27M depletion increases differentiation and extends latency of diffuse intrinsic pontine glioma growth in vivo. <i>Acta Neuropathologica</i> , 2019, 137, 637-655.	3.9	85
45	The global clonal complexity of the murine blood system declines throughout life and after serial transplantation. <i>Blood</i> , 2019, 133, 1927-1942.	0.6	45
46	Germline deletion of ETV6 in familial acute lymphoblastic leukemia. <i>Blood Advances</i> , 2019, 3, 1039-1046.	2.5	21
47	Exome sequencing in amyotrophic lateral sclerosis implicates a novel gene, DNAJC7, encoding a heat-shock protein. <i>Nature Neuroscience</i> , 2019, 22, 1966-1974.	7.1	101
48	Histone H3.3 K27M Accelerates Spontaneous Brainstem Glioma and Drives Restricted Changes in Bivalent Gene Expression. <i>Cancer Cell</i> , 2019, 35, 140-155.e7.	7.7	194
49	Structure and evolution of double minutes in diagnosis and relapse brain tumors. <i>Acta Neuropathologica</i> , 2019, 137, 123-137.	3.9	63
50	SAT-LB058 Effect of a Genetic Modifier of Cancer Risk in TP53 Mutation Carriers. <i>Journal of the Endocrine Society</i> , 2019, 3, .	0.1	0
51	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2018, 33, 937-948.e8.	7.7	142
52	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. <i>Journal of the National Cancer Institute</i> , 2018, 110, 895-904.	3.0	19
53	Germline Lysine-Specific Demethylase 1 (<i>LSD1/KDM1A</i>) Mutations Confer Susceptibility to Multiple Myeloma. <i>Cancer Research</i> , 2018, 78, 2747-2759.	0.4	56
54	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. <i>Neuron</i> , 2018, 97, 1268-1283.e6.	3.8	517

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55	Identification of compound heterozygous variants in <i>OPTN</i> in an ALS-FTD patient from the CReATe consortium: a case report. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2018, 19, 469-471.	1.1	15
56	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. <i>Journal of Clinical Oncology</i> , 2018, 36, 2078-2087.	0.8	105
57	Polygenic Determinants for Subsequent Breast Cancer Risk in Survivors of Childhood Cancer: The St Jude Lifetime Cohort Study (SJLIFE). <i>Clinical Cancer Research</i> , 2018, 24, 6230-6235.	3.2	18
58	Integrating somatic variant data and biomarkers for germline variant classification in cancer predisposition genes. <i>Human Mutation</i> , 2018, 39, 1542-1552.	1.1	40
59	UMI-count modeling and differential expression analysis for single-cell RNA sequencing. <i>Genome Biology</i> , 2018, 19, 70.	3.8	91
60	Clonal dynamics of donor-derived myelodysplastic syndrome after unrelated hematopoietic cell transplantation for high-risk pediatric B-lymphoblastic leukemia. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002980.	0.5	7
61	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. <i>Acta Neuropathologica</i> , 2018, 136, 211-226.	3.9	199
62	Data Access and Interactive Visualization of Whole Genome Sequence of Sickle Cell Patients within the St. Jude Cloud. <i>Blood</i> , 2018, 132, 723-723.	0.6	2
63	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. <i>Blood</i> , 2018, 132, 3641-3641.	0.6	3
64	Frequent epigenetic alterations in polycomb repressive complex 2 in osteosarcoma cell lines. <i>Oncotarget</i> , 2018, 9, 27087-27091.	0.8	15
65	Insulin-like Growth Factor Binding Protein-3 (IGFBP3) Induces Fetal Hemoglobin in Hematopoietic Stem and Progenitor Cells from Patients with Sickle Cell Anemia. <i>Blood</i> , 2018, 132, 722-722.	0.6	0
66	Accurate Prediction of RH Genotypes Using Whole Genome Sequencing Data. <i>Blood</i> , 2018, 132, 2332-2332.	0.6	0
67	Inactivation of Ezh2 Upregulates Gfi1 and Drives Aggressive Myc-Driven Group 3 Medulloblastoma. <i>Cell Reports</i> , 2017, 18, 2907-2917.	2.9	61
68	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
69	Genetic evolution of influenza H9N2 viruses isolated from various hosts in China from 1994 to 2013. <i>Emerging Microbes and Infections</i> , 2017, 6, 1-11.	3.0	56
70	The genomic landscape of pediatric myelodysplastic syndromes. <i>Nature Communications</i> , 2017, 8, 1557.	5.8	143
71	Simultaneous noninvasive recording of skin sympathetic nerve activity and electrocardiogram. <i>Heart Rhythm</i> , 2017, 14, 25-33.	0.3	105
72	The neoepitope landscape in pediatric cancers. <i>Genome Medicine</i> , 2017, 9, 78.	3.6	77

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73	Exome sequencing analysis of murine medulloblastoma models identifies WDR11 as a potential tumor suppressor in Group 3 tumors. <i>Oncotarget</i> , 2017, 8, 64685-64697.	0.8	10
74	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).. <i>Journal of Clinical Oncology</i> , 2017, 35, 10502-10502.	0.8	1
75	JUMPg: An Integrative Proteogenomics Pipeline Identifying Unannotated Proteins in Human Brain and Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 2309-2320.	1.8	76
76	Effects of stepwise denervation of the stellate ganglion: Novel insights from an acute canine study. <i>Heart Rhythm</i> , 2016, 13, 1395-1401.	0.3	11
77	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. <i>EBioMedicine</i> , 2016, 8, 173-183.	2.7	241
78	Telomerase Expression by Aberrant Methylation of the TERT Promoter in Melanoma Arising in Giant Congenital Nevi. <i>Journal of Investigative Dermatology</i> , 2016, 136, 339-342.	0.3	36
79	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2016, 48, 1481-1489.	9.4	231
80	The genomic landscape of core-binding factor acute myeloid leukemias. <i>Nature Genetics</i> , 2016, 48, 1551-1556.	9.4	215
81	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016, 131, 833-845.	3.9	288
82	The landscape of fusion transcripts in spitzoid melanoma and biologically indeterminate spitzoid tumors by RNA sequencing. <i>Modern Pathology</i> , 2016, 29, 359-369.	2.9	61
83	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (<i>PRKCA</i>) Fusion. <i>JAMA Dermatology</i> , 2016, 152, 318.	2.0	33
84	Exploring genomic alteration in pediatric cancer using ProteinPaint. <i>Nature Genetics</i> , 2016, 48, 4-6.	9.4	275
85	Antigenic evolution of H9N2 chicken influenza viruses isolated in China during 2009-2013 and selection of a candidate vaccine strain with broad cross-reactivity. <i>Veterinary Microbiology</i> , 2016, 182, 1-7.	0.8	37
86	Comprehensive Functional Characterization of Germline ETV6 Variants Associated with Inherited Predisposition to Acute Lymphoblastic Leukemia in Children. <i>Blood</i> , 2016, 128, 1085-1085.	0.6	1
87	The Genomic Landscape of Pediatric Myelodysplastic Syndromes. <i>Blood</i> , 2016, 128, 956-956.	0.6	1
88	Erythroid miRNA-144/451 Binds Many mRNAs but Regulates Only a Small Subset. <i>Blood</i> , 2016, 128, 1198-1198.	0.6	0
89	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. <i>Blood</i> , 2015, 125, 3609-3617.	0.6	72
90	Gorlin syndrome and desmoplastic medulloblastoma: Report of 3 cases with unfavorable clinical course and novel mutations. <i>Pediatric Blood and Cancer</i> , 2015, 62, 1855-1858.	0.8	6

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91	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. <i>PLoS Genetics</i> , 2015, 11, e1005262.	1.5	128
92	The Genomic Contributions of Avian H1N1 Influenza A Viruses to the Evolution of Mammalian Strains. <i>PLoS ONE</i> , 2015, 10, e0133795.	1.1	7
93	Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 548-553.	3.3	287
94	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015, 373, 2336-2346.	13.9	949
95	The Genomic Landscape of Childhood and Adolescent Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 816-823.	0.3	148
96	Critical Role for the DNA Sensor AIM2 in Stem Cell Proliferation and Cancer. <i>Cell</i> , 2015, 162, 45-58.	13.5	266
97	Vismodegib Exerts Targeted Efficacy Against Recurrent Sonic Hedgehog Subgroup Medulloblastoma: Results From Phase II Pediatric Brain Tumor Consortium Studies PBTC-025B and PBTC-032. <i>Journal of Clinical Oncology</i> , 2015, 33, 2646-2654.	0.8	368
98	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. <i>Nature Communications</i> , 2015, 6, 6553.	5.8	90
99	Integrated Analysis of Transcriptomic and Proteomic Datasets Reveals Information on Protein Expressivity and Factors Affecting Translational Efficiency. <i>Methods in Molecular Biology</i> , 2015, 1375, 123-136.	0.4	11
100	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2015, 6, 6604.	5.8	281
101	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. <i>Nature Genetics</i> , 2015, 47, 330-337.	9.4	405
102	CONCERTING: integrating copy-number analysis with structural-variation detection. <i>Nature Methods</i> , 2015, 12, 527-530.	9.0	68
103	The CYP2C19 Intron 2 Branch Point SNP is the Ancestral Polymorphism Contributing to the Poor Metabolizer Phenotype in Livers with CYP2C19*35 and CYP2C19*2 Alleles. <i>Drug Metabolism and Disposition</i> , 2015, 43, 1226-1235.	1.7	23
104	Germline genetic variation in ETV6 and risk of childhood acute lymphoblastic leukaemia: a systematic genetic study. <i>Lancet Oncology</i> , The, 2015, 16, 1659-1666.	5.1	161
105	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 693-693.	0.6	1
106	Genomic Landscape of Relapsed Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 692-692.	0.6	3
107	Germline Genetic Variation in ETV6 and Predisposition to Childhood Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015, 126, 695-695.	0.6	2
108	Viral suppressors of the RIG-I-mediated interferon response are pre-packaged in influenza virions. <i>Nature Communications</i> , 2014, 5, 5645.	5.8	55

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109	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. <i>Neuro-Oncology</i> , 2014, 16, iii16-iii16.	0.6	1
110	Histone H3 Mutations in Pediatric Brain Tumors. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018689-a018689.	2.3	29
111	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. <i>Nature Communications</i> , 2014, 5, 3630.	5.8	342
112	C11orf95-RELA fusions drive oncogenic NF- κ B signalling in ependymoma. <i>Nature</i> , 2014, 506, 451-455.	13.7	559
113	PTEN action in leukaemia dictated by the tissue microenvironment. <i>Nature</i> , 2014, 510, 402-406.	13.7	40
114	An integrated systems genetics screen reveals the transcriptional structure of inherited predisposition to metastatic disease. <i>Genome Research</i> , 2014, 24, 227-240.	2.4	37
115	Barcoding Influenza Virus to Decode Transmission. <i>Cell Host and Microbe</i> , 2014, 16, 559-561.	5.1	5
116	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. <i>Cancer Discovery</i> , 2014, 4, 1342-1353.	7.7	418
117	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. <i>New England Journal of Medicine</i> , 2014, 371, 1005-1015.	13.9	1,161
118	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. <i>Bioinformatics</i> , 2014, 30, 1400-1408.	1.8	10
119	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. <i>Nature Genetics</i> , 2014, 46, 444-450.	9.4	871
120	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. <i>Cell Reports</i> , 2014, 7, 104-112.	2.9	583
121	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. <i>Scientific Reports</i> , 2014, 4, 7455.	1.6	13
122	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. <i>Blood</i> , 2014, 124, 127-127.	0.6	9
123	Cross-species transcriptional network analysis reveals conservation and variation in response to metal stress in cyanobacteria. <i>BMC Genomics</i> , 2013, 14, 112.	1.2	32
124	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1226-1231.	9.4	270
125	Tyrosine kinome sequencing of pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group TARGET Project. <i>Blood</i> , 2013, 121, 485-488.	0.6	156
126	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. <i>Cancer Cell</i> , 2013, 24, 710-724.	7.7	252

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127	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. <i>Nature Genetics</i> , 2013, 45, 602-612.	9.4	704
128	Systematic characterization of hypothetical proteins in <i>Synechocystis</i> sp. PCC 6803 reveals proteins functionally relevant to stress responses. <i>Gene</i> , 2013, 512, 6-15.	1.0	26
129	The genomic landscape of hypodiploid acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 242-252.	9.4	588
130	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. <i>Blood</i> , 2013, 122, 824-824.	0.6	4
131	Identification of Molecular Pathway Aberrations in Uterine Serous Carcinoma by Genome-wide Analyses. <i>Journal of the National Cancer Institute</i> , 2012, 104, 1503-1513.	3.0	231
132	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 683-697.	7.7	213
133	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. <i>Genome Biology</i> , 2012, 13, R113.	13.9	31
134	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. <i>Nature Genetics</i> , 2012, 44, 251-253.	9.4	1,402
135	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. <i>Nature</i> , 2012, 481, 157-163.	13.7	1,430
136	A novel retinoblastoma therapy from genomic and epigenetic analyses. <i>Nature</i> , 2012, 481, 329-334.	13.7	442
137	Novel mutations target distinct subgroups of medulloblastoma. <i>Nature</i> , 2012, 488, 43-48.	13.7	742
138	Integrated cross-species transcriptional network analysis of metastatic susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3184-3189.	3.3	50
139	Analysis of MDM2 and MDM4 Single Nucleotide Polymorphisms, mRNA Splicing and Protein Expression in Retinoblastoma. <i>PLoS ONE</i> , 2012, 7, e42739.	1.1	68
140	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. <i>Blood</i> , 2011, 118, 3080-3087.	0.6	255
141	Prediction and Characterization of Missing Proteomic Data in <i>Desulfovibrio vulgaris</i> . <i>Comparative and Functional Genomics</i> , 2011, 2011, 1-16.	2.0	16
142	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. <i>Blood</i> , 2011, 118, 69-69.	0.6	6
143	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. <i>Blood</i> , 2011, 118, 68-68.	0.6	0
144	Integrative Analyses of Posttranscriptional Regulation in the Yeast <i>Saccharomyces cerevisiae</i> Using Transcriptomic and Proteomic Data. <i>Current Microbiology</i> , 2008, 57, 18-22.	1.0	67

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145	Statistical Application and Challenges in Global Gel-Free Proteomic Analysis by Mass Spectrometry. <i>Critical Reviews in Biotechnology</i> , 2008, 28, 297-307.	5.1	19
146	SGDB: a database of synthetic genes re-designed for optimizing protein over-expression. <i>Nucleic Acids Research</i> , 2007, 35, D76-D79.	6.5	32
147	Optimal encoding rules for synthetic genes: the need for a community effort. <i>Molecular Systems Biology</i> , 2007, 3, 134.	3.2	21
148	Integrative Analysis of Transcriptomic and Proteomic Data: Challenges, Solutions and Applications. <i>Critical Reviews in Biotechnology</i> , 2007, 27, 63-75.	5.1	224
149	Evolution of the syntrophic interaction between <i>Desulfovibrio vulgaris</i> and <i>Methanosarcina barkeri</i> : Involvement of an ancient horizontal gene transfer. <i>Biochemical and Biophysical Research Communications</i> , 2007, 352, 48-54.	1.0	53
150	The effects of differential gene expression on coding sequence features: Analysis by one-way ANOVA. <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 1108-1113.	1.0	10
151	Simplified gene synthesis: A one-step approach to PCR-based gene construction. <i>Journal of Biotechnology</i> , 2006, 124, 496-503.	1.9	51
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