Gang Wu

List of Publications by Year
in descending order

160	21,157	23567 58	10445 139
papers	citations	h-index	g-index

171	171	171	28673
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Revealing the Mutational Spectrum in Southern Africans With Amyotrophic Lateral Sclerosis. Neurology: Genetics, 2022, 8, e654.	1.9	10
2	Antigen cross-presentation in young tumor-bearing hosts promotes CD8 ⁺ T cell terminal differentiation. Science Immunology, 2022, 7, eabf6136.	11.9	5
3	Somatic and Germline Variant Calling from Next-Generation Sequencing Data. Advances in Experimental Medicine and Biology, 2022, 1361, 37-54.	1.6	2
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	The molecular characteristics of lowâ€grade and highâ€grade areas in desmoplastic infantile astrocytoma/ganglioglioma. Neuropathology and Applied Neurobiology, 2022, 48, .	3.2	5
6	Genomic profiling identifies genes and pathways dysregulated by HEY1â€“NCOA2 fusion and shines a light on mesenchymal chondrosarcoma tumorigenesis. Journal of Pathology, 2022, 257, 579-592.	4.5	7
7	ZNF384 Fusion Oncoproteins Drive Lineage Aberrancy in Acute Leukemia. Blood Cancer Discovery, 2022, 3, 240-263.	5.0	11
8	SARS-CoV-2 antigen exposure history shapes phenotypes and specificity of memory CD8+ T cells. Nature Immunology, 2022, 23, 781-790.	14.5	116
9	A rare variant analysis framework using public genotype summary counts to prioritize disease-predisposition genes. Nature Communications, 2022, 13, 2592.	12.8	6
10	Acute lymphoblastic leukemia displays a distinct highly methylated genome. Nature Cancer, 2022, 3, 768-782.	13.2	15
11	Targeting KDM4 for treating PAX3-FOXO1â€“driven alveolar rhabdomyosarcoma. Science Translational Medicine, 2022, 14, .	12.4	16
12	Molecular basis of ETV6-mediated predisposition to childhood acute lymphoblastic leukemia. Blood, 2021, 137, 364-373.	1.4	37
13	Outcome and molecular analysis of young children with choroid plexus carcinoma treated with non-myeloablative therapy: results from the SJYC07 trial. Neuro-Oncology Advances, 2021, 3, vdaa168.	0.7	6
14	The acquisition of molecular drivers in pediatric therapy-related myeloid neoplasms. Nature Communications, 2021, 12, 985.	12.8	31
15	Relevance of Molecular Groups in Children with Newly Diagnosed Atypical Teratoid Rhabdoid Tumor: Results from Prospective St. Jude Multi-institutional Trials. Clinical Cancer Research, 2021, 27, 2879-2889.	7.0	35
16	Molecular classification improves risk assessment in adult BCR-ABL1â€“negative B-ALL. Blood, 2021, 138, 948-958.	1.4	59
17	Repeats expansions in ATXN2, NOP56, NIPA1 and ATXN1 are not associated with ALS in Africans. IBRO Neuroscience Reports, 2021, 10, 130-135.	1.6	6
18	Enhancer Hijacking Drives Oncogenic BCL11B Expression in Lineage-Ambiguous Stem Cell Leukemia. Cancer Discovery, 2021, 11, 2846-2867.	9.4	83

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19	Patient-derived models recapitulate heterogeneity of molecular signatures and drug response in pediatric high-grade glioma. Nature Communications, 2021, 12, 4089.	12.8	27
20	Retinoblastoma from human stem cell-derived retinal organoids. Nature Communications, 2021, 12, 4535.	12.8	48
21	Comprehensive molecular characterization of pediatric radiation-induced high-grade glioma. Nature Communications, 2021, 12, 5531.	12.8	31
22	St. Jude Cloud: A Pediatric Cancer Genomic Data-Sharing Ecosystem. Cancer Discovery, 2021, 11, 1082-1099.	9.4	109
23	Machine learning suggests polygenic risk for cognitive dysfunction in amyotrophic lateral sclerosis. EMBO Molecular Medicine, 2021, 13, e12595.	6.9	13
24	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
25	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
26	ChIPseqSpikeInFree: a ChIP-seq normalization approach to reveal global changes in histone modifications without spike-in. Bioinformatics, 2020, 36, 1270-1272.	4.1	25
27	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
28	Dasatinib induces a dramatic response in a child with refractory juvenile xanthogranuloma with a novel MRC1-PDGFRB fusion. Blood Advances, 2020, 4, 2991-2995.	5.2	10
29	A novel algorithm comprehensively characterizes human RH genes using whole-genome sequencing data. Blood Advances, 2020, 4, 4347-4357.	5.2	9
30	Patient-derived orthotopic xenografts of pediatric brain tumors: a St. Jude resource. Acta Neuropathologica, 2020, 140, 209-225.	7.7	45
31	XAF1 as a modifier of p53 function and cancer susceptibility. Science Advances, 2020, 6, eaba3231.	10.3	37
32	Germline Variants in Phosphodiesterase Genes and Genetic Predisposition to Pediatric Adrenocortical Tumors. Cancers, 2020, 12, 506.	3.7	17
33	An ABC Transporter Drives Medulloblastoma Pathogenesis by Regulating Sonic Hedgehog Signaling. Cancer Research, 2020, 80, 1524-1537.	0.9	10
34	Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia. Blood Cancer Discovery, 2020, 1, 96-111.	5.0	93
35	A comparison of methods accounting for batch effects in differential expression analysis of UMI count based single cell RNA sequencing. Computational and Structural Biotechnology Journal, 2020, 18, 861-873.	4.1	28
36	Enhancer Hijacking of BCL11B Defines a Subtype of Lineage Ambiguous Acute Leukemia. Blood, 2020, 136, LBA-3-LBA-3.	1.4	2

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37	Genomic Analysis of Congenital Myeloid Sarcoma Identifies Significant Bone Marrow Involvement in the Absence of Morphologic Blasts. Blood, 2020, 136, 41-41.	1.4	0
38	Stellate ganglion block and cardiac sympathetic denervation in patients with inappropriate sinus tachycardia. Journal of Cardiovascular Electrophysiology, 2019, 30, 2920-2928.	1.7	12
39	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
40	The Clonal Evolution of Metastatic Osteosarcoma as Shaped by Cisplatin Treatment. Molecular Cancer Research, 2019, 17, 895-906.	3.4	40
41	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
42	Children with sickle cell anemia and APOL1 genetic variants develop albuminuria early in life. Haematologica, 2019, 104, e385-e387.	3.5	26
43	Regulation of gene expression by miR-144/451 during mouse erythropoiesis. Blood, 2019, 133, 2518-2528.	1.4	33
44	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
45	The global clonal complexity of the murine blood system declines throughout life and after serial transplantation. Blood, 2019, 133, 1927-1942.	1.4	45
46	Germline deletion of ETV6 in familial acute lymphoblastic leukemia. Blood Advances, 2019, 3, 1039-1046.	5.2	21
47	Exome sequencing in amyotrophic lateral sclerosis implicates a novel gene, DNAJC7, encoding a heat-shock protein. Nature Neuroscience, 2019, 22, 1966-1974.	14.8	101
48	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
49	Structure and evolution of double minutes in diagnosis and relapse brain tumors. Acta Neuropathologica, 2019, 137, 123-137.	7.7	63
50	SAT-LB058 Effect of a Genetic Modifier of Cancer Risk in TP53 Mutation Carriers. Journal of the Endocrine Society, 2019, 3, .	0.2	0
51	Germline Genetic IKZF1 Variation and Predisposition to Childhood Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 33, 937-948.e8.	16.8	142
52	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
53	Germline Lysine-Specific Demethylase 1 (LSD1/KDM1A) Mutations Confer Susceptibility to Multiple Myeloma. Cancer Research, 2018, 78, 2747-2759.	0.9	56
54	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. Neuron, 2018, 97, 1268-1283.e6.	8.1	517

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55	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
56	Genetic Risk for Subsequent Neoplasms Among Long-Term Survivors of Childhood Cancer. Journal of Clinical Oncology, 2018, 36, 2078-2087.	1.6	105
57	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
58	Integrating somatic variant data and biomarkers for germline variant classification in cancer predisposition genes. Human Mutation, 2018, 39, 1542-1552.	2.5	40
59	UMI-count modeling and differential expression analysis for single-cell RNA sequencing. Genome Biology, 2018, 19, 70.	8.8	91
60	Clonal dynamics of donor-derived myelodysplastic syndrome after unrelated hematopoietic cell transplantation for high-risk pediatric B-lymphoblastic leukemia. Journal of Physical Education and Sports Management, 2018, 4, a002980.	1.2	7
61	Molecular heterogeneity and CXorf67 alterations in posterior fossa group A (PFA) ependymomas. Acta Neuropathologica, 2018, 136, 211-226.	7.7	199
62	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
63	Precision Medicine for Sickle Cell Disease through Whole Genome Sequencing. Blood, 2018, 132, 3641-3641.	1.4	3
64	Frequent epigenetic alterations in polycomb repressive complex 2 in osteosarcoma cell lines. Oncotarget, 2018, 9, 27087-27091.	1.8	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. Blood, 2018, 132, 722-722.	1.4	0
66	Accurate Prediction of RH Genotypes Using Whole Genome Sequencing Data. Blood, 2018, 132, 2332-2332.	1.4	0
67	Inactivation of Ezh2 Upregulates Gfi1 and Drives Aggressive Myc-Driven Group 3 Medulloblastoma. Cell Reports, 2017, 18, 2907-2917.	6.4	61
68	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
69	Genetic evolution of influenza H9N2 viruses isolated from various hosts in China from 1994 to 2013. Emerging Microbes and Infections, 2017, 6, 1-11.	6.5	56
70	The genomic landscape of pediatric myelodysplastic syndromes. Nature Communications, 2017, 8, 1557.	12.8	143
71	Simultaneous noninvasive recording of skin sympathetic nerve activity and electrocardiogram. Heart Rhythm, 2017, 14, 25-33.	0.7	105
72	The neoepitope landscape in pediatric cancers. Genome Medicine, 2017, 9, 78.	8.2	77

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73	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
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).. Journal of Clinical Oncology, 2017, 35, 10502-10502.	1.6	1
75	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
76	Effects of stepwise denervation of the stellate ganglion: Novel insights from an acute canine study. Heart Rhythm, 2016, 13, 1395-1401.	0.7	11
77	Genomic Profiling of Adult and Pediatric B-cell Acute Lymphoblastic Leukemia. EBioMedicine, 2016, 8, 173-183.	6.1	241
78	Telomerase Expression by Aberrant Methylation of the TERT Promoter in Melanoma Arising in Giant Congenital Nevi. Journal of Investigative Dermatology, 2016, 136, 339-342.	0.7	36
79	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
80	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
81	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
82	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
83	Pigment-Synthesizing Melanocytic Neoplasm With Protein Kinase C Alpha (PRKCA) Fusion. JAMA Dermatology, 2016, 152, 318.	4.1	33
84	Exploring genomic alteration in pediatric cancer using ProteinPaint. Nature Genetics, 2016, 48, 4-6.	21.4	275
85	Antigenic evolution of H9N2 chicken influenza viruses isolated in China during 2009â€“2013 and selection of a candidate vaccine strain with broad cross-reactivity. Veterinary Microbiology, 2016, 182, 1-7.	1.9	37
86	Comprehensive Functional Characterization of Germline ETV6 Variants Associated with Inherited Predisposition to Acute Lymphoblastic Leukemia in Children. Blood, 2016, 128, 1085-1085.	1.4	1
87	The Genomic Landscape of Pediatric Myelodysplastic Syndromes. Blood, 2016, 128, 956-956.	1.4	1
88	Erythroid miRNA-144/451 Binds Many mRNAs but Regulates Only a Small Subset. Blood, 2016, 128, 1198-1198.	1.4	0
89	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	1.4	72
90	Gorlin syndrome and desmoplastic medulloblastoma: Report of 3 cases with unfavorable clinical course and novel mutations. Pediatric Blood and Cancer, 2015, 62, 1855-1858.	1.5	6

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91	Germline ETV6 Mutations Confer Susceptibility to Acute Lymphoblastic Leukemia and Thrombocytopenia. PLoS Genetics, 2015, 11, e1005262.	3.5	128
92	The Genomic Contributions of Avian H1N1 Influenza A Viruses to the Evolution of Mammalian Strains. PLoS ONE, 2015, 10, e0133795.	2.5	7
93	Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 548-553.	7.1	287
94	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
95	The Genomic Landscape of Childhood and Adolescent Melanoma. Journal of Investigative Dermatology, 2015, 135, 816-823.	0.7	148
96	Critical Role for the DNA Sensor AIM2 in Stem Cell Proliferation and Cancer. Cell, 2015, 162, 45-58.	28.9	266
97	Vismodegib Exerts Targeted Efficacy Against Recurrent Sonic Hedgehogâ€“Subgroup Medulloblastoma: Results From Phase II Pediatric Brain Tumor Consortium Studies PBTC-025B and PBTC-032. Journal of Clinical Oncology, 2015, 33, 2646-2654.	1.6	368
98	Mammalian adaptation of influenza A(H7N9) virus is limited by a narrow genetic bottleneck. Nature Communications, 2015, 6, 6553.	12.8	90
99	Integrated Analysis of Transcriptomic and Proteomic Datasets Reveals Information on Protein Expressivity and Factors Affecting Translational Efficiency. Methods in Molecular Biology, 2015, 1375, 123-136.	0.9	11
100	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	12.8	281
101	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
102	CONSERTING: integrating copy-number analysis with structural-variation detection. Nature Methods, 2015, 12, 527-530.	19.0	68
103	TheCYP2C19Intron 2 Branch Point SNP is the Ancestral Polymorphism Contributing to the Poor Metabolizer Phenotype in Livers withCYP2C19*35andCYP2C19*2Alleles. Drug Metabolism and Disposition, 2015, 43, 1226-1235.	3.3	23
104	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
105	Expression of an Oncogenic ERG isoform Characterizes a Distinct Subtype of B-Progenitor Acute Lymphoblastic Leukemia. Blood, 2015, 126, 693-693.	1.4	1
106	Genomic Landscape of Relapsed Acute Lymphoblastic Leukemia. Blood, 2015, 126, 692-692.	1.4	3
107	Germline Genetic Variation in ETV6 and Predisposition to Childhood Acute Lymphoblastic Leukemia. Blood, 2015, 126, 695-695.	1.4	2
108	Viral suppressors of the RIG-I-mediated interferon response are pre-packaged in influenza virions. Nature Communications, 2014, 5, 5645.	12.8	55

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109	C11ORF95-RELA FUSIONS DRIVE ONCOGENIC NF-KB SIGNALING IN EPENDYMOMA. Neuro-Oncology, 2014, 16, iii16-iii16.	1.2	1
110	Histone H3 Mutations in Pediatric Brain Tumors. Cold Spring Harbor Perspectives in Biology, 2014, 6, a018689-a018689.	5.5	29
111	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
112	C11orf95â€"RELA fusions drive oncogenic NF-ÎºB signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
113	PTEN action in leukaemia dictated by the tissue microenvironment. Nature, 2014, 510, 402-406.	27.8	40
114	An integrated systems genetics screen reveals the transcriptional structure of inherited predisposition to metastatic disease. Genome Research, 2014, 24, 227-240.	5.5	37
115	Barcoding Influenza Virus to Decode Transmission. Cell Host and Microbe, 2014, 16, 559-561.	11.0	5
116	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	9.4	418
117	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	27.0	1,161
118	The most informative spacing test effectively discovers biologically relevant outliers or multiple modes in expression. Bioinformatics, 2014, 30, 1400-1408.	4.1	10
119	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
120	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
121	Survival analysis of infected mice reveals pathogenic variations in the genome of avian H1N1 viruses. Scientific Reports, 2014, 4, 7455.	3.3	13
122	Incidence of Germline Mutations in Cancer-Predisposition Genes in Children with Hematologic Malignancies: a Report from the Pediatric Cancer Genome Project. Blood, 2014, 124, 127-127.	1.4	9
123	Cross-species transcriptional network analysis reveals conservation and variation in response to metal stress in cyanobacteria. BMC Genomics, 2013, 14, 112.	2.8	32
124	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	21.4	270
125	Tyrosine kinome sequencing of pediatric acute lymphoblastic leukemia: a report from the Children's Oncology Group TARGET Project. Blood, 2013, 121, 485-488.	1.4	156
126	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252

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127	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
128	Systematic characterization of hypothetical proteins in Synechocystis sp. PCC 6803 reveals proteins functionally relevant to stress responses. Gene, 2013, 512, 6-15.	2.2	26
129	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
130	Comparison Of Mutational Profiles Of Diagnosis and Relapsed Pediatric B-Acute Lymphoblastic Leukemia: A Report From The COG ALL Target Project. Blood, 2013, 122, 824-824.	1.4	4
131	Identification of Molecular Pathway Aberrations in Uterine Serous Carcinoma by Genome-wide Analyses. Journal of the National Cancer Institute, 2012, 104, 1503-1513.	6.3	231
132	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
133	Assessing telomeric DNA content in pediatric cancers using whole-genome sequencing data. Genome Biology, 2012, 13, R113.	9.6	31
134	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. Nature Genetics, 2012, 44, 251-253.	21.4	1,402
135	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
136	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
137	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742
138	Integrated cross-species transcriptional network analysis of metastatic susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3184-3189.	7.1	50
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	Key pathways are frequently mutated in high-risk childhood acute lymphoblastic leukemia: a report from the Children's Oncology Group. Blood, 2011, 118, 3080-3087.	1.4	255
141	Prediction and Characterization of Missing Proteomic Data inDesulfovibrio vulgaris. Comparative and Functional Genomics, 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 Childrenâ€˜s Research Hospital - Washington University Pediatric Cancer Genome Project. Blood, 2011, 118, 69-69.	1.4	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. Blood, 2011, 118, 68-68.	1.4	0
144	Integrative Analyses of Posttranscriptional Regulation in the Yeast Saccharomyces cerevisiae Using Transcriptomic and Proteomic Data. Current Microbiology, 2008, 57, 18-22.	2.2	67

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145	Statistical Application and Challenges in Global Gel-Free Proteomic Analysis by Mass Spectrometry. Critical Reviews in Biotechnology, 2008, 28, 297-307.	9.0	19
146	SGDB: a database of synthetic genes re-designed for optimizing protein over-expression. Nucleic Acids Research, 2007, 35, D76-D79.	14.5	32
147	Optimal encoding rules for synthetic genes: the need for a community effort. Molecular Systems Biology, 2007, 3, 134.	7.2	21
148	Integrative Analysis of Transcriptomic and Proteomic Data: Challenges, Solutions and Applications. Critical Reviews in Biotechnology, 2007, 27, 63-75.	9.0	224
149	Evolution of the syntrophic interaction between Desulfovibrio vulgaris and Methanosarcina barkeri: Involvement of an ancient horizontal gene transfer. Biochemical and Biophysical Research Communications, 2007, 352, 48-54.	2.1	53
150	The effects of differential gene expression on coding sequence features: Analysis by one-way ANOVA. Biochemical and Biophysical Research Communications, 2007, 358, 1108-1113.	2.1	10
151	Simplified gene synthesis: A one-step approach to PCR-based gene construction. Journal of Biotechnology, 2006, 124, 496-503.	3.8	51
152	Correlation between mRNA and protein abundance in Desulfovibrio vulgaris: A multiple regression to identify sources of variations. Biochemical and Biophysical Research Communications, 2006, 339, 603-610.	2.1	159
153	Relation between mRNA expression and sequence information in Desulfovibrio vulgaris: Combinatorial contributions of upstream regulatory motifs and coding sequence features to variations in mRNA abundance. Biochemical and Biophysical Research Communications, 2006, 344, 114-121.	2.1	7
154	The Synthetic Gene Designer: A flexible web platform to explore sequence manipulation for heterologous expression. Protein Expression and Purification, 2006, 47, 441-445.	1.3	64
155	Predicted highly expressed genes in Nocardia farcinica and the implication for its primary metabolism and nocardial virulence. Antonie Van Leeuwenhoek, 2006, 89, 135-146.	1.7	33
156	Two-Component Signal Transduction Systems of Desulfovibrio vulgaris: Structural and Phylogenetic Analysis and Deduction of Putative Cognate Pairs. Journal of Molecular Evolution, 2006, 62, 473-487.	1.8	12
157	Integrated analysis of transcriptomic and proteomic data of Desulfovibrio vulgaris: zero-inflated Poisson regression models to predict abundance of undetected proteins. Bioinformatics, 2006, 22, 1641-1647.	4.1	51
158	Correlation of mRNA Expression and Protein Abundance Affected by Multiple Sequence Features Related to Translational Efficiency in Desulfovibrio vulgaris: A Quantitative Analysis. Genetics, 2006, 174, 2229-2243.	2.9	183
159	Predicted highly expressed genes in the genomes of Streptomyces coelicolor and Streptomyces avermitilis and the implications for their metabolism. Microbiology (United Kingdom), 2005, 151, 2175-2187.	1.8	115
160	Consistency of unitary shapes in dual lead recordings from myelinated fibres in human peripheral nerves: evidence for extracellular single-unit recordings in microneurography. Experimental Brain Research, 1998, 120, 470-478.	1.5	8