Jianjun Chen

List of Publications by Year in descending order

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147 papers	17,041 citations	19608 61 h-index	16127 124 g-index
154 all docs	154 docs citations	154 times ranked	16999 citing authors

#	Article	IF	Citations
1	Crosstalk between epitranscriptomic and epigenetic mechanisms in gene regulation. Trends in Genetics, 2022, 38, 182-193.	2.9	108
2	YTHDF1 promotes mRNA degradation via YTHDF1â€AGO2 interaction and phase separation. Cell Proliferation, 2022, 55, e13157.	2.4	36
3	DNA N6-methyldeoxyadenosine in mammals and human disease. Trends in Genetics, 2022, 38, 454-467.	2.9	23
4	Opioid receptor signaling suppresses leukemia through both catalytic and non-catalytic functions of TET2. Cell Reports, 2022, 38, 110253.	2.9	6
5	METTL16 exerts an m6A-independent function to facilitate translation and tumorigenesis. Nature Cell Biology, 2022, 24, 205-216.	4.6	143
6	FTO in cancer: functions, molecular mechanisms, and therapeutic implications. Trends in Cancer, 2022, 8, 598-614.	3.8	61
7	m6A RNA modifications are measured at single-base resolution across the mammalian transcriptome. Nature Biotechnology, 2022, 40, 1210-1219.	9.4	115
8	RNA-binding proteins in regulating mRNA stability and translation: roles and mechanisms in cancer. Seminars in Cancer Biology, 2022, 86, 664-677.	4.3	29
9	YTHDF1 Promotes Gastric Carcinogenesis by Controlling Translation of FZD7. Cancer Research, 2021, 81, 2651-2665.	0.4	150
10	N(6)â€methyladenosineâ€binding protein YTHDF1 suppresses EBV replication and promotes EBV RNA decay. EMBO Reports, 2021, 22, e50128.	2.0	59
11	Cytoplasmic DROSHA and non-canonical mechanisms of MiR-155 biogenesis in FLT3-ITD acute myeloid leukemia. Leukemia, 2021, 35, 2285-2298.	3.3	10
12	YBX1 is required for maintaining myeloid leukemia cell survival by regulating BCL2 stability in an m6A-dependent manner. Blood, 2021, 138, 71-85.	0.6	87
13	R-2-hydroxyglutarate attenuates aerobic glycolysis in leukemia by targeting the FTO/m6A/PFKP/LDHB axis. Molecular Cell, 2021, 81, 922-939.e9.	4.5	157
14	Targeting differentiation blockade in AML: New hope from cell-surface-based CRISPR screens. Cell Stem Cell, 2021, 28, 585-587.	5.2	4
15	Ten-eleven translocation protein 1 modulates medulloblastoma progression. Genome Biology, 2021, 22, 125.	3.8	3
16	RNA Modification in Cancer. FASEB Journal, 2021, 35, .	0.2	0
17	Evaluation of glycolytic rates in human hematopoietic stem/progenitor cells after target gene depletion. STAR Protocols, 2021, 2, 100603.	0.5	1
18	RNA modifications in hematopoietic malignancies: a new research frontier. Blood, 2021, 138, 637-648.	0.6	24

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19	The RNA m6A reader YTHDF2 controls NK cell antitumor and antiviral immunity. Journal of Experimental Medicine, 2021, 218, .	4.2	82
20	Transcriptional regulation of N6-methyladenosine orchestrates sex-dimorphic metabolic traits. Nature Metabolism, 2021, 3, 940-953.	5.1	24
21	High-resolution characterization of gene function using single-cell CRISPR tiling screen. Nature Communications, 2021, 12, 4063.	5.8	23
22	Targeting FTO for cancer therapy and more. Aging, 2021, 13, 19080-19082.	1.4	4
23	Lysine acetylation restricts mutant IDH2 activity to optimize transformation in AML cells. Molecular Cell, 2021, 81, 3833-3847.e11.	4.5	10
24	Glycoproteome remodeling in MLL-rearranged B-cell precursor acute lymphoblastic leukemia. Theranostics, 2021, 11, 9519-9537.	4.6	8
25	METTL3 Dysregulates RNA Splicing by Translational Control of Splicing Factors via m 6A Modification in CLL. Blood, 2021, 138, 499-499.	0.6	0
26	Homoharringtonine exhibits potent anti-tumor effect and modulates DNA epigenome in acute myeloid leukemia by targeting SP1/TET1/5hmC. Haematologica, 2020, 105, 148-160.	1.7	41
27	RNA Modifications in Cancer: Functions, Mechanisms, and Therapeutic Implications. Annual Review of Cancer Biology, 2020, 4, 221-240.	2.3	60
28	The Biogenesis and Precise Control of RNA m6A Methylation. Trends in Genetics, 2020, 36, 44-52.	2.9	198
29	Signalling input from divergent pathways subverts BÂcell transformation. Nature, 2020, 583, 845-851.	13.7	37
30	miR-550-1 functions as a tumor suppressor in acute myeloid leukemia via the hippo signaling pathway. International Journal of Biological Sciences, 2020, 16, 2853-2867.	2.6	11
31	Co-culture Systems of Drug-Treated Acute Myeloid Leukemia Cells and T Cells for In Vitro and In Vivo Study. STAR Protocols, 2020, 1, 100097.	0.5	2
32	IFITM3 functions as a PIP3 scaffold to amplify PI3K signalling in BÂcells. Nature, 2020, 588, 491-497.	13.7	57
33	RNA Demethylase ALKBH5 Selectively Promotes Tumorigenesis and Cancer Stem Cell Self-Renewal in Acute Myeloid Leukemia. Cell Stem Cell, 2020, 27, 64-80.e9.	5.2	225
34	Frequency and spectrum of disease-causing variants in 1892 patients with suspected genetic HLH disorders. Blood Advances, 2020, 4, 2578-2594.	2.5	29
35	Targeting FTO Suppresses Cancer Stem Cell Maintenance and Immune Evasion. Cancer Cell, 2020, 38, 79-96.e11.	7.7	389
36	m6A Modification in Coding and Non-coding RNAs: Roles and Therapeutic Implications in Cancer. Cancer Cell, 2020, 37, 270-288.	7.7	688

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37	FTO-Dependent N⁶-Methyladenosine Modifications Inhibit Ovarian Cancer Stem Cell Self-Renewal by Blocking cAMP Signaling. Cancer Research, 2020, 80, 3200-3214.	0.4	128
38	FOXM1 regulates leukemia stem cell quiescence and survival in MLL-rearranged AML. Nature Communications, 2020, 11, 928.	5.8	54
39	RNA N6-methyladenosine modification in solid tumors: new therapeutic frontiers. Cancer Gene Therapy, 2020, 27, 625-633.	2.2	22
40	Epitranscriptomics in liver disease: Basic concepts and therapeutic potential. Journal of Hepatology, 2020, 73, 664-679.	1.8	92
41	Integrative Transcriptome and Quantitative Proteome Analyses Identify METTL3 As a Key Regulator for Aberrant RNA Processing in Chronic Lymphocytic Leukemia. Blood, 2020, 136, 12-12.	0.6	0
42	Rationale for targeting BCL6 in MLL-rearranged acute lymphoblastic leukemia. Genes and Development, 2019, 33, 1265-1279.	2.7	17
43	Targeting PRMT1-mediated FLT3 methylation disrupts maintenance of MLL-rearranged acute lymphoblastic leukemia. Blood, 2019, 134, 1257-1268.	0.6	30
44	EGR1 recruits TET1 to shape the brain methylome during development and upon neuronal activity. Nature Communications, 2019, 10, 3892.	5.8	95
45	Breast Cancer Riskâ€“Associated SNPs in the mTOR Promoter Form De Novo KLF5- and ZEB1-Binding Sites that Influence the Cellular Response to Paclitaxel. Molecular Cancer Research, 2019, 17, 2244-2256.	1.5	8
46	Small-Molecule Targeting of Oncogenic FTO Demethylase in Acute Myeloid Leukemia. Cancer Cell, 2019, 35, 677-691.e10.	7.7	516
47	Histone H3 trimethylation at lysine 36 guides m6A RNA modification co-transcriptionally. Nature, 2019, 567, 414-419.	13.7	452
48	Hypoxiaâ€inducible factorâ€2Î± directly promotes <scp>BCRP</scp> expression and mediates the resistance of ovarian cancer stem cells to adriamycin. Molecular Oncology, 2019, 13, 403-421.	2.1	47
49	IGF2BP1 promotes SRF-dependent transcription in cancer in a m6A- and miRNA-dependent manner. Nucleic Acids Research, 2019, 47, 375-390.	6.5	256
50	RNA N 6-Methyladenosine Modification in Normal and Malignant Hematopoiesis. Advances in Experimental Medicine and Biology, 2019, 1143, 75-93.	0.8	35
51	Effective Novel Fto Inhibitors Show Potent Anti-Cancer Efficacy and Suppress Drug Resistance. Blood, 2019, 134, 233-233.	0.6	5
52	TET1 Modulates DNA Replication in Leukemia Cells Via a Catalytic-Independent Mechanism through Cooperating with KAT8. Blood, 2019, 134, 1249-1249.	0.6	0
53	Ifitm3 Is Essential for PI(3,4,5)P3-Dependent B-Cell Activation and Leukemogenesis. Blood, 2019, 134, 2782-2782.	0.6	1
54	Identification of ZNF217 As an Essential Oncogenic Gene in B-Cell Acute Lymphoblastic Leukemia By CRISPR/Cas9-Based Library Screening. Blood, 2019, 134, 1465-1465.	0.6	0

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55	Recognition of RNA N6-methyladenosine by IGF2BP proteins enhances mRNA stability and translation. Nature Cell Biology, 2018, 20, 285-295.	4.6	1,650
56	RNA N6-methyladenosine modification in cancers: current status and perspectives. Cell Research, 2018, 28, 507-517.	5.7	586
57	METTL14 Inhibits Hematopoietic Stem/Progenitor Differentiation and Promotes Leukemogenesis via mRNA m6A Modification. Cell Stem Cell, 2018, 22, 191-205.e9.	5.2	749
58	Role of N6-methyladenosine modification in cancer. Current Opinion in Genetics and Development, 2018, 48, 1-7.	1.5	178
59	R-2HG Exhibits Anti-tumor Activity by Targeting FTO/m6A/MYC/CEBPA Signaling. Cell, 2018, 172, 90-105.e23.	13.5	794
60	HIF-2Î± promotes conversion to a stem cell phenotype and induces chemoresistance in breast cancer cells by activating Wnt and Notch pathways. Journal of Experimental and Clinical Cancer Research, 2018, 37, 256.	3.5	124
61	Differential m6A, m6Am, and m1A Demethylation Mediated by FTO in the Cell Nucleus and Cytoplasm. Molecular Cell, 2018, 71, 973-985.e5.	4.5	506
62	Critical Enzymatic Functions of FTO in Obesity and Cancer. Frontiers in Endocrinology, 2018, 9, 396.	1.5	102
63	Downregulation of Mir-142 Promotes Leukemia Growth in Philadelphia Chromosome-Positive (Ph+) Acute Lymphoblastic Leukemia (ALL): A Possible Novel Therapeutic Target?. Blood, 2018, 132, 1338-1338.	0.6	0
64	ALKBH5 Functions As an Oncogene in Acute Myeloid Leukemia. Blood, 2018, 132, 3910-3910.	0.6	0
65	ALOX5 exhibits anti-tumor and drug-sensitizing effects in MLL-rearranged leukemia. Scientific Reports, 2017, 7, 1853.	1.6	26
66	FTO Plays an Oncogenic Role in Acute Myeloid Leukemia as a N 6 -Methyladenosine RNA Demethylase. Cancer Cell, 2017, 31, 127-141.	7.7	1,139
67	The IRF4 Gene Regulatory Module Functions as a Read-Write Integrator to Dynamically Coordinate TÂHelper Cell Fate. Immunity, 2017, 47, 481-497.e7.	6.6	104
68	Targeted inhibition of STAT/TET1 axis as a therapeutic strategy for acute myeloid leukemia. Nature Communications, 2017, 8, 2099.	5.8	45
69	Sensitizing leukemia stem cells to NF-ÎºB inhibitor treatment in vivo by inactivation of both TNF and IL-1 signaling. Oncotarget, 2017, 8, 8420-8435.	0.8	29
70	Targeted Inhibition of STAT/TET1 Axis As a Potent Therapeutic Strategy for Acute Myeloid Leukemia. Blood, 2017, 130, 857-857.	0.6	1
71	Identification of a circulating MicroRNA signature to distinguish recurrence in breast cancer patients. Oncotarget, 2016, 7, 55231-55248.	0.8	70
72	miR-22 has a potent anti-tumour role with therapeutic potential in acute myeloid leukaemia. Nature Communications, 2016, 7, 11452.	5.8	113

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73	Eradication of Acute Myeloid Leukemia with FLT3 Ligandâ€“Targeted miR-150 Nanoparticles. Cancer Research, 2016, 76, 4470-4480.	0.4	48
74	Identification of MLL-fusion/MYCâŠ£miR-26âŠ£TET1 signaling circuit in MLL-rearranged leukemia. Cancer Letters, 2016, 372, 157-165.	3.2	25
75	PBX3 and MEIS1 Cooperate in Hematopoietic Cells to Drive Acute Myeloid Leukemias Characterized by a Core Transcriptome of the MLL-Rearranged Disease. Cancer Research, 2016, 76, 619-629.	0.4	45
76	The N6-Adenine Methyltransferase METTL14 Plays an Oncogenic Role in Acute Myeloid Leukemia. Blood, 2016, 128, 1536-1536.	0.6	1
77	Alox5 Functions As Both Tumor Suppressor and Drug Sensitizer in AML. Blood, 2016, 128, 2851-2851.	0.6	0
78	Overexpression and knockout of miR-126 both promote leukemogenesis. Blood, 2015, 126, 2005-2015.	0.6	65
79	Systematic computation with functional gene-sets among leukemic and hematopoietic stem cells reveals a favorable prognostic signature for acute myeloid leukemia. BMC Bioinformatics, 2015, 16, 97.	1.2	11
80	TRAIL pathway is associated with inhibition of colon cancer by protopanaxadiol. Journal of Pharmacological Sciences, 2015, 127, 83-91.	1.1	20
81	The pathological role and prognostic impact of miR-181 in acute myeloid leukemia. Cancer Genetics, 2015, 208, 225-229.	0.2	49
82	Overexpression and Knockout of Mir-126 Both Promote Leukemogenesis through Targeting Distinct Gene Signaling. Blood, 2015, 126, 3667-3667.	0.6	1
83	MicroRNAs in cancer biology and therapy: Current status and perspectives. Genes and Diseases, 2014, 1, 53-63.	1.5	111
84	The dynamics of DNA methylation fidelity during mouse embryonic stem cell self-renewal and differentiation. Genome Research, 2014, 24, 1296-1307.	2.4	72
85	Co-inhibition of NF-Î²B and JNK is synergistic in TNF-expressing human AML. Journal of Experimental Medicine, 2014, 211, 1093-1108.	4.2	80
86	Therapeutic antagonists of microRNAs deplete leukemia-initiating cell activity. Journal of Clinical Investigation, 2014, 124, 222-236.	3.9	66
87	Identification of a 24-Gene Prognostic Signature That Improves the European LeukemiaNet Risk Classification of Acute Myeloid Leukemia: An International Collaborative Study. Journal of Clinical Oncology, 2013, 31, 1172-1181.	0.8	164
88	An Extensive Network of TET2-Targeting MicroRNAs Regulates Malignant Hematopoiesis. Cell Reports, 2013, 5, 471-481.	2.9	139
89	PBX3 is an important cofactor of HOXA9 in leukemogenesis. Blood, 2013, 121, 1422-1431.	0.6	116
90	miR-9 is an essential oncogenic microRNA specifically overexpressed in mixed lineage leukemia â€“rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11511-11516.	3.3	97

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91	HMGA2/TET1/HOXA9 signaling pathway regulates breast cancer growth and metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9920-9925.	3.3	231
92	Critical role of miR-9 in myelopoiesis and EVI1-induced leukemogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5594-5599.	3.3	68
93	TET1 plays an essential oncogenic role in MLL -rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11994-11999.	3.3	185
94	AML Cells Utilize TNF-Driven JNK Signaling As a Critical NF-ÎºB-Independent Survival Signal. Blood, 2013, 122, 2890-2890.	0.6	0
95	MLL-Rearranged Acute Myeloid Leukemias Drive Expression Of Mir-9, a Critical Oncogene In Leukemogenesis. Blood, 2013, 122, 3740-3740.	0.6	0
96	Young intragenic miRNAs are less coexpressed with host genes than old ones: implications of miRNAâ€“host gene coevolution. Nucleic Acids Research, 2012, 40, 4002-4012.	6.5	63
97	miR-196b directly targets both HOXA9/MEIS1 oncogenes and FAS tumour suppressor in MLL-rearranged leukaemia. Nature Communications, 2012, 3, 688.	5.8	138
98	miR-495 is a tumor-suppressor microRNA down-regulated in MLL -rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19397-19402.	3.3	109
99	Crosstalk Between DNA and Histones: Tetâ€™s New Role in Embryonic Stem Cells. Current Genomics, 2012, 13, 603-608.	0.7	14
100	Blockade of miR-150 Maturation by MLL-Fusion/MYC/LIN-28 Is Required for MLL-Associated Leukemia. Cancer Cell, 2012, 22, 524-535.	7.7	154
101	Up-regulation of a HOXA-PBX3 homeobox-gene signature following down-regulation of miR-181 is associated with adverse prognosis in patients with cytogenetically abnormal AML. Blood, 2012, 119, 2314-2324.	0.6	145
102	Two isoforms of HOXA9 function differently but work synergistically in human MLL-rearranged leukemia. Blood Cells, Molecules, and Diseases, 2012, 49, 102-106.	0.6	11
103	miR-150: targeting MLL leukemia. Oncotarget, 2012, 3, 1268-1269.	0.8	3
104	Blockade of Mir-150 Maturation by MLL-Fusion/MYC/Lin-28 Is Required for MLL-Associated Leukemia. Blood, 2012, 120, 3499-3499.	0.6	1
105	The HOXA/PBX3 Pathway Is an Attractive Therapeutic Target in MLL-Rearranged Acute Leukemia. Blood, 2012, 120, 3522-3522.	0.6	0
106	MLL-Associated Leukemias Drive Expression of MiR-9, Required for Tumorigenesis. Blood, 2012, 120, 525-525.	0.6	0
107	In Vitro Functional Study of miR-126 in Leukemia. Methods in Molecular Biology, 2011, 676, 185-195.	0.4	22
108	MIR29B regulates expression of MLLT11 (AF1Q), an MLL fusion partner, and low MIR29B expression associates with adverse cytogenetics and poor overall survival in AML. British Journal of Haematology, 2011, 153, 753-757.	1.2	38

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109	Repression of Mir-495, a Microrna Associated with Favorable Outcome of Acute Myeloid Leukemia Patients, Is Required for the MLL-Associated Leukemogenesis,. Blood, 2011, 118, 3462-3462.	0.6	0
110	Activation of a Mir-181-Targeting HOXA-PBX3 Homeobox Gene Signature Is Associated with Adverse Prognosis of Cytogenetically Abnormal Acute Myeloid Leukemia. Blood, 2011, 118, 236-236.	0.6	0
111	Leukaemogenesis: more than mutant genes. Nature Reviews Cancer, 2010, 10, 23-36.	12.8	286
112	Aberrant overexpression and function of the miR-17-92 cluster in MLL -rearranged acute leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3710-3715.	3.3	141
113	Cytoplasmic FANCA-FANCC Complex Interacts and Stabilizes the Cytoplasm-dislocalized Leukemic Nucleophosmin Protein (NPMc). Journal of Biological Chemistry, 2010, 285, 37436-37444.	1.6	12
114	MicroRNAs expression signatures are associated with lineage and survival in acute leukemias. Blood Cells, Molecules, and Diseases, 2010, 44, 191-197.	0.6	132
115	Consistent Deregulation of Gene Expression between Human and Murine MLL Rearrangement Leukemias. Cancer Research, 2009, 69, 1109-1116.	0.4	81
116	Regulation of mir-196b by MLL and its overexpression by MLL fusions contributes to immortalization. Blood, 2009, 113, 3314-3322.	0.6	208
117	miR-21 plays a pivotal role in gastric cancer pathogenesis and progression. Laboratory Investigation, 2008, 88, 1358-1366.	1.7	434
118	Distinct microRNA expression profiles in acute myeloid leukemia with common translocations. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15535-15540.	3.3	418
119	MicroRNA expression signatures accurately discriminate acute lymphoblastic leukemia from acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19971-19976.	3.3	435
120	Recent Patents on the Identification and Clinical Application of microRNAs and Target Genes. Recent Patents on DNA & Gene Sequences, 2007, 1, 116-24.	0.7	4
121	MicroRNA Expression Profiles in Acute Myeloid Leukemia with Common Translocations.. Blood, 2007, 110, 3181-3181.	0.6	0
122	MicroRNA and cancer: Current status and prospective. International Journal of Cancer, 2006, 120, 953-960.	2.3	231
123	Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcriptionand organismic complexity. Genome Research, 2006, 16, 922-933.	2.4	40
124	Gene expression profiles in acute myeloid leukemia with common translocations using SAGE. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1030-1035.	3.3	32
125	Identification of Genes Abnormally Expressed in Human MLL-AF4 Leukemia.. Blood, 2006, 108, 4314-4314.	0.6	0
126	Identification of Genes Abnormally Expressed in Both Human and Murine MLL-ELL and/or MLL-ENL Leukemia.. Blood, 2006, 108, 2249-2249.	0.6	0

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127	Human antisense genes have unusually short introns: evidence for selection for rapid transcription. Trends in Genetics, 2005, 21, 203-207.	2.9	60
128	Genome-wide analysis of coordinate expression and evolution of human encoded sense-antisense transcripts. Trends in Genetics, 2005, 21, 326-329.	2.9	133
129	The Small Introns of Antisense Genes Are Better Explained by Selection for Rapid Transcription Than by â€œGenomic Designâ€. Genetics, 2005, 171, 2151-2155.	1.2	17
130	Evidence for a preferential targeting of 3'-UTRs by cis-encoded natural antisense transcripts. Nucleic Acids Research, 2005, 33, 5533-5543.	6.5	78
131	Gene Expression Profiles in Acute Myeloid Leukemia (AML): From Diagnosis to Prognosis.. Blood, 2005, 106, 2996-2996.	0.6	0
132	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. Nucleic Acids Research, 2004, 32, e94-e94.	6.5	12
133	Over 20% of human transcripts might form sense-antisense pairs. Nucleic Acids Research, 2004, 32, 4812-4820.	6.5	287
134	SAGE is far more sensitive than EST for detecting low-abundance transcripts. BMC Genomics, 2004, 5, 1.	1.2	98
135	PRDX4, a member of the peroxiredoxin family, is fused toAML1 (RUNX1) in an acute myeloid leukemia patient with a t(X;21)(p22;q22). Genes Chromosomes and Cancer, 2004, 40, 365-370.	1.5	31
136	Characterization of genomic breakpoints inMLL andCBP in leukemia patients with t(11;16). Genes Chromosomes and Cancer, 2004, 41, 257-265.	1.5	26
137	Analysis of translocations that involve theNUP98 gene in patients with 11p15 chromosomal rearrangements. Genes Chromosomes and Cancer, 2004, 41, 339-352.	1.5	36
138	Construction of novel tumor necrosis factor-alpha mutants with reduced toxicity and higher cytotoxicity on human tumor cells. Science in China Series C: Life Sciences, 2003, 46, 1-9.	1.3	6
139	Duplexes of 21-nucleotide RNAs mediate RNA interference in differentiated mouse ES cells. Biology of the Cell, 2003, 95, 365-371.	0.7	33
140	Oligo(dT) primer generates a high frequency of truncated cDNAs through internal poly(A) priming during reverse transcription. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6152-6156.	3.3	168
141	Genomic DNA breakpoints in AML1/RUNX1 and ETO cluster with topoisomerase II DNA cleavage and DNase I hypersensitive sites in t(8;21) leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3070-3075.	3.3	100
142	Identifying novel transcripts and novel genes in the human genome by using novel SAGE tags. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12257-12262.	3.3	143
143	Molecular portraits of B cell lineage commitment. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10014-10019.	3.3	39
144	Correct Identification of Genes from Serial Analysis of Gene Expression Tag Sequences. Genomics, 2002, 79, 598-602.	1.3	28

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145	High-throughput GLGI procedure for converting a large number of serial analysis of gene expression tag sequences into 3? complementary DNAs. Genes Chromosomes and Cancer, 2002, 33, 252-261.	1.5	51
146	The Pattern of Gene Expression in Mouse Gr-1+ Myeloid Progenitor Cells. Genomics, 2001, 77, 149-162.	1.3	9
147	Epitranscriptomics in myeloid malignancies. Blood Science, 0, Publish Ahead of Print, .	0.4	0