San Ming Wang

List of Publications by Year
in descending order

38 papers	**1,850** citations	304743 **22** h-index	345221 **36** g-index
38 all docs	**38** docs citations	**38** times ranked	**3061** citing authors

#	ARTICLE	IF	CITATIONS
1	Conserved expression of natural antisense transcripts in mammals. BMC Genomics, 2013, 14, 243.	2.8	40
2	Alternatively Expressed Genes Identified in the CD4⁺ T Cells of Allograft Rejection Mice. Cell Transplantation, 2011, 20, 333-350.	2.5	12
3	Transcriptome study for early hematopoiesis—achievement, challenge and new opportunity. Journal of Cellular Physiology, 2010, 223, 549-552.	4.1	2
4	Reply to "Evolutionary flux of canonical microRNAs and mirtrons in Drosophila". Nature Genetics, 2010, 42, 9-10.	21.4	27
5	The transcriptome of human CD34⁺ hematopoietic stem-progenitor cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8278-8283.	7.1	28
6	Consistent Deregulation of Gene Expression between Human and Murine *MLL* Rearrangement Leukemias. Cancer Research, 2009, 69, 1109-1116.	0.9	81
7	Transcriptome analysis of the zebrafish mind bomb mutant. Molecular Genetics and Genomics, 2009, 281, 77-85.	2.1	10
8	The birth and death of microRNA genes in Drosophila. Nature Genetics, 2008, 40, 351-355.	21.4	240
9	Scanning the human genome at kilobase resolution. Genome Research, 2008, 18, 751-762.	5.5	16
10	Long-Short-Long Games in mRNA Identification: The Length Matters. Current Pharmaceutical Biotechnology, 2008, 9, 362-367.	1.6	5
11	Poly A- Transcripts Expressed in HeLa Cells. PLoS ONE, 2008, 3, e2803.	2.5	78
12	Understanding SAGE data. Trends in Genetics, 2007, 23, 42-50.	6.7	74
13	Pan-genome isolation of low abundance transcripts using SAGE tag. FEBS Letters, 2006, 580, 6721-6729.	2.8	10
14	Annotating nonspecific SAGE tags with microarray data. Genomics, 2006, 87, 173-180.	2.9	7
15	Applying the SAGE technique to study the effects of electromagnetic field on biological systems. Proteomics, 2006, 6, 4765-4768.	2.2	5
16	SAGE detects microRNA precursors. BMC Genomics, 2006, 7, 285.	2.8	12
17	A large quantity of novel human antisense transcripts detected by LongSAGE. Bioinformatics, 2006, 22, 2475-2479.	4.1	49
18	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.	7.1	32

#	Article	IF	Citations
19	Detecting novel low-abundant transcripts in Drosophila. Rna, 2005, 11, 939-946.	3.5	34
20	Serial Analysis of Gene Expression Study of a Hybrid Rice Strain (LYP9) and Its Parental Cultivars. Plant Physiology, 2005, 138, 1216-1231.	4.8	86
21	2.45 GHz radiofrequency fields alter gene expression in cultured human cells. FEBS Letters, 2005, 579, 4829-4836.	2.8	79
22	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. Genomics, 2005, 86, 127-141.	2.9	230
23	Stage-dependent gene expression profiles during natural killer cell development. Genomics, 2005, 86, 551-565.	2.9	14
24	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. Nucleic Acids Research, 2004, 32, e94-e94.	14.5	12
25	SAGE is far more sensitive than EST for detecting low-abundance transcripts. BMC Genomics, 2004, 5, 1.	2.8	98
26	Response: The new role of SAGE in gene discovery. Trends in Biotechnology, 2003, 21, 57-58.	9.3	10
27	Generation of Longer cDNA Fragments from SAGE Tags for Gene Identification. , 2003, 221, 207-222.		4
28	Screening Poly [dA/dT(-)] cDNA for Gene Identification. , 2003, 221, 197-206.		0
29	Computational Analysis of Gene Identification with SAGE. Journal of Computational Biology, 2002, 9, 513-526.	1.6	13
30	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.	7.1	168
31	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.	7.1	143
32	Silencing of B Cell Receptor Signals in Human Naive B Cells. Journal of Experimental Medicine, 2002, 196, 1291-1305.	8.5	48
33	Molecular portraits of B cell lineage commitment. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10014-10019.	7.1	39
34	Correct Identification of Genes from Serial Analysis of Gene Expression Tag Sequences. Genomics, 2002, 79, 598-602.	2.9	28
35	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.	2.8	51
36	The Pattern of Gene Expression in Mouse Gr-1+ Myeloid Progenitor Cells. Genomics, 2001, 77, 149-162.	2.9	9

#	Article	IF	Citations
37	Generation of High-Quantity and Quality Tag/Ditag cDNAs for SAGE Analysis. BioTechniques, 2001, 31, 348-354.	1.8	27
38	A method for the quantitative analysis of human heat shock gene expression using a multiplex RT-PCR assay. Cell Stress and Chaperones, 1999, 4, 153.	2.9	29