

# San Ming Wang

## List of Publications by Year in descending order

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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	The birth and death of microRNA genes in Drosophila. <i>Nature Genetics</i> , 2008, 40, 351-355.	21.4	240
2	Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. <i>Genomics</i> , 2005, 86, 127-141.	2.9	230
3	Oligo(dT) primer generates a high frequency of truncated cDNAs through internal poly(A) priming during reverse transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6152-6156.	7.1	168
4	Identifying novel transcripts and novel genes in the human genome by using novel SAGE tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12257-12262.	7.1	143
5	SAGE is far more sensitive than EST for detecting low-abundance transcripts. <i>BMC Genomics</i> , 2004, 5, 1.	2.8	98
6	Serial Analysis of Gene Expression Study of a Hybrid Rice Strain (LYP9) and Its Parental Cultivars. <i>Plant Physiology</i> , 2005, 138, 1216-1231.	4.8	86
7	Consistent Deregulation of Gene Expression between Human and Murine <i>c-MYC</i> Rearrangement Leukemias. <i>Cancer Research</i> , 2009, 69, 1109-1116.	0.9	81
8	2.45 GHz radiofrequency fields alter gene expression in cultured human cells. <i>FEBS Letters</i> , 2005, 579, 4829-4836.	2.8	79
9	Poly A- Transcripts Expressed in HeLa Cells. <i>PLoS ONE</i> , 2008, 3, e2803.	2.5	78
10	Understanding SAGE data. <i>Trends in Genetics</i> , 2007, 23, 42-50.	6.7	74
11	High-throughput GLGI procedure for converting a large number of serial analysis of gene expression tag sequences into 3' complementary DNAs. <i>Genes Chromosomes and Cancer</i> , 2002, 33, 252-261.	2.8	51
12	A large quantity of novel human antisense transcripts detected by LongSAGE. <i>Bioinformatics</i> , 2006, 22, 2475-2479.	4.1	49
13	Silencing of B Cell Receptor Signals in Human Naive B Cells. <i>Journal of Experimental Medicine</i> , 2002, 196, 1291-1305.	8.5	48
14	Conserved expression of natural antisense transcripts in mammals. <i>BMC Genomics</i> , 2013, 14, 243.	2.8	40
15	Molecular portraits of B cell lineage commitment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 10014-10019.	7.1	39
16	Detecting novel low-abundant transcripts in Drosophila. <i>Rna</i> , 2005, 11, 939-946.	3.5	34
17	Gene expression profiles in acute myeloid leukemia with common translocations using SAGE. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1030-1035.	7.1	32
18	A method for the quantitative analysis of human heat shock gene expression using a multiplex RT-PCR assay. <i>Cell Stress and Chaperones</i> , 1999, 4, 153.	2.9	29

#	ARTICLE	IF	CITATIONS
19	Correct Identification of Genes from Serial Analysis of Gene Expression Tag Sequences. <i>Genomics</i> , 2002, 79, 598-602.	2.9	28
20	The transcriptome of human CD34 <sup>+</sup> hematopoietic stem-progenitor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8278-8283.	7.1	28
21	Generation of High-Quantity and Quality Tag/Ditag cDNAs for SAGE Analysis. <i>BioTechniques</i> , 2001, 31, 348-354.	1.8	27
22	Reply to "Evolutionary flux of canonical microRNAs and mirtrons in <i>Drosophila</i> ". <i>Nature Genetics</i> , 2010, 42, 9-10.	21.4	27
23	Scanning the human genome at kilobase resolution. <i>Genome Research</i> , 2008, 18, 751-762.	5.5	16
24	Stage-dependent gene expression profiles during natural killer cell development. <i>Genomics</i> , 2005, 86, 551-565.	2.9	14
25	Computational Analysis of Gene Identification with SAGE. <i>Journal of Computational Biology</i> , 2002, 9, 513-526.	1.6	13
26	Generation of longer 3' cDNA fragments from massively parallel signature sequencing tags. <i>Nucleic Acids Research</i> , 2004, 32, e94-e94.	14.5	12
27	SAGE detects microRNA precursors. <i>BMC Genomics</i> , 2006, 7, 285.	2.8	12
28	Alternatively Expressed Genes Identified in the CD4 <sup>+</sup> T Cells of Allograft Rejection Mice. <i>Cell Transplantation</i> , 2011, 20, 333-350.	2.5	12
29	Response: The new role of SAGE in gene discovery. <i>Trends in Biotechnology</i> , 2003, 21, 57-58.	9.3	10
30	Pan-genome isolation of low abundance transcripts using SAGE tag. <i>FEBS Letters</i> , 2006, 580, 6721-6729.	2.8	10
31	Transcriptome analysis of the zebrafish mind bomb mutant. <i>Molecular Genetics and Genomics</i> , 2009, 281, 77-85.	2.1	10
32	The Pattern of Gene Expression in Mouse Gr-1 <sup>+</sup> Myeloid Progenitor Cells. <i>Genomics</i> , 2001, 77, 149-162.	2.9	9
33	Annotating nonspecific SAGE tags with microarray data. <i>Genomics</i> , 2006, 87, 173-180.	2.9	7
34	Applying the SAGE technique to study the effects of electromagnetic field on biological systems. <i>Proteomics</i> , 2006, 6, 4765-4768.	2.2	5
35	Long-Short-Long Games in mRNA Identification: The Length Matters. <i>Current Pharmaceutical Biotechnology</i> , 2008, 9, 362-367.	1.6	5
36	Generation of Longer cDNA Fragments from SAGE Tags for Gene Identification. , 2003, 221, 207-222.		4

#	ARTICLE	IF	CITATIONS
37	Transcriptome study for early hematopoiesisâ€™ achievement, challenge and new opportunity. Journal of Cellular Physiology, 2010, 223, 549-552.	4.1	2
38	Screening Poly [dA/dT(-)] cDNA for Gene Identification. , 2003, 221, 197-206.		0