

Kazunori Waki

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

12,611
citations

623699

14
h-index

888047

17
g-index

17
all docs

17
docs citations

17
times ranked

16228
citing authors

#	ARTICLE	IF	CITATIONS
1	The RIKEN integrated database of mammals. <i>Nucleic Acids Research</i> , 2011, 39, D861-D870.	14.5	23
2	SDOP-DB: a comparative standardized-protocol database for mouse phenotypic analyses. <i>Bioinformatics</i> , 2010, 26, 1133-1134.	4.1	3
3	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	21.4	731
4	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
5	Introduction to the Japan Mouse Clinic at the RIKEN BioResource Center. <i>Experimental Animals</i> , 2009, 58, 443-450.	1.1	30
6	A Resource for Transcriptomic Analysis in the Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3012.	2.5	11
7	Antisense Transcription in the Mammalian Transcriptome. <i>Science</i> , 2005, 309, 1564-1566.	12.6	1,553
8	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	27.8	3,365
9	Cytoskeletal Rearrangements in Synovial Fibroblasts as a Novel Pathophysiological Determinant of Modeled Rheumatoid Arthritis. <i>PLoS Genetics</i> , 2005, 1, e48.	3.5	49
10	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
11	Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas. <i>Nature Methods</i> , 2004, 1, 233-239.	19.0	45
12	Cap analysis gene expression for high-throughput analysis of transcriptional starting point and identification of promoter usage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15776-15781.	7.1	673
13	Targeting a Complex Transcriptome: The Construction of the Mouse Full-Length cDNA Encyclopedia. <i>Genome Research</i> , 2003, 13, 1273-1289.	5.5	154
14	Subtraction of cap-trapped full-length cDNA libraries to select rare transcripts. <i>BioTechniques</i> , 2003, 35, 510-518.	1.8	12
15	A Comprehensive Rice Transcript Map Containing 6591 Expressed Sequence Tag Sites. <i>Plant Cell</i> , 2002, 14, 525-535.	6.6	260
16	The genome sequence and structure of rice chromosome 1. <i>Nature</i> , 2002, 420, 312-316.	27.8	519
17	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. <i>Nature</i> , 2002, 420, 563-573.	27.8	1,548