Wei Chen

List of Publications by Year
in descending order

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67 papers	17,710 citations	57631 44 h-index	98622 67 g-index
72 all docs	72 docs citations	72 times ranked	32796 citing authors

#	Article	IF	Citations
1	DeeReCT-APA: Prediction of Alternative Polyadenylation Site Usage Through Deep Learning. Genomics, Proteomics and Bioinformatics, 2022, 20, 483-495.	3.0	20
2	CRISPR-iPAS: a novel dCAS13-based method for alternative polyadenylation interference. Nucleic Acids Research, 2022, 50, e26-e26.	6.5	10
3	Mammalian splicing divergence is shaped by drift, buffering in trans, and a scaling law. Life Science Alliance, 2022, 5, e202101333.	1.3	3
4	QAUST: Protein Function Prediction Using Structure Similarity, Protein Interaction, and Functional Motifs. Genomics, Proteomics and Bioinformatics, 2021, 19, 998-1011.	3.0	14
5	CASB: a concanavalin Aâ€based sample barcoding strategy for singleâ€cell sequencing. Molecular Systems Biology, 2021, 17, e10060.	3.2	14
6	Translational control by DHX36 binding to 5â€²UTR G-quadruplex is essential for muscle stem-cell regenerative functions. Nature Communications, 2021, 12, 5043.	5.8	36
7	Rbm10 facilitates heterochromatin assembly via the Clr6 HDAC complex. Epigenetics and Chromatin, 2021, 14, 8.	1.8	6
8	CIGARâ€seq, a CRISPR/Casâ€based method for unbiased screening of novel mRNA modification regulators. Molecular Systems Biology, 2020, 16, e10025.	3.2	17
9	Splicing-accessible coding 3â€²UTRs control protein stability and interaction networks. Genome Biology, 2020, 21, 186.	3.8	13
10	Panâ€tissue analysis of allelic alternative polyadenylation suggests widespread functional regulation. Molecular Systems Biology, 2020, 16, e9367.	3.2	5
11	Integrative multi-omics analysis of a colon cancer cell line with heterogeneous Wnt activity revealed RUNX2 as an epigenetic regulator of EMT. Oncogene, 2020, 39, 5152-5164.	2.6	33
12	Inhibiting WNT and NOTCH in renal cancer stem cells and the implications for human patients. Nature Communications, 2020, 11, 929.	5.8	113
13	A deep learning framework to predict binding preference of RNA constituents on protein surface. Nature Communications, 2019, 10, 4941.	5.8	69
14	Full-length transcriptome reconstruction reveals a large diversity of RNA and protein isoforms in rat hippocampus. Nature Communications, 2019, 10, 5009.	5.8	43
15	Deep Learning Deepens the Analysis of Alternative Splicing. Genomics, Proteomics and Bioinformatics, 2019, 17, 219-221.	3.0	2
16	The dynamic proteome of influenza A virus infection identifies M segment splicing as a host range determinant. Nature Communications, 2019, 10, 5518.	5.8	34
17	An Integrated Understanding of the Molecular Mechanisms of How Adipose Tissue Metabolism Affects Long-term Body Weight Maintenance. Diabetes, 2019, 68, 57-65.	0.3	23
18	Metabolic Labeling of Newly Synthesized RNA with 4sU to in Parallel Assess RNA Transcription and Decay. Methods in Molecular Biology, 2018, 1720, 25-34.	0.4	4

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19	The IÎºB kinase complex is a regulator of <scp>mRNA</scp> stability. EMBO Journal, 2018, 37, .	3.5	21
20	The evolution of posttranscriptional regulation. Wiley Interdisciplinary Reviews RNA, 2018, 9, e1485.	3.2	45
21	Global analysis of regulatory divergence in the evolution of mouse alternative polyadenylation. Molecular Systems Biology, 2016, 12, 890.	3.2	23
22	Pervasive isoformâ€specific translational regulation via alternative transcription start sites in mammals. Molecular Systems Biology, 2016, 12, 875.	3.2	83
23	Circular RNAs in Brain and Other Tissues: A Functional Enigma. Trends in Neurosciences, 2016, 39, 597-604.	4.2	181
24	Widespread splicing changes in human brain development and aging. Molecular Systems Biology, 2013, 9, 633.	3.2	183
25	Retargeting transposon insertions by the adeno-associated virus Rep protein. Nucleic Acids Research, 2012, 40, 6693-6712.	6.5	57
26	miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. Nucleic Acids Research, 2012, 40, 37-52.	6.5	2,624
27	A Unilateral Negative Feedback Loop BetweenmiR-200microRNAs and Sox2/E2F3 Controls Neural Progenitor Cell-Cycle Exit and Differentiation. Journal of Neuroscience, 2012, 32, 13292-13308.	1.7	98
28	Dynamic epigenetic enhancer signatures reveal key transcription factors associated with monocytic differentiation states. Blood, 2012, 119, e161-e171.	0.6	139
29	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. Cell, 2012, 151, 671-683.	13.5	513
30	Extension of cortical synaptic development distinguishes humans from chimpanzees and macaques. Genome Research, 2012, 22, 611-622.	2.4	224
31	Gene expression of pluripotency determinants is conserved between mammalian and planarian stem cells. EMBO Journal, 2012, 31, 2755-2769.	3.5	136
32	Retargeting Sleeping Beauty Transposon Insertions by Engineered Zinc Finger DNA-binding Domains. Molecular Therapy, 2012, 20, 1852-1862.	3.7	59
33	Integrated Epigenome Profiling of Repressive Histone Modifications, DNA Methylation and Gene Expression in Normal and Malignant Urothelial Cells. PLoS ONE, 2012, 7, e32750.	1.1	34
34	Deep sequencing reveals 50 novel genes for recessive cognitive disorders. Nature, 2011, 478, 57-63.	13.7	805
35	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. Blood, 2011, 117, 2827-2838.	0.6	120
36	Next generation sequencing in a family with autosomal recessive Kahrizi syndrome (OMIM 612713) reveals a homozygous frameshift mutation in SRD5A3. European Journal of Human Genetics, 2011, 19, 115-117.	1.4	52

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37	Hybridisation-based resequencing of 17 X-linked intellectual disability genes in 135 patients reveals novel mutations in ATRX, SLC6A8 and PQBP1. European Journal of Human Genetics, 2011, 19, 717-720.	1.4	21
38	Global quantification of mammalian gene expression control. Nature, 2011, 473, 337-342.	13.7	5,498
39	ST3GAL3 Mutations Impair the Development of Higher Cognitive Functions. American Journal of Human Genetics, 2011, 89, 407-414.	2.6	89
40	Comparative Genomic Integration Profiling of Sleeping Beauty Transposons Mobilized With High Efficacy From Integrase-defective Lentiviral Vectors in Primary Human Cells. Molecular Therapy, 2011, 19, 1499-1510.	3.7	73
41	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. Genome Research, 2011, 21, 1193-1200.	2.4	100
42	Widespread expression of piRNA-like molecules in somatic tissues. Nucleic Acids Research, 2011, 39, 6596-6607.	6.5	182
43	MicroRNA-Driven Developmental Remodeling in the Brain Distinguishes Humans from Other Primates. PLoS Biology, 2011, 9, e1001214.	2.6	198
44	MicroRNA Expression and Regulation in Human, Chimpanzee, and Macaque Brains. PLoS Genetics, 2011, 7, e1002327.	1.5	126
45	Deciphering the porcine intestinal microRNA transcriptome. BMC Genomics, 2010, 11, 275.	1.2	71
46	Comprehensive survey of human brain microRNA by deep sequencing. BMC Genomics, 2010, 11, 409.	1.2	142
47	Breakpoint analysis of balanced chromosome rearrangements by next-generation paired-end sequencing. European Journal of Human Genetics, 2010, 18, 539-543.	1.4	61
48	The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. Nature Immunology, 2010, 11, 1057-1062.	7.0	304
49	Genomic analysis of miRNAs in an extreme mammalian hibernator, the Arctic ground squirrel. Physiological Genomics, 2010, 42A, 39-51.	1.0	40
50	MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain. Genome Research, 2010, 20, 1207-1218.	2.4	283
51	Tumor Necrosis Factor Receptor Superfamily Member 19 (TNFRSF19) Regulates Differentiation Fate of Human Mesenchymal (Stromal) Stem Cells through Canonical Wnt Signaling and C/EBP. Journal of Biological Chemistry, 2010, 285, 14438-14449.	1.6	63
52	Intergenic and Repeat Transcription in Human, Chimpanzee and Macaque Brains Measured by RNA-Seq. PLoS Computational Biology, 2010, 6, e1000843.	1.5	62
53	Comparative Analysis of Transposable Element Vector Systems in Human Cells. Molecular Therapy, 2010, 18, 1200-1209.	3.7	205
54	Altered Histone Acetylation Is Associated with Age-Dependent Memory Impairment in Mice. Science, 2010, 328, 753-756.	6.0	851

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55	Estimating accuracy of RNA-Seq and microarrays with proteomics. BMC Genomics, 2009, 10, 161.	1.2	240
56	Sequence features associated with microRNA strand selection in humans and flies. BMC Genomics, 2009, 10, 413.	1.2	139
57	Large-scale sorting of C. elegans embryos reveals the dynamics of small RNA expression. Nature Methods, 2009, 6, 745-751.	9.0	91
58	A Human snoRNA with MicroRNA-Like Functions. Molecular Cell, 2008, 32, 519-528.	4.5	738
59	Discovering microRNAs from deep sequencing data using miRDeep. Nature Biotechnology, 2008, 26, 407-415.	9.4	1,102
60	Mapping translocation breakpoints by next-generation sequencing. Genome Research, 2008, 18, 1143-1149.	2.4	118
61	Comparative genome hybridization suggests a role for NRXN1 and APBA2 in schizophrenia. Human Molecular Genetics, 2007, 17, 458-465.	1.4	344
62	Array CGH identifies reciprocal 16p13.1 duplications and deletions that predispose to autism and/or mental retardation. Human Mutation, 2007, 28, 674-682.	1.1	263
63	Mutation screening of brain-expressed X-chromosomal miRNA genes in 464 patients with nonsyndromic X-linked mental retardation. European Journal of Human Genetics, 2007, 15, 375-378.	1.4	23
64	Homozygosity mapping in consanguineous families reveals extreme heterogeneity of non-syndromic autosomal recessive mental retardation and identifies 8 novel gene loci. Human Genetics, 2007, 121, 43-48.	1.8	92
65	A novel X-linked recessive mental retardation syndrome comprising macrocephaly and ciliary dysfunction is allelic to oralâ€“facialâ€“digital type I syndrome. Human Genetics, 2006, 120, 171-178.	1.8	166
66	Impact of low copy repeats on the generation of balanced and unbalanced chromosomal aberrations in mental retardation. Cytogenetic and Genome Research, 2006, 115, 247-253.	0.6	65
67	CGHPRO -- a comprehensive data analysis tool for array CGH. BMC Bioinformatics, 2005, 6, 85.	1.2	97