

Xuebing Wu

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

18,217
citations

21
h-index

33
g-index

33
ext. papers

21,766
ext. citations

26.8
avg, IF

6.4
L-index

#	Paper	IF	Citations
30	Transcriptional Pause Sites Delineate Stable Nucleosome-Associated Premature Polyadenylation Suppressed by U1 snRNP. <i>Molecular Cell</i> , 2018 , 69, 648-663.e7	17.6	65
29	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018 , 172, 979-992.e6	56.2	239
28	Pairwise library screen systematically interrogates Staphylococcus aureus Cas9 specificity in human cells. <i>Nature Communications</i> , 2018 , 9, 2962	17.4	18
27	A genetic program mediates cold-warming response and promotes stress-induced phenoptosis in. <i>ELife</i> , 2018 , 7,	8.9	10
26	Combined effects of octreotide and cisplatin on the proliferation of side population cells from anaplastic thyroid cancer cell lines. <i>Oncology Letters</i> , 2018 , 16, 4033-4042	2.6	7
25	Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d. <i>Cell</i> , 2018 , 175, 212-223.e17	56.2	96
24	Widespread Influence of 3eEnd Structures on Mammalian mRNA Processing and Stability. <i>Cell</i> , 2017 , 169, 905-917.e11	56.2	69
23	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. <i>Nucleic Acids Research</i> , 2017 , 45, W534-W538	20.1	47
22	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. <i>Cell</i> , 2016 , 166, 1147-1162.e15	56.2	159
21	Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016 , 167, 233-247.e17	56.2	690
20	In vivo genome editing using Staphylococcus aureus Cas9. <i>Nature</i> , 2015 , 520, 186-91	50.4	1700
19	Characterizing Polyadenylated uaRNAs Suggests a Potential Role for Pabpn1. <i>FASEB Journal</i> , 2015 , 29, 562.25	0.9	
18	Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells. <i>Nature Biotechnology</i> , 2014 , 32, 670-6	44.5	666
17	Global microRNA depletion suppresses tumor angiogenesis. <i>Genes and Development</i> , 2014 , 28, 1054-67	12.6	52
16	Target specificity of the CRISPR-Cas9 system. <i>Quantitative Biology</i> , 2014 , 2, 59-70	3.9	184
15	DNA targeting specificity of RNA-guided Cas9 nucleases. <i>Nature Biotechnology</i> , 2013 , 31, 827-32	44.5	3056
14	Single-molecule mRNA detection and counting in mammalian tissue. <i>Nature Protocols</i> , 2013 , 8, 1743-58	18.8	148

13	Divergent transcription: a driving force for new gene origination?. <i>Cell</i> , 2013 , 155, 990-6	56.2	118
12	Integrating human omics data to prioritize candidate genes. <i>BMC Medical Genomics</i> , 2013 , 6, 57	3.7	21
11	Multiplex genome engineering using CRISPR/Cas systems. <i>Science</i> , 2013 , 339, 819-23	33.3	9746
10	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. <i>Nature</i> , 2013 , 499, 360-350.4	294	
9	Cancer Gene Prediction Using a Network Approach. <i>Chapman & Hall/CRC Mathematical and Computational Biology Series</i> , 2010 , 191-212		4
8	Accelerating Genome-Wide Association Studies Using CUDA Compatible Graphics Processing Units 2009 ,		5
7	Align human interactome with phenome to identify causative genes and networks underlying disease families. <i>Bioinformatics</i> , 2009 , 25, 98-104	7.2	80
6	A random forest approach to the detection of epistatic interactions in case-control studies. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S65	3.6	180
5	A Comparative Study of Ensemble Learning Approaches in the Classification of Breast Cancer Metastasis 2009 ,		11
4	Epistatic module detection for case-control studies: a Bayesian model with a Gibbs sampling strategy. <i>PLoS Genetics</i> , 2009 , 5, e1000464	6	75
3	Network-based global inference of human disease genes. <i>Molecular Systems Biology</i> , 2008 , 4, 189	12.2	475
2	RNA-guided cell targeting with CRISPR/RfxCas13d collateral activity in human cells		1
1	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences		1