Xuebing Wu

List of Publications by Year
in descending order

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27 papers	24,013 citations	279487 23 h-index	580395 25 g-index
33 all docs	33 docs citations	33 times ranked	34062 citing authors

#	Article	IF	Citations
1	Multiplex Genome Engineering Using CRISPR/Cas Systems. Science, 2013, 339, 819-823.	6.0	12,725
2	DNA targeting specificity of RNA-guided Cas9 nucleases. Nature Biotechnology, 2013, 31, 827-832.	9.4	3,953
3	In vivo genome editing using Staphylococcus aureus Cas9. Nature, 2015, 520, 186-191.	13.7	2,237
4	Editing DNA Methylation in the Mammalian Genome. Cell, 2016, 167, 233-247.e17.	13.5	932
5	Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells. Nature Biotechnology, 2014, 32, 670-676.	9.4	829
6	Networkâ€based global inference of human disease genes. Molecular Systems Biology, 2008, 4, 189.	3.2	583
7	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. Nature, 2013, 499, 360-363.	13.7	361
8	Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. Cell, 2018, 172, 979-992.e6.	13.5	351
9	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. Cell, 2016, 166, 1147-1162.e15.	13.5	276
10	Target specificity of the CRISPRâ€Cas9 system. Quantitative Biology, 2014, 2, 59-70.	0.3	262
11	A random forest approach to the detection of epistatic interactions in case-control studies. BMC Bioinformatics, 2009, 10, S65.	1.2	225
12	Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d. Cell, 2018, 175, 212-223.e17.	13.5	195
13	Single-molecule mRNA detection and counting in mammalian tissue. Nature Protocols, 2013, 8, 1743-1758.	5.5	187
14	Divergent Transcription: A Driving Force for New Gene Origination?. Cell, 2013, 155, 990-996.	13.5	156
15	Widespread Influence of 3â€²-End Structures on Mammalian mRNA Processing and Stability. Cell, 2017, 169, 905-917.e11.	13.5	123
16	Transcriptional Pause Sites Delineate Stable Nucleosome-Associated Premature Polyadenylation Suppressed by U1 snRNP. Molecular Cell, 2018, 69, 648-663.e7.	4.5	103
17	Epistatic Module Detection for Case-Control Studies: A Bayesian Model with a Gibbs Sampling Strategy. PLoS Genetics, 2009, 5, e1000464.	1.5	100
18	kpLogo: positional k-mer analysis reveals hidden specificity in biological sequences. Nucleic Acids Research, 2017, 45, W534-W538.	6.5	91

#	Article	IF	Citations
19	Align human interactome with phenome to identify causative genes and networks underlying disease families. Bioinformatics, 2009, 25, 98-104.	1.8	90
20	Global microRNA depletion suppresses tumor angiogenesis. Genes and Development, 2014, 28, 1054-1067.	2.7	66
21	A genetic program mediates cold-warming response and promotes stress-induced phenoptosis in C. elegans. ELife, 2018, 7, .	2.8	37
22	Integrating human omics data to prioritize candidate genes. BMC Medical Genomics, 2013, 6, 57.	0.7	36
23	Pairwise library screen systematically interrogates Staphylococcus aureus Cas9 specificity in human cells. Nature Communications, 2018, 9, 2962.	5.8	32
24	A Comparative Study of Ensemble Learning Approaches in the Classification of Breast Cancer Metastasis. , 2009, , .		20
25	Combined effects of octreotide and cisplatin on the proliferation of side population cells from anaplastic thyroid cancer cell lines. Oncology Letters, 2018, 16, 4033-4042.	0.8	9
26	Accelerating Genome-Wide Association Studies Using CUDA Compatible Graphics Processing Units. , 2009, , .		5
27	Characterizing Polyadenylated uaRNAs Suggests a Potential Role for Pabpn1. FASEB Journal, 2015, 29, 562.25.	0.2	0