Jin-Wu Nam

List of Publications by Year
in descending order

28 papers	8,386 citations	430874 18 h-index	477307 29 g-index
35 all docs	35 docs citations	35 times ranked	16208 citing authors

#	Article	IF	Citations
1	Predicting effective microRNA target sites in mammalian mRNAs. ELife, 2015, 4, .	6.0	5,779
2	Expanding the MicroRNA Targeting Code: Functional Sites with Centered Pairing. Molecular Cell, 2010, 38, 789-802.	9.7	534
3	In vivo high-throughput profiling of CRISPR–Cpf1 activity. Nature Methods, 2017, 14, 153-159.	19.0	305
4	Global Analyses of the Effect of Different Cellular Contexts on MicroRNA Targeting. Molecular Cell, 2014, 53, 1031-1043.	9.7	276
5	Long noncoding RNAs in *C. elegans*. Genome Research, 2012, 22, 2529-2540.	5.5	191
6	The small peptide world in long noncoding RNAs. Briefings in Bioinformatics, 2019, 20, 1853-1864.	6.5	183
7	The present and future of *de novo* whole-genome assembly. Briefings in Bioinformatics, 2018, 19, bbw096.	6.5	139
8	A single-cell survey of Drosophila blood. ELife, 2020, 9, .	6.0	134
9	The long noncoding RNA LUCAT1 promotes tumorigenesis by controlling ubiquitination and stability of DNA methyltransferase 1 in esophageal squamous cell carcinoma. Cancer Letters, 2018, 417, 47-57.	7.2	112
10	Single-cell transcriptome maps of myeloid blood cell lineages in Drosophila. Nature Communications, 2020, 11, 4483.	12.8	100
11	Incredible RNA: Dual Functions of Coding and Noncoding. Molecules and Cells, 2016, 39, 367-374.	2.6	89
12	Tumor immune microenvironment lncRNAs. Briefings in Bioinformatics, 2022, 23, .	6.5	77
13	High-confidence coding and noncoding transcriptome maps. Genome Research, 2017, 27, 1050-1062.	5.5	58
14	The regulatory impact of RNA-binding proteins on microRNA targeting. Nature Communications, 2021, 12, 5057.	12.8	54
15	Global estimation of the 3′ untranslated region landscape using RNA sequencing. Methods, 2015, 83, 111-117.	3.8	48
16	HERES, a lncRNA that regulates canonical and noncanonical Wnt signaling pathways via interaction with EZH2. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24620-24629.	7.1	45
17	*En bloc* and segmental deletions of human *XIST* reveal X chromosome inactivation-involving RNA elements. Nucleic Acids Research, 2019, 47, 3875-3887.	14.5	28
18	Whole genome and transcriptome maps of the entirely black native Korean chicken breed Yeonsan Ogye. GigaScience, 2018, 7, .	6.4	20

#	Article	IF	Citations
19	UPF1/SMG7-dependent microRNA-mediated gene regulation. Nature Communications, 2019, 10, 4181.	12.8	20
20	Comprehensive genome and transcriptome analyses reveal genetic relationship, selection signature, and transcriptome landscape of small-sized Korean native Jeju horse. Scientific Reports, 2019, 9, 16672.	3.3	18
21	Degradome sequencing reveals an endogenous microRNA target in <i>C. elegans</i>. FEBS Letters, 2013, 587, 964-969.	2.8	17
22	Preoperative immune landscape predisposes adverse outcomes in hepatocellular carcinoma patients with liver transplantation. Npj Precision Oncology, 2021, 5, 27.	5.4	11
23	TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA-binding protein association. BMC Bioinformatics, 2018, 19, 41.	2.6	8
24	hnRNPC induces isoform shifts in miR-21-5p leading to cancer development. Experimental and Molecular Medicine, 2022, 54, 812-824.	7.7	8
25	Non-Coding Transcriptome Maps across Twenty Tissues of the Korean Black Chicken, Yeonsan Ogye. International Journal of Molecular Sciences, 2018, 19, 2359.	4.1	6
26	HuR stabilizes a polyadenylated form of replicationâ€dependent histone mRNAs under stress conditions. FASEB Journal, 2019, 33, 2680-2693.	0.5	6
27	CGD: Comprehensive guide designer for CRISPR-Cas systems. Computational and Structural Biotechnology Journal, 2020, 18, 814-820.	4.1	6
28	Pseudo-Reference-Based Assembly of Vertebrate Transcriptomes. Genes, 2016, 7, 10.	2.4	2