

Hojoong Kwak

List of Publications by Citations

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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.

19
papers

1,873
citations

14
h-index

21
g-index

21
ext. papers

2,524
ext. citations

17.8
avg, IF

4.98
L-index

#	Paper	IF	Citations
19	Precise maps of RNA polymerase reveal how promoters direct initiation and pausing. <i>Science</i> , 2013 , 339, 950-3	33.3	466
18	Control of transcriptional elongation. <i>Annual Review of Genetics</i> , 2013 , 47, 483-508	14.5	285
17	mA enhances the phase separation potential of mRNA. <i>Nature</i> , 2019 , 571, 424-428	50.4	241
16	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016 , 11, 1455-76	18.8	208
15	Defining the status of RNA polymerase at promoters. <i>Cell Reports</i> , 2012 , 2, 1025-35	10.6	163
14	Systematic Characterization of Stress-Induced RNA Granulation. <i>Molecular Cell</i> , 2018 , 70, 175-187.e8	17.6	96
13	Aspm knockout ferret reveals an evolutionary mechanism governing cerebral cortical size. <i>Nature</i> , 2018 , 556, 370-375	50.4	77
12	The Hmr and Lhr hybrid incompatibility genes suppress a broad range of heterochromatic repeats. <i>PLoS Genetics</i> , 2014 , 10, e1004240	6	60
11	Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. <i>Nature Genetics</i> , 2018 , 50, 1553-1564	36.3	56
10	Defining NELF-E RNA binding in HIV-1 and promoter-proximal pause regions. <i>PLoS Genetics</i> , 2014 , 10, e1004090	6	48
9	High-Resolution Mapping of RNA Polymerases Identifies Mechanisms of Sensitivity and Resistance to BET Inhibitors in t(8;21) AML. <i>Cell Reports</i> , 2016 , 16, 2003-16	10.6	48
8	RNA-DNA differences are generated in human cells within seconds after RNA exits polymerase II. <i>Cell Reports</i> , 2014 , 6, 906-15	10.6	44
7	TED-Seq Identifies the Dynamics of Poly(A) Length during ER Stress. <i>Cell Reports</i> , 2018 , 24, 3630-3641.e7	10.6	25
6	Chromatin Architecture of the Pitx2 Locus Requires CTCF- and Pitx2-Dependent Asymmetry that Mirrors Embryonic Gut Laterality. <i>Cell Reports</i> , 2015 , 13, 337-49	10.6	24
5	Population-scale study of eRNA transcription reveals bipartite functional enhancer architecture. <i>Nature Communications</i> , 2020 , 11, 5963	17.4	13
4	Single-Cell Transcriptome Analysis of Colon Cancer Cell Response to 5-Fluorouracil-Induced DNA Damage. <i>Cell Reports</i> , 2020 , 32, 108077	10.6	10
3	Population-scale study of eRNA transcription reveals bipartite functional enhancer architecture		6

2 Nascent RNA sequencing of peripheral blood leukocytes reveal gene expression diversity 3

1 Genome-Wide Identification of Polyadenylation Dynamics with TED-Seq. *Methods in Molecular Biology*, **2022**, 2404, 281-298 1.4