

Namshik Han

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

1,822
citations

566801

15
h-index

794141

19
g-index

25
all docs

25
docs citations

25
times ranked

3575
citing authors

#	ARTICLE	IF	CITATIONS
1	Current and prospective computational approaches and challenges for developing COVID-19 vaccines. <i>Advanced Drug Delivery Reviews</i> , 2021, 172, 249-274.	6.6	30
2	Identification of SARS-CoV-2-induced pathways reveals drug repurposing strategies. <i>Science Advances</i> , 2021, 7, .	4.7	34
3	Methylation of histone H3 at lysine 37 by Set1 and Set2 prevents spurious DNA replication. <i>Molecular Cell</i> , 2021, 81, 2793-2807.e8.	4.5	18
4	Identification of potential pan-coronavirus therapies using a computational drug repurposing platform. <i>Methods</i> , 2021, , .	1.9	1
5	Differential Expression of Soluble Receptor for Advanced Glycation End-products in Mice Susceptible or Resistant to Chronic Colitis. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 360-368.	0.9	9
6	A novel long noncoding RNA Linc-ASEN represses cellular senescence through multileveled reduction of p21 expression. <i>Cell Death and Differentiation</i> , 2020, 27, 1844-1861.	5.0	23
7	Inflammatory Signals Induce AT2 Cell-Derived Damage-Associated Transient Progenitors that Mediate Alveolar Regeneration. <i>Cell Stem Cell</i> , 2020, 27, 366-382.e7.	5.2	303
8	Long non-coding RNA ChRO1 facilitates ATRX/DAXX-dependent H3.3 deposition for transcription-associated heterochromatin reorganization. <i>Nucleic Acids Research</i> , 2018, 46, 11759-11775.	6.5	37
9	<sc>DDX</sc>3X <sc>RNA</sc> helicase affects breast cancer cell cycle progression by regulating expression of <sc>KLF</sc>4. <i>FEBS Letters</i> , 2018, 592, 2308-2322.	1.3	32
10	Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci. <i>Genome Biology</i> , 2018, 19, 32.	3.8	114
11	Promoter-bound METTL3 maintains myeloid leukaemia by m6A-dependent translation control. <i>Nature</i> , 2017, 552, 126-131.	13.7	833
12	TIGERi: modeling and visualizing the responses to perturbation of a transcription factor network. <i>BMC Bioinformatics</i> , 2017, 18, 260.	1.2	2
13	Deregulation of the FOXM1 target gene network and its coregulatory partners in oesophageal adenocarcinoma. <i>Molecular Cancer</i> , 2015, 14, 69.	7.9	30
14	The forkhead transcription factor FOXK2 acts as a chromatin targeting factor for the BAP1-containing histone deubiquitinase complex. <i>Nucleic Acids Research</i> , 2014, 42, 6232-6242.	6.5	66
15	The Forkhead Transcription Factor FOXM1 Controls Cell Cycle-Dependent Gene Expression through an Atypical Chromatin Binding Mechanism. <i>Molecular and Cellular Biology</i> , 2013, 33, 227-236.	1.1	185
16	The FOXM1-PLK1 axis is commonly upregulated in oesophageal adenocarcinoma. <i>British Journal of Cancer</i> , 2012, 107, 1766-1775.	2.9	34
17	Protein Kinase C Regulates Late Cell Cycle-Dependent Gene Expression. <i>Molecular and Cellular Biology</i> , 2012, 32, 4651-4661.	1.1	20
18	Progressive lung cancer determined by expression profiling and transcriptional regulation. <i>International Journal of Oncology</i> , 2012, 41, 242-52.	1.4	6

#	ARTICLE	IF	CITATIONS
19	Ultradian Cortisol Pulsatility Encodes a Distinct, Biologically Important Signal. PLoS ONE, 2011, 6, e15766.	1.1	44