

Varun Narendra

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11340244/publications.pdf>

Version: 2024-02-01

13
papers

1,497
citations

840119

11
h-index

1058022

14
g-index

17
all docs

17
docs citations

17
times ranked

3170
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPR and biochemical screens identify MAZ as a cofactor in CTCF-mediated insulation at Hox clusters. <i>Nature Genetics</i> , 2022, 54, 202-212.	9.4	37
2	Oncologic immunomodulatory agents in patients with cancer and COVID-19. <i>Scientific Reports</i> , 2021, 11, 4814.	1.6	11
3	Neutropenia in adult acute myeloid leukemia patients represents a powerful risk factor for COVID-19 related mortality. <i>Leukemia and Lymphoma</i> , 2021, 62, 1940-1948.	0.6	7
4	Chemotherapy and COVID-19 Outcomes in Patients With Cancer. <i>Journal of Clinical Oncology</i> , 2020, 38, 3538-3546.	0.8	195
5	Capturing the Onset of PRC2-Mediated Repressive Domain Formation. <i>Molecular Cell</i> , 2018, 70, 1149-1162.e5.	4.5	222
6	CTCF-mediated topological boundaries during development foster appropriate gene regulation. <i>Genes and Development</i> , 2016, 30, 2657-2662.	2.7	161
7	Co-repressor CBFA2T2 regulates pluripotency and germline development. <i>Nature</i> , 2016, 534, 387-390.	13.7	61
8	USP7 Cooperates with SCML2 To Regulate the Activity of PRC1. <i>Molecular and Cellular Biology</i> , 2015, 35, 1157-1168.	1.1	50
9	CTCF establishes discrete functional chromatin domains at the <i>Hox</i> clusters during differentiation. <i>Science</i> , 2015, 347, 1017-1021.	6.0	490
10	Erk1/2 Activity Promotes Chromatin Features and RNAPII Phosphorylation at Developmental Promoters in Mouse ESCs. <i>Cell</i> , 2014, 156, 678-690.	13.5	144
11	In Vivo Proximity Labeling for the Detection of Protein-Protein and Protein-RNA Interactions. <i>Journal of Proteome Research</i> , 2014, 13, 6135-6143.	1.8	22
12	Interactions with RNA direct the Polycomb group protein SCML2 to chromatin where it represses target genes. <i>ELife</i> , 2014, 3, e02637.	2.8	46
13	A comprehensive assessment of methods for de-novo reverse-engineering of genome-scale regulatory networks. <i>Genomics</i> , 2011, 97, 7-18.	1.3	45