

# Suresh Cuddapah

## List of Publications by Year in descending order

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23  
papers

8,599  
citations

430442

18  
h-index

676716

22  
g-index

25  
all docs

25  
docs citations

25  
times ranked

12860  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptional repression of E-cadherin in nickel-exposed lung epithelial cells mediated by loss of Sp1 binding at the promoter. <i>Molecular Carcinogenesis</i> , 2022, 61, 99-110.	1.3	6
2	Epithelial-mesenchymal transition: Insights into nickel-induced lung diseases. <i>Seminars in Cancer Biology</i> , 2021, 76, 99-109.	4.3	40
3	Cadmium exposure upregulates SNAIL through miR-30 repression in human lung epithelial cells. <i>Toxicology and Applied Pharmacology</i> , 2019, 373, 1-9.	1.3	26
4	Nickel-induced transcriptional changes persist after exposure through epigenetic reprogramming. <i>Epigenetics and Chromatin</i> , 2019, 12, 75.	1.8	22
5	Role of CTCF in DNA damage response. <i>Mutation Research - Reviews in Mutation Research</i> , 2019, 780, 61-68.	2.4	18
6	Nickel exposure induces persistent mesenchymal phenotype in human lung epithelial cells through epigenetic activation of ZEB1. <i>Molecular Carcinogenesis</i> , 2018, 57, 794-806.	1.3	44
7	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. <i>Scientific Reports</i> , 2017, 7, 39785.	1.6	39
8	Identification of a unique gene expression signature in mercury and 2,3,7,8-tetrachlorodibenzo-p-dioxin co-exposed cells. <i>Toxicology Research</i> , 2017, 6, 312-323.	0.9	9
9	Nuclear Factor $\kappa$ B1/RelA Mediates Inflammation in Human Lung Epithelial Cells at Atmospheric Oxygen Levels. <i>Journal of Cellular Physiology</i> , 2016, 231, 1611-1620.	2.0	9
10	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the epigenetic landscape. <i>Cellular and Molecular Immunology</i> , 2016, 13, 502-513.	4.8	99
11	Oxidative Stress Under Ambient and Physiological Oxygen Tension in Tissue Culture. <i>Current Pharmacology Reports</i> , 2016, 2, 64-72.	1.5	100
12	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14631-14636.	3.3	39
13	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in Drosophila. <i>PLoS ONE</i> , 2012, 7, e36365.	1.1	24
14	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. <i>Molecular and Cellular Biology</i> , 2011, 31, 700-709.	1.1	44
15	Epigenomics of T cell activation, differentiation, and memory. <i>Current Opinion in Immunology</i> , 2010, 22, 341-347.	2.4	91
16	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. <i>Genome Research</i> , 2009, 19, 24-32.	2.4	587
17	Native Chromatin Preparation and Illumina/Solexa Library Construction. <i>Cold Spring Harbor Protocols</i> , 2009, 2009, pdb.prot5237.	0.2	26
18	Transcriptional enhancer factor 1 (TEF/TEAD1) mediates activation of <i>IFITM3</i> gene by BRG1. <i>FEBS Letters</i> , 2008, 582, 391-397.	1.3	8

#	ARTICLE	IF	CITATIONS
19	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from CHIP-Seq data. Nucleic Acids Research, 2008, 36, 5221-5231.	6.5	500
20	High-Resolution Profiling of Histone Methylations in the Human Genome. Cell, 2007, 129, 823-837.	13.5	6,036
21	Genome-wide Mapping of Histone Modifications by GMAT. Biotechnology and Genetic Engineering Reviews, 2006, 23, 93-104.	2.4	0
22	The genomic landscape of histone modifications in human T cells. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15782-15787.	3.3	432
23	Active chromatin domains are defined by acetylation islands revealed by genome-wide mapping. Genes and Development, 2005, 19, 542-552.	2.7	398