Suresh Cuddapah

List of Publications by Year in descending order

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SUDESH CUDDADAH

#	Article	IF	CITATIONS
1	Transcriptional repression of Eâ€eadherin in nickelâ€exposed lung epithelial cells mediated by loss of Sp1 binding at the promoter. Molecular Carcinogenesis, 2022, 61, 99-110.	2.7	6
2	Epithelial-mesenchymal transition: Insights into nickel-induced lung diseases. Seminars in Cancer Biology, 2021, 76, 99-109.	9.6	40
3	Cadmium exposure upregulates SNAIL through miR-30 repression in human lung epithelial cells. Toxicology and Applied Pharmacology, 2019, 373, 1-9.	2.8	26
4	Nickel-induced transcriptional changes persist Âpost exposure through epigenetic reprogramming. Epigenetics and Chromatin, 2019, 12, 75.	3.9	22
5	Role of CTCF in DNA damage response. Mutation Research - Reviews in Mutation Research, 2019, 780, 61-68.	5.5	18
6	Nickel exposure induces persistent mesenchymal phenotype in human lung epithelial cells through epigenetic activation of ZEB1. Molecular Carcinogenesis, 2018, 57, 794-806.	2.7	44
7	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. Scientific Reports, 2017, 7, 39785.	3.3	39
8	ldentification of a unique gene expression signature in mercury and 2,3,7,8-tetrachlorodibenzo-p-dioxin co-exposed cells. Toxicology Research, 2017, 6, 312-323.	2.1	9
9	Nuclear Factor κB1/RelA Mediates Inflammation in Human Lung Epithelial Cells at Atmospheric Oxygen Levels. Journal of Cellular Physiology, 2016, 231, 1611-1620.	4.1	9
10	Lineage relationship of CD8+ T cell subsets is revealed by progressive changes in the epigenetic landscape. Cellular and Molecular Immunology, 2016, 13, 502-513.	10.5	99
11	Oxidative Stress Under Ambient and Physiological Oxygen Tension in Tissue Culture. Current Pharmacology Reports, 2016, 2, 64-72.	3.0	100
12	Epigenetic dysregulation by nickel through repressive chromatin domain disruption. Proceedings of the United States of America, 2014, 111, 14631-14636.	7.1	39
13	A Novel Human Polycomb Binding Site Acts As a Functional Polycomb Response Element in Drosophila. PLoS ONE, 2012, 7, e36365.	2.5	24
14	Genomic Profiling of HMGN1 Reveals an Association with Chromatin at Regulatory Regions. Molecular and Cellular Biology, 2011, 31, 700-709.	2.3	44
15	Epigenomics of T cell activation, differentiation, and memory. Current Opinion in Immunology, 2010, 22, 341-347.	5.5	91
16	Global analysis of the insulator binding protein CTCF in chromatin barrier regions reveals demarcation of active and repressive domains. Genome Research, 2009, 19, 24-32.	5.5	587
17	Native Chromatin Preparation and Illumina/Solexa Library Construction. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5237.	0.3	26
18	Transcriptional enhancer factor 1 (TEFâ€1/TEAD1) mediates activation of <i>IFITM3</i> gene by BRGI. FEBS Letters, 2008, 582, 391-397.	2.8	8

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19	Genome-wide identification of <i>in vivo</i> protein-DNA binding sites from ChIP-Seq data. Nucleic Acids Research, 2008, 36, 5221-5231.	14.5	500
20	High-Resolution Profiling of Histone Methylations in the Human Genome. Cell, 2007, 129, 823-837.	28.9	6,036
21	Genome-wide Mapping of Histone Modifications by GMAT. Biotechnology and Genetic Engineering Reviews, 2006, 23, 93-104.	6.2	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.	7.1	432
23	Active chromatin domains are defined by acetylation islands revealed by genome-wide mapping. Genes and Development, 2005, 19, 542-552.	5.9	398