

Kuljeet Singh Sandhu

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

18,195
citations

566801

15
h-index

552369

26
g-index

32
all docs

32
docs citations

32
times ranked

36608
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent evolution of a genomic rearrangement may explain cancer resistance in hystrico- and sciurumorpha rodents. <i>Npj Aging and Mechanisms of Disease</i> , 2021, 7, 20.	4.5	2
2	CTCF-Mediated Genome Architecture Regulates the Dosage of Mitotically Stable Mono-allelic Expression of Autosomal Genes. <i>Cell Reports</i> , 2020, 33, 108302.	2.9	4
3	Biased visibility in Hi-C datasets marks dynamically regulated condensed and decondensed chromatin states genome-wide. <i>BMC Genomics</i> , 2020, 21, 175.	1.2	11
4	Does genome surveillance explain the global discrepancy between binding and effect of chromatin factors?. <i>FEBS Letters</i> , 2020, 594, 1339-1353.	1.3	0
5	Evolutionary Loss of Genomic Proximity to Conserved Noncoding Elements Impacted the Gene Expression Dynamics During Mammalian Brain Development. <i>Genetics</i> , 2019, 211, 1239-1254.	1.2	3
6	Three Dimensional Organization of Genome Might Have Guided the Dynamics of Gene Order Evolution in Eukaryotes. <i>Genome Biology and Evolution</i> , 2016, 8, 946-954.	1.1	9
7	Spatially coordinated replication and minimization of expression noise constrain three-dimensional organization of yeast genome. <i>DNA Research</i> , 2016, 23, 155-169.	1.5	4
8	High Resolution Mapping of Enhancer-Promoter Interactions. <i>PLoS ONE</i> , 2015, 10, e0122420.	1.1	3
9	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. <i>Molecular BioSystems</i> , 2014, 10, 1469.	2.9	4
10	DNase Iâ€“hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013, 45, 852-859.	9.4	112
11	Did the modulation of expression noise shape the evolution of three dimensional genome organizations in eukaryotes?. <i>Nucleus</i> , 2012, 3, 286-289.	0.6	3
12	Disordered Proteins and Network Disorder in Network Descriptions of Protein Structure, Dynamics and Function: Hypotheses and a Comprehensive Review. <i>Current Protein and Peptide Science</i> , 2012, 13, 19-33.	0.7	49
13	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. <i>Cell Reports</i> , 2012, 2, 1207-1219.	2.9	102
14	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
15	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. <i>Cell</i> , 2012, 148, 84-98.	13.5	1,096
16	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011, 112, 2218-2221.	1.2	18
17	Female-biased expression of long non-coding RNAs in domains that escape X-inactivation in mouse. <i>BMC Genomics</i> , 2010, 11, 614.	1.2	77
18	Systems properties of proteins encoded by imprinted genes. <i>Epigenetics</i> , 2010, 5, 627-636.	1.3	26

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19	Nonallelic transvection of multiple imprinted loci is organized by the <i>H19</i> imprinting control region during germline development. <i>Genes and Development</i> , 2009, 23, 2598-2603.	2.7	87
20	Intrinsic disorder explains diverse nuclear roles of chromatin remodeling proteins. <i>Journal of Molecular Recognition</i> , 2009, 22, 1-8.	1.1	42
21	<i>Spirulina</i> nitrate-assimilating enzymes (NR, NiR, GS) have higher specific activities and are more stable than those of rice. <i>Physiology and Molecular Biology of Plants</i> , 2008, 14, 179-182.	1.4	12
22	GASCO: genetic algorithm simulation for codon optimization. <i>In Silico Biology</i> , 2008, 8, 187-92.	0.4	18
23	A whole genome analysis of 5â€² regulatory regions of human genes for putative cis-acting modulators of nucleosome positioning. <i>Gene</i> , 2007, 391, 242-251.	1.0	14
24	Dynamic Î±-helices: Conformations that do not conform. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 109-122.	1.5	21
25	Structural assessment of glycol mutations in invariantly conserved motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 617-632.	1.5	1
26	Conformational flexibility may explain multiple cellular roles of PEST motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 727-732.	1.5	17
27	Circular chromosome conformation capture (4C) uncovers extensive networks of epigenetically regulated intra- and interchromosomal interactions. <i>Nature Genetics</i> , 2006, 38, 1341-1347.	9.4	857
28	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 309-315.	1.5	86