

Kuljeet Singh Sandhu

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1260428/kuljeet-singh-sandhu-publications-by-citations.pdf>

Version: 2024-04-19

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28

papers

13,741

citations

15

h-index

32

g-index

32

ext. papers

16,766

ext. citations

10.4

avg, IF

8.05

L-index

#	Paper	IF	Citations
28	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
27	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
26	Circular chromosome conformation capture (4C) uncovers extensive networks of epigenetically regulated intra- and interchromosomal interactions. <i>Nature Genetics</i> , 2006 , 38, 1341-7	36.3	718
25	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. <i>Nature Genetics</i> , 2013 , 45, 852-9	36.3	94
24	Large-scale functional organization of long-range chromatin interaction networks. <i>Cell Reports</i> , 2012 , 2, 1207-19	10.6	84
23	Nonallelic transvection of multiple imprinted loci is organized by the H19 imprinting control region during germline development. <i>Genes and Development</i> , 2009 , 23, 2598-603	12.6	81
22	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 309-15	4.2	79
21	Female-biased expression of long non-coding RNAs in domains that escape X-inactivation in mouse. <i>BMC Genomics</i> , 2010 , 11, 614	4.5	70
20	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	2.8	44
19	Intrinsic disorder explains diverse nuclear roles of chromatin remodeling proteins. <i>Journal of Molecular Recognition</i> , 2009 , 22, 1-8	2.6	38
18	Systems properties of proteins encoded by imprinted genes. <i>Epigenetics</i> , 2010 , 5, 627-36	5.7	20
17	GASCO: genetic algorithm simulation for codon optimization. <i>In Silico Biology</i> , 2008 , 8, 187-92	2	17
16	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 2218-21	4.7	15
15	Dynamic alpha-helices: conformations that do not conform. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 68, 109-22	4.2	15
14	Conformational flexibility may explain multiple cellular roles of PEST motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 63, 727-32	4.2	14
13	A whole genome analysis of 5bregulatory regions of human genes for putative cis-acting modulators of nucleosome positioning. <i>Gene</i> , 2007 , 391, 242-51	3.8	10
12	Spirulina 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, 179-82	2.8	9

11	Three Dimensional Organization of Genome Might Have Guided the Dynamics of Gene Order Evolution in Eukaryotes. <i>Genome Biology and Evolution</i> , 2016 , 8, 946-54	3.9	7
10	Biased visibility in Hi-C datasets marks dynamically regulated condensed and decondensed chromatin states genome-wide. <i>BMC Genomics</i> , 2020 , 21, 175	4.5	6
9	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. <i>Molecular BioSystems</i> , 2014 , 10, 1469-80		3
8	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	4	2
7	Spatially coordinated replication and minimization of expression noise constrain three-dimensional organization of yeast genome. <i>DNA Research</i> , 2016 , 23, 155-69	4.5	2
6	High resolution mapping of enhancer-promoter interactions. <i>PLoS ONE</i> , 2015 , 10, e0122420	3.7	2
5	Did the modulation of expression noise shape the evolution of three dimensional genome organizations in eukaryotes?. <i>Nucleus</i> , 2012 , 3, 286-9	3.9	2
4	CTCF-Mediated Genome Architecture Regulates the Dosage of Mitotically Stable Mono-allelic Expression of Autosomal Genes. <i>Cell Reports</i> , 2020 , 33, 108302	10.6	0
3	Convergent evolution of a genomic rearrangement may explain cancer resistance in hystrico- and sciuromorpha rodents. <i>Npj Aging and Mechanisms of Disease</i> , 2021 , 7, 20	5.5	0
2	Does genome surveillance explain the global discrepancy between binding and effect of chromatin factors?. <i>FEBS Letters</i> , 2020 , 594, 1339-1353	3.8	
1	Structural assessment of glycyI mutations in invariantly conserved motifs. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 617-32	4.2	