Kuljeet Singh Sandhu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1260428/publications.pdf Version: 2024-02-01

		567281	552781
28	18,195	15	26
papers	citations	h-index	g-index
32	32	32	36608
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	28.9	1,096
3	Circular chromosome conformation capture (4C) uncovers extensive networks of epigenetically regulated intra- and interchromosomal interactions. Nature Genetics, 2006, 38, 1341-1347.	21.4	857
4	DNase l–hypersensitive exons colocalize with promoters and distal regulatory elements. Nature Genetics, 2013, 45, 852-859.	21.4	112
5	Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. Cell Reports, 2012, 2, 1207-1219.	6.4	102
6	Nonallelic transvection of multiple imprinted loci is organized by the <i>H19</i> imprinting control region during germline development. Genes and Development, 2009, 23, 2598-2603.	5.9	87
7	Intrinsic unstructuredness and abundance of PEST motifs in eukaryotic proteomes. Proteins: Structure, Function and Bioinformatics, 2005, 62, 309-315.	2.6	86
8	Female-biased expression of long non-coding RNAs in domains that escape X-inactivation in mouse. BMC Genomics, 2010, 11, 614.	2.8	77
9	Disordered Proteins and Network Disorder in Network Descriptions of Protein Structure, Dynamics and Function: Hypotheses and a Comprehensive Review. Current Protein and Peptide Science, 2012, 13, 19-33.	1.4	49
10	Intrinsic disorder explains diverse nuclear roles of chromatin remodeling proteins. Journal of Molecular Recognition, 2009, 22, 1-8.	2.1	42
11	Systems properties of proteins encoded by imprinted genes. Epigenetics, 2010, 5, 627-636.	2.7	26
12	Dynamic α-helices: Conformations that do not conform. Proteins: Structure, Function and Bioinformatics, 2007, 68, 109-122.	2.6	21
13	Chromatin interaction networks and higher order architectures of eukaryotic genomes. Journal of Cellular Biochemistry, 2011, 112, 2218-2221.	2.6	18
14	GASCO: genetic algorithm simulation for codon optimization. In Silico Biology, 2008, 8, 187-92.	0.9	18
15	Conformational flexibility may explain multiple cellular roles of PEST motifs. Proteins: Structure, Function and Bioinformatics, 2006, 63, 727-732.	2.6	17
16	A whole genome analysis of 5′ regulatory regions of human genes for putative cis-acting modulators of nucleosome positioning. Gene, 2007, 391, 242-251.	2.2	14
17	Spirulina nitrate-assimilating enzymes (NR, NiR, GS) have higher specific activities and are more stable than those of rice. Physiology and Molecular Biology of Plants, 2008, 14, 179-182.	3.1	12
18	Biased visibility in Hi-C datasets marks dynamically regulated condensed and decondensed chromatin states genome-wide. BMC Genomics, 2020, 21, 175.	2.8	11

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19	Three Dimensional Organization of Genome Might Have Guided the Dynamics of Gene Order Evolution in Eukaryotes. Genome Biology and Evolution, 2016, 8, 946-954.	2.5	9
20	Evolutionarily conserved and conformationally constrained short peptides might serve as DNA recognition elements in intrinsically disordered regions. Molecular BioSystems, 2014, 10, 1469.	2.9	4
21	Spatially coordinated replication and minimization of expression noise constrain three-dimensional organization of yeast genome. DNA Research, 2016, 23, 155-169.	3.4	4
22	CTCF-Mediated Genome Architecture Regulates the Dosage of Mitotically Stable Mono-allelic Expression of Autosomal Genes. Cell Reports, 2020, 33, 108302.	6.4	4
23	Did the modulation of expression noise shape the evolution of three dimensional genome organizations in eukaryotes?. Nucleus, 2012, 3, 286-289.	2.2	3
24	High Resolution Mapping of Enhancer-Promoter Interactions. PLoS ONE, 2015, 10, e0122420.	2.5	3
25	Evolutionary Loss of Genomic Proximity to Conserved Noncoding Elements Impacted the Gene Expression Dynamics During Mammalian Brain Development. Genetics, 2019, 211, 1239-1254.	2.9	3
26	Convergent evolution of a genomic rearrangement may explain cancer resistance in hystrico- and sciuromorpha rodents. Npj Aging and Mechanisms of Disease, 2021, 7, 20.	4.5	2
27	Structural assessment of glycyl mutations in invariantly conserved motifs. Proteins: Structure, Function and Bioinformatics, 2007, 69, 617-632.	2.6	1
28	Does genome surveillance explain the global discrepancy between binding and effect of chromatin factors?. FEBS Letters, 2020, 594, 1339-1353.	2.8	0