Dhirendra Kumar

List of Publications by Year
in descending order

27 papers	1,254 citations	471509 17 h-index	552781 26 g-index
30 all docs	30 docs citations	30 times ranked	2326 citing authors

#	Article	IF	Citations
1	False discovery rate: the Achilles' heel of proteogenomics. Briefings in Bioinformatics, 2022, 23, .	6.5	11
2	Decoding the function of bivalent chromatin in development and cancer. Genome Research, 2021, 31, 2170-2184.	5.5	48
3	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. Nature Communications, 2019, 10, 3072.	12.8	53
4	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell Systems, 2019, 8, 427-445.e10.	6.2	111
5	GLIS3 Transcriptionally Activates WNT Genes to Promote Differentiation of Human Embryonic Stem Cells into Posterior Neural Progenitors. Stem Cells, 2019, 37, 202-215.	3.2	21
6	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1549, 17-29.	0.9	25
7	Intragenic Enhancers Attenuate Host Gene Expression. Molecular Cell, 2017, 68, 104-117.e6.	9.7	85
8	GLIS3 is indispensable for TSH/TSHR-dependent thyroid hormone biosynthesis and follicular cell proliferation. Journal of Clinical Investigation, 2017, 127, 4326-4337.	8.2	47
9	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. Proteomics, 2016, 16, 226-240.	2.2	12
10	Integrating transcriptome and proteome profiling: Strategies and applications. Proteomics, 2016, 16, 2533-2544.	2.2	147
11	Proteogenomic Tools and Approaches to Explore Protein Coding Landscapes of Eukaryotic Genomes. Advances in Experimental Medicine and Biology, 2016, 926, 1-10.	1.6	10
12	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. Molecular and Cellular Proteomics, 2016, 15, 329-339.	3.8	35
13	Expression profiling of lymph nodes in tuberculosis patients reveal inflammatory milieu at site of infection. Scientific Reports, 2015, 5, 15214.	3.3	43
14	Polyketide Quinones Are Alternate Intermediate Electron Carriers during Mycobacterial Respiration in Oxygen-Deficient Niches. Molecular Cell, 2015, 60, 637-650.	9.7	53
15	Transcriptome and venom proteome of the box jellyfish Chironex fleckeri. BMC Genomics, 2015, 16, 407.	2.8	103
16	Probing the Missing Human Proteome: A Computational Perspective. Journal of Proteome Research, 2015, 14, 4949-4958.	3.7	6
17	Gene-Rich Large Deletions Are Overrepresented in POAG Patients of Indian and Caucasian Origins. , 2014, 55, 3258.		9
18	Extensive Copy Number Variations in Admixed Indian Population of African Ancestry: Potential Involvement in Adaptation. Genome Biology and Evolution, 2014, 6, 3171-3181.	2.5	23

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19	Discovery of rare protein‚Äîcoding genes in model methylotroph <i>Methylobacterium extorquens</i> AM1. Proteomics, 2014, 14, 2790-2794.	2.2	17
20	ProteoStats‚Äî"a library for estimating false discovery rates in proteomics pipelines. Bioinformatics, 2013, 29, 2799-2800.	4.1	18
21	Proteogenomic Analysis of Bradyrhizobium japonicum USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. Molecular and Cellular Proteomics, 2013, 12, 3388-3397.	3.8	39
22	Integration Host Factor of Mycobacterium tuberculosis, mIHF, Compacts DNA by a Bending Mechanism. PLoS ONE, 2013, 8, e69985.	2.5	21
23	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. Human Genetics, 2012, 131, 131-143.	3.8	17
24	Learning from Decoys to Improve the Sensitivity and Specificity of Proteomics Database Search Results. PLoS ONE, 2012, 7, e50651.	2.5	17
25	MassWiz: A Novel Scoring Algorithm with Target-Decoy Based Analysis Pipeline for Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 2154-2160.	3.7	46
26	Proteogenomic Analysis of Mycobacterium tuberculosis By High Resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.011445.	3.8	145
27	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. PLoS ONE, 2011, 6, e24442.	2.5	87