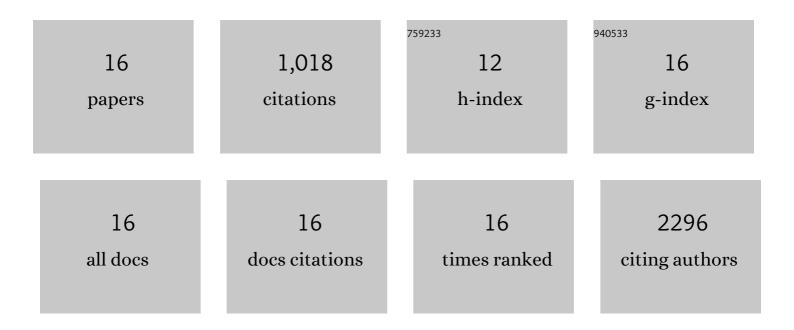
Deepak K Jha

List of Publications by Year in descending order

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Πεεσλκ Κ Ιμλ

#	Article	IF	CITATIONS
1	Haematopoietic stem and progenitor cells from human pluripotent stem cells. Nature, 2017, 545, 432-438.	27.8	395
2	An RNA polymerase II-coupled function for histone H3K36 methylation in checkpoint activation and DSB repair. Nature Communications, 2014, 5, 3965.	12.8	104
3	A high-resolution transcriptome map of cell cycle reveals novel connections between periodic genes and cancer. Cell Research, 2016, 26, 946-962.	12.0	84
4	Reconstruction of complex single-cell trajectories using CellRouter. Nature Communications, 2018, 9, 892.	12.8	78
5	Regulation of embryonic haematopoietic multipotency by EZH1. Nature, 2018, 553, 506-510.	27.8	70
6	Association of Taf14 with acetylated histone H3 directs gene transcription and the DNA damage response. Genes and Development, 2015, 29, 1795-1800.	5.9	65
7	Structure/Function Analysis of Recurrent Mutations in SETD2 Protein Reveals a Critical and Conserved Role for a SET Domain Residue in Maintaining Protein Stability and Histone H3 Lys-36 Trimethylation. Journal of Biological Chemistry, 2016, 291, 21283-21295.	3.4	64
8	Histone H3K36 methylation regulates pre-mRNA splicing in <i>Saccharomyces cerevisiae</i> . RNA Biology, 2016, 13, 412-426.	3.1	46
9	The developmental stage of the hematopoietic niche regulates lineage in <i>MLL-</i> rearranged leukemia. Journal of Experimental Medicine, 2019, 216, 527-538.	8.5	27
10	SET-ting the stage for DNA repair. Nature Structural and Molecular Biology, 2014, 21, 655-657.	8.2	25
11	Set2 methyltransferase facilitates cell cycle progression by maintaining transcriptional fidelity. Nucleic Acids Research, 2018, 46, 1331-1344.	14.5	23
12	Redundant Functions for Nap1 and Chz1 in H2A.Z Deposition. Scientific Reports, 2017, 7, 10791.	3.3	13
13	LIN28B alters ribosomal dynamics to promote metastasis in MYCN-driven malignancy. Journal of Clinical Investigation, 2021, 131, .	8.2	12
14	Transcriptome Dynamics of Hematopoietic Stem Cell Formation Revealed Using a Combinatorial Runx1 and Ly6a Reporter System. Stem Cell Reports, 2020, 14, 956-971.	4.8	8
15	Hematopoietic Stem and Progenitor Cells from Human Pluripotent Stem Cells Via Transcription Factor Conversion of Hemogenic Endothelium. Blood, 2016, 128, 371-371.	1.4	3
16	Novel Epigenetic Vulnerabilities for Diffuse Large B-Cell Lymphoma. Blood, 2018, 132, 2600-2600.	1.4	1