

# Sachin Pundhir

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1939318/publications.pdf>

Version: 2024-02-01

19  
papers

602  
citations

933447

10  
h-index

794594

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

1647  
citing authors

#	ARTICLE	IF	CITATIONS
1	H3K9 dimethylation safeguards cancer cells against activation of the interferon pathway. <i>Science Advances</i> , 2022, 8, eabf8627.	10.3	10
2	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. <i>Cell Reports</i> , 2022, 39, 110793.	6.4	3
3	Transcription factor-driven coordination of cell cycle exit and lineage-specification in vivo during granulocytic differentiation. <i>Nature Communications</i> , 2022, 13, .	12.8	16
4	The ASXL1-G643W variant accelerates the development of CEBPA mutant acute myeloid leukemia. <i>Haematologica</i> , 2021, 106, 1000-1007.	3.5	9
5	Ancestrally Duplicated Conserved Noncoding Element Suggests Dual Regulatory Roles of HOTAIR in cis and trans. <i>IScience</i> , 2020, 23, 101008.	4.1	9
6	Mutant CEBPA directly drives the expression of the targetable tumor-promoting factor CD73 in AML. <i>Science Advances</i> , 2019, 5, eaaw4304.	10.3	28
7	The splicing factor RBM25 controls MYC activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 172.	12.8	42
8	Epigenetic and Transcriptomic Characterization of Pure Adipocyte Fractions From Obese Pigs Identifies Candidate Pathways Controlling Metabolism. <i>Frontiers in Genetics</i> , 2019, 10, 1268.	2.3	9
9	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in <i>Cebpa</i> null Progenitors. <i>Cell Reports</i> , 2018, 23, 2744-2757.	6.4	45
10	Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. <i>Cell Reports</i> , 2018, 24, 766-780.	6.4	40
11	Peak-valley-peak pattern of histone modifications delineates active regulatory elements and their directionality. <i>Nucleic Acids Research</i> , 2016, 44, 4037-4051.	14.5	26
12	BloodSpot: a database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis. <i>Nucleic Acids Research</i> , 2016, 44, D917-D924.	14.5	242
13	Differential and coherent processing patterns from small RNAs. <i>Scientific Reports</i> , 2015, 5, 12062.	3.3	22
14	Emerging applications of read profiles towards the functional annotation of the genome. <i>Frontiers in Genetics</i> , 2015, 6, 188.	2.3	9
15	Spatially conserved regulatory elements identified within human and mouse <i>Cd247</i> gene using high-throughput sequencing data from the ENCODE project. <i>Gene</i> , 2014, 545, 80-87.	2.2	6
16	MicroRNA discovery by similarity search to a database of RNA-seq profiles. <i>Frontiers in Genetics</i> , 2013, 4, 133.	2.3	8
17	deepBlockAlign: a tool for aligning RNA-seq profiles of read block patterns. <i>Bioinformatics</i> , 2012, 28, 17-24.	4.1	19
18	SSPred: A prediction server based on SVM for the identification and classification of proteins involved in bacterial secretion systems. <i>Bioinformatics</i> , 2011, 6, 380-382.	0.5	18

#	ARTICLE	IF	CITATIONS
19	PredictBias: a server for the identification of genomic and pathogenicity islands in prokaryotes. In <i>Silico Biology</i> , 2008, 8, 223-34.	0.9	40