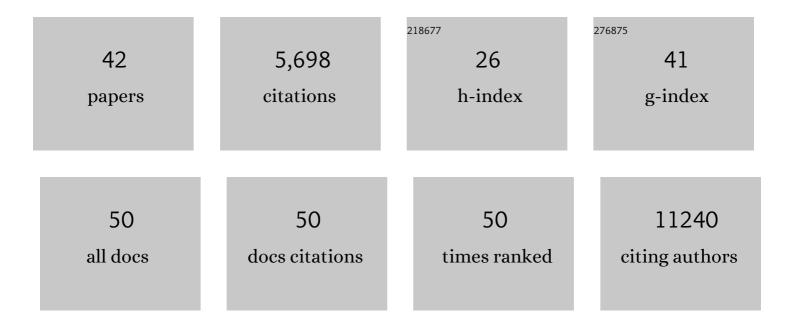
## Kunal Rai

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8292445/publications.pdf Version: 2024-02-01



Κιινία Ραι

#	Article	IF	CITATIONS
1	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
2	DNA Demethylation in Zebrafish Involves the Coupling of a Deaminase, a Glycosylase, and Gadd45. Cell, 2008, 135, 1201-1212.	28.9	594
3	A Two-Step Model for Colon Adenoma Initiation and Progression Caused by APC Loss. Cell, 2009, 137, 623-634.	28.9	262
4	Ketone Body Signaling Mediates Intestinal Stem Cell Homeostasis and Adaptation to Diet. Cell, 2019, 178, 1115-1131.e15.	28.9	231
5	Dnmt2 functions in the cytoplasm to promote liver, brain, and retina development in zebrafish. Genes and Development, 2007, 21, 261-266.	5.9	179
6	Mutations in the SWI/SNF complex induce a targetable dependence on oxidative phosphorylation in lung cancer. Nature Medicine, 2018, 24, 1047-1057.	30.7	175
7	Zebra Fish Dnmt1 and Suv39h1 Regulate Organ-Specific Terminal Differentiation during Development. Molecular and Cellular Biology, 2006, 26, 7077-7085.	2.3	143
8	Accumulation of long-chain fatty acids in the tumor microenvironment drives dysfunction in in intrapancreatic CD8+ T cells. Journal of Experimental Medicine, 2020, 217, .	8.5	142
9	KMT2D Deficiency Impairs Super-Enhancers to Confer a Glycolytic Vulnerability in Lung Cancer. Cancer Cell, 2020, 37, 599-617.e7.	16.8	137
10	Identification of EMT signaling cross-talk and gene regulatory networks by single-cell RNA sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	134
11	Dnmt3 and C9a Cooperate for Tissue-specific Development in Zebrafish. Journal of Biological Chemistry, 2010, 285, 4110-4121.	3.4	114
12	microRNA Regulatory Network Inference Identifies miR-34a as a Novel Regulator of TGF-Î <sup>2</sup> Signaling in Glioblastoma. Cancer Discovery, 2012, 2, 736-749.	9.4	99
13	DNA Demethylase Activity Maintains Intestinal Cells in an Undifferentiated State Following Loss of APC. Cell, 2010, 142, 930-942.	28.9	96
14	Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. Cell Reports, 2017, 19, 875-889.	6.4	78
15	PRKCI promotes immune suppression in ovarian cancer. Genes and Development, 2017, 31, 1109-1121.	5.9	75
16	TRIM28 and Interacting KRAB-ZNFs Control Self-Renewal of Human Pluripotent Stem Cells through Epigenetic Repression of Pro-differentiation Genes. Stem Cell Reports, 2017, 9, 2065-2080.	4.8	62
17	Truncating PREX2 mutations activate its GEF activity and alter gene expression regulation in NRAS-mutant melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1296-305.	7.1	59
18	Dual Roles of RNF2 in Melanoma Progression. Cancer Discovery, 2015, 5, 1314-1327.	9.4	57

Kunal Rai

#	Article	IF	CITATIONS
19	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. Nature Communications, 2021, 12, 6071.	12.8	44
20	Telomere dysfunction activates YAP1 to drive tissue inflammation. Nature Communications, 2020, 11, 4766.	12.8	42
21	Dual roles for adenomatous polyposis coli in regulating retinoic acid biosynthesis and Wnt during ocular development. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13409-13414.	7.1	39
22	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. Nature Communications, 2018, 9, 2496.	12.8	39
23	Enhancer Reprogramming Confers Dependence on Glycolysis and IGF Signaling in KMT2D Mutant Melanoma. Cell Reports, 2020, 33, 108293.	6.4	39
24	Atypical plant homeodomain of UBR7 functions as an H2BK120Ub ligase and breast tumor suppressor. Nature Communications, 2019, 10, 1398.	12.8	35
25	Positive Regulation of Transcription by Human ZMYND8 through Its Association with P-TEFb Complex. Cell Reports, 2018, 24, 2141-2154.e6.	6.4	30
26	Increased H3K9me3 drives dedifferentiated phenotype via KLF6 repression in liposarcoma. Journal of Clinical Investigation, 2015, 125, 2965-2978.	8.2	29
27	Chromatin state dynamics confers specific therapeutic strategies in enhancer subtypes of colorectal cancer. Gut, 2022, 71, 938-949.	12.1	25
28	An Integrated Platform for Genome-wide Mapping of Chromatin States Using High-throughput ChIP-sequencing in Tumor Tissues. Journal of Visualized Experiments, 2018, , .	0.3	24
29	Reprogramming of H3K9bhb at regulatory elements is a key feature of fasting in the small intestine. Cell Reports, 2021, 37, 110044.	6.4	22
30	Reprogramming of bivalent chromatin states in NRAS mutant melanoma suggests PRC2 inhibition as a therapeutic strategy. Cell Reports, 2021, 36, 109410.	6.4	17
31	Machine Learning in Epigenomics: Insights into Cancer Biology and Medicine. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188588.	7.4	14
32	The androgen receptor is a therapeutic target in desmoplastic small round cell sarcoma. Nature Communications, 2022, 13, .	12.8	14
33	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. Acta Neuropathologica, 2021, 142, 565-590.	7.7	12
34	Immune landscape of a genetically engineered murine model of glioma compared with human glioma. JCI Insight, 2022, 7, .	5.0	10
35	Multi-modal molecular programs regulate melanoma cell state. Nature Communications, 2022, 13, .	12.8	9
36	Experimental models of undifferentiated pleomorphic sarcoma and malignant peripheral nerve sheath tumor. Laboratory Investigation, 2022, 102, 658-666.	3.7	7

Kunal Rai

#	Article	IF	CITATIONS
37	Loss of histone acetylation and H3K4 methylation promotes melanocytic malignant transformation. Molecular and Cellular Oncology, 2018, 5, e1359229.	0.7	5
38	Personalized Cancer Therapy: YES1 Is the New Kid on the Block. Cancer Research, 2019, 79, 5702-5703.	0.9	5
39	Methylation-eQTL analysis in cancer research. Bioinformatics, 2021, 37, 4014-4022.	4.1	5
40	H3K9me3-mediated repression of KLF6: Discovering a novel tumor suppressor in liposarcoma using a systematic epigenomic approach. Molecular and Cellular Oncology, 2016, 3, e1093691.	0.7	2
41	Computational Analysis of Epigenetic Modifications in Melanoma. , 2019, , 327-342.		1
42	Single-Cell Characterization of Acute Myeloid Leukemia (AML) and Its Microenvironment Identifies Signatures of Resistance to PD-1 Blockade Based Therapy. Blood, 2020, 136, 29-31.	1.4	0