

# Jung Kim

## List of Publications by Year in descending order

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36  
papers

2,016  
citations

394421

19  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

3966  
citing authors

#	ARTICLE	IF	CITATIONS
1	LncRNA HOTAIR enhances ER signaling and confers tamoxifen resistance in breast cancer. <i>Oncogene</i> , 2016, 35, 2746-2755.	5.9	359
2	LncRNA HOTAIR Enhances the Androgen-Receptor-Mediated Transcriptional Program and Drives Castration-Resistant Prostate Cancer. <i>Cell Reports</i> , 2015, 13, 209-221.	6.4	291
3	Polycomb- and Methylation-Independent Roles of EZH2 as a Transcription Activator. <i>Cell Reports</i> , 2018, 25, 2808-2820.e4.	6.4	201
4	Cooperativity and equilibrium with FOXA1 define the androgen receptor transcriptional program. <i>Nature Communications</i> , 2014, 5, 3972.	12.8	147
5	FOXA1 inhibits prostate cancer neuroendocrine differentiation. <i>Oncogene</i> , 2017, 36, 4072-4080.	5.9	101
6	Activation of MAPK Signaling by CXCR7 Leads to Enzalutamide Resistance in Prostate Cancer. <i>Cancer Research</i> , 2019, 79, 2580-2592.	0.9	85
7	ERG Is a Critical Regulator of Wnt/LEF1 Signaling in Prostate Cancer. <i>Cancer Research</i> , 2013, 73, 6068-6079.	0.9	81
8	CD95/Fas Increases Stemness in Cancer Cells by Inducing a STAT1-Dependent Type I Interferon Response. <i>Cell Reports</i> , 2017, 18, 2373-2386.	6.4	81
9	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	21.4	81
10	The prevalence of <i>DICER1</i> pathogenic variation in population databases. <i>International Journal of Cancer</i> , 2017, 141, 2030-2036.	5.1	75
11	Variable population prevalence estimates of germline <i>TP53</i> variants: A gnomAD-based analysis. <i>Human Mutation</i> , 2019, 40, 97-105.	2.5	66
12	Androgen receptor genomic regulation. <i>Translational Andrology and Urology</i> , 2013, 2, 157-177.	1.4	63
13	FOXA1 acts upstream of GATA2 and AR in hormonal regulation of gene expression. <i>Oncogene</i> , 2016, 35, 4335-4344.	5.9	55
14	FOXA1 potentiates lineage-specific enhancer activation through modulating TET1 expression and function. <i>Nucleic Acids Research</i> , 2016, 44, 8153-8164.	14.5	53
15	TMPRSS2-ERG gene fusions induce prostate tumorigenesis by modulating microRNA miR-200c. <i>Oncogene</i> , 2014, 33, 5183-5192.	5.9	43
16	Posttranslational regulation of FOXA1 by Polycomb and BUB3/USP7 deubiquitin complex in prostate cancer. <i>Science Advances</i> , 2021, 7, .	10.3	37
17	Pathogenic Germline Variants in Cancer Susceptibility Genes in Children and Young Adults With Rhabdomyosarcoma. <i>JCO Precision Oncology</i> , 2021, 5, 75-87.	3.0	27
18	A Genome-First Approach to Characterize <i>DICER1</i> Pathogenic Variant Prevalence, Penetrance, and Phenotype. <i>JAMA Network Open</i> , 2021, 4, e210112.	5.9	25

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19	The prevalence of germline <i>DICER1</i> pathogenic variation in cancer populations. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e555.	1.2	24
20	Polycomb-Mediated Disruption of an Androgen Receptor Feedback Loop Drives Castration-Resistant Prostate Cancer. <i>Cancer Research</i> , 2017, 77, 412-422.	0.9	23
21	Altered chromatin recruitment by FOXA1 mutations promotes androgen independence and prostate cancer progression. <i>Cell Research</i> , 2019, 29, 773-775.	12.0	20
22	Prevalence of pathogenic/likely pathogenic variants in the 24 cancer genes of the ACMG Secondary Findings v2.0 list in a large cancer cohort and ethnicity-matched controls. <i>Genome Medicine</i> , 2018, 10, 99.	8.2	15
23	Interrogating genomic and epigenomic data to understand prostate cancer. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2012, 1825, 186-196.	7.4	14
24	Frequency of Pathogenic Germline Variants in Cancer-Susceptibility Genes in the Childhood Cancer Survivor Study. <i>JNCI Cancer Spectrum</i> , 2021, 5, p1ab007.	2.9	11
25	Population Frequency of Fanconi Pathway Gene Variants and Their Association with Survival After Hematopoietic Cell Transplantation for Severe Aplastic Anemia. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, 817-822.	2.0	6
26	A Genome-First Approach to Estimate Prevalence of Germline Pathogenic Variants and Risk of Pancreatic Cancer in Select Cancer Susceptibility Genes. <i>Cancers</i> , 2022, 14, 3257.	3.7	6
27	Endemic Burkitt Lymphoma in second-degree relatives in Northern Uganda: in-depth genome-wide analysis suggests clues about genetic susceptibility. <i>Leukemia</i> , 2021, 35, 1209-1213.	7.2	5
28	Unusual phenotypes in patients with a pathogenic germline variant in <i>DICER1</i> . <i>Familial Cancer</i> , 2021, , 1.	1.9	5
29	Rare germline deleterious variants increase susceptibility for lung cancer. <i>Human Molecular Genetics</i> , 2022, 31, 3558-3565.	2.9	5
30	Influence of oncogenic transcription factors on chromatin conformation and implications in prostate cancer. <i>The Application of Clinical Genetics</i> , 2014, 7, 81.	3.0	3
31	In search of genetic factors predisposing to familial hairy cell leukemia (HCL): exome-sequencing of four multiplex HCL pedigrees. <i>Leukemia</i> , 2020, 34, 1934-1938.	7.2	3
32	Identification of Genetic Risk Factors for Familial Urinary Bladder Cancer: An Exome Sequencing Study. <i>JCO Precision Oncology</i> , 2021, 5, 1830-1839.	3.0	3
33	Response to: Concern regarding classification of germline TP53 variants as likely pathogenic. <i>Human Mutation</i> , 2019, 40, 832-833.	2.5	1
34	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. <i>Familial Cancer</i> , 2022, 21, 347-355.	1.9	1
35	Lack of pathogenic germline <i>DICER1</i> variants in males with testicular germ-cell tumors. <i>Cancer Genetics</i> , 2020, 248-249, 49-56.	0.4	0
36	Whole Exome Sequencing in Severe Aplastic Anemia Identifies Unrecognized Inherited Subset with Inferior Survival after Hematopoietic Cell Transplant. <i>Blood</i> , 2021, 138, 605-605.	1.4	0