

# Jung Kyoon Choi

## List of Publications by Year in descending order

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Version: 2024-02-01

39  
papers

1,403  
citations

516710

16  
h-index

377865

34  
g-index

40  
all docs

40  
docs citations

40  
times ranked

2969  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. <i>Nature Genetics</i> , 2020, 52, 594-603.	21.4	380
2	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019, 10, 4278.	12.8	263
3	Contrasting chromatin organization of CpG islands and exons in the human genome. <i>Genome Biology</i> , 2010, 11, R70.	9.6	98
4	SET7/9 Methylation of the Pluripotency Factor LIN28A Is a Nucleolar Localization Mechanism that Blocks let-7 Biogenesis in Human ESCs. <i>Cell Stem Cell</i> , 2014, 15, 735-749.	11.1	65
5	Matrix stiffness epigenetically regulates the oncogenic activation of the Yes-associated protein in gastric cancer. <i>Nature Biomedical Engineering</i> , 2021, 5, 114-123.	22.5	65
6	The mutational landscape of ocular marginal zone lymphoma identifies frequent alterations in <i>TNFAIP3</i> followed by mutations in <i>TBL1XR1</i> and <i>CREBBP</i> . <i>Oncotarget</i> , 2017, 8, 17038-17049.	1.8	55
7	Genome-wide methylation patterns predict clinical benefit of immunotherapy in lung cancer. <i>Clinical Epigenetics</i> , 2020, 12, 119.	4.1	53
8	Immune signatures correlate with L1 retrotransposition in gastrointestinal cancers. <i>Genome Research</i> , 2018, 28, 1136-1146.	5.5	44
9	Histone variant H3F3A promotes lung cancer cell migration through intronic regulation. <i>Nature Communications</i> , 2016, 7, 12914.	12.8	43
10	Predicting clinical benefit of immunotherapy by antigenic or functional mutations affecting tumour immunogenicity. <i>Nature Communications</i> , 2020, 11, 951.	12.8	34
11	L1 retrotransposons exploit RNA m6A modification as an evolutionary driving force. <i>Nature Communications</i> , 2021, 12, 880.	12.8	32
12	Chromatin structure-based prediction of recurrent noncoding mutations in cancer. <i>Nature Genetics</i> , 2016, 48, 1321-1326.	21.4	29
13	Serine metabolism in the brain regulates starvation-induced sleep suppression in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7129-7134.	7.1	29
14	Comprehensive characterisation of intronic mis-splicing mutations in human cancers. <i>Oncogene</i> , 2021, 40, 1347-1361.	5.9	28
15	A long-range interactive DNA methylation marker panel for the promoters of HOXA9 and HOXA10 predicts survival in breast cancer patients. <i>Clinical Epigenetics</i> , 2017, 9, 73.	4.1	25
16	Frequent hypermethylation of orphan CpG islands with enhancer activity in cancer. <i>BMC Medical Genomics</i> , 2016, 9, 38.	1.5	23
17	Novel cancer gene variants and gene fusions of triple-negative breast cancers (TNBCs) reveal their molecular diversity conserved in the patient-derived xenograft (PDX) model. <i>Cancer Letters</i> , 2018, 428, 127-138.	7.2	19
18	Functional fine-mapping of noncoding risk variants in amyotrophic lateral sclerosis utilizing convolutional neural network. <i>Scientific Reports</i> , 2020, 10, 12872.	3.3	11

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19	Predicting the recurrence of noncoding regulatory mutations in cancer. BMC Bioinformatics, 2016, 17, 492.	2.6	10
20	Non-coding de novo mutations in chromatin interactions are implicated in autism spectrum disorder. Molecular Psychiatry, 2022, 27, 4680-4694.	7.9	9
21	Global mapping of the regulatory interactions of histone residues. FEBS Letters, 2015, 589, 4061-4070.	2.8	8
22	Selected heterozygosity at cis-regulatory sequences increases the expression homogeneity of a cell population in humans. Genome Biology, 2016, 17, 164.	8.8	7
23	Functional annotation of noncoding causal variants in autoimmune diseases. Genomics, 2020, 112, 1208-1213.	2.9	7
24	Computational inference of cancer-specific vulnerabilities in clinical samples. Genome Biology, 2020, 21, 155.	8.8	7
25	Aberrant Transcript Usage Is Associated with Homologous Recombination Deficiency and Predicts Therapeutic Response. Cancer Research, 2022, 82, 142-154.	0.9	7
26	Global transcription network incorporating distal regulator binding reveals selective cooperation of cancer drivers and risk genes. Nucleic Acids Research, 2015, 43, 5716-5729.	14.5	6
27	Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. PLoS Genetics, 2018, 14, e1007311.	3.5	6
28	Convolutional neural network model to predict causal risk factors that share complex regulatory features. Nucleic Acids Research, 2019, 47, e146-e146.	14.5	6
29	LncRNA HSPA7 in human atherosclerotic plaques sponges miR-223 and promotes the proinflammatory vascular smooth muscle cell transition. Experimental and Molecular Medicine, 2021, 53, 1842-1849.	7.7	6
30	Network perturbation by recurrent regulatory variants in cancer. PLoS Computational Biology, 2017, 13, e1005449.	3.2	5
31	Intersection of genetics and epigenetics in monozygotic twin genomes. Methods, 2016, 102, 50-56.	3.8	4
32	Genetic variants beyond amyloid and tau associated with cognitive decline. Neurology, 2020, 95, e2366-e2377.	1.1	4
33	Understanding Epistatic Interactions between Genes Targeted by Non-coding Regulatory Elements in Complex Diseases. Genomics and Informatics, 2014, 12, 181.	0.8	4
34	Whole-Genome and Transcriptome Sequencing Identified NOTCH2 and HES1 as Potential Markers of Response to Imatinib in Desmoid Tumor (Aggressive Fibromatosis): A Phase II Trial Study. Cancer Research and Treatment, 2022, 54, 1240-1255.	3.0	4
35	The emerging genetic diversity of hereditary spastic paraplegia in Korean patients. Genomics, 2021, 113, 4136-4148.	2.9	3
36	Accelerated Evolution of the Regulatory Sequences of Brain Development in the Human Genome. Molecules and Cells, 2020, 43, 331-339.	2.6	3

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37	Genetic Architecture of Transcription and Chromatin Regulation. <i>Genomics and Informatics</i> , 2015, 13, 40.	0.8	1
38	Predictive long-range allele-specific mapping of regulatory variants and target transcripts. <i>PLoS ONE</i> , 2017, 12, e0175768.	2.5	0
39	Gene essentiality for tumour growth influences neoantigen-directed immunoediting. <i>Clinical and Translational Medicine</i> , 2022, 12, e714.	4.0	0