Jung Kyoon Choi

List of Publications by Year in descending order

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	Aberrant Transcript Usage Is Associated with Homologous Recombination Deficiency and Predicts Therapeutic Response. Cancer Research, 2022, 82, 142-154.	0.9	7
2	Gene essentiality for tumour growth influences neoantigenâ€directed immunoediting. Clinical and Translational Medicine, 2022, 12, e714.	4.0	0
3	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
4	Non-coding de novo mutations in chromatin interactions are implicated in autism spectrum disorder. Molecular Psychiatry, 2022, 27, 4680-4694.	7.9	9
5	Matrix stiffness epigenetically regulates the oncogenic activation of the Yes-associated protein in gastric cancer. Nature Biomedical Engineering, 2021, 5, 114-123.	22.5	65
6	Comprehensive characterisation of intronic mis-splicing mutations in human cancers. Oncogene, 2021, 40, 1347-1361.	5.9	28
7	L1 retrotransposons exploit RNA m6A modification as an evolutionary driving force. Nature Communications, 2021, 12, 880.	12.8	32
8	The emerging genetic diversity of hereditary spastic paraplegia in Korean patients. Genomics, 2021, 113, 4136-4148.	2.9	3
9	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
10	Functional annotation of noncoding causal variants in autoimmune diseases. Genomics, 2020, 112, 1208-1213.	2.9	7
11	Genome-wide methylation patterns predict clinical benefit of immunotherapy in lung cancer. Clinical Epigenetics, 2020, 12, 119.	4.1	53
12	Functional fine-mapping of noncoding risk variants in amyotrophic lateral sclerosis utilizing convolutional neural network. Scientific Reports, 2020, 10, 12872.	3.3	11
13	Genetic variants beyond amyloid and tau associated with cognitive decline. Neurology, 2020, 95, e2366-e2377.	1.1	4
14	Computational inference of cancer-specific vulnerabilities in clinical samples. Genome Biology, 2020, 21, 155.	8.8	7
15	Predicting clinical benefit of immunotherapy by antigenic or functional mutations affecting tumour immunogenicity. Nature Communications, 2020, 11, 951.	12.8	34
16	Lineage-dependent gene expression programs influence the immune landscape of colorectal cancer. Nature Genetics, 2020, 52, 594-603.	21.4	380
17	Accelerated Evolution of the Regulatory Sequences of Brain Development in the Human Genome. Molecules and Cells, 2020, 43, 331-339.	2.6	3
18	Convolutional neural network model to predict causal risk factors that share complex regulatory features. Nucleic Acids Research, 2019, 47, e146-e146.	14.5	6

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19	DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. Nature Communications, 2019, 10, 4278.	12.8	263
20	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. Cancer Letters, 2018, 428, 127-138.	7.2	19
21	Immune signatures correlate with L1 retrotransposition in gastrointestinal cancers. Genome Research, 2018, 28, 1136-1146.	5.5	44
22	Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. PLoS Genetics, 2018, 14, e1007311.	3.5	6
23	Serine metabolism in the brain regulates starvation-induced sleep suppression in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7129-7134.	7.1	29
24	The mutational landscape of ocular marginal zone lymphoma identifies frequent alterations in TNFAIP3 followed by mutations in TBL1XR1 and CREBBP. Oncotarget, 2017, 8, 17038-17049.	1.8	55
25	Network perturbation by recurrent regulatory variants in cancer. PLoS Computational Biology, 2017, 13, e1005449.	3.2	5
26	A long-range interactive DNA methylation marker panel for the promoters of HOXA9 and HOXA10 predicts survival in breast cancer patients. Clinical Epigenetics, 2017, 9, 73.	4.1	25
27	Predictive long-range allele-specific mapping of regulatory variants and target transcripts. PLoS ONE, 2017, 12, e0175768.	2.5	0
28	Selected heterozygosity at cis-regulatory sequences increases the expression homogeneity of a cell population in humans. Genome Biology, 2016, 17, 164.	8.8	7
29	Frequent hypermethylation of orphan CpG islands with enhancer activity in cancer. BMC Medical Genomics, 2016, 9, 38.	1.5	23
30	Chromatin structureâ€“based prediction of recurrent noncoding mutations in cancer. Nature Genetics, 2016, 48, 1321-1326.	21.4	29
31	Histone variant H3F3A promotes lung cancer cell migration through intronic regulation. Nature Communications, 2016, 7, 12914.	12.8	43
32	Predicting the recurrence of noncoding regulatory mutations in cancer. BMC Bioinformatics, 2016, 17, 492.	2.6	10
33	Intersection of genetics and epigenetics in monozygotic twin genomes. Methods, 2016, 102, 50-56.	3.8	4
34	Global mapping of the regulatory interactions of histone residues. FEBS Letters, 2015, 589, 4061-4070.	2.8	8
35	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
36	Genetic Architecture of Transcription and Chromatin Regulation. Genomics and Informatics, 2015, 13, 40.	0.8	1

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37	SET7/9 Methylation of the Pluripotency Factor LIN28A Is a Nucleolar Localization Mechanism that Blocks let-7 Biogenesis in Human ESCs. Cell Stem Cell, 2014, 15, 735-749.	11.1	65
38	Understanding Epistatic Interactions between Genes Targeted by Non-coding Regulatory Elements in Complex Diseases. Genomics and Informatics, 2014, 12, 181.	0.8	4
39	Contrasting chromatin organization of CpG islands and exons in the human genome. Genome Biology, 2010, 11, R70.	9.6	98