

# Inkyung Jung

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5212643/publications.pdf>

Version: 2024-02-01

37  
papers

6,443  
citations

430874

18  
h-index

330143

37  
g-index

43  
all docs

43  
docs citations

43  
times ranked

14247  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hi-C as a molecular rangefinder to examine genomic rearrangements. <i>Seminars in Cell and Developmental Biology</i> , 2022, 121, 161-170.	5.0	7
2	HLA-I-restricted CD8+ T cell immunity may accelerate tumorigenesis in conjunction with VHL inactivation. <i>IScience</i> , 2022, 25, 104467.	4.1	1
3	Functional annotation of lung cancer-associated genetic variants by cell type-specific epigenome and long-range chromatin interactome. <i>Genomics and Informatics</i> , 2021, 19, e3.	0.8	0
4	covNorm: An R package for coverage based normalization of Hi-C and capture Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3149-3159.	4.1	5
5	3DIV update for 2021: a comprehensive resource of 3D genome and 3D cancer genome. <i>Nucleic Acids Research</i> , 2021, 49, D38-D46.	14.5	23
6	A compendium of chromatin contact maps reflecting regulation by chromatin remodelers in budding yeast. <i>Nature Communications</i> , 2021, 12, 6380.	12.8	6
7	CHD4 Conceals Aberrant CTCF-Binding Sites at TAD Interiors by Regulating Chromatin Accessibility in Mouse Embryonic Stem Cells. <i>Molecules and Cells</i> , 2021, 44, 805-829.	2.6	7
8	DNA Methylation of Intragenic CpG Islands are Required for Differentiation from iPSC to NPC. <i>Stem Cell Reviews and Reports</i> , 2020, 16, 1316-1327.	3.8	6
9	Long-range chromatin interactions in pathogenic gene expression control. <i>Transcription</i> , 2020, 11, 211-216.	3.1	5
10	Chromatin Interaction Changes during the iPSC-NPC Model to Facilitate the Study of Biologically Significant Genes Involved in Differentiation. <i>Genes</i> , 2020, 11, 1176.	2.4	2
11	Persistence of Fear Memory Depends on a Delayed Elevation of BAF53b and FGF1 Expression in the Lateral Amygdala. <i>Journal of Neuroscience</i> , 2020, 40, 7133-7141.	3.6	3
12	Immunophenotyping of COVID-19 and influenza highlights the role of type I interferons in development of severe COVID-19. <i>Science Immunology</i> , 2020, 5, .	11.9	689
13	NEUROD1 Intrinsically Initiates Differentiation of Induced Pluripotent Stem Cells into Neural Progenitor Cells. <i>Molecules and Cells</i> , 2020, 43, 1011-1022.	2.6	9
14	VEGF-A drives TOX-dependent T cell exhaustion in anti-PD-1-resistant microsatellite stable colorectal cancers. <i>Science Immunology</i> , 2019, 4, .	11.9	148
15	A compendium of promoter-centered long-range chromatin interactions in the human genome. <i>Nature Genetics</i> , 2019, 51, 1442-1449.	21.4	267
16	A new class of constitutively active super-enhancers is associated with fast recovery of 3D chromatin loops. <i>BMC Bioinformatics</i> , 2019, 20, 127.	2.6	13
17	Characterization of Structural Variations in the Context of 3D Chromatin Structure. <i>Molecules and Cells</i> , 2019, 42, 512-522.	2.6	12
18	The human noncoding genome defined by genetic diversity. <i>Nature Genetics</i> , 2018, 50, 333-337.	21.4	137

#	ARTICLE	IF	CITATIONS
19	3DIV: A 3D-genome Interaction Viewer and database. <i>Nucleic Acids Research</i> , 2018, 46, D52-D57.	14.5	110
20	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. <i>Nature Methods</i> , 2017, 14, 629-635.	19.0	217
21	Broad histone H3K4me3 domains in mouse oocytes modulate maternal-to-zygotic transition. <i>Nature</i> , 2016, 537, 548-552.	27.8	484
22	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. <i>Cell Reports</i> , 2016, 17, 2042-2059.	6.4	745
23	A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. <i>Genome Research</i> , 2016, 26, 397-405.	5.5	111
24	Global mapping of the regulatory interactions of histone residues. <i>FEBS Letters</i> , 2015, 589, 4061-4070.	2.8	8
25	Identification of novel trans-crosstalk between histone modifications via genome-wide analysis of maximal deletion effect. <i>Genes and Genomics</i> , 2015, 37, 693-701.	1.4	1
26	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	27.8	605
27	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	27.8	201
28	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	27.8	1,442
29	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. <i>Cell</i> , 2015, 162, 900-910.	28.9	846
30	LinkNMF: Identification of histone modification modules in the human genome using nonnegative matrix factorization. <i>Gene</i> , 2013, 518, 215-221.	2.2	4
31	H2B monoubiquitylation is a 5â€²-enriched active transcription mark and correlates with exonâ€™intron structure in human cells. <i>Genome Research</i> , 2012, 22, 1026-1035.	5.5	60
32	Human Histone H3K79 Methyltransferase DOT1L Methyltransferase Binds Actively Transcribing RNA Polymerase II to Regulate Gene Expression. <i>Journal of Biological Chemistry</i> , 2012, 287, 39698-39709.	3.4	96
33	Histone modification profiles characterize function-specific gene regulation. <i>Journal of Theoretical Biology</i> , 2012, 310, 132-142.	1.7	12
34	Expression profiles of miRNAs in human embryonic stem cells during hepatocyte differentiation. <i>Hepatology Research</i> , 2011, 41, 170-183.	3.4	83
35	PostMod: sequence based prediction of kinase-specific phosphorylation sites with indirect relationship. <i>BMC Bioinformatics</i> , 2010, 11, S10.	2.6	36
36	SIMPRO: simple protein homology detection method by using indirect signals. <i>Bioinformatics</i> , 2009, 25, 729-735.	4.1	8

#	ARTICLE	IF	CITATIONS
37	Application of nonnegative matrix factorization to improve profile-profile alignment features for fold recognition and remote homolog detection. BMC Bioinformatics, 2008, 9, 298.	2.6	15