

# Jung Kyoon Choi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10833838/publications.pdf>

Version: 2024-02-01

18  
papers

1,365  
citations

687220

13  
h-index

887953

17  
g-index

18  
all docs

18  
docs citations

18  
times ranked

2294  
citing authors

#	ARTICLE	IF	CITATIONS
1	Combining multiple microarray studies and modeling interstudy variation. <i>Bioinformatics</i> , 2003, 19, i84-i90.	1.8	360
2	Differential coexpression analysis using microarray data and its application to human cancer. <i>Bioinformatics</i> , 2005, 21, 4348-4355.	1.8	233
3	Intrinsic variability of gene expression encoded in nucleosome positioning sequences. <i>Nature Genetics</i> , 2009, 41, 498-503.	9.4	136
4	Contrasting chromatin organization of CpG islands and exons in the human genome. <i>Genome Biology</i> , 2010, 11, R70.	13.9	98
5	Epigenetic regulation and the variability of gene expression. <i>Nature Genetics</i> , 2008, 40, 141-147.	9.4	95
6	Genome-wide profiles of H2AX and $\gamma$ -H2AX differentiate endogenous and exogenous DNA damage hotspots in human cells. <i>Nucleic Acids Research</i> , 2012, 40, 5965-5974.	6.5	90
7	Integrative analysis of multiple gene expression profiles applied to liver cancer study. <i>FEBS Letters</i> , 2004, 565, 93-100.	1.3	81
8	Nucleosome deposition and DNA methylation at coding region boundaries. <i>Genome Biology</i> , 2009, 10, R89.	13.9	76
9	Environmental Effects on Gene Expression Phenotype Have Regional Biases in the Human Genome. <i>Genetics</i> , 2007, 175, 1607-1613.	1.2	55
10	HBx induces hypomethylation of distal intragenic CpG islands required for active expression of developmental regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9555-9560.	3.3	55
11	Genome-wide reorganization of histone H2AX toward particular fragile sites on cell activation. <i>Nucleic Acids Research</i> , 2014, 42, 1016-1025.	6.5	25
12	Genetic Landscape of Open Chromatin in Yeast. <i>PLoS Genetics</i> , 2013, 9, e1003229.	1.5	22
13	Stochastic and Regulatory Role of Chromatin Silencing in Genomic Response to Environmental Changes. <i>PLoS ONE</i> , 2008, 3, e3002.	1.1	18
14	Implications of the nucleosome code in regulatory variation, adaptation and evolution. <i>Epigenetics</i> , 2009, 4, 291-295.	1.3	10
15	Global mapping of the regulatory interactions of histone residues. <i>FEBS Letters</i> , 2015, 589, 4061-4070.	1.3	8
16	Controlling transcriptional programs for cellular adaptation by chromatin regulation. <i>Molecular BioSystems</i> , 2011, 7, 1713.	2.9	2
17	Genetic Architecture of Transcription and Chromatin Regulation. <i>Genomics and Informatics</i> , 2015, 13, 40.	0.4	1
18	Conference Scene: An international showcase of the rapid expansion of epigenetics. <i>Epigenomics</i> , 2009, 1, 235-237.	1.0	0