

# Kyoung-Jae Won

## List of Publications by Year in Descending Order

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**Version:** 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

82 papers	4,486 citations	34 h-index	66 g-index
96 ext. papers	5,706 ext. citations	12.8 avg, IF	5.38 L-index

#	Paper	IF	Citations
82	Aberrant qNSC activity mediates decreased active neurogenesis in the Shank3 deficient Autism development. <i>Molecular Psychiatry</i> , <b>2022</b> , 27, 2637-2637	15.1	
81	Targeted inhibition of cooperative mutation- and therapy-induced AKT activation in AML effectively enhances response to chemotherapy. <i>Leukemia</i> , <b>2021</b> , 35, 2030-2042	10.7	7
80	Flower lose, a cell fitness marker, predicts COVID-19 prognosis. <i>EMBO Molecular Medicine</i> , <b>2021</b> , 13, e13714	11.4	0
79	VeTra: a tool for trajectory inference based on RNA velocity. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	3
78	TENET: gene network reconstruction using transfer entropy reveals key regulatory factors from single cell transcriptomic data. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e1	20.1	8
77	Cell competition in intratumoral and tumor microenvironment interactions. <i>EMBO Journal</i> , <b>2021</b> , 40, e107271	13	9
76	A Critical Role for Estrogen-Related Receptor Signaling in Cardiac Maturation. <i>Circulation Research</i> , <b>2020</b> , 126, 1685-1702	15.7	18
75	SHARP: hyperfast and accurate processing of single-cell RNA-seq data via ensemble random projection. <i>Genome Research</i> , <b>2020</b> , 30, 205-213	9.7	21
74	Mapping Cellular Coordinates through Advances in Spatial Transcriptomics Technology. <i>Molecules and Cells</i> , <b>2020</b> , 43, 591-599	3.5	6
73	Pontin arginine methylation by CARM1 is crucial for epigenetic regulation of autophagy. <i>Nature Communications</i> , <b>2020</b> , 11, 6297	17.4	10
72	A PRDM16-Driven Metabolic Signal from Adipocytes Regulates Precursor Cell Fate. <i>Cell Metabolism</i> , <b>2019</b> , 30, 174-189.e5	24.6	73
71	Genomic architecture of Shh-dependent cochlear morphogenesis. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	10
70	MondoA drives muscle lipid accumulation and insulin resistance. <i>JCI Insight</i> , <b>2019</b> , 5,	9.9	14
69	Single Cell RNA-Sequencing for the Study of Atherosclerosis. <i>Journal of Lipid and Atherosclerosis</i> , <b>2019</b> , 8, 152-161	3	3
68	PKC $\epsilon$ SD1-NF- $\kappa$ B-Signaling Cascade Is Crucial for Epigenetic Control of the Inflammatory Response. <i>Molecular Cell</i> , <b>2018</b> , 69, 398-411.e6	17.6	39
67	Transcriptomic Analysis Reveals Novel Mechanisms Mediating Islet Dysfunction in the Intrauterine Growth-Restricted Rat. <i>Endocrinology</i> , <b>2018</b> , 159, 1035-1049	4.8	10
66	Rev-erb $\alpha$ dynamically modulates chromatin looping to control circadian gene transcription. <i>Science</i> , <b>2018</b> , 359, 1274-1277	33.3	102

65	Defiant: (DMRs: easy, fast, identification and ANnoTation) identifies differentially Methylated regions from iron-deficient rat hippocampus. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 31	3.6	17
64	CellBIC: bimodality-based top-down clustering of single-cell RNA sequencing data reveals hierarchical structure of the cell type. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e124	20.1	11
63	Shared nucleotide flanks confer transcriptional competency to bZip core motifs. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 8371-8384	20.1	4
62	Distinct macrophage populations direct inflammatory versus physiological changes in adipose tissue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E5096-E5105	11.5	150
61	EBF2 transcriptionally regulates brown adipogenesis via the histone reader DPF3 and the BAF chromatin remodeling complex. <i>Genes and Development</i> , <b>2017</b> , 31, 660-673	12.6	38
60	Single cell transcriptomic profiling of mouse pancreatic progenitors. <i>Physiological Genomics</i> , <b>2017</b> , 49, 105-114	3.6	26
59	PRDM16 represses the type I interferon response in adipocytes to promote mitochondrial and thermogenic programing. <i>EMBO Journal</i> , <b>2017</b> , 36, 1528-1542	13	35
58	Histone deacetylase 3 prepares brown adipose tissue for acute thermogenic challenge. <i>Nature</i> , <b>2017</b> , 546, 544-548	50.4	88
57	DNA hypermethylation induced by Epstein-Barr virus in the development of Epstein-Barr virus-associated gastric carcinoma. <i>Archives of Pharmacal Research</i> , <b>2017</b> , 40, 894-905	6.1	14
56	LIM domain-binding 1 maintains the terminally differentiated state of pancreatic $\beta$ cells. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 215-229	15.9	43
55	Targeting PPAR $\alpha$ in the epigenome rescues genetic metabolic defects in mice. <i>Journal of Clinical Investigation</i> , <b>2017</b> , 127, 1451-1462	15.9	31
54	Epigenetic regulation of intestinal stem cells by Tet1-mediated DNA hydroxymethylation. <i>Genes and Development</i> , <b>2016</b> , 30, 2433-2442	12.6	37
53	The Nuclear Receptor Rev-erb $\beta$ Regulates Adipose Tissue-specific FGF21 Signaling. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 10867-75	5.4	23
52	EBF2 promotes the recruitment of beige adipocytes in white adipose tissue. <i>Molecular Metabolism</i> , <b>2016</b> , 5, 57-65	8.8	59
51	AMPK-SKP2-CARM1 signalling cascade in transcriptional regulation of autophagy. <i>Nature</i> , <b>2016</b> , 534, 553-7	50.4	249
50	Single-Cell Transcriptomics of the Human Endocrine Pancreas. <i>Diabetes</i> , <b>2016</b> , 65, 3028-38	0.9	223
49	Histone H4 acetylation and the epigenetic reader Brd4 are critical regulators of pluripotency in embryonic stem cells. <i>BMC Genomics</i> , <b>2016</b> , 17, 95	4.5	34
48	Prenatal Choline Supplementation Diminishes Early-Life Iron Deficiency-Induced Reprogramming of Molecular Networks Associated with Behavioral Abnormalities in the Adult Rat Hippocampus. <i>Journal of Nutrition</i> , <b>2016</b> , 146, 484-93	4.1	32

47	The CSB chromatin remodeler and CTCF architectural protein cooperate in response to oxidative stress. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 2125-35	20.1	28
46	EBNA2 Drives Formation of New Chromosome Binding Sites and Target Genes for B-Cell Master Regulatory Transcription Factors RBP-j $\kappa$ and EBF1. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005339	7.6	34
45	Targeting ACLY sensitizes castration-resistant prostate cancer cells to AR antagonism by impinging on an ACLY-AMPK-AR feedback mechanism. <i>Oncotarget</i> , <b>2016</b> , 7, 43713-43730	3.3	40
44	Threshold-Dependent Cooperativity of Pdx1 and Oc1 in Pancreatic Progenitors Establishes Competency for Endocrine Differentiation and $\beta$ Cell Function. <i>Cell Reports</i> , <b>2016</b> , 15, 2637-2650	10.6	7
43	Genetic Variation Determines PPAR $\alpha$ Function and Anti-diabetic Drug Response In Vivo. <i>Cell</i> , <b>2015</b> , 162, 33-44	56.2	90
42	HEART DEVELOPMENT. Integration of Bmp and Wnt signaling by Hopx specifies commitment of cardiomyoblasts. <i>Science</i> , <b>2015</b> , 348, aaa6071	33.3	89
41	Proteogenomics analysis reveals specific genomic orientations of distal regulatory regions composed by non-canonical histone variants. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 13	5.8	8
40	Genomic redistribution of GR monomers and dimers mediates transcriptional response to exogenous glucocorticoid in vivo. <i>Genome Research</i> , <b>2015</b> , 25, 836-44	9.7	113
39	A stationary wavelet entropy-based clustering approach accurately predicts gene expression. <i>Journal of Computational Biology</i> , <b>2015</b> , 22, 236-49	1.7	7
38	Nonparametric Tests for Differential Histone Enrichment with ChIP-Seq Data. <i>Cancer Informatics</i> , <b>2015</b> , 14, 11-22	2.4	2
37	ATF4 licenses C/EBP $\beta$ activity in human mesenchymal stem cells primed for adipogenesis. <i>ELife</i> , <b>2015</b> , 4, e06821	8.9	31
36	Transcriptomic Profiling and H3K27me3 Distribution Reveal Both Demethylase-Dependent and Independent Regulation of Developmental Gene Transcription in Cell Differentiation. <i>PLoS ONE</i> , <b>2015</b> , 10, e0135276	3.7	13
35	PRDM16 binds MED1 and controls chromatin architecture to determine a brown fat transcriptional program. <i>Genes and Development</i> , <b>2015</b> , 29, 298-307	12.6	86
34	Prdm16 is required for the maintenance of brown adipocyte identity and function in adult mice. <i>Cell Metabolism</i> , <b>2014</b> , 19, 593-604	24.6	229
33	A wavelet-based method to exploit epigenomic language in the regulatory region. <i>Bioinformatics</i> , <b>2014</b> , 30, 908-14	7.2	6
32	Anti-diabetic rosiglitazone remodels the adipocyte transcriptome by redistributing transcription to PPAR $\alpha$ -driven enhancers. <i>Genes and Development</i> , <b>2014</b> , 28, 1018-28	12.6	73
31	Epigenetic regulation of the DLK1-MEG3 microRNA cluster in human type 2 diabetic islets. <i>Cell Metabolism</i> , <b>2014</b> , 19, 135-45	24.6	241
30	Akt-dependent metabolic reprogramming regulates tumor cell histone acetylation. <i>Cell Metabolism</i> , <b>2014</b> , 20, 306-319	24.6	340

29	Ebf2 is a selective marker of brown and beige adipogenic precursor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 14466-71	11.5	135
28	5-hydroxymethylcytosine represses the activity of enhancers in embryonic stem cells: a new epigenetic signature for gene regulation. <i>BMC Genomics</i> , <b>2014</b> , 15, 670	4.5	23
27	The sequence-specific transcription factor c-Jun targets Cockayne syndrome protein B to regulate transcription and chromatin structure. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004284	6	25
26	RBPJ, the major transcriptional effector of Notch signaling, remains associated with chromatin throughout mitosis, suggesting a role in mitotic bookmarking. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004204	6	53
25	A wavelet approach to detect enriched regions and explore epigenomic landscapes. <i>Journal of Computational Biology</i> , <b>2014</b> , 21, 846-54	1.7	4
24	Histone deacetylase 3 coordinates commensal-bacteria-dependent intestinal homeostasis. <i>Nature</i> , <b>2013</b> , 504, 153-7	50.4	154
23	Deacetylase-independent function of HDAC3 in transcription and metabolism requires nuclear receptor corepressor. <i>Molecular Cell</i> , <b>2013</b> , 52, 769-82	17.6	168
22	Nuclear receptor co-repressors are required for the histone-deacetylase activity of HDAC3 in vivo. <i>Nature Structural and Molecular Biology</i> , <b>2013</b> , 20, 182-7	17.6	131
21	Dynamic chromatin remodeling mediated by polycomb proteins orchestrates pancreatic differentiation of human embryonic stem cells. <i>Cell Stem Cell</i> , <b>2013</b> , 12, 224-37	18	179
20	An iPSC line from human pancreatic ductal adenocarcinoma undergoes early to invasive stages of pancreatic cancer progression. <i>Cell Reports</i> , <b>2013</b> , 3, 2088-99	10.6	125
19	An iPSC Line from Human Pancreatic Ductal Adenocarcinoma Undergoes Early to Invasive Stages of Pancreatic Cancer Progression. <i>Cell Reports</i> , <b>2013</b> , 4, 403	10.6	2
18	EBF2 determines and maintains brown adipocyte identity. <i>Cell Metabolism</i> , <b>2013</b> , 17, 562-74	24.6	244
17	Evolving fisher kernels for biological sequence classification. <i>Evolutionary Computation</i> , <b>2013</b> , 21, 83-105	4.3	2
16	Comparative annotation of functional regions in the human genome using epigenomic data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 4423-32	20.1	37
15	Zfp423 binds autoregulatory sites in p19 cell culture model. <i>PLoS ONE</i> , <b>2013</b> , 8, e66514	3.7	10
14	Human Transcriptome and Chromatin Modifications: An ENCODE Perspective. <i>Genomics and Informatics</i> , <b>2013</b> , 11, 60-7	1.9	4
13	Adhesion regulates MAP kinase/ternary complex factor exchange to control a proliferative transcriptional switch. <i>Current Biology</i> , <b>2012</b> , 22, 2017-26	6.3	28
12	Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 8199-209	20.1	8

11	Genome-wide prediction of transcription factor binding sites using an integrated model. <i>Genome Biology</i> , <b>2010</b> , 11, R7	18.3	87
10	An integrated approach to identifying cis-regulatory modules in the human genome. <i>PLoS ONE</i> , <b>2009</b> , 4, e5501	3.7	14
9	Prediction of regulatory elements in mammalian genomes using chromatin signatures. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 547	3.6	75
8	Modeling promoter grammars with evolving hidden Markov models. <i>Bioinformatics</i> , <b>2008</b> , 24, 1669-75	7.2	11
7	An evolutionary method for learning HMM structure: prediction of protein secondary structure. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 357	3.6	35
6	Evolving the structure of hidden Markov models. <i>IEEE Transactions on Evolutionary Computation</i> , <b>2006</b> , 10, 39-49	15.6	9
5	Training HMM structure with genetic algorithm for biological sequence analysis. <i>Bioinformatics</i> , <b>2004</b> , 20, 3613-9	7.2	33
4	VeTra: a tool for trajectory inference based on RNA velocity		1
3	SHARP: Single-cell RNA-seq Hyper-fast and Accurate Processing via Ensemble Random Projection		2
2	Decreased KATP channel activity contributes to the low glucose threshold for insulin secretion of rat neonatal islets		1
1	Postnatal activation of hypoxia pathway disrupts $\beta$ -cell functional maturation		1