

# Dongjun Chung

## List of Publications by Year in Descending Order

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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.

71  
papers

1,465  
citations

18  
h-index

37  
g-index

86  
ext. papers

1,985  
ext. citations

5.7  
avg, IF

4.66  
L-index

#	Paper	IF	Citations
71	Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology.. <i>Journal of Hematology and Oncology</i> , <b>2022</b> , 15, 5	22.4	2
70	Androgen conspires with the CD8 T cell exhaustion program and contributes to sex bias in cancer.. <i>Science Immunology</i> , <b>2022</b> ,	28	4
69	Brown adipose tissue involution associated with progressive restriction in progenitor competence.. <i>Cell Reports</i> , <b>2022</b> , 39, 110575	10.6	3
68	Association of Referral Source and Substance Use with Hepatitis C Virus Outcomes at a Southern Academic Medical Center. <i>Southern Medical Journal</i> , <b>2022</b> , 115, 352-357	0.6	
67	Gene Expression Differences Between Young Adults Based on Trauma History and Post-traumatic Stress Disorder. <i>Frontiers in Psychiatry</i> , <b>2021</b> , 12, 581093	5	
66	Genotype Does Not Associate with CD4 T-Cell Recovery in People Living with Human Immunodeficiency Virus. <i>AIDS Research and Human Retroviruses</i> , <b>2021</b> , 37, 184-188	1.6	1
65	IRIS-FGM: an integrative single-cell RNA-Seq interpretation system for functional gene module analysis. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	2
64	Differential immune signatures in the tumor microenvironment are associated with colon cancer racial disparities. <i>Cancer Medicine</i> , <b>2021</b> , 10, 1805-1814	4.8	8
63	Trefoil factor 2 secreted from damaged hepatocytes activates hepatic stellate cells to induce fibrogenesis. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 297, 100887	5.4	0
62	IMMUNOLOGICAL INSIGHTS INTO THE THERAPEUTIC ROLES OF CD24Fc AGAINST SEVERE COVID-19 <b>2021</b> ,		1
61	Remodeling Translation Primes CD8 T-cell Antitumor Immunity. <i>Cancer Immunology Research</i> , <b>2020</b> , 8, 587-595	12.5	6
60	RNA binding protein PCBP1 is an intracellular immune checkpoint for shaping T cell responses in cancer immunity. <i>Science Advances</i> , <b>2020</b> , 6, eaaz3865	14.3	13
59	hubViz: A Novel Tool for Hub-centric Visualization. <i>Chemometrics and Intelligent Laboratory Systems</i> , <b>2020</b> , 203, 104071-104071	3.8	
58	OGT suppresses S6K1-mediated macrophage inflammation and metabolic disturbance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 16616-16625	11.5	15
57	Ranking subjects based on paired compositional data with application to age-related hearing loss subtyping. <i>Communications for Statistical Applications and Methods</i> , <b>2020</b> , 27, 225-239	0.4	
56	New Insights for Early Warning and Countermeasures to Aquatic Pollution <b>2020</b> , 431-445		1
55	Sparse Linear Discriminant Analysis using the Prior-Knowledge-Guided Block Covariance Matrix. <i>Chemometrics and Intelligent Laboratory Systems</i> , <b>2020</b> , 206,	3.8	2

54	PALMER: improving pathway annotation based on the biomedical literature mining with a constrained latent block model. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 432	3.6	2
53	BiMM tree: A decision tree method for modeling clustered and longitudinal binary outcomes. <i>Communications in Statistics Part B: Simulation and Computation</i> , <b>2020</b> , 49, 1004-1023	0.6	8
52	BiMM forest: A random forest method for modeling clustered and longitudinal binary outcomes. <i>Chemometrics and Intelligent Laboratory Systems</i> , <b>2019</b> , 185, 122-134	3.8	17
51	Molecular Profiling of RNA Tumors Using High-Throughput RNA Sequencing: From Raw Data to Systems Level Analyses. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1908, 185-204	1.4	5
50	Predicting daily outcomes in acetaminophen-induced acute liver failure patients with machine learning techniques. <i>Computer Methods and Programs in Biomedicine</i> , <b>2019</b> , 175, 111-120	6.9	11
49	Defects in the Exocyst-Cilia Machinery Cause Bicuspid Aortic Valve Disease and Aortic Stenosis. <i>Circulation</i> , <b>2019</b> , 140, 1331-1341	16.7	18
48	GAIL: An interactive webserver for inference and dynamic visualization of gene-gene associations based on gene ontology guided mining of biomedical literature. <i>PLoS ONE</i> , <b>2019</b> , 14, e0219195	3.7	4
47	O-GlcNAc transferase suppresses necroptosis and liver fibrosis. <i>JCI Insight</i> , <b>2019</b> , 4,	9.9	24
46	Title: SNP Microarray Reveals Predicted Outcomes of a Novel High Risk AML Subgroup with ERG Amplification. <i>Blood</i> , <b>2019</b> , 134, 2737-2737	2.2	
45	Transcriptomic analysis of short-term 17β-ethynylestradiol exposure in two Californian sentinel fish species sardine ( <i>Sardinops sagax</i> ) and mackerel ( <i>Scomber japonicus</i> ). <i>Environmental Pollution</i> , <b>2019</b> , 244, 926-937	9.3	3
44	Semi-supervised identification of cancer subgroups using survival outcomes and overlapping grouping information. <i>Statistical Methods in Medical Research</i> , <b>2019</b> , 28, 2137-2149	2.3	2
43	Systems Analysis of the Liver Transcriptome in Adult Male Zebrafish Exposed to the Plasticizer (2-Ethylhexyl) Phthalate (DEHP). <i>Scientific Reports</i> , <b>2018</b> , 8, 2118	4.9	29
42	Improving SNP prioritization and pleiotropic architecture estimation by incorporating prior knowledge using graph-GPA. <i>Bioinformatics</i> , <b>2018</b> , 34, 2139-2141	7.2	3
41	Effects of diethylene glycol dibenzoate and Bisphenol A on the lipid metabolism of <i>Danio rerio</i> . <i>Science of the Total Environment</i> , <b>2018</b> , 636, 641-655	10.2	35
40	Sex as a predictor of response to cancer immunotherapy. <i>Lancet Oncology</i> , <b>2018</b> , 19, e379	21.7	3
39	Sex Differences in Using Systemic Inflammatory Markers to Prognosticate Patients with Head and Neck Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2018</b> , 27, 1176-1185	4	7
38	ShinyGPA: An interactive visualization toolkit for investigating pleiotropic architecture using GWAS datasets. <i>PLoS ONE</i> , <b>2018</b> , 13, e0190949	3.7	2
37	Identification of Pathway-Modulating Genes Using the Biomedical Literature Mining. <i>ICSA Book Series in Statistics</i> , <b>2018</b> , 345-363	0.3	

36	Lipid Metabolism Alteration by Endocrine Disruptors in Animal Models: An Overview. <i>Frontiers in Endocrinology</i> , <b>2018</b> , 9, 654	5.7	39
35	miRmapper: A Tool for Interpretation of miRNA-mRNA Interaction Networks. <i>Genes</i> , <b>2018</b> , 9,	4.2	12
34	Genomics pipelines and data integration: challenges and opportunities in the research setting. <i>Expert Review of Molecular Diagnostics</i> , <b>2017</b> , 17, 225-237	3.8	38
33	graph-GPA: A graphical model for prioritizing GWAS results and investigating pleiotropic architecture. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005388	5	8
32	Relationships between GAT1 and PTSD, Depression, and Substance Use Disorder. <i>Brain Sciences</i> , <b>2017</b> , 7,	3.4	5
31	A statistical framework for biomedical literature mining. <i>Statistics in Medicine</i> , <b>2017</b> , 36, 3461-3474	2.3	7
30	The LZIP: A Bayesian latent factor model for correlated zero-inflated counts. <i>Biometrics</i> , <b>2017</b> , 73, 185-196	6	
29	Data exploration, quality control and statistical analysis of CHIP-exo/nexus experiments. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e145	20.1	2
28	The Plasticizer Bisphenol A Perturbs the Hepatic Epigenome: A Systems Level Analysis of the miRNome. <i>Genes</i> , <b>2017</b> , 8,	4.2	26
27	BPA-Induced Deregulation Of Epigenetic Patterns: Effects On Female Zebrafish Reproduction. <i>Scientific Reports</i> , <b>2016</b> , 6, 21982	4.9	105
26	GPA-MDS: A Visualization Approach to Investigate Genetic Architecture among Phenotypes Using GWAS Results. <i>International Journal of Genomics</i> , <b>2016</b> , 2016, 6589843	2.5	3
25	Bisphenol A Induces Fatty Liver by an Endocannabinoid-Mediated Positive Feedback Loop. <i>Endocrinology</i> , <b>2016</b> , 157, 1751-63	4.8	50
24	Metabolic Regulation of Gene Expression by Histone Lysine $\epsilon$ -Hydroxybutyrylation. <i>Molecular Cell</i> , <b>2016</b> , 62, 194-206	17.6	240
23	Accurate ensemble pruning with PL-bagging. <i>Computational Statistics and Data Analysis</i> , <b>2015</b> , 83, 1-13	1.6	9
22	Implications of pleiotropy: challenges and opportunities for mining Big Data in biomedicine. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 229	4.5	28
21	Impact of Anaerobiosis on Expression of the Iron-Responsive Fur and RyhB Regulons. <i>MBio</i> , <b>2015</b> , 6, e01947-15	37	
20	Statistical issues in binding site identification through CLIP-seq. <i>Statistics and Its Interface</i> , <b>2015</b> , 8, 419-436	0	
19	A developmental hepatotoxicity study of dietary bisphenol A in <i>Sparus aurata</i> juveniles. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , <b>2014</b> , 166, 1-13	3.2	26

18	GPA: a statistical approach to prioritizing GWAS results by integrating pleiotropy and annotation. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004787	6	137
17	MOSAICS-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data <b>2014</b> , 277-295		2
16	dPeak: high resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003246	5	12
15	Genome-scale analysis of escherichia coli FNR reveals complex features of transcription factor binding. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003565	6	120
14	Statistical analysis of ChIP-seq data with MOSAICS. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1038, 193-212	1.4	16
13	Evidence of social contextual effects on adolescent smoking in South Korea. <i>Asia-Pacific Journal of Public Health</i> , <b>2013</b> , 25, 260-70	2	13
12	A Statistical Framework for the Analysis of ChIP-Seq Data. <i>Journal of the American Statistical Association</i> , <b>2011</b> , 106, 891-903	2.8	82
11	Robust classification ensemble method for microarray data. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2011</b> , 5, 504-18	0.5	3
10	Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-Seq data. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1002111	5	60
9	eQTL Mapping for Functional Classes of <i>Saccharomyces cerevisiae</i> Genes with Multivariate Sparse Partial Least Squares Regression <b>2011</b> , 283-298		
8	Sparse partial least squares classification for high dimensional data. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2010</b> , 9, Article17	1.2	100
7	Developmental craniofacial anthropometry: Assessment of race effects. <i>Clinical Anatomy</i> , <b>2009</b> , 22, 800-8.5		14
6	Measurement consistency from magnetic resonance images. <i>Academic Radiology</i> , <b>2008</b> , 15, 1322-30	4.3	8
5	Co-author.Keyword Network and its Two Culture Appearance in Health Policy Fields in Korea: Analysis of articles in the Korean Journal of Health Policy and Administration, 1991~2006. <i>Health Policy and Management</i> , <b>2008</b> , 18, 86-106		1
4	Distinct CD8+ T Cell Programming in the Tumor Microenvironment Contributes to Sex Bias in Bladder Cancer Outcome		2
3	A Bayesian Multivariate Mixture Model for Spatial Transcriptomics Data		1
2	Introduction to statistical methods in genome-wide association studies26-52		
1	Define and visualize pathological architectures of human tissues from spatially resolved transcriptomics using deep learning		1

