

Dongjun Chung

List of Publications by Citations

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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	Metabolic Regulation of Gene Expression by Histone Lysine ϵ -Hydroxybutyrylation. <i>Molecular Cell</i> , 2016 , 62, 194-206	17.6	240
70	GPA: a statistical approach to prioritizing GWAS results by integrating pleiotropy and annotation. <i>PLoS Genetics</i> , 2014 , 10, e1004787	6	137
69	Genome-scale analysis of escherichia coli FNR reveals complex features of transcription factor binding. <i>PLoS Genetics</i> , 2013 , 9, e1003565	6	120
68	BPA-Induced Deregulation Of Epigenetic Patterns: Effects On Female Zebrafish Reproduction. <i>Scientific Reports</i> , 2016 , 6, 21982	4.9	105
67	Sparse partial least squares classification for high dimensional data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010 , 9, Article17	1.2	100
66	A Statistical Framework for the Analysis of ChIP-Seq Data. <i>Journal of the American Statistical Association</i> , 2011 , 106, 891-903	2.8	82
65	Discovering transcription factor binding sites in highly repetitive regions of genomes with multi-read analysis of ChIP-Seq data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002111	5	60
64	Bisphenol A Induces Fatty Liver by an Endocannabinoid-Mediated Positive Feedback Loop. <i>Endocrinology</i> , 2016 , 157, 1751-63	4.8	50
63	Lipid Metabolism Alteration by Endocrine Disruptors in Animal Models: An Overview. <i>Frontiers in Endocrinology</i> , 2018 , 9, 654	5.7	39
62	Genomics pipelines and data integration: challenges and opportunities in the research setting. <i>Expert Review of Molecular Diagnostics</i> , 2017 , 17, 225-237	3.8	38
61	Impact of Anaerobiosis on Expression of the Iron-Responsive Fur and RyhB Regulons. <i>MBio</i> , 2015 , 6, e01947-15	3.7	37
60	Effects of diethylene glycol dibenzoate and Bisphenol A on the lipid metabolism of Danio rerio. <i>Science of the Total Environment</i> , 2018 , 636, 641-655	10.2	35
59	Systems Analysis of the Liver Transcriptome in Adult Male Zebrafish Exposed to the Plasticizer (2-Ethylhexyl) Phthalate (DEHP). <i>Scientific Reports</i> , 2018 , 8, 2118	4.9	29
58	Implications of pleiotropy: challenges and opportunities for mining Big Data in biomedicine. <i>Frontiers in Genetics</i> , 2015 , 6, 229	4.5	28
57	A developmental hepatotoxicity study of dietary bisphenol A in Sparus aurata juveniles. <i>Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology</i> , 2014 , 166, 1-13	3.2	26
56	The Plasticizer Bisphenol A Perturbs the Hepatic Epigenome: A Systems Level Analysis of the miRNome. <i>Genes</i> , 2017 , 8,	4.2	26
55	O-GlcNAc transferase suppresses necroptosis and liver fibrosis. <i>JCI Insight</i> , 2019 , 4,	9.9	24

54	Defects in the Exocyst-Cilia Machinery Cause Bicuspid Aortic Valve Disease and Aortic Stenosis. <i>Circulation</i> , 2019 , 140, 1331-1341	16.7	18
53	BiMM forest: A random forest method for modeling clustered and longitudinal binary outcomes. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2019 , 185, 122-134	3.8	17
52	Statistical analysis of ChIP-seq data with MOSAiCS. <i>Methods in Molecular Biology</i> , 2013 , 1038, 193-212	1.4	16
51	OGT suppresses S6K1-mediated macrophage inflammation and metabolic disturbance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16616-16625	11.5	15
50	Developmental craniofacial anthropometry: Assessment of race effects. <i>Clinical Anatomy</i> , 2009 , 22, 800-805	8.5	14
49	RNA binding protein PCBP1 is an intracellular immune checkpoint for shaping T cell responses in cancer immunity. <i>Science Advances</i> , 2020 , 6, eaaz3865	14.3	13
48	Evidence of social contextual effects on adolescent smoking in South Korea. <i>Asia-Pacific Journal of Public Health</i> , 2013 , 25, 260-70	2	13
47	dPeak: high resolution identification of transcription factor binding sites from PET and SET ChIP-Seq data. <i>PLoS Computational Biology</i> , 2013 , 9, e1003246	5	12
46	miRmapper: A Tool for Interpretation of miRNA-mRNA Interaction Networks. <i>Genes</i> , 2018 , 9,	4.2	12
45	Predicting daily outcomes in acetaminophen-induced acute liver failure patients with machine learning techniques. <i>Computer Methods and Programs in Biomedicine</i> , 2019 , 175, 111-120	6.9	11
44	Accurate ensemble pruning with PL-bagging. <i>Computational Statistics and Data Analysis</i> , 2015 , 83, 1-13	1.6	9
43	graph-GPA: A graphical model for prioritizing GWAS results and investigating pleiotropic architecture. <i>PLoS Computational Biology</i> , 2017 , 13, e1005388	5	8
42	Measurement consistency from magnetic resonance images. <i>Academic Radiology</i> , 2008 , 15, 1322-30	4.3	8
41	BiMM tree: A decision tree method for modeling clustered and longitudinal binary outcomes. <i>Communications in Statistics Part B: Simulation and Computation</i> , 2020 , 49, 1004-1023	0.6	8
40	Differential immune signatures in the tumor microenvironment are associated with colon cancer racial disparities. <i>Cancer Medicine</i> , 2021 , 10, 1805-1814	4.8	8
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> , 2018 , 27, 1176-1185	4	7
38	A statistical framework for biomedical literature mining. <i>Statistics in Medicine</i> , 2017 , 36, 3461-3474	2.3	7
37	Remodeling Translation Primes CD8 T-cell Antitumor Immunity. <i>Cancer Immunology Research</i> , 2020 , 8, 587-595	12.5	6

36	The LZIP: A Bayesian latent factor model for correlated zero-inflated counts. <i>Biometrics</i> , 2017 , 73, 185-196		6
35	Molecular Profiling of RNA Tumors Using High-Throughput RNA Sequencing: From Raw Data to Systems Level Analyses. <i>Methods in Molecular Biology</i> , 2019 , 1908, 185-204	1.4	5
34	Relationships between GAT1 and PTSD, Depression, and Substance Use Disorder. <i>Brain Sciences</i> , 2017 , 7,	3.4	5
33	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> , 2019 , 14, e0219195	3.7	4
32	Androgen conspires with the CD8 T cell exhaustion program and contributes to sex bias in cancer.. <i>Science Immunology</i> , 2022 ,	2.8	4
31	Improving SNP prioritization and pleiotropic architecture estimation by incorporating prior knowledge using graph-GPA. <i>Bioinformatics</i> , 2018 , 34, 2139-2141	7.2	3
30	Sex as a predictor of response to cancer immunotherapy. <i>Lancet Oncology, The</i> , 2018 , 19, e379	21.7	3
29	Robust classification ensemble method for microarray data. <i>International Journal of Data Mining and Bioinformatics</i> , 2011 , 5, 504-18	0.5	3
28	GPA-MDS: A Visualization Approach to Investigate Genetic Architecture among Phenotypes Using GWAS Results. <i>International Journal of Genomics</i> , 2016 , 2016, 6589843	2.5	3
27	Transcriptomic analysis of short-term 17 β ethynylestradiol exposure in two Californian sentinel fish species sardine (<i>Sardinops sagax</i>) and mackerel (<i>Scomber japonicus</i>). <i>Environmental Pollution</i> , 2019 , 244, 926-937	9.3	3
26	Brown adipose tissue involution associated with progressive restriction in progenitor competence.. <i>Cell Reports</i> , 2022 , 39, 110575	10.6	3
25	Data exploration, quality control and statistical analysis of ChIP-exo/nexus experiments. <i>Nucleic Acids Research</i> , 2017 , 45, e145	20.1	2
24	Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology.. <i>Journal of Hematology and Oncology</i> , 2022 , 15, 5	22.4	2
23	ShinyGPA: An interactive visualization toolkit for investigating pleiotropic architecture using GWAS datasets. <i>PLoS ONE</i> , 2018 , 13, e0190949	3.7	2
22	MOSAICS-HMM: A Model-Based Approach for Detecting Regions of Histone Modifications from ChIP-Seq Data 2014 , 277-295		2
21	Distinct CD8+ T Cell Programming in the Tumor Microenvironment Contributes to Sex Bias in Bladder Cancer Outcome		2
20	Sparse Linear Discriminant Analysis using the Prior-Knowledge-Guided Block Covariance Matrix. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020 , 206,	3.8	2
19	PALMER: improving pathway annotation based on the biomedical literature mining with a constrained latent block model. <i>BMC Bioinformatics</i> , 2020 , 21, 432	3.6	2

18	Semi-supervised identification of cancer subgroups using survival outcomes and overlapping grouping information. <i>Statistical Methods in Medical Research</i> , 2019 , 28, 2137-2149	2.3	2
17	IRIS-FGM: an integrative single-cell RNA-Seq interpretation system for functional gene module analysis. <i>Bioinformatics</i> , 2021 ,	7.2	2
16	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> , 2008 , 18, 86-106		1
15	New Insights for Early Warning and Countermeasures to Aquatic Pollution 2020 , 431-445		1
14	A Bayesian Multivariate Mixture Model for Spatial Transcriptomics Data		1
13	Genotype Does Not Associate with CD4 T-Cell Recovery in People Living with Human Immunodeficiency Virus. <i>AIDS Research and Human Retroviruses</i> , 2021 , 37, 184-188	1.6	1
12	Define and visualize pathological architectures of human tissues from spatially resolved transcriptomics using deep learning		1
11	IMMUNOLOGICAL INSIGHTS INTO THE THERAPEUTIC ROLES OF CD24Fc AGAINST SEVERE COVID-19 2021 ,		1
10	Statistical issues in binding site identification through CLIP-seq. <i>Statistics and Its Interface</i> , 2015 , 8, 419-436	4.6	0
9	Trefoil factor 2 secreted from damaged hepatocytes activates hepatic stellate cells to induce fibrogenesis. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100887	5.4	0
8	hubViz: A Novel Tool for Hub-centric Visualization. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020 , 203, 104071-104071	3.8	
7	Ranking subjects based on paired compositional data with application to age-related hearing loss subtyping. <i>Communications for Statistical Applications and Methods</i> , 2020 , 27, 225-239	0.4	
6	Identification of Pathway-Modulating Genes Using the Biomedical Literature Mining. <i>ICSA Book Series in Statistics</i> , 2018 , 345-363	0.3	
5	Title: SNP Microarray Reveals Predicted Outcomes of a Novel High Risk AML Subgroup with ERG Amplification. <i>Blood</i> , 2019 , 134, 2737-2737	2.2	
4	eQTL Mapping for Functional Classes of <i>Saccharomyces cerevisiae</i> Genes with Multivariate Sparse Partial Least Squares Regression 2011 , 283-298		
3	Gene Expression Differences Between Young Adults Based on Trauma History and Post-traumatic Stress Disorder. <i>Frontiers in Psychiatry</i> , 2021 , 12, 581093	5	
2	Introduction to statistical methods in genome-wide association studies26-52		
1	Association of Referral Source and Substance Use with Hepatitis C Virus Outcomes at a Southern Academic Medical Center. <i>Southern Medical Journal</i> , 2022 , 115, 352-357	0.6	

