

Sek Won Kong

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.

75
papers

5,449
citations

34
h-index

73
g-index

82
ext. papers

6,273
ext. citations

6.9
avg, IF

5.17
L-index

#	Paper	IF	Citations
75	Inhibition of mevalonate metabolism by statins augments the immunoregulatory phenotype of vascular endothelial cells and inhibits the costimulation of CD4 T cells. <i>American Journal of Transplantation</i> , 2021 ,	8.7	1
74	Plasma metabolomics of autism spectrum disorder and influence of shared components in proband families. 2021 , 1, osab004		0
73	Genetic variation analyses indicate conserved SARS-CoV-2-host interaction and varied genetic adaptation in immune response factors in modern human evolution. <i>Development Growth and Differentiation</i> , 2021 , 63, 219-227	3	2
72	WEScover: selection between clinical whole exome sequencing and gene panel testing. <i>BMC Bioinformatics</i> , 2021 , 22, 259	3.6	2
71	GenoPheno: cataloging large-scale phenotypic and next-generation sequencing data within human datasets. <i>Briefings in Bioinformatics</i> , 2021 , 22, 55-65	13.4	3
70	A two-step gas chromatography-tandem mass spectrometry method for measurement of multiple environmental pollutants in human plasma. <i>Environmental Science and Pollution Research</i> , 2021 , 28, 3266-3279	5.1	2
69	Two macrophages, osteoclasts and microglia: from development to pleiotropy. <i>Bone Research</i> , 2021 , 9, 11	13.3	7
68	Investigation of genetic variants in SARS-CoV-2-interacting molecules of ACE2, TMPRSS2 and TLR3/7/8 across populations. <i>Proceedings for Annual Meeting of the Japanese Pharmacological Society</i> , 2021 , 94, 1-P2-36	0	
67	Human autologous iPSC-derived dopaminergic progenitors restore motor function in Parkinson's disease models. <i>Journal of Clinical Investigation</i> , 2020 , 130, 904-920	15.9	55
66	Assessment of coverage for endogenous metabolites and exogenous chemical compounds using an untargeted metabolomics platform. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020 , 25, 587-598	1.3	2
65	The Clinical Genome and Ancestry Report: An interactive web application for prioritizing clinically implicated variants from genome sequencing data with ancestry composition. <i>Human Mutation</i> , 2020 , 41, 387-396	4.7	
64	A survey of genetic variants in SARS-CoV-2 interacting domains of ACE2, TMPRSS2 and TLR3/7/8 across populations. <i>Infection, Genetics and Evolution</i> , 2020 , 85, 104507	4.5	15
63	The Genomics Research and Innovation Network: creating an interoperable, federated, genomics learning system. <i>Genetics in Medicine</i> , 2020 , 22, 371-380	8.1	19
62	An Improved Prediction Model for Ovarian Cancer Using Urinary Biomarkers and a Novel Validation Strategy. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	8
61	T Cell-Specific Adaptor Protein Regulates Mitochondrial Function and CD4 T Regulatory Cell Activity In Vivo following Transplantation. <i>Journal of Immunology</i> , 2019 , 203, 2328-2338	5.3	4
60	A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. <i>American Journal of Human Genetics</i> , 2019 , 104, 1060-1072	11	39
59	Comparative analysis of whole-genome sequencing pipelines to minimize false negative findings. <i>Scientific Reports</i> , 2019 , 9, 3219	4.9	29

58	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. <i>Developmental Cell</i> , 2019 , 49, 10-29	10.2	39
57	DEPTOR modulates activation responses in CD4 T cells and enhances immunoregulation following transplantation. <i>American Journal of Transplantation</i> , 2019 , 19, 77-88	8.7	6
56	Highly differentiated cytotoxic T cells in inclusion body myositis. <i>Brain</i> , 2019 , 142, 2590-2604	11.2	22
55	Concordance between gene expression in peripheral whole blood and colonic tissue in children with inflammatory bowel disease. <i>PLoS ONE</i> , 2019 , 14, e0222952	3.7	9
54	Co-inhibitory T cell receptor KLRG1: human cancer expression and efficacy of neutralization in murine cancer models. <i>Oncotarget</i> , 2019 , 10, 1399-1406	3.3	17
53	A whole genome approach for discovering the genetic basis of blood group antigens: independent confirmation for P1 and Xg. <i>Transfusion</i> , 2019 , 59, 908-915	2.9	9
52	Solving for X: Evidence for sex-specific autism biomarkers across multiple transcriptomic studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019 , 180, 377-389	3.5	3
51	Measuring coverage and accuracy of whole-exome sequencing in clinical context. <i>Genetics in Medicine</i> , 2018 , 20, 1617-1626	8.1	23
50	Pluripotent stem cell-based therapy for Parkinson's disease: Current status and future prospects. <i>Progress in Neurobiology</i> , 2018 , 168, 1-20	10.9	47
49	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. <i>Lancet Haematology</i> , 2018 , 5, e241-e251	14.6	35
48	Learning a Comorbidity-Driven Taxonomy of Pediatric Pulmonary Hypertension. <i>Circulation Research</i> , 2017 , 121, 341-353	15.7	12
47	Comprehensive Analysis of Tissue-wide Gene Expression and Phenotype Data Reveals Tissues Affected in Rare Genetic Disorders. <i>Cell Systems</i> , 2017 , 5, 140-148.e2	10.6	8
46	Altered vulnerability to asthma at various levels of ambient Benzo[a]Pyrene by CTLA4, STAT4 and CYP2E1 polymorphisms. <i>Environmental Pollution</i> , 2017 , 231, 1134-1144	9.3	15
45	Blood transcriptomic comparison of individuals with and without autism spectrum disorder: A combined-samples mega-analysis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017 , 174, 181-201	3.5	34
44	Development of the Precision Link Biobank at Boston Children's Hospital: Challenges and Opportunities. <i>Journal of Personalized Medicine</i> , 2017 , 7,	3.6	13
43	A model-driven methodology for exploring complex disease comorbidities applied to autism spectrum disorder and inflammatory bowel disease. <i>Journal of Biomedical Informatics</i> , 2016 , 63, 366-378 ^{10.2}	10.2	9
42	ksRepo: a generalized platform for computational drug repositioning. <i>BMC Bioinformatics</i> , 2016 , 17, 78	3.6	34
41	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016 , 98, 1051-1066	11	107

40	Mitf is a master regulator of the v-ATPase, forming a control module for cellular homeostasis with v-ATPase and TORC1. <i>Journal of Cell Science</i> , 2015 , 128, 2938-50	5.3	49
39	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. <i>Genetics in Medicine</i> , 2015 , 17, 536-44	8.1	30
38	Gene expression analysis in Fmr1KO mice identifies an immunological signature in brain tissue and mGluR5-related signaling in primary neuronal cultures. <i>Molecular Autism</i> , 2015 , 6, 66	6.5	11
37	I148M variant in PNPLA3 reduces central adiposity and metabolic disease risks while increasing nonalcoholic fatty liver disease. <i>Liver International</i> , 2015 , 35, 2537-46	7.9	24
36	Return of genomic results to research participants: the floor, the ceiling, and the choices in between. <i>American Journal of Human Genetics</i> , 2014 , 94, 818-26	11	283
35	Prioritizing disease-linked variants, genes, and pathways with an interactive whole-genome analysis pipeline. <i>Human Mutation</i> , 2014 , 35, 537-47	4.7	18
34	Reducing false-positive incidental findings with ensemble genotyping and logistic regression based variant filtering methods. <i>Human Mutation</i> , 2014 , 35, 936-44	4.7	6
33	Divergent dysregulation of gene expression in murine models of fragile X syndrome and tuberous sclerosis. <i>Molecular Autism</i> , 2014 , 5, 16	6.5	15
32	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. <i>Trials</i> , 2014 , 15, 85	2.8	103
31	Pathway-based outlier method reveals heterogeneous genomic structure of autism in blood transcriptome. <i>BMC Medical Genomics</i> , 2013 , 6, 34	3.7	20
30	Cytosolic 5Vnucleotidase 1A autoimmunity in sporadic inclusion body myositis. <i>Annals of Neurology</i> , 2013 , 73, 408-18	9.4	174
29	Polycomb repressive complex 2 regulates normal development of the mouse heart. <i>Circulation Research</i> , 2012 , 110, 406-15	15.7	155
28	Characteristics and predictive value of blood transcriptome signature in males with autism spectrum disorders. <i>PLoS ONE</i> , 2012 , 7, e49475	3.7	106
27	Taxonomizing, sizing, and overcoming the incidentalome. <i>Genetics in Medicine</i> , 2012 , 14, 399-404	8.1	93
26	gSearch: a fast and flexible general search tool for whole-genome sequencing. <i>Bioinformatics</i> , 2012 , 28, 2176-7	7.2	7
25	CompleteMOTIFs: DNA motif discovery platform for transcription factor binding experiments. <i>Bioinformatics</i> , 2011 , 27, 715-7	7.2	42
24	Co-occupancy by multiple cardiac transcription factors identifies transcriptional enhancers active in heart. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5632-7 ^{11.5}		276
23	Heart failure-associated changes in RNA splicing of sarcomere genes. <i>Circulation: Cardiovascular Genetics</i> , 2010 , 3, 138-46		91

22	Interferon-stimulated gene 15 (ISG15) conjugates proteins in dermatomyositis muscle with perifascicular atrophy. <i>Annals of Neurology</i> , 2010 , 67, 53-63	9.4	121
21	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. <i>Bioinformatics</i> , 2009 , 25, 3121-7	7.2	17
20	MicroRNA-1 negatively regulates expression of the hypertrophy-associated calmodulin and Mef2a genes. <i>Molecular and Cellular Biology</i> , 2009 , 29, 2193-204	4.8	320
19	Fast-twitch sarcomeric and glycolytic enzyme protein loss in inclusion body myositis. <i>Muscle and Nerve</i> , 2009 , 39, 739-53	3.4	38
18	Fog2 is critical for cardiac function and maintenance of coronary vasculature in the adult mouse heart. <i>Journal of Clinical Investigation</i> , 2009 , 119, 1462-76	15.9	55
17	Analysis of the Otd-dependent transcriptome supports the evolutionary conservation of CRX/OTX/OTD functions in flies and vertebrates. <i>Developmental Biology</i> , 2008 , 315, 521-34	3.1	34
16	GATA4 is a direct transcriptional activator of cyclin D2 and Cdk4 and is required for cardiomyocyte proliferation in anterior heart field-derived myocardium. <i>Molecular and Cellular Biology</i> , 2008 , 28, 5420-31	4.8	98
15	Integrative analysis reveals the direct and indirect interactions between DNA copy number aberrations and gene expression changes. <i>Bioinformatics</i> , 2008 , 24, 889-96	7.2	62
14	Phenotypic diversity and altered environmental plasticity in <i>Arabidopsis thaliana</i> with reduced Hsp90 levels. <i>PLoS ONE</i> , 2007 , 2, e648	3.7	121
13	Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. <i>Arthritis and Rheumatism</i> , 2007 , 56, 3784-92		212
12	Altered microRNA expression in human heart disease. <i>Physiological Genomics</i> , 2007 , 31, 367-73	3.6	501
11	Network-based analysis of affected biological processes in type 2 diabetes models. <i>PLoS Genetics</i> , 2007 , 3, e96	6	142
10	Statistical methods in cardiac gene expression profiling: from image to function. <i>Methods in Molecular Biology</i> , 2007 , 366, 75-105	1.4	1
9	A multivariate approach for integrating genome-wide expression data and biological knowledge. <i>Bioinformatics</i> , 2006 , 22, 2373-80	7.2	106
8	Development of heart valves requires Gata4 expression in endothelial-derived cells. <i>Development (Cambridge)</i> , 2006 , 133, 3607-18	6.6	144
7	Gata4 is required for maintenance of postnatal cardiac function and protection from pressure overload-induced heart failure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14471-6	11.5	147
6	Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. <i>Physiological Genomics</i> , 2005 , 21, 34-42	3.6	98
5	CrossChip: a system supporting comparative analysis of different generations of Affymetrix arrays. <i>Bioinformatics</i> , 2005 , 21, 2116-7	7.2	15

4	Discovering statistically significant pathways in expression profiling studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13544-9	11.5	503
3	The insulin-like growth factor 1 receptor induces physiological heart growth via the phosphoinositide 3-kinase(p110alpha) pathway. <i>Journal of Biological Chemistry</i> , 2004 , 279, 4782-93	5.4	287
2	Mouse cardiac surgery: comprehensive techniques for the generation of mouse models of human diseases and their application for genomic studies. <i>Physiological Genomics</i> , 2004 , 16, 349-60	3.6	250
1	Combining gene expression data from different generations of oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2004 , 5, 159	3.6	42