Sek Won Kong

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.

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	Discovering statistically significant pathways in expression profiling studies. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 13544-9	11.5	503
74	Altered microRNA expression in human heart disease. *Physiological Genomics*, **2007**, 31, 367-73	3.6	501
73	MicroRNA-1 negatively regulates expression of the hypertrophy-associated calmodulin and Mef2a genes. *Molecular and Cellular Biology*, **2009**, 29, 2193-204	4.8	320
72	The insulin-like growth factor 1 receptor induces physiological heart growth via the phosphoinositide 3-kinase(p110alpha) pathway. *Journal of Biological Chemistry*, **2004**, 279, 4782-93	5.4	287
71	Return of genomic results to research participants: the floor, the ceiling, and the choices in between. *American Journal of Human Genetics*, **2014**, 94, 818-26	11	283
70	Co-occupancy by multiple cardiac transcription factors identifies transcriptional enhancers active in heart. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 5632-7	11.5	276
69	Mouse cardiac surgery: comprehensive techniques for the generation of mouse models of human diseases and their application for genomic studies. *Physiological Genomics*, **2004**, 16, 349-60	3.6	250
68	Type I interferon-inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. *Arthritis and Rheumatism*, **2007**, 56, 3784-92		212
67	Cytosolic 5∀nucleotidase 1A autoimmunity in sporadic inclusion body myositis. *Annals of Neurology*, **2013**, 73, 408-18	9.4	174
66	Polycomb repressive complex 2 regulates normal development of the mouse heart. *Circulation Research*, **2012**, 110, 406-15	15.7	155
65	Gata4 is required for maintenance of postnatal cardiac function and protection from pressure overload-induced heart failure. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 14471-6	11.5	147
64	Development of heart valves requires Gata4 expression in endothelial-derived cells. *Development (Cambridge)*, **2006**, 133, 3607-18	6.6	144
63	Network-based analysis of affected biological processes in type 2 diabetes models. *PLoS Genetics*, **2007**, 3, e96	6	142
62	Interferon-stimulated gene 15 (ISG15) conjugates proteins in dermatomyositis muscle with perifascicular atrophy. *Annals of Neurology*, **2010**, 67, 53-63	9.4	121
61	Phenotypic diversity and altered environmental plasticity in Arabidopsis thaliana with reduced Hsp90 levels. *PLoS ONE*, **2007**, 2, e648	3.7	121
60	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. *American Journal of Human Genetics*, **2016**, 98, 1051-1066	11	107
59	Characteristics and predictive value of blood transcriptome signature in males with autism spectrum disorders. *PLoS ONE*, **2012**, 7, e49475	3.7	106

58	A multivariate approach for integrating genome-wide expression data and biological knowledge. *Bioinformatics*, **2006**, 22, 2373-80	7.2	106
57	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. *Trials*, **2014**, 15, 85	2.8	103
56	GATA4 is a direct transcriptional activator of cyclin D2 and Cdk4 and is required for cardiomyocyte proliferation in anterior heart field-derived myocardium. *Molecular and Cellular Biology*, **2008**, 28, 5420-31	4.8	98
55	Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. *Physiological Genomics*, **2005**, 21, 34-42	3.6	98
54	Taxonomizing, sizing, and overcoming the incidentalome. *Genetics in Medicine*, **2012**, 14, 399-404	8.1	93
53	Heart failure-associated changes in RNA splicing of sarcomere genes. *Circulation: Cardiovascular Genetics*, **2010**, 3, 138-46		91
52	Integrative analysis reveals the direct and indirect interactions between DNA copy number aberrations and gene expression changes. *Bioinformatics*, **2008**, 24, 889-96	7.2	62
51	Human autologous iPSC-derived dopaminergic progenitors restore motor function in Parkinson's disease models. *Journal of Clinical Investigation*, **2020**, 130, 904-920	15.9	55
50	Fog2 is critical for cardiac function and maintenance of coronary vasculature in the adult mouse heart. *Journal of Clinical Investigation*, **2009**, 119, 1462-76	15.9	55
49	Mitf is a master regulator of the v-ATPase, forming a control module for cellular homeostasis with v-ATPase and TORC1. *Journal of Cell Science*, **2015**, 128, 2938-50	5.3	49
48	Pluripotent stem cell-based therapy for Parkinson's disease: Current status and future prospects. *Progress in Neurobiology*, **2018**, 168, 1-20	10.9	47
47	CompleteMOTIFs: DNA motif discovery platform for transcription factor binding experiments. *Bioinformatics*, **2011**, 27, 715-7	7.2	42
46	Combining gene expression data from different generations of oligonucleotide arrays. *BMC Bioinformatics*, **2004**, 5, 159	3.6	42
45	A Recurrent Missense Variant in AP2M1 Impairs Clathrin-Mediated Endocytosis and Causes Developmental and Epileptic Encephalopathy. *American Journal of Human Genetics*, **2019**, 104, 1060-1072	11	39
44	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. *Developmental Cell*, **2019**, 49, 10-29	10.2	39
43	Fast-twitch sarcomeric and glycolytic enzyme protein loss in inclusion body myositis. *Muscle and Nerve*, **2009**, 39, 739-53	3.4	38
42	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. *Lancet Haematology,the*, **2018**, 5, e241-e251	14.6	35
41	ksRepo: a generalized platform for computational drug repositioning. *BMC Bioinformatics*, **2016**, 17, 78	3.6	34

40	Blood transcriptomic comparison of individuals with and without autism spectrum disorder: A combined-samples mega-analysis. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 181-201	3.5	34
39	Analysis of the Otd-dependent transcriptome supports the evolutionary conservation of CRX/OTX/OTD functions in flies and vertebrates. *Developmental Biology*, **2008**, 315, 521-34	3.1	34
38	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. *Genetics in Medicine*, **2015**, 17, 536-44	8.1	30
37	Comparative analysis of whole-genome sequencing pipelines to minimize false negative findings. *Scientific Reports*, **2019**, 9, 3219	4.9	29
36	I148M variant in PNPLA3 reduces central adiposity and metabolic disease risks while increasing nonalcoholic fatty liver disease. *Liver International*, **2015**, 35, 2537-46	7.9	24
35	Measuring coverage and accuracy of whole-exome sequencing in clinical context. *Genetics in Medicine*, **2018**, 20, 1617-1626	8.1	23
34	Highly differentiated cytotoxic T cells in inclusion body myositis. *Brain*, **2019**, 142, 2590-2604	11.2	22
33	Pathway-based outlier method reveals heterogeneous genomic structure of autism in blood transcriptome. *BMC Medical Genomics*, **2013**, 6, 34	3.7	20
32	The Genomics Research and Innovation Network: creating an interoperable, federated, genomics learning system. *Genetics in Medicine*, **2020**, 22, 371-380	8.1	19
31	Prioritizing disease-linked variants, genes, and pathways with an interactive whole-genome analysis pipeline. *Human Mutation*, **2014**, 35, 537-47	4.7	18
30	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. *Bioinformatics*, **2009**, 25, 3121-7	7.2	17
29	Co-inhibitory T cell receptor KLRG1: human cancer expression and efficacy of neutralization in murine cancer models. *Oncotarget*, **2019**, 10, 1399-1406	3.3	17
28	Divergent dysregulation of gene expression in murine models of fragile X syndrome and tuberous sclerosis. *Molecular Autism*, **2014**, 5, 16	6.5	15
27	Altered vulnerability to asthma at various levels of ambient Benzo[a]Pyrene by CTLA4, STAT4 and CYP2E1 polymorphisms. *Environmental Pollution*, **2017**, 231, 1134-1144	9.3	15
26	CrossChip: a system supporting comparative analysis of different generations of Affymetrix arrays. *Bioinformatics*, **2005**, 21, 2116-7	7.2	15
25	A survey of genetic variants in SARS-CoV-2 interacting domains of ACE2, TMPRSS2 and TLR3/7/8 across populations. *Infection, Genetics and Evolution*, **2020**, 85, 104507	4.5	15
24	Development of the Precision Link Biobank at Boston Children's Hospital: Challenges and Opportunities. *Journal of Personalized Medicine*, **2017**, 7,	3.6	13
23	Learning a Comorbidity-Driven Taxonomy of Pediatric Pulmonary Hypertension. *Circulation Research*, **2017**, 121, 341-353	15.7	12

22	Gene expression analysis in Fmr1KO mice identifies an immunological signature in brain tissue and mGluR5-related signaling in primary neuronal cultures. *Molecular Autism*, **2015**, 6, 66	6.5	11
21	A model-driven methodology for exploring complex disease comorbidities applied to autism spectrum disorder and inflammatory bowel disease. *Journal of Biomedical Informatics*, **2016**, 63, 366-378	10.2	9
20	Concordance between gene expression in peripheral whole blood and colonic tissue in children with inflammatory bowel disease. *PLoS ONE*, **2019**, 14, e0222952	3.7	9
19	A whole genome approach for discovering the genetic basis of blood group antigens: independent confirmation for P1 and Xg. *Transfusion*, **2019**, 59, 908-915	2.9	9
18	An Improved Prediction Model for Ovarian Cancer Using Urinary Biomarkers and a Novel Validation Strategy. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	8
17	Comprehensive Analysis of Tissue-wide Gene Expression and Phenotype Data Reveals Tissues Affected in Rare Genetic Disorders. *Cell Systems*, **2017**, 5, 140-148.e2	10.6	8
16	gSearch: a fast and flexible general search tool for whole-genome sequencing. *Bioinformatics*, **2012**, 28, 2176-7	7.2	7
15	Two macrophages, osteoclasts and microglia: from development to pleiotropy. *Bone Research*, **2021**, 9, 11	13.3	7
14	DEPTOR modulates activation responses in CD4 T cells and enhances immunoregulation following transplantation. *American Journal of Transplantation*, **2019**, 19, 77-88	8.7	6
13	Reducing false-positive incidental findings with ensemble genotyping and logistic regression based variant filtering methods. *Human Mutation*, **2014**, 35, 936-44	4.7	6
12	T Cell-Specific Adaptor Protein Regulates Mitochondrial Function and CD4 T Regulatory Cell Activity In Vivo following Transplantation. *Journal of Immunology*, **2019**, 203, 2328-2338	5.3	4
11	Solving for X: Evidence for sex-specific autism biomarkers across multiple transcriptomic studies. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 377-389	3.5	3
10	GenoPheno: cataloging large-scale phenotypic and next-generation sequencing data within human datasets. *Briefings in Bioinformatics*, **2021**, 22, 55-65	13.4	3
9	Assessment of coverage for endogenous metabolites and exogenous chemical compounds using an untargeted metabolomics platform. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2020**, 25, 587-598	1.3	2
8	Genetic variation analyses indicate conserved SARS-CoV-2-host interaction and varied genetic adaptation in immune response factors in modern human evolution. *Development Growth and Differentiation*, **2021**, 63, 219-227	3	2
7	WEScover: selection between clinical whole exome sequencing and gene panel testing. *BMC Bioinformatics*, **2021**, 22, 259	3.6	2
6	A two-step gas chromatography-tandem mass spectrometry method for measurement of multiple environmental pollutants in human plasma. *Environmental Science and Pollution Research*, **2021**, 28, 3266-3279	5.1	2
5	Inhibition of mevalonate metabolism by statins augments the immunoregulatory phenotype of vascular endothelial cells and inhibits the costimulation of CD4 T cells. *American Journal of Transplantation*, **2021**,	8.7	1

4	Statistical methods in cardiac gene expression profiling: from image to function. *Methods in Molecular Biology*, **2007**, 366, 75-105	1.4	1
3	Plasma metabolomics of autism spectrum disorder and influence of shared components in proband families. **2021**, 1, osab004		0
2	The Clinical Genome and Ancestry Report: An interactive web application for prioritizing clinically implicated variants from genome sequencing data with ancestry composition. *Human Mutation*, **2020**, 41, 387-396	4.7	
1	Investigation of genetic variants in SARS-CoV-2-interacting molecules of ACE2, TMPRSS2 and TLR3/7/8 across populations. *Proceedings for Annual Meeting of the Japanese Pharmacological Society*, **2021**, 94, 1-P2-36	0	