Sek Won Kong

List of Publications by Year
in descending order

77 papers	6,862 citations	87888 38 h-index	76900 74 g-index
82 all docs	82 docs citations	82 times ranked	12247 citing authors

#	Article	IF	Citations
1	Discovering statistically significant pathways in expression profiling studies. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13544-13549.	7.1	583
2	Altered microRNA expression in human heart disease. Physiological Genomics, 2007, 31, 367-373.	2.3	564
3	MicroRNA-1 Negatively Regulates Expression of the Hypertrophy-Associated Calmodulin and Mef2a Genes. Molecular and Cellular Biology, 2009, 29, 2193-2204.	2.3	358
4	The Insulin-like Growth Factor 1 Receptor Induces Physiological Heart Growth via the Phosphoinositide 3-Kinase(p110Î±) Pathway. Journal of Biological Chemistry, 2004, 279, 4782-4793.	3.4	350
5	Return of Genomic Results to Research Participants: The Floor, the Ceiling, and the Choices In Between. American Journal of Human Genetics, 2014, 94, 818-826.	6.2	342
6	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, 5632-5637.	7.1	316
7	Mouse cardiac surgery: comprehensive techniques for the generation of mouse models of human diseases and their application for genomic studies. Physiological Genomics, 2004, 16, 349-360.	2.3	291
8	Type I interferonâ€“inducible gene expression in blood is present and reflects disease activity in dermatomyositis and polymyositis. Arthritis and Rheumatism, 2007, 56, 3784-3792.	6.7	264
9	Cytosolic 5â€²â€nucleotidase 1A autoimmunity in sporadic inclusion body myositis. Annals of Neurology, 2013, 73, 408-418.	5.3	230
10	Polycomb Repressive Complex 2 Regulates Normal Development of the Mouse Heart. Circulation Research, 2012, 110, 406-415.	4.5	188
11	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, 14471-14476.	7.1	170
12	Network-Based Analysis of Affected Biological Processes in Type 2 Diabetes Models. PLoS Genetics, 2007, 3, e96.	3.5	166
13	Development of heart valves requires Gata4 expression in endothelial-derived cells. Development (Cambridge), 2006, 133, 3607-3618.	2.5	163
14	Phenotypic Diversity and Altered Environmental Plasticity in Arabidopsis thaliana with Reduced Hsp90 Levels. PLoS ONE, 2007, 2, e648.	2.5	159
15	Interferonâ€stimulated gene 15 (ISG15) conjugates proteins in dermatomyositis muscle with perifascicular atrophy. Annals of Neurology, 2010, 67, 53-63.	5.3	153
16	Characteristics and Predictive Value of Blood Transcriptome Signature in Males with Autism Spectrum Disorders. PLoS ONE, 2012, 7, e49475.	2.5	151
17	Heart Failureâ€“Associated Changes in RNA Splicing of Sarcomere Genes. Circulation: Cardiovascular Genetics, 2010, 3, 138-146.	5.1	137
18	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137

#	Article	IF	Citations
19	A multivariate approach for integrating genome-wide expression data and biological knowledge. Bioinformatics, 2006, 22, 2373-2380.	4.1	122
20	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. Trials, 2014, 15, 85.	1.6	122
21	Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. Physiological Genomics, 2005, 21, 34-42.	2.3	108
22	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, 5420-5431.	2.3	107
23	Taxonomizing, sizing, and overcoming the incidentalome. Genetics in Medicine, 2012, 14, 399-404.	2.4	102
24	Human autologous iPSCâ€“derived dopaminergic progenitors restore motor function in Parkinsonâ€™s disease models. Journal of Clinical Investigation, 2020, 130, 904-920.	8.2	102
25	Pluripotent stem cell-based therapy for Parkinsonâ€™s disease: Current status and future prospects. Progress in Neurobiology, 2018, 168, 1-20.	5.7	84
26	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.	6.2	78
27	Highly differentiated cytotoxic T cells in inclusion body myositis. Brain, 2019, 142, 2590-2604.	7.6	73
28	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. Lancet Haematology,the, 2018, 5, e241-e251.	4.6	70
29	Integrative analysis reveals the direct and indirect interactions between DNA copy number aberrations and gene expression changes. Bioinformatics, 2008, 24, 889-896.	4.1	68
30	Mitf is a master regulator of the v-ATPase forming an Mitf/v-ATPase/TORC1 control module for cellular homeostasis. Journal of Cell Science, 2015, 128, 2938-50.	2.0	68
31	Fog2 is critical for cardiac function and maintenance of coronary vasculature in the adult mouse heart. Journal of Clinical Investigation, 2009, 119, 1462-1476.	8.2	64
32	Comparative analysis of whole-genome sequencing pipelines to minimize false negative findings. Scientific Reports, 2019, 9, 3219.	3.3	57
33	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
34	Blood transcriptomic comparison of individuals with and without autism spectrum disorder: A combinedâ€samples megaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 181-201.	1.7	54
35	Combining gene expression data from different generations of oligonucleotide arrays. BMC Bioinformatics, 2004, 5, 159.	2.6	52
36	Measuring coverage and accuracy of whole-exome sequencing in clinical context. Genetics in Medicine, 2018, 20, 1617-1626.	2.4	50

#	Article	IF	Citations
37	ksRepo: a generalized platform for computational drug repositioning. BMC Bioinformatics, 2016, 17, 78.	2.6	46
38	CompleteMOTIFs: DNA motif discovery platform for transcription factor binding experiments. Bioinformatics, 2011, 27, 715-717.	4.1	43
39	Fastâ€twitch sarcomeric and glycolytic enzyme protein loss in inclusion body myositis. Muscle and Nerve, 2009, 39, 739-753.	2.2	41
40	Analysis of the Otd-dependent transcriptome supports the evolutionary conservation of CRX/OTX/OTD functions in flies and vertebrates. Developmental Biology, 2008, 315, 521-534.	2.0	39
41	Co-inhibitory T cell receptor KLRG1: human cancer expression and efficacy of neutralization in murine cancer models. Oncotarget, 2019, 10, 1399-1406.	1.8	35
42	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. Genetics in Medicine, 2015, 17, 536-544.	2.4	34
43	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.	2.3	31
44	The Genomics Research and Innovation Network: creating an interoperable, federated, genomics learning system. Genetics in Medicine, 2020, 22, 371-380.	2.4	30
45	Concordance between gene expression in peripheral whole blood and colonic tissue in children with inflammatory bowel disease. PLoS ONE, 2019, 14, e0222952.	2.5	28
46	I148<scp>M</scp> variant in <scp>PNPLA</scp>3 reduces central adiposity and metabolic disease risks while increasing nonalcoholic fatty liver disease. Liver International, 2015, 35, 2537-2546.	3.9	27
47	Pathway-based outlier method reveals heterogeneous genomic structure of autism in blood transcriptome. BMC Medical Genomics, 2013, 6, 34.	1.5	24
48	Altered vulnerability to asthma at various levels of ambient Benzo[a]Pyrene by CTLA4, STAT4 and CYP2E1 polymorphisms. Environmental Pollution, 2017, 231, 1134-1144.	7.5	24
49	Prioritizing Disease-Linked Variants, Genes, and Pathways with an Interactive Whole-Genome Analysis Pipeline. Human Mutation, 2014, 35, 537-547.	2.5	23
50	Two macrophages, osteoclasts and microglia: from development to pleiotropy. Bone Research, 2021, 9, 11.	11.4	22
51	Learning a Comorbidity-Driven Taxonomy of Pediatric Pulmonary Hypertension. Circulation Research, 2017, 121, 341-353.	4.5	21
52	Integration of heterogeneous expression data sets extends the role of the retinol pathway in diabetes and insulin resistance. Bioinformatics, 2009, 25, 3121-3127.	4.1	20
53	Development of the Precision Link Biobank at Boston Childrenâ€™s Hospital: Challenges and Opportunities. Journal of Personalized Medicine, 2017, 7, 21.	2.5	20
54	Divergent dysregulation of gene expression in murine models of fragile X syndrome and tuberous sclerosis. Molecular Autism, 2014, 5, 16.	4.9	18

#	Article	IF	Citations
55	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.	4.9	18
56	Comprehensive Analysis of Tissue-wide Gene Expression and Phenotype Data Reveals Tissues Affected in Rare Genetic Disorders. Cell Systems, 2017, 5, 140-148.e2.	6.2	18
57	CrossChip: a system supporting comparative analysis of different generations of Affymetrix arrays. Bioinformatics, 2005, 21, 2116-2117.	4.1	17
58	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.	4.3	14
59	A whole genome approach for discovering the genetic basis of blood group antigens: independent confirmation for P1 and Xg^a. Transfusion, 2019, 59, 908-915.	1.6	13
60	DEPTOR modulates activation responses in CD4+ T cells and enhances immunoregulation following transplantation. American Journal of Transplantation, 2019, 19, 77-88.	4.7	12
61	Reducing False-Positive Incidental Findings with Ensemble Genotyping and Logistic Regression Based Variant Filtering Methods. Human Mutation, 2014, 35, 936-944.	2.5	10
62	An Improved Prediction Model for Ovarian Cancer Using Urinary Biomarkers and a Novel Validation Strategy. International Journal of Molecular Sciences, 2019, 20, 4938.	4.1	10
63	Genetic variation analyses indicate conserved SARSâ€CoVâ€2â€“host interaction and varied genetic adaptation in immune response factors in modern human evolution. Development Growth and Differentiation, 2021, 63, 219-227.	1.5	10
64	Solving for X: Evidence for sexâ€specific autism biomarkers across multiple transcriptomic studies. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 377-389.	1.7	8
65	GenoPheno: cataloging large-scale phenotypic and next-generation sequencing data within human datasets. Briefings in Bioinformatics, 2021, 22, 55-65.	6.5	8
66	gSearch: a fast and flexible general search tool for whole-genome sequencing. Bioinformatics, 2012, 28, 2176-2177.	4.1	7
67	T Cellâ€“Specific Adaptor Protein Regulates Mitochondrial Function and CD4+ T Regulatory Cell Activity In Vivo following Transplantation. Journal of Immunology, 2019, 203, 2328-2338.	0.8	5
68	Plasma metabolomics of autism spectrum disorder and influence of shared components in proband families. Exposome, 2021, 1, osab004.	2.8	5
69	Assessment of coverage for endogenous metabolites and exogenous chemical compounds using an untargeted metabolomics platform. , 2019, , .		5
70	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.	5.3	4
71	WEScover: selection between clinical whole exome sequencing and gene panel testing. BMC Bioinformatics, 2021, 22, 259.	2.6	4
72	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, 2022, 22, 947-954.	4.7	3

#	Article	IF	Citations
73	Increased Prevalence of Familial Autoimmune Disease in Children With Opsoclonus-Myoclonus Syndrome. Neurology: Neuroimmunology and NeuroInflammation, 2021, 8, e1079.	6.0	2
74	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.	0.7	2
75	Statistical Methods in Cardiac Gene Expression Profiling. Methods in Molecular Biology, 2007, 366, 75-105.	0.9	1
76	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.	2.5	0
77	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.	0.0	0