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	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
2	GenoPheno: cataloging large-scale phenotypic and next-generation sequencing data within human datasets. Briefings in Bioinformatics, 2021, 22, 55-65.	6.5	8
3	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
4	Two macrophages, osteoclasts and microglia: from development to pleiotropy. Bone Research, 2021, 9, 11.	11.4	22
5	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
6	WEScover: selection between clinical whole exome sequencing and gene panel testing. BMC Bioinformatics, 2021, 22, 259.	2.6	4
7	Increased Prevalence of Familial Autoimmune Disease in Children With Opsoclonus-Myoclonus Syndrome. Neurology: Neuroimmunology and NeuroInflammation, 2021, 8, e1079.	6.0	2
8	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
9	Plasma metabolomics of autism spectrum disorder and influence of shared components in proband families. Exposome, 2021, 1, osab004.	2.8	5
10	The Genomics Research and Innovation Network: creating an interoperable, federated, genomics learning system. Genetics in Medicine, 2020, 22, 371-380.	2.4	30
11	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
12	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
13	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
14	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
15	DEPTOR modulates activation responses in CD4+ T cells and enhances immunoregulation following transplantation. American Journal of Transplantation, 2019, 19, 77-88.	4.7	12
16	Highly differentiated cytotoxic T cells in inclusion body myositis. Brain, 2019, 142, 2590-2604.	7.6	73
17	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
18	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

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19	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
20	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
21	Comparative analysis of whole-genome sequencing pipelines to minimize false negative findings. Scientific Reports, 2019, 9, 3219.	3.3	57
22	The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. Developmental Cell, 2019, 49, 10-29.	7.0	57
23	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
24	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
25	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
26	Assessment of coverage for endogenous metabolites and exogenous chemical compounds using an untargeted metabolomics platform. , 2019, , .		5
27	Measuring coverage and accuracy of whole-exome sequencing in clinical context. Genetics in Medicine, 2018, 20, 1617-1626.	2.4	50
28	Pluripotent stem cell-based therapy for Parkinsonâ€™s disease: Current status and future prospects. Progress in Neurobiology, 2018, 168, 1-20.	5.7	84
29	Automated typing of red blood cell and platelet antigens: a whole-genome sequencing study. Lancet Haematology,the, 2018, 5, e241-e251.	4.6	70
30	Learning a Comorbidity-Driven Taxonomy of Pediatric Pulmonary Hypertension. Circulation Research, 2017, 121, 341-353.	4.5	21
31	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
32	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
33	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
34	Development of the Precision Link Biobank at Boston Childrenâ€™s Hospital: Challenges and Opportunities. Journal of Personalized Medicine, 2017, 7, 21.	2.5	20
35	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. American Journal of Human Genetics, 2016, 98, 1051-1066.	6.2	137
36	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

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37	ksRepo: a generalized platform for computational drug repositioning. BMC Bioinformatics, 2016, 17, 78.	2.6	46
38	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
39	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
40	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
41	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. Genetics in Medicine, 2015, 17, 536-544.	2.4	34
42	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
43	Prioritizing Disease-Linked Variants, Genes, and Pathways with an Interactive Whole-Genome Analysis Pipeline. Human Mutation, 2014, 35, 537-547.	2.5	23
44	Reducing False-Positive Incidental Findings with Ensemble Genotyping and Logistic Regression Based Variant Filtering Methods. Human Mutation, 2014, 35, 936-944.	2.5	10
45	Divergent dysregulation of gene expression in murine models of fragile X syndrome and tuberous sclerosis. Molecular Autism, 2014, 5, 16.	4.9	18
46	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. Trials, 2014, 15, 85.	1.6	122
47	Pathway-based outlier method reveals heterogeneous genomic structure of autism in blood transcriptome. BMC Medical Genomics, 2013, 6, 34.	1.5	24
48	Cytosolic 5â€²â€nucleotidase 1A autoimmunity in sporadic inclusion body myositis. Annals of Neurology, 2013, 73, 408-418.	5.3	230
49	Taxonomizing, sizing, and overcoming the incidentalome. Genetics in Medicine, 2012, 14, 399-404.	2.4	102
50	gSearch: a fast and flexible general search tool for whole-genome sequencing. Bioinformatics, 2012, 28, 2176-2177.	4.1	7
51	Polycomb Repressive Complex 2 Regulates Normal Development of the Mouse Heart. Circulation Research, 2012, 110, 406-415.	4.5	188
52	Characteristics and Predictive Value of Blood Transcriptome Signature in Males with Autism Spectrum Disorders. PLoS ONE, 2012, 7, e49475.	2.5	151
53	CompleteMOTIFs: DNA motif discovery platform for transcription factor binding experiments. Bioinformatics, 2011, 27, 715-717.	4.1	43
54	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

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55	Interferonâ€stimulated gene 15 (ISG15) conjugates proteins in dermatomyositis muscle with perifascicular atrophy. Annals of Neurology, 2010, 67, 53-63.	5.3	153
56	Heart Failureâ€"Associated Changes in RNA Splicing of Sarcomere Genes. Circulation: Cardiovascular Genetics, 2010, 3, 138-146.	5.1	137
57	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
58	MicroRNA-1 Negatively Regulates Expression of the Hypertrophy-Associated Calmodulin and Mef2a Genes. Molecular and Cellular Biology, 2009, 29, 2193-2204.	2.3	358
59	Fastâ€twitch sarcomeric and glycolytic enzyme protein loss in inclusion body myositis. Muscle and Nerve, 2009, 39, 739-753.	2.2	41
60	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
61	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
62	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
63	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
64	Network-Based Analysis of Affected Biological Processes in Type 2 Diabetes Models. PLoS Genetics, 2007, 3, e96.	3.5	166
65	Phenotypic Diversity and Altered Environmental Plasticity in Arabidopsis thaliana with Reduced Hsp90 Levels. PLoS ONE, 2007, 2, e648.	2.5	159
66	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
67	Altered microRNA expression in human heart disease. Physiological Genomics, 2007, 31, 367-373.	2.3	564
68	Statistical Methods in Cardiac Gene Expression Profiling. Methods in Molecular Biology, 2007, 366, 75-105.	0.9	1
69	A multivariate approach for integrating genome-wide expression data and biological knowledge. Bioinformatics, 2006, 22, 2373-2380.	4.1	122
70	Development of heart valves requires Gata4 expression in endothelial-derived cells. Development (Cambridge), 2006, 133, 3607-3618.	2.5	163
71	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
72	Genetic expression profiles during physiological and pathological cardiac hypertrophy and heart failure in rats. Physiological Genomics, 2005, 21, 34-42.	2.3	108

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73	CrossChip: a system supporting comparative analysis of different generations of Affymetrix arrays. Bioinformatics, 2005, 21, 2116-2117.	4.1	17
74	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
75	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
76	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
77	Combining gene expression data from different generations of oligonucleotide arrays. BMC Bioinformatics, 2004, 5, 159.	2.6	52