

Kouichi Ozaki

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.

77
papers

4,678
citations

30
h-index

68
g-index

88
ext. papers

5,499
ext. citations

9.8
avg, IF

4.47
L-index

#	Paper	IF	Citations
77	A functional variant of SHARPIN confers increased risk of late-onset Alzheimer's disease. <i>Journal of Human Genetics</i> , 2021 ,	4.3	1
76	JAMIR-eQTL: Japanese genome-wide identification of microRNA expression quantitative trait loci across dementia types. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	1
75	Dementia subtype prediction models constructed by penalized regression methods for multiclass classification using serum microRNA expression data. <i>Scientific Reports</i> , 2021 , 11, 20947	4.9	1
74	Ethnic and trans-ethnic genome-wide association studies identify new loci influencing Japanese Alzheimer's disease risk. <i>Translational Psychiatry</i> , 2021 , 11, 151	8.6	7
73	Structural and numerical Y chromosomal variations in elderly men identified through multiplex ligation-dependent probe amplification. <i>Journal of Human Genetics</i> , 2021 , 66, 1181-1184	4.3	1
72	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002670	5.2	9
71	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020 , 52, 669-679	36.3	85
70	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimer's disease patients. <i>PLoS ONE</i> , 2020 , 15, e0239196	3.7	2
69	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <i>Nature Genetics</i> , 2020 , 52, 1169-1177	36.3	51
68	Identification of potential blood biomarkers for early diagnosis of Alzheimer's disease through RNA sequencing analysis. <i>Alzheimers Research and Therapy</i> , 2020 , 12, 87	9	18
67	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimer's disease created by integrative analysis of multi-omics data. <i>Alzheimers Research and Therapy</i> , 2020 , 12, 145	9	9
66	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimer's disease patients 2020 , 15, e0239196		
65	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimer's disease patients 2020 , 15, e0239196		
64	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimer's disease patients 2020 , 15, e0239196		
63	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimer's disease patients 2020 , 15, e0239196		
62	A rare functional variant of SHARPIN attenuates the inflammatory response and associates with increased risk of late-onset Alzheimer's disease. <i>Molecular Medicine</i> , 2019 , 25, 20	6.2	22
61	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. <i>Communications Biology</i> , 2019 , 2, 77	6.7	27

60	Pathway analysis with genome-wide association study (GWAS) data detected the association of atrial fibrillation with the mTOR signaling pathway. <i>IJC Heart and Vasculature</i> , 2019 , 24, 100383	2.4	2
59	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data. <i>BMC Medical Genomics</i> , 2019 , 12, 150	3.7	13
58	Genetics of Coronary Disease 2019 , 21-36		
57	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis. <i>Scientific Reports</i> , 2018 , 8, 5608	4.9	15
56	Clinical utility and functional analysis of variants in atrial fibrillation-associated locus 4q25. <i>Journal of Cardiology</i> , 2017 , 70, 366-373	3	3
55	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. <i>Nature Genetics</i> , 2017 , 49, 953-958	36.3	89
54	Molecular genetics of coronary artery disease. <i>Journal of Human Genetics</i> , 2016 , 61, 71-7	4.3	47
53	A functional SNP in FLT1 increases risk of coronary artery disease in a Japanese population. <i>Journal of Human Genetics</i> , 2016 , 61, 435-41	4.3	8
52	Variations in ORAI1 Gene Associated with Kawasaki Disease. <i>PLoS ONE</i> , 2016 , 11, e0145486	3.7	30
51	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. <i>European Journal of Human Genetics</i> , 2015 , 23, 374-80	5.3	39
50	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. <i>PLoS ONE</i> , 2015 , 10, e0130329	3.7	20
49	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. <i>PLoS ONE</i> , 2015 , 10, e0139262	3.7	24
48	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. <i>Journal of the American College of Cardiology</i> , 2014 , 63, 1200-1210	15.1	102
47	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. <i>Circulation</i> , 2014 , 130, 1225-35	16.7	143
46	Novel calmodulin mutations associated with congenital arrhythmia susceptibility. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 466-74		133
45	Reduced risk of recurrent myocardial infarction in homozygous carriers of the chromosome 9p21 rs1333049 C risk allele in the contemporary percutaneous coronary intervention era: a prospective observational study. <i>BMJ Open</i> , 2014 , 4, e005438	3	8
44	Renin-angiotensin-aldosterone system polymorphisms and 5-year mortality in survivors of acute myocardial infarction: a report from the Osaka Acute Coronary Insufficiency Study. <i>International Heart Journal</i> , 2014 , 55, 190-6	1.8	7
43	Decreased mortality associated with statin treatment in patients with acute myocardial infarction and lymphotoxin-alpha C804A polymorphism. <i>Atherosclerosis</i> , 2013 , 227, 373-9	3.1	3

42	A genome-wide association study identifies three new risk loci for Kawasaki disease. <i>Nature Genetics</i> , 2012 , 44, 517-21	36.3	217
41	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012 , 44, 670-5	36.3	429
40	Haplotypes with copy number and single nucleotide polymorphisms in CYP2A6 locus are associated with smoking quantity in a Japanese population. <i>PLoS ONE</i> , 2012 , 7, e44507	3.7	42
39	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. <i>Journal of Human Genetics</i> , 2011 , 56, 47-51	4.3	26
38	BRAP Activates Inflammatory Cascades and Increases the Risk for Carotid Atherosclerosis. <i>Molecular Medicine</i> , 2011 , 17, 1065-74	6.2	33
37	Common variants in a novel gene, FONG on chromosome 2q33.1 confer risk of osteoporosis in Japanese. <i>PLoS ONE</i> , 2011 , 6, e19641	3.7	27
36	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. <i>Human Molecular Genetics</i> , 2011 , 20, 3684-92	5.6	42
35	Genetic Background of Myocardial Infarction 2011 , 113-120		
34	Prediction model for knee osteoarthritis based on genetic and clinical information. <i>Arthritis Research and Therapy</i> , 2010 , 12, R187	5.7	40
33	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. <i>Nature Genetics</i> , 2009 , 41, 329-33	36.3	83
32	Association of the tag SNPs in the human SKT gene (KIAA1217) with lumbar disc herniation. <i>Journal of Bone and Mineral Research</i> , 2009 , 24, 1537-43	6.3	33
31	Lymphotoxin-alpha3 mediates monocyte-endothelial interaction by TNFR I/NF-kappaB signaling. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 379, 374-8	3.4	5
30	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. <i>Nature Genetics</i> , 2008 , 40, 994-8	36.3	116
29	A functional polymorphism in THBS2 that affects alternative splicing and MMP binding is associated with lumbar-disc herniation. <i>American Journal of Human Genetics</i> , 2008 , 82, 1122-9	11	82
28	A functional SNP in EDG2 increases susceptibility to knee osteoarthritis in Japanese. <i>Human Molecular Genetics</i> , 2008 , 17, 1790-7	5.6	37
27	Genetic backgrounds of myocardial infarction. <i>Current Cardiovascular Risk Reports</i> , 2007 , 1, 427-431	0.9	
26	A functional polymorphism in COL11A1, which encodes the alpha 1 chain of type XI collagen, is associated with susceptibility to lumbar disc herniation. <i>American Journal of Human Genetics</i> , 2007 , 81, 1271-7	11	114
25	A functional SNP in ITIH3 is associated with susceptibility to myocardial infarction. <i>Journal of Human Genetics</i> , 2007 , 52, 220-229	4.3	27

24	Impact of atherosclerosis-related gene polymorphisms on mortality and recurrent events after myocardial infarction. <i>Atherosclerosis</i> , 2006 , 185, 400-5	3.1	30
23	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. <i>Nature Genetics</i> , 2006 , 38, 921-5	36.3	91
22	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. <i>Journal of Human Genetics</i> , 2006 , 51, 1087-1099	4.3	491
21	Inflammation as a risk factor for myocardial infarction. <i>Journal of Human Genetics</i> , 2006 , 51, 595-604	4.3	27
20	Genome-wide association study to identify single-nucleotide polymorphisms conferring risk of myocardial infarction. <i>Methods in Molecular Medicine</i> , 2006 , 128, 173-80		5
19	Genome-wide association study to identify SNPs conferring risk of myocardial infarction and their functional analyses. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 1804-13	10.3	41
18	Fine-scale SNP map of an 11-kb genomic region at 22q13.1 containing the galectin-1 gene. <i>Journal of Human Genetics</i> , 2005 , 50, 42-45	4.3	10
17	Functional variation in LGALS2 confers risk of myocardial infarction and regulates lymphotoxin-alpha secretion in vitro. <i>Nature</i> , 2004 , 429, 72-5	50.4	206
16	Identification of 46 novel SNPs in the 130-kb region containing a myocardial infarction susceptibility gene on chromosomal band 6p21. <i>Journal of Human Genetics</i> , 2003 , 48, 476-479	4.3	8
15	Functional SNPs in the lymphotoxin-alpha gene that are associated with susceptibility to myocardial infarction. <i>Nature Genetics</i> , 2002 , 32, 650-4	36.3	755
14	High-density single-nucleotide polymorphism (SNP) map in the 96-kb region containing the entire human DiGeorge syndrome critical region 2 (DGCR2) gene at 22q11.2. <i>Journal of Human Genetics</i> , 2001 , 46, 604-8	4.3	7
13	A high-throughput SNP typing system for genome-wide association studies. <i>Journal of Human Genetics</i> , 2001 , 46, 471-7	4.3	405
12	Isolation of a novel human lung-specific gene, LUNX, a potential molecular marker for detection of micrometastasis in non-small-cell lung cancer. <i>International Journal of Cancer</i> , 2001 , 91, 433-7	7.5	88
11	Complete cDNA sequence and genomic organization of a human pancreas-specific gene homologous to <i>Caenorhabditis elegans</i> sel-1. <i>Journal of Human Genetics</i> , 1999 , 44, 330-6	4.3	30
10	Isolation and mapping of a human lung-specific gene, TSA1902, encoding a novel chitinase family member. <i>Gene</i> , 1999 , 239, 325-31	3.8	27
9	Isolation and characterization of a novel human pancreas-specific gene, pancpin, that is down-regulated in pancreatic cancer cells 1998 , 22, 179-185		30
8	Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin. <i>Journal of Human Genetics</i> , 1998 , 43, 169-77	4.3	63
7	Isolation and mapping of a novel human kidney- and liver-specific gene homologous to the bacterial acetyltransferases. <i>Journal of Human Genetics</i> , 1998 , 43, 255-8	4.3	11

- 6 Isolation and characterization of a novel human lung-specific gene homologous to lysosomal membrane glycoproteins 1 and 2: significantly increased expression in cancers of various tissues. *Cancer Research*, **1998**, 58, 3499-503 10.1 34
- 5 Isolation of a novel gene showing reduced expression in metastatic colorectal carcinoma cell lines and carcinomas. *Japanese Journal of Cancer Research*, **1997**, 88, 725-31 6
- 4 Isolation of three testis-specific genes (TSA303, TSA806, TSA903) by a differential mRNA display method. *Genomics*, **1996**, 36, 316-9 4.3 34
- 3 Purification and some properties of ribonuclease from *Xenopus laevis* eggs. *Biological and Pharmaceutical Bulletin*, **1993**, 16, 353-6 2.3
- 2 Identification of myocardial infarction-susceptible genes and their functional analyses79-88
- 1 Molecular Genetics of Coronary Artery Disease1-10