Kouichi Ozaki

List of Publications by Year
in descending order

79 papers	6,156 citations	117571 34 h-index	88593 70 g-index
88 all docs	88 docs citations	88 times ranked	9704 citing authors

#	Article	IF	Citations
1	Functional SNPs in the lymphotoxin-Î± gene that are associated with susceptibility to myocardial infarction. Nature Genetics, 2002, 32, 650-654.	9.4	878
2	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. Journal of Human Genetics, 2006, 51, 1087-1099.	1.1	597
3	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	9.4	533
4	A high-throughput SNP typing system for genome-wide association studies. Journal of Human Genetics, 2001, 46, 471-477.	1.1	421
5	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	9.4	304
6	A genome-wide association study identifies three new risk loci for Kawasaki disease. Nature Genetics, 2012, 44, 517-521.	9.4	284
7	Functional variation in LGALS2 confers risk of myocardial infarction and regulates lymphotoxin-Î± secretion in vitro. Nature, 2004, 429, 72-75.	13.7	236
8	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. Nature Genetics, 2020, 52, 1169-1177.	9.4	206
9	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. Circulation, 2014, 130, 1225-1235.	1.6	183
10	Novel Calmodulin Mutations Associated With Congenital Arrhythmia Susceptibility. Circulation: Cardiovascular Genetics, 2014, 7, 466-474.	5.1	165
11	A Functional Polymorphism in COL11A1, Which Encodes the Î±1 Chain of Type XI Collagen, Is Associated with Susceptibility to Lumbar Disc Herniation. American Journal of Human Genetics, 2007, 81, 1271-1277.	2.6	144
12	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. Nature Genetics, 2017, 49, 953-958.	9.4	136
13	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. Nature Genetics, 2008, 40, 994-998.	9.4	134
14	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	1.2	127
15	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. Nature Genetics, 2006, 38, 921-925.	9.4	102
16	A Functional Polymorphism in THBS2 that Affects Alternative Splicing and MMP Binding Is Associated with Lumbar-Disc Herniation. American Journal of Human Genetics, 2008, 82, 1122-1129.	2.6	102
17	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. Nature Genetics, 2009, 41, 329-333.	9.4	102
18	Isolation of a novel human lung-specific gene,LUNX, a potential molecular marker for detection of micrometastasis in non-small-cell lung cancer. International Journal of Cancer, 2001, 91, 433-437.	2.3	94

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19	Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin. Journal of Human Genetics, 1998, 43, 169-177.	1.1	78
20	Molecular genetics of coronary artery disease. Journal of Human Genetics, 2016, 61, 71-77.	1.1	69
21	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. Human Molecular Genetics, 2011, 20, 3684-3692.	1.4	53
22	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. Communications Biology, 2019, 2, 77.	2.0	50
23	Prediction model for knee osteoarthritis based on genetic and clinical information. Arthritis Research and Therapy, 2010, 12, R187.	1.6	49
24	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. European Journal of Human Genetics, 2015, 23, 374-380.	1.4	48
25	Identification of potential blood biomarkers for early diagnosis of Alzheimerâ€™s disease through RNA sequencing analysis. Alzheimer's Research and Therapy, 2020, 12, 87.	3.0	48
26	Genome-wide association study to identify SNPs conferring risk of myocardial infarction and their functional analyses. Cellular and Molecular Life Sciences, 2005, 62, 1804-1813.	2.4	47
27	Haplotypes with Copy Number and Single Nucleotide Polymorphisms in CYP2A6 Locus Are Associated with Smoking Quantity in a Japanese Population. PLoS ONE, 2012, 7, e44507.	1.1	45
28	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002670.	1.6	44
29	Association of the Tag SNPs in the Human SKT Gene (KIAA1217) With Lumbar Disc Herniation. Journal of Bone and Mineral Research, 2009, 24, 1537-1543.	3.1	43
30	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. Journal of Human Genetics, 2011, 56, 47-51.	1.1	41
31	Variations in ORAI1 Gene Associated with Kawasaki Disease. PLoS ONE, 2016, 11, e0145486.	1.1	41
32	A functional SNP in EDG2 increases susceptibility to knee osteoarthritis in Japanese. Human Molecular Genetics, 2008, 17, 1790-1797.	1.4	40
33	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.	0.4	39
34	A functional SNP in ITIH3 is associated with susceptibility to myocardial infarction. Journal of Human Genetics, 2007, 52, 220-229.	1.1	38
35	BRAP Activates Inflammatory Cascades and Increases the Risk for Carotid Atherosclerosis. Molecular Medicine, 2011, 17, 1065-1074.	1.9	36
36	Isolation of Three Testis-Specific Genes (TSA303, TSA806, TSA903) by a Differential mRNA Display Method. Genomics, 1996, 36, 316-319.	1.3	35

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37	Common Variants in a Novel Gene, FONG on Chromosome 2q33.1 Confer Risk of Osteoporosis in Japanese. PLoS ONE, 2011, 6, e19641.	1.1	35
38	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. PLoS ONE, 2015, 10, e0139262.	1.1	35
39	Isolation and characterization of a novel human pancreas-specific gene,pancpin, that is down-regulated in pancreatic cancer cells. , 1998, 22, 179-185.		34
40	Ethnic and trans-ethnic genome-wide association studies identify new loci influencing Japanese Alzheimerâ€™s disease risk. Translational Psychiatry, 2021, 11, 151.	2.4	34
41	Complete cDNA sequence and genomic organization of a human pancreas-specific gene homologous to Caenorhabditis elegans sel-1. Journal of Human Genetics, 1999, 44, 330-336.	1.1	33
42	Impact of atherosclerosis-related gene polymorphisms on mortality and recurrent events after myocardial infarction. Atherosclerosis, 2006, 185, 400-405.	0.4	33
43	A rare functional variant of SHARPIN attenuates the inflammatory response and associates with increased risk of late-onset Alzheimerâ€™s disease. Molecular Medicine, 2019, 25, 20.	1.9	33
44	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimerâ€™s disease created by integrative analysis of multi-omics data. Alzheimer's Research and Therapy, 2020, 12, 145.	3.0	33
45	Inflammation as a risk factor for myocardial infarction. Journal of Human Genetics, 2006, 51, 595-604.	1.1	31
46	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. PLoS ONE, 2015, 10, e0130329.	1.1	30
47	Isolation and mapping of a human lung-specific gene, TSA1902, encoding a novel chitinase family member. Gene, 1999, 239, 325-331.	1.0	28
48	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data. BMC Medical Genomics, 2019, 12, 150.	0.7	22
49	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis. Scientific Reports, 2018, 8, 5608.	1.6	20
50	Lower DNA methylation levels in CpG island shores of CR1, CLU, and PICALM in the blood of Japanese Alzheimerâ€™s disease patients. PLoS ONE, 2020, 15, e0239196.	1.1	18
51	Whole-genome sequencing reveals novel ethnicity-specific rare variants associated with Alzheimerâ€™s disease. Molecular Psychiatry, 2022, 27, 2554-2562.	4.1	14
52	Fine-scale SNP map of an 11-kb genomic region at 22q13.1 containing the galectin-1 gene. Journal of Human Genetics, 2005, 50, 42-45.	1.1	12
53	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. BMJ Open, 2014, 4, e005438-e005438.	0.8	12
54	Isolation and mapping of a novel human kidney- and liver-specific gene homologous to the bacterial acetyltransferases. Journal of Human Genetics, 1998, 43, 255-258.	1.1	11

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55	A functional SNP in FLT1 increases risk of coronary artery disease in a Japanese population. Journal of Human Genetics, 2016, 61, 435-441.	1.1	10
56	Identification of 46 novel SNPs in the 130-kb region containing a myocardial infarction susceptibility gene on chromosomal band 6p21. Journal of Human Genetics, 2003, 48, 476-479.	1.1	9
57	Renin-Angiotensin-Aldosterone System Polymorphisms and 5-Year Mortality in Survivors of Acute Myocardial Infarction. International Heart Journal, 2014, 55, 190-196.	0.5	9
58	Lymphotoxin-Î±3 mediates monocyteâ€“endothelial interaction by TNFR I/NF-ÎºB signaling. Biochemical and Biophysical Research Communications, 2009, 379, 374-378.	1.0	8
59	A functional variant of SHARPIN confers increased risk of late-onset Alzheimerâ€™s disease. Journal of Human Genetics, 2022, 67, 203-208.	1.1	8
60	Isolation of a Novel Gene Showing Reduced Expression in Metastatic Colorectal Carcinoma Cell Lines and Carcinomas. Japanese Journal of Cancer Research, 1997, 88, 725-731.	1.7	7
61	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. Journal of Human Genetics, 2001, 46, 604-608.	1.1	7
62	Pathway analysis with genome-wide association study (GWAS) data detected the association of atrial fibrillation with the mTOR signaling pathway. IJC Heart and Vasculature, 2019, 24, 100383.	0.6	5
63	Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms Conferring Risk of Myocardial Infarction. Methods in Molecular Medicine, 2006, 128, 173-180.	0.8	5
64	Dementia subtype prediction models constructed by penalized regression methods for multiclass classification using serum microRNA expression data. Scientific Reports, 2021, 11, 20947.	1.6	5
65	Decreased mortality associated with statin treatment in patients with acute myocardial infarction and lymphotoxin-alpha C804A polymorphism. Atherosclerosis, 2013, 227, 373-379.	0.4	4
66	Clinical utility and functional analysis of variants in atrial fibrillation-associated locus 4q25. Journal of Cardiology, 2017, 70, 366-373.	0.8	4
67	JAMIR-eQTL: Japanese genome-wide identification of microRNA expression quantitative trait loci across dementia types. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	4
68	Structural and numerical Y chromosomal variations in elderly men identified through multiplex ligation-dependent probe amplification. Journal of Human Genetics, 2021, 66, 1181-1184.	1.1	3
69	Purification and Some Properties of Ribonuclease from Xenopus laevis Eggs.. Biological and Pharmaceutical Bulletin, 1993, 16, 353-356.	0.6	1
70	Networkâ€based metaâ€analysis and the candidate gene association studies reveal novel ethnicityâ€specific variants in <scp> MFSD3 </scp> and <scp> MRPL43 </scp> associated with dementia with Lewy bodies. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 0, , .	1.1	1
71	Genetic backgrounds of myocardial infarction. Current Cardiovascular Risk Reports, 2007, 1, 427-431.	0.8	0
72	Identification of myocardial infarction-susceptible genes and their functional analyses. , 0, , 79-88.		0

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73	Genetic Background of Myocardial Infarction. , 2011, , 113-120.		0
74	Genetics of Coronary Disease. , 2019, , 21-36.		0
75	Title is missing!. , 2020, 15, e0239196.		0
76	Title is missing!. , 2020, 15, e0239196.		0
77	Title is missing!. , 2020, 15, e0239196.		0
78	Title is missing!. , 2020, 15, e0239196.		0
79	Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms Conferring Risk of Myocardial Infarction. , 0, , 173-180.		0