Norihiro Kato

List of Publications by Year
in descending order

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85	9,805	57719	51562
papers	citations	44 h-index	86 g-index

89	89	89	15411
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
2	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
3	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	9.4	545
4	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nature Genetics, 2011, 43, 531-538.	9.4	516
5	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
6	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
7	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	9.4	372
8	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
9	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
10	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
11	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
12	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
13	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
14	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. Nature Genetics, 2012, 44, 302-306.	9.4	240
15	Confirmation of Multiple Risk Loci and Genetic Impacts by a Genome-Wide Association Study of Type 2 Diabetes in the Japanese Population. Diabetes, 2009, 58, 1690-1699.	0.3	216
16	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	1.4	192
17	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189
18	Blood Pressure and Hypertension Are Associated With 7 Loci in the Japanese Population. Circulation, 2010, 121, 2302-2309.	1.6	174

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19	Genome-wide association study of coronary artery disease in the Japanese. European Journal of Human Genetics, 2012, 20, 333-340.	1.4	156
20	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	1.4	135
21	Confirmation of ALDH2 as a Major Locus of Drinking Behavior and of Its Variants Regulating Multiple Metabolic Phenotypes in a Japanese Population. Circulation Journal, 2011, 75, 911-918.	0.7	128
22	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
23	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
24	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
25	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
26	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
27	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
28	Association of genetic variants for susceptibility to obesity with type 2 diabetes in Japanese individuals. Diabetologia, 2011, 54, 1350-1359.	2.9	70
29	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. Human Molecular Genetics, 2014, 23, 1108-1119.	1.4	68
30	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	2.0	68
31	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. Communications Biology, 2019, 2, 115.	2.0	66
32	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
33	Deletion of CDKAL1 Affects Mitochondrial ATP Generation and First-Phase Insulin Exocytosis. PLoS ONE, 2010, 5, e15553.	1.1	64
34	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. Human Molecular Genetics, 2013, 22, 2303-2311.	1.4	63
35	Genome-Wide Association Study Meta-Analysis Reveals Transethnic Replication of Mean Arterial and Pulse Pressure Loci. Hypertension, 2013, 62, 853-859.	1.3	63
36	Absence of Cd36 mutation in the original spontaneously hypertensive rats with insulin resistance. Nature Genetics, 1999, 22, 226-228.	9.4	59

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37	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.3	59
38	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. Scientific Reports, 2016, 6, 17958.	1.6	58
39	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. European Heart Journal, 2022, 43, 1702-1711.	1.0	58
40	High-density association study and nomination of susceptibility genes for hypertension in the Japanese National Project. Human Molecular Genetics, 2007, 17, 617-627.	1.4	53
41	Ethnic differences in genetic predisposition to hypertension. Hypertension Research, 2012, 35, 574-581.	1.5	51
42	Insights into the genetic basis of type 2 diabetes. Journal of Diabetes Investigation, 2013, 4, 233-244.	1.1	51
43	Non-alcoholic fatty liver disease in a rural, physically active, low income population in Sri Lanka. BMC Research Notes, 2011, 4, 513.	0.6	49
44	Geneâ€“environmental interaction regarding alcohol-metabolizing enzymes in the Japanese general population. Hypertension Research, 2009, 32, 207-213.	1.5	46
45	Reevaluation of the association of seven candidate genes with blood pressure and hypertension: a replication study and meta-analysis with a larger sample size. Hypertension Research, 2012, 35, 825-831.	1.5	44
46	Association of Genetic Variants Influencing Lipid Levels with Coronary Artery Disease in Japanese Individuals. PLoS ONE, 2012, 7, e46385.	1.1	43
47	Genetic Analysis in Human Hypertension.. Hypertension Research, 2002, 25, 319-327.	1.5	40
48	Isolation of a Chromosome 1 Region Affecting Blood Pressure and Vascular Disease Traits in the Stroke-Prone Rat Model. Hypertension, 2003, 42, 1191-1197.	1.3	37
49	The stroke-prone spontaneously hypertensive rat: still a useful model for post-GWAS genetic studies?. Hypertension Research, 2012, 35, 477-484.	1.5	36
50	Identification of Quantitative Trait Loci for Serum Cholesterol Levels in Stroke-Prone Spontaneously Hypertensive Rats. Arteriosclerosis, Thrombosis, and Vascular Biology, 2000, 20, 223-229.	1.1	32
51	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
52	Analysis of KRAP expression and localization, and genes regulated by KRAP in a human colon cancer cell line. Journal of Human Genetics, 2007, 52, 978-984.	1.1	29
53	SLC15A4 mediates M1-prone metabolic shifts in macrophages and guards immune cells from metabolic stress. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	29
54	The fine-scale genetic structure and evolution of the Japanese population. PLoS ONE, 2017, 12, e0185487.	1.1	27

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55	Genome-wide searches for blood pressure quantitative trait loci in the stroke-prone spontaneously hypertensive rat of a Japanese colony. Journal of Hypertension, 2003, 21, 295-303.	0.3	26
56	Lysosome biogenesis regulated by the amino-acid transporter SLC15A4 is critical for functional integrity of mast cells. International Immunology, 2017, 29, 551-566.	1.8	26
57	Deletion of CDKAL1 Affects High-Fat Dietâ€"Induced Fat Accumulation and Glucose-Stimulated Insulin Secretion in Mice, Indicating Relevance to Diabetes. PLoS ONE, 2012, 7, e49055.	1.1	25
58	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. European Journal of Preventive Cardiology, 2017, 24, 492-504.	0.8	22
59	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
60	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	2.0	21
61	Genome-wide linkage analysis of type 2 diabetes mellitus reconfirms the susceptibility locus on 11p13â€"p12 in Japanese. Journal of Human Genetics, 2004, 49, 629-634.	1.1	18
62	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
63	LOX-1 (Lectin-Like Oxidized Low-Density Lipoprotein Receptor-1) Deletion Has Protective Effects on Stroke in the Genetic Background of Stroke-Prone Spontaneously Hypertensive Rat. Stroke, 2020, 51, 1835-1843.	1.0	16
64	Identification of Quantitative Trait Loci for Cardiac Hypertrophy in Two Different Strains of the Spontaneously Hypertensive Rat. Hypertension Research, 2005, 28, 273-281.	1.5	14
65	Identification of a genetic variant at 2q12.1 associated with blood pressure in East-Asians by genome-wide scan including gene-environment interactions. BMC Medical Genetics, 2014, 15, 65.	2.1	14
66	Systemic evaluation of gene expression changes in major target organs induced by atorvastatin. European Journal of Pharmacology, 2008, 584, 376-389.	1.7	12
67	Clinical Implication of Smoking-Related Aryl-Hydrocarbon Receptor Repressor (<i>AHRR</i>) Hypomethylation in Japanese Adults. Circulation Journal, 2022, 86, 986-992.	0.7	12
68	Systematic Fine-Mapping of Association with BMI and Type 2 Diabetes at the FTO Locus by Integrating Results from Multiple Ethnic Groups. PLoS ONE, 2014, 9, e101329.	1.1	11
69	Further dissection of QTLs for salt-induced stroke and identification of candidate genes in the stroke-prone spontaneously hypertensive rat. Scientific Reports, 2018, 8, 9403.	1.6	10
70	Investigation of Functional Genes at Homologous Loci Identified Based on Genome-wide Association Studies of Blood Lipids via High-fat Diet Intervention in Rats using an in vivo Approach. Journal of Atherosclerosis and Thrombosis, 2015, 22, 455-480.	0.9	9
71	Diseaseâ€associated polymorphisms in 9p21 are not associated with extreme longevity. Geriatrics and Gerontology International, 2015, 15, 797-803.	0.7	9
72	Proposition of a Feasible Protocol to Evaluate Salt Sensitivity in a Population-Based Setting.. Hypertension Research, 2002, 25, 801-809.	1.5	9

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73	Evaluation of insulin resistance linkage to rat chromosome 4 in SHR of a Japanese colony. Biochemical and Biophysical Research Communications, 2005, 329, 879-887.	1.0	7
74	HapMap coverage for SNPs in the Japanese population. Journal of Human Genetics, 2008, 53, 96-99.	1.1	6
75	Heterogeneous Effects of Association Between Blood Pressure Loci and Coronary Artery Disease in East Asian Individuals. Circulation Journal, 2015, 79, 830-838.	0.7	6
76	Alterations of lipid metabolism, blood pressure and fatty liver in spontaneously hypertensive rats transgenic for human cholesteryl ester transfer protein. Hypertension Research, 2020, 43, 655-666.	1.5	6
77	Integrative genomic analysis of blood pressure and related phenotypes in rats. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	6
78	Transcriptomic Response in the Heart and Kidney to Different Types of Antihypertensive Drug Administration. Hypertension, 2022, 79, 413-423.	1.3	6
79	Ethnic diversity in type 2 diabetes genetics between East Asians and Europeans. Journal of Diabetes Investigation, 2012, 3, 349-351.	1.1	5
80	Effects of maternal and fetal choline concentrations on the fetal growth and placental <scp>DNA</scp> methylation of 12 target genes related to fetal growth, adipogenesis, and energy metabolism. Journal of Obstetrics and Gynaecology Research, 2021, 47, 734-744.	0.6	5
81	Candesartan-Induced Gene Expression in Five Organs of Stroke-Prone Spontaneously Hypertensive Rats. Hypertension Research, 2008, 31, 1963-1975.	1.5	3
82	Dynamic changes of the renin-angiotensin and associated systems in the rat after pharmacological and dietary interventions in vivo. Physiological Genomics, 2008, 35, 330-340.	1.0	3
83	Nonlinear ridge regression improves cell-type-specific differential expression analysis. BMC Bioinformatics, 2021, 22, 141.	1.2	3
84	Venous thromboembolism is caused by prothrombin p.Arg541Trp mutation in Japanese individuals. Human Genome Variation, 2021, 8, 13.	0.4	2
85	Candidate genes revisited in the genetics of hypertension and blood pressure. Hypertension Research, 2013, 36, 1032-1034.	1.5	1