

Norihiro Kato

List of Publications by Year in descending order

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85
papers

9,805
citations

57758

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51608

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89
all docs

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docs citations

89
times ranked

15411
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptomic Response in the Heart and Kidney to Different Types of Antihypertensive Drug Administration. <i>Hypertension</i> , 2022, 79, 413-423.	2.7	6
2	Clinical Implication of Smoking-Related Aryl-Hydrocarbon Receptor Repressor (<i>AHRR&/i>) Hypomethylation in Japanese Adults. <i>Circulation Journal</i> , 2022, 86, 986-992.	1.6	12
3	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. <i>European Heart Journal</i> , 2022, 43, 1702-1711.	2.2	58
4	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	4.4	21
5	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
6	Effects of maternal and fetal choline concentrations on the fetal growth and placental ^{DNA} methylation of 12 target genes related to fetal growth, adipogenesis, and energy metabolism. <i>Journal of Obstetrics and Gynaecology Research</i> , 2021, 47, 734-744.	1.3	5
7	Venous thromboembolism is caused by prothrombin p.Arg541Trp mutation in Japanese individuals. <i>Human Genome Variation</i> , 2021, 8, 13.	0.7	2
8	Nonlinear ridge regression improves cell-type-specific differential expression analysis. <i>BMC Bioinformatics</i> , 2021, 22, 141.	2.6	3
9	Integrative genomic analysis of blood pressure and related phenotypes in rats. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	2.4	6
10	SLC15A4 mediates M1-prone metabolic shifts in macrophages and guards immune cells from metabolic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	29
11	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
12	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
13	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	282
14	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. <i>Stroke</i> , 2020, 51, 1835-1843.	2.0	16
15	Alterations of lipid metabolism, blood pressure and fatty liver in spontaneously hypertensive rats transgenic for human cholesteryl ester transfer protein. <i>Hypertension Research</i> , 2020, 43, 655-666.	2.7	6
16	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
17	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
18	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , 2019, 2, 115.	4.4	66

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19	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	2.9	31
20	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
21	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
22	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	12.8	75
23	Further dissection of QTLs for salt-induced stroke and identification of candidate genes in the stroke-prone spontaneously hypertensive rat. <i>Scientific Reports</i> , 2018, 8, 9403.	3.3	10
24	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
25	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
26	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	21.4	492
27	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. <i>European Journal of Preventive Cardiology</i> , 2017, 24, 492-504.	1.8	22
28	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. <i>Circulation Research</i> , 2017, 121, 81-88.	4.5	68
29	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , 2017, 26, 1770-1784.	2.9	135
30	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
31	Lysosome biogenesis regulated by the amino-acid transporter SLC15A4 is critical for functional integrity of mast cells. <i>International Immunology</i> , 2017, 29, 551-566.	4.0	26
32	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , 2017, 12, e0185487.	2.5	27
33	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
34	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , 2016, 6, 17958.	3.3	58
35	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	2.9	21
36	Heterogeneous Effects of Association Between Blood Pressure Loci and Coronary Artery Disease in East Asian Individuals. <i>Circulation Journal</i> , 2015, 79, 830-838.	1.6	6

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37	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 <i>in vivo</i> Approach. <i>Journal of Atherosclerosis and Thrombosis</i> , 2015, 22, 455-480.	2.0	9
38	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. <i>Diabetes</i> , 2015, 64, 291-298.	0.6	59
39	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294
40	Disease-associated polymorphisms in 9p21 are not associated with extreme longevity. <i>Geriatrics and Gerontology International</i> , 2015, 15, 797-803.	1.5	9
41	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015, 24, 1791-1800.	2.9	105
42	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504.	2.9	192
43	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. <i>Human Molecular Genetics</i> , 2014, 23, 1108-1119.	2.9	68
44	Identification of a genetic variant at 2q12.1 associated with blood pressure in East-Asians by genome-wide scan including gene-environment interactions. <i>BMC Medical Genetics</i> , 2014, 15, 65.	2.1	14
45	Systematic Fine-Mapping of Association with BMI and Type 2 Diabetes at the FTO Locus by Integrating Results from Multiple Ethnic Groups. <i>PLoS ONE</i> , 2014, 9, e101329.	2.5	11
46	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554.	6.2	189
47	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , 2013, 22, 2303-2311.	2.9	63
48	Insights into the genetic basis of type 2 diabetes. <i>Journal of Diabetes Investigation</i> , 2013, 4, 233-244.	2.4	51
49	Candidate genes revisited in the genetics of hypertension and blood pressure. <i>Hypertension Research</i> , 2013, 36, 1032-1034.	2.7	1
50	Genome-Wide Association Study Meta-Analysis Reveals Transethnic Replication of Mean Arterial and Pulse Pressure Loci. <i>Hypertension</i> , 2013, 62, 853-859.	2.7	63
51	Ethnic differences in genetic predisposition to hypertension. <i>Hypertension Research</i> , 2012, 35, 574-581.	2.7	51
52	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. <i>Nature Genetics</i> , 2012, 44, 302-306.	21.4	240
53	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , 2012, 44, 67-72.	21.4	545
54	The stroke-prone spontaneously hypertensive rat: still a useful model for post-GWAS genetic studies?. <i>Hypertension Research</i> , 2012, 35, 477-484.	2.7	36

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55	Reevaluation of the association of seven candidate genes with blood pressure and hypertension: a replication study and meta-analysis with a larger sample size. <i>Hypertension Research</i> , 2012, 35, 825-831.	2.7	44
56	Ethnic diversity in type 2 diabetes genetics between East Asians and Europeans. <i>Journal of Diabetes Investigation</i> , 2012, 3, 349-351.	2.4	5
57	Genome-wide association study of coronary artery disease in the Japanese. <i>European Journal of Human Genetics</i> , 2012, 20, 333-340.	2.8	156
58	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012, 44, 307-311.	21.4	372
59	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , 2012, 44, 904-909.	21.4	254
60	Association of Genetic Variants Influencing Lipid Levels with Coronary Artery Disease in Japanese Individuals. <i>PLoS ONE</i> , 2012, 7, e46385.	2.5	43
61	Deletion of CDKAL1 Affects High-Fat Diet-Induced Fat Accumulation and Glucose-Stimulated Insulin Secretion in Mice, Indicating Relevance to Diabetes. <i>PLoS ONE</i> , 2012, 7, e49055.	2.5	25
62	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 984-989.	21.4	481
63	Non-alcoholic fatty liver disease in a rural, physically active, low income population in Sri Lanka. <i>BMC Research Notes</i> , 2011, 4, 513.	1.4	49
64	Confirmation of ALDH2 as a Major Locus of Drinking Behavior and of Its Variants Regulating Multiple Metabolic Phenotypes in a Japanese Population. <i>Circulation Journal</i> , 2011, 75, 911-918.	1.6	128
65	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. <i>Nature Genetics</i> , 2011, 43, 531-538.	21.4	516
66	Association of genetic variants for susceptibility to obesity with type 2 diabetes in Japanese individuals. <i>Diabetologia</i> , 2011, 54, 1350-1359.	6.3	70
67	Blood Pressure and Hypertension Are Associated With 7 Loci in the Japanese Population. <i>Circulation</i> , 2010, 121, 2302-2309.	1.6	174
68	Deletion of CDKAL1 Affects Mitochondrial ATP Generation and First-Phase Insulin Exocytosis. <i>PLoS ONE</i> , 2010, 5, e15553.	2.5	64
69	Confirmation of Multiple Risk Loci and Genetic Impacts by a Genome-Wide Association Study of Type 2 Diabetes in the Japanese Population. <i>Diabetes</i> , 2009, 58, 1690-1699.	0.6	216
70	Gene-environmental interaction regarding alcohol-metabolizing enzymes in the Japanese general population. <i>Hypertension Research</i> , 2009, 32, 207-213.	2.7	46
71	HapMap coverage for SNPs in the Japanese population. <i>Journal of Human Genetics</i> , 2008, 53, 96-99.	2.3	6
72	Systemic evaluation of gene expression changes in major target organs induced by atorvastatin. <i>European Journal of Pharmacology</i> , 2008, 584, 376-389.	3.5	12

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73	Candesartan-Induced Gene Expression in Five Organs of Stroke-Prone Spontaneously Hypertensive Rats. <i>Hypertension Research</i> , 2008, 31, 1963-1975.	2.7	3
74	Dynamic changes of the renin-angiotensin and associated systems in the rat after pharmacological and dietary interventions in vivo. <i>Physiological Genomics</i> , 2008, 35, 330-340.	2.3	3
75	High-density association study and nomination of susceptibility genes for hypertension in the Japanese National Project. <i>Human Molecular Genetics</i> , 2007, 17, 617-627.	2.9	53
76	Analysis of KRAP expression and localization, and genes regulated by KRAP in a human colon cancer cell line. <i>Journal of Human Genetics</i> , 2007, 52, 978-984.	2.3	29
77	Evaluation of insulin resistance linkage to rat chromosome 4 in SHR of a Japanese colony. <i>Biochemical and Biophysical Research Communications</i> , 2005, 329, 879-887.	2.1	7
78	Identification of Quantitative Trait Loci for Cardiac Hypertrophy in Two Different Strains of the Spontaneously Hypertensive Rat. <i>Hypertension Research</i> , 2005, 28, 273-281.	2.7	14
79	Genome-wide linkage analysis of type 2 diabetes mellitus reconfirms the susceptibility locus on 11p13-p12 in Japanese. <i>Journal of Human Genetics</i> , 2004, 49, 629-634.	2.3	18
80	Isolation of a Chromosome 1 Region Affecting Blood Pressure and Vascular Disease Traits in the Stroke-Prone Rat Model. <i>Hypertension</i> , 2003, 42, 1191-1197.	2.7	37
81	Genome-wide searches for blood pressure quantitative trait loci in the stroke-prone spontaneously hypertensive rat of a Japanese colony. <i>Journal of Hypertension</i> , 2003, 21, 295-303.	0.5	26
82	Genetic Analysis in Human Hypertension.. <i>Hypertension Research</i> , 2002, 25, 319-327.	2.7	40
83	Proposition of a Feasible Protocol to Evaluate Salt Sensitivity in a Population-Based Setting.. <i>Hypertension Research</i> , 2002, 25, 801-809.	2.7	9
84	Identification of Quantitative Trait Loci for Serum Cholesterol Levels in Stroke-Prone Spontaneously Hypertensive Rats. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2000, 20, 223-229.	2.4	32
85	Absence of Cd36 mutation in the original spontaneously hypertensive rats with insulin resistance. <i>Nature Genetics</i> , 1999, 22, 226-228.	21.4	59