

# Norihiro Kato

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/3560781/norihiro-kato-publications-by-year.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85  
papers

6,440  
citations

38  
h-index

80  
g-index

89  
ext. papers

8,308  
ext. citations

11.3  
avg, IF

4.44  
L-index

#	Paper	IF	Citations
85	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study.. <i>European Heart Journal</i> , <b>2022</b> ,	9.5	3
84	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. <i>Communications Biology</i> , <b>2022</b> , 5, 329	6.7	2
83	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , <b>2022</b> ,	36.3	7
82	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , <b>2021</b> , 26, 2111-2125	15.1	3
81	Transcriptomic Response in the Heart and Kidney to Different Types of Antihypertensive Drug Administration. <i>Hypertension</i> , <b>2021</b> , HYPERTENSIONAHA12118026	8.5	2
80	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , <b>2021</b> ,	50.4	24
79	Nonlinear ridge regression improves cell-type-specific differential expression analysis. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 141	3.6	3
78	Integrative genomic analysis of blood pressure and related phenotypes in rats. <i>DMM Disease Models and Mechanisms</i> , <b>2021</b> , 14,	4.1	2
77	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> , <b>2021</b> , 47, 734-744	1.9	2
76	Venous thromboembolism is caused by prothrombin p.Arg541Trp mutation in Japanese individuals. <i>Human Genome Variation</i> , <b>2021</b> , 8, 13	1.8	1
75	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> , <b>2021</b> , 118,	11.5	4
74	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , <b>2020</b> , 582, 240-245	50.4	89
73	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> , <b>2020</b> , 51, 1835-1843	6.7	6
72	Alterations of lipid metabolism, blood pressure and fatty liver in spontaneously hypertensive rats transgenic for human cholesteryl ester transfer protein. <i>Hypertension Research</i> , <b>2020</b> , 43, 655-666	4.7	4
71	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1033-1054	3.8	39
70	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , <b>2019</b> , 10, 376	17.4	41
69	Genome-wide meta-analysis identifies multiple novel loci associated with serum uric acid levels in Japanese individuals. <i>Communications Biology</i> , <b>2019</b> , 2, 115	6.7	42

68	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> , <b>2019</b> , 28, 2615-2633	5.6	14
67	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , <b>2019</b> , 51, 636-648	36.3	59
66	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> , <b>2018</b> , 102, 375-400	11	59
65	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , <b>2018</b> , 13, e0198166	3.7	31
64	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , <b>2018</b> , 50, 524-537	36.3	536
63	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , <b>2018</b> , 9, 5052	17.4	29
62	Further dissection of QTLs for salt-induced stroke and identification of candidate genes in the stroke-prone spontaneously hypertensive rat. <i>Scientific Reports</i> , <b>2018</b> , 8, 9403	4.9	4
61	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 403-415	36.3	313
60	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. <i>European Journal of Preventive Cardiology</i> , <b>2017</b> , 24, 492-504	3.9	16
59	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. <i>Circulation Research</i> , <b>2017</b> , 121, 81-88	15.7	48
58	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> , <b>2017</b> , 26, 1770-1784	5.6	90
57	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , <b>2017</b> , 541, 81-86	50.4	511
56	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , <b>2017</b> , 12, e0185487	3.7	21
55	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> , <b>2017</b> , 14, e1002383	11.6	223
54	Lysosome biogenesis regulated by the amino-acid transporter SLC15A4 is critical for functional integrity of mast cells. <i>International Immunology</i> , <b>2017</b> , 29, 551-566	4.9	10
53	Genome-wide association studies in East Asians identify new loci for waist-hip ratio and waist circumference. <i>Scientific Reports</i> , <b>2016</b> , 6, 17958	4.9	48
52	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 2070-2081	5.6	20
51	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , <b>2015</b> , 47, 1282-1293	36.3	223

50	Disease-associated polymorphisms in 9p21 are not associated with extreme longevity. <i>Geriatrics and Gerontology International</i> , <b>2015</b> , 15, 797-803	2.9	6
49	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 1791-800	5.6	71
48	Heterogeneous effects of association between blood pressure loci and coronary artery disease in east Asian individuals. <i>Circulation Journal</i> , <b>2015</b> , 79, 830-8	2.9	2
47	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. <i>Journal of Atherosclerosis and Thrombosis</i> , <b>2015</b> , 22, 455-80	4	7
46	Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. <i>Diabetes</i> , <b>2015</b> , 64, 291-8	0.9	43
45	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> , <b>2014</b> , 15, 65	2.1	12
44	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> , <b>2014</b> , 23, 5492-504	5.6	141
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> , <b>2014</b> , 23, 1108-19	5.6	53
42	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> , <b>2014</b> , 9, e101329	3.7	7
41	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> , <b>2013</b> , 93, 545-54	11	145
40	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 2303-11	5.6	48
39	Insights into the genetic basis of type 2 diabetes. <i>Journal of Diabetes Investigation</i> , <b>2013</b> , 4, 233-44	3.9	44
38	Candidate genes revisited in the genetics of hypertension and blood pressure. <i>Hypertension Research</i> , <b>2013</b> , 36, 1032-4	4.7	1
37	Genome-wide association study meta-analysis reveals transethnic replication of mean arterial and pulse pressure loci. <i>Hypertension</i> , <b>2013</b> , 62, 853-9	8.5	60
36	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. <i>Nature Genetics</i> , <b>2012</b> , 44, 302-6	36.3	192
35	The stroke-prone spontaneously hypertensive rat: still a useful model for post-GWAS genetic studies?. <i>Hypertension Research</i> , <b>2012</b> , 35, 477-84	4.7	21
34	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> , <b>2012</b> , 35, 825-31	4.7	38
33	Ethnic diversity in type 2 diabetes genetics between East Asians and Europeans. <i>Journal of Diabetes Investigation</i> , <b>2012</b> , 3, 349-51	3.9	4

32	Genome-wide association study of coronary artery disease in the Japanese. <i>European Journal of Human Genetics</i> , <b>2012</b> , 20, 333-40	5.3	123
31	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , <b>2012</b> , 44, 307-11	36.3	301
30	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , <b>2012</b> , 44, 904-9	36.3	201
29	Ethnic differences in genetic predisposition to hypertension. <i>Hypertension Research</i> , <b>2012</b> , 35, 574-81	4.7	41
28	Association of genetic variants influencing lipid levels with coronary artery disease in Japanese individuals. <i>PLoS ONE</i> , <b>2012</b> , 7, e46385	3.7	38
27	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> , <b>2012</b> , 7, e49055	3.7	22
26	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , <b>2011</b> , 44, 67-72	36.3	475
25	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , <b>2011</b> , 43, 984-9	36.3	406
24	Non-alcoholic fatty liver disease in a rural, physically active, low income population in Sri Lanka. <i>BMC Research Notes</i> , <b>2011</b> , 4, 513	2.3	38
23	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> , <b>2011</b> , 75, 911-8	2.9	104
22	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. <i>Nature Genetics</i> , <b>2011</b> , 43, 531-8	36.3	442
21	Association of genetic variants for susceptibility to obesity with type 2 diabetes in Japanese individuals. <i>Diabetologia</i> , <b>2011</b> , 54, 1350-9	10.3	58
20	Blood pressure and hypertension are associated with 7 loci in the Japanese population. <i>Circulation</i> , <b>2010</b> , 121, 2302-9	16.7	147
19	Deletion of CDKAL1 affects mitochondrial ATP generation and first-phase insulin exocytosis. <i>PLoS ONE</i> , <b>2010</b> , 5, e15553	3.7	57
18	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> , <b>2009</b> , 58, 1690-9	0.9	196
17	Gene-environmental interaction regarding alcohol-metabolizing enzymes in the Japanese general population. <i>Hypertension Research</i> , <b>2009</b> , 32, 207-13	4.7	42
16	Systemic evaluation of gene expression changes in major target organs induced by atorvastatin. <i>European Journal of Pharmacology</i> , <b>2008</b> , 584, 376-89	5.3	9
15	Candesartan-induced gene expression in five organs of stroke-prone spontaneously hypertensive rats. <i>Hypertension Research</i> , <b>2008</b> , 31, 1963-75	4.7	3

14	Dynamic changes of the renin-angiotensin and associated systems in the rat after pharmacological and dietary interventions in vivo. <i>Physiological Genomics</i> , <b>2008</b> , 35, 330-40	3.6	3
13	HapMap coverage for SNPs in the Japanese population. <i>Journal of Human Genetics</i> , <b>2008</b> , 53, 96-99	4.3	6
12	High-density association study and nomination of susceptibility genes for hypertension in the Japanese National Project. <i>Human Molecular Genetics</i> , <b>2008</b> , 17, 617-27	5.6	44
11	Analysis of KRAP expression and localization, and genes regulated by KRAP in a human colon cancer cell line. <i>Journal of Human Genetics</i> , <b>2007</b> , 52, 978-984	4.3	24
10	Evaluation of insulin resistance linkage to rat chromosome 4 in SHR of a Japanese colony. <i>Biochemical and Biophysical Research Communications</i> , <b>2005</b> , 329, 879-87	3.4	6
9	Identification of quantitative trait loci for cardiac hypertrophy in two different strains of the spontaneously hypertensive rat. <i>Hypertension Research</i> , <b>2005</b> , 28, 273-81	4.7	13
8	Genome-wide linkage analysis of type 2 diabetes mellitus reconfirms the susceptibility locus on 11p13-p12 in Japanese. <i>Journal of Human Genetics</i> , <b>2004</b> , 49, 629-634	4.3	18
7	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> , <b>2003</b> , 21, 295-303	1.9	24
6	Isolation of a chromosome 1 region affecting blood pressure and vascular disease traits in the stroke-prone rat model. <i>Hypertension</i> , <b>2003</b> , 42, 1191-7	8.5	36
5	Genetic analysis in human hypertension. <i>Hypertension Research</i> , <b>2002</b> , 25, 319-27	4.7	34
4	Proposition of a feasible protocol to evaluate salt sensitivity in a population-based setting. <i>Hypertension Research</i> , <b>2002</b> , 25, 801-9	4.7	8
3	Identification of quantitative trait loci for serum cholesterol levels in stroke-prone spontaneously hypertensive rats. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2000</b> , 20, 223-9	9.4	31
2	Absence of Cd36 mutation in the original spontaneously hypertensive rats with insulin resistance. <i>Nature Genetics</i> , <b>1999</b> , 22, 226-8	36.3	54
1	Identification of type 2 diabetes loci in 433,540 East Asian individuals		4