

Fumihiko Takeuchi

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

11,818
citations

81900
39
h-index

76900
74
g-index

85
all docs

85
docs citations

85
times ranked

20404
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	27.8	2,625
2	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
3	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
4	A Genome-Wide Association Study Confirms VKORC1, CYP2C9, and CYP4F2 as Principal Genetic Determinants of Warfarin Dose. <i>PLoS Genetics</i> , 2009, 5, e1000433.	3.5	554
5	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
6	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
7	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
8	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
10	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
11	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
12	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	282
13	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
14	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
15	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
16	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
17	Blood Pressure and Hypertension Are Associated With 7 Loci in the Japanese Population. <i>Circulation</i> , 2010, 121, 2302-2309.	1.6	174
18	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

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19	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
20	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
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	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
23	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
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	Common variants at the GCK, GCKR, G6PC2-ABC11 and MTNR1B loci are associated with fasting glucose in two Asian populations. <i>Diabetologia</i> , 2010, 53, 299-308.	6.3	85
26	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
27	Effects of bowel preparation on the human gut microbiome and metabolome. <i>Scientific Reports</i> , 2019, 9, 4042.	3.3	78
28	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	12.8	75
29	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
30	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
31	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. <i>Diabetes</i> , 2014, 63, 2551-2562.	0.6	61
32	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
33	Common polymorphism near the MC4R gene is associated with type 2 diabetes: data from a meta-analysis of 123,373 individuals. <i>Diabetologia</i> , 2012, 55, 2660-2666.	6.3	58
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	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
36	Human Papillomavirus Genotype Distribution in Cervical Intraepithelial Neoplasia Grade 2/3 and Invasive Cervical Cancer in Japanese Women. <i>Japanese Journal of Clinical Oncology</i> , 2014, 44, 910-917.	1.3	55

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37	Gene-environmental interaction regarding alcohol-metabolizing enzymes in the Japanese general population. <i>Hypertension Research</i> , 2009, 32, 207-213.	2.7	46
38	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
39	Association of Genetic Variants Influencing Lipid Levels with Coronary Artery Disease in Japanese Individuals. <i>PLoS ONE</i> , 2012, 7, e46385.	2.5	43
40	Search for type 2 diabetes susceptibility genes on chromosomes 1q, 3q and 12q. <i>Journal of Human Genetics</i> , 2008, 53, 314-324.	2.3	40
41	Genome-wide association study of cervical cancer suggests a role for <i>ARRDC3</i> gene in human papillomavirus infection. <i>Human Molecular Genetics</i> , 2019, 28, 341-348.	2.9	33
42	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
43	The Mitochondrial Genomes of a Myxozoan Genus <i>Kudoa</i> Are Extremely Divergent in Metazoa. <i>PLoS ONE</i> , 2015, 10, e0132030.	2.5	29
44	Evaluation of Pharmacogenetic Algorithm for Warfarin Dose Requirements in Japanese Patients. <i>Circulation Journal</i> , 2010, 74, 977-982.	1.6	28
45	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , 2017, 12, e0185487.	2.5	27
46	Linkage Disequilibrium Grouping of Single Nucleotide Polymorphisms (SNPs) Reflecting Haplotype Phylogeny for Efficient Selection of Tag SNPs. <i>Genetics</i> , 2005, 170, 291-304.	2.9	26
47	Evaluation of genetic loci influencing adult height in the Japanese population. <i>Journal of Human Genetics</i> , 2009, 54, 749-752.	2.3	25
48	Genetic variants of <i>Kudoa septempunctata</i> (Myxozoa: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td (<sc>M</sc>yxozoa:) <i>Journal of Human Genetics</i> , 2016, 39, 667-672.	1.9	24
49	Characterising private and shared signatures of positive selection in 37 Asian populations. <i>European Journal of Human Genetics</i> , 2017, 25, 499-508.	2.8	22
50	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
51	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
52	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	4.4	21
53	Genetic Impact on Uric Acid Concentration and Hyperuricemia in the Japanese Population. <i>Journal of Atherosclerosis and Thrombosis</i> , 2013, 20, 351-367.	2.0	20
54	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

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55	Detection of common single nucleotide polymorphisms synthesizing quantitative trait association of rarer causal variants. <i>Genome Research</i> , 2011, 21, 1122-1130.	5.5	16
56	Effects of storage temperature, storage time, and Cary-Blair transport medium on the stability of the gut microbiota. <i>Drug Discoveries and Therapeutics</i> , 2019, 13, 256-260.	1.5	16
57	Effectiveness of realistic vaccination strategies for contact networks of various degree distributions. <i>Journal of Theoretical Biology</i> , 2006, 243, 39-47.	1.7	15
58	Search of type 2 diabetes susceptibility gene on chromosome 20q. <i>Biochemical and Biophysical Research Communications</i> , 2007, 357, 1100-1106.	2.1	14
59	Clinical Implication of Smoking-Related Aryl-Hydrocarbon Receptor Repressor (<i>AHR</i>) Hypomethylation in Japanese Adults. <i>Circulation Journal</i> , 2022, 86, 986-992.	1.6	12
60	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
61	Statistics of trinucleotides in coding sequences and evolution. <i>Journal of Theoretical Biology</i> , 2003, 222, 139-149.	1.7	9
62	Fine Mapping of the Major Histocompatibility Complex Region and Association of the HLA-B*52:01 Allele With Cervical Cancer in Japanese Women. <i>JAMA Network Open</i> , 2020, 3, e2023248.	5.9	7
63	HapMap coverage for SNPs in the Japanese population. <i>Journal of Human Genetics</i> , 2008, 53, 96-99.	2.3	6
64	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
65	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
66	Integrative genomic analysis of blood pressure and related phenotypes in rats. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	2.4	6
67	Transcriptomic Response in the Heart and Kidney to Different Types of Antihypertensive Drug Administration. <i>Hypertension</i> , 2022, 79, 413-423.	2.7	6
68	Nonlinear ridge regression improves cell-type-specific differential expression analysis. <i>BMC Bioinformatics</i> , 2021, 22, 141.	2.6	3
69	Population Dependency of Measles, Syphilis, and Amebiasis in Japan and Community Evolution. <i>Japanese Journal of Infectious Diseases</i> , 2017, 70, 263-269.	1.2	2
70	Attack Rates of Norovirus and <i>Campylobacter</i> Food Poisonings that Cannot Be Represented by Numeric Constant but by Plotting the Attack Rate against the Number of Patients per Incident in Cartesian Coordinates. <i>Japanese Journal of Infectious Diseases</i> , 2017, 70, 609-615.	1.2	2
71	Venous thromboembolism is caused by prothrombin p.Arg541Trp mutation in Japanese individuals. <i>Human Genome Variation</i> , 2021, 8, 13.	0.7	2
72	P2-326 Comparison of urban diabetics with optimal and suboptimal control. <i>Journal of Epidemiology and Community Health</i> , 2011, 65, A312-A312.	3.7	1

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73	Case Report of Left Ventricular Noncompaction Cardiomyopathy Characterized by Undulating Phenotypes in Adult Patients. <i>International Heart Journal</i> , 2021, 62, 1420-1429.	1.0	1