

Atsushi Takahashi

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

18,609
citations

53794

45
h-index

53230

85
g-index

99
all docs

99
docs citations

99
times ranked

30393
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	27.8	1,974
3	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. <i>Nature Genetics</i> , 2015, 47, 979-986.	21.4	1,965
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
5	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <i>Nature Genetics</i> , 2018, 50, 390-400.	21.4	613
6	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. <i>Journal of Human Genetics</i> , 2006, 51, 1087-1099.	2.3	597
7	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015, 47, 1449-1456.	21.4	529
8	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678.	21.4	440
9	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018, 50, 42-53.	21.4	426
10	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	21.4	408
11	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. <i>Nature Genetics</i> , 2017, 49, 1458-1467.	21.4	380
12	Genome-wide association study identifies eight new susceptibility loci for atopic dermatitis in the Japanese population. <i>Nature Genetics</i> , 2012, 44, 1222-1226.	21.4	310
13	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. <i>Nature Genetics</i> , 2020, 52, 669-679.	21.4	304
14	Genome-wide association study identifies three new susceptibility loci for adult asthma in the Japanese population. <i>Nature Genetics</i> , 2011, 43, 893-896.	21.4	296
15	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.	27.8	282
16	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021, 53, 65-75.	21.4	264
17	Genome-wide association study identifies five new susceptibility loci for prostate cancer in the Japanese population. <i>Nature Genetics</i> , 2010, 42, 751-754.	21.4	258
18	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

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19	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
20	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
21	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. <i>Nature Communications</i> , 2017, 8, 15539.	12.8	230
22	A genome-wide association study identifies genetic variants in the CDKN2BAS locus associated with endometriosis in Japanese. <i>Nature Genetics</i> , 2010, 42, 707-710.	21.4	227
23	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014, 46, 533-542.	21.4	212
24	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <i>Nature Genetics</i> , 2020, 52, 1169-1177.	21.4	206
25	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016, 7, 10531.	12.8	149
26	Genome-wide association study of clinically defined gout identifies multiple risk loci and its association with clinical subtypes. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 652-659.	0.9	144
27	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. <i>Nature Genetics</i> , 2017, 49, 953-958.	21.4	136
28	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. <i>Nature Genetics</i> , 2014, 46, 886-890.	21.4	135
29	Association of VKORC1 and CYP2C9 polymorphisms with warfarin dose requirements in Japanese patients. <i>Journal of Human Genetics</i> , 2006, 51, 249-253.	2.3	125
30	Characterizing rare and low-frequency height-associated variants in the Japanese population. <i>Nature Communications</i> , 2019, 10, 4393.	12.8	123
31	A PAX1 enhancer locus is associated with susceptibility to idiopathic scoliosis in females. <i>Nature Communications</i> , 2015, 6, 6452.	12.8	122
32	Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. <i>Nature Genetics</i> , 2015, 47, 798-802.	21.4	119
33	A Functional SNP in BNC2 Is Associated with Adolescent Idiopathic Scoliosis. <i>American Journal of Human Genetics</i> , 2015, 97, 337-342.	6.2	119
34	A genome-wide association study identifies susceptibility loci for ossification of the posterior longitudinal ligament of the spine. <i>Nature Genetics</i> , 2014, 46, 1012-1016.	21.4	115
35	Common variants at 11q12, 10q26 and 3p11.2 are associated with prostate cancer susceptibility in Japanese. <i>Nature Genetics</i> , 2012, 44, 426-429.	21.4	98
36	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. <i>Nature Human Behaviour</i> , 2020, 4, 308-316.	12.0	80

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37	A meta-analysis identifies adolescent idiopathic scoliosis association with <i>LBX1</i> locus in multiple ethnic groups. <i>Journal of Medical Genetics</i> , 2014, 51, 401-406.	3.2	79
38	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018, 9, 5052.	12.8	75
39	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. <i>Nature Medicine</i> , 2020, 26, 542-548.	30.7	74
40	A genomewide linkage analysis of Kawasaki disease: evidence for linkage to chromosome 12. <i>Journal of Human Genetics</i> , 2007, 52, 179-190.	2.3	72
41	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. <i>Nature Communications</i> , 2019, 10, 5175.	12.8	69
42	A Genome-Wide Association Study of Nephrolithiasis in the Japanese Population Identifies Novel Susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. <i>PLoS Genetics</i> , 2012, 8, e1002541.	3.5	63
43	Association between endometriosis and the interleukin 1A (IL1A) locus. <i>Human Reproduction</i> , 2015, 30, 239-248.	0.9	58
44	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
45	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. <i>Nature Human Behaviour</i> , 2019, 3, 471-477.	12.0	54
46	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. <i>Carcinogenesis</i> , 2018, 39, 652-660.	2.8	52
47	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. <i>Nature Communications</i> , 2015, 6, 8469.	12.8	51
48	Genetic characteristics of inflammatory bowel disease in a Japanese population. <i>Journal of Gastroenterology</i> , 2016, 51, 672-681.	5.1	51
49	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. <i>Nature Communications</i> , 2019, 10, 4422.	12.8	49
50	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. <i>European Journal of Human Genetics</i> , 2015, 23, 374-380.	2.8	48
51	Genome-wide association study of recalcitrant atopic dermatitis in Korean children. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 678-684.e4.	2.9	45
52	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. <i>Journal of the American Heart Association</i> , 2016, 5, .	3.7	45
53	Haplotypes with Copy Number and Single Nucleotide Polymorphisms in CYP2A6 Locus Are Associated with Smoking Quantity in a Japanese Population. <i>PLoS ONE</i> , 2012, 7, e44507.	2.5	45
54	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002670.	3.6	44

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55	Low-frequency coding variants in <i>CETP</i> and <i>CFB</i> are associated with susceptibility of exudative age-related macular degeneration in the Japanese population. <i>Human Molecular Genetics</i> , 2016, 25, ddw335.	2.9	42
56	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2016, 25, 3361-3371.	2.9	40
57	Genome-wide association study identifies gastric cancer susceptibility loci at 12q24.11 and 20q11.21. <i>Cancer Science</i> , 2018, 109, 4015-4024.	3.9	39
58	A functional SNP in <i>ITIH3</i> is associated with susceptibility to myocardial infarction. <i>Journal of Human Genetics</i> , 2007, 52, 220-229.	2.3	38
59	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. <i>Human Molecular Genetics</i> , 2015, 24, 1177-1184.	2.9	38
60	Impact of <i>LDLR</i> and <i>PCSK9</i> pathogenic variants in Japanese heterozygous familial hypercholesterolemia patients. <i>Atherosclerosis</i> , 2019, 289, 101-108.	0.8	37
61	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. <i>Human Genetics</i> , 2021, 140, 529-552.	3.8	36
62	<i>HLA-DQB1*03</i> Confers Susceptibility to Chronic Hepatitis C in Japanese: A Genome-Wide Association Study. <i>PLoS ONE</i> , 2013, 8, e84226.	2.5	35
63	Reproducibility, Performance, and Clinical Utility of a Genetic Risk Prediction Model for Prostate Cancer in Japanese. <i>PLoS ONE</i> , 2012, 7, e46454.	2.5	30
64	Variants near the <i>HLA</i> complex group 22 gene (<i>HCG22</i>) confer increased susceptibility to late-onset asthma in Japanese populations. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 138, 281-283.e13.	2.9	28
65	Novel Risk Loci Identified in a Genome-Wide Association Study of Urolithiasis in a Japanese Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 855-864.	6.1	25
66	<i>HLA-DQ</i> and <i>RBFOX1</i> as susceptibility genes for an outbreak of hydrolyzed wheat allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 1354-1363.	2.9	24
67	High-resolution SNP and haplotype maps of the human gamma-glutamyl carboxylase gene (<i>GGCX</i>) and association study between polymorphisms in <i>GGCX</i> and the warfarin maintenance dose requirement of the Japanese population. <i>Journal of Human Genetics</i> , 2007, 52, 856-864.	2.3	21
68	Disease susceptibility genes shared by primary biliary cirrhosis and Crohn's disease in the Japanese population. <i>Journal of Human Genetics</i> , 2015, 60, 525-531.	2.3	20
69	The schizophrenia genetics knowledgebase: a comprehensive update of findings from candidate gene studies. <i>Translational Psychiatry</i> , 2019, 9, 205.	4.8	19
70	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. <i>Human Molecular Genetics</i> , 2021, 30, 356-369.	2.9	19
71	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. <i>Human Reproduction</i> , 2022, 37, 366-383.	0.9	19
72	The first Japanese cases of familial hypercholesterolemia due to a known pathogenic <i>APOB</i> gene variant, c.10580G>A: p.(Arg3527Gln). <i>Journal of Clinical Lipidology</i> , 2020, 14, 482-486.	1.5	18

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73	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. <i>Human Genetics</i> , 2021, 140, 1353-1365.	3.8	18
74	Genetic risk score based on the prevalence of vertebral fracture in Japanese women with osteoporosis. <i>Bone Reports</i> , 2016, 5, 168-172.	0.4	15
75	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020, 112, 1223-1232.	2.9	15
76	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. <i>Scientific Reports</i> , 2020, 10, 1197.	3.3	14
77	A cross-ethnic survey of CFB and SLC44A4, Indian ulcerative colitis GWAS hits, underscores their potential role in disease susceptibility. <i>European Journal of Human Genetics</i> , 2017, 25, 111-122.	2.8	13
78	Genome-wide association studies identify two novel loci conferring susceptibility to diabetic retinopathy in Japanese patients with type 2 diabetes. <i>Human Molecular Genetics</i> , 2021, 30, 716-726.	2.9	13
79	Association of the MSX2 gene polymorphisms with ankylosing spondylitis in Japanese. <i>Journal of Human Genetics</i> , 2008, 53, 419-424.	2.3	9
80	Genome-wide association study of epilepsy in a Japanese population identified an associated region at chromosome 12q24. <i>Epilepsia</i> , 2021, 62, 1391-1400.	5.1	9
81	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. <i>PLoS ONE</i> , 2018, 13, e0209096.	2.5	8
82	Influence of Genetic Variants in EGF and Other Genes on Hematological Traits in Korean Populations by a Genome-Wide Approach. <i>BioMed Research International</i> , 2015, 2015, 1-9.	1.9	6
83	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. <i>Human Immunology</i> , 2019, 80, 731-738.	2.4	5
84	IDDF2019-ABS-0253 Explained variance and predictability of inflammatory bowel diseases by genetic risk score in five asian populations (results from the international IBD genetics consortium). , 2019, , .		0
85	Reproducibility, performance, and clinical utility of a genetic risk prediction model for prostate cancer in Japanese patients.. <i>Journal of Clinical Oncology</i> , 2012, 30, 10520-10520.	1.6	0
86	Abstract 33: A Meta-analysis Of Three Genome-wide Association Studies Identifies A Novel Susceptibility Locus For Kawasaki Disease.. <i>Circulation</i> , 2015, 131, .	1.6	0
87	Identification of a novel large duplication (exon2_6dup): copy number variation in the LDLR gene in a large family with familial hypercholesterolemia by whole-genome sequencing. <i>Journal of Clinical Lipidology</i> , 2022, , .	1.5	0