Atsushi Takahashi

List of Publications by Year
in descending order

87 papers	18,609 citations	61687 45 h-index	60403 85 g-index
99 all docs	99 docs citations	99 times ranked	33168 citing authors

#	Article	IF	Citations
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
2	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. Journal of Clinical Lipidology, 2022, , .	0.6	0
3	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
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
5	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
6	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. Human Genetics, 2021, 140, 529-552.	1.8	36
7	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
8	Genome-wide association studies identify two novel loci conferring susceptibility to diabetic retinopathy in Japanese patients with type 2 diabetes. Human Molecular Genetics, 2021, 30, 716-726.	1.4	13
9	Transethnic analysis of the human leukocyte antigen region for ulcerative colitis reveals not only shared but also ethnicity-specific disease associations. Human Molecular Genetics, 2021, 30, 356-369.	1.4	19
10	Genomeâ€wide association study of epilepsy in a Japanese population identified an associated region at chromosome 12q24. Epilepsia, 2021, 62, 1391-1400.	2.6	9
11	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. Human Genetics, 2021, 140, 1353-1365.	1.8	18
12	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	1.3	15
13	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. Nature Genetics, 2020, 52, 1169-1177.	9.4	206
14	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
15	Transethnic Meta-Analysis of Genome-Wide Association Studies Identifies Three New Loci and Characterizes Population-Specific Differences for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2020, 13, e002670.	1.6	44
16	The first Japanese cases of familial hypercholesterolemia due to a known pathogenic APOB gene variant, c.10580ÂG>A: p.(Arg3527Gln). Journal of Clinical Lipidology, 2020, 14, 482-486.	0.6	18
17	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	9.4	304
18	Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. Nature Medicine, 2020, 26, 542-548.	15.2	74

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19	GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. Nature Human Behaviour, 2020, 4, 308-316.	6.2	80
20	Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. Scientific Reports, 2020, 10, 1197.	1.6	14
21	The schizophrenia genetics knowledgebase: a comprehensive update of findings from candidate gene studies. Translational Psychiatry, 2019, 9, 205.	2.4	19
22	Impact of LDLR and PCSK9 pathogenic variants in Japanese heterozygous familial hypercholesterolemia patients. Atherosclerosis, 2019, 289, 101-108.	0.4	37
23	HLA-DQ and RBFOX1 as susceptibility genes for an outbreak of hydrolyzed wheat allergy. Journal of Allergy and Clinical Immunology, 2019, 144, 1354-1363.	1.5	24
24	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. Nature Communications, 2019, 10, 4422.	5.8	49
25	Characterizing rare and low-frequency height-associated variants in the Japanese population. Nature Communications, 2019, 10, 4393.	5.8	123
26	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. Human Immunology, 2019, 80, 731-738.	1.2	5
27	Novel Risk Loci Identified in a Genome-Wide Association Study of Urolithiasis in a Japanese Population. Journal of the American Society of Nephrology: JASN, 2019, 30, 855-864.	3.0	25
28	GWAS of smoking behaviour in 165,436 Japanese people reveals seven new loci and shared genetic architecture. Nature Human Behaviour, 2019, 3, 471-477.	6.2	54
29	IDDF2019-ABS-0253â€...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
30	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
31	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. Nature Communications, 2019, 10, 5175.	5.8	69
32	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. Carcinogenesis, 2018, 39, 652-660.	1.3	52
33	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. Nature Genetics, 2018, 50, 390-400.	9.4	613
34	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
35	Genome-wide association study (GWAS) of ovarian cancer in Japanese predicted regulatory variants in 22q13.1. PLoS ONE, 2018, 13, e0209096.	1.1	8
36	Genomeâ€wide association study identifies gastric cancer susceptibility loci at 12q24.11â€12 and 20q11.21. Cancer Science, 2018, 109, 4015-4024.	1.7	39

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37	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	5.8	75
38	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. Nature Genetics, 2017, 49, 953-958.	9.4	136
39	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
40	Genome-wide association study identifies 112 new loci for body mass index in the Japanese population. Nature Genetics, 2017, 49, 1458-1467.	9.4	380
41	A cross-ethnic survey of CFB and SLC44A4, Indian ulcerative colitis GWAS hits, underscores their potential role in disease susceptibility. European Journal of Human Genetics, 2017, 25, 111-122.	1.4	13
42	Genetic risk score based on the prevalence of vertebral fracture in Japanese women with osteoporosis. Bone Reports, 2016, 5, 168-172.	0.2	15
43	Low-frequency coding variants inCETPandCFBare associated with susceptibility of exudative age-related macular degeneration in the Japanese population. Human Molecular Genetics, 2016, 25, ddw335.	1.4	42
44	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45
45	Variants near the HLA complex group 22 gene (HCG22) confer increased susceptibility to late-onset asthma in Japanese populations. Journal of Allergy and Clinical Immunology, 2016, 138, 281-283.e13.	1.5	28
46	Genome-wide association study in East Asians identifies two novel breast cancer susceptibility loci. Human Molecular Genetics, 2016, 25, 3361-3371.	1.4	40
47	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	5.8	149
48	Genetic characteristics of inflammatory bowel disease in a Japanese population. Journal of Gastroenterology, 2016, 51, 672-681.	2.3	51
49	Genome-wide association study of clinically defined gout identifies multiple risk loci and its association with clinical subtypes. Annals of the Rheumatic Diseases, 2016, 75, 652-659.	0.5	144
50	Influence of Genetic Variants in EGF and Other Genes on Hematological Traits in Korean Populations by a Genome-Wide Approach. BioMed Research International, 2015, 2015, 1-9.	0.9	6
51	Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. Nature Genetics, 2015, 47, 798-802.	9.4	119
52	Association between endometriosis and the interleukin 1A (IL1A) locus. Human Reproduction, 2015, 30, 239-248.	0.4	58
53	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. European Journal of Human Genetics, 2015, 23, 374-380.	1.4	48
54	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823

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55	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. Nature Genetics, 2015, 47, 979-986.	9.4	1,965
56	A PAX1 enhancer locus is associated with susceptibility to idiopathic scoliosis in females. Nature Communications, 2015, 6, 6452.	5.8	122
57	A Functional SNP in BNC2 Is Associated with Adolescent Idiopathic Scoliosis. American Journal of Human Genetics, 2015, 97, 337-342.	2.6	119
58	Disease susceptibility genes shared by primary biliary cirrhosis and Crohnâ€™s disease in the Japanese population. Journal of Human Genetics, 2015, 60, 525-531.	1.1	20
59	Genome-wide association study of recalcitrant atopic dermatitis in Korean children. Journal of Allergy and Clinical Immunology, 2015, 136, 678-684.e4.	1.5	45
60	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	9.4	529
61	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. Nature Communications, 2015, 6, 8469.	5.8	51
62	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. Human Molecular Genetics, 2015, 24, 1177-1184.	1.4	38
63	Abstract 33: A Meta-analysis Of Three Genome-wide Association Studies Identifies A Novel Susceptibility Locus For Kawasaki Disease.. Circulation, 2015, 131, .	1.6	0
64	A genome-wide association study identifies susceptibility loci for ossification of the posterior longitudinal ligament of the spine. Nature Genetics, 2014, 46, 1012-1016.	9.4	115
65	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. Nature Genetics, 2014, 46, 533-542.	9.4	212
66	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	13.7	1,974
67	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	9.4	135
68	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
69	A meta-analysis identifies adolescent idiopathic scoliosis association withLBX1locus in multiple ethnic groups. Journal of Medical Genetics, 2014, 51, 401-406.	1.5	79
70	HLA-DQB1*03 Confers Susceptibility to Chronic Hepatitis C in Japanese: A Genome-Wide Association Study. PLoS ONE, 2013, 8, e84226.	1.1	35
71	A Genome-Wide Association Study of Nephrolithiasis in the Japanese Population Identifies Novel Susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. PLoS Genetics, 2012, 8, e1002541.	1.5	63
72	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

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73	Genome-wide association study identifies eight new susceptibility loci for atopic dermatitis in the Japanese population. Nature Genetics, 2012, 44, 1222-1226.	9.4	310
74	Common variants at 11q12, 10q26 and 3p11.2 are associated with prostate cancer susceptibility in Japanese. Nature Genetics, 2012, 44, 426-429.	9.4	98
75	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
76	Haplotypes with Copy Number and Single Nucleotide Polymorphisms in CYP2A6 Locus Are Associated with Smoking Quantity in a Japanese Population. PLoS ONE, 2012, 7, e44507.	1.1	45
77	Reproducibility, Performance, and Clinical Utility of a Genetic Risk Prediction Model for Prostate Cancer in Japanese. PLoS ONE, 2012, 7, e46454.	1.1	30
78	Reproducibility, performance, and clinical utility of a genetic risk prediction model for prostate cancer in Japanese patients.. Journal of Clinical Oncology, 2012, 30, 10520-10520.	0.8	0
79	Genome-wide association study identifies three new susceptibility loci for adult asthma in the Japanese population. Nature Genetics, 2011, 43, 893-896.	9.4	296
80	A genome-wide association study identifies genetic variants in the CDKN2BAS locus associated with endometriosis in Japanese. Nature Genetics, 2010, 42, 707-710.	9.4	227
81	Genome-wide association study identifies five new susceptibility loci for prostate cancer in the Japanese population. Nature Genetics, 2010, 42, 751-754.	9.4	258
82	Association of the MSX2 gene polymorphisms with ankylosing spondylitis in Japanese. Journal of Human Genetics, 2008, 53, 419-424.	1.1	9
83	A functional SNP in ITIH3 is associated with susceptibility to myocardial infarction. Journal of Human Genetics, 2007, 52, 220-229.	1.1	38
84	A genomewide linkage analysis of Kawasaki disease: evidence for linkage to chromosome 12. Journal of Human Genetics, 2007, 52, 179-190.	1.1	72
85	High-resolution SNP and haplotype maps of the human gamma-glutamyl carboxylase gene (GGCX) and association study between polymorphisms in GGCX and the warfarin maintenance dose requirement of the Japanese population. Journal of Human Genetics, 2007, 52, 856-864.	1.1	21
86	Association of VKORC1 and CYP2C9 polymorphisms with warfarin dose requirements in Japanese patients. Journal of Human Genetics, 2006, 51, 249-253.	1.1	125
87	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. Journal of Human Genetics, 2006, 51, 1087-1099.	1.1	597