

Michael Inouye

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

21,349
citations

28190

55
h-index

24915

109
g-index

157
all docs

157
docs citations

157
times ranked

35571
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	13.7	2,625
2	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. <i>Nature Genetics</i> , 2007, 39, 1329-1337.	9.4	1,298
3	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	9.4	1,179
4	The developmental pathway for CD103+CD8+ tissue-resident memory T cells of skin. <i>Nature Immunology</i> , 2013, 14, 1294-1301.	7.0	1,037
5	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014, 6, 90.	3.6	953
6	The diploid genome sequence of an Asian individual. <i>Nature</i> , 2008, 456, 60-65.	13.7	834
7	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	9.4	742
8	The Infant Nasopharyngeal Microbiome Impacts Severity of Lower Respiratory Infection and Risk of Asthma Development. <i>Cell Host and Microbe</i> , 2015, 17, 704-715.	5.1	721
9	Variants in MTNR1B influence fasting glucose levels. <i>Nature Genetics</i> , 2009, 41, 77-81.	9.4	662
10	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults. <i>Journal of the American College of Cardiology</i> , 2018, 72, 1883-1893.	1.2	557
11	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. <i>Nature Genetics</i> , 2012, 44, 269-276.	9.4	516
12	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
13	Towards clinical utility of polygenic risk scores. <i>Human Molecular Genetics</i> , 2019, 28, R133-R142.	1.4	381
14	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 2264-2276.	1.1	369
15	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351
16	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009, 41, 657-665.	9.4	345
17	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. <i>Nature Genetics</i> , 2010, 42, 869-873.	9.4	332
18	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015, 16, 663-673.	7.0	332

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19	LDL-cholesterol concentrations: a genome-wide association study. <i>Lancet</i> , The, 2008, 371, 483-491.	6.3	329
20	FlashPCA2: principal component analysis of Biobank-scale genotype datasets. <i>Bioinformatics</i> , 2017, 33, 2776-2778.	1.8	300
21	The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. <i>Nature Genetics</i> , 2021, 53, 420-425.	9.4	293
22	Genomic prediction of coronary heart disease. <i>European Heart Journal</i> , 2016, 37, 3267-3278.	1.0	277
23	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	13.7	265
24	Fast Principal Component Analysis of Large-Scale Genome-Wide Data. <i>PLoS ONE</i> , 2014, 9, e93766.	1.1	255
25	Recovery from severe H7N9 disease is associated with diverse response mechanisms dominated by CD8+ T cells. <i>Nature Communications</i> , 2015, 6, 6833.	5.8	241
26	Meta-Analysis of Genome-Wide Scans for Human Adult Stature Identifies Novel Loci and Associations with Measures of Skeletal Frame Size. <i>PLoS Genetics</i> , 2009, 5, e1000445.	1.5	237
27	Metabonomic, transcriptomic, and genomic variation of a population cohort. <i>Molecular Systems Biology</i> , 2010, 6, 441.	3.2	230
28	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. <i>Nature Medicine</i> , 2021, 27, 1876-1884.	15.2	214
29	A genotype calling algorithm for the Illumina BeadArray platform. <i>Bioinformatics</i> , 2007, 23, 2741-2746.	1.8	209
30	FastSpar: rapid and scalable correlation estimation for compositional data. <i>Bioinformatics</i> , 2019, 35, 1064-1066.	1.8	190
31	The Biomarker GlycA Is Associated with Chronic Inflammation and Predicts Long-Term Risk of Severe Infection. <i>Cell Systems</i> , 2015, 1, 293-301.	2.9	179
32	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. <i>PLoS Genetics</i> , 2012, 8, e1002907.	1.5	171
33	Frequent transmission of the <i>Mycobacterium tuberculosis</i> Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam. <i>Nature Genetics</i> , 2018, 50, 849-856.	9.4	167
34	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. <i>Nature Genetics</i> , 2022, 54, 134-142.	9.4	164
35	Recent Advances in Characterizing the Gastrointestinal Microbiome in Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	0.9	157
36	An exposome perspective: Early-life events and immune development in a changing world. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 24-40.	1.5	149

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37	Airway Microbiota Dynamics Uncover a Critical Window for Interplay of Pathogenic Bacteria and Allergy in Childhood Respiratory Disease. <i>Cell Host and Microbe</i> , 2018, 24, 341-352.e5.	5.1	146
38	Green Algorithms: Quantifying the Carbon Footprint of Computation. <i>Advanced Science</i> , 2021, 8, 2100707.	5.6	131
39	The transcription factors IRF8 and PU.1 negatively regulate plasma cell differentiation. <i>Journal of Experimental Medicine</i> , 2014, 211, 2169-2181.	4.2	126
40	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. <i>Nature Communications</i> , 2019, 10, 5819.	5.8	124
41	An Immune Response Network Associated with Blood Lipid Levels. <i>PLoS Genetics</i> , 2010, 6, e1001113.	1.5	112
42	Insights into the Genetic Architecture of Early Stage Age-Related Macular Degeneration: A Genome-Wide Association Study Meta-Analysis. <i>PLoS ONE</i> , 2013, 8, e53830.	1.1	108
43	Performance and Robustness of Penalized and Unpenalized Methods for Genetic Prediction of Complex Human Disease. <i>Genetic Epidemiology</i> , 2013, 37, 184-195.	0.6	107
44	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	1.2	106
45	Genomic risk prediction of complex human disease and its clinical application. <i>Current Opinion in Genetics and Development</i> , 2015, 33, 10-16.	1.5	97
46	Accurate and Robust Genomic Prediction of Celiac Disease Using Statistical Learning. <i>PLoS Genetics</i> , 2014, 10, e1004137.	1.5	95
47	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. <i>PLoS Medicine</i> , 2021, 18, e1003498.	3.9	95
48	Power, false discovery rate and Winner's Curse in eQTL studies. <i>Nucleic Acids Research</i> , 2018, 46, e133-e133.	6.5	92
49	Post-infectious group A streptococcal autoimmune syndromes and the heart. <i>Autoimmunity Reviews</i> , 2015, 14, 710-725.	2.5	91
50	Microbial Factors Associated with Postoperative Crohn's Disease Recurrence. <i>Journal of Crohn's and Colitis</i> , 2017, 11, 191-203.	0.6	86
51	Short read sequence typing (SRST): multi-locus sequence types from short reads. <i>BMC Genomics</i> , 2012, 13, 338.	1.2	84
52	Vitamin D over the first decade and susceptibility to childhood allergy and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 472-481.e9.	1.5	76
53	Validation of a Genome-Wide Polygenic Score for Coronary Artery Disease in South Asians. <i>Journal of the American College of Cardiology</i> , 2020, 76, 703-714.	1.2	76
54	Polygenic scores in biomedical research. <i>Nature Reviews Genetics</i> , 2022, 23, 524-532.	7.7	69

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55	Association Between the Gut Microbiota and Blood Pressure in a Population Cohort of 6953 Individuals. <i>Journal of the American Heart Association</i> , 2020, 9, e016641.	1.6	67
56	Developmental patterns in the nasopharyngeal microbiome during infancy are associated with asthma risk. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 1683-1691.	1.5	61
57	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFox1, a regulator of tissue-specific splicing, associated with refractive error. <i>Human Molecular Genetics</i> , 2013, 22, 2754-2764.	1.4	60
58	Genome-Wide Analysis of Genetic Risk Factors for Rheumatic Heart Disease in Aboriginal Australians Provides Support for Pathogenic Molecular Mimicry. <i>Journal of Infectious Diseases</i> , 2017, 216, 1460-1470.	1.9	60
59	Experimental and Human Evidence for Lipocalin-2 (Neutrophil Gelatinase-Associated Lipocalin [NGAL]) in the Development of Cardiac Hypertrophy and Heart Failure. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	59
60	Genetic loci associated with coronary artery disease harbor evidence of selection and antagonistic pleiotropy. <i>PLoS Genetics</i> , 2017, 13, e1006328.	1.5	58
61	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. <i>Nature Communications</i> , 2021, 12, 2671.	5.8	55
62	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. <i>Genome Research</i> , 2010, 20, 1344-1351.	2.4	52
63	Comparative analysis reveals a role for TGF- β 2 in shaping the residency-related transcriptional signature in tissue-resident memory CD8+ T cells. <i>PLoS ONE</i> , 2019, 14, e0210495.	1.1	49
64	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , 2016, 3, 71-82.	2.9	48
65	Gut Microbiome Composition Is Predictive of Incident Type 2 Diabetes in a Population Cohort of 5,572 Finnish Adults. <i>Diabetes Care</i> , 2022, 45, 811-818.	4.3	47
66	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <i>Genome Biology</i> , 2017, 18, 146.	3.8	46
67	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. <i>Nature Metabolism</i> , 2021, 3, 1476-1483.	5.1	43
68	Associations of healthy food choices with gut microbiota profiles. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 605-616.	2.2	42
69	Links between gut microbiome composition and fatty liver disease in a large population sample. <i>Gut Microbes</i> , 2021, 13, 1-22.	4.3	41
70	Metabolomics in epidemiology: from metabolite concentrations to integrative reaction networks. <i>International Journal of Epidemiology</i> , 2016, 45, 1319-1328.	0.9	40
71	SparSNP: Fast and memory-efficient analysis of all SNPs for phenotype prediction. <i>BMC Bioinformatics</i> , 2012, 13, 88.	1.2	38
72	Biomarker Glycoprotein Acetyls Is Associated With the Risk of a Wide Spectrum of Incident Diseases and Stratifies Mortality Risk in Angiography Patients. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002234.	1.6	38

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73	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	7.2	35
74	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
75	Identification of expression quantitative trait loci associated with schizophrenia and affective disorders in normal brain tissue. <i>PLoS Genetics</i> , 2018, 14, e1007607.	1.5	34
76	Genome-wide association studies and systems biology: together at last. <i>Trends in Genetics</i> , 2011, 27, 493-498.	2.9	33
77	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. <i>American Journal of Human Genetics</i> , 2019, 105, 1076-1090.	2.6	31
78	The intersect of genetics, environment, and microbiota in asthma—perspectives and challenges. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 781-793.	1.5	31
79	The Carbon Footprint of Bioinformatics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	29
80	Genetic Loci for Retinal Arteriolar Microcirculation. <i>PLoS ONE</i> , 2013, 8, e65804.	1.1	27
81	Ten simple rules to make your computing more environmentally sustainable. <i>PLoS Computational Biology</i> , 2021, 17, e1009324.	1.5	27
82	Genetic Determinants of Major Blood Lipids in Pakistanis Compared With Europeans. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 348-357.	5.1	25
83	Genomic prediction of celiac disease targeting HLA-positive individuals. <i>Genome Medicine</i> , 2015, 7, 72.	3.6	25
84	High performance computing enabling exhaustive analysis of higher order single nucleotide polymorphism interaction in Genome Wide Association Studies. <i>Health Information Science and Systems</i> , 2015, 3, S3.	3.4	24
85	Systems biology and big data in asthma and allergy: recent discoveries and emerging challenges. <i>European Respiratory Journal</i> , 2020, 55, 1900844.	3.1	22
86	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. <i>Nature Communications</i> , 2020, 11, 3761.	5.8	22
87	Luminal microbiota related to Crohn's disease recurrence after surgery. <i>Gut Microbes</i> , 2020, 11, 1713-1728.	4.3	22
88	Trajectories of childhood immune development and respiratory health relevant to asthma and allergy. <i>ELife</i> , 2018, 7, .	2.8	22
89	Workshop proceedings: GWAS summary statistics standards and sharing. <i>Cell Genomics</i> , 2021, 1, 100004.	3.0	22
90	Towards a Molecular Systems Model of Coronary Artery Disease. <i>Current Cardiology Reports</i> , 2014, 16, 488.	1.3	19

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91	Risk Prediction Using Polygenic Risk Scores for Prevention of Stroke and Other Cardiovascular Diseases. <i>Stroke</i> , 2021, 52, 2983-2991.	1.0	19
92	Acute effects of active breaks during prolonged sitting on subcutaneous adipose tissue gene expression: an ancillary analysis of a randomised controlled trial. <i>Scientific Reports</i> , 2019, 9, 3847.	1.6	18
93	Elucidation of Pathways Driving Asthma Pathogenesis: Development of a Systems-Level Analytic Strategy. <i>Frontiers in Immunology</i> , 2014, 5, 447.	2.2	16
94	Interactions within the MHC contribute to the genetic architecture of celiac disease. <i>PLoS ONE</i> , 2017, 12, e0172826.	1.1	16
95	Deletion of Trim28 in committed adipocytes promotes obesity but preserves glucose tolerance. <i>Nature Communications</i> , 2021, 12, 74.	5.8	16
96	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
97	Predictive Performance of a Polygenic Risk Score for Incident Ischemic Stroke in a Healthy Older Population. <i>Stroke</i> , 2021, 52, 2882-2891.	1.0	15
98	Elevated serum alpha-1 antitrypsin is a major component of GlycA-associated risk for future morbidity and mortality. <i>PLoS ONE</i> , 2019, 14, e0223692.	1.1	14
99	Whole genome "amplified" DNA: insights and imputation. <i>Nature Methods</i> , 2008, 5, 279-280.	9.0	13
100	Prognostic Value of a Polygenic Risk Score for Coronary Heart Disease in Individuals Aged 70 Years and Older. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003429.	1.6	13
101	Genomic risk scores for juvenile idiopathic arthritis and its subtypes. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1572-1579.	0.5	12
102	Loss of the long non-coding RNA OIP5-AS1 exacerbates heart failure in a sex-specific manner. <i>IScience</i> , 2021, 24, 102537.	1.9	12
103	A plasma metabolite score of three eicosanoids predicts incident type 2 diabetes: a prospective study in three independent cohorts. <i>BMJ Open Diabetes Research and Care</i> , 2022, 10, e002519.	1.2	10
104	GeneMates: an R package for detecting horizontal gene co-transfer between bacteria using gene-gene associations controlled for population structure. <i>BMC Genomics</i> , 2020, 21, 658.	1.2	9
105	Machine learning optimized polygenic scores for blood cell traits identify sex-specific trajectories and genetic correlations with disease. <i>Cell Genomics</i> , 2022, 2, 100086.	3.0	9
106	A Versatile Big Data Health System for Australia: Driving Improvements in Cardiovascular Health. <i>Heart Lung and Circulation</i> , 2021, 30, 1467-1476.	0.2	8
107	New Cardiovascular Risk Assessment Techniques for Primary Prevention. <i>Journal of the American College of Cardiology</i> , 2022, 80, 373-387.	1.2	5
108	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. <i>Breast Cancer Research</i> , 2021, 23, 94.	2.2	4

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109	Known allosteric proteins have central roles in genetic disease. PLoS Computational Biology, 2022, 18, e1009806.	1.5	2
110	Look, no hands! Spectral biomarkers from genetic association studies. Genome Medicine, 2013, 5, 14.	3.6	0
111	Gene Regulatory Networks to Explain Coronary Artery Disease Heritability. Journal of the American College of Cardiology, 2019, 73, 2958-2960.	1.2	0
112	Reference exome data for Australian Aboriginal populations to support health-based research. Scientific Data, 2020, 7, 129.	2.4	0
113	Depression and genetic susceptibility to cardiometabolic diseases. , 2022, 1, 102-103.		0