

Michael Inouye

List of Publications by Year in descending order

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Version: 2024-02-01

113
papers

21,349
citations

32410

55
h-index

28425

109
g-index

157
all docs

157
docs citations

157
times ranked

39171
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	The Carbon Footprint of Bioinformatics. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	29
4	Known allosteric proteins have central roles in genetic disease. <i>PLoS Computational Biology</i> , 2022, 18, e1009806.	1.5	2
5	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
6	Depression and genetic susceptibility to cardiometabolic diseases. , 2022, 1, 102-103.		0
7	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
8	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
9	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
10	Polygenic scores in biomedical research. <i>Nature Reviews Genetics</i> , 2022, 23, 524-532.	7.7	69
11	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
12	New Cardiovascular Risk Assessment Techniques for Primary Prevention. <i>Journal of the American College of Cardiology</i> , 2022, 80, 373-387.	1.2	5
13	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
14	Deletion of Trim28 in committed adipocytes promotes obesity but preserves glucose tolerance. <i>Nature Communications</i> , 2021, 12, 74.	5.8	16
15	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. <i>PLoS Medicine</i> , 2021, 18, e1003498.	3.9	95
16	The intersect of genetics, environment, and microbiota in asthmaâ€”perspectives and challenges. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 147, 781-793.	1.5	31
17	The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. <i>Nature Genetics</i> , 2021, 53, 420-425.	9.4	293
18	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	13.7	265

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19	Associations of healthy food choices with gut microbiota profiles. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 605-616.	2.2	42
20	Green Algorithms: Quantifying the Carbon Footprint of Computation. <i>Advanced Science</i> , 2021, 8, 2100707.	5.6	131
21	Taxonomic signatures of cause-specific mortality risk in human gut microbiome. <i>Nature Communications</i> , 2021, 12, 2671.	5.8	55
22	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
23	Ten simple rules to make your computing more environmentally sustainable. <i>PLoS Computational Biology</i> , 2021, 17, e1009324.	1.5	27
24	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
25	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
26	Risk Prediction Using Polygenic Risk Scores for Prevention of Stroke and Other Cardiovascular Diseases. <i>Stroke</i> , 2021, 52, 2983-2991.	1.0	19
27	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
28	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
29	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
30	Workshop proceedings: GWAS summary statistics standards and sharing. <i>Cell Genomics</i> , 2021, 1, 100004.	3.0	22
31	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. <i>Nature Metabolism</i> , 2021, 3, 1476-1483.	5.1	43
32	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
33	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
34	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
35	Reference exome data for Australian Aboriginal populations to support health-based research. <i>Scientific Data</i> , 2020, 7, 129.	2.4	0
36	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

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37	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
38	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. <i>Nature Communications</i> , 2020, 11, 3761.	5.8	22
39	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
40	Genomic risk scores for juvenile idiopathic arthritis and its subtypes. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1572-1579.	0.5	12
41	Luminal microbiota related to Crohn's disease recurrence after surgery. <i>Gut Microbes</i> , 2020, 11, 1713-1728.	4.3	22
42	Towards clinical utility of polygenic risk scores. <i>Human Molecular Genetics</i> , 2019, 28, R133-R142.	1.4	381
43	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
44	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
45	FastSpar: rapid and scalable correlation estimation for compositional data. <i>Bioinformatics</i> , 2019, 35, 1064-1066.	1.8	190
46	Gene Regulatory Networks to Explain Coronary Artery Disease Heritability. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2958-2960.	1.2	0
47	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
48	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
49	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. <i>Nature Communications</i> , 2019, 10, 5819.	5.8	124
50	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
51	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
52	Power, false discovery rate and Winner's Curse in eQTL studies. <i>Nucleic Acids Research</i> , 2018, 46, e133-e133.	6.5	92
53	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
54	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

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55	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
56	Trajectories of childhood immune development and respiratory health relevant to asthma and allergy. <i>ELife</i> , 2018, 7, .	2.8	22
57	Experimental and Human Evidence for Lipocalinâ€² (Neutrophil Gelatinaseâ€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
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	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
60	Microbial Factors Associated with Postoperative Crohnâ€™s Disease Recurrence. <i>Journal of Crohn's and Colitis</i> , 2017, 11, 191-203.	0.6	86
61	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
62	Interactions within the MHC contribute to the genetic architecture of celiac disease. <i>PLoS ONE</i> , 2017, 12, e0172826.	1.1	16
63	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <i>Genome Biology</i> , 2017, 18, 146.	3.8	46
64	FlashPCA2: principal component analysis of Biobank-scale genotype datasets. <i>Bioinformatics</i> , 2017, 33, 2776-2778.	1.8	300
65	Genetic loci associated with coronary artery disease harbor evidence of selection and antagonistic pleiotropy. <i>PLoS Genetics</i> , 2017, 13, e1006328.	1.5	58
66	Genomic prediction of coronary heart disease. <i>European Heart Journal</i> , 2016, 37, 3267-3278.	1.0	277
67	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
68	Mergeomics: multidimensional data integration to identify pathogenic perturbations to biological systems. <i>BMC Genomics</i> , 2016, 17, 874.	1.2	106
69	Metabolomics in epidemiology: from metabolite concentrations to integrative reaction networks. <i>International Journal of Epidemiology</i> , 2016, 45, 1319-1328.	0.9	40
70	Recent Advances in Characterizing the Gastrointestinal Microbiome in Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2015, 21, 1.	0.9	157
71	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
72	Genomic prediction of celiac disease targeting HLA-positive individuals. <i>Genome Medicine</i> , 2015, 7, 72.	3.6	25

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73	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
74	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
75	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
76	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
77	Post-infectious group A streptococcal autoimmune syndromes and the heart. <i>Autoimmunity Reviews</i> , 2015, 14, 710-725.	2.5	91
78	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
79	Fast Principal Component Analysis of Large-Scale Genome-Wide Data. <i>PLoS ONE</i> , 2014, 9, e93766.	1.1	255
80	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014, 6, 90.	3.6	953
81	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	1.5	351
82	Accurate and Robust Genomic Prediction of Celiac Disease Using Statistical Learning. <i>PLoS Genetics</i> , 2014, 10, e1004137.	1.5	95
83	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
84	Towards a Molecular Systems Model of Coronary Artery Disease. <i>Current Cardiology Reports</i> , 2014, 16, 488.	1.3	19
85	Elucidation of Pathways Driving Asthma Pathogenesis: Development of a Systems-Level Analytic Strategy. <i>Frontiers in Immunology</i> , 2014, 5, 447.	2.2	16
86	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
87	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
88	Look, no hands! Spectral biomarkers from genetic association studies. <i>Genome Medicine</i> , 2013, 5, 14.	3.6	0
89	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
90	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

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91	Genetic Loci for Retinal Arteriolar Microcirculation. PLoS ONE, 2013, 8, e65804.	1.1	27
92	Novel Loci for Metabolic Networks and Multi-Tissue Expression Studies Reveal Genes for Atherosclerosis. PLoS Genetics, 2012, 8, e1002907.	1.5	171
93	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. Nature Genetics, 2012, 44, 269-276.	9.4	516
94	SparSNP: Fast and memory-efficient analysis of all SNPs for phenotype prediction. BMC Bioinformatics, 2012, 13, 88.	1.2	38
95	Short read sequence typing (SRST): multi-locus sequence types from short reads. BMC Genomics, 2012, 13, 338.	1.2	84
96	Genome-wide association studies and systems biology: together at last. Trends in Genetics, 2011, 27, 493-498.	2.9	33
97	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
98	Genome-wide association study of migraine implicates a common susceptibility variant on 8q22.1. Nature Genetics, 2010, 42, 869-873.	9.4	332
99	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. Genome Research, 2010, 20, 1344-1351.	2.4	52
100	Genetic Variants Influencing Circulating Lipid Levels and Risk of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 2264-2276.	1.1	369
101	An Immune Response Network Associated with Blood Lipid Levels. PLoS Genetics, 2010, 6, e1001113.	1.5	112
102	Genetic Determinants of Major Blood Lipids in Pakistanis Compared With Europeans. Circulation: Cardiovascular Genetics, 2010, 3, 348-357.	5.1	25
103	Metabonomic, transcriptomic, and genomic variation of a population cohort. Molecular Systems Biology, 2010, 6, 441.	3.2	230
104	Meta-Analysis of Genome-Wide Scans for Human Adult Stature Identifies Novel Loci and Associations with Measures of Skeletal Frame Size. PLoS Genetics, 2009, 5, e1000445.	1.5	237
105	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
106	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	9.4	345
107	The diploid genome sequence of an Asian individual. Nature, 2008, 456, 60-65.	13.7	834
108	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742

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109	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
110	Whole genome amplified DNA: insights and imputation. <i>Nature Methods</i> , 2008, 5, 279-280.	9.0	13
111	LDL-cholesterol concentrations: a genome-wide association study. <i>Lancet</i> , The, 2008, 371, 483-491.	6.3	329
112	A genotype calling algorithm for the Illumina BeadArray platform. <i>Bioinformatics</i> , 2007, 23, 2741-2746.	1.8	209
113	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