Robert P Igo

List of Publications by Year
in descending order

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100 papers	7,279 citations	81900 39 h-index	66911 78 g-index
106 all docs	106 docs citations	106 times ranked	10249 citing authors

#	Article	IF	Citations
1	Gene Set Enrichment Analsyes Identify Pathways Involved in Genetic Risk for Diabetic Retinopathy. American Journal of Ophthalmology, 2022, 233, 111-123.	3.3	7
2	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virusâ€“Infected Individuals From East Africa. Journal of Infectious Diseases, 2021, 224, 695-704.	4.0	1
3	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	12.8	196
4	Association of Rare CYP39A1 Variants With Exfoliation Syndrome Involving the Anterior Chamber of the Eye. JAMA - Journal of the American Medical Association, 2021, 325, 753.	7.4	16
5	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. JAMA Ophthalmology, 2021, 139, 601.	2.5	22
6	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. Npj Genomic Medicine, 2021, 6, 64.	3.8	7
7	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration. JAMA Ophthalmology, 2021, 139, 1299.	2.5	29
8	Genetic risk scores in complex eye disorders. , 2020, , 259-275.		6
9	Statistical driver genes as a means to uncover missing heritability for age-related macular degeneration. BMC Medical Genomics, 2020, 13, 95.	1.5	0
10	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	4.4	10
11	HSD3B1 genotype identifies glucocorticoid responsiveness in severe asthma. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2187-2193.	7.1	27
12	Association of APOE With Primary Open-Angle Glaucoma Suggests a Protective Effect for APOE Îµ4. , 2020, 61, 3.		23
13	Multitrait analysis of glaucoma identifies new risk loci and enables polygenic prediction of disease susceptibility and progression. Nature Genetics, 2020, 52, 160-166.	21.4	192
14	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. PLoS Genetics, 2020, 16, e1008728.	3.5	40
15	Fine-mapping analysis of a chromosome 2 region linked to resistance to Mycobacterium tuberculosis infection in Uganda reveals potential regulatory variants. Genes and Immunity, 2019, 20, 473-483.	4.1	18
16	AMISH EYE STUDY. Retina, 2019, 39, 1540-1550.	1.7	17
17	Rare variants and loci for age-related macular degeneration in the Ohio and Indiana Amish. Human Genetics, 2019, 138, 1171-1182.	3.8	7
18	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 1682.	7.4	50

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19	Pathway Analysis Integrating Genome-Wide and Functional Data Identifies PLCG2 as a Candidate Gene for Age-Related Macular Degeneration. , 2019, 60, 4041.		10
20	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	3.3	12
21	Myocilin Mutations in Patients With Normal-Tension Glaucoma. JAMA Ophthalmology, 2019, 137, 559.	2.5	17
22	Genetic Risk Scores. Current Protocols in Human Genetics, 2019, 104, e95.	3.5	69
23	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.6	54
24	Differential Long-Term Outcomes for Individuals With Histories of Preschool Speech Sound Disorders. American Journal of Speech-Language Pathology, 2019, 28, 1582-1596.	1.8	13
25	Genetically-guided algorithm development and sample size optimization for age-related macular degeneration cases and controls in electronic health records from the VA Million Veteran Program. AMIA Summits on Translational Science Proceedings, 2019, 2019, 153-162.	0.4	0
26	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.6	136
27	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
28	Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. Nature Genetics, 2018, 50, 778-782.	21.4	214
29	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
30	AmpliSeq transcriptome analysis of human alveolar and monocyte-derived macrophages over time in response to Mycobacterium tuberculosis infection. PLoS ONE, 2018, 13, e0198221.	2.5	50
31	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
32	Genome-wide association study identifies three novel loci in Fuchs endothelial corneal dystrophy. Nature Communications, 2017, 8, 14898.	12.8	101
33	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
34	Age at natural menopause genetic risk score in relation to age at natural menopause and primary open-angle glaucoma in a US-based sample. Menopause, 2017, 24, 150-156.	2.0	6
35	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	28.9	121
36	A chromosome 5q31.1 locus associates with tuberculin skin test reactivity in HIV-positive individuals from tuberculosis hyper-endemic regions in east Africa. PLoS Genetics, 2017, 13, e1006710.	3.5	28

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37	Autosomal dominant hereditary spastic paraplegia with axonal sensory motor polyneuropathy maps to chromosome 21q 22.3. International Journal of Neuroscience, 2016, 126, 1-7.	1.6	0
38	A Common Variant in MIR182 Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium. , 2016, 57, 4528.		42
39	Quality Control for the Illumina HumanExome BeadChip. Current Protocols in Human Genetics, 2016, 90, 2.14.1-2.14.16.	3.5	9
40	Genetic Risk Scores. Current Protocols in Human Genetics, 2016, 91, 1.29.1-1.29.9.	3.5	42
41	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
42	Selecting SNPs informative for African, American Indian and European Ancestry: application to the Family Investigation of Nephropathy and Diabetes (FIND). BMC Genomics, 2016, 17, 325.	2.8	1
43	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. American Journal of Human Genetics, 2016, 98, 514-524.	6.2	78
44	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	21.4	1,167
45	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
46	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). PLoS Genetics, 2015, 11, e1005352.	3.5	118
47	Polymorphisms in TICAM2 and IL1B are associated with TB. Genes and Immunity, 2015, 16, 127-133.	4.1	49
48	Practical Barriers and Ethical Challenges in Genetic Data Sharing. International Journal of Environmental Research and Public Health, 2014, 11, 8383-8398.	2.6	20
49	Genetic Evidence for Role of Carotenoids in Age-Related Macular Degeneration in the Carotenoids in Age-Related Eye Disease Study (CAREDS). , 2014, 55, 587.		109
50	Mitochondrial Polymorphism A10398G and Haplogroup I Are Associated With Fuchs' Endothelial Corneal Dystrophy. , 2014, 55, 4577.		12
51	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
52	Association between AVPR1A, DRD2, and ASPM and endophenotypes of communication disorders. Psychiatric Genetics, 2014, 24, 191-200.	1.1	7
53	Clinical and epidemiological characteristics of individuals resistant to M. tuberculosis infection in a longitudinal TB household contact study in Kampala, Uganda. BMC Infectious Diseases, 2014, 14, 352.	2.9	47
54	Rare and common variants in extracellular matrix gene Fibrillin 2 (FBN2) are associated with macular degeneration. Human Molecular Genetics, 2014, 23, 5827-5837.	2.9	52

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55	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	6.2	139
56	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
57	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
58	Genetic Determinants of Macular Pigments in Women of the Carotenoids in Age-Related Eye Disease Study. , 2013, 54, 2333.		78
59	Vitamin D Intake and Season Modify the Effects of the GC and CYP2R1 Genes on 25-Hydroxyvitamin D Concentrations. Journal of Nutrition, 2013, 143, 17-26.	2.9	62
60	Association of Smoking and Other Risk Factors With Fuchs' Endothelial Corneal Dystrophy Severity and Corneal Thickness. , 2013, 54, 5829.		55
61	A Genome-Wide Search for Linkage of Estimated Glomerular Filtration Rate (eGFR) in the Family Investigation of Nephropathy and Diabetes (FIND). PLoS ONE, 2013, 8, e81888.	2.5	24
62	A Multicenter Study to Map Genes for Fuchs Endothelial Corneal Dystrophy: Baseline Characteristics and Heritability. Cornea, 2012, 31, 26-35.	1.7	78
63	Comparison of Requirements and Capabilities of Major Multipurpose Software Packages. Methods in Molecular Biology, 2012, 850, 539-558.	0.9	1
64	Differing Roles for TCF4 and COL8A2 in Central Corneal Thickness and Fuchs Endothelial Corneal Dystrophy. PLoS ONE, 2012, 7, e46742.	2.5	43
65	Genetic susceptibility to tuberculosis associated with cathepsin Z haplotype in a Ugandan household contact study. Human Immunology, 2011, 72, 426-430.	2.4	22
66	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. PLoS ONE, 2011, 6, e25598.	2.5	46
67	Analysis of positional candidate genes in the AAA1 susceptibility locus for abdominal aortic aneurysms on chromosome 19. BMC Medical Genetics, 2011, 12, 14.	2.1	18
68	Genomewide Linkage Scan for Diabetic Renal Failure and Albuminuria: The FIND Study. American Journal of Nephrology, 2011, 33, 381-389.	3.1	52
69	Some Capabilities for Model-Based and Model-Free Linkage Analysis using the Program Package S.A.G.E. (Statistical Analysis for Genetic Epidemiology). Human Heredity, 2011, 72, 237-246.	0.8	33
70	Linkage and association analyses identify a candidate region for apoB level on chromosome 4q32.3 in FCHL families. Human Genetics, 2010, 127, 705-719.	3.8	13
71	Genome-wide association identifies SKIV2L and MYRIP as protective factors for age-related macular degeneration. Genes and Immunity, 2010, 11, 609-621.	4.1	55
72	Association mapping by generalized linear regression with densityâ€based haplotype clustering. Genetic Epidemiology, 2009, 33, 16-26.	1.3	6

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73	Bayesian intervals for linkage locations. Genetic Epidemiology, 2009, 33, 604-616.	1.3	6
74	Genomeâ€wide linkage scans for type 2 diabetes mellitus in four ethnically diverse populationsâ€”significant evidence for linkage on chromosome 4q in African Americans: the Family Investigation of Nephropathy and Diabetes Research Group. Diabetes/Metabolism Research and Reviews, 2009, 25, 740-747.	4.0	12
75	Markov Chain Monte Carlo Linkage Analysis Methods. , 2009, , 147-169.		0
76	Genome Scan of a Nonword Repetition Phenotype in Families with Dyslexia: Evidence for Multiple Loci. Behavior Genetics, 2008, 38, 462-475.	2.1	29
77	Empirical significance values for linkage analysis: trait simulation using posterior model distributions from MCMC oligogenic segregation analysis. Genetic Epidemiology, 2008, 32, 119-131.	1.3	18
78	Heritability of the Severity of Diabetic Retinopathy: The FIND-Eye Study. , 2008, 49, 3839.		163
79	Density-based clustering in haplotype analysis for association mapping. BMC Proceedings, 2007, 1, S27.	1.6	5
80	Issues in association mapping with high-density SNP data and diverse family structures. Genetic Epidemiology, 2007, 31, S22-S33.	1.3	4
81	Genomewide scan for real-word reading subphenotypes of dyslexia: Novel chromosome 13 locus and genetic complexity. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 15-27.	1.7	43
82	Segregation Analysis of a Complex Quantitative Trait: Approaches for Identifying Influential Data Points. Human Heredity, 2006, 61, 80-86.	0.8	11
83	A genome scan in multigenerational families with dyslexia: Identification of a novel locus on chromosome 2q that contributes to phonological decoding efficiency. Molecular Psychiatry, 2005, 10, 699-711.	7.9	61
84	In Vitro Assays for Kinetoplastid U Insertion-Deletion Editing and Associated Activities. , 2004, 265, 251-272.		2
85	Low-Density Lipoprotein Particle Size Loci in Familial Combined Hyperlipidemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 1942-1950.	2.4	37
86	Linkage analyses of four regions previously implicated in dyslexia: Confirmation of a locus on chromosome 15q. American Journal of Medical Genetics Part A, 2004, 131B, 67-75.	2.4	76
87	Kinetoplastid RNA editing ligases: complex association, characterization, and substrate requirements. Molecular and Biochemical Parasitology, 2003, 127, 161-167.	1.1	34
88	TbMP57 Is a 3â€² Terminal Uridylyl Transferase (TUTase) of the Trypanosoma brucei Editosome. Molecular Cell, 2003, 11, 1525-1536.	9.7	111
89	Role of Uridylate-Specific Exoribonuclease Activity in Trypanosoma brucei RNA Editing. Eukaryotic Cell, 2002, 1, 112-118.	3.4	68
90	RNA Sequence and Base Pairing Effects on Insertion Editing in Trypanosoma brucei. Molecular and Cellular Biology, 2002, 22, 1567-1576.	2.3	45

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91	Endoribonuclease activities of Trypanosoma brucei mitochondria. Molecular and Biochemical Parasitology, 2002, 120, 23-31.	1.1	22
92	The specificity of nucleotide removal during RNA editing in Trypanosoma brucei. Rna, 2001, 7, 1793-1802.	3.5	19
93	Association of Two Novel Proteins, TbMP52 and TbMP48, with the Trypanosoma brucei RNA Editing Complex. Molecular and Cellular Biology, 2001, 21, 380-389.	2.3	120
94	Four Related Proteins of the Trypanosoma brucei RNA Editing Complex. Molecular and Cellular Biology, 2001, 21, 6833-6840.	2.3	107
95	An RNA Ligase Essential for RNA Editing and Survival of the Bloodstream Form of Trypanosoma brucei. Science, 2001, 291, 2159-2162.	12.6	187
96	Uridylate Addition and RNA Ligation Contribute to the Specificity of Kinetoplastid Insertion RNA Editing. Molecular and Cellular Biology, 2000, 20, 8447-8457.	2.3	101
97	New mutations and phenotypes associated with glutamate and aspartate transport in Chinese hamster ovary (CHO-K1) cells. Somatic Cell and Molecular Genetics, 1996, 22, 87-103.	0.7	9
98	Novel regulations of glutamate and aspartate uptake by HeLa cells. Biochimica Et Biophysica Acta - Biomembranes, 1995, 1233, 153-162.	2.6	5
99	Selection of Chinese hamster ovary cells (CHO-K1) with reduced glutamate and aspartate uptake. Somatic Cell and Molecular Genetics, 1993, 19, 231-243.	0.7	8
100	Numerical analysis reveals complexities of glutamate transport. Biochimica Et Biophysica Acta - Biomembranes, 1993, 1149, 109-118.	2.6	8