Mark Seielstad

List of Publications by Year
in descending order

118 papers	25,858 citations	20759 60 h-index	19136 118 g-index
123 all docs	123 docs citations	123 times ranked	34790 citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
2	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
3	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	9.4	1,201
4	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	9.4	1,132
5	Patterns of linkage disequilibrium in the human genome. Nature Reviews Genetics, 2002, 3, 299-309.	7.7	994
6	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
7	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
8	Y chromosome sequence variation and the history of human populations. Nature Genetics, 2000, 26, 358-361.	9.4	935
9	Population growth of human Y chromosomes: a study of Y chromosome microsatellites. Molecular Biology and Evolution, 1999, 16, 1791-1798.	3.5	842
10	TRAF1â€“C5as a Risk Locus for Rheumatoid Arthritis â€” A Genomewide Study. New England Journal of Medicine, 2007, 357, 1199-1209.	13.9	729
11	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. Nature Genetics, 2010, 42, 332-337.	9.4	572
12	Genetic evidence for a higher female migration rate in humans. Nature Genetics, 1998, 20, 278-280.	9.4	562
13	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557
14	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	9.4	545
15	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nature Genetics, 2011, 43, 531-538.	9.4	516
16	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
17	Common variants at CD40 and other loci confer risk of rheumatoid arthritis. Nature Genetics, 2008, 40, 1216-1223.	9.4	476
18	The Distribution of Human Genetic Diversity: A Comparison of Mitochondrial, Autosomal, and Y-Chromosome Data. American Journal of Human Genetics, 2000, 66, 979-988.	2.6	469

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19	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. Nature, 2014, 506, 97-101.	13.7	439
20	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
21	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	9.4	372
22	Genetic Structure of the Han Chinese Population Revealed by Genome-wide SNP Variation. American Journal of Human Genetics, 2009, 85, 775-785.	2.6	316
23	African Origin of Modern Humans in East Asia: A Tale of 12,000 Y Chromosomes. Science, 2001, 292, 1151-1153.	6.0	310
24	Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. Nature Genetics, 2009, 41, 1313-1318.	9.4	306
25	High-density mapping of the MHC identifies a shared role for HLA-DRB1*01:03 in inflammatory bowel diseases and heterozygous advantage in ulcerative colitis. Nature Genetics, 2015, 47, 172-179.	9.4	280
26	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
27	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
28	Y chromosome haplotypes reveal prehistorical migrations to the Himalayas. Human Genetics, 2000, 107, 582-590.	1.8	242
29	A genome-wide association study suggests contrasting associations in ACPA-positive versus ACPA-negative rheumatoid arthritis. Annals of the Rheumatic Diseases, 2011, 70, 259-265.	0.5	238
30	Genetic Association and Expression Studies Indicate a Role of Toll-Like Receptor 8 in Pulmonary Tuberculosis. PLoS Genetics, 2008, 4, e1000218.	1.5	228
31	Genome-Wide Expression Profiling Identifies Type 1 Interferon Response Pathways in Active Tuberculosis. PLoS ONE, 2012, 7, e45839.	1.1	213
32	Testing for Population Subdivision and Association in Four Case-Control Studies. American Journal of Human Genetics, 2002, 71, 304-311.	2.6	210
33	Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics, 2010, 6, e1001127.	1.5	193
34	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	1.4	192
35	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189
36	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	5.8	154

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37	FTO Variants Are Associated With Obesity in the Chinese and Malay Populations in Singapore. Diabetes, 2008, 57, 2851-2857.	0.3	152
38	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	3.3	152
39	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2016, 48, 556-562.	9.4	147
40	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. Genome Research, 2009, 19, 2154-2162.	2.4	146
41	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Human Molecular Genetics, 2011, 20, 649-658.	1.4	140
42	Identification of Tuberculosis Susceptibility Genes with Human Macrophage Gene Expression Profiles. PLoS Pathogens, 2008, 4, e1000229.	2.1	134
43	Transferability of Type 2 Diabetes Implicated Loci in Multi-Ethnic Cohorts from Southeast Asia. PLoS Genetics, 2011, 7, e1001363.	1.5	131
44	Genome-Wide Association Studies Reveal Genetic Variants in CTNND2 for High Myopia in Singapore Chinese. Ophthalmology, 2011, 118, 368-375.	2.5	118
45	Different patterns of associations with antiâ€“citrullinated protein antibodyâ€“positive and antiâ€“citrullinated protein antibodyâ€“negative rheumatoid arthritis in the extended major histocompatibility complex region. Arthritis and Rheumatism, 2009, 60, 30-38.	6.7	113
46	A genome-wide association study of hepatitis B vaccine response in an Indonesian population reveals multiple independent risk variants in the HLA region. Human Molecular Genetics, 2011, 20, 3893-3898.	1.4	113
47	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
48	A Novel Y-Chromosome Variant Puts an Upper Limit on the Timing of First Entry into the Americas. American Journal of Human Genetics, 2003, 73, 700-705.	2.6	99
49	Genetic Variants on Chromosome 1q41 Influence Ocular Axial Length and High Myopia. PLoS Genetics, 2012, 8, e1002753.	1.5	95
50	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
51	Comparative analyses of seven algorithms for copy number variant identification from single nucleotide polymorphism arrays. Nucleic Acids Research, 2010, 38, e105-e105.	6.5	94
52	Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Human Molecular Genetics, 2011, 20, 1864-1872.	1.4	91
53	A View of Modern Human Origins from Y Chromosome Microsatellite Variation. Genome Research, 1999, 9, 558-567.	2.4	91
54	A genome wide association study of pulmonary tuberculosis susceptibility in Indonesians. BMC Medical Genetics, 2012, 13, 5.	2.1	90

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55	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
56	Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. International Journal of Obesity, 2012, 36, 159-163.	1.6	83
57	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. Journal of Molecular Evolution, 1997, 45, 265-270.	0.8	82
58	New genetic associations detected in a host response study to hepatitis B vaccine. Genes and Immunity, 2010, 11, 232-238.	2.2	78
59	Polymorphisms Identified through Genome-Wide Association Studies and Their Associations with Type 2 Diabetes in Chinese, Malays, and Asian-Indians in Singapore. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 390-397.	1.8	77
60	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 437-445.	1.4	69
61	Association of Cardiovascular and Metabolic Disease Genes with Psoriasis. Journal of Investigative Dermatology, 2013, 133, 836-839.	0.3	62
62	A whole genome long-range haplotype (WGLRH) test for detecting imprints of positive selection in human populations. Bioinformatics, 2006, 22, 2122-2128.	1.8	61
63	Analysis of association of the TIRAP (MAL) S180L variant and tuberculosis in three populations. Nature Genetics, 2008, 40, 261-262.	9.4	61
64	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.3	59
65	Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. Journal of Lipid Research, 2009, 50, 514-520.	2.0	53
66	Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. Human Molecular Genetics, 2011, 20, 3693-3698.	1.4	51
67	Genetic variation in Northern Thailand Hill Tribes: origins and relationships with social structure and linguistic differences. BMC Evolutionary Biology, 2007, 7, S12.	3.2	49
68	Geographic clustering of human Y-chromosome haplotypes. Annals of Human Genetics, 1996, 60, 401-408.	0.3	47
69	On the Usage of HWE for Identifying Genotyping Errors. Annals of Human Genetics, 2007, 71, 701-703.	0.3	47
70	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
71	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. PLoS ONE, 2011, 6, e25598.	1.1	46
72	Asymmetries in the Maternal and Paternal Genetic Histories of Colombian Populations. American Journal of Human Genetics, 2000, 67, 1062-1066.	2.6	45

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73	Genome Wide Association Study (GWAS) of Chagas Cardiomyopathy in Trypanosoma cruzi Seropositive Subjects. PLoS ONE, 2013, 8, e79629.	1.1	44
74	Genome-Wide Meta-Analysis of Five Asian Cohorts Identifies PDGFRA as a Susceptibility Locus for Corneal Astigmatism. PLoS Genetics, 2011, 7, e1002402.	1.5	35
75	Blood Gene Signatures of Chagas Cardiomyopathy With or Without Ventricular Dysfunction. Journal of Infectious Diseases, 2017, 215, 387-395.	1.9	32
76	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
77	Genetic evidence supports linguistic affinity of Mlabri - a hunter-gatherer group in Thailand. BMC Genetics, 2010, 11, 18.	2.7	30
78	Pathway-based analysis using reduced gene subsets in genome-wide association studies. BMC Bioinformatics, 2011, 12, 17.	1.2	30
79	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	0.8	30
80	Meta-analysis of the TNFAIP3 region in psoriasis reveals a risk haplotype that is distinct from other autoimmune diseases. Genes and Immunity, 2015, 16, 120-126.	2.2	29
81	A view of modern human origins from Y chromosome microsatellite variation. Genome Research, 1999, 9, 558-67.	2.4	29
82	Genetic structure of the Mon-Khmer speaking groups and their affinity to the neighbouring Tai populations in Northern Thailand. BMC Genetics, 2011, 12, 56.	2.7	28
83	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
84	Relation of Age-related Cataract With Obesity and Obesity Genes in an Asian Population. American Journal of Epidemiology, 2009, 169, 1267-1274.	1.6	27
85	SgD-CNV, a database for common and rare copy number variants in three Asian populations. Human Mutation, 2011, 32, 1341-1349.	1.1	27
86	Genomic copy number variations in three Southeast Asian populations. Human Mutation, 2010, 31, 851-857.	1.1	26
87	Polymorphisms Identified through Genome-Wide Association Studies and Their Associations with Type 2 Diabetes in Chinese, Malays, and Asian-Indians in Singapore. Endocrine Reviews, 2009, 30, 926-926.	8.9	24
88	The PRL â€“1149 G/T polymorphism and rheumatoid arthritis susceptibility. Arthritis and Rheumatism, 2009, 60, 1250-1254.	6.7	23
89	Association of Skin Barrier Genes within the PSORS4 Locus Is Enriched in Singaporean Chinese with Early-Onset Psoriasis. Journal of Investigative Dermatology, 2009, 129, 606-614.	0.3	23
90	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	1.1	22

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91	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
92	Analysis of 39 CrohnÊ¼s Disease Risk loci in Swedish Inflammatory Bowel Disease Patients. Inflammatory Bowel Diseases, 2010, 16, 907-909.	0.9	20
93	Support for TGFB1 as a Susceptibility Gene for High Myopia in Individuals of Chinese Descent. JAMA Ophthalmology, 2010, 128, 1081.	2.6	20
94	A Novel, 5-Transcript, Whole-blood Gene-expression Signature for Tuberculosis Screening Among People Living With Human Immunodeficiency Virus. Clinical Infectious Diseases, 2019, 69, 77-83.	2.9	20
95	Genetic affinity and admixture of northern Thai people along their migration route in northern Thailand: evidence from autosomal STR loci. Journal of Human Genetics, 2011, 56, 130-137.	1.1	19
96	Polymorphisms in SP110 are not associated with pulmonary tuberculosis in Indonesians. Infection, Genetics and Evolution, 2012, 12, 1319-1323.	1.0	18
97	Allele frequency and genotype distribution of polymorphisms within disease-related genes is influenced by ethnic population sub-structuring in Sudan. Genetica, 2003, 119, 57-63.	0.5	16
98	Title is missing!. ScienceAsia, 2007, 33, 443.	0.2	16
99	Epiregulin (EREG) variation is associated with susceptibility to tuberculosis. Genes and Immunity, 2012, 13, 275-281.	2.2	16
100	Joint Effects of Known Type 2 Diabetes Susceptibility Loci in Genome-Wide Association Study of Singapore Chinese: The Singapore Chinese Health Study. PLoS ONE, 2014, 9, e87762.	1.1	15
101	Identification of genetic variants associated with susceptibility to West Nile virus neuroinvasive disease. Genes and Immunity, 2016, 17, 298-304.	2.2	14
102	Whole genomeâ€“amplified DNA: insights and imputation. Nature Methods, 2008, 5, 279-280.	9.0	13
103	Methylation changes in the peripheral blood of filipinos with type 2 diabetes suggest spurious transcription initiation at TXNIP. Human Molecular Genetics, 2019, 28, 4208-4218.	1.4	12
104	Y chromosomal evidence on the origin of northern Thai people. PLoS ONE, 2017, 12, e0181935.	1.1	10
105	Cw * 1701 defines a divergent African HLA-C allelic lineage. Immunogenetics, 1997, 46, 173-180.	1.2	9
106	Multi-platform segmentation for joint detection of copy number variants. Bioinformatics, 2011, 27, 1555-1561.	1.8	8
107	Whole genome sequencing to identify host genetic risk factors for severe outcomes of hepatitis a virus infection. Journal of Medical Virology, 2014, 86, 1661-1668.	2.5	8
108	Admixed Origin of the Kayah (Red Karen) in Northern Thailand Revealed by Biparental and Paternal Markers. Annals of Human Genetics, 2015, 79, 108-121.	0.3	6

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109	Genomewide association study of HLA alloimmunization in previously pregnant blood donors. Transfusion, 2018, 58, 402-412.	0.8	5
110	Whiffs of selection. Nature Genetics, 2000, 26, 131-132.	9.4	3
111	Detection of Novel ALAD Gene Polymorphisms Using Denaturing High-Performance Liquid Chromatography. Human Biology, 2001, 73, 429-442.	0.4	3
112	Hepatocyte Growth Factor and Retinal Arteriolar Diameter in Singapore Chinese. Ophthalmology, 2010, 117, 939-945.	2.5	3
113	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 4365-4365.	1.4	2
114	Y-CHROMOSOMAL VARIATION IN UXORILOCAL AND PATRILOCAL POPULATIONS IN THAILAND. , 2001, , .		2
115	Copy number polymorphisms in new HapMap III and Singapore populations. Journal of Human Genetics, 2011, 56, 552-560.	1.1	1
116	HIV, Stigma, and Rates of Infection: Absence of Evidence. PLoS Medicine, 2007, 4, e54.	3.9	0
117	OR.103. Combined Analysis of Three Genome-wide Scans Reveals Additional Loci Associated with Rheumatoid Arthritis. Clinical Immunology, 2008, 127, S41.	1.4	0
118	The Singapore Genome Variation Project. European Journal of Cancer, Supplement, 2008, 6, 200.	2.2	0