Mark Seielstad

List of Publications by Year
in descending order

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118 papers	25,858 citations	20797 60 h-index	19169 118 g-index
123 all docs	123 docs citations	123 times ranked	34790 citing authors

#	Article	IF	Citations
1	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
2	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
3	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
4	Development and evaluation of a transfusion medicine genome wide genotyping array. Transfusion, 2019, 59, 101-111.	0.8	30
5	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
6	Genomewide association study of HLA alloimmunization in previously pregnant blood donors. Transfusion, 2018, 58, 402-412.	0.8	5
7	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	1.6	89
8	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
9	Blood Gene Signatures of Chagas Cardiomyopathy With or Without Ventricular Dysfunction. Journal of Infectious Diseases, 2017, 215, 387-395.	1.9	32
10	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
11	Y chromosomal evidence on the origin of northern Thai people. PLoS ONE, 2017, 12, e0181935.	1.1	10
12	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
13	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2016, 48, 556-562.	9.4	147
14	Identification of genetic variants associated with susceptibility to West Nile virus neuroinvasive disease. Genes and Immunity, 2016, 17, 298-304.	2.2	14
15	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
16	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. Nature Communications, 2015, 6, 6916.	5.8	154
17	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.3	59
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. Nature, 2014, 506, 97-101.	13.7	439
27	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
28	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
29	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
30	Association of Cardiovascular and Metabolic Disease Genes with Psoriasis. Journal of Investigative Dermatology, 2013, 133, 836-839.	0.3	62
31	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	1.1	22
32	Genome Wide Association Study (GWAS) of Chagas Cardiomyopathy in Trypanosoma cruzi Seropositive Subjects. PLoS ONE, 2013, 8, e79629.	1.1	44
33	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
34	Genetic Variants on Chromosome 1q41 Influence Ocular Axial Length and High Myopia. PLoS Genetics, 2012, 8, e1002753.	1.5	95
35	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
36	Epiregulin (EREG) variation is associated with susceptibility to tuberculosis. Genes and Immunity, 2012, 13, 275-281.	2.2	16

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37	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
38	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
39	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	9.4	372
40	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
41	Genome-Wide Expression Profiling Identifies Type 1 Interferon Response Pathways in Active Tuberculosis. PLoS ONE, 2012, 7, e45839.	1.1	213
42	Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. International Journal of Obesity, 2012, 36, 159-163.	1.6	83
43	Polymorphisms in SP110 are not associated with pulmonary tuberculosis in Indonesians. Infection, Genetics and Evolution, 2012, 12, 1319-1323.	1.0	18
44	A genome wide association study of pulmonary tuberculosis susceptibility in Indonesians. BMC Medical Genetics, 2012, 13, 5.	2.1	90
45	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
46	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
47	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
48	Genome-Wide Association Studies Reveal Genetic Variants in CTNND2 for High Myopia in Singapore Chinese. Ophthalmology, 2011, 118, 368-375.	2.5	118
49	A 32 kb Critical Region Excluding Y402H in CFH Mediates Risk for Age-Related Macular Degeneration. PLoS ONE, 2011, 6, e25598.	1.1	46
50	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
51	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
52	Pathway-based analysis using reduced gene subsets in genome-wide association studies. BMC Bioinformatics, 2011, 12, 17.	1.2	30
53	SgD-CNV, a database for common and rare copy number variants in three Asian populations. Human Mutation, 2011, 32, 1341-1349.	1.1	27
54	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

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55	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
56	Multi-platform segmentation for joint detection of copy number variants. Bioinformatics, 2011, 27, 1555-1561.	1.8	8
57	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Human Molecular Genetics, 2011, 20, 649-658.	1.4	140
58	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
59	Copy number polymorphisms in new HapMap III and Singapore populations. Journal of Human Genetics, 2011, 56, 552-560.	1.1	1
60	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
61	Transferability of Type 2 Diabetes Implicated Loci in Multi-Ethnic Cohorts from Southeast Asia. PLoS Genetics, 2011, 7, e1001363.	1.5	131
62	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
63	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
64	Genomic copy number variations in three Southeast Asian populations. Human Mutation, 2010, 31, 851-857.	1.1	26
65	Analysis of 39 CrohnÊ¼s Disease Risk loci in Swedish Inflammatory Bowel Disease Patients. Inflammatory Bowel Diseases, 2010, 16, 907-909.	0.9	20
66	Genetic evidence supports linguistic affinity of Mlabri - a hunter-gatherer group in Thailand. BMC Genetics, 2010, 11, 18.	2.7	30
67	New genetic associations detected in a host response study to hepatitis B vaccine. Genes and Immunity, 2010, 11, 232-238.	2.2	78
68	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
69	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. Nature Genetics, 2010, 42, 332-337.	9.4	572
70	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. Nature Genetics, 2010, 42, 508-514.	9.4	1,132
71	Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics, 2010, 6, e1001127.	1.5	193
72	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

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73	Support for TGFB1 as a Susceptibility Gene for High Myopia in Individuals of Chinese Descent. JAMA Ophthalmology, 2010, 128, 1081.	2.6	20
74	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
75	Hepatocyte Growth Factor and Retinal Arteriolar Diameter in Singapore Chinese. Ophthalmology, 2010, 117, 939-945.	2.5	3
76	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
77	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. Genome Research, 2009, 19, 2154-2162.	2.4	146
78	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
79	The PRL â€“1149 G/T polymorphism and rheumatoid arthritis susceptibility. Arthritis and Rheumatism, 2009, 60, 1250-1254.	6.7	23
80	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
81	Genetic variants at CD28, PRDM1 and CD2/CD58 are associated with rheumatoid arthritis risk. Nature Genetics, 2009, 41, 1313-1318.	9.4	306
82	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
83	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
84	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557
85	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
86	Common variants at CD40 and other loci confer risk of rheumatoid arthritis. Nature Genetics, 2008, 40, 1216-1223.	9.4	476
87	Analysis of association of the TIRAP (MAL) S180L variant and tuberculosis in three populations. Nature Genetics, 2008, 40, 261-262.	9.4	61
88	Whole genomeâ€“amplified DNA: insights and imputation. Nature Methods, 2008, 5, 279-280.	9.0	13
89	OR.103. Combined Analysis of Three Genome-wide Scans Reveals Additional Loci Associated with Rheumatoid Arthritis. Clinical Immunology, 2008, 127, S41.	1.4	0
90	The Singapore Genome Variation Project. European Journal of Cancer, Supplement, 2008, 6, 200.	2.2	0

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91	FTO Variants Are Associated With Obesity in the Chinese and Malay Populations in Singapore. Diabetes, 2008, 57, 2851-2857.	0.3	152
92	Genetic Association and Expression Studies Indicate a Role of Toll-Like Receptor 8 in Pulmonary Tuberculosis. PLoS Genetics, 2008, 4, e1000218.	1.5	228
93	Identification of Tuberculosis Susceptibility Genes with Human Macrophage Gene Expression Profiles. PLoS Pathogens, 2008, 4, e1000229.	2.1	134
94	HIV, Stigma, and Rates of Infection: Absence of Evidence. PLoS Medicine, 2007, 4, e54.	3.9	0
95	TRAF1â€“C5as a Risk Locus for Rheumatoid Arthritis â€” A Genomewide Study. New England Journal of Medicine, 2007, 357, 1199-1209.	13.9	729
96	Title is missing!. ScienceAsia, 2007, 33, 443.	0.2	16
97	On the Usage of HWE for Identifying Genotyping Errors. Annals of Human Genetics, 2007, 71, 701-703.	0.3	47
98	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
99	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
100	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
101	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
102	Testing for Population Subdivision and Association in Four Case-Control Studies. American Journal of Human Genetics, 2002, 71, 304-311.	2.6	210
103	Patterns of linkage disequilibrium in the human genome. Nature Reviews Genetics, 2002, 3, 299-309.	7.7	994
104	African Origin of Modern Humans in East Asia: A Tale of 12,000 Y Chromosomes. Science, 2001, 292, 1151-1153.	6.0	310
105	Detection of Novel ALAD Gene Polymorphisms Using Denaturing High-Performance Liquid Chromatography. Human Biology, 2001, 73, 429-442.	0.4	3
106	Y-CHROMOSOMAL VARIATION IN UXORILOCAL AND PATRILOCAL POPULATIONS IN THAILAND. , 2001, , .		2
107	Whiffs of selection. Nature Genetics, 2000, 26, 131-132.	9.4	3
108	Y chromosome sequence variation and the history of human populations. Nature Genetics, 2000, 26, 358-361.	9.4	935

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109	Y chromosome haplotypes reveal prehistorical migrations to the Himalayas. Human Genetics, 2000, 107, 582-590.	1.8	242
110	Asymmetries in the Maternal and Paternal Genetic Histories of Colombian Populations. American Journal of Human Genetics, 2000, 67, 1062-1066.	2.6	45
111	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
112	Population growth of human Y chromosomes: a study of Y chromosome microsatellites. Molecular Biology and Evolution, 1999, 16, 1791-1798.	3.5	842
113	A view of modern human origins from Y chromosome microsatellite variation. Genome Research, 1999, 9, 558-67.	2.4	29
114	A View of Modern Human Origins from Y Chromosome Microsatellite Variation. Genome Research, 1999, 9, 558-567.	2.4	91
115	Genetic evidence for a higher female migration rate in humans. Nature Genetics, 1998, 20, 278-280.	9.4	562
116	Population Genetics of Y-Chromosome Short Tandem Repeats in Humans. Journal of Molecular Evolution, 1997, 45, 265-270.	0.8	82
117	Cw * 1701 defines a divergent African HLA-C allelic lineage. Immunogenetics, 1997, 46, 173-180.	1.2	9
118	Geographic clustering of human Y-chromosome haplotypes. Annals of Human Genetics, 1996, 60, 401-408.	0.3	47