

Catherine M Stein

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104
papers

2,399
citations

28
h-index

44
g-index

115
ext. papers

2,979
ext. citations

5.2
avg, IF

4.7
L-index

#	Paper	IF	Citations
104	Genome scan of human systemic lupus erythematosus by regression modeling: evidence of linkage and epistasis at 4p16-15.2. <i>American Journal of Human Genetics</i> , 2000 , 67, 1460-9	11	126
103	Polymorphisms in Toll-like receptor 9 influence the clinical course of HIV-1 infection. <i>Aids</i> , 2007 , 21, 441-5	6.5	122
102	Immunological mechanisms of human resistance to persistent Mycobacterium tuberculosis infection. <i>Nature Reviews Immunology</i> , 2018 , 18, 575-589	36.5	118
101	IFN- γ -Independent immune markers of Mycobacterium tuberculosis exposure. <i>Nature Medicine</i> , 2019 , 25, 977-987	50.5	104
100	Pleiotropic effects of a chromosome 3 locus on speech-sound disorder and reading. <i>American Journal of Human Genetics</i> , 2004 , 74, 283-97	11	100
99	Genome scan of M. tuberculosis infection and disease in Ugandans. <i>PLoS ONE</i> , 2008 , 3, e4094	3.7	94
98	Triglyceride levels and not adipokine concentrations are closely related to severity of nonalcoholic fatty liver disease in an obesity surgery cohort. <i>Obesity</i> , 2009 , 17, 1696-701	8	70
97	The genetic bases of speech sound disorders: evidence from spoken and written language. <i>Journal of Speech, Language, and Hearing Research</i> , 2006 , 49, 1294-312	2.8	62
96	Linkage and association analysis of candidate genes for TB and TNF α cytokine expression: evidence for association with IFNGR1, IL-10, and TNF receptor 1 genes. <i>Human Genetics</i> , 2007 , 121, 663-73	6.3	56
95	Genetic epidemiology of tuberculosis susceptibility: impact of study design. <i>PLoS Pathogens</i> , 2011 , 7, e1001189	7.6	55
94	Contact investigation for active tuberculosis among child contacts in Uganda. <i>Clinical Infectious Diseases</i> , 2013 , 57, 1685-92	11.6	54
93	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. <i>American Journal of Human Genetics</i> , 2016 , 98, 514-524	11	53
92	Adolescent outcomes of children with early speech sound disorders with and without language impairment. <i>American Journal of Speech-Language Pathology</i> , 2015 , 24, 150-63	3.1	51
91	The aromatase gene CYP19A1: several genetic and functional lines of evidence supporting a role in reading, speech and language. <i>Behavior Genetics</i> , 2012 , 42, 509-27	3.2	51
90	Dimensions of early speech sound disorders: A factor analytic study. <i>Journal of Communication Disorders</i> , 2006 , 39, 139-57	1.9	51
89	Heritability analysis of cytokines as intermediate phenotypes of tuberculosis. <i>Journal of Infectious Diseases</i> , 2003 , 187, 1679-85	7	49
88	Speech sound disorder influenced by a locus in 15q14 region. <i>Behavior Genetics</i> , 2006 , 36, 858-68	3.2	42

87	Resistance and Susceptibility to Mycobacterium tuberculosis Infection and Disease in Tuberculosis Households in Kampala, Uganda. <i>American Journal of Epidemiology</i> , 2018 , 187, 1477-1489	3.8	41
86	Polymorphisms in TICAM2 and IL1B are associated with TB. <i>Genes and Immunity</i> , 2015 , 16, 127-133	4.4	41
85	Literacy outcomes of children with early childhood speech sound disorders: impact of endophenotypes. <i>Journal of Speech, Language, and Hearing Research</i> , 2011 , 54, 1628-43	2.8	40
84	Transcriptional networks are associated with resistance to Mycobacterium tuberculosis infection. <i>PLoS ONE</i> , 2017 , 12, e0175844	3.7	38
83	Narrative ability of children with speech sound disorders and the prediction of later literacy skills. <i>Language, Speech, and Hearing Services in Schools</i> , 2011 , 42, 561-79	2.3	38
82	Clinical and epidemiological characteristics of individuals resistant to M. tuberculosis infection in a longitudinal TB household contact study in Kampala, Uganda. <i>BMC Infectious Diseases</i> , 2014 , 14, 352	4	36
81	Structural equation modeling. <i>Methods in Molecular Biology</i> , 2012 , 850, 495-512	1.4	35
80	Innate and adaptive immune responses during acute M. tuberculosis infection in adult household contacts in Kampala, Uganda. <i>American Journal of Tropical Medicine and Hygiene</i> , 2012 , 86, 690-7	3.2	33
79	Evidence for a major gene influence on tumor necrosis factor-alpha expression in tuberculosis: path and segregation analysis. <i>Human Heredity</i> , 2005 , 60, 109-18	1.1	32
78	Further evidence of pleiotropy influencing speech and language: analysis of the DYX8 region. <i>Human Heredity</i> , 2007 , 63, 47-58	1.1	30
77	Subtyping Children With Speech Sound Disorders by Endophenotypes. <i>Topics in Language Disorders</i> , 2011 , 31, 112-127	1.3	29
76	Whole blood interferon-gamma responses to mycobacterium tuberculosis antigens in young household contacts of persons with tuberculosis in Uganda. <i>PLoS ONE</i> , 2008 , 3, e3407	3.7	27
75	Structural equation model-based genome scan for the metabolic syndrome. <i>BMC Genetics</i> , 2003 , 4 Suppl 1, S99	2.6	27
74	Increased prevalence of renal disease in systemic lupus erythematosus families with affected male relatives. <i>Arthritis and Rheumatism</i> , 2002 , 46, 428-35		26
73	Lean tissue mass wasting is associated with increased risk of mortality among women with pulmonary tuberculosis in urban Uganda. <i>Annals of Epidemiology</i> , 2012 , 22, 466-73	6.4	25
72	Mendelian Randomization. <i>Methods in Molecular Biology</i> , 2017 , 1666, 581-628	1.4	22
71	Genomics of human pulmonary tuberculosis: from genes to pathways. <i>Current Genetic Medicine Reports</i> , 2017 , 5, 149-166	2.2	21
70	Structural Equation Modeling. <i>Methods in Molecular Biology</i> , 2017 , 1666, 557-580	1.4	19

69	Association of symptoms and severity of rift valley fever with genetic polymorphisms in human innate immune pathways. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003584	4.8	19
68	Genetic and shared environmental influences on interferon- γ production in response to Mycobacterium tuberculosis antigens in a Ugandan population. <i>American Journal of Tropical Medicine and Hygiene</i> , 2013 , 89, 169-73	3.2	19
67	Genetic susceptibility to tuberculosis associated with cathepsin Z haplotype in a Ugandan household contact study. <i>Human Immunology</i> , 2011 , 72, 426-30	2.3	19
66	A chromosome 5q31.1 locus associates with tuberculin skin test reactivity in HIV-positive individuals from tuberculosis hyper-endemic regions in east Africa. <i>PLoS Genetics</i> , 2017 , 13, e1006710	6	19
65	Long-term Stability of Resistance to Latent Mycobacterium tuberculosis Infection in Highly Exposed Tuberculosis Household Contacts in Kampala, Uganda. <i>Clinical Infectious Diseases</i> , 2019 , 68, 1705-1712	11.6	19
64	Association of Toll-like receptor polymorphisms with HIV status in North Americans. <i>Genes and Immunity</i> , 2014 , 15, 569-77	4.4	18
63	Tuberculosis as a complex trait: impact of genetic epidemiological study design. <i>Mammalian Genome</i> , 2011 , 22, 91-9	3.2	18
62	Defining genetic determinants of the Metabolic Syndrome in the Framingham Heart Study using association and structural equation modeling methods. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S50	2.3	18
61	Novel polymorphisms in and associated with tuberculosis progression phenotypes in Ethiopian populations. <i>Global Health, Epidemiology and Genomics</i> , 2018 , 3, e1	2.9	17
60	Psychosocial co-morbidities in adolescents and adults with histories of communication disorders. <i>Journal of Communication Disorders</i> , 2016 , 61, 60-70	1.9	17
59	The household contact study design for genetic epidemiological studies of infectious diseases. <i>Frontiers in Genetics</i> , 2013 , 4, 61	4.5	17
58	Practical barriers and ethical challenges in genetic data sharing. <i>International Journal of Environmental Research and Public Health</i> , 2014 , 11, 8383-98	4.6	16
57	Finding genes underlying human disease. <i>Clinical Genetics</i> , 2009 , 75, 101-6	4	16
56	AmpliSeq transcriptome analysis of human alveolar and monocyte-derived macrophages over time in response to Mycobacterium tuberculosis infection. <i>PLoS ONE</i> , 2018 , 13, e0198221	3.7	15
55	Reading skills of students with speech sound disorders at three stages of literacy development. <i>Language, Speech, and Hearing Services in Schools</i> , 2013 , 44, 360-73	2.3	15
54	Reading Outcomes for Individuals With Histories of Suspected Childhood Apraxia of Speech. <i>American Journal of Speech-Language Pathology</i> , 2019 , 28, 1432-1447	3.1	15
53	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. <i>PLoS Genetics</i> , 2020 , 16, e1008728	6	14
52	Effectiveness of WHO@ pragmatic screening algorithm for child contacts of tuberculosis cases in resource-constrained settings: a prospective cohort study in Uganda. <i>Lancet Respiratory Medicine</i> , 2018 , 6, 276-286	35.1	13

51	Heritability and longitudinal outcomes of spelling skills in individuals with histories of early speech and language disorders. <i>Learning and Individual Differences</i> , 2018 , 65, 1-11	3.1	13
50	Wasting among Uganda men with pulmonary tuberculosis is associated with linear regain in lean tissue mass during and after treatment in contrast to women with wasting who regain fat tissue mass: prospective cohort study. <i>BMC Infectious Diseases</i> , 2014 , 14, 24	4	13
49	A framework for structural equation models in general pedigrees. <i>Human Heredity</i> , 2010 , 70, 278-86	1.1	13
48	Multivariate analysis of complex gene expression and clinical phenotypes with genetic marker data. <i>Genetic Epidemiology</i> , 2007 , 31 Suppl 1, S103-9	2.6	12
47	Fine-mapping analysis of a chromosome 2 region linked to resistance to Mycobacterium tuberculosis infection in Uganda reveals potential regulatory variants. <i>Genes and Immunity</i> , 2019 , 20, 473-483	4.4	11
46	Heritability estimation for speech-sound traits with developmental trajectories. <i>Behavior Genetics</i> , 2011 , 41, 184-91	3.2	11
45	Modeling the complex gene x environment interplay in the simulated rheumatoid arthritis GAW15 data using latent variable structural equation modeling. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S118	2.3	11
44	CCR2, CCR5, and CXCL12 variation and HIV/AIDS in Papua New Guinea. <i>Infection, Genetics and Evolution</i> , 2015 , 36, 165-173	4.5	10
43	Genetics and evolution of tuberculosis pathogenesis: New perspectives and approaches. <i>Infection, Genetics and Evolution</i> , 2020 , 81, 104204	4.5	10
42	Impact of geographic distance on appraisal delay for active TB treatment seeking in Uganda: a network analysis of the Kawempe Community Health Cohort Study. <i>BMC Public Health</i> , 2018 , 18, 798	4.1	10
41	Comparison of affected sibling-pair linkage methods to identify gene x gene interaction in GAW15 simulated data. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S66	2.3	10
40	Tuberculin skin test reversion following isoniazid preventive therapy reflects diversity of immune response to primary Mycobacterium tuberculosis infection. <i>PLoS ONE</i> , 2014 , 9, e96613	3.7	10
39	Speech-Sound Disorders and Attention-Deficit/Hyperactivity Disorder Symptoms. <i>Topics in Language Disorders</i> , 2012 , 32, 247-263	1.3	9
38	A tuberculosis ontology for host systems biology. <i>Tuberculosis</i> , 2015 , 95, 570-4	2.6	8
37	Identification of Host Proteins Predictive of Early Stage Mycobacterium tuberculosis Infection. <i>EBioMedicine</i> , 2017 , 21, 150-157	8.8	8
36	An autosome-wide search using longitudinal data for loci linked to type 2 diabetes progression. <i>BMC Genetics</i> , 2003 , 4 Suppl 1, S8	2.6	8
35	Differential Long-Term Outcomes for Individuals With Histories of Preschool Speech Sound Disorders. <i>American Journal of Speech-Language Pathology</i> , 2019 , 28, 1582-1596	3.1	8
34	Joint modeling of longitudinal data and discrete-time survival outcome. <i>Statistical Methods in Medical Research</i> , 2016 , 25, 1512-26	2.3	7

33	Calculating asymptotic significance levels of the constrained likelihood ratio test with application to multivariate genetic linkage analysis. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009 , 8, Article 39	1.2	7
32	Structural equation modeling with latent variables for longitudinal blood pressure traits using general pedigrees. <i>BMC Proceedings</i> , 2016 , 10, 303-307	2.3	6
31	Tuberculosis case finding in first-degree relative contacts not living with index tuberculosis cases in Kampala, Uganda. <i>Clinical Epidemiology</i> , 2015 , 7, 411-9	5.9	6
30	Association between AVPR1A, DRD2, and ASPM and endophenotypes of communication disorders. <i>Psychiatric Genetics</i> , 2014 , 24, 191-200	2.9	6
29	Genetic variation in TLR genes in Ugandan and South African populations and comparison with HapMap data. <i>PLoS ONE</i> , 2012 , 7, e47597	3.7	6
28	Mendelian randomization in family data. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S45	2.3	6
27	Discussing gene-gene interaction: warning--translating equations to English may result in jabberwocky. <i>Genetic Epidemiology</i> , 2007 , 31 Suppl 1, S61-7	2.6	6
26	strum: an R package for structural modeling of latent variables for general pedigrees. <i>BMC Genetics</i> , 2015 , 16, 35	2.6	5
25	Feature-driven classification reveals potential comorbid subtypes within childhood apraxia of speech. <i>BMC Pediatrics</i> , 2020 , 20, 519	2.6	5
24	Associations of Toll-Like Receptor and ðDefensin Polymorphisms with Measures of Periodontal Disease (PD) in HIV+ North American Adults: An Exploratory Study. <i>PLoS ONE</i> , 2016 , 11, e0164075	3.7	5
23	Genetic variability and consequence of Mycobacterium tuberculosis lineage 3 in Kampala-Uganda. <i>PLoS ONE</i> , 2019 , 14, e0221644	3.7	4
22	Experiences and perspectives on the return of secondary findings among genetic epidemiologists. <i>Genetics in Medicine</i> , 2019 , 21, 1541-1547	8.1	4
21	The DYS2 locus and neurochemical signaling genes contribute to speech sound disorder and related neurocognitive domains. <i>Genes, Brain and Behavior</i> , 2015 , 14, 377-85	3.6	3
20	Psychosocial Comorbidities in Adolescents With Histories of Childhood Apraxia of Speech. <i>American Journal of Speech-Language Pathology</i> , 2021 , 30, 2572-2588	3.1	3
19	Importance of Study Design and Phenotype Definition in Ongoing Studies of Resistance to Latent Mycobacterium tuberculosis Infection. <i>Journal of Infectious Diseases</i> , 2020 , 221, 1025-1026	7	3
18	Model-Free Linkage Analysis of a Quantitative Trait. <i>Methods in Molecular Biology</i> , 2017 , 1666, 327-342	1.4	2
17	A Prospective Validation of a Clinical Algorithm to Detect Tuberculosis in Child Contacts. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 197, 1214-1216	10.2	2
16	Genetics of Susceptibility to Tuberculosis 2012 ,		2

15	The fa leptin receptor mutation and the heritability of respiratory frequency in a Brown Norway and Zucker intercross. <i>Journal of Applied Physiology</i> , 2004 , 97, 811-20	3.7	2
14	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. <i>Npj Genomic Medicine</i> , 2021 , 6, 64	6.2	2
13	Model-free linkage analysis of a quantitative trait. <i>Methods in Molecular Biology</i> , 2012 , 850, 301-16	1.4	1
12	Comparison of univariate and multivariate linkage analysis of traits related to hypertension. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S99	2.3	1
11	Transmission/disequilibrium test analysis of total serum IgE levels in the Hutterite and Collaborative Study on the Genetics of Asthma data sets. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S298-302	3.6	1
10	Interaction between host genes and M. tuberculosis lineage can affect tuberculosis severity: evidence for coevolution		1
9	Challenges of Genetic Data Sharing in African Studies. <i>Trends in Genetics</i> , 2020 , 36, 895-896	8.5	1
8	HDAC3 inhibitor RGFP966 controls bacterial growth and modulates macrophage signaling during Mycobacterium tuberculosis infection. <i>Tuberculosis</i> , 2021 , 127, 102062	2.6	1
7	Phenotype Definition for "Resisters" to Infection in the Literature-A Review and Recommendations. <i>Frontiers in Immunology</i> , 2021 , 12, 619988	8.4	1
6	Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon- γ release assay conversion. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	1
5	Identifying Genes Underlying Human Inherited Disease		1
4	Resistance to TST/IGRA conversion in Uganda: Heritability and Genome-Wide Association Study. <i>EBioMedicine</i> , 2021 , 74, 103727	8.8	0
3	Immune cells in bronchoalveolar lavage fluid of Ugandan adults who resist versus those who develop latent Mycobacterium tuberculosis infection. <i>PLoS ONE</i> , 2021 , 16, e0249477	3.7	0
2	Identifying Genes Underlying Human Inherited Disease1-7		
1	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virus-Infected Individuals From East Africa. <i>Journal of Infectious Diseases</i> , 2021 , 224, 695-704	7	