## **Catherine M Stein**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Immunological mechanisms of human resistance to persistent Mycobacterium tuberculosis infection. Nature Reviews Immunology, 2018, 18, 575-589.	10.6	241
2	IFN-γ-independent immune markers of Mycobacterium tuberculosis exposure. Nature Medicine, 2019, 25, 977-987.	15.2	186
3	Polymorphisms in Toll-like receptor 9 influence the clinical course of HIV-1 infection. Aids, 2007, 21, 441-446.	1.0	139
4	Genome Scan of Human Systemic Lupus Erythematosus by Regression Modeling: Evidence of Linkage and Epistasis at 4p16-15.2. American Journal of Human Genetics, 2000, 67, 1460-1469.	2.6	135
5	Pleiotropic Effects of a Chromosome 3 Locus on Speech-Sound Disorder and Reading. American Journal of Human Genetics, 2004, 74, 283-297.	2.6	124
6	Genome Scan of M. tuberculosis Infection and Disease in Ugandans. PLoS ONE, 2008, 3, e4094.	1.1	113
7	Triglyceride Levels and Not Adipokine Concentrations Are Closely Related to Severity of Nonalcoholic Fatty Liver Disease in an Obesity Surgery Cohort. Obesity, 2009, 17, 1696-1701.	1.5	92
8	A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. American Journal of Human Genetics, 2016, 98, 514-524.	2.6	78
9	Genetic Epidemiology of Tuberculosis Susceptibility: Impact of Study Design. PLoS Pathogens, 2011, 7, e1001189.	2.1	77
10	The Genetic Bases of Speech Sound Disorders: Evidence From Spoken and Written Language. Journal of Speech, Language, and Hearing Research, 2006, 49, 1294-1312.	0.7	71
11	Adolescent Outcomes of Children With Early Speech Sound Disorders With and Without Language Impairment. American Journal of Speech-Language Pathology, 2015, 24, 150-163.	0.9	70
12	Structural Equation Modeling. Methods in Molecular Biology, 2012, 850, 495-512.	0.4	70
13	Contact Investigation for Active Tuberculosis Among Child Contacts in Uganda. Clinical Infectious Diseases, 2013, 57, 1685-1692.	2.9	69
14	Resistance and Susceptibility to Mycobacterium tuberculosis Infection and Disease in Tuberculosis Households in Kampala, Uganda. American Journal of Epidemiology, 2018, 187, 1477-1489.	1.6	69
15	Mendelian Randomization. Methods in Molecular Biology, 2017, 1666, 581-628.	0.4	65
16	Transcriptional networks are associated with resistance to Mycobacterium tuberculosis infection. PLoS ONE, 2017, 12, e0175844.	1.1	64
17	The Aromatase Gene CYP19A1: Several Genetic and Functional Lines of Evidence Supporting a Role in Reading, Speech and Language. Behavior Genetics, 2012, 42, 509-527.	1.4	60
18	Linkage and association analysis of candidate genes for TB and TNFα cytokine expression: evidence for association with IFNGR1, IL-10, and TNF receptor 1 genes. Human Genetics, 2007, 121, 663-673.	1.8	58

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19	Dimensions of early speech sound disorders: A factor analytic study. Journal of Communication Disorders, 2006, 39, 139-157.	0.8	57
20	Structural Equation Modeling. Methods in Molecular Biology, 2017, 1666, 557-580.	0.4	57
21	Heritability Analysis of Cytokines as Intermediate Phenotypes of Tuberculosis. Journal of Infectious Diseases, 2003, 187, 1679-1685.	1.9	56
22	Literacy Outcomes of Children With Early Childhood Speech Sound Disorders: Impact of Endophenotypes. Journal of Speech, Language, and Hearing Research, 2011, 54, 1628-1643.	0.7	50
23	AmpliSeq transcriptome analysis of human alveolar and monocyte-derived macrophages over time in response to Mycobacterium tuberculosis infection. PLoS ONE, 2018, 13, e0198221.	1.1	50
24	Polymorphisms in TICAM2 and IL1B are associated with TB. Genes and Immunity, 2015, 16, 127-133.	2.2	49
25	Speech Sound Disorder Influenced by a Locus in 15q14 Region. Behavior Genetics, 2006, 36, 858-868.	1.4	48
26	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.	1.3	47
27	Narrative Ability of Children With Speech Sound Disorders and the Prediction of Later Literacy Skills. Language, Speech, and Hearing Services in Schools, 2011, 42, 561-579.	0.7	46
28	Long-term Stability of Resistance to Latent Mycobacterium tuberculosis Infection in Highly Exposed Tuberculosis Household Contacts in Kampala, Uganda. Clinical Infectious Diseases, 2019, 68, 1705-1712.	2.9	46
29	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. PLoS Genetics, 2020, 16, e1008728.	1.5	40
30	Novel polymorphisms in <i>TICAM2</i> and <i>NOD1</i> associated with tuberculosis progression phenotypes in Ethiopian populations. Global Health, Epidemiology and Genomics, 2018, 3, e1.	0.2	38
31	Subtyping Children With Speech Sound Disorders by Endophenotypes. Topics in Language Disorders, 2011, 31, 112-127.	0.9	36
32	Innate and Adaptive Immune Responses during Acute M. tuberculosis Infection in Adult Household Contacts in Kampala, Uganda. American Journal of Tropical Medicine and Hygiene, 2012, 86, 690-697.	0.6	36
33	Further Evidence of Pleiotropy Influencing Speech and Language: Analysis of the DYX8 Region. Human Heredity, 2007, 63, 47-58.	0.4	35
34	Structural equation model-based genome scan for the metabolic syndrome. BMC Genetics, 2003, 4, S99.	2.7	34
35	Evidence for a Major Gene Influence on Tumor Necrosis Factor-α Expression in Tuberculosis: Path and Segregation Analysis. Human Heredity, 2005, 60, 109-118.	0.4	34
36	Whole Blood Interferon-Gamma Responses to Mycobacterium tuberculosis Antigens in Young Household Contacts of Persons with Tuberculosis in Uganda. PLoS ONE, 2008, 3, e3407.	1.1	34

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37	Association of Symptoms and Severity of Rift Valley Fever with Genetic Polymorphisms in Human Innate Immune Pathways. PLoS Neglected Tropical Diseases, 2015, 9, e0003584.	1.3	30
38	Genomics of Human Pulmonary Tuberculosis: from Genes to Pathways. Current Genetic Medicine Reports, 2017, 5, 149-166.	1.9	30
39	Increased prevalence of renal disease in systemic lupus erythematosus families with affected male relatives. Arthritis and Rheumatism, 2002, 46, 428-435.	6.7	29
40	Reading Outcomes for Individuals With Histories of Suspected Childhood Apraxia of Speech. American Journal of Speech-Language Pathology, 2019, 28, 1432-1447.	0.9	29
41	Lean Tissue Mass Wasting is Associated With Increased Risk of Mortality Among Women With Pulmonary Tuberculosis in Urban Uganda. Annals of Epidemiology, 2012, 22, 466-473.	0.9	28
42	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.	1.5	28
43	Defining genetic determinants of the Metabolic Syndrome in the Framingham Heart Study using association and structural equation modeling methods. BMC Proceedings, 2009, 3, S50.	1.8	27
44	Genetics and evolution of tuberculosis pathogenesis: New perspectives and approaches. Infection, Genetics and Evolution, 2020, 81, 104204.	1.0	24
45	Effectiveness of WHO's pragmatic screening algorithm for child contacts of tuberculosis cases in resource-constrained settings: a prospective cohort study in Uganda. Lancet Respiratory Medicine,the, 2018, 6, 276-286.	5.2	23
46	Genetic susceptibility to tuberculosis associated with cathepsin Z haplotype in a Ugandan household contact study. Human Immunology, 2011, 72, 426-430.	1.2	22
47	Association of Toll-like receptor polymorphisms with HIV status in North Americans. Genes and Immunity, 2014, 15, 569-577.	2.2	22
48	Finding genes underlying human disease. Clinical Genetics, 2009, 75, 101-106.	1.0	21
49	Genetic and Shared Environmental Influences on Interferon-Î <sup>3</sup> Production in Response to Mycobacterium tuberculosis Antigens in a Ugandan Population. American Journal of Tropical Medicine and Hygiene, 2013, 89, 169-173.	0.6	21
50	Practical Barriers and Ethical Challenges in Genetic Data Sharing. International Journal of Environmental Research and Public Health, 2014, 11, 8383-8398.	1.2	20
51	Psychosocial co-morbidities in adolescents and adults with histories of communication disorders. Journal of Communication Disorders, 2016, 61, 60-70.	0.8	20
52	Tuberculosis as a complex trait: impact of genetic epidemiological study design. Mammalian Genome, 2011, 22, 91-99.	1.0	19
53	The household contact study design for genetic epidemiological studies of infectious diseases. Frontiers in Genetics, 2013, 4, 61.	1.1	19
54	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. BMC Infectious Diseases, 2014, 14, 24.	1.3	19

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55	Speech-Sound Disorders and Attention-Deficit/Hyperactivity Disorder Symptoms. Topics in Language Disorders, 2012, 32, 247-263.	0.9	18
56	Heritability and longitudinal outcomes of spelling skills in individuals with histories of early speech and language disorders. Learning and Individual Differences, 2018, 65, 1-11.	1.5	18
57	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.	2.2	18
58	Multivariate analysis of complex gene expression and clinical phenotypes with genetic marker data. Genetic Epidemiology, 2007, 31, S103-S109.	0.6	17
59	Reading Skills of Students With Speech Sound Disorders at Three Stages of Literacy Development. Language, Speech, and Hearing Services in Schools, 2013, 44, 360-373.	0.7	17
60	Impact of geographic distance on appraisal delay for active TB treatment seeking in Uganda: a network analysis of the Kawempe Community Health Cohort Study. BMC Public Health, 2018, 18, 798.	1.2	15
61	Feature-driven classification reveals potential comorbid subtypes within childhood apraxia of speech. BMC Pediatrics, 2020, 20, 519.	0.7	15
62	A Framework for Structural Equation Models in General Pedigrees. Human Heredity, 2010, 70, 278-286.	0.4	14
63	Identification of Host Proteins Predictive of Early Stage Mycobacterium tuberculosis Infection. EBioMedicine, 2017, 21, 150-157.	2.7	13
64	Phenotype Definition for "Resisters―to Mycobacterium tuberculosis Infection in the Literature—A Review and Recommendations. Frontiers in Immunology, 2021, 12, 619988.	2.2	13
65	Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon-Î <sup>3</sup> release assay conversion. Journal of Clinical Investigation, 2021, 131, .	3.9	13
66	Tuberculin Skin Test Reversion following Isoniazid Preventive Therapy Reflects Diversity of Immune Response to Primary Mycobacterium tuberculosis Infection. PLoS ONE, 2014, 9, e96613.	1.1	13
67	Differential Long-Term Outcomes for Individuals With Histories of Preschool Speech Sound Disorders. American Journal of Speech-Language Pathology, 2019, 28, 1582-1596.	0.9	13
68	Heritability Estimation for Speech-Sound Traits with Developmental Trajectories. Behavior Genetics, 2011, 41, 184-191.	1.4	12
69	Modeling the complex gene × environment interplay in the simulated rheumatoid arthritis GAW15 data using latent variable structural equation modeling. BMC Proceedings, 2007, 1, S118.	1.8	11
70	A tuberculosis ontology for host systems biology. Tuberculosis, 2015, 95, 570-574.	0.8	11
71	CCR2 , CCR5 , and CXCL12 variation and HIV/AIDS in Papua New Guinea. Infection, Genetics and Evolution, 2015, 36, 165-173.	1.0	11
72	Joint modeling of longitudinal data and discrete-time survival outcome. Statistical Methods in Medical Research, 2016, 25, 1512-1526.	0.7	11

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73	HDAC3 inhibitor RGFP966 controls bacterial growth and modulates macrophage signaling during Mycobacterium tuberculosis infection. Tuberculosis, 2021, 127, 102062.	0.8	11
74	Comparison of affected sibling-pair linkage methods to identify gene × gene interaction in GAW15 simulated data. BMC Proceedings, 2007, 1, S66.	1.8	10
75	Genetic variability and consequence of Mycobacterium tuberculosis lineage 3 in Kampala-Uganda. PLoS ONE, 2019, 14, e0221644.	1.1	10
76	Tuberculosis case finding in first-degree relative contacts not living with index tuberculosis cases in Kampala, Uganda. Clinical Epidemiology, 2015, 7, 411.	1.5	9
77	Structural equation modeling with latent variables for longitudinal blood pressure traits using general pedigrees. BMC Proceedings, 2016, 10, 303-307.	1.8	9
78	Psychosocial Comorbidities in Adolescents With Histories of Childhood Apraxia of Speech. American Journal of Speech-Language Pathology, 2021, 30, 1-17.	0.9	9
79	Resistance to TST/IGRA conversion in Uganda: Heritability and Genome-Wide Association Study. EBioMedicine, 2021, 74, 103727.	2.7	9
80	An autosome-wide search using longitudinal data for loci linked to type 2 diabetes progression. BMC Genetics, 2003, 4, S8.	2.7	8
81	Calculating Asymptotic Significance Levels of the Constrained Likelihood Ratio Test with Application to Multivariate Genetic Linkage Analysis. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-32.	0.2	8
82	The <scp>DYX2</scp> locus and neurochemical signaling genes contribute to speech sound disorder and related neurocognitive domains. Genes, Brain and Behavior, 2015, 14, 377-385.	1.1	8
83	Monocyte Transcriptional Responses to Mycobacterium tuberculosis Associate with Resistance to Tuberculin Skin Test and Interferon Gamma Release Assay Conversion. MSphere, 2022, 7, .	1.3	8
84	Discussing gene-gene interaction: Warning — translating equations to English may result in Jabberwocky. Genetic Epidemiology, 2007, 31, S61-S67.	0.6	7
85	Mendelian randomization in family data. BMC Proceedings, 2009, 3, S45.	1.8	7
86	Genetic Variation in TLR Genes in Ugandan and South African Populations and Comparison with HapMap Data. PLoS ONE, 2012, 7, e47597.	1.1	7
87	Association between AVPR1A, DRD2, and ASPM and endophenotypes of communication disorders. Psychiatric Genetics, 2014, 24, 191-200.	0.6	7
88	Associations of Toll-Like Receptor and β-Defensin Polymorphisms with Measures of Periodontal Disease (PD) in HIV+ North American Adults: An Exploratory Study. PLoS ONE, 2016, 11, e0164075.	1.1	7
89	Challenges of Genetic Data Sharing in African Studies. Trends in Genetics, 2020, 36, 895-896.	2.9	7
90	Association between genes regulating neural pathways for quantitative traits of speech and language disorders. Npj Genomic Medicine, 2021, 6, 64.	1.7	7

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91	strum: an R package for structural modeling of latent variables for general pedigrees. BMC Genetics, 2015, 16, 35.	2.7	6
92	Experiences and perspectives on the return of secondary findings among genetic epidemiologists. Genetics in Medicine, 2019, 21, 1541-1547.	1.1	6
93	Immune cells in bronchoalveolar lavage fluid of Ugandan adults who resist versus those who develop latent Mycobacterium tuberculosis infection. PLoS ONE, 2021, 16, e0249477.	1.1	6
94	Importance of Study Design and Phenotype Definition in Ongoing Studies of Resistance to Latent Mycobacterium tuberculosis Infection. Journal of Infectious Diseases, 2020, 221, 1025-1026.	1.9	5
95	Interaction between M. tuberculosis Lineage and Human Genetic Variants Reveals Novel Pathway Associations with Severity of TB. Pathogens, 2021, 10, 1487.	1.2	5
96	Novel HLA associations with outcomes of <i>Mycobacterium tuberculosis</i> exposure and sarcoidosis in individuals of African ancestry using nearestâ€neighbor feature selection. Genetic Epidemiology, 2022, 46, 463-474.	0.6	5
97	Model-Free Linkage Analysis of a Quantitative Trait. Methods in Molecular Biology, 2017, 1666, 327-342.	0.4	4
98	A Prospective Validation of a Clinical Algorithm to Detect Tuberculosis in Child Contacts. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1214-1216.	2.5	4
99	The fa leptin receptor mutation and the heritability of respiratory frequency in a Brown Norway and Zucker intercross. Journal of Applied Physiology, 2004, 97, 811-820.	1.2	3
100	Comparison of univariate and multivariate linkage analysis of traits related to hypertension. BMC Proceedings, 2009, 3, S99.	1.8	3
101	Model-Free Linkage Analysis of a Quantitative Trait. Methods in Molecular Biology, 2012, 850, 301-316.	0.4	2
102	Transmission/Disequilibrium Test Analysis of Total Serum IgE Levels in the Hutterite and Collaborative Study on the Genetics of Asthma Data Sets. Genetic Epidemiology, 2001, 21, S298-302.	0.6	1
103	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virus–Infected Individuals From East Africa. Journal of Infectious Diseases, 2021, 224, 695-704.	1.9	1