Christoph Lange

List of Publications by Year
in descending order

238 papers	15,194 citations	20036 63 h-index	23173 116 g-index
254 all docs	254 docs citations	254 times ranked	19990 citing authors

#	ARTICLE	IF	CITATIONS
1	A Common Genetic Variant Is Associated with Adult and Childhood Obesity. Science, 2006, 312, 279-283.	6.0	652
2	Treatment correlates of successful outcomes in pulmonary multidrug-resistant tuberculosis: an individual patient data meta-analysis. Lancet, The, 2018, 392, 821-834.	6.3	452
3	Genome-wide Association Analysis Reveals Putative Alzheimer's Disease Susceptibility Loci in Addition to APOE. American Journal of Human Genetics, 2008, 83, 623-632.	2.6	423
4	Family-based designs in the age of large-scale gene-association studies. Nature Reviews Genetics, 2006, 7, 385-394.	7.7	397
5	Variants in FAM13A are associated with chronic obstructive pulmonary disease. Nature Genetics, 2010, 42, 200-202.	9.4	348
6	Genomewide Association between GLCCI1 and Response to Glucocorticoid Therapy in Asthma. New England Journal of Medicine, 2011, 365, 1173-1183.	13.9	342
7	Genome‐wide association scan of quantitative traits for attention deficit hyperactivity disorder identifies novel associations and confirms candidate gene associations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1345-1354.	1.1	335
8	MMP12, Lung Function, and COPD in High-Risk Populations. New England Journal of Medicine, 2009, 361, 2599-2608.	13.9	315
9	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	9.4	311
10	Genome-wide Association Analysis Identifies PDE4D as an Asthma-Susceptibility Gene. American Journal of Human Genetics, 2009, 84, 581-593.	2.6	296
11	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. Lancet Respiratory Medicine,the, 2014, 2, 214-225.	5.2	291
12	PBAT: Tools for Family-Based Association Studies. American Journal of Human Genetics, 2004, 74, 367-369.	2.6	262
13	Management of patients with multidrug-resistant/extensively drug-resistant tuberculosis in Europe: a TBNET consensus statement. European Respiratory Journal, 2014, 44, 23-63.	3.1	256
14	Association of Vitamin D Receptor Gene Polymorphisms with Childhood and Adult Asthma. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 1057-1065.	2.5	232
15	Family-Based Association between Alzheimer's Disease and Variants in UBQLN1. New England Journal of Medicine, 2005, 352, 884-894.	13.9	232
16	Genome‐wide association scan of attention deficit hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1337-1344.	1.1	228
17	Genetic model testing and statistical power in population-based association studies of quantitative traits. Genetic Epidemiology, 2007, 31, 358-362.	0.6	224
18	Combined Analysis from Eleven Linkage Studies of Bipolar Disorder Provides Strong Evidence of Susceptibility Loci on Chromosomes 6q and 8q. American Journal of Human Genetics, 2005, 77, 582-595.	2.6	218

#	ARTICLE	IF	CITATIONS
19	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. Human Molecular Genetics, 2012, 21, 947-957.	1.4	216
20	The risk of tuberculosis in transplant candidates and recipients: a TBNET consensus statement. European Respiratory Journal, 2012, 40, 990-1013.	3.1	211
21	The transforming growth factor-Â1 (TGFB1) gene is associated with chronic obstructive pulmonary disease (COPD). Human Molecular Genetics, 2004, 13, 1649-1656.	1.4	203
22	Attempted Replication of Reported Chronic Obstructive Pulmonary Disease Candidate Gene Associations. American Journal of Respiratory Cell and Molecular Biology, 2005, 33, 71-78.	1.4	185
23	A multivariate family-based association test using generalized estimating equations: FBAT-GEE. Biostatistics, 2003, 4, 195-206.	0.9	181
24	Genetic association analysis of copy-number variation (CNV) in human disease pathogenesis. Genomics, 2009, 93, 22-26.	1.3	177
25	Genomic screening and replication using the same data set in family-based association testing. Nature Genetics, 2005, 37, 683-691.	9.4	173
26	Most antiviral CD8 T cells during chronic viral infection do not express high levels of perforin and are not directly cytotoxic. Blood, 2003, 101, 226-235.	0.6	167
27	The SERPINE2 Gene Is Associated with Chronic Obstructive Pulmonary Disease. American Journal of Human Genetics, 2006, 78, 253-264.	2.6	167
28	Drug-associated adverse events in the treatment of multidrug-resistant tuberculosis: an individual patient data meta-analysis. Lancet Respiratory Medicine,the, 2020, 8, 383-394.	5.2	155
29	Polymorphisms in Toll-Like Receptor 4 Are Not Associated with Asthma or Atopy-related Phenotypes. American Journal of Respiratory and Critical Care Medicine, 2002, 166, 1449-1456.	2.5	154
30	Rapid Diagnosis of Smear-negative Tuberculosis by Bronchoalveolar Lavage Enzyme-linked Immunospot. American Journal of Respiratory and Critical Care Medicine, 2006, 174, 1048-1054.	2.5	148
31	CD8 T cells specific for human immunodeficiency virus, Epstein-Barr virus, and cytomegalovirus lack molecules for homing to lymphoid sites of infection. Blood, 2001, 98, 156-164.	0.6	147
32	A New Testing Strategy to Identify Rare Variants with Either Risk or Protective Effect on Disease. PLoS Genetics, 2011, 7, e1001289.	1.5	141
33	Integration of Genomic and Genetic Approaches Implicates IREB2 as a COPD Susceptibility Gene. American Journal of Human Genetics, 2009, 85, 493-502.	2.6	139
34	Power and Design Considerations for a General Class of Family-Based Association Tests: Quantitative Traits. American Journal of Human Genetics, 2002, 71, 1330-1341.	2.6	138
35	HIV-1 Infection Impairs the Bronchoalveolar T-Cell Response to Mycobacteria. American Journal of Respiratory and Critical Care Medicine, 2009, 180, 1262-1270.	2.5	138
36	Blood eosinophil count thresholds and exacerbations in patients with chronic obstructive pulmonary disease. Journal of Allergy and Clinical Immunology, 2018, 141, 2037-2047.e10.	1.5	138

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37	Beyond the IFN-Â horizon: biomarkers for immunodiagnosis of infection with Mycobacterium tuberculosis. European Respiratory Journal, 2014, 43, 1472-1486.	3.1	135
38	The Association of a SNP Upstream of INSIG2 with Body Mass Index is Reproduced in Several but Not All Cohorts. PLoS Genetics, 2007, 3, e61.	1.5	134
39	TOLL-like Receptor 10 Genetic Variation Is Associated with Asthma in Two Independent Samples. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 594-600.	2.5	133
40	On the Replication of Genetic Associations: Timing Can Be Everything!. American Journal of Human Genetics, 2008, 82, 849-858.	2.6	130
41	Advances in the diagnosis of tuberculosis. Respirology, 2010, 15, 220-240.	1.3	130
42	Bronchoalveolar Lavage Enzyme-linked Immunospot for a Rapid Diagnosis of Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2009, 180, 666-673.	2.5	125
43	*ARG1* Is a Novel Bronchodilator Response Gene. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 688-694.	2.5	121
44	Family-based association analysis of Î²2-adrenergic receptor polymorphisms in the childhood asthma management program. Journal of Allergy and Clinical Immunology, 2003, 112, 870-876.	1.5	119
45	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. BMC Genetics, 2015, 16, 138.	2.7	119
46	Power Calculations for a General Class of Family-Based Association Tests: Dichotomous Traits. American Journal of Human Genetics, 2002, 71, 575-584.	2.6	118
47	ADAM33 polymorphisms and phenotype associations in childhood asthma. Journal of Allergy and Clinical Immunology, 2004, 113, 1071-1078.	1.5	115
48	Multidrug- and Extensively Drug-Resistant Tuberculosis, Germany. Emerging Infectious Diseases, 2008, 14, 1700-1706.	2.0	113
49	On a general class of conditional tests for family-based association studies in genetics: the asymptotic distribution, the conditional power, and optimality considerations. Genetic Epidemiology, 2002, 23, 165-180.	0.6	108
50	Polymorphisms in IL13, total IgE, eosinophilia, and asthma exacerbations in childhood. Journal of Allergy and Clinical Immunology, 2007, 120, 84-90.	1.5	105
51	Genomeâ€wide association scan of the time to onset of attention deficit hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1355-1358.	1.1	103
52	Assessing the Reproducibility of Asthma Candidate Gene Associations, Using Genome-wide Data. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 1084-1090.	2.5	99
53	Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. Human Molecular Genetics, 2010, 19, 4745-4757.	1.4	98
54	Extensively Drug-resistant Tuberculosis, Italy and Germany. Emerging Infectious Diseases, 2007, 13, 780-782.	2.0	96

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55	Genomewide Weighted Hypothesis Testing in Family-Based Association Studies, with an Application to a 100K Scan. American Journal of Human Genetics, 2007, 81, 607-614.	2.6	94
56	Accuracy of Immunodiagnostic Tests for Active Tuberculosis Using Single and Combined Results: A Multicenter TBNET-Study. PLoS ONE, 2008, 3, e3417.	1.1	88
57	IL10 gene polymorphisms are associated with asthma phenotypes in children. Genetic Epidemiology, 2004, 26, 155-165.	0.6	86
58	Comprehensive Testing of Positionally Cloned Asthma Genes in Two Populations. American Journal of Respiratory and Critical Care Medicine, 2007, 176, 849-857.	2.5	82
59	Using the Noninformative Families in Family-Based Association Tests: A Powerful New Testing Strategy. American Journal of Human Genetics, 2003, 73, 801-811.	2.6	80
60	The IL12B Gene Is Associated with Asthma. American Journal of Human Genetics, 2004, 75, 709-715.	2.6	79
61	A Family-Based Association Test for Repeatedly Measured Quantitative Traits Adjusting for Unknown Environmental and/or Polygenic Effects. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-27.	0.2	78
62	Familyâ€Based Methods for Linkage and Association Analysis. Advances in Genetics, 2008, 60, 219-252.	0.8	71
63	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. Human Genetics, 2013, 132, 431-441.	1.8	69
64	Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 677-690.	2.5	66
65	Assessment of Alzheimerâ€™s disease caseâ€"control associations using family-based methods. Neurogenetics, 2009, 10, 19-25.	0.7	65
66	Multidrug-Resistant and Extensively Drug-Resistant Tuberculosis in the West. Europe and United States: Epidemiology, Surveillance, and Control. Clinics in Chest Medicine, 2009, 30, 637-665.	0.8	64
67	PBAT: A comprehensive software package for genome-wide association analysis of complex family-based studies. Human Genomics, 2005, 2, 67.	1.4	63
68	Meta-Analysis of the INSIG2 Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. PLoS Genetics, 2009, 5, e1000694.	1.5	62
69	Genome-wide Linkage of Forced Mid-expiratory Flow in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 1294-1301.	2.5	61
70	Estimating the number of unseen variants in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5008-5013.	3.3	61
71	PLD3 gene variants and Alzheimer's disease. Nature, 2015, 520, E7-E8.	13.7	60
72	Increased expression of the natural killer cell inhibitory receptor CD85j/ILT2 on antigen-specific effector CD8 T cells and its impact on CD8 T-cell function. Immunology, 2004, 112, 531-542.	2.0	57

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73	Luzzu—A Methodology and Framework for Linked Data Quality Assessment. Journal of Data and Information Quality, 2016, 8, 1-32.	1.5	56
74	Genetic Association and Risk Scores in a Chronic Obstructive Pulmonary Disease Meta-analysis of 16,707 Subjects. American Journal of Respiratory Cell and Molecular Biology, 2017, 57, 35-46.	1.4	55
75	Standardised shorter regimens *versus* individualised longer regimens for rifampin- or multidrug-resistant tuberculosis. European Respiratory Journal, 2020, 55, 1901467.	3.1	55
76	A New Powerful Non-Parametric Two-Stage Approach for Testing Multiple Phenotypes in Family-Based Association Studies. Human Heredity, 2003, 56, 10-17.	0.4	54
77	Ontologies and languages for representing mathematical knowledge on the Semantic Web. Semantic Web, 2013, 4, 119-158.	1.1	53
78	Chromosome 12q harbors multiple genetic loci related to asthma and asthma-related phenotypes. Human Molecular Genetics, 2003, 12, 1973-1979.	1.4	52
79	On the analysis of copy-number variations in genome-wide association studies: a translation of the family-based association test. Genetic Epidemiology, 2008, 32, 273-284.	0.6	52
80	Extended Haplotype in the Tumor Necrosis Factor Gene Cluster Is Associated with Asthma and Asthma-related Phenotypes. American Journal of Respiratory and Critical Care Medicine, 2005, 172, 687-692.	2.5	51
81	Genome-Wide Association Analysis of Body Mass in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2011, 45, 304-310.	1.4	50
82	Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development. Alzheimer's and Dementia, 2021, 17, 1509-1527.	0.4	50
83	Association of corticotropin-releasing hormone receptor-2 genetic variants with acute bronchodilator response in asthma. Pharmacogenetics and Genomics, 2008, 18, 373-382.	0.7	49
84	On the adjustment for covariates in genetic association analysis: a novel, simple principle to infer direct causal effects. Genetic Epidemiology, 2009, 33, 394-405.	0.6	49
85	*IL1B* polymorphisms modulate cystic fibrosis lung disease. Pediatric Pulmonology, 2009, 44, 580-593.	1.0	49
86	Testing for non-random mating: evidence for ancestry-related assortative mating in the Framingham heart study. Genetic Epidemiology, 2010, 34, 674-679.	0.6	49
87	Paternal History of Asthma and Airway Responsiveness in Children with Asthma. American Journal of Respiratory and Critical Care Medicine, 2005, 172, 552-558.	2.5	46
88	Exome Sequencing Analysis in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2016, 193, 1353-1363.	2.5	46
89	Family-based association tests for survival and times-to-onset analysis. Statistics in Medicine, 2004, 23, 179-189.	0.8	45
90	On the simultaneous association analysis of large genomic regions: a massive multi-locus association test. Bioinformatics, 2014, 30, 157-164.	1.8	45

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91	Mapping Quantitative Trait Loci Using Generalized Estimating Equations. Genetics, 2001, 159, 1325-1337.	1.2	45
92	Machine Learning Characterization of COPD Subtypes. Chest, 2020, 157, 1147-1157.	0.4	44
93	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. Human Molecular Genetics, 2015, 24, 1200-1210.	1.4	43
94	Utilizing the Jaccard index to reveal population stratification in sequencing data: a simulation study and an application to the 1000 Genomes Project. Bioinformatics, 2016, 32, 1366-1372.	1.8	43
95	Using Canonical Correlation Analysis to Discover Genetic Regulatory Variants. PLoS ONE, 2010, 5, e10395.	1.1	41
96	Family-based association analysis of a statistically derived quantitative traits for ADHD reveal an association inDRD4 with inattentive symptoms in ADHD individuals. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 100-106.	1.1	40
97	Diagnosis and treatment of latent infection with *Mycobacterium tuberculosis*. Respirology, 2013, 18, 205-216.	1.3	40
98	The rare *TREM2* R47H variant exerts only a modest effect on Alzheimer disease risk. Neurology, 2014, 83, 1353-1358.	1.5	40
99	Natriuretic Peptide System Gene Variants Are Associated with Ventricular Dysfunction after Coronary Artery Bypass Grafting. Anesthesiology, 2009, 110, 738-747.	1.3	40
100	On the Analysis of Genome-Wide Association Studies in Family-Based Designs: A Universal, Robust Analysis Approach and an Application to Four Genome-Wide Association Studies. PLoS Genetics, 2009, 5, e1000741.	1.5	40
101	Evaluating the quality of the LOD cloud: An empirical investigation. Semantic Web, 2018, 9, 859-901.	1.1	37
102	Testing and Estimating Gene–Environment Interactions in Family–Based Association Studies. Biometrics, 2008, 64, 458-467.	0.8	36
103	False-negative interferon-γ release assay results in active tuberculosis: a TBNET study. European Respiratory Journal, 2015, 45, 279-283.	3.1	36
104	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. Chest, 2018, 153, 65-76.	0.4	36
105	Cross-reactive immunity against the SARS-CoV-2 Omicron variant is low in pediatric patients with prior COVID-19 or MIS-C. Nature Communications, 2022, 13, .	5.8	36
106	Extensively Drug-Resistant Tuberculosis Is Worse than Multidrug-Resistant Tuberculosis: Different Methodology and Settings, Same Results. Clinical Infectious Diseases, 2008, 46, 958-959.	2.9	35
107	Association between Tuberculin Skin Test Reactivity, the Memory CD4 Cell Subset, and Circulating FoxP3-Expressing Cells in HIV-Infected Persons. Journal of Infectious Diseases, 2009, 199, 702-710.	1.9	34
108	FARVAT: a family-based rare variant association test. Bioinformatics, 2014, 30, 3197-3205.	1.8	34

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109	Recovering unused information in genome-wide association studies: the benefit of analyzing SNPs out of Hardy–Weinberg equilibrium. European Journal of Human Genetics, 2009, 17, 1676-1682.	1.4	32
110	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	1.4	32
111	Gene–environment interaction tests for dichotomous traits in trios and sibships. Genetic Epidemiology, 2009, 33, 691-699.	0.6	31
112	Increased frequencies of pulmonary regulatory T-cells in latent *Mycobacterium tuberculosis* infection. European Respiratory Journal, 2012, 40, 1450-1457.	3.1	31
113	Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. Scientific Reports, 2020, 10, 5029.	1.6	31
114	On Genome-wide Association Studies for Family-Based Designs: An Integrative Analysis Approach Combining Ascertained Family Samples with Unselected Controls. American Journal of Human Genetics, 2010, 86, 573-580.	2.6	30
115	On Prediction of Genetic Values in Marker-Assisted Selection. Genetics, 2001, 159, 1375-1381.	1.2	27
116	Screening and Replication using the Same Data Set: Testing Strategies for Family-Based Studies in which All Probands Are Affected. PLoS Genetics, 2008, 4, e1000197.	1.5	26
117	Potential Role for IL-2 ELISpot in Differentiating Recent and Remote Infection in Tuberculosis Contact Tracing. PLoS ONE, 2010, 5, e11670.	1.1	25
118	Plasmacytoid Dendritic Cells Infiltrate the Skin in Positive Tuberculin Skin Test Indurations. Journal of Investigative Dermatology, 2012, 132, 114-123.	0.3	24
119	Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within *Gremlin-1*, a component of the bone morphogenetic protein 4 pathway. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 493-498.	1.6	24
120	The Role of Family-Based Designs in Genome-Wide Association Studies. Statistical Science, 2009, 24, .	1.6	23
121	'Location, Location, Location': a spatial approach for rare variant analysis and an application to a study on non-syndromic cleft lip with or without cleft palate. Bioinformatics, 2012, 28, 3027-3033.	1.8	22
122	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 614-622.	1.4	22
123	Rapid immunodiagnosis of tuberculosis in a woman receiving anti-TNF therapy. Nature Clinical Practice Rheumatology, 2007, 3, 528-534.	3.2	21
124	Antimycobacterial immune responses in patients with pulmonary sarcoidosis. Clinical Respiratory Journal, 2009, 3, 229-238.	0.6	21
125	The Planetary System: Web 3.0 & Active Documents for STEM. Procedia Computer Science, 2011, 4, 598-607.	1.2	21
126	Common genetic variation in the GAD1 gene and the entire family of DLX homeobox genes and autism spectrum disorders. , 2011, 156, 233-239.		20

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127	Intention to Test Is Intention to Treat. American Journal of Respiratory and Critical Care Medicine, 2011, 183, 3-4.	2.5	20
128	Attitudes about Tuberculosis Prevention in the Elimination Phase: A Survey among Physicians in Germany. PLoS ONE, 2014, 9, e112681.	1.1	20
129	P2BAT: a massive parallel implementation of PBAT for genome-wide association studies in R. Bioinformatics, 2006, 22, 3103-3105.	1.8	19
130	Common Genetic Variants Associated with Resting Oxygenation in Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2014, 51, 678-687.	1.4	19
131	Identification of genetic outliers due to sub-structure and cryptic relationships. Bioinformatics, 2017, 33, 1972-1979.	1.8	19
132	Family-based association test for time-to-onset data with time-dependent differences between the hazard functions. Genetic Epidemiology, 2006, 30, 124-132.	0.6	18
133	Genomics and genome-wide association studies: An integrative approach to expression QTL mapping. Genomics, 2008, 92, 129-133.	1.3	18
134	Vitamin D and Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 740-742.	2.5	18
135	Beyond GWAS in COPD: Probing the Landscape between Gene-Set Associations, Genome-Wide Associations and Protein-Protein Interaction Networks. Human Heredity, 2014, 78, 131-139.	0.4	18
136	Integrating Multiple Correlated Phenotypes for Genetic Association Analysis by Maximizing Heritability. Human Heredity, 2015, 79, 93-104.	0.4	18
137	Asthma-susceptibility variants identified using probands in case-control and family-based analyses. BMC Medical Genetics, 2010, 11, 122.	2.1	17
138	High Rates of Treatment Success in Pulmonary Multidrug-Resistant Tuberculosis by Individually Tailored Treatment Regimens. Annals of the American Thoracic Society, 2016, 13, 1271-1278.	1.5	17
139	A general approach to testing for pleiotropy with rare and common variants. Genetic Epidemiology, 2017, 41, 163-170.	0.6	17
140	Of Blind Men and Elephants: Making Sense of Extensively Drug-resistant Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 1000-1001.	2.5	16
141	Representing dataset quality metadata using multi-dimensional views. , 2014, , .		16
142	Exploring candidate gene associations with neuropsychological performance. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2007, 144B, 987-991.	1.1	15
143	Association of SERPINE2 With Asthma. Chest, 2011, 140, 667-674.	0.4	15
144	Tbnet â€" Collaborative research on tuberculosis in Europe. European Journal of Microbiology and Immunology, 2012, 2, 264-274.	1.5	15

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145	Integrative Genomics Analysis Identifies ACVR1B as a Candidate Causal Gene of Emphysema Distribution. American Journal of Respiratory Cell and Molecular Biology, 2019, 60, 388-398.	1.4	15
146	Caution against examining the role of reverse causality in Mendelian Randomization. Genetic Epidemiology, 2021, 45, 445-454.	0.6	15
147	Causation and causal inference for genetic effects. Human Genetics, 2012, 131, 1665-1676.	1.8	14
148	Handling the data management needs of high-throughput sequencing data: SpeedGene, a compression algorithm for the efficient storage of genetic data. BMC Bioinformatics, 2012, 13, 100.	1.2	14
149	Geneâ€based segregation method for identifying rare variants in familyâ€based sequencing studies. Genetic Epidemiology, 2017, 41, 309-319.	0.6	14
150	Genomeâ€wide association analysis of COVIDâ€19 mortality risk in SARSâ€CoVâ€2 genomes identifies mutation in the SARSâ€CoVâ€2 spike protein that colocalizes with P.1 of the Brazilian strain. Genetic Epidemiology, 2021, 45, 685-693.	0.6	14
151	A doubly robust test for gene-environment interaction in family-based studies of affected offspring. Biostatistics, 2010, 11, 213-225.	0.9	13
152	Bringing Mathematics to the Web of Data: The Case of the Mathematics Subject Classification. Lecture Notes in Computer Science, 2012, , 763-777.	1.0	13
153	A general framework for robust and efficient association analysis in familyâ€based designs: quantitative and dichotomous phenotypes. Statistics in Medicine, 2013, 32, 4482-4498.	0.8	12
154	Investigation of the role of <i>TCF4</i> rare sequence variants in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 354-362.	1.1	12
155	Rapid diagnosis of pulmonary tuberculosis by combined molecular and immunological methods. European Respiratory Journal, 2018, 51, 1702189.	3.1	12
156	Quality Assessment of Linked Datasets Using Probabilistic Approximation. Lecture Notes in Computer Science, 2015, , 221-236.	1.0	12
157	Single-Nucleotide Polymorphism rs498055 on Chromosome 10q24 Is Not Associated with Alzheimer Disease in Two Independent Family Samples. American Journal of Human Genetics, 2006, 79, 180-183.	2.6	11
158	STEX+. , 2010, , .		11
159	An alternative hypothesis testing strategy for secondary phenotype data in case-control genetic association studies. Frontiers in Genetics, 2014, 5, 188.	1.1	11
160	Combined Antigen-Specific Interferon-Î³ and Interleukin-2 Release Assay (FluoroSpot) for the Diagnosis of Mycobacterium tuberculosis Infection. PLoS ONE, 2015, 10, e0120006.	1.1	11
161	Comment on: Daily 300 mg dose of linezolid for the treatment of intractable multidrug-resistant and extensively drug-resistant tuberculosis. Journal of Antimicrobial Chemotherapy, 2009, 64, 879-883.	1.3	10
162	Development of a Pharmacogenetic Predictive Test in asthma: proof of concept. Pharmacogenetics and Genomics, 2010, 20, 86-93.	0.7	10

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163	On the association analysis of genome‐sequencing data: A spatial clustering approach for partitioning the entire genome into nonoverlapping windows. Genetic Epidemiology, 2017, 41, 332-340.	0.6	10
164	A Mathematical Approach to Ontology Authoring and Documentation. Lecture Notes in Computer Science, 2009, , 389-404.	1.0	10
165	New Powerful Approaches for Family‐based Association Tests with Longitudinal Measurements. Annals of Human Genetics, 2009, 73, 74-83.	0.3	9
166	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. BMC Medical Genetics, 2015, 16, 62.	2.1	9
167	On Quality Control Measures in Genome-Wide Association Studies: A Test to Assess the Genotyping Quality of Individual Probands in Family-Based Association Studies and an Application to the HapMap Data. PLoS Genetics, 2009, 5, e1000572.	1.5	9
168	Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimer's disease-associated genes: DTNB and DLG2. Molecular Psychiatry, 2022, 27, 1963-1969.	4.1	9
169	On dichotomizing phenotypes in family-based association tests: quantitative phenotypes are not always the optimal choice. Genetic Epidemiology, 2007, 31, 376-382.	0.6	8
170	Pulmonary immune responses to Mycobacterium tuberculosis in exposed individuals. PLoS ONE, 2017, 12, e0187882.	1.1	8
171	locStra: Fast analysis of regional/global stratification in whole‐genome sequencing studies. Genetic Epidemiology, 2021, 45, 82-98.	0.6	8
172	Generalized estimating equations: A hybrid approach for mean parameters in multivariate regression models. Statistical Modelling, 2002, 2, 163-181.	0.5	7
173	Recommendations for using standardised phenotypes in genetic association studies. Human Genomics, 2009, 3, 308.	1.4	7
174	An omnibus test for family-based association studies with multiple SNPs and multiple phenotypes. European Journal of Human Genetics, 2010, 18, 720-725.	1.4	7
175	Combining Disease Models to Test for Gene-Environment Interaction in Nuclear Families. Biometrics, 2011, 67, 1260-1270.	0.8	7
176	Quantitative trait prediction based on genetic marker-array data, a simulation study. Bioinformatics, 2011, 27, 745-748.	1.8	7
177	Differentiating Population Stratification from Genotyping Error Using Family Data. Annals of Human Genetics, 2012, 76, 42-52.	0.3	7
178	A comparison of popular TDT‐generalizations for family‐based association analysis. Genetic Epidemiology, 2019, 43, 300-317.	0.6	7
179	A unifying framework for rare variant association testing in family-based designs, including higher criticism approaches, SKATs, and burden tests. Bioinformatics, 2021, 36, 5432-5438.	1.8	7
180	Consensus Not Yet Reached on Key Drugs for Extensively Drug‐Resistant Tuberculosis Treatment. Clinical Infectious Diseases, 2009, 49, 315-316.	2.9	6

#	Article	IF	Citations
181	On the genome‐wide analysis of copy number variants in family‐based designs: methods for combining family‐based and population‐based information for testing dichotomous or quantitative traits, or completely ascertained samples. Genetic Epidemiology, 2010, 34, 582-590.	0.6	6
182	On the Meta-Analysis of Genome-Wide Association Studies: A Robust and Efficient Approach to Combine Population and Family-Based Studies. Human Heredity, 2012, 73, 35-46.	0.4	6
183	Dendritic cell recruitment in response to skin antigen tests in HIV-1-infected individuals correlates with the level of T-cell infiltration. Aids, 2013, 27, 1071-1080.	1.0	6
184	Unsupervised cluster analysis of SARS‐CoV‐2 genomes reflects its geographic progression and identifies distinct genetic subgroups of SARS‐CoV‐2 virus. Genetic Epidemiology, 2021, 45, 316-323.	0.6	6
185	The influence of unmeasured confounding on the MR Steiger approach. Genetic Epidemiology, 2022, 46, 139-141.	0.6	6
186	FBAT-SNP-PC: An Approach for Multiple Markers and Single Trait in Family-Based Association Tests. Human Heredity, 2008, 66, 122-126.	0.4	5
187	Maximizing the Power of Genome-Wide Association Studies: A Novel Class of Powerful Family-Based Association Tests. Statistics in Biosciences, 2009, 1, 125-143.	0.6	5
188	Two-Stage Testing Strategies for Genome-Wide Association Studies in Family-Based Designs. Methods in Molecular Biology, 2010, 620, 485-496.	0.4	5
189	Inferring genetic causal effects on survival data with associated endo-phenotypes. Genetic Epidemiology, 2011, 35, 119-124.	0.6	5
190	PolyGEE: a generalized estimating equation approach to the efficient and robust estimation of polygenic effects in large-scale association studies. Biostatistics, 2018, 19, 295-306.	0.9	5
191	Mycobacterium Growth Inhibition Assay of Human Alveolar Macrophages as a Correlate of Immune Protection Following Mycobacterium bovis Bacille Calmette–Guérin Vaccination. Frontiers in Immunology, 2018, 9, 1708.	2.2	5
192	Effect of population stratification on SNP‐by‐environment interaction. Genetic Epidemiology, 2019, 43, 1046-1055.	0.6	5
193	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.4	5
194	The effects of misspecification of the mediator and outcome in mediation analysis. Genetic Epidemiology, 2020, 44, 400-403.	0.6	5
195	Reimplementing the Mathematics Subject Classification (MSC) as a Linked Open Dataset. Lecture Notes in Computer Science, 2012, , 458-462.	1.0	5
196	On the parsing of statistical information in family-based association testing. Nature Genetics, 2007, 39, 281-282.	9.4	4
197	A Bayesian approach to genetic association studies with family-based designs. Genetic Epidemiology, 2010, 34, 569-574.	0.6	4
198	On the follow-up of genome-wide association studies: an overall test for the most promising SNPs. Genetic Epidemiology, 2011, 35, 303-309.	0.6	4

#	Article	IF	Citations
199	Immunological Evidence of Incipient Pulmonary Tuberculosis. Journal of Infectious Diseases, 2012, 206, 1630-1631.	1.9	4
200	Family-based tests for associating haplotypes with general phenotype data. Genetic Epidemiology, 2018, 42, 123-126.	0.6	4
201	A flexible and nearly optimal sequential testing approach to randomized testing: QUICKâ€STOP. Genetic Epidemiology, 2020, 44, 139-147.	0.6	4
202	Genomic screening in family-based association testing. BMC Genetics, 2005, 6, S115.	2.7	3
203	Comparison of linkage and association strategies for quantitative traits using the COGA dataset. BMC Genetics, 2005, 6, S96.	2.7	3
204	Response to Macgregor. American Journal of Human Genetics, 2008, 82, 799-800.	2.6	3
205	Impact of Population Stratification on Family-Based Association Tests with Longitudinal Measurements. Statistical Applications in Genetics and Molecular Biology, 2009, 8, 1-17.	0.2	3
206	Genome-Wide Association Studies of Family Data in Pharmacogenetics: A Case Study. Current Pharmaceutical Design, 2009, 15, 3764-3772.	0.9	3
207	CGene: an R package for implementation of causal genetic analyses. European Journal of Human Genetics, 2011, 19, 1292-1294.	1.4	3
208	Testing for direct genetic effects using a screening step in family-based association studies. Frontiers in Genetics, 2013, 4, 243.	1.1	3
209	A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. Genetic Epidemiology, 2014, 38, 714-721.	0.6	3
210	Quantitative Pulmonary T-Cell Responses for the Diagnosis of Active Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 289-290.	2.5	2
211	TB or not TB: The role of immunodiagnosis. European Journal of Immunology, 2012, 42, 2840-2843.	1.6	2
212	A general semi-parametric approach to the analysis of genetic association studies in population-based designs. BMC Genetics, 2013, 14, 13.	2.7	2
213	metaFARVAT: An Efficient Tool for Meta-Analysis of Family-Based, Case-Control, and Population-Based Rare Variant Association Studies. Frontiers in Genetics, 2019, 10, 572.	1.1	2
214	Novel recessive locus for body mass index in childhood asthma. Thorax, 2021, 76, 1227-1230.	2.7	2
215	Authoring and Publishing Units and Quantities in Semantic Documents. Lecture Notes in Computer Science, 2012, , 202-216.	1.0	2
216	Testing for association in genetic studies. , 2005, , 27-46.		2

#	Article	IF	Citations
217	Assessing the contribution of rare genetic variants to phenotypes of chronic obstructive pulmonary disease using whole-genome sequence data. Human Molecular Genetics, 2022, 31, 3873-3885.	1.4	2
218	Parsing the Effects of Individual SNPs in Candidate Genes with Family Data. Human Heredity, 2010, 69, 91-103.	0.4	1
219	Association Analysis in Family Designs. Statistics in the Health Sciences, 2011, , 139-159.	0.2	1
220	Principal components methods for narrow–sense heritability in the analysis of multidimensional longitudinal cognitive phenotypes. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 770-778.	1.1	1
221	Revisiting Healthcare Workers as a Risk Group for Progression toward Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2015, 192, 1021-1022.	2.5	1
222	Rapid Diagnosis of Smear-negative Tuberculosis by Bronchoalveolar Lavage Enzyme-linked Immunospot. American Journal of Respiratory and Critical Care Medicine, 2007, 176, 317-317.	2.5	0
223	Vitamin D and Active Tuberculosis: A Futile Quest?. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 95-95.	2.5	0
224	Stronger Evidence for Replication of NPPA Using Genome-wide Genotyping Data. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 96-96.	2.5	0
225	The Basics of Genetic Association Analysis. Statistics in the Health Sciences, 2011, , 99-124.	0.2	0
226	Genome Wide Association Studies. Statistics in the Health Sciences, 2011, , 175-189.	0.2	0
227	Family-based Association Methods. , 2011, , 231-250.		0
228	Mashups Using Mathematical Knowledge. , 2013, , 171-204.		0
229	On Association Analysis of Rare Variants Under Population Substructure: An Approach for the Detection of Subjects That Can Cause Bias in the Analysis—T$_{opt}$: An Outlier Detection Method. Genetic Epidemiology, 2013, 37, 431-439.	0.6	0
230	On Rare-Variant Analysis in Population-Based Designs: Decomposing the Likelihood to Two Informative Components. Human Heredity, 2013, 76, 76-85.	0.4	0
231	The Opening Scholarly Communication in Social Sciences project OSCOSS. , 2017, , 433-444.		0
232	The Role of SNP Interactions when Determining Independence of Novel Signals in Genetic Association Studies—An Application to ARG1 and Bronchodilator Response. Journal of Personalized Medicine, 2021, 11, 145.	1.1	0
233	Does B-type Natriuretic Peptide or Its Gene Polymorphism Predict Patient Outcome after Coronary Artery Bypass Graft Surgery?. Anesthesiology, 2009, 111, 1378-1379.	1.3	0
234	What About Existing Databases?. Deutsches A&#x0308;rzteblatt International, 2010, 107, 435-6; author reply 436.	0.6	0

#	Article	IF	Citations
235	Using Network Methodology to Infer Population Substructure. PLoS ONE, 2015, 10, e0130708.	1.1	0
236	On the Recombination Rate Estimation in the Presence of Population Substructure. PLoS ONE, 2015, 10, e0145152.	1.1	0
237	Selection bias when inferring the effect direction in Mendelian randomization. Genetic Epidemiology, 2022, 46, 341-343.	0.6	0
238	Covariate adjustment of spirometric and smoking phenotypes: The potential of neural network models. PLoS ONE, 2022, 17, e0266752.	1.1	0