Christoph Lange

List of Publications by Year
in descending order

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238	15,194	20036	23173
papers	citations	63 h-index	116 g-index

254	254	254	19990
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The influence of unmeasured confounding on the MR Steiger approach. Genetic Epidemiology, 2022, 46, 139-141.	0.6	6
2	Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimerâ€™s disease-associated genes: DTNB and DLG2. Molecular Psychiatry, 2022, 27, 1963-1969.	4.1	9
3	Selection bias when inferring the effect direction in Mendelian randomization. Genetic Epidemiology, 2022, 46, 341-343.	0.6	0
4	Covariate adjustment of spirometric and smoking phenotypes: The potential of neural network models. PLoS ONE, 2022, 17, e0266752.	1.1	0
5	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
6	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
7	locStra: Fast analysis of regional/global stratification in wholeâ€genome sequencingÂstudies. Genetic Epidemiology, 2021, 45, 82-98.	0.6	8
8	Unsupervised cluster analysis of SARSâ€CoVâ€2 genomes reflects its geographic progression and identifies distinct genetic subgroups of SARSâ€CoVâ€2 virus. Genetic Epidemiology, 2021, 45, 316-323.	0.6	6
9	The Role of SNP Interactions when Determining Independence of Novel Signals in Genetic Association Studiesâ€”An Application to ARG1 and Bronchodilator Response. Journal of Personalized Medicine, 2021, 11, 145.	1.1	0
10	Novel recessive locus for body mass index in childhood asthma. Thorax, 2021, 76, 1227-1230.	2.7	2
11	Wholeâ€genome sequencing reveals new Alzheimer's diseaseâ€“associated rare variants in loci related to synaptic function and neuronal development. Alzheimer's and Dementia, 2021, 17, 1509-1527.	0.4	50
12	Caution against examining the role of reverse causality in Mendelian Randomization. Genetic Epidemiology, 2021, 45, 445-454.	0.6	15
13	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
14	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
15	Machine Learning Characterization of COPD Subtypes. Chest, 2020, 157, 1147-1157.	0.4	44
16	A flexible and nearly optimal sequential testing approach to randomized testing: QUICKâ€STOP. Genetic Epidemiology, 2020, 44, 139-147.	0.6	4
17	Standardised shorter regimens versus individualised longer regimens for rifampin- or multidrug-resistant tuberculosis. European Respiratory Journal, 2020, 55, 1901467.	3.1	55
18	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

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19	The effects of misspecification of the mediator and outcome in mediation analysis. Genetic Epidemiology, 2020, 44, 400-403.	0.6	5
20	Identification of Novel Alzheimerâ€™s Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. Scientific Reports, 2020, 10, 5029.	1.6	31
21	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
22	Effect of population stratification on SNPâ€byâ€environment interaction. Genetic Epidemiology, 2019, 43, 1046-1055.	0.6	5
23	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.4	5
24	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
25	A comparison of popular TDTâ€generalizations for familyâ€based association analysis. Genetic Epidemiology, 2019, 43, 300-317.	0.6	7
26	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
27	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
28	Rapid diagnosis of pulmonary tuberculosis by combined molecular and immunological methods. European Respiratory Journal, 2018, 51, 1702189.	3.1	12
29	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. Chest, 2018, 153, 65-76.	0.4	36
30	Family-based tests for associating haplotypes with general phenotype data. Genetic Epidemiology, 2018, 42, 123-126.	0.6	4
31	Evaluating the quality of the LOD cloud: AnÂempirical investigation. Semantic Web, 2018, 9, 859-901.	1.1	37
32	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
33	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
34	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. American Journal of Respiratory Cell and Molecular Biology, 2018, 59, 614-622.	1.4	22
35	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. Human Molecular Genetics, 2018, 27, 3801-3812.	1.4	32
36	Mycobacterium Growth Inhibition Assay of Human Alveolar Macrophages as a Correlate of Immune Protection Following Mycobacterium bovis Bacille Calmetteâ€“GuÃ©rin Vaccination. Frontiers in Immunology, 2018, 9, 1708.	2.2	5

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37	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
38	Geneâ€based segregation method for identifying rare variants in familyâ€based sequencing studies. Genetic Epidemiology, 2017, 41, 309-319.	0.6	14
39	A general approach to testing for pleiotropy with rare and common variants. Genetic Epidemiology, 2017, 41, 163-170.	0.6	17
40	On the association analysis of genomeâ€sequencing data: A spatial clustering approach for partitioning the entire genome into nonoverlapping windows. Genetic Epidemiology, 2017, 41, 332-340.	0.6	10
41	Identification of genetic outliers due to sub-structure and cryptic relationships. Bioinformatics, 2017, 33, 1972-1979.	1.8	19
42	The Opening Scholarly Communication in Social Sciences project OSCOSS. , 2017, , 433-444.		0
43	Pulmonary immune responses to Mycobacterium tuberculosis in exposed individuals. PLoS ONE, 2017, 12, e0187882.	1.1	8
44	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
45	Luzzuâ€"A Methodology and Framework for Linked Data Quality Assessment. Journal of Data and Information Quality, 2016, 8, 1-32.	1.5	56
46	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
47	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
48	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
49	Investigation of the role of TCF4 rare sequence variants in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 354-362.	1.1	12
50	False-negative interferon-Î³ release assay results in active tuberculosis: a TBNET study. European Respiratory Journal, 2015, 45, 279-283.	3.1	36
51	PLD3 gene variants and Alzheimer's disease. Nature, 2015, 520, E7-E8.	13.7	60
52	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. BMC Medical Genetics, 2015, 16, 62.	2.1	9
53	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
54	Integrating Multiple Correlated Phenotypes for Genetic Association Analysis by Maximizing Heritability. Human Heredity, 2015, 79, 93-104.	0.4	18

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55	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. Human Molecular Genetics, 2015, 24, 1200-1210.	1.4	43
56	Quality Assessment of Linked Datasets Using Probabilistic Approximation. Lecture Notes in Computer Science, 2015, , 221-236.	1.0	12
57	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
58	Using Network Methodology to Infer Population Substructure. PLoS ONE, 2015, 10, e0130708.	1.1	0
59	On the Recombination Rate Estimation in the Presence of Population Substructure. PLoS ONE, 2015, 10, e0145152.	1.1	0
60	Attitudes about Tuberculosis Prevention in the Elimination Phase: A Survey among Physicians in Germany. PLoS ONE, 2014, 9, e112681.	1.1	20
61	An alternative hypothesis testing strategy for secondary phenotype data in case-control genetic association studies. Frontiers in Genetics, 2014, 5, 188.	1.1	11
62	The rare TREM2 R47H variant exerts only a modest effect on Alzheimer disease risk. Neurology, 2014, 83, 1353-1358.	1.5	40
63	Representing dataset quality metadata using multi-dimensional views. , 2014, , .		16
64	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
65	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
66	Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within Gremlinâ€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
67	A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. Genetic Epidemiology, 2014, 38, 714-721.	0.6	3
68	On the simultaneous association analysis of large genomic regions: a massive multi-locus association test. Bioinformatics, 2014, 30, 157-164.	1.8	45
69	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
70	FARVAT: a family-based rare variant association test. Bioinformatics, 2014, 30, 3197-3205.	1.8	34
71	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
72	Beyond the IFN-Â horizon: biomarkers for immunodiagnosis of infection with Mycobacterium tuberculosis. European Respiratory Journal, 2014, 43, 1472-1486.	3.1	135

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73	A general semi-parametric approach to the analysis of genetic association studies in population-based designs. BMC Genetics, 2013, 14, 13.	2.7	2
74	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. Human Genetics, 2013, 132, 431-441.	1.8	69
75	Diagnosis and treatment of latent infection with <scp>M</scp>ycobacterium tuberculosis. Respirology, 2013, 18, 205-216.	1.3	40
76	Mashups Using Mathematical Knowledge. , 2013, , 171-204.		0
77	On Association Analysis of Rare Variants Under Population Substructure: An Approach for the Detection of Subjects That Can Cause Bias in the Analysisâ€"T_{opt}: An Outlier Detection Method. Genetic Epidemiology, 2013, 37, 431-439.	0.6	0
78	Principal components methods for narrowâ€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
79	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
80	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
81	Ontologies and languages for representing mathematical knowledge on the Semantic Web. Semantic Web, 2013, 4, 119-158.	1.1	53
82	On Rare-Variant Analysis in Population-Based Designs: Decomposing the Likelihood to Two Informative Components. Human Heredity, 2013, 76, 76-85.	0.4	0
83	Testing for direct genetic effects using a screening step in family-based association studies. Frontiers in Genetics, 2013, 4, 243.	1.1	3
84	Plasmacytoid Dendritic Cells Infiltrate the Skin in Positive Tuberculin Skin Test Indurations. Journal of Investigative Dermatology, 2012, 132, 114-123.	0.3	24
85	â€˜Location, Location, Locationâ€™: 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
86	The risk of tuberculosis in transplant candidates and recipients: a TBNET consensus statement. European Respiratory Journal, 2012, 40, 990-1013.	3.1	211
87	Immunological Evidence of Incipient Pulmonary Tuberculosis. Journal of Infectious Diseases, 2012, 206, 1630-1631.	1.9	4
88	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
89	Increased frequencies of pulmonary regulatory T-cells in latentMycobacterium tuberculosisinfection. European Respiratory Journal, 2012, 40, 1450-1457.	3.1	31
90	TB or not TB: The role of immunodiagnosis. European Journal of Immunology, 2012, 42, 2840-2843.	1.6	2

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91	Causation and causal inference for genetic effects. Human Genetics, 2012, 131, 1665-1676.	1.8	14
92	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. Human Molecular Genetics, 2012, 21, 947-957.	1.4	216
93	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
94	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
95	Tbnet â€" Collaborative research on tuberculosis in Europe. European Journal of Microbiology and Immunology, 2012, 2, 264-274.	1.5	15
96	Differentiating Population Stratification from Genotyping Error Using Family Data. Annals of Human Genetics, 2012, 76, 42-52.	0.3	7
97	Authoring and Publishing Units and Quantities in Semantic Documents. Lecture Notes in Computer Science, 2012, , 202-216.	1.0	2
98	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
99	Reimplementing the Mathematics Subject Classification (MSC) as a Linked Open Dataset. Lecture Notes in Computer Science, 2012, , 458-462.	1.0	5
100	The Basics of Genetic Association Analysis. Statistics in the Health Sciences, 2011, , 99-124.	0.2	0
101	Association Analysis in Family Designs. Statistics in the Health Sciences, 2011, , 139-159.	0.2	1
102	Genome Wide Association Studies. Statistics in the Health Sciences, 2011, , 175-189.	0.2	0
103	Family-based Association Methods. , 2011, , 231-250.		0
104	Combining Disease Models to Test for Gene-Environment Interaction in Nuclear Families. Biometrics, 2011, 67, 1260-1270.	0.8	7
105	Common genetic variation in the GAD1 gene and the entire family of DLX homeobox genes and autism spectrum disorders. , 2011, 156, 233-239.		20
106	Inferring genetic causal effects on survival data with associated endo-phenotypes. Genetic Epidemiology, 2011, 35, 119-124.	0.6	5
107	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
108	The Planetary System: Web 3.0 & Active Documents for STEM. Procedia Computer Science, 2011, 4, 598-607.	1.2	21

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109	Genomewide Association betweenGLCCI1and Response to Glucocorticoid Therapy in Asthma. New England Journal of Medicine, 2011, 365, 1173-1183.	13.9	342
110	Intention to Test Is Intention to Treat. American Journal of Respiratory and Critical Care Medicine, 2011, 183, 3-4.	2.5	20
111	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
112	Quantitative trait prediction based on genetic marker-array data, a simulation study. Bioinformatics, 2011, 27, 745-748.	1.8	7
113	Association of SERPINE2 With Asthma. Chest, 2011, 140, 667-674.	0.4	15
114	A New Testing Strategy to Identify Rare Variants with Either Risk or Protective Effect on Disease. PLoS Genetics, 2011, 7, e1001289.	1.5	141
115	CGene: an R package for implementation of causal genetic analyses. European Journal of Human Genetics, 2011, 19, 1292-1294.	1.4	3
116	Vitamin D and Active Tuberculosis: A Futile Quest?. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 95-95.	2.5	0
117	Development of a Pharmacogenetic Predictive Test in asthma: proof of concept. Pharmacogenetics and Genomics, 2010, 20, 86-93.	0.7	10
118	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
119	A Bayesian approach to genetic association studies with family-based designs. Genetic Epidemiology, 2010, 34, 569-574.	0.6	4
120	On the genomeâ€wide analysis of copy number variants in familyâ€based designs: methods for combining familyâ€based and populationâ€based information for testing dichotomous or quantitative traits, or completely ascertained samples. Genetic Epidemiology, 2010, 34, 582-590.	0.6	6
121	Testing for nonâ€random mating: evidence for ancestryâ€related assortative mating in the Framingham heart study. Genetic Epidemiology, 2010, 34, 674-679.	0.6	49
122	Asthma-susceptibility variants identified using probands in case-control and family-based analyses. BMC Medical Genetics, 2010, 11, 122.	2.1	17
123	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
124	Variants in FAM13A are associated with chronic obstructive pulmonary disease. Nature Genetics, 2010, 42, 200-202.	9.4	348
125	Advances in the diagnosis of tuberculosis. Respirology, 2010, 15, 220-240.	1.3	130
126	Potential Role for IL-2 ELISpot in Differentiating Recent and Remote Infection in Tuberculosis Contact Tracing. PLoS ONE, 2010, 5, e11670.	1.1	25

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127	A doubly robust test for gene-environment interaction in family-based studies of affected offspring. Biostatistics, 2010, 11, 213-225.	0.9	13
128	STEX+. , 2010, , .		11
129	Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. Human Molecular Genetics, 2010, 19, 4745-4757.	1.4	98
130	Parsing the Effects of Individual SNPs in Candidate Genes with Family Data. Human Heredity, 2010, 69, 91-103.	0.4	1
131	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
132	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
133	Two-Stage Testing Strategies for Genome-Wide Association Studies in Family-Based Designs. Methods in Molecular Biology, 2010, 620, 485-496.	0.4	5
134	Using Canonical Correlation Analysis to Discover Genetic Regulatory Variants. PLoS ONE, 2010, 5, e10395.	1.1	41
135	What About Existing Databases?. Deutsches Ärzteblatt International, 2010, 107, 435-6; author reply 436.	0.6	0
136	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
137	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
138	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
139	MMP12,Lung Function, and COPD in High-Risk Populations. New England Journal of Medicine, 2009, 361, 2599-2608.	13.9	315
140	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
141	Vitamin D and Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 740-742.	2.5	18
142	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
143	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
144	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

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145	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
146	Consensus Not Yet Reached on Key Drugs for Extensively Drugâ€Resistant Tuberculosis Treatment. Clinical Infectious Diseases, 2009, 49, 315-316.	2.9	6
147	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
148	Geneâ€environment interaction tests for dichotomous traits in trios and sibships. Genetic Epidemiology, 2009, 33, 691-699.	0.6	31
149	Assessment of Alzheimerâ€™s disease caseâ€“control associations using family-based methods. Neurogenetics, 2009, 10, 19-25.	0.7	65
150	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
151	IL1B polymorphisms modulate cystic fibrosis lung disease. Pediatric Pulmonology, 2009, 44, 580-593.	1.0	49
152	Recovering unused information in genome-wide association studies: the benefit of analyzing SNPs out of Hardyâ€“Weinberg equilibrium. European Journal of Human Genetics, 2009, 17, 1676-1682.	1.4	32
153	Antimycobacterial immune responses in patients with pulmonary sarcoidosis. Clinical Respiratory Journal, 2009, 3, 229-238.	0.6	21
154	New Powerful Approaches for Familyâ€based Association Tests with Longitudinal Measurements. Annals of Human Genetics, 2009, 73, 74-83.	0.3	9
155	Genome-wide Association Analysis Identifies PDE4D as an Asthma-Susceptibility Gene. American Journal of Human Genetics, 2009, 84, 581-593.	2.6	296
156	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
157	Genetic association analysis of copy-number variation (CNV) in human disease pathogenesis. Genomics, 2009, 93, 22-26.	1.3	177
158	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
159	The Role of Family-Based Designs in Genome-Wide Association Studies. Statistical Science, 2009, 24, .	1.6	23
160	Recommendations for using standardised phenotypes in genetic association studies. Human Genomics, 2009, 3, 308.	1.4	7
161	Genome-Wide Association Studies of Family Data in Pharmacogenetics: A Case Study. Current Pharmaceutical Design, 2009, 15, 3764-3772.	0.9	3
162	A Mathematical Approach to Ontology Authoring and Documentation. Lecture Notes in Computer Science, 2009, , 389-404.	1.0	10

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163	Natriuretic Peptide System Gene Variants Are Associated with Ventricular Dysfunction after Coronary Artery Bypass Grafting. Anesthesiology, 2009, 110, 738-747.	1.3	40
164	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
165	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
166	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
167	On the analysis of copyâ€number variations in genomeâ€wide association studies: a translation of the familyâ€based association test. Genetic Epidemiology, 2008, 32, 273-284.	0.6	52
168	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
169	Genomeâ€wide association scan of attention deficit hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 1337-1344.	1.1	228
170	Genomeâ€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
171	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
172	Response to Macgregor. American Journal of Human Genetics, 2008, 82, 799-800.	2.6	3
173	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
174	Testing and Estimating Geneâ€“Environment Interactions in Familyâ€Based Association Studies. Biometrics, 2008, 64, 458-467.	0.8	36
175	Familyâ€Based Methods for Linkage and Association Analysis. Advances in Genetics, 2008, 60, 219-252.	0.8	71
176	On the Replication of Genetic Associations: Timing Can Be Everything!. American Journal of Human Genetics, 2008, 82, 849-858.	2.6	130
177	Genomics and genome-wide association studies: An integrative approach to expression QTL mapping. Genomics, 2008, 92, 129-133.	1.3	18
178	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
179	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
180	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

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