Christoph Lange

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

239 papers	12,498 citations	60 h-index	107 g-index
254 ext. papers	14,030 ext. citations	7.3 avg, IF	5.83 L-index

#	Paper	IF	Citations
239	The influence of unmeasured confounding on the MR Steiger approach.. *Genetic Epidemiology*, **2022** ,	2.6	1
238	Covariate adjustment of spirometric and smoking phenotypes: The potential of neural network models.. *PLoS ONE*, **2022**, 17, e0266752	3.7	
237	Novel recessive locus for body mass index in childhood asthma. *Thorax*, **2021**, 76, 1227-1230	7.3	0
236	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	1.2	15
235	Caution against examining the role of reverse causality in Mendelian Randomization. *Genetic Epidemiology*, **2021**, 45, 445-454	2.6	4
234	Genome-wide association analysis of COVID-19 mortality risk in SARS-CoV-2 genomes identifies mutation in the SARS-CoV-2 spike protein that colocalizes with P.1 of the Brazilian strain. *Genetic Epidemiology*, **2021**, 45, 685-693	2.6	2
233	locStra: Fast analysis of regional/global stratification in whole-genome sequencing´studies. *Genetic Epidemiology*, **2021**, 45, 82-98	2.6	5
232	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	2.6	2
231	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	35.1	58
230	The effects of misspecification of the mediator and outcome in mediation analysis. *Genetic Epidemiology*, **2020**, 44, 400-403	2.6	2
229	Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. *Scientific Reports*, **2020**, 10, 5029	4.9	16
228	Unsupervised cluster analysis of SARS-CoV-2 genomes reflects its geographic progression and identifies distinct genetic subgroups of SARS-CoV-2 virus **2020**,		3
227	A unifying framework for rare variant association testing in family-based designs, including higher criticism approaches, SKATs, and burden tests. *Bioinformatics*, **2020**,	7.2	1
226	Unsupervised cluster analysis of SARS-CoV-2 genomes indicates that recent (June 2020) cases in Beijing are from a genetic subgroup that consists of mostly European and South(east) Asian samples, of which the latter are the most recent **2020**,		5
225	Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development **2020**,		3
224	Machine Learning Characterization of COPD Subtypes: Insights From the COPDGene Study. *Chest*, **2020**, 157, 1147-1157	5.3	18
223	A flexible and nearly optimal sequential testing approach to randomized testing: QUICK-STOP. *Genetic Epidemiology*, **2020**, 44, 139-147	2.6	2

222	Standardised shorter regimens individualised longer regimens for rifampin- or multidrug-resistant tuberculosis. *European Respiratory Journal*, **2020**, 55,	13.6	27
221	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	4.5	
220	Effect of population stratification on SNP-by-environment interaction. *Genetic Epidemiology*, **2019**, 43, 1046-1055	2.6	2
219	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. *Chest*, **2019**, 156, 1068-1079	5.3	3
218	Genetic Advances in Chronic Obstructive Pulmonary Disease. Insights from COPDGene. *American Journal of Respiratory and Critical Care Medicine*, **2019**, 200, 677-690	10.2	31
217	A comparison of popular TDT-generalizations for family-based association analysis. *Genetic Epidemiology*, **2019**, 43, 300-317	2.6	2
216	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	5.7	9
215	Blood eosinophil count thresholds and exacerbations in patients with chronic obstructive pulmonary disease. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 2037-2047.e10	11.5	95
214	Rapid diagnosis of pulmonary tuberculosis by combined molecular and immunological methods. *European Respiratory Journal*, **2018**, 51,	13.6	5
213	Lobar Emphysema Distribution Is Associated With 5-Year Radiological Disease Progression. *Chest*, **2018**, 153, 65-76	5.3	23
212	Whole exome sequencing analysis in severe chronic obstructive pulmonary disease. *Human Molecular Genetics*, **2018**, 27, 3801-3812	5.6	19
211	Growth Inhibition Assay of Human Alveolar Macrophages as a Correlate of Immune Protection Following Mycobacterium bovis Bacille Calmette-Guﬀin Vaccination. *Frontiers in Immunology*, **2018**, 9, 1708	8.4	4
210	Family-based tests for associating haplotypes with general phenotype data: Improving the FBAT-haplotype algorithm. *Genetic Epidemiology*, **2018**, 42, 123-126	2.6	2
209	Tuberkulose Standards der Diagnostik und Therapie 2018. *Pneumo News*, **2018**, 10, 38-50	0	
208	Evaluating the quality of the LOD cloud: An´empirical investigation. *Semantic Web*, **2018**, 9, 859-901	2.4	29
207	Treatment correlates of successful outcomes in pulmonary multidrug-resistant tuberculosis: an individual patient data meta-analysis. *Lancet, The*, **2018**, 392, 821-834	40	281
206	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	3.7	4
205	Whole-Genome Sequencing in Severe Chronic Obstructive Pulmonary Disease. *American Journal of Respiratory Cell and Molecular Biology*, **2018**, 59, 614-622	5.7	14

204	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	5.7	37
203	Gene-based segregation method for identifying rare variants in family-based sequencing studies. *Genetic Epidemiology*, **2017**, 41, 309-319	2.6	11
202	A general approach to testing for pleiotropy with rare and common variants. *Genetic Epidemiology*, **2017**, 41, 163-170	2.6	12
201	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	2.6	8
200	Pulmonary immune responses to Mycobacterium tuberculosis in exposed individuals. *PLoS ONE*, **2017**, 12, e0187882	3.7	6
199	Identification of genetic outliers due to sub-structure and cryptic relationships. *Bioinformatics*, **2017**, 33, 1972-1979	7.2	11
198	Luzzu□ Methodology and Framework for Linked Data Quality Assessment. *Journal of Data and Information Quality*, **2016**, 8, 1-32	2.5	33
197	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, 1366-72	7.2	29
196	Exome Sequencing Analysis in Severe, Early-Onset Chronic Obstructive Pulmonary Disease. *American Journal of Respiratory and Critical Care Medicine*, **2016**, 193, 1353-63	10.2	35
195	High Rates of Treatment Success in Pulmonary Multidrug-Resistant Tuberculosis by Individually Tailored Treatment Regimens. *Annals of the American Thoracic Society*, **2016**, 13, 1271-8	4.7	11
194	PLD3 gene variants and Alzheimer□ disease. *Nature*, **2015**, 520, E7-8	50.4	51
193	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. *BMC Medical Genetics*, **2015**, 16, 62	2.1	7
192	Revisiting Healthcare Workers as a Risk Group for Progression toward Tuberculosis. *American Journal of Respiratory and Critical Care Medicine*, **2015**, 192, 1021-2	10.2	0
191	Integrating Multiple Correlated Phenotypes for Genetic Association Analysis by Maximizing Heritability. *Human Heredity*, **2015**, 79, 93-104	1.1	11
190	Genetic control of gene expression at novel and established chronic obstructive pulmonary disease loci. *Human Molecular Genetics*, **2015**, 24, 1200-10	5.6	33
189	A genome-wide association study identifies risk loci for spirometric measures among smokers of European and African ancestry. *BMC Genetics*, **2015**, 16, 138	2.6	84
188	Investigation of the role of TCF4 rare sequence variants in schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2015**, 168B, 354-62	3.5	10
187	False-negative interferon-□release assay results in active tuberculosis: a TBNET study. *European Respiratory Journal*, **2015**, 45, 279-83	13.6	27

186	Combined antigen-specific interferon-γ and interleukin-2 release assay (FluoroSpot) for the diagnosis of Mycobacterium tuberculosis infection. *PLoS ONE*, **2015**, 10, e0120006	3.7	10
185	Quality Assessment of Linked Datasets Using Probabilistic Approximation. *Lecture Notes in Computer Science*, **2015**, 221-236	0.9	11
184	Using Network Methodology to Infer Population Substructure. *PLoS ONE*, **2015**, 10, e0130708	3.7	
183	On the Recombination Rate Estimation in the Presence of Population Substructure. *PLoS ONE*, **2015**, 10, e0145152	3.7	
182	FARVAT: a family-based rare variant association test. *Bioinformatics*, **2014**, 30, 3197-205	7.2	20
181	Risk loci for chronic obstructive pulmonary disease: a genome-wide association study and meta-analysis. *Lancet Respiratory Medicine,the*, **2014**, 2, 214-25	35.1	208
180	Beyond the IFN-γ horizon: biomarkers for immunodiagnosis of infection with Mycobacterium tuberculosis. *European Respiratory Journal*, **2014**, 43, 1472-86	13.6	103
179	Attitudes about tuberculosis prevention in the elimination phase: a survey among physicians in Germany. *PLoS ONE*, **2014**, 9, e112681	3.7	15
178	An alternative hypothesis testing strategy for secondary phenotype data in case-control genetic association studies. *Frontiers in Genetics*, **2014**, 5, 188	4.5	9
177	The rare TREM2 R47H variant exerts only a modest effect on Alzheimer disease risk. *Neurology*, **2014**, 83, 1353-8	6.5	35
176	Representing dataset quality metadata using multi-dimensional views **2014**,		13
175	Beyond GWAS in COPD: probing the landscape between gene-set associations, genome-wide associations and protein-protein interaction networks. *Human Heredity*, **2014**, 78, 131-9	1.1	15
174	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, 493-8		16
173	A novel method for detecting association between DNA methylation and diseases using spatial information. *Genetic Epidemiology*, **2014**, 38, 714-21	2.6	3
172	On the simultaneous association analysis of large genomic regions: a massive multi-locus association test. *Bioinformatics*, **2014**, 30, 157-64	7.2	45
171	Common genetic variants associated with resting oxygenation in chronic obstructive pulmonary disease. *American Journal of Respiratory Cell and Molecular Biology*, **2014**, 51, 678-87	5.7	17
170	A general semi-parametric approach to the analysis of genetic association studies in population-based designs. *BMC Genetics*, **2013**, 14, 13	2.6	1
169	Dissecting direct and indirect genetic effects on chronic obstructive pulmonary disease (COPD) susceptibility. *Human Genetics*, **2013**, 132, 431-41	6.3	59

168	Diagnosis and treatment of latent infection with Mycobacterium tuberculosis. *Respirology*, **2013**, 18, 205-16	3.6	28
167	Mashups Using Mathematical Knowledge **2013**, 171-204		
166	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, 431-9	2.6	
165	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**, 162B, 770-8	3.5	1
164	A general framework for robust and efficient association analysis in family-based designs: quantitative and dichotomous phenotypes. *Statistics in Medicine*, **2013**, 32, 4482-98	2.3	10
163	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, 1071-80	3.5	6
162	Ontologies and languages for representing mathematical knowledge on the Semantic Web. *Semantic Web*, **2013**, 4, 119-158	2.4	31
161	On rare-variant analysis in population-based designs: decomposing the likelihood to two informative components. *Human Heredity*, **2013**, 76, 76-85	1.1	
160	Testing for direct genetic effects using a screening step in family-based association studies. *Frontiers in Genetics*, **2013**, 4, 243	4.5	2
159	Increased frequencies of pulmonary regulatory T-cells in latent Mycobacterium tuberculosis infection. *European Respiratory Journal*, **2012**, 40, 1450-7	13.6	24
158	TB or not TB: the role of immunodiagnosis. *European Journal of Immunology*, **2012**, 42, 2840-3	6.1	2
157	Causation and causal inference for genetic effects. *Human Genetics*, **2012**, 131, 1665-76	6.3	12
156	A genome-wide association study of COPD identifies a susceptibility locus on chromosome 19q13. *Human Molecular Genetics*, **2012**, 21, 947-57	5.6	181
155	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	3.6	14
154	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. *Nature Genetics*, **2012**, 44, 968-71	36.3	246
153	TBNET - Collaborative research on tuberculosis in Europe. *European Journal of Microbiology and Immunology*, **2012**, 2, 264-74	4.6	13
152	Differentiating population stratification from genotyping error using family data. *Annals of Human Genetics*, **2012**, 76, 42-52	2.2	5
151	Plasmacytoid dendritic cells infiltrate the skin in positive tuberculin skin test indurations. *Journal of Investigative Dermatology*, **2012**, 132, 114-23	4.3	19

150	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, 3027-33	7.2	19
149	The risk of tuberculosis in transplant candidates and recipients: a TBNET consensus statement. *European Respiratory Journal*, **2012**, 40, 990-1013	13.6	163
148	Immunological evidence of incipient pulmonary tuberculosis. *Journal of Infectious Diseases*, **2012**, 206, 1630-1; author reply 1631-2	7	2
147	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	1.1	5
146	Authoring and Publishing Units and Quantities in Semantic Documents. *Lecture Notes in Computer Science*, **2012**, 202-216	0.9	2
145	Bringing Mathematics to the Web of Data: The Case of the Mathematics Subject Classification. *Lecture Notes in Computer Science*, **2012**, 763-777	0.9	8
144	Reimplementing the Mathematics Subject Classification (MSC) as a Linked Open Dataset. *Lecture Notes in Computer Science*, **2012**, 458-462	0.9	3
143	The Fundamentals of Modern Statistical Genetics **2011**,		42
142	The Basics of Genetic Association Analysis **2011**, 99-124		
141	Association Analysis in Family Designs **2011**, 139-159		1
140	Genome Wide Association Studies **2011**, 175-189		
139	Family-based Association Methods **2011**, 231-250		
138	Combining disease models to test for gene-environment interaction in nuclear families. *Biometrics*, **2011**, 67, 1260-70	1.8	4
137	Common genetic variation in the GAD1 gene and the entire family of DLX homeobox genes and autism spectrum disorders. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156, 233-9	3.5	17
136	Inferring genetic causal effects on survival data with associated endo-phenotypes. *Genetic Epidemiology*, **2011**, 35, 119-24	2.6	4
135	On the follow-up of genome-wide association studies: an overall test for the most promising SNPs. *Genetic Epidemiology*, **2011**, 35, 303-9	2.6	4
134	The Planetary System: Web 3.0 & Active Documents for STEM. *Procedia Computer Science*, **2011**, 4, 598-607	1.6	19
133	Genomewide association between GLCCI1 and response to glucocorticoid therapy in asthma. *New England Journal of Medicine*, **2011**, 365, 1173-83	59.2	277

132	Genome-wide association analysis of body mass in chronic obstructive pulmonary disease. *American Journal of Respiratory Cell and Molecular Biology*, **2011**, 45, 304-10	5.7	43
131	Quantitative trait prediction based on genetic marker-array data, a simulation study. *Bioinformatics*, **2011**, 27, 745-8	7.2	5
130	Association of SERPINE2 with asthma. *Chest*, **2011**, 140, 667-674	5.3	14
129	A new testing strategy to identify rare variants with either risk or protective effect on disease. *PLoS Genetics*, **2011**, 7, e1001289	6	121
128	CGene: an R package for implementation of causal genetic analyses. *European Journal of Human Genetics*, **2011**, 19, 1292-4	5.3	3
127	An omnibus test for family-based association studies with multiple SNPs and multiple phenotypes. *European Journal of Human Genetics*, **2010**, 18, 720-5	5.3	7
126	Variants in FAM13A are associated with chronic obstructive pulmonary disease. *Nature Genetics*, **2010**, 42, 200-2	36.3	295
125	Advances in the diagnosis of tuberculosis. *Respirology*, **2010**, 15, 220-40	3.6	102
124	Potential role for IL-2 ELISpot in differentiating recent and remote infection in tuberculosis contact tracing. *PLoS ONE*, **2010**, 5, e11670	3.7	21
123	A doubly robust test for gene-environment interaction in family-based studies of affected offspring. *Biostatistics*, **2010**, 11, 213-25	3.7	11
122	STEX+ **2010**,		7
121	Mapping of numerous disease-associated expression polymorphisms in primary peripheral blood CD4+ lymphocytes. *Human Molecular Genetics*, **2010**, 19, 4745-57	5.6	94
120	Parsing the effects of individual SNPs in candidate genes with family data. *Human Heredity*, **2010**, 69, 91-103	1.1	1
119	Stronger evidence for replication of NPPA using genome-wide genotyping data. *American Journal of Respiratory and Critical Care Medicine*, **2010**, 181, 96	10.2	
118	Quantitative Pulmonary T-Cell Responses for the Diagnosis of Active Tuberculosis. *American Journal of Respiratory and Critical Care Medicine*, **2010**, 181, 289-290	10.2	1
117	Two-stage testing strategies for genome-wide association studies in family-based designs. *Methods in Molecular Biology*, **2010**, 620, 485-96	1.4	5
116	Vitamin D and Active Tuberculosis: A Futile Quest?. *American Journal of Respiratory and Critical Care Medicine*, **2010**, 181, 95-95	10.2	
115	Development of a Pharmacogenetic Predictive Test in asthma: proof of concept. *Pharmacogenetics and Genomics*, **2010**, 20, 86-93	1.9	9

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, 573-80	11	28
113	A Bayesian approach to genetic association studies with family-based designs. *Genetic Epidemiology* , **2010**, 34, 569-74	2.6	4
112	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, 582-90	2.6	6
111	Testing for non-random mating: evidence for ancestry-related assortative mating in the Framingham heart study. *Genetic Epidemiology*, **2010**, 34, 674-9	2.6	36
110	Asthma-susceptibility variants identified using probands in case-control and family-based analyses. *BMC Medical Genetics*, **2010**, 11, 122	2.1	16
109	Using canonical correlation analysis to discover genetic regulatory variants. *PLoS ONE*, **2010**, 5, e10395	3.7	30
108	What about existing databases?. *Deutsches Ärzteblatt International*, **2010**, 107, 435-6; author reply 436	2.5	
107	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, 5008-13	11.5	51
106	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, 702-10	7	28
105	HIV-1 infection impairs the bronchoalveolar T-cell response to mycobacteria. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 180, 1262-70	10.2	121
104	MMP12, lung function, and COPD in high-risk populations. *New England Journal of Medicine*, **2009**, 361, 2599-608	59.2	257
103	Assessing the reproducibility of asthma candidate gene associations, using genome-wide data. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 179, 1084-90	10.2	87
102	Vitamin d and tuberculosis: new light on a potent biologic therapy?. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 179, 740-2	10.2	17
101	Bronchoalveolar lavage enzyme-linked immunospot for a rapid diagnosis of tuberculosis: a Tuberculosis Network European Trialsgroup study. *American Journal of Respiratory and Critical Care Medicine*, **2009**, 180, 666-73	10.2	103
100	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	6	54
99	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, 879-83; author reply 883-4	5.1	8
98	Impact of population stratification on family-based association tests with longitudinal measurements. *Statistical Applications in Genetics and Molecular Biology*, **2009**, 8, Article 17	1.2	3
97	Consensus not yet reached on key drugs for extensively drug-resistant tuberculosis treatment. *Clinical Infectious Diseases*, **2009**, 49, 315-6; author reply 317	11.6	5

96	On the adjustment for covariates in genetic association analysis: a novel, simple principle to infer direct causal effects. *Genetic Epidemiology*, **2009**, 33, 394-405	2.6	39
95	Gene-environment interaction tests for dichotomous traits in trios and sibships. *Genetic Epidemiology*, **2009**, 33, 691-9	2.6	27
94	Assessment of Alzheimer's disease case-control associations using family-based methods. *Neurogenetics*, **2009**, 10, 19-25	3	60
93	Maximizing the Power of Genome-Wide Association Studies: A Novel Class of Powerful Family-Based Association Tests. *Statistics in Biosciences*, **2009**, 1, 125-143	1.5	5
92	IL1B polymorphisms modulate cystic fibrosis lung disease. *Pediatric Pulmonology*, **2009**, 44, 580-93	3.5	43
91	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, 1676-82	5.3	28
90	Antimycobacterial immune responses in patients with pulmonary sarcoidosis. *Clinical Respiratory Journal*, **2009**, 3, 229-38	1.7	19
89	New powerful approaches for family-based association tests with longitudinal measurements. *Annals of Human Genetics*, **2009**, 73, 74-83	2.2	8
88	Genome-wide association analysis identifies PDE4D as an asthma-susceptibility gene. *American Journal of Human Genetics*, **2009**, 84, 581-93	11	264
87	Integration of genomic and genetic approaches implicates IREB2 as a COPD susceptibility gene. *American Journal of Human Genetics*, **2009**, 85, 493-502	11	118
86	Genetic association analysis of copy-number variation (CNV) in human disease pathogenesis. *Genomics*, **2009**, 93, 22-6	4.3	145
85	Multidrug-resistant and extensively drug-resistant tuberculosis in the West. Europe and United States: epidemiology, surveillance, and control. *Clinics in Chest Medicine*, **2009**, 30, 637-65, vii	5.3	53
84	The Role of Family-Based Designs in Genome-Wide Association Studies. *Statistical Science*, **2009**, 24,	2.4	19
83	Recommendations for using standardised phenotypes in genetic association studies. *Human Genomics*, **2009**, 3, 308-19	6.8	6
82	Genome-wide association studies of family data in pharmacogenetics: a case study. *Current Pharmaceutical Design*, **2009**, 15, 3764-72	3.3	1
81	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	6	6
80	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	6	37
79	Integrating Web Services into Active Mathematical Documents. *Lecture Notes in Computer Science*, **2009**, 279-293	0.9	14

78	A Mathematical Approach to Ontology Authoring and Documentation. *Lecture Notes in Computer Science*, **2009**, 389-404	0.9	7
77	Natriuretic peptide system gene variants are associated with ventricular dysfunction after coronary artery bypass grafting. *Anesthesiology*, **2009**, 110, 738-47	4.3	35
76	Does B-type natriuretic peptide or its gene polymorphism predict patient outcome after coronary artery bypass graft surgery?. *Anesthesiology*, **2009**, 111, 1378-9; author reply 1378-9	4.3	
75	Family-based methods for linkage and association analysis. *Advances in Genetics*, **2008**, 60, 219-52	3.3	63
74	On the replication of genetic associations: timing can be everything!. *American Journal of Human Genetics*, **2008**, 82, 849-58	11	119
73	Genomics and genome-wide association studies: an integrative approach to expression QTL mapping. *Genomics*, **2008**, 92, 129-33	4.3	18
72	Extensively drug-resistant tuberculosis is worse than multidrug-resistant tuberculosis: different methodology and settings, same results. *Clinical Infectious Diseases*, **2008**, 46, 958-9	11.6	30
71	FBAT-SNP-PC: an approach for multiple markers and single trait in family-based association tests. *Human Heredity*, **2008**, 66, 122-6	1.1	5
70	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	6	24
69	Of blind men and elephants: making sense of extensively drug-resistant tuberculosis. *American Journal of Respiratory and Critical Care Medicine*, **2008**, 178, 1000-1	10.2	12
68	Multidrug- and extensively drug-resistant tuberculosis, Germany. *Emerging Infectious Diseases*, **2008** , 14, 1700-6	10.2	81
67	Association of corticotropin-releasing hormone receptor-2 genetic variants with acute bronchodilator response in asthma. *Pharmacogenetics and Genomics*, **2008**, 18, 373-82	1.9	39
66	On the analysis of copy-number variations in genome-wide association studies: a translation of the family-based association test. *Genetic Epidemiology*, **2008**, 32, 273-84	2.6	49
65	Family-based association analysis of a statistically derived quantitative traits for ADHD reveal an association in DRD4 with inattentive symptoms in ADHD individuals. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 100-6	3.5	35
64	Genome-wide association scan of attention deficit hyperactivity disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1337-44	3.5	201
63	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, 1345-54	3.5	299
62	Genome-wide association scan of the time to onset of attention deficit hyperactivity disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1355-8	3.5	92
61	Response to Macgregor. *American Journal of Human Genetics*, **2008**, 82, 799-800	11	3

60	Genome-wide association analysis reveals putative Alzheimer disease susceptibility loci in addition to APOE. *American Journal of Human Genetics*, **2008**, 83, 623-32	11	363
59	Testing and estimating gene-environment interactions in family-based association studies. *Biometrics*, **2008**, 64, 458-67	1.8	34
58	ARG1 is a novel bronchodilator response gene: screening and replication in four asthma cohorts. *American Journal of Respiratory and Critical Care Medicine*, **2008**, 178, 688-94	10.2	98
57	Accuracy of immunodiagnostic tests for active tuberculosis using single and combined results: a multicenter TBNET-Study. *PLoS ONE*, **2008**, 3, e3417	3.7	68
56	Polymorphisms in IL13, total IgE, eosinophilia, and asthma exacerbations in childhood. *Journal of Allergy and Clinical Immunology*, **2007**, 120, 84-90	11.5	93
55	Extensively drug-resistant tuberculosis, Italy and Germany. *Emerging Infectious Diseases*, **2007**, 13, 780-2	10.2	60
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2	Two mutations in the SARS-CoV-2 spike protein and RNA polymerase complex are associated with COVID-19 mortality risk		3
1	Family-Based Association Test (FBAT)1-8		1