Heike BickebÃ¶ller

List of Publications by Year
in descending order

171	8,189	44069	56724
papers	citations	48 h-index	83 g-index

193	193	193	13799
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. Human Molecular Genetics, 2022, 31, 2831-2843.	2.9	4
2	Geneâ€“gene interaction of AhRwith and within the Wntcascade affects susceptibility to lung cancer. European Journal of Medical Research, 2022, 27, 14.	2.2	1
3	Iam hiQâ€”a novel pair of accuracy indices for imputed genotypes. BMC Bioinformatics, 2022, 23, 50.	2.6	2
4	Stability over time of scores on psychiatric rating scales, questionnaires and cognitive tests in healthy controls. BJPsych Open, 2022, 8, e55.	0.7	2
5	A Large-Scale Genome-Wide Gene-Gene Interaction Study of Lung Cancer Susceptibility in Europeans With a Trans-Ethnic Validation in Asians. Journal of Thoracic Oncology, 2022, 17, 974-990.	1.1	18
6	Integration of multiomic annotation data to prioritize and characterize inflammation and immuneâ€related risk variants in squamous cell lung cancer. Genetic Epidemiology, 2021, 45, 99-114.	1.3	7
7	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. International Journal of Cancer, 2021, 148, 1077-1086.	5.1	73
8	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. Frontiers of Medicine, 2021, 15, 275-291.	3.4	21
9	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.9	50
10	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	3.5	19
11	A genome-wide association study of the longitudinal course of executive functions. Translational Psychiatry, 2021, 11, 386.	4.8	7
12	Transcriptomeâ€wide association study reveals candidate causal genes for lung cancer. International Journal of Cancer, 2020, 146, 1862-1878.	5.1	33
13	Genomeâ€wide association study of INDELs identified four novel susceptibility loci associated with lung cancer risk. International Journal of Cancer, 2020, 146, 2855-2864.	5.1	7
14	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	12.8	23
15	Candidate-gene association analysis for a continuous phenotype with a spike at zero using parent-offspring trios. Journal of Applied Statistics, 2020, 47, 2066-2080.	1.3	1
16	Review of Genetic Variation as a Predictive Biomarker for Chronic Graft-Versus-Host-Disease After Allogeneic Stem Cell Transplantation. Frontiers in Immunology, 2020, 11, 575492.	4.8	11
17	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
18	Association Analysis of Driver Geneâ€“Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1423-1429.	2.5	6

#	Article	IF	Citations
19	Lung Cancer Risk in Never-Smokers of European Descent is Associated With Genetic Variation in the 5p15.33 TERT-CLPTM1Ll Region. Journal of Thoracic Oncology, 2019, 14, 1360-1369.	1.1	27
20	Polygenic burden associated to oligodendrocyte precursor cells and radial glia influences the hippocampal volume changes induced by aerobic exercise in schizophrenia patients. Translational Psychiatry, 2019, 9, 284.	4.8	14
21	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
22	Global, pathway and gene coverage of three Illumina arrays with respect to inflammatory and immune-related pathways. European Journal of Human Genetics, 2019, 27, 1716-1723.	2.8	4
23	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. Oncotarget, 2019, 10, 1760-1774.	1.8	25
24	Mendelian Randomization and mediation analysis of leukocyte telomere length and risk of lung and head and neck cancers. International Journal of Epidemiology, 2019, 48, 751-766.	1.9	32
25	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.7	7
26	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. Carcinogenesis, 2018, 39, 336-346.	2.8	29
27	Novel genetic variants in the P38MAPK pathway gene ZAK and susceptibility to lung cancer. Molecular Carcinogenesis, 2018, 57, 216-224.	2.7	9
28	Relating drug response to epigenetic and genetic markers using a region-based kernel score test. BMC Proceedings, 2018, 12, 47.	1.6	1
29	Detecting responses to treatment with fenofibrate in pedigrees. BMC Genetics, 2018, 19, 64.	2.7	1
30	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature Communications, 2018, 9, 3927.	12.8	43
31	Genetic modifiers of radon-induced lung cancer risk: a genome-wide interaction study in former uranium miners. International Archives of Occupational and Environmental Health, 2018, 91, 937-950.	2.3	27
32	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
33	Pathwayâ€analysis of published genomeâ€wide association studies of lung cancer: A potential role for the CYP4F3 locus. Molecular Carcinogenesis, 2017, 56, 1663-1672.	2.7	13
34	Genetic variants of PTPN2 are associated with lung cancer risk: a re-analysis of eight GWASs in the TRICL-ILCCO consortium. Scientific Reports, 2017, 7, 825.	3.3	10
35	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	12.8	40
36	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472

#	Article	IF	Citations
37	Functional variants in DCAF4 associated with lung cancer risk in European populations. Carcinogenesis, 2017, 38, 541-551.	2.8	16
38	Associations between genetic variants in mRNA splicing-related genes and risk of lung cancer: a pathway-based analysis from published GWASs. Scientific Reports, 2017, 7, 44634.	3.3	10
39	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	5.1	28
40	Investigating the genetic relationship between Alzheimerâ€™s disease and cancer using GWAS summary statistics. Human Genetics, 2017, 136, 1341-1351.	3.8	46
41	Polygenic risk has an impact on the structural plasticity of hippocampal subfields during aerobic exercise combined with cognitive remediation in multi-episode schizophrenia. Translational Psychiatry, 2017, 7, e1159-e1159.	4.8	56
42	Susceptibility loci of CNOT6 in the general mRNA degradation pathway and lung cancer riskâ€”A reâ€analysis of eight GWASs. Molecular Carcinogenesis, 2017, 56, 1227-1238.	2.7	10
43	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
44	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.3	126
45	Pathway-Based Kernel Boosting for the Analysis of Genome-Wide Association Studies. Computational and Mathematical Methods in Medicine, 2017, 2017, 1-17.	1.3	6
46	Gene-set meta-analysis of lung cancer identifies pathway related to systemic lupus erythematosus. PLoS ONE, 2017, 12, e0173339.	2.5	15
47	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	2.5	79
48	Abstract 2292: Lung function and lung cancer risk: a Mendelian randomization study of UK Biobank cohort and the International Lung Cancer Consortium. , 2017, , .		0
49	Impact of the MICA-129Met/Val Dimorphism on NKG2D-Mediated Biological Functions and Disease Risks. Frontiers in Immunology, 2016, 7, 588.	4.8	55
50	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
51	Genetic Risk Can Be Decreased: Quitting Smoking Decreases and Delays Lung Cancer for Smokers With High and Low CHRNA5 Risk Genotypes â€” A Meta-Analysis. EBioMedicine, 2016, 11, 219-226.	6.1	40
52	Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk. Cancer Research, 2016, 76, 5768-5776.	0.9	57
53	Impact of genomic risk factors on survival after haematopoietic stem cell transplantation for patients with acute leukaemia. International Journal of Immunogenetics, 2016, 43, 404-412.	1.8	4
54	A Novel Genetic Variant in Long Non-coding RNA Gene NEXN-AS1 is Associated with Risk of Lung Cancer. Scientific Reports, 2016, 6, 34234.	3.3	48

#	Article	IF	Citations
55	Comparing strategies for combined testing of rare and common variants in whole sequence and genome-wide genotype data. BMC Proceedings, 2016, 10, 269-273.	1.6	5
56	Genetic variant in DNA repair geneGTF2H4is associated with lung cancer risk: a large-scale analysis of six published GWAS datasets in the TRICL consortium. Carcinogenesis, 2016, 37, 888-896.	2.8	15
57	Polymorphisms of the centrosomal gene (FGFR1OP) and lung cancer risk: a meta-analysis of 14 463 cases and 44 188 controls. Carcinogenesis, 2016, 37, 280-289.	2.8	7
58	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. PLoS Medicine, 2016, 13, e1002118.	8.4	69
59	Abstract 2569: A genome wide association study of lung cancer identifies 11 novel susceptibility loci. , 2016, , .		0
60	The MICAâ€129 dimorphism affects NKG2D signaling and outcome of hematopoietic stem cell transplantation. EMBO Molecular Medicine, 2015, 7, 1480-1502.	6.9	81
61	Genome-wide meta-analysis reveals common splice site acceptor variant in CHRNA4 associated with nicotine dependence. Translational Psychiatry, 2015, 5, e651-e651.	4.8	86
62	Informed Genomeâ€Wide Association Analysis With Family History As a Secondary Phenotype Identifies Novel Loci of Lung Cancer. Genetic Epidemiology, 2015, 39, 197-206.	1.3	11
63	Predicting survival using clinical risk scores and non-HLA immunogenetics. Bone Marrow Transplantation, 2015, 50, 1445-1452.	2.4	14
64	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
65	CHRNA5 Risk Variant Predicts Delayed Smoking Cessation and Earlier Lung Cancer Diagnosisâ€”A Meta-Analysis. Journal of the National Cancer Institute, 2015, 107, .	6.3	72
66	Identification of lung cancer histology-specific variants applying Bayesian framework variant prioritization approaches within the TRICL and ILCCO consortia. Carcinogenesis, 2015, 36, 1314-1326.	2.8	15
67	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. Human Molecular Genetics, 2015, 24, 7406-7420.	2.9	17
68	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	6.3	63
69	META-GSA: Combining Findings from Gene-Set Analyses across Several Genome-Wide Association Studies. PLoS ONE, 2015, 10, e0140179.	2.5	3
70	Abstract 4597: A novel variant in DNA repair gene GTF2H4 is associated with lung cancer risk: A reanalysis of GWAS datasets from the TRICL consortium. , 2015, , .		0
71	Controversial association results for INSIG2 on body mass index may be explained by interactions with age and with MC4R. European Journal of Human Genetics, 2014, 22, 1217-1224.	2.8	8
72	Pleiotropic Associations of Risk Variants Identified for Other Cancers With Lung Cancer Risk: The PAGE and TRICL Consortia. Journal of the National Cancer Institute, 2014, 106, dju061.	6.3	35

#	Article	IF	Citations
73	Comparison of three summary statistics for ranking genes in genome-wide association studies. Statistics in Medicine, 2014, 33, 1828-1841.	1.6	2
74	Genetic factors in individual radiation sensitivity. DNA Repair, 2014, 16, 54-65.	2.8	34
75	Coverage and efficiency in current SNP chips. European Journal of Human Genetics, 2014, 22, 1124-1130.	2.8	68
76	Genetic Analysis Workshop 18: Methods and strategies for analyzing human sequence and phenotype data in members of extended pedigrees. BMC Proceedings, 2014, 8, S1.	1.6	12
77	Kernel score statistic for dependent data. BMC Proceedings, 2014, 8, S41.	1.6	7
78	Hierarchical modeling identifies novel lung cancer susceptibility variants in inflammation pathways among 10,140 cases and 11,012 controls. Human Genetics, 2013, 132, 579-589.	3.8	29
79	Odor naming and interpretation performance in 881 schizophrenia subjects: association with clinical parameters. BMC Psychiatry, 2013, 13, 218.	2.6	15
80	Empirical Hierarchical Bayes Approach to Geneâ€Environment Interactions: Development and Application to Genomeâ€Wide Association Studies of Lung Cancer in TRICL. Genetic Epidemiology, 2013, 37, 551-559.	1.3	7
81	A Network-Based Kernel Machine Test for the Identification of Risk Pathways in Genome-Wide Association Studies. Human Heredity, 2013, 76, 64-75.	0.8	25
82	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	3.5	78
83	Influence of common genetic variation on lung cancer risk: meta-analysis of 14 900 cases and 29 485 controls. Human Molecular Genetics, 2012, 21, 4980-4995.	2.9	196
84	Asthma and lung cancer risk: a systematic investigation by the International Lung Cancer Consortium. Carcinogenesis, 2012, 33, 587-597.	2.8	69
85	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. Archives of General Psychiatry, 2012, 69, 854.	12.3	71
86	A Novel Kernel for Correcting Size Bias in the Logistic Kernel Machine Test with an Application to Rheumatoid Arthritis. Human Heredity, 2012, 74, 97-108.	0.8	7
87	Previous Lung Diseases and Lung Cancer Risk: A Pooled Analysis From the International Lung Cancer Consortium. American Journal of Epidemiology, 2012, 176, 573-585.	3.4	160
88	Increased risk of lung cancer in individuals with a family history of the disease: A pooled analysis from the International Lung Cancer Consortium. European Journal of Cancer, 2012, 48, 1957-1968.	2.8	143
89	Comparison of Pathway Analysis Approaches Using Lung Cancer GWAS Data Sets. PLoS ONE, 2012, 7, e31816.	2.5	38
90	Heritability of Radiation Response in Lung Cancer Families. Genes, 2012, 3, 248-260.	2.4	8

#	Article	IF	Citations
91	Validation of a fully automated COMET assay: 1.75 million single cells measured over a 5 year period. DNA Repair, 2011, 10, 322-337.	2.8	19
92	Aspirin and NSAID use and lung cancer risk: a pooled analysis in the International Lung Cancer Consortium (ILCCO). Cancer Causes and Control, 2011, 22, 1709-1720.	1.8	47
93	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.6	6
94	Dealing with high dimensionality for the identification of common and rare variants as main effects and for geneâ€environment interaction. Genetic Epidemiology, 2011, 35, S35-40.	1.3	5
95	A CAG repeat polymorphism of KCNN3 predicts SK3 channel function and cognitive performance in schizophrenia. EMBO Molecular Medicine, 2011, 3, 309-319.	6.9	63
96	Prevention, Diagnosis, Therapy, and Follow-up of Lung Cancer. Pneumologie, 2011, 65, 39-59.	0.1	133
97	Dissociation of accumulated genetic risk and disease severity in patients with schizophrenia. Translational Psychiatry, 2011, 1, e45-e45.	4.8	13
98	Inverse Relationship Between Cerebrovascular Lesions and Severity of Lewy Body Pathology in Patients With Lewy Body Diseases. Journal of Neuropathology and Experimental Neurology, 2010, 69, 442-448.	1.7	71
99	Impact of genomic risk factors on outcome after hematopoietic stem cell transplantation for patients with chronic myeloid leukemia. Haematologica, 2010, 95, 922-927.	3.5	24
100	The endogenous danger signals HSP70 and MICA cooperate in the activation of cytotoxic effector functions of NK cells. Journal of Cellular and Molecular Medicine, 2010, 14, 992-1002.	3.6	36
101	The longitudinal nonparametric test as a new tool to explore geneâ€gene and geneâ€time effects in cohorts. Genetic Epidemiology, 2010, 34, 469-478.	1.3	9
102	Genetic polymorphisms of MPO, GSTT1, GSTM1, GSTP1, EPHX1 and NQO1 as risk factors of earlyâ€onset lung cancer. International Journal of Cancer, 2010, 127, 1547-1561.	5.1	48
103	Complexin2 null mutation requires a â€˜second hitâ€™ for induction of phenotypic changes relevant to schizophrenia. Genes, Brain and Behavior, 2010, 9, 592-602.	2.2	27
104	Replication of Lung Cancer Susceptibility Loci at Chromosomes 15q25, 5p15, and 6p21: A Pooled Analysis From the International Lung Cancer Consortium. Journal of the National Cancer Institute, 2010, 102, 959-971.	6.3	174
105	Modification of Cognitive Performance in Schizophrenia by Complexin 2 Gene Polymorphisms. Archives of General Psychiatry, 2010, 67, 879.	12.3	86
106	International Lung Cancer Consortium: Coordinated association study of 10 potential lung cancer susceptibility variants. Carcinogenesis, 2010, 31, 625-633.	2.8	56
107	A Common MLP (Muscle LIM Protein) Variant Is Associated With Cardiomyopathy. Circulation Research, 2010, 106, 695-704.	4.5	90
108	GPC5 rs2352028 variant and risk of lung cancer in never smokers. Lancet Oncology, The, 2010, 11, 714-716.	10.7	15

#	Article	IF	Citations
109	Abstract 4826: International Lung Cancer Consortium: Pooled analysis of previous lung diseases and lung cancer risk. , 2010, , .		0
110	CYP450 polymorphisms as risk factors for early-onset lung cancer: gender-specific differences. Carcinogenesis, 2009, 30, 1161-1169.	2.8	66
111	Integration of a priori gene set information into genome-wide association studies. BMC Proceedings, 2009, 3, S95.	1.6	9
112	Genetic Analysis Workshop 16: Strategies for genome-wide association study analyses. BMC Proceedings, 2009, 3, S1.	1.6	8
113	Tests for candidate-gene interaction for longitudinal quantitative traits measured in a large cohort. BMC Proceedings, 2009, 3, S80.	1.6	12
114	Functional impact of endotoxin receptor CD14 polymorphisms on transcriptional activity. Journal of Molecular Medicine, 2009, 87, 815-824.	3.9	17
115	GENESTAT: an information portal for design and analysis of genetic association studies. European Journal of Human Genetics, 2009, 17, 533-536.	2.8	5
116	KIR genes and KIR ligands affect occurrence of acute GVHD after unrelated, 12/12 HLA matched, hematopoietic stem cell transplantation. Bone Marrow Transplantation, 2009, 44, 97-103.	2.4	45
117	A multiplex real-time PCR method for detection of GSTM1 and GSTT1 copy numbers. Clinical Biochemistry, 2009, 42, 500-509.	1.9	18
118	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	6.2	489
119	Minor ABO-Mismatches are Risk Factors for Acute Graft-versus-Host Disease in Hematopoietic Stem Cell Transplant Patients. Biology of Blood and Marrow Transplantation, 2009, 15, 1400-1406.	2.0	27
120	Association of HLA-E Polymorphism With the Outcome of Hematopoietic Stem-Cell Transplantation With Unrelated Donors. Transplantation, 2009, 88, 1227-1228.	1.0	36
121	Clinical and Genetic Risk Assessment for Overall Survival in Haematopoietic Stem Cell Transplantation (HSCT).. Blood, 2009, 114, 1189-1189.	1.4	0
122	Quantifying the contribution of genetic variants for survival phenotypes. Genetic Epidemiology, 2008, 32, 574-585.	1.3	2
123	Impact of HLAâ€ÐPB1 allelic and single amino acid mismatches on HSCT. British Journal of Haematology, 2008, 142, 436-443.	2.5	32
124	Early onset lung cancer, cigarette smoking and the SNP309 of the murine double minute-2 (MDM2) gene. BMC Cancer, 2008, 8, 113.	2.6	16
125	Do genetic factors protect for early onset lung cancer? A case control study before the age of 50 years. BMC Cancer, 2008, 8, 60.	2.6	52
126	Detection of ATM Gene Mutations in Young Lung Cancer Patients: A Population-based Control Study. Archives of Medical Research, 2008, 39, 226-231.	3.3	13

#	Article	IF	Citations
127	Case-control study of genetic susceptibility in early onset lung cancer: Investigation of Matrix Metalloproteinase-1 (MMP1). European Journal of Cancer, Supplement, 2008, 6, 205.	2.2	0
128	Matrix Metalloproteinase 1 (MMP1) Is Associated with Early-Onset Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1127-1135.	2.5	127
129	Correlation of Hsp70-1 and Hsp70-2 Gene Expression With the Degree of Graft-Versus-Host Reaction in a Rat Skin Explant Model. Transplantation, 2008, 85, 1809-1816.	1.0	14
130	The Tumorigenicity of Mouse Embryonic Stem Cells and In Vitro Differentiated Neuronal Cells Is Controlled by the Recipients' Immune Response. PLoS ONE, 2008, 3, e2622.	2.5	94
131	The Heat Shock Protein HSP70 Promotes Mouse NK Cell Activity against Tumors That Express Inducible NKG2D Ligands. Journal of Immunology, 2007, 179, 5523-5533.	0.8	128
132	Strategy for Detecting Susceptibility Genes with Weak or No Marginal Effect. Human Heredity, 2007, 63, 85-92.	0.8	40
133	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. BMC Proceedings, 2007, 1, S1.	1.6	8
134	Case-control studies with affected sibships. BMC Proceedings, 2007, 1, S29.	1.6	3
135	Issues in association mapping with high-density SNP data and diverse family structures. Genetic Epidemiology, 2007, 31, S22-S33.	1.3	4
136	Meta analysis of whole-genome linkage scans with data uncertainty: an application to Parkinson's disease. BMC Genetics, 2007, 8, 44.	2.7	2
137	German cattle allergy study (CAS): public health relevance of cattle-allergic farmers. International Archives of Occupational and Environmental Health, 2007, 81, 201-208.	2.3	21
138	Dendritic Cells in Multiple Sclerosis Lesions: Maturation Stage, Myelin Uptake, and Interaction With Proliferating T Cells. Journal of Neuropathology and Experimental Neurology, 2006, 65, 124-141.	1.7	185
139	Relationship of Apolipoprotein E and Age at Onset to Parkinson Disease Neuropathology. Journal of Neuropathology and Experimental Neurology, 2006, 65, 116-123.	1.7	132
140	Interferon regulatory factor-1 promoter polymorphism and the outcome of hepatitis C virus infection. European Journal of Gastroenterology and Hepatology, 2006, 18, 991-997.	1.6	24
141	Caseâ€Control Association Tests Correcting for Population Stratification. Annals of Human Genetics, 2006, 70, 98-115.	0.8	32
142	Hidden population substructures in an apparently homogeneous population bias association studies. European Journal of Human Genetics, 2006, 14, 236-244.	2.8	18
143	Significant association of a M129V independent polymorphism in the 5' UTR of the PRNP gene with sporadic Creutzfeldt-Jakob disease in a large German case-control study. Journal of Medical Genetics, 2006, 43, e53-e53.	3.2	56
144	A functional polymorphism within plasminogen activator urokinase (PLAU) is associated with Alzheimer's disease. Human Molecular Genetics, 2006, 15, 2446-2456.	2.9	37

#	Article	IF	Citations
145	High factor VIII levels in venous thromboembolism show linkage to imprinted loci on chromosomes 5 and 11. Blood, 2005, 105, 638-644.	1.4	34
146	Dissection of heterogeneous phenotypes for quantitative trait mapping. Genetic Epidemiology, 2005, 29, S41-S47.	1.3	2
147	Application of genomewide SNP arrays for detection of simulated susceptibility loci. Human Mutation, 2005, 25, 557-565.	2.5	6
148	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC Genetics, 2005, 6, S1.	2.7	10
149	Surrogate phenotype definition for alcohol use disorders: a genome-wide search for linkage and association. BMC Genetics, 2005, 6, S55.	2.7	3
150	NAD(P)H Oxidase and Multidrug Resistance Protein Genetic Polymorphisms Are Associated With Doxorubicin-Induced Cardiotoxicity. Circulation, 2005, 112, 3754-3762.	1.6	423
151	Post-genome respiratory epidemiology: a multidisciplinary challenge. European Respiratory Journal, 2004, 24, 471-480.	6.7	26
152	O3-02-02 The chromosome 10 locus and AD: recent progress of the German national genome network initiative. Neurobiology of Aging, 2004, 25, S54.	3.1	0
153	Modeling and dissection of longitudinal blood pressure and hypertension phenotypes in genetic epidemiological studies. Genetic Epidemiology, 2003, 25, S72-S77.	1.3	5
154	Nonparametric longitudinal allele-sharing model. BMC Genetics, 2003, 4, S85.	2.7	2
155	Angiotensin converting enzyme gene polymorphism and myocardial infarction a large association and linkage study. International Journal of Biochemistry and Cell Biology, 2003, 35, 955-962.	2.8	19
156	Weighting Schemes in Pooled Linkage Analysis. Genetic Epidemiology, 2001, 21, S142-7.	1.3	17
157	Fine mapping and single nucleotide polymorphism association results of candidate genes for asthma and related phenotypes. Human Mutation, 2001, 18, 327-336.	2.5	54
158	Investigation of Linkage and Association-Issues on Study Design. International Statistical Review, 2000, 68, 75-81.	1.9	3
159	Association of Î²₂-Adrenoreceptor Variants with Bronchial Hyperresponsiveness. American Journal of Respiratory and Critical Care Medicine, 2000, 161, 469-474.	5.6	65
160	Analysis of principal component based quantitative phenotypes for alcoholism. Genetic Epidemiology, 1999, 17, S313-S318.	1.3	3
161	Incorporating larger families in identityâ€byâ€descent based linkage analysis. Genetic Epidemiology, 1999, 17, S235-40.	1.3	0
162	Genetic control of lipoprotein(a) concentrations is different in Africans and Caucasians. European Journal of Human Genetics, 1999, 7, 169-178.	2.8	65

#	Article	IF	Citations
163	A Genome-wide Search for Linkage to Asthma22See the Appendix.. Genomics, 1999, 58, 1-8.	2.9	332
164	Systematic search for susceptibility genes in different populations. Genetic Epidemiology, 1999, 17, S709-S714.	1.3	0
165	Investigation of the candidate genes ACTHR and Golf for bipolar illness by the transmission/disequilibrium test. , 1997, 14, 575-580.		8
166	Distribution of Genome Shared IBD by Half-Sibs: Approximation by the Poisson Clumping Heuristic. Theoretical Population Biology, 1996, 50, 66-90.	1.1	27
167	Systematic search of susceptibility loci with methods using gametic disequilibrium. Genetic Epidemiology, 1995, 12, 577-582.	1.3	5
168	Comparing the power of linkage detection by the transmission disequilibrium test and the identityâ€byâ€descent test. Genetic Epidemiology, 1995, 12, 583-588.	1.3	22
169	Statistical properties of the allelic and genotypic transmission/disequilibrium test for multiallelic markers. Genetic Epidemiology, 1995, 12, 865-870.	1.3	84
170	Linkage analysis of Alzheimer's disease with methods using relative pairs. Genetic Epidemiology, 1993, 10, 377-382.	1.3	4
171	Linkage analysis of malignant melanoma with the chromosome 1 markers D1S47 and PND. Cytogenetic and Genome Research, 1992, 59, 182-184.	1.1	2