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	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
2	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
3	NAD(P)H Oxidase and Multidrug Resistance Protein Genetic Polymorphisms Are Associated With Doxorubicin-Induced Cardiotoxicity. Circulation, 2005, 112, 3754-3762.	1.6	423
4	A Genome-wide Search for Linkage to Asthma22See the Appendix.. Genomics, 1999, 58, 1-8.	2.9	332
5	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
6	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
7	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
8	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
9	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
10	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
11	Prevention, Diagnosis, Therapy, and Follow-up of Lung Cancer. Pneumologie, 2011, 65, 39-59.	0.1	133
12	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
13	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
14	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
15	Matrix Metalloproteinase 1 (MMP1) Is Associated with Early-Onset Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1127-1135.	2.5	127
16	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.3	126
17	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
18	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

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19	A Common MLP (Muscle LIM Protein) Variant Is Associated With Cardiomyopathy. Circulation Research, 2010, 106, 695-704.	4.5	90
20	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
21	Modification of Cognitive Performance in Schizophrenia by Complexin 2 Gene Polymorphisms. Archives of General Psychiatry, 2010, 67, 879.	12.3	86
22	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
23	Statistical properties of the allelic and genotypic transmission/disequilibrium test for multiallelic markers. Genetic Epidemiology, 1995, 12, 865-870.	1.3	84
24	The MICAâ€129 dimorphism affects NKG2D signaling and outcome of hematopoietic stem cell transplantation. EMBO Molecular Medicine, 2015, 7, 1480-1502.	6.9	81
25	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	2.5	79
26	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. PLoS Genetics, 2012, 8, e1003032.	3.5	78
27	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
28	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
29	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
30	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. Archives of General Psychiatry, 2012, 69, 854.	12.3	71
31	Asthma and lung cancer risk: a systematic investigation by the International Lung Cancer Consortium. Carcinogenesis, 2012, 33, 587-597.	2.8	69
32	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
33	Coverage and efficiency in current SNP chips. European Journal of Human Genetics, 2014, 22, 1124-1130.	2.8	68
34	CYP450 polymorphisms as risk factors for early-onset lung cancer: gender-specific differences. Carcinogenesis, 2009, 30, 1161-1169.	2.8	66
35	Genetic control of lipoprotein(a) concentrations is different in Africans and Caucasians. European Journal of Human Genetics, 1999, 7, 169-178.	2.8	65
36	Association of Î²₂-Adrenoreceptor Variants with Bronchial Hyperresponsiveness. American Journal of Respiratory and Critical Care Medicine, 2000, 161, 469-474.	5.6	65

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37	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
38	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
39	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
40	Novel Association of Genetic Markers Affecting CYP2A6 Activity and Lung Cancer Risk. Cancer Research, 2016, 76, 5768-5776.	0.9	57
41	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
42	International Lung Cancer Consortium: Coordinated association study of 10 potential lung cancer susceptibility variants. Carcinogenesis, 2010, 31, 625-633.	2.8	56
43	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
44	Impact of the MICA-129Met/Val Dimorphism on NKG2D-Mediated Biological Functions and Disease Risks. Frontiers in Immunology, 2016, 7, 588.	4.8	55
45	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
46	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
47	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.9	50
48	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
49	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
50	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
51	Investigating the genetic relationship between Alzheimerâ€™s disease and cancer using GWAS summary statistics. Human Genetics, 2017, 136, 1341-1351.	3.8	46
52	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
53	Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature Communications, 2018, 9, 3927.	12.8	43
54	Strategy for Detecting Susceptibility Genes with Weak or No Marginal Effect. Human Heredity, 2007, 63, 85-92.	0.8	40

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55	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
56	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
57	Comparison of Pathway Analysis Approaches Using Lung Cancer GWAS Data Sets. PLoS ONE, 2012, 7, e31816.	2.5	38
58	A functional polymorphism within plasminogen activator urokinase (PLAU) is associated with Alzheimer's disease. Human Molecular Genetics, 2006, 15, 2446-2456.	2.9	37
59	Association of HLA-E Polymorphism With the Outcome of Hematopoietic Stem-Cell Transplantation With Unrelated Donors. Transplantation, 2009, 88, 1227-1228.	1.0	36
60	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
61	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
62	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
63	Genetic factors in individual radiation sensitivity. DNA Repair, 2014, 16, 54-65.	2.8	34
64	Transcriptomeâ€wide association study reveals candidate causal genes for lung cancer. International Journal of Cancer, 2020, 146, 1862-1878.	5.1	33
65	Caseâ€Control Association Tests Correcting for Population Stratification. Annals of Human Genetics, 2006, 70, 98-115.	0.8	32
66	Impact of HLAâ€DPB1 allelic and single amino acid mismatches on HSCT. British Journal of Haematology, 2008, 142, 436-443.	2.5	32
67	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
68	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
69	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
70	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
71	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
72	Distribution of Genome Shared IBD by Half-Sibs: Approximation by the Poisson Clumping Heuristic. Theoretical Population Biology, 1996, 50, 66-90.	1.1	27

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73	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
74	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
75	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
76	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
77	Post-genome respiratory epidemiology: a multidisciplinary challenge. European Respiratory Journal, 2004, 24, 471-480.	6.7	26
78	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
79	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. Oncotarget, 2019, 10, 1760-1774.	1.8	25
80	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
81	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
82	Immune-mediated genetic pathways resulting in pulmonary function impairment increase lung cancer susceptibility. Nature Communications, 2020, 11, 27.	12.8	23
83	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
84	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
85	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
86	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
87	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
88	Genome-wide association meta-analysis identifies pleiotropic risk loci for aerodigestive squamous cell cancers. PLoS Genetics, 2021, 17, e1009254.	3.5	19
89	Hidden population substructures in an apparently homogeneous population bias association studies. European Journal of Human Genetics, 2006, 14, 236-244.	2.8	18
90	A multiplex real-time PCR method for detection of GSTM1 and GSTT1 copy numbers. Clinical Biochemistry, 2009, 42, 500-509.	1.9	18

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91	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
92	Weighting Schemes in Pooled Linkage Analysis. Genetic Epidemiology, 2001, 21, S142-7.	1.3	17
93	Functional impact of endotoxin receptor CD14 polymorphisms on transcriptional activity. Journal of Molecular Medicine, 2009, 87, 815-824.	3.9	17
94	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
95	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
96	Functional variants in DCAF4 associated with lung cancer risk in European populations. Carcinogenesis, 2017, 38, 541-551.	2.8	16
97	GPC5 rs2352028 variant and risk of lung cancer in never smokers. Lancet Oncology, The, 2010, 11, 714-716.	10.7	15
98	Odor naming and interpretation performance in 881 schizophrenia subjects: association with clinical parameters. BMC Psychiatry, 2013, 13, 218.	2.6	15
99	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
100	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
101	Gene-set meta-analysis of lung cancer identifies pathway related to systemic lupus erythematosus. PLoS ONE, 2017, 12, e0173339.	2.5	15
102	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
103	Predicting survival using clinical risk scores and non-HLA immunogenetics. Bone Marrow Transplantation, 2015, 50, 1445-1452.	2.4	14
104	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
105	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
106	Dissociation of accumulated genetic risk and disease severity in patients with schizophrenia. Translational Psychiatry, 2011, 1, e45-e45.	4.8	13
107	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
108	Tests for candidate-gene interaction for longitudinal quantitative traits measured in a large cohort. BMC Proceedings, 2009, 3, S80.	1.6	12

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109	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
110	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
111	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
112	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC Genetics, 2005, 6, S1.	2.7	10
113	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
114	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
115	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
116	Integration of a priori gene set information into genome-wide association studies. BMC Proceedings, 2009, 3, S95.	1.6	9
117	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
118	Novel genetic variants in the P38MAPK pathway gene ZAK and susceptibility to lung cancer. Molecular Carcinogenesis, 2018, 57, 216-224.	2.7	9
119	Investigation of the candidate genes ACTHR and Golf for bipolar illness by the transmission/disequilibrium test. , 1997, 14, 575-580.		8
120	Genetic Analysis Workshop 15: gene expression analysis and approaches to detecting multiple functional loci. BMC Proceedings, 2007, 1, S1.	1.6	8
121	Genetic Analysis Workshop 16: Strategies for genome-wide association study analyses. BMC Proceedings, 2009, 3, S1.	1.6	8
122	Heritability of Radiation Response in Lung Cancer Families. Genes, 2012, 3, 248-260.	2.4	8
123	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
124	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
125	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
126	Kernel score statistic for dependent data. BMC Proceedings, 2014, 8, S41.	1.6	7

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127	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
128	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. European Neuropsychopharmacology, 2019, 29, 156-170.	0.7	7
129	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
130	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
131	A genome-wide association study of the longitudinal course of executive functions. Translational Psychiatry, 2021, 11, 386.	4.8	7
132	Application of genomewide SNP arrays for detection of simulated susceptibility loci. Human Mutation, 2005, 25, 557-565.	2.5	6
133	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.6	6
134	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
135	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
136	Systematic search of susceptibility loci with methods using gametic disequilibrium. Genetic Epidemiology, 1995, 12, 577-582.	1.3	5
137	Modeling and dissection of longitudinal blood pressure and hypertension phenotypes in genetic epidemiological studies. Genetic Epidemiology, 2003, 25, S72-S77.	1.3	5
138	GENESTAT: an information portal for design and analysis of genetic association studies. European Journal of Human Genetics, 2009, 17, 533-536.	2.8	5
139	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
140	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
141	Linkage analysis of Alzheimer's disease with methods using relative pairs. Genetic Epidemiology, 1993, 10, 377-382.	1.3	4
142	Issues in association mapping with high-density SNP data and diverse family structures. Genetic Epidemiology, 2007, 31, S22-S33.	1.3	4
143	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
144	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

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145	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
146	Analysis of principal component based quantitative phenotypes for alcoholism. Genetic Epidemiology, 1999, 17, S313-S318.	1.3	3
147	Investigation of Linkage and Association-Issues on Study Design. International Statistical Review, 2000, 68, 75-81.	1.9	3
148	Surrogate phenotype definition for alcohol use disorders: a genome-wide search for linkage and association. BMC Genetics, 2005, 6, S55.	2.7	3
149	Case-control studies with affected sibships. BMC Proceedings, 2007, 1, S29.	1.6	3
150	META-GSA: Combining Findings from Gene-Set Analyses across Several Genome-Wide Association Studies. PLoS ONE, 2015, 10, e0140179.	2.5	3
151	Linkage analysis of malignant melanoma with the chromosome 1 markers D1S47 and PND. Cytogenetic and Genome Research, 1992, 59, 182-184.	1.1	2
152	Nonparametric longitudinal allele-sharing model. BMC Genetics, 2003, 4, S85.	2.7	2
153	Dissection of heterogeneous phenotypes for quantitative trait mapping. Genetic Epidemiology, 2005, 29, S41-S47.	1.3	2
154	Meta analysis of whole-genome linkage scans with data uncertainty: an application to Parkinson's disease. BMC Genetics, 2007, 8, 44.	2.7	2
155	Quantifying the contribution of genetic variants for survival phenotypes. Genetic Epidemiology, 2008, 32, 574-585.	1.3	2
156	Comparison of three summary statistics for ranking genes in genome-wide association studies. Statistics in Medicine, 2014, 33, 1828-1841.	1.6	2
157	Iam hiQâ€”a novel pair of accuracy indices for imputed genotypes. BMC Bioinformatics, 2022, 23, 50.	2.6	2
158	Stability over time of scores on psychiatric rating scales, questionnaires and cognitive tests in healthy controls. BJPsych Open, 2022, 8, e55.	0.7	2
159	Relating drug response to epigenetic and genetic markers using a region-based kernel score test. BMC Proceedings, 2018, 12, 47.	1.6	1
160	Detecting responses to treatment with fenofibrate in pedigrees. BMC Genetics, 2018, 19, 64.	2.7	1
161	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
162	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

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163	Incorporating larger families in identityâ€byâ€descent based linkage analysis. Genetic Epidemiology, 1999, 17, S235-40.	1.3	0
164	Systematic search for susceptibility genes in different populations. Genetic Epidemiology, 1999, 17, S709-S714.	1.3	0
165	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
166	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
167	Clinical and Genetic Risk Assessment for Overall Survival in Haematopoietic Stem Cell Transplantation (HSCT).. Blood, 2009, 114, 1189-1189.	1.4	0
168	Abstract 4826: International Lung Cancer Consortium: Pooled analysis of previous lung diseases and lung cancer risk. , 2010, , .		0
169	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
170	Abstract 2569: A genome wide association study of lung cancer identifies 11 novel susceptibility loci. , 2016, , .		0
171	Abstract 2292: Lung function and lung cancer risk: a Mendelian randomization study of UK Biobank cohort and the International Lung Cancer Consortium. , 2017, , .		0