Andreas Ziegler

List of Publications by Year
in descending order

271	33,025	10650 74	4853 174
papers	citations	h-index	g-index

292	292	292	45379
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
3	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
4	Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453.	13.9	1,865
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
6	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
7	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
8	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	9.4	990
9	Gene map of the extended human MHC. Nature Reviews Genetics, 2004, 5, 889-899.	7.7	949
10	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
11	Genetics and Beyond â€“ The Transcriptome of Human Monocytes and Disease Susceptibility. PLoS ONE, 2010, 5, e10693.	1.1	539
12	BRCA2 Germline Mutations in Familial Pancreatic Carcinoma. Journal of the National Cancer Institute, 2003, 95, 214-221.	3.0	457
13	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
14	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. Nature Genetics, 2009, 41, 283-285.	9.4	427
15	Avoidance of mechanical ventilation by surfactant treatment of spontaneously breathing preterm infants (AMV): an open-label, randomised, controlled trial. Lancet, The, 2011, 378, 1627-1634.	6.3	408
16	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
17	Repeated Replication and a Prospective Meta-Analysis of the Association Between Chromosome 9p21.3 and Coronary Artery Disease. Circulation, 2008, 117, 1675-1684.	1.6	356
18	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. Nature Genetics, 2010, 42, 739-741.	9.4	332

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19	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302
20	Predicting functional outcome and survival after acute ischemic stroke. Journal of Neurology, 2002, 249, 888-895.	1.8	272
21	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
22	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
23	The behaviour of random forest permutation-based variable importance measures under predictor correlation. BMC Bioinformatics, 2010, 11, 110.	1.2	254
24	Photodynamic Diagnosis in Nonâ€“Muscle-Invasive Bladder Cancer: A Systematic Review and Cumulative Analysis of Prospective Studies. European Urology, 2010, 57, 595-606.	0.9	250
25	Predicting Long-Term Outcome After Acute Ischemic Stroke. Stroke, 2008, 39, 1821-1826.	1.0	242
26	Genome-wide association study indicates two novel resistance loci for severe malaria. Nature, 2012, 489, 443-446.	13.7	227
27	On safari to Random Jungle: a fast implementation of Random Forests for high-dimensional data. Bioinformatics, 2010, 26, 1752-1758.	1.8	216
28	Strong Genetic Evidence of DCDC2 as a Susceptibility Gene for Dyslexia. American Journal of Human Genetics, 2006, 78, 52-62.	2.6	211
29	Candidate biomarkers for discrimination between infection and disease caused by Mycobacterium tuberculosis. Journal of Molecular Medicine, 2007, 85, 613-621.	1.7	211
30	Genetic Variants Associated With Cardiac Structure and Function. JAMA - Journal of the American Medical Association, 2009, 302, 168.	3.8	202
31	A point mutation in PTPRC is associated with the development of multiple sclerosis. Nature Genetics, 2000, 26, 495-499.	9.4	197
32	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	9.4	191
33	Personalized medicine using DNA biomarkers: a review. Human Genetics, 2012, 131, 1627-1638.	1.8	169
34	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
35	CDKN2A Germline Mutations in Familial Pancreatic Cancer. Annals of Surgery, 2002, 236, 730-737.	2.1	157
36	The Generalised Estimating Equations: An Annotated Bibliography. Biometrical Journal, 1998, 40, 115-139.	0.6	143

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37	Phenotypes in Three Pedigrees with Autosomal Dominant Obesity Caused by Haploinsufficiency Mutations in the Melanocortin-4 Receptor Gene. American Journal of Human Genetics, 1999, 65, 1501-1507.	2.6	143
38	Mining data with random forests: current options for realâ€world applications. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2014, 4, 55-63.	4.6	140
39	Statistical analysis of rare sequence variants: an overview of collapsing methods. Genetic Epidemiology, 2011, 35, S12-7.	0.6	139
40	Consumer credit risk: Individual probability estimates using machine learning. Expert Systems With Applications, 2013, 40, 5125-5131.	4.4	138
41	Lifelong Reduction of LDL-Cholesterol Related to a Common Variant in the LDL-Receptor Gene Decreases the Risk of Coronary Artery Diseaseâ€"A Mendelian Randomisation Study. PLoS ONE, 2008, 3, e2986.	1.1	137
42	Biostatistical Aspects of Genomeâ€Wide Association Studies. Biometrical Journal, 2008, 50, 8-28.	0.6	136
43	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678.	4.7	133
44	A Genome-Wide Association Study Identifies LIPA as a Susceptibility Gene for Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2011, 4, 403-412.	5.1	130
45	Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. PLoS Genetics, 2011, 7, e1002367.	1.5	126
46	Genome-wide association study identifies a new locus for coronary artery disease on chromosome 10p11.23. European Heart Journal, 2011, 32, 158-168.	1.0	124
47	SNP-Based Analysis of Genetic Substructure in the German Population. Human Heredity, 2006, 62, 20-29.	0.4	121
48	Multi-organ assessment in mainly non-hospitalized individuals after SARS-CoV-2 infection: The Hamburg City Health Study COVID programme. European Heart Journal, 2022, 43, 1124-1137.	1.0	111
49	Promoter Polymorphisms of the Genes Encoding Tumor Necrosis Factor-Î± and Interleukin-1Î² are Associated with Different Subtypes of Psoriasis Characterized by Early and Late Disease Onset. Journal of Investigative Dermatology, 2002, 118, 155-163.	0.3	110
50	Unbiased split variable selection for random survival forests using maximally selected rank statistics. Statistics in Medicine, 2017, 36, 1272-1284.	0.8	110
51	Risk estimation and risk prediction using machine-learning methods. Human Genetics, 2012, 131, 1639-1654.	1.8	107
52	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	3.9	106
53	Female choice and the MHC. Trends in Immunology, 2005, 26, 496-502.	2.9	104
54	Removing Batch Effects from Longitudinal Gene Expression - Quantile Normalization Plus ComBat as Best Approach for Microarray Transcriptome Data. PLoS ONE, 2016, 11, e0156594.	1.1	101

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55	Less invasive surfactant administration is associated with improved pulmonary outcomes in spontaneously breathing preterm infants. Acta Paediatrica, International Journal of Paediatrics, 2015, 104, 241-246.	0.7	100
56	Expression profiling of laser-microdissected intrapulmonary arteries in hypoxia-induced pulmonary hypertension. Respiratory Research, 2005, 6, 109.	1.4	99
57	Next-Generation Phenotyping Using theParkinExample. JAMA Neurology, 2013, 70, 1186.	4.5	99
58	Assessment of 3 xeroderma pigmentosum group C gene polymorphisms and risk of cutaneous melanoma: a caseâ€“control study. Carcinogenesis, 2005, 26, 1085-1090.	1.3	98
59	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
60	Cytokine gene polymorphisms in allergiccontact dermatitis. Contact Dermatitis, 2003, 48, 93-98.	0.8	97
61	Association of allergic contact dermatitis with a promoter polymorphism in the IL16 gene. Journal of Allergy and Clinical Immunology, 2003, 112, 1191-1194.	1.5	97
62	Sepsis syndrome and death in trauma patients are associated with variation in the gene encoding tumor necrosis factor*. Critical Care Medicine, 2008, 36, 1456-e6.	0.4	94
63	Do little interactions get lost in dark random forests?. BMC Bioinformatics, 2016, 17, 145.	1.2	94
64	Association between c135G/A genotype and RET proto-oncogene germline mutations and phenotype of Hirschsprung's disease. Lancet, The, 2002, 359, 1200-1205.	6.3	93
65	Internal Limiting Membrane Peeling With Indocyanine Green or Trypan Blue in Macular Hole Surgery. JAMA Ophthalmology, 2007, 125, 326.	2.6	93
66	How to Include Chromosome X in Your Genomeâ€Wide Association Study. Genetic Epidemiology, 2014, 38, 97-103.	0.6	91
67	Anterior chamber angle measurement with optical coherence tomography: Intraobserver and interobserver variability. Journal of Cataract and Refractive Surgery, 2006, 32, 1803-1808.	0.7	90
68	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. International Journal of Cancer, 2009, 124, 420-428.	2.3	84
69	Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies. Journal of the American College of Cardiology, 2010, 56, 1552-1563.	1.2	84
70	BiomarCaRE: rationale and design of the European BiomarCaRE project including 300,000 participants from 13 European countries. European Journal of Epidemiology, 2014, 29, 777-790.	2.5	83
71	p16INK4a is a Prognostic Marker in Resected Ductal Pancreatic Cancer. Annals of Surgery, 2002, 235, 51-59.	2.1	80
72	The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. Journal of Molecular Medicine, 2008, 86, 1233-1241.	1.7	80

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73	Individual Radiosensitivity Measured With Lymphocytes May Predict the Risk of Acute Reaction After Radiotherapy. International Journal of Radiation Oncology Biology Physics, 2008, 71, 256-264.	0.4	79
74	Prevalence of familial pancreatic cancer in Germany. International Journal of Cancer, 2004, 110, 902-906.	2.3	78
75	Genome Scan for Childhood and Adolescent Obesity in German Families. Pediatrics, 2003, 111, 321-327.	1.0	74
76	EPIBLASTER-fast exhaustive two-locus epistasis detection strategy using graphical processing units. European Journal of Human Genetics, 2011, 19, 465-471.	1.4	74
77	Analyzing Illumina Gene Expression Microarray Data from Different Tissues: Methodological Aspects of Data Analysis in the MetaXpress Consortium. PLoS ONE, 2012, 7, e50938.	1.1	71
78	Genetic Predisposition to Higher Blood Pressure Increases Coronary Artery Disease Risk. Hypertension, 2013, 61, 995-1001.	1.3	70
79	Association of single nucleotide polymorphisms in ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with clinical and cellular radiosensitivity. Radiotherapy and Oncology, 2010, 97, 26-32.	0.3	69
80	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
81	Functional haplotypes of the RET proto-oncogene promoter are associated with Hirschsprung disease (HSCR). Human Molecular Genetics, 2003, 12, 3207-3214.	1.4	67
82	Probability estimation with machine learning methods for dichotomous and multicategory outcome: Theory. Biometrical Journal, 2014, 56, 534-563.	0.6	67
83	Polymorphisms in the human surfactant protein-D (SFTPD) gene: strong evidence that serum levels of surfactant protein-D (SP-D) are genetically influenced. Immunogenetics, 2005, 57, 1-7.	1.2	65
84	Mendelian Randomization. Methods in Molecular Biology, 2017, 1666, 581-628.	0.4	65
85	Triple Target Treatment (3T) Is More Effective Than Biofeedback Alone for Anal Incontinence: The 3T-AI Study. Diseases of the Colon and Rectum, 2010, 53, 1007-1016.	0.7	64
86	Further evidence for DYX1C1 as a susceptibility factor for dyslexia. Psychiatric Genetics, 2009, 19, 59-63.	0.6	62
87	Independent Confirmation of a Major Locus for Obesity on Chromosome 10. Journal of Clinical Endocrinology and Metabolism, 2000, 85, 2962-2965.	1.8	60
88	Investigating Hardyâ€“Weinberg equilibrium in caseâ€“control or cohort studies or meta-analysis. Breast Cancer Research and Treatment, 2011, 128, 197-201.	1.1	60
89	On the use of Harrellâ€™s C for clinical risk prediction via random survival forests. Expert Systems With Applications, 2016, 63, 450-459.	4.4	60
90	GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm. PLoS Genetics, 2013, 9, e1003657.	1.5	58

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91	Genome-Wide Linkage Analysis of Malaria Infection Intensity and Mild Disease. PLoS Genetics, 2007, 3, e48.	1.5	57
92	Psychosocial benefits of insulin pump therapy in children with diabetes type 1 and their families: The pumpkin multicenter randomized controlled trial. Pediatric Diabetes, 2018, 19, 1471-1480.	1.2	57
93	Treatment choices and neuropsychological symptoms of a large cohort of early MS. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e446.	3.1	54
94	Genome-Wide Haplotype Analysis of Cis Expression Quantitative Trait Loci in Monocytes. PLoS Genetics, 2013, 9, e1003240.	1.5	53
95	Genomeâ€wide association study in musician's dystonia: A risk variant at the arylsulfatase G locus?. Movement Disorders, 2014, 29, 921-927.	2.2	53
96	MDR1 variants and risk of Parkinson disease. Journal of Neurology, 2009, 256, 115-120.	1.8	51
97	Hypofractionation with simultaneous integrated boost for early breast cancer. Strahlentherapie Und Onkologie, 2014, 190, 646-653.	1.0	51
98	No evidence for involvement of polymorphisms of the dopamine D4 receptor gene in anorexia nervosa, underweight, and obesity. , 1999, 88, 594-597.		50
99	Lisch corneal dystrophy is genetically distinct from Meesmann corneal dystrophy and maps to Xp22.3. American Journal of Ophthalmology, 2000, 130, 461-468.	1.7	50
100	Tissue Inhibitor of Metalloproteinases-1, â”2, and â”3 Polymorphisms in a White Population With Intracranial Aneurysms. Stroke, 2003, 34, 2817-2821.	1.0	49
101	Developmental Dyslexia â€“ Recurrence Risk Estimates from a German Bi-Center Study Using the Single Proband Sib Pair Design. Human Heredity, 2005, 59, 136-143.	0.4	49
102	Association of a polymorphism of the ACVRL1 gene with sporadic arteriovenous malformations of the central nervous system. Journal of Neurosurgery, 2006, 104, 945-949.	0.9	48
103	Investigation of the DCDC2 intron 2 deletion/compound short tandem repeat polymorphism in a large German dyslexia sample. Psychiatric Genetics, 2008, 18, 310-312.	0.6	46
104	Lack of Association Between the MEF2A Gene and Myocardial Infarction. Circulation, 2008, 117, 185-191.	1.6	44
105	Association of a functional polymorphism in the CYP4A11 gene with systolic blood pressure in survivors of myocardial infarction. Journal of Hypertension, 2006, 24, 1965-1970.	0.3	42
106	Probability estimation with machine learning methods for dichotomous and multicategory outcome: Applications. Biometrical Journal, 2014, 56, 564-583.	0.6	42
107	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. Journal of Neural Transmission, 2008, 115, 1587-1589.	1.4	41
108	Association of polymorphisms in the human surfactant proteinâ€Ð (SFTPD) gene and postnatal pulmonary adaptation in the preterm infant. Acta Paediatrica, International Journal of Paediatrics, 2009, 98, 112-117.	0.7	41

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109	Electrical stimulation and biofeedback for the treatment of fecal incontinence: a systematic review. International Journal of Colorectal Disease, 2013, 28, 1567-1577.	1.0	41
110	Treatment with an Anti-CD44v10-Specific Antibody Inhibits the Onset of Alopecia Areata in C3H/HeJ Mice. Journal of Investigative Dermatology, 2000, 115, 653-657.	0.3	40
111	Extensive alterations of the whole-blood transcriptome are associated with body mass index: results of an mRNA profiling study involving two large population-based cohorts. BMC Medical Genomics, 2015, 8, 65.	0.7	40
112	Gitelmanâ€™s syndrome is genetically distinct from other forms of Bartterâ€™s syndrome. Pediatric Nephrology, 1996, 10, 551-554.	0.9	39
113	Incidence of therapy-related acute leukaemia in mitoxantrone-treated multiple sclerosis patients in Germany. Therapeutic Advances in Neurological Disorders, 2012, 5, 75-79.	1.5	39
114	No association between three xeroderma pigmentosum group C and one group G gene polymorphisms and risk of cutaneous melanoma. European Journal of Human Genetics, 2005, 13, 253-255.	1.4	38
115	What Do We Mean by â€˜Replicationâ€™ and â€˜Validationâ€™ in Genome-Wide Association Studies?. Human Heredity, 2009, 67, 66-68.	0.4	38
116	Novel intronic polymorphisms in theRET proto-oncogene and their association with Hirschsprung disease. Human Mutation, 2003, 22, 177-177.	1.1	37
117	Observation and execution of upper-limb movements as a tool for rehabilitation of motor deficits in paretic stroke patients: protocol of a randomized clinical trial. BMC Neurology, 2012, 12, 42.	0.8	37
118	Variations of the melanocortin-1 receptor and the glutathione-S transferase T1 and M1 genes in cutaneous malignant melanoma. Archives of Dermatological Research, 2006, 298, 371-379.	1.1	36
119	Association Tests for X-Chromosomal Markers â€“ A Comparison of Different Test Statistics. Human Heredity, 2011, 71, 23-36.	0.4	36
120	Calibrating random forests for probability estimation. Statistics in Medicine, 2016, 35, 3949-3960.	0.8	36
121	Update of Familial Pancreatic Cancer in Germany. Pancreatology, 2001, 1, 510-516.	0.5	35
122	A novel mutation in PTPRC interferes with splicing and alters the structure of the human CD45 molecule. Immunogenetics, 2002, 54, 158-163.	1.2	35
123	A Genotype-Based Approach to Assessing the Association between Single Nucleotide Polymorphisms. Human Heredity, 2009, 67, 128-139.	0.4	35
124	An omics-based strategy using coenzyme Q10 in patients with Parkinsonâ€™s disease: concept evaluation in a double-blind randomized placebo-controlled parallel group trial. Neurological Research and Practice, 2019, 1, 31.	1.0	35
125	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	1.3	34
126	Rasâ€Associated Small GTPase 33A, a Novel T Cell Factor, Is Downâ€Regulated in Patients with Tuberculosis. Journal of Infectious Diseases, 2005, 192, 1211-1218.	1.9	33

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127	Association of single nucleotide polymorphisms in the genes ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with risk of severe erythema after breast conserving radiotherapy. Radiation Oncology, 2012, 7, 65.	1.2	33
128	Genetic variation in the arachidonate 5-lipoxygenase-activating protein (ALOX5AP) is associated with myocardial infarction in the German population. Clinical Science, 2008, 115, 309-315.	1.8	32
129	High Frequency of Aneuploidy Defines Ulcerative Colitis-Associated Carcinomas. Annals of Surgery, 2010, 252, 74-83.	2.1	30
130	Reduced body fat in long-term followed-up female patients with anorexia nervosa. Journal of Psychiatric Research, 2000, 34, 83-88.	1.5	28
131	Extended Single Nucleotide Polymorphism and Haplotype Analysis of the elastin Gene in Caucasians with Intracranial Aneurysms Provides Evidence for Racially/Ethnically Based Differences. Cerebrovascular Diseases, 2004, 18, 104-110.	0.8	28
132	Picking single-nucleotide polymorphisms in forests. BMC Proceedings, 2007, 1, S59.	1.8	28
133	Data mining, neural nets, trees â€" Problems 2 and 3 of Genetic Analysis Workshop 15. Genetic Epidemiology, 2007, 31, S51-S60.	0.6	28
134	Analysis of the base excision repair genes MTH1, OGG1 and MUTYH in patients with squamous oral carcinomas. Oral Oncology, 2007, 43, 791-795.	0.8	28
135	TLR4 and ILâ€18 gene variants in aggressive periodontitis. Journal of Clinical Periodontology, 2008, 35, 1020-1026.	2.3	28
136	Transmission disequilibrium and sequence variants at the leptin receptor gene in extremely obese German children and adolescents. Human Genetics, 1998, 103, 540-546.	1.8	27
137	Generalized estimating equations and regression diagnostics for longitudinal controlled clinical trials: A case study. Computational Statistics and Data Analysis, 2012, 56, 1232-1242.	0.7	27
138	GEE approaches to marginal regression models for medical diagnostic tests. Statistics in Medicine, 2004, 23, 1377-1398.	0.8	26
139	Mapping for dyslexia and related cognitive trait loci provides strong evidence for further risk genes on chromosome 6p21. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 36-43.	1.1	26
140	Polymorphisms of the NADPH Oxidase p22phox Gene in a Caucasian Population with Intracranial Aneurysms. Cerebrovascular Diseases, 2003, 16, 363-368.	0.8	25
141	Development and Validation of a Melanoma Risk Score Based on Pooled Data from 16 Caseâ€"Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 817-824.	1.1	25
142	Multiple primaries in pancreatic cancer patients: indicator of a genetic predisposition?. International Journal of Epidemiology, 2000, 29, 999-1003.	0.9	24
143	SNPtoGO: characterizing SNPs by enriched GO terms. Bioinformatics, 2008, 24, 146-148.	1.8	24
144	Triple-Target Treatment Versus Low-Frequency Electrostimulation for Anal Incontinence. Deutsches Ärzteblatt International, 2011, 108, 653-60.	0.6	24

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145	The Promise and Limitations of Genome-wide Association Studies. JAMA - Journal of the American Medical Association, 2012, 308, 1867.	3.8	24
146	Comparison of SCAphoid fracture osteosynthesis by MAGnesium-based headless Herbert screws with titanium Herbert screws: protocol for the randomized controlled SCAMAG clinical trial. BMC Musculoskeletal Disorders, 2019, 20, 357.	0.8	24
147	Osteosynthesis of the Mandibular Condyle With Magnesium-Based Biodegradable Headless Compression Screws Show Good Clinical Results During a 1-Year Follow-Up Period. Journal of Oral and Maxillofacial Surgery, 2021, 79, 637-643.	0.5	24
148	Compound effect of PHOX2B and RET gene variants in congenital central hypoventilation syndrome combined with Hirschsprung disease. American Journal of Medical Genetics, Part A, 2008, 146A, 1486-1489.	0.7	23
149	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. Genomics, 2011, 98, 320-326.	1.3	23
150	The Choice of the Filtering Method in Microarrays Affects the Inference Regarding Dosage Compensation of the Active X-Chromosome. PLoS ONE, 2011, 6, e23956.	1.1	23
151	Sleep but not hyperventilation increases the sensitivity of the EEG in patients with temporal lobe epilepsy. Epilepsy Research, 2003, 56, 43-49.	0.8	22
152	Effects of common atopy-associated amino acid substitutions in the IL-4 receptor alpha chain on IL-4 induced phenotypes. Immunogenetics, 2005, 56, 808-817.	1.2	22
153	Passive rotary dynamic sitting at the workplace by office-workers with lumbar pain: a randomized multicenter study. Spine Journal, 2007, 7, 531-540.	0.6	22
154	Predicting recovery after intracerebral hemorrhage â€“ An external validation in patients from controlled clinical trials. Journal of Neurology, 2009, 256, 464-469.	1.8	22
155	From GWAS to clinical utility in Parkinson's disease. Lancet, The, 2011, 377, 613-614.	6.3	22
156	Metachronous metastasis- and survival-analysis show prognostic importance of lymphadenectomy for colon carcinomas. BMC Gastroenterology, 2012, 12, 24.	0.8	22
157	Molecular Characterization of the NLRC4 Expression in Relation to Interleukin-18 Levels. Circulation: Cardiovascular Genetics, 2015, 8, 717-726.	5.1	22
158	Detection Rates for Genotyping Errors in SNPs Using the Trio Design. Human Heredity, 2002, 54, 111-117.	0.4	21
159	Human Genetic Resistance toOnchocerca volvulus:Evidence for Linkage to Chromosome 2p from an Autosomeâ€Wide Scan. Journal of Infectious Diseases, 2008, 198, 427-433.	1.9	21
160	Aberrant protein expression and frequent allelic loss of MSH3 in colorectal cancer with low-level microsatellite instability. International Journal of Colorectal Disease, 2012, 27, 911-919.	1.0	20
161	Identifying influential families using regression diagnostics for generalized estimating equations. , 1998, 15, 341-353.		19
162	Brain-derived neurotrophic factor: A genetic risk factor for obsessive-compulsive disorder and Tourette syndrome?. Movement Disorders, 2006, 21, 881-883.	2.2	19

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163	Association of Parkinson disease to PARK16 in a Chilean sample. Parkinsonism and Related Disorders, 2011, 17, 70-71.	1.1	19
164	Reduction of Vascular Noradrenaline Sensitivity by AT1Antagonists Depends on Functional Sympathetic Innervation. Hypertension, 2004, 44, 346-351.	1.3	18
165	Polymorphisms of Homocysteine Metabolism Are Associated with Intracranial Aneurysms. Cerebrovascular Diseases, 2008, 26, 425-429.	0.8	18
166	Identification of genetic association of multiple rare variants using collapsing methods. Genetic Epidemiology, 2011, 35, S101-6.	0.6	18
167	Mendelian Randomization versus Path Models: Making Causal Inferences in Genetic Epidemiology. Human Heredity, 2015, 79, 194-204.	0.4	18
168	Update of the effect estimates for common variants associated with carotid intima media thickness within four independent samples: The Bonn IMT Family Study, the Heinz Nixdorf Recall Study, the SAPHIR Study and the Bruneck Study. Atherosclerosis, 2016, 249, 83-87.	0.4	18
169	Familial associations of lipid profiles: a generalized estimating equations approach. Statistics in Medicine, 2000, 19, 3345-3357.	0.8	17
170	Variations in the genes encoding the peroxisome proliferator-activated receptors ? and ? in psoriasis. Archives of Dermatological Research, 2004, 296, 1-5.	1.1	17
171	Assessing the impact of a combined analysis of four common low-risk genetic variants on autism risk. Molecular Autism, 2010, 1, 4.	2.6	17
172	HDAC2 and TXNL1 distinguish aneuploid from diploid colorectal cancers. Cellular and Molecular Life Sciences, 2011, 68, 3261-3274.	2.4	17
173	Lessons learned from Genetic Analysis Workshop 17: transitioning from genomeâ€wide association studies to wholeâ€genome statistical genetic analysis. Genetic Epidemiology, 2011, 35, S107-14.	0.6	17
174	A unifying framework for robust association testing, estimation, and genetic model selection using the generalized linear model. European Journal of Human Genetics, 2013, 21, 1442-1448.	1.4	17
175	Optimized Group Sequential Study Designs for Tests of Genetic Linkage and Association in Complex Diseases. American Journal of Human Genetics, 2001, 69, 590-600.	2.6	16
176	Lifespan effects of mitochondrial mutations. Nature, 2016, 540, E13-E14.	13.7	16
177	Analysis of pregnancy and other factors on detection of human papilloma virus (HPV) infection using weighted estimating equations for follow-up data. Statistics in Medicine, 2003, 22, 2217-2233.	0.8	15
178	Further evidence for a susceptibility locus contributing to reading disability on chromosome 15q15â€“q21. Psychiatric Genetics, 2008, 18, 137-142.	0.6	15
179	A Confidenceâ€Limitâ€Based Approach to the Assessment of Hardyâ€“Weinberg Equilibrium. Biometrical Journal, 2010, 52, 253-270.	0.6	15
180	The potential role of G2- but not of G0-radiosensitivity for predisposition of prostate cancer. Radiotherapy and Oncology, 2010, 96, 19-24.	0.3	15

#	Article	IF	Citations
181	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. Genetic Epidemiology, 2015, 39, 601-608.	0.6	15
182	Sample size calculations for linkage analysis using extreme sib pairs based on segregation analysis with the quantitative phenotype body weight as an example. , 1998, 15, 577-593.		14
183	Variations in the peroxisome proliferator-activated receptor-Î³ gene and melanoma risk. Cancer Letters, 2007, 246, 218-223.	3.2	14
184	Evaluating diagnostic accuracy of genetic profiles in affected offspring families. Statistics in Medicine, 2010, 29, 2359-2368.	0.8	14
185	FCGR2A functional genetic variant associated with susceptibility to severe malarial anaemia in Ghanaian children. Journal of Medical Genetics, 2010, 47, 471-475.	1.5	14
186	A â^'436C>A Polymorphism in the Human FAS Gene Promoter Associated with Severe Childhood Malaria. PLoS Genetics, 2011, 7, e1002066.	1.5	14
187	A comprehensive evaluation of collapsing methods using simulated and real data: excellent annotation of functionality and large sample sizes required. Frontiers in Genetics, 2014, 5, 323.	1.1	14
188	The Generalised Estimating Equations: A Comparison of Procedures Available in Commercial Statistical Software Packages. Biometrical Journal, 1998, 40, 245-260.	0.6	13
189	Comments on â€˜Mendelian randomization: using genes as instruments for making causal inferences in epidemiologyâ€™ by Debbie A. Lawlor, R. M. Harbord, J. A. Sterne, N. Timpson and G. Davey Smith, Statistics in Medicine, DOI: 10.1002/sim.3034. Statistics in Medicine, 2008, 27, 2974-2976.	0.8	13
190	Comparison of pre-processing methods for multiplex bead-based immunoassays. BMC Genomics, 2016, 17, 601.	1.2	13
191	Media Stories on NICU Outbreaks Lead to an Increased Prescription Rate of Third-Line Antibiotics in the Community of Neonatal Care. Infection Control and Hospital Epidemiology, 2016, 37, 924-930.	1.0	13
192	Comprehension of the Description of Side Effects in Drug Information Leaflets. Deutsches Ärzteblatt International, 2013, 110, 669-73.	0.6	13
193	Sequential Designs for Genetic Epidemiological Linkage or Association Studies A Review of the Literature. Biometrical Journal, 2001, 43, 501-525.	0.6	12
194	Cochran-Armitage Test versus Logistic Regression in the Analysis of Genetic Association Studies. Human Heredity, 2012, 73, 14-17.	0.4	12
195	Association between SNPs in defined functional pathways and risk of early or late toxicity as well as individual radiosensitivity. Strahlentherapie Und Onkologie, 2015, 191, 59-66.	1.0	12
196	Haplotypes and haplotype-tagging single-nucleotide polymorphism: Presentation Group 8 of Genetic Analysis Workshop 14. Genetic Epidemiology, 2005, 29, S59-S71.	0.6	11
197	Pulsed Electromagnetic Field Therapy Improves Osseous Consolidation after High Tibial Osteotomy in Elderly Patientsâ€”A Randomized, Placebo-Controlled, Double-Blind Trial. Journal of Clinical Medicine, 2019, 8, 2008.	1.0	11
198	No evidence for involvement of the calpain-10 gene `high-risk' haplotype combination for non-insulin-dependent diabetes mellitus in early onset obesity. Molecular Genetics and Metabolism, 2002, 76, 152-156.	0.5	10

#	Article	IF	Citations
199	A Statistical Model for the Evaluation of Sensory Tests in Glaucoma, Depending on Optic Disc Damage. , 2003, 44, 2879.		10
200	Group Sequential Study Designs in Genetic-Epidemiological Case-Control Studies. Human Heredity, 2003, 56, 63-72.	0.4	10
201	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC Genetics, 2005, 6, S1.	2.7	10
202	Assessment of transmission distortion on chromosome 6p in healthy individuals using tagSNPs. European Journal of Human Genetics, 2009, 17, 1182-1189.	1.4	10
203	Study designs and methods post genome-wide association studies. Human Genetics, 2012, 131, 1525-1531.	1.8	10
204	A novel integrated care concept (NICC) versus standard care in the treatment of chronic cardiovascular diseases: protocol for the randomized controlled trial CardioCare MV. Trials, 2018, 19, 120.	0.7	10
205	Genotype Calling for the Affymetrix Platform. Methods in Molecular Biology, 2012, 850, 513-523.	0.4	10
206	Effects of covariates: A summary of Group 5 contributions. Genetic Epidemiology, 2003, 25, S43-S49.	0.6	9
207	ACPA: automated cluster plot analysis of genotype data. BMC Proceedings, 2009, 3, S58.	1.8	9
208	Adapting the logical basis of tests for Hardyâ€Weinberg Equilibrium to the real needs of association studies in human and medical genetics. Genetic Epidemiology, 2009, 33, 569-580.	0.6	9
209	Detection of divergent genes in microbial aCGH experiments. BMC Bioinformatics, 2006, 7, 181.	1.2	8
210	Protein profiling of genomic instability in endometrial cancer. Cellular and Molecular Life Sciences, 2012, 69, 325-333.	2.4	8
211	Nerve Conduction Velocity Is Regulated by the Inositol Polyphosphate-4-Phosphatase II Gene. American Journal of Pathology, 2014, 184, 2420-2429.	1.9	8
212	Comprehensive Exploration of the Effects of miRNA SNPs on Monocyte Gene Expression. PLoS ONE, 2012, 7, e45863.	1.1	8
213	Practical considerations of the jackknife estimator of variance for generalized estimating equations. Statistical Papers, 1997, 38, 363-369.	0.7	7
214	Multipoint development of the weighted pairwise correlation (WPC) linkage method for pedigrees of arbitrary size and application to the analysis of breast cancer and alcoholism familial data. Genetic Epidemiology, 2001, 21, 40-52.	0.6	7
215	The New Haseman-Elston Method and the Weighted Pairwise Correlation Statistic Are Variations on the Same Theme. Biometrical Journal, 2001, 43, 697.	0.6	7
216	Multiple test procedures using an upper bound of the number of true hypotheses and their use for evaluating high-dimensional EEG data. Journal of Neuroscience Methods, 2008, 170, 158-164.	1.3	7

#	Article	IF	Citations
217	Evaluation of single-nucleotide polymorphism imputation using random forests. BMC Proceedings, 2009, 3, S65.	1.8	7
218	Introduction to genetic analysis workshop 17 summaries. Genetic Epidemiology, 2011, 35, S1-4.	0.6	7
219	Linkage and Association Analysis Identifies TRAF1 Influencing Common Carotid Intimaâ€“Media Thickness. Stroke, 2016, 47, 2904-2909.	1.0	7
220	Empirical analysis of the text structure of original research articles in medical journals. PLoS ONE, 2020, 15, e0240288.	1.1	7
221	Reducing sample sizes in genome scans: Group sequential study designs with futility stops. Genetic Epidemiology, 2003, 25, 339-349.	0.6	6
222	Data Rotation Improves Genomotyping Efficiency. Biometrical Journal, 2005, 47, 585-598.	0.6	6
223	Weighting Affected Sib Pairs by Marker Informativity. American Journal of Human Genetics, 2005, 77, 230-241.	2.6	6
224	Lack of association of genetic variants in the LRP8 gene with familial and sporadic myocardial infarction. Journal of Molecular Medicine, 2008, 86, 1163-1170.	1.7	6
225	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
226	Sampling strategies for model free linkage analyses of quantitative traits: Implications for sib pair studies of reading and spelling disabilities to minimize the total study cost. European Child and Adolescent Psychiatry, 1999, 8, S35-S39.	2.8	5
227	Analysis of SNPs in pooled DNA: A decision theoretic model. Genetic Epidemiology, 2004, 26, 31-43.	0.6	5
228	Haplotype-sharing analysis for alcohol dependence based on quantitative traits and the Mantel statistic. BMC Genetics, 2005, 6, S75.	2.7	5
229	On Confidence Intervals for Genotype Relative Risks and Attributable Risks from Case Parent Trio Designs for Candidate-Gene Studies. Human Heredity, 2005, 60, 81-88.	0.4	5
230	Look who is calling: a comparison of genotype calling algorithms. BMC Proceedings, 2009, 3, S59.	1.8	5
231	Comparison of collapsing methods for the statistical analysis of rare variants. BMC Proceedings, 2011, 5, S115.	1.8	5
232	Adrenal cortex expression quantitative trait loci in a German Holstein Ã— Charolais cross. BMC Genetics, 2016, 17, 135.	2.7	5
233	Generalized estimating equations with stabilized working correlation structure. Computational Statistics and Data Analysis, 2017, 106, 1-11.	0.7	5
234	On the total expected study cost in two-stage genome-wide search designs for linkage analysis using the mean test for affected sib pairs. Genetic Epidemiology, 2001, 20, 397-400.	0.6	4

#	Article	IF	Citations
235	A General Approach for Sample Size and Power Calculations Based on the Hasemanâ€“Elston Method. Biometrical Journal, 2008, 50, 257-269.	0.6	4
236	More powerful haplotype sharing by accounting for the mode of inheritance. Genetic Epidemiology, 2009, 33, 228-236.	0.6	4
237	Adaptive linear rank tests for eQTL studies. Statistics in Medicine, 2013, 32, 524-537.	0.8	4
238	Generalized Estimating Equations. , 2014, , 1337-1376.		4
239	Testing for goodness rather than lack of fit of an Xâ€“chromosomal SNP to the Hardy-Weinberg model. PLoS ONE, 2019, 14, e0212344.	1.1	4
240	Statistical analysis plan for the randomized controlled trial CardioCare MV investigating a novel integrated care concept (NICC) for patients suffering from chronic cardiovascular disease. Trials, 2020, 21, 131.	0.7	4
241	The Use of Sequential Designs in Genome Scans for Asthma Susceptibility Loci With Affected Sib Pairs. Genetic Epidemiology, 2001, 21, S49-54.	0.6	3
242	A Bivariate Hasemanâ€Elston Method and Application to the Analysis of Asthmaâ€Related Phenotypes on Chromosome 5q. Genetic Epidemiology, 2001, 21, S216-21.	0.6	3
243	Haseman-Elston weighted by marker informativity. BMC Genetics, 2005, 6, S50.	2.7	3
244	Estimating Disequilibrium Coefficients. Methods in Molecular Biology, 2017, 1666, 117-132.	0.4	3
245	Non-invasive Degradation Tracking of Mg Implants in Humans: A Measurement Approach. Jom, 2020, 72, 1845-1850.	0.9	3
246	Comments on: Association Study between Coronary Artery Disease and rs1333049 and rs10757274 Polymorphisms at 9p21 Locus in South-West Iran. Cell Journal, 2016, 17, 756.	0.2	3
247	A Clinically Orientated Approach for Combining Discordant and Concordant Sib Pairs. Biometrical Journal, 1997, 39, 263-272.	0.6	2
248	On the Use of the Terms Repeatability and Reproducibility Regarding â€œReproducibility of genotypes as measured by the Affymetrix GeneChip(R) 100ÂK Human Mapping Array Setâ€•by Fridley and colleagues (2008) Comput. Stat. Data Anal. 52:5367-74. Computational Statistics and Data Analysis, 2010, 54, 803.	0.7	2
249	A comparison of two collapsing methods in different approaches. BMC Proceedings, 2014, 8, S8.	1.8	2
250	Celebrating the 30th Anniversary ofGenetic Epidemiology: How to Define Our Scope?â€. Genetic Epidemiology, 2014, 38, 379-380.	0.6	2
251	Analyzing Illumina Gene Expression Microarray Data Obtained From Human Whole Blood Cell and Blood Monocyte Samples. Methods in Molecular Biology, 2016, 1368, 85-97.	0.4	2
252	Evidence-based recommendations for increasing the citation frequency of original articles. Scientometrics, 2022, 127, 3367-3381.	1.6	2

#	Article	IF	Citations
253	50 Years Biometrical Journal. Biometrical Journal, 2008, 50, 5-7.	0.6	1
254	Rare Human IFNG Variants. Journal of Interferon and Cytokine Research, 2010, 30, 219-222.	0.5	1
255	Does the new HapMap throw the baby out with the bath water?. European Journal of Human Genetics, 2011, 19, 733-734.	1.4	1
256	Analysis of Stathmin gene variation in patients with panic disorder and agoraphobia. Psychiatric Genetics, 2013, 23, 43-44.	0.6	1
257	Triple Target Treatment (3T) vs Biofeedback. Diseases of the Colon and Rectum, 2013, 56, e35-e36.	0.7	1
258	Rejoinder. Biometrical Journal, 2014, 56, 607-613.	0.6	1
259	Genetic Prediction in the Genetic Analysis Workshop 18 Sequencing Data. Genetic Epidemiology, 2014, 38, S57-62.	0.6	1
260	No evidence for involvement of polymorphisms of the dopamine D4 receptor gene in anorexia nervosa, underweight, and obesity. American Journal of Medical Genetics Part A, 1999, 88, 594-597.	2.4	1
261	Estimating Disequilibrium Coefficients. Methods in Molecular Biology, 2012, 850, 103-117.	0.4	1
262	Distribution of RET protoâ€oncogene variants in children with appendicitis. Molecular Genetics & Genomic Medicine, 2022, , e1864.	0.6	1
263	Alterations in magnetic resonance imaging characteristics of bioabsorbable magnesium screws over time in humans: a retrospective single center study. Innovative Surgical Sciences, 2022, 6, 105-113.	0.4	1
264	Significant evidence for linkage of a simulated trait to D1G024â€“A conclusion reached using multiallelic transmission/disequilibrium tests. Genetic Epidemiology, 1999, 17, S785-9.	0.6	0
265	How to Predict the Risk of Parkinson Disease in Relatives of Parkin Mutation Carriers. Archives of Neurology, 2008, 65, 443.	4.9	0
266	A Modular Approach to Combine Postmarket Clinical Follow-Up Studies and Postmarket Surveillance Studies. Methods of Information in Medicine, 2021, 60, 116-122.	0.7	0
267	In Reply. Deutsches Ärzteblatt International, 2014, 111, 68.	0.6	0
268	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
269	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
270	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0

#	Article	IF	Citations
271	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0