Andreas Ziegler

List of Publications by Year in Descending Order

271 papers	27,198 citations	67 h-index	162 g-index
292 ext. papers	30,705 ext. citations	7.3 avg, IF	5.9 L-index

#	Paper	IF	Citations
271	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	0.8	
270	Distribution of RET proto-oncogene variants in children with appendicitis.. *Molecular Genetics & Genomic Medicine*, **2022**, e1864	2.3	1
269	Multi-organ assessment in mainly non-hospitalized individuals after SARS-CoV-2 infection: The Hamburg City Health Study COVID programme.. *European Heart Journal*, **2022**,	9.5	21
268	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	1.8	8
267	A Modular Approach to Combine Postmarket Clinical Follow-Up Studies and Postmarket Surveillance Studies. *Methods of Information in Medicine*, **2021**, 60, 116-122	1.5	
266	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	2.8	1
265	Non-invasive Degradation Tracking of Mg Implants in Humans: A Measurement Approach. *Jom*, **2020**, 72, 1845-1850	2.1	1
264	Empirical analysis of the text structure of original research articles in medical journals. *PLoS ONE*, **2020**, 15, e0240288	3.7	3
263	Empirical analysis of the text structure of original research articles in medical journals **2020**, 15, e0240288		
262	Empirical analysis of the text structure of original research articles in medical journals **2020**, 15, e0240288		
261	Empirical analysis of the text structure of original research articles in medical journals **2020**, 15, e0240288		
260	Empirical analysis of the text structure of original research articles in medical journals **2020**, 15, e0240288		
259	An omics-based strategy using coenzyme Q10 in patients with Parkinson's disease: concept evaluation in a double-blind randomized placebo-controlled parallel group trial. *Neurological Research and Practice*, **2019**, 1, 31	3.2	16
258	Testing for goodness rather than lack of fit of an X-chromosomal SNP to the Hardy-Weinberg model. *PLoS ONE*, **2019**, 14, e0212344	3.7	2
257	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	2.8	12
256	Pulsed Electromagnetic Field Therapy Improves Osseous Consolidation after High Tibial Osteotomy in Elderly Patients-A Randomized, Placebo-Controlled, Double-Blind Trial. *Journal of Clinical Medicine*, **2019**, 8,	5.1	8
255	Treatment choices and neuropsychological symptoms of a large cohort of early MS. *Neurology: Neuroimmunology and NeuroInflammation*, **2018**, 5, e446	9.1	40

254	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	2.8	6
253	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	3.6	35
252	Neuroimmunologische Register in Deutschland. *Aktuelle Neurologie*, **2018**, 45, 7-23		0
251	Unbiased split variable selection for random survival forests using maximally selected rank statistics. *Statistics in Medicine*, **2017**, 36, 1272-1284	2.3	59
250	Mendelian Randomization. *Methods in Molecular Biology*, **2017**, 1666, 581-628	1.4	22
249	Estimating Disequilibrium Coefficients. *Methods in Molecular Biology*, **2017**, 1666, 117-132	1.4	2
248	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. *Hypertension*, **2017**, 70, 743-750	8.5	21
247	Generalized estimating equations with stabilized working correlation structure. *Computational Statistics and Data Analysis*, **2017**, 106, 1-11	1.6	4
246	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
245	On the use of Harrell C for clinical risk prediction via random survival forests. *Expert Systems With Applications*, **2016**, 63, 450-459	7.8	37
244	Linkage and Association Analysis Identifies TRAF1 Influencing Common Carotid Intima-Media Thickness. *Stroke*, **2016**, 47, 2904-2909	6.7	6
243	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. *Science Advances*, **2016**, 2, e1501678	14.3	75
242	Adrenal cortex expression quantitative trait loci in a German Holstein Charolais cross. *BMC Genetics*, **2016**, 17, 135	2.6	4
241	Calibrating random forests for probability estimation. *Statistics in Medicine*, **2016**, 35, 3949-60	2.3	26
240	Analyzing Illumina Gene Expression Microarray Data Obtained From Human Whole Blood Cell and Blood Monocyte Samples. *Methods in Molecular Biology*, **2016**, 1368, 85-97	1.4	2
239	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	2.4	2
238	Comparison of pre-processing methods for multiplex bead-based immunoassays. *BMC Genomics*, **2016**, 17, 601	4.5	10
237	Removing Batch Effects from Longitudinal Gene Expression - Quantile Normalization Plus ComBat as Best Approach for Microarray Transcriptome Data. *PLoS ONE*, **2016**, 11, e0156594	3.7	53

236	Lifespan effects of mitochondrial mutations. *Nature*, **2016**, 540, E13-E14	50.4	11
235	Do little interactions get lost in dark random forests?. *BMC Bioinformatics*, **2016**, 17, 145	3.6	57
234	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, 83-7	3.1	14
233	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	2	6
232	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	4.3	11
231	Mendelian Randomization versus Path Models: Making Causal Inferences in Genetic Epidemiology. *Human Heredity*, **2015**, 79, 194-204	1.1	9
230	Molecular Characterization of the NLRC4 Expression in Relation to Interleukin-18 Levels. *Circulation: Cardiovascular Genetics*, **2015**, 8, 717-26		18
229	Less invasive surfactant administration is associated with improved pulmonary outcomes in spontaneously breathing preterm infants. *Acta Paediatrica, International Journal of Paediatrics*, **2015**, 104, 241-6	3.1	79
228	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	3.7	16
227	Successful Replication of GWAS Hits for Multiple Sclerosis in 10,000 Germans Using the Exome Array. *Genetic Epidemiology*, **2015**, 39, 601-8	2.6	9
226	Development and validation of a melanoma risk score based on pooled data from 16 case-control studies. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 817-24	4	18
225	Generalized Estimating Equations **2014**, 1337-1376		0
224	Shared genetic susceptibility to ischemic stroke and coronary artery disease: a genome-wide analysis of common variants. *Stroke*, **2014**, 45, 24-36	6.7	245
223	Genetic prediction in the Genetic Analysis Workshop 18 sequencing data. *Genetic Epidemiology*, **2014**, 38 Suppl 1, S57-62	2.6	1
222	How to include chromosome X in your genome-wide association study. *Genetic Epidemiology*, **2014**, 38, 97-103	2.6	55
221	Mining data with random forests: current options for real-world applications. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, **2014**, 4, 55-63	6.9	74
220	Nerve conduction velocity is regulated by the inositol polyphosphate-4-phosphatase II gene. *American Journal of Pathology*, **2014**, 184, 2420-9	5.8	5
219	A comparison of two collapsing methods in different approaches. *BMC Proceedings*, **2014**, 8, S8	2.3	2

218	Hypofractionation with simultaneous integrated boost for early breast cancer: results of the German multicenter phase II trial (ARO-2010-01). *Strahlentherapie Und Onkologie*, **2014**, 190, 646-53	4.3	44
217	BiomarCaRE: rationale and design of the European BiomarCaRE project including 300,000 participants from 13 European countries. *European Journal of Epidemiology*, **2014**, 29, 777-90	12.1	63
216	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	4.5	9
215	Genome-wide association study in musician's dystonia: a risk variant at the arylsulfatase G locus?. *Movement Disorders*, **2014**, 29, 921-7	7	35
214	Probability estimation with machine learning methods for dichotomous and multicategory outcome: theory. *Biometrical Journal*, **2014**, 56, 534-63	1.5	55
213	Rejoinder. *Biometrical Journal*, **2014**, 56, 607-13	1.5	0
212	Probability estimation with machine learning methods for dichotomous and multicategory outcome: applications. *Biometrical Journal*, **2014**, 56, 564-83	1.5	28
211	In reply. *Deutsches Ärzteblatt International*, **2014**, 111, 68	2.5	
210	Electrical stimulation and biofeedback for the treatment of fecal incontinence: a systematic review. *International Journal of Colorectal Disease*, **2013**, 28, 1567-77	3	29
209	Consumer credit risk: Individual probability estimates using machine learning. *Expert Systems With Applications*, **2013**, 40, 5125-5131	7.8	102
208	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
207	A unifying framework for robust association testing, estimation, and genetic model selection using the generalized linear model. *European Journal of Human Genetics*, **2013**, 21, 1442-8	5.3	14
206	Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001	8.5	55
205	Adaptive linear rank tests for eQTL studies. *Statistics in Medicine*, **2013**, 32, 524-37	2.3	4
204	Genome-wide haplotype analysis of cis expression quantitative trait loci in monocytes. *PLoS Genetics*, **2013**, 9, e1003240	6	47
203	GUESS-ing polygenic associations with multiple phenotypes using a GPU-based evolutionary stochastic search algorithm. *PLoS Genetics*, **2013**, 9, e1003657	6	45
202	Analysis of Stathmin gene variation in patients with panic disorder and agoraphobia. *Psychiatric Genetics*, **2013**, 23, 43-4	2.9	1
201	Next-generation phenotyping using the parkin example: time to catch up with genetics. *JAMA Neurology*, **2013**, 70, 1186-91	17.2	75

200	Triple target treatment (3T) vs biofeedback. *Diseases of the Colon and Rectum*, **2013**, 56, e35-6	3.1	1
199	Comprehension of the description of side effects in drug information leaflets: a survey of doctors, pharmacists and lawyers. *Deutsches Ärzteblatt International*, **2013**, 110, 669-73	2.5	9
198	Generalized estimating equations and regression diagnostics for longitudinal controlled clinical trials: A case study. *Computational Statistics and Data Analysis*, **2012**, 56, 1232-1242	1.6	21
197	Protein profiling of genomic instability in endometrial cancer. *Cellular and Molecular Life Sciences*, **2012**, 69, 325-33	10.3	8
196	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
195	The Promise and Limitations of Genome-wide Association Studies. *JAMA - Journal of the American Medical Association*, **2012**, 308, 1867	27.4	18
194	Personalized medicine using DNA biomarkers: a review. *Human Genetics*, **2012**, 131, 1627-38	6.3	131
193	Risk estimation and risk prediction using machine-learning methods. *Human Genetics*, **2012**, 131, 1639-54	6.3	82
192	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, 100-12		84
191	Metachronous metastasis- and survival-analysis show prognostic importance of lymphadenectomy for colon carcinomas. *BMC Gastroenterology*, **2012**, 12, 24	3	18
190	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	3.1	28
189	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
188	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *American Journal of Human Genetics*, **2012**, 91, 744-53	11	58
187	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	4.2	30
186	Analyzing illumina gene expression microarray data from different tissues: methodological aspects of data analysis in the metaxpress consortium. *PLoS ONE*, **2012**, 7, e50938	3.7	54
185	Aberrant protein expression and frequent allelic loss of MSH3 in colorectal cancer with low-level microsatellite instability. *International Journal of Colorectal Disease*, **2012**, 27, 911-9	3	17
184	Cochran-Armitage test versus logistic regression in the analysis of genetic association studies. *Human Heredity*, **2012**, 73, 14-7	1.1	12
183	Genome-wide association study indicates two novel resistance loci for severe malaria. *Nature*, **2012**, 489, 443-6	50.4	173

182	Incidence of therapy-related acute leukaemia in mitoxantrone-treated multiple sclerosis patients in Germany. *Therapeutic Advances in Neurological Disorders*, **2012**, 5, 75-9	6.6	32
181	Comprehensive exploration of the effects of miRNA SNPs on monocyte gene expression. *PLoS ONE*, **2012**, 7, e45863	3.7	8
180	Genotype calling for the Affymetrix platform. *Methods in Molecular Biology*, **2012**, 850, 513-23	1.4	8
179	Estimating disequilibrium coefficients. *Methods in Molecular Biology*, **2012**, 850, 103-17	1.4	1
178	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. *Genomics*, **2011**, 98, 320-6	4.3	21
177	Association of Parkinson disease to PARK16 in a Chilean sample. *Parkinsonism and Related Disorders* , **2011**, 17, 70-1	3.6	15
176	From GWAS to clinical utility in Parkinson's disease. *Lancet, The*, **2011**, 377, 613-4	40	16
175	Avoidance of mechanical ventilation by surfactant treatment of spontaneously breathing preterm infants (AMV): an open-label, randomised, controlled trial. *Lancet, The*, **2011**, 378, 1627-34	40	314
174	Triple-target treatment versus low-frequency electrostimulation for anal incontinence: a randomized, controlled trial. *Deutsches Ärzteblatt International*, **2011**, 108, 653-60	2.5	21
173	The choice of the filtering method in microarrays affects the inference regarding dosage compensation of the active X-chromosome. *PLoS ONE*, **2011**, 6, e23956	3.7	19
172	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
171	EPIBLASTER-fast exhaustive two-locus epistasis detection strategy using graphical processing units. *European Journal of Human Genetics*, **2011**, 19, 465-71	5.3	66
170	Does the new HapMap throw the baby out with the bath water?. *European Journal of Human Genetics*, **2011**, 19, 733-4	5.3	1
169	Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. *Circulation*, **2011**, 124, 2855-64	16.7	213
168	Genome-wide association study identifies a new locus for coronary artery disease on chromosome 10p11.23. *European Heart Journal*, **2011**, 32, 158-68	9.5	92
167	A genome-wide association study identifies LIPA as a susceptibility gene for coronary artery disease. *Circulation: Cardiovascular Genetics*, **2011**, 4, 403-12		98
166	Investigating Hardy-Weinberg equilibrium in case-control or cohort studies or meta-analysis. *Breast Cancer Research and Treatment*, **2011**, 128, 197-201	4.4	52
165	HDAC2 and TXNL1 distinguish aneuploid from diploid colorectal cancers. *Cellular and Molecular Life Sciences*, **2011**, 68, 3261-74	10.3	15

164	Identifying rare variants from exome scans: the GAW17 experience. *BMC Proceedings*, **2011**, 5 Suppl 9, S1	2.3	5
163	Comparison of collapsing methods for the statistical analysis of rare variants. *BMC Proceedings*, **2011**, 5 Suppl 9, S115	2.3	4
162	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**, 156B, 36-43	3.5	23
161	Introduction to genetic analysis workshop 17 summaries. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S1-4	2.6	6
160	Statistical analysis of rare sequence variants: an overview of collapsing methods. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S12-7	2.6	132
159	Identification of genetic association of multiple rare variants using collapsing methods. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S101-6	2.6	13
158	Lessons learned from Genetic Analysis Workshop 17: transitioning from genome-wide association studies to whole-genome statistical genetic analysis. *Genetic Epidemiology*, **2011**, 35 Suppl 1, S107-14	2.6	15
157	Association tests for X-chromosomal markers--a comparison of different test statistics. *Human Heredity*, **2011**, 71, 23-36	1.1	29
156	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, 940-7	36.3	168
155	Integrating genome-wide genetic variations and monocyte expression data reveals trans-regulated gene modules in humans. *PLoS Genetics*, **2011**, 7, e1002367	6	99
154	A -436C>A polymorphism in the human FAS gene promoter associated with severe childhood malaria. *PLoS Genetics*, **2011**, 7, e1002066	6	10
153	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
152	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. *Nature*, **2010**, 467, 460-4	50.4	224
151	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
150	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
149	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. *Nature Genetics*, **2010**, 42, 739-741	36.3	276
148	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
147	Genetics and beyond--the transcriptome of human monocytes and disease susceptibility. *PLoS ONE*, **2010**, 5, e10693	3.7	482

146	FCGR2A functional genetic variant associated with susceptibility to severe malarial anaemia in Ghanaian children. *Journal of Medical Genetics*, **2010**, 47, 471-5	5.8	13
145	Rare human IFNG variants. *Journal of Interferon and Cytokine Research*, **2010**, 30, 219-22	3.5	1
144	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, 1552-63	15.1	75
143	On safari to Random Jungle: a fast implementation of Random Forests for high-dimensional data. *Bioinformatics*, **2010**, 26, 1752-8	7.2	176
142	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	5.3	57
141	The potential role of G2- but not of G0-radiosensitivity for predisposition of prostate cancer. *Radiotherapy and Oncology*, **2010**, 96, 19-24	5.3	13
140	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study: A Genome-wide association meta-analysis involving more than 22 000 cases and 60 000 controls. *Circulation: Cardiovascular Genetics*, **2010**, 3, 475-83		135
139	High Frequency of Aneuploidy Defines Ulcerative Colitis-Associated Carcinomas: A Prognostic Comparison to Sporadic Colorectal Carcinomas. *Annals of Surgery*, **2010**, 252, 74-83	7.8	28
138	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, 1007-16	3.1	53
137	The behaviour of random forest permutation-based variable importance measures under predictor correlation. *BMC Bioinformatics*, **2010**, 11, 110	3.6	172
136	Photodynamic diagnosis in non-muscle-invasive bladder cancer: a systematic review and cumulative analysis of prospective studies. *European Urology*, **2010**, 57, 595-606	10.2	188
135	A confidence-limit-based approach to the assessment of Hardy-Weinberg equilibrium. *Biometrical Journal*, **2010**, 52, 253-70	1.5	13
134	On the Use of the Terms Repeatability and Reproducibility Regarding Reproducibility of genotypes as measured by the Affymetrix GeneChip(R) 100K Human Mapping Array Set by Fridley and colleagues (2008) Comput. Stat. Data Anal. 52:5367-74. *Computational Statistics and Data Analysis*, **2010**, 54, 803	1.6	1
133	Assessing the impact of a combined analysis of four common low-risk genetic variants on autism risk. *Molecular Autism*, **2010**, 1, 4	6.5	15
132	Evaluating diagnostic accuracy of genetic profiles in affected offspring families. *Statistics in Medicine*, **2010**, 29, 2359-68	2.3	11
131	**2010**,		49
130	What do we mean by 'replication' and 'validation' in genome-wide association studies?. *Human Heredity*, **2009**, 67, 66-8	1.1	33
129	A genotype-based approach to assessing the association between single nucleotide polymorphisms. *Human Heredity*, **2009**, 67, 128-39	1.1	29

128	Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA - Journal of the American Medical Association*, **2009**, 302, 168-78	27.4	164
127	Look who is calling: a comparison of genotype calling algorithms. *BMC Proceedings*, **2009**, 3 Suppl 7, S59	2.3	3
126	ACPA: automated cluster plot analysis of genotype data. *BMC Proceedings*, **2009**, 3 Suppl 7, S58	2.3	5
125	Evaluation of single-nucleotide polymorphism imputation using random forests. *BMC Proceedings*, **2009**, 3 Suppl 7, S65	2.3	6
124	Association of polymorphisms in the human surfactant protein-D (SFTPD) gene and postnatal pulmonary adaptation in the preterm infant. *Acta Paediatrica, International Journal of Paediatrics*, **2009**, 98, 112-7	3.1	32
123	More powerful haplotype sharing by accounting for the mode of inheritance. *Genetic Epidemiology*, **2009**, 33, 228-36	2.6	4
122	Adapting the logical basis of tests for Hardy-Weinberg Equilibrium to the real needs of association studies in human and medical genetics. *Genetic Epidemiology*, **2009**, 33, 569-80	2.6	6
121	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. *International Journal of Cancer*, **2009**, 124, 420-8	7.5	72
120	MDR1 variants and risk of Parkinson disease. Association with pesticide exposure?. *Journal of Neurology*, **2009**, 256, 115-20	5.5	42
119	Predicting recovery after intracerebral hemorrhage--an external validation in patients from controlled clinical trials. *Journal of Neurology*, **2009**, 256, 464-9	5.5	20
118	Assessment of transmission distortion on chromosome 6p in healthy individuals using tagSNPs. *European Journal of Human Genetics*, **2009**, 17, 1182-9	5.3	10
117	New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nature Genetics*, **2009**, 41, 280-2	36.3	389
116	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. *Nature Genetics*, **2009**, 41, 283-5	36.3	374
115	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nature Genetics*, **2009**, 41, 334-41	36.3	884
114	Further evidence for DYX1C1 as a susceptibility factor for dyslexia. *Psychiatric Genetics*, **2009**, 19, 59-63	2.9	55
113	SNPtoGO: characterizing SNPs by enriched GO terms. *Bioinformatics*, **2008**, 24, 146-8	7.2	24
112	Human genetic resistance to Onchocerca volvulus: evidence for linkage to chromosome 2p from an autosome-wide scan. *Journal of Infectious Diseases*, **2008**, 198, 427-33	7	18
111	Predicting long-term outcome after acute ischemic stroke: a simple index works in patients from controlled clinical trials. *Stroke*, **2008**, 39, 1821-6	6.7	198

110	Polymorphisms of homocysteine metabolism are associated with intracranial aneurysms. *Cerebrovascular Diseases*, **2008**, 26, 425-9	3.2	16
109	Lack of association between the MEF2A gene and myocardial infarction. *Circulation*, **2008**, 117, 185-91	16.7	38
108	Repeated replication and a prospective meta-analysis of the association between chromosome 9p21.3 and coronary artery disease. *Circulation*, **2008**, 117, 1675-84	16.7	312
107	Genetic variation in the arachidonate 5-lipoxygenase-activating protein (ALOX5AP) is associated with myocardial infarction in the German population. *Clinical Science*, **2008**, 115, 309-15	6.5	27
106	Sepsis syndrome and death in trauma patients are associated with variation in the gene encoding tumor necrosis factor. *Critical Care Medicine*, **2008**, 36, 1456-62, e1-6	1.4	80
105	Further evidence for a susceptibility locus contributing to reading disability on chromosome 15q15-q21. *Psychiatric Genetics*, **2008**, 18, 137-42	2.9	14
104	Investigation of the DCDC2 intron 2 deletion/compound short tandem repeat polymorphism in a large German dyslexia sample. *Psychiatric Genetics*, **2008**, 18, 310-2	2.9	41
103	Lifelong reduction of LDL-cholesterol related to a common variant in the LDL-receptor gene decreases the risk of coronary artery disease--a Mendelian Randomisation study. *PLoS ONE*, **2008**, 3, e2986	3.7	117
102	Lack of association of genetic variants in the LRP8 gene with familial and sporadic myocardial infarction. *Journal of Molecular Medicine*, **2008**, 86, 1163-70	5.5	4
101	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, 1233-41	5.5	69
100	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. *Journal of Neural Transmission*, **2008**, 115, 1587-9	4.3	36
99	Comments on 'Mendelian randomization: using genes as instruments for making causal inferences in epidemiology' 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, 2974-6; author reply 2976-8	2.3	3
98	50 Years Biometrical Journal. *Biometrical Journal*, **2008**, 50, 5-7	1.5	0
97	Biostatistical aspects of genome-wide association studies. *Biometrical Journal*, **2008**, 50, 8-28	1.5	111
96	A general approach for sample size and power calculations based on the Haseman-Elston method. *Biometrical Journal*, **2008**, 50, 257-69	1.5	2
95	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, 1486-9	2.5	17
94	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, 158-64	3	7
93	Individual radiosensitivity measured with lymphocytes may predict the risk of acute reaction after radiotherapy. *International Journal of Radiation Oncology Biology Physics*, **2008**, 71, 256-64	4	65

92	TLR4 and IL-18 gene variants in aggressive periodontitis. *Journal of Clinical Periodontology*, **2008**, 35, 1020-6	7.7	24
91	Passive rotary dynamic sitting at the workplace by office-workers with lumbar pain: a randomized multicenter study. *Spine Journal*, **2007**, 7, 531-40; discussion 540	4	18
90	Picking single-nucleotide polymorphisms in forests. *BMC Proceedings*, **2007**, 1 Suppl 1, S59	2.3	25
89	Data mining, neural nets, trees--problems 2 and 3 of Genetic Analysis Workshop 15. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S51-60	2.6	21
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