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	Distribution of RET protoâ€oncogene variants in children with appendicitis. Molecular Genetics & Genomic Medicine, 2022, , e1864.	0.6	1
2	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
3	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
4	Evidence-based recommendations for increasing the citation frequency of original articles. Scientometrics, 2022, 127, 3367-3381.	1.6	2
5	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
6	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
7	Empirical analysis of the text structure of original research articles in medical journals. PLoS ONE, 2020, 15, e0240288.	1.1	7
8	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
9	Non-invasive Degradation Tracking of Mg Implants in Humans: A Measurement Approach. Jom, 2020, 72, 1845-1850.	0.9	3
10	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
11	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
12	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
13	Empirical analysis of the text structure of original research articles in medical journals. , 2020, 15, e0240288.		0
14	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
15	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
16	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
17	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
18	Treatment choices and neuropsychological symptoms of a large cohort of early MS. Neurology: Neuroimmunology and NeuroInflammation, 2018, 5, e446.	3.1	54

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19	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
20	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
21	Unbiased split variable selection for random survival forests using maximally selected rank statistics. Statistics in Medicine, 2017, 36, 1272-1284.	0.8	110
22	Mendelian Randomization. Methods in Molecular Biology, 2017, 1666, 581-628.	0.4	65
23	Estimating Disequilibrium Coefficients. Methods in Molecular Biology, 2017, 1666, 117-132.	0.4	3
24	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	1.3	34
25	Generalized estimating equations with stabilized working correlation structure. Computational Statistics and Data Analysis, 2017, 106, 1-11.	0.7	5
26	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
27	Comparison of pre-processing methods for multiplex bead-based immunoassays. BMC Genomics, 2016, 17, 601.	1.2	13
28	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
29	Lifespan effects of mitochondrial mutations. Nature, 2016, 540, E13-E14.	13.7	16
30	Do little interactions get lost in dark random forests?. BMC Bioinformatics, 2016, 17, 145.	1.2	94
31	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
32	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
33	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
34	Linkage and Association Analysis Identifies TRAF1 Influencing Common Carotid Intimaâ€“Media Thickness. Stroke, 2016, 47, 2904-2909.	1.0	7
35	Novel multiple sclerosis susceptibility loci implicated in epigenetic regulation. Science Advances, 2016, 2, e1501678.	4.7	133
36	Adrenal cortex expression quantitative trait loci in a German Holstein Ã— Charolais cross. BMC Genetics, 2016, 17, 135.	2.7	5

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37	Calibrating random forests for probability estimation. Statistics in Medicine, 2016, 35, 3949-3960.	0.8	36
38	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
39	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
40	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
41	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
42	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
43	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
44	Mendelian Randomization versus Path Models: Making Causal Inferences in Genetic Epidemiology. Human Heredity, 2015, 79, 194-204.	0.4	18
45	Molecular Characterization of the NLRC4 Expression in Relation to Interleukin-18 Levels. Circulation: Cardiovascular Genetics, 2015, 8, 717-726.	5.1	22
46	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
47	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
48	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
49	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
50	Probability estimation with machine learning methods for dichotomous and multicategory outcome: Theory. Biometrical Journal, 2014, 56, 534-563.	0.6	67
51	Rejoinder. Biometrical Journal, 2014, 56, 607-613.	0.6	1
52	Probability estimation with machine learning methods for dichotomous and multicategory outcome: Applications. Biometrical Journal, 2014, 56, 564-583.	0.6	42
53	Generalized Estimating Equations. , 2014, , 1337-1376.		4
54	Shared Genetic Susceptibility to Ischemic Stroke and Coronary Artery Disease. Stroke, 2014, 45, 24-36.	1.0	302

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55	Genetic Prediction in the Genetic Analysis Workshop 18 Sequencing Data. Genetic Epidemiology, 2014, 38, S57-62.	0.6	1
56	How to Include Chromosome X in Your Genomeâ€Wide Association Study. Genetic Epidemiology, 2014, 38, 97-103.	0.6	91
57	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
58	Nerve Conduction Velocity Is Regulated by the Inositol Polyphosphate-4-Phosphatase II Gene. American Journal of Pathology, 2014, 184, 2420-2429.	1.9	8
59	A comparison of two collapsing methods in different approaches. BMC Proceedings, 2014, 8, S8.	1.8	2
60	Hypofractionation with simultaneous integrated boost for early breast cancer. Strahlentherapie Und Onkologie, 2014, 190, 646-653.	1.0	51
61	Celebrating the 30th Anniversary ofGenetic Epidemiology: How to Define Our Scope?â€. Genetic Epidemiology, 2014, 38, 379-380.	0.6	2
62	In Reply. Deutsches Ärzteblatt International, 2014, 111, 68.	0.6	0
63	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
64	Consumer credit risk: Individual probability estimates using machine learning. Expert Systems With Applications, 2013, 40, 5125-5131.	4.4	138
65	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
66	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
67	Genetic Predisposition to Higher Blood Pressure Increases Coronary Artery Disease Risk. Hypertension, 2013, 61, 995-1001.	1.3	70
68	Adaptive linear rank tests for eQTL studies. Statistics in Medicine, 2013, 32, 524-537.	0.8	4
69	Genome-Wide Haplotype Analysis of Cis Expression Quantitative Trait Loci in Monocytes. PLoS Genetics, 2013, 9, e1003240.	1.5	53
70	GUESS-ing Polygenic Associations with Multiple Phenotypes Using a GPU-Based Evolutionary Stochastic Search Algorithm. PLoS Genetics, 2013, 9, e1003657.	1.5	58
71	Analysis of Stathmin gene variation in patients with panic disorder and agoraphobia. Psychiatric Genetics, 2013, 23, 43-44.	0.6	1
72	Next-Generation Phenotyping Using theParkinExample. JAMA Neurology, 2013, 70, 1186.	4.5	99

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73	Triple Target Treatment (3T) vs Biofeedback. Diseases of the Colon and Rectum, 2013, 56, e35-e36.	0.7	1
74	Comprehension of the Description of Side Effects in Drug Information Leaflets. Deutsches Ärzteblatt International, 2013, 110, 669-73.	0.6	13
75	Cochran-Armitage Test versus Logistic Regression in the Analysis of Genetic Association Studies. Human Heredity, 2012, 73, 14-17.	0.4	12
76	Genome-wide association study indicates two novel resistance loci for severe malaria. Nature, 2012, 489, 443-446.	13.7	227
77	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
78	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
79	The Promise and Limitations of Genome-wide Association Studies. JAMA - Journal of the American Medical Association, 2012, 308, 1867.	3.8	24
80	Personalized medicine using DNA biomarkers: a review. Human Genetics, 2012, 131, 1627-1638.	1.8	169
81	Risk estimation and risk prediction using machine-learning methods. Human Genetics, 2012, 131, 1639-1654.	1.8	107
82	Study designs and methods post genome-wide association studies. Human Genetics, 2012, 131, 1525-1531.	1.8	10
83	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
84	Metachronous metastasis- and survival-analysis show prognostic importance of lymphadenectomy for colon carcinomas. BMC Gastroenterology, 2012, 12, 24.	0.8	22
85	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
86	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
87	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
88	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
89	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
90	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

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91	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
92	Protein profiling of genomic instability in endometrial cancer. Cellular and Molecular Life Sciences, 2012, 69, 325-333.	2.4	8
93	Genotype Calling for the Affymetrix Platform. Methods in Molecular Biology, 2012, 850, 513-523.	0.4	10
94	Estimating Disequilibrium Coefficients. Methods in Molecular Biology, 2012, 850, 103-117.	0.4	1
95	Comprehensive Exploration of the Effects of miRNA SNPs on Monocyte Gene Expression. PLoS ONE, 2012, 7, e45863.	1.1	8
96	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. Genomics, 2011, 98, 320-326.	1.3	23
97	Association of Parkinson disease to PARK16 in a Chilean sample. Parkinsonism and Related Disorders, 2011, 17, 70-71.	1.1	19
98	From GWAS to clinical utility in Parkinson's disease. Lancet, The, 2011, 377, 613-614.	6.3	22
99	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
100	Triple-Target Treatment Versus Low-Frequency Electrostimulation for Anal Incontinence. Deutsches Ärzteblatt International, 2011, 108, 653-60.	0.6	24
101	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
102	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	9.4	1,685
103	EPIBLASTER-fast exhaustive two-locus epistasis detection strategy using graphical processing units. European Journal of Human Genetics, 2011, 19, 465-471.	1.4	74
104	Does the new HapMap throw the baby out with the bath water?. European Journal of Human Genetics, 2011, 19, 733-734.	1.4	1
105	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
106	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
107	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
108	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

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109	HDAC2 and TXNL1 distinguish aneuploid from diploid colorectal cancers. Cellular and Molecular Life Sciences, 2011, 68, 3261-3274.	2.4	17
110	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.8	6
111	Comparison of collapsing methods for the statistical analysis of rare variants. BMC Proceedings, 2011, 5, S115.	1.8	5
112	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
113	Introduction to genetic analysis workshop 17 summaries. Genetic Epidemiology, 2011, 35, S1-4.	0.6	7
114	Statistical analysis of rare sequence variants: an overview of collapsing methods. Genetic Epidemiology, 2011, 35, S12-7.	0.6	139
115	Identification of genetic association of multiple rare variants using collapsing methods. Genetic Epidemiology, 2011, 35, S101-6.	0.6	18
116	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
117	Association Tests for X-Chromosomal Markers â€“ A Comparison of Different Test Statistics. Human Heredity, 2011, 71, 23-36.	0.4	36
118	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
119	Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. PLoS Genetics, 2011, 7, e1002367.	1.5	126
120	A â˜’436C>A Polymorphism in the Human FAS Gene Promoter Associated with Severe Childhood Malaria. PLoS Genetics, 2011, 7, e1002066.	1.5	14
121	High Frequency of Aneuploidy Defines Ulcerative Colitis-Associated Carcinomas. Annals of Surgery, 2010, 252, 74-83.	2.1	30
122	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
123	The behaviour of random forest permutation-based variable importance measures under predictor correlation. BMC Bioinformatics, 2010, 11, 110.	1.2	254
124	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
125	A Confidenceâ€Limitâ€Based Approach to the Assessment of Hardyâ€“Weinberg Equilibrium. Biometrical Journal, 2010, 52, 253-270.	0.6	15
126	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

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127	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
128	Evaluating diagnostic accuracy of genetic profiles in affected offspring families. Statistics in Medicine, 2010, 29, 2359-2368.	0.8	14
129	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
130	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464.	13.7	271
131	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
132	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
133	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. Nature Genetics, 2010, 42, 739-741.	9.4	332
134	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
135	Genetics and Beyond â€“ The Transcriptome of Human Monocytes and Disease Susceptibility. PLoS ONE, 2010, 5, e10693.	1.1	539
136	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
137	Rare Human IFNG Variants. Journal of Interferon and Cytokine Research, 2010, 30, 219-222.	0.5	1
138	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
139	On safari to Random Jungle: a fast implementation of Random Forests for high-dimensional data. Bioinformatics, 2010, 26, 1752-1758.	1.8	216
140	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
141	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
142	Design of the Coronary ARtery DIsease Genome-Wide Replication And Meta-Analysis (CARDIoGRAM) Study. Circulation: Cardiovascular Genetics, 2010, 3, 475-483.	5.1	159
143	What Do We Mean by â€˜Replicationâ€™ and â€˜Validationâ€™ in Genome-Wide Association Studies?. Human Heredity, 2009, 67, 66-68.	0.4	38
144	A Genotype-Based Approach to Assessing the Association between Single Nucleotide Polymorphisms. Human Heredity, 2009, 67, 128-139.	0.4	35

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145	Genetic Variants Associated With Cardiac Structure and Function. JAMA - Journal of the American Medical Association, 2009, 302, 168.	3.8	202
146	Look who is calling: a comparison of genotype calling algorithms. BMC Proceedings, 2009, 3, S59.	1.8	5
147	ACPA: automated cluster plot analysis of genotype data. BMC Proceedings, 2009, 3, S58.	1.8	9
148	Evaluation of single-nucleotide polymorphism imputation using random forests. BMC Proceedings, 2009, 3, S65.	1.8	7
149	Association of polymorphisms in the human surfactant proteinâ€D (SFTPD) gene and postnatal pulmonary adaptation in the preterm infant. Acta Paediatrica, International Journal of Paediatrics, 2009, 98, 112-117.	0.7	41
150	More powerful haplotype sharing by accounting for the mode of inheritance. Genetic Epidemiology, 2009, 33, 228-236.	0.6	4
151	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
152	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
153	MDR1 variants and risk of Parkinson disease. Journal of Neurology, 2009, 256, 115-120.	1.8	51
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	Assessment of transmission distortion on chromosome 6p in healthy individuals using tagSNPs. European Journal of Human Genetics, 2009, 17, 1182-1189.	1.4	10
156	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
157	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
158	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
159	Further evidence for DYX1C1 as a susceptibility factor for dyslexia. Psychiatric Genetics, 2009, 19, 59-63.	0.6	62
160	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
161	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
162	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. Journal of Neural Transmission, 2008, 115, 1587-1589.	1.4	41

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163	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
164	50 Years Biometrical Journal. Biometrical Journal, 2008, 50, 5-7.	0.6	1
165	Biostatistical Aspects of Genomeâ€Wide Association Studies. Biometrical Journal, 2008, 50, 8-28.	0.6	136
166	A General Approach for Sample Size and Power Calculations Based on the Hasemanâ€“Elston Method. Biometrical Journal, 2008, 50, 257-269.	0.6	4
167	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
168	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
169	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
170	TLR4 and ILâ€1 gene variants in aggressive periodontitis. Journal of Clinical Periodontology, 2008, 35, 1020-1026.	2.3	28
171	How to Predict the Risk of Parkinson Disease in Relatives of Parkin Mutation Carriers. Archives of Neurology, 2008, 65, 443.	4.9	0
172	SNPtoGO: characterizing SNPs by enriched GO terms. Bioinformatics, 2008, 24, 146-148.	1.8	24
173	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
174	Predicting Long-Term Outcome After Acute Ischemic Stroke. Stroke, 2008, 39, 1821-1826.	1.0	242
175	Polymorphisms of Homocysteine Metabolism Are Associated with Intracranial Aneurysms. Cerebrovascular Diseases, 2008, 26, 425-429.	0.8	18
176	Lack of Association Between the MEF2A Gene and Myocardial Infarction. Circulation, 2008, 117, 185-191.	1.6	44
177	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
178	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
179	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
180	Further evidence for a susceptibility locus contributing to reading disability on chromosome 15q15â€“q21. Psychiatric Genetics, 2008, 18, 137-142.	0.6	15

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