Michael Krawczak

List of Publications by Year
in descending order

286 papers	26,258 citations	11235 73 h-index	8212 153 g-index
300 all docs	300 docs citations	300 times ranked	37573 citing authors

#	Article	IF	Citations
1	Correspondence on â€œScreening for autosomal recessive and X-linked conditions during pregnancy and preconception: A practice resource of the American College of Medical Genetics and Genomics (ACMG)â€•by Gregg etÂal. Genetics in Medicine, 2022, 24, 1156-1157.	1.1	4
2	Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. Gut Microbes, 2022, 14, 2024415.	4.3	5
3	PanelDesign: Integrating Epidemiological Information into the Design of Diagnostic NGS Gene Panels. Genes, 2022, 13, 684.	1.0	1
4	Severity, predictors and clinical correlates of Post-COVID syndrome (PCS) in Germany: A prospective, multi-centre, population-based cohort study. EClinicalMedicine, 2022, 51, 101549.	3.2	66
5	The germlines of male monozygotic (MZ) twins: Very similar, but not identical. Forensic Science International: Genetics, 2021, 50, 102408.	1.6	10
6	Secondary research use of personal medical data: attitudes from patient and population surveys in The Netherlands and Germany. European Journal of Human Genetics, 2021, 29, 495-502.	1.4	26
7	The copy number variation and stroke (CaNVAS) risk and outcome study. PLoS ONE, 2021, 16, e0248791.	1.1	2
8	Genotype imputation in case-only studies of gene-environment interaction: validity and power. Human Genetics, 2021, 140, 1217-1228.	1.8	3
9	Balancing scientific interests and the rights of participants in designing a recall by genotype study. European Journal of Human Genetics, 2021, 29, 1146-1157.	1.4	6
10	Validity and Prognostic Value of a Polygenic Risk Score for Parkinsonâ€™s Disease. Genes, 2021, 12, 1859.	1.0	15
11	Secondary research use of personal medical data: patient attitudes towards data donation. BMC Medical Ethics, 2021, 22, 164.	1.0	18
12	Case-only analysis of geneâ€“gene interactions in inflammatory bowel disease. Scandinavian Journal of Gastroenterology, 2020, 55, 897-906.	0.6	2
13	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. Movement Disorders, 2020, 35, 1245-1248.	2.2	37
14	Private variants in PRKN are associated with late-onset Parkinson's disease. Parkinsonism and Related Disorders, 2020, 75, 24-26.	1.1	4
15	Role of rhesus macaque IFITM3(2) in simian immunodeficiency virus infection of macaques. PLoS ONE, 2019, 14, e0224082.	1.1	1
16	Comparison of Markov Chain Monte Carlo Software for the Evolutionary Analysis of Y-Chromosomal Microsatellite Data. Computational and Structural Biotechnology Journal, 2019, 17, 1082-1090.	1.9	1
17	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. Gut, 2019, 68, 854-865.	6.1	84
18	Patient views on research use of clinical data without consent: Legal, but also acceptable?. European Journal of Human Genetics, 2019, 27, 841-847.	1.4	48

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19	Genetic Imbalance Is Associated With Functional Outcome After Ischemic Stroke. Stroke, 2019, 50, 298-304.	1.0	16
20	Missense variants in NOX1 and p22phox in a case of very-early-onset inflammatory bowel disease are functionally linked to NOD2. Journal of Physical Education and Sports Management, 2019, 5, a002428.	0.5	13
21	Does big data require a methodological change in medical research?. BMC Medical Research Methodology, 2019, 19, 125.	1.4	17
22	Linking pre-existing biorepositories for medical research: the PopGen 2.0 Network. Journal of Community Genetics, 2019, 10, 523-530.	0.5	10
23	VarWatchâ€"A stand-alone software tool for variant matching. PLoS ONE, 2019, 14, e0215618.	1.1	0
24	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. Human Genetics, 2019, 138, 375-388.	1.8	6
25	Thanks for opening an overdue discussion on GWAS of BMI: a reply to Prof. Speakman et al.. International Journal of Obesity, 2019, 43, 217-218.	1.6	0
26	Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. Nature Communications, 2018, 9, 327.	5.8	94
27	Phenotypes of organ involvement in sarcoidosis. European Respiratory Journal, 2018, 51, 1700991.	3.1	146
28	Biobanks in the Era of Digital Medicine. Clinical Pharmacology and Therapeutics, 2018, 103, 761-762.	2.3	11
29	Broad consent for health careâ€"embedded biobanking: understanding and reasons to donate in a large patient sample. Genetics in Medicine, 2018, 20, 76-82.	1.1	45
30	Predictive values in Forensic DNA Phenotyping are not necessarily prevalence-dependent. Forensic Science International: Genetics, 2018, 33, e7-e8.	1.6	10
31	Distinguishing genetically between the germlines of male monozygotic twins. PLoS Genetics, 2018, 14, e1007756.	1.5	7
32	Match probabilities for Y-chromosomal profiles: A paradigm shift. Forensic Science International: Genetics, 2018, 37, 200-203.	1.6	8
33	Epigenomic map of human liver reveals principles of zonated morphogenic and metabolic control. Nature Communications, 2018, 9, 4150.	5.8	65
34	Low-Frequency Blood Group Antigens in Switzerland. Transfusion Medicine and Hemotherapy, 2018, 45, 239-250.	0.7	8
35	The case of GWAS of obesity: does body weight control play by the rules?. International Journal of Obesity, 2018, 42, 1395-1405.	1.6	45
36	Genetic Profiles of Clinical Features in Sarcoidosis. , 2018, , .		1

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37	IMHOTEPâ€"a composite score integrating popular tools for predicting the functional consequences of non-synonymous sequence variants. Nucleic Acids Research, 2017, 45, gkw886.	6.5	10
38	Uncoupling of mucosal gene regulation, mRNA splicing and adherent microbiota signatures in inflammatory bowel disease. Gut, 2017, 66, 2087-2097.	6.1	81
39	Likelihood ratio and posterior odds in forensic genetics: Two sides of the same coin. Forensic Science International: Genetics, 2017, 28, 203-210.	1.6	12
40	Genetic Factors Interact With Tobacco Smoke to Modify Risk for Inflammatory Bowel Disease in Humans and Mice. Gastroenterology, 2017, 153, 550-565.	0.6	68
41	Insights into early pig domestication provided by ancient DNA analysis. Scientific Reports, 2017, 7, 44550.	1.6	19
42	Increased Tryptophan Metabolism Is Associated With Activity of Inflammatory Bowel Diseases. Gastroenterology, 2017, 153, 1504-1516.e2.	0.6	338
43	Vector Order Determines Protection against Pathogenic Simian Immunodeficiency Virus Infection in a Triple-Component Vaccine by Balancing CD4 ⁺ and CD8 ⁺ T-Cell Responses. Journal of Virology, 2017, 91, .	1.5	6
44	Genome-wide association and targeted analysis of copy number variants with psoriatic arthritis in German patients. BMC Medical Genetics, 2017, 18, 92.	2.1	8
45	Rhesus macaque IFITM3 gene polymorphisms and SIV infection. PLoS ONE, 2017, 12, e0172847.	1.1	7
46	Prospective evaluation of a patented DNA test for canine hip dysplasia (CHD). PLoS ONE, 2017, 12, e0182093.	1.1	6
47	Genetic Imbalance in Patients with Cervical Artery Dissection. Current Genomics, 2017, 18, 206-213.	0.7	28
48	The Slavic NBN Founder Mutation: A Role for Reproductive Fitness?. PLoS ONE, 2016, 11, e0167984.	1.1	21
49	Distinct metabolic network states manifest in the gene expression profiles of pediatric inflammatory bowel disease patients and controls. Scientific Reports, 2016, 6, 32584.	1.6	17
50	Genetic studies on the Cayo Santiago rhesus macaques: A review of 40 years of research. American Journal of Primatology, 2016, 78, 44-62.	0.8	80
51	Genetic mapping of 15 human X chromosomal forensic short tandem repeat (STR) loci by means of multi-core parallelization. Forensic Science International: Genetics, 2016, 25, 39-44.	1.6	21
52	Probability and Likelihood. Security Science and Technology, 2016, , 61-80.	0.5	2
53	Interdisciplinary approach towards a systems medicine toolbox using the example of inflammatory diseases. Briefings in Bioinformatics, 2016, 18, bbw024.	3.2	13
54	The more the merrier? How a few SNPs predict pigmentation phenotypes in the Northern German population. European Journal of Human Genetics, 2016, 24, 739-747.	1.4	9

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55	Family-Based Benchmarking of Copy Number Variation Detection Software. PLoS ONE, 2015, 10, e0133465.	1.1	9
56	The role of linkage disequilibrium in case-only studies of geneâ€“environment interactions. Human Genetics, 2015, 134, 89-96.	1.8	5
57	A Candidate Gene Association Study Identifies DAPL1 as a Female-Specific Susceptibility Locus for Age-Related Macular Degeneration (AMD). NeuroMolecular Medicine, 2015, 17, 111-120.	1.8	30
58	Allowing for population stratification in case-only studies of geneâ€“environment interaction, using genomic control. Human Genetics, 2015, 134, 1117-1125.	1.8	2
59	No shortcut solution to the problem of Y-STR match probability calculation. Forensic Science International: Genetics, 2015, 15, 69-75.	1.6	23
60	Mutations Causing Complex Disease May under Certain Circumstances Be Protective in an Epidemiological Sense. PLoS ONE, 2015, 10, e0132150.	1.1	4
61	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. European Heart Journal, 2014, 35, 1069-1077.	1.0	137
62	Genome-wide analysis associates familial colorectal cancer with increases in copy number variations and a rare structural variation at 12p12.3. Carcinogenesis, 2014, 35, 315-323.	1.3	31
63	Molecular genetic epidemiology of human diseases: from patterns to predictions. Human Genetics, 2014, 133, 425-430.	1.8	10
64	Causality of incest: a reply to ten Kate. International Journal of Legal Medicine, 2014, 128, 747-747.	1.2	0
65	Evaluation of genome-wide loci of iron metabolism in hereditary hemochromatosis identifies PCSK7 as a host risk factor of liver cirrhosis. Human Molecular Genetics, 2014, 23, 3883-3890.	1.4	50
66	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	1.6	214
67	Adjustment for smoking does not alter the FOXO3A association with longevity. Age, 2014, 36, 911-921.	3.0	12
68	GrabBlur - a framework to facilitate the secure exchange of whole-exome and -genome SNV data using VCF files. BMC Genomics, 2014, 15, S8.	1.2	6
69	Recurrence of gallstones after cholecystectomy is associated with ABCG5/8 genotype. Journal of Gastroenterology, 2013, 48, 391-396.	2.3	19
70	DNA Methylation Analysis in Nonalcoholic Fatty Liver Disease Suggests Distinct Disease-Specific and Remodeling Signatures after Bariatric Surgery. Cell Metabolism, 2013, 18, 296-302.	7.2	424
71	Where genotype is not predictive of phenotype: towards an understanding of the molecular basis of reduced penetrance in human inherited disease. Human Genetics, 2013, 132, 1077-1130.	1.8	528
72	Genetic characterization of northeastern Italian population isolates in the context of broader European genetic diversity. European Journal of Human Genetics, 2013, 21, 659-665.	1.4	64

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73	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	0.6	149
74	Y-chromosomal analysis identifies the skeletal remains of Swiss national hero JÃ¶rg Jenatsch (1596â€“1639). Forensic Science International: Genetics, 2013, 7, 610-617.	1.6	27
75	Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54.	1.6	24
76	Genome-wide investigation of geneâ€“environment interactions in colorectal cancer. Human Genetics, 2013, 132, 219-231.	1.8	38
77	Estimating trace-suspect match probabilities for singleton Y-STR haplotypes using coalescent theory. Forensic Science International: Genetics, 2013, 7, 264-271.	1.6	35
78	Genetic investigation of FOXO3A requires special attention due to sequence homology with FOXO3B. European Journal of Human Genetics, 2013, 21, 240-242.	1.4	18
79	Continent-Wide Decoupling of Y-Chromosomal Genetic Variation from Language and Geography in Native South Americans. PLoS Genetics, 2013, 9, e1003460.	1.5	89
80	Higher Fetuin-A Level Is Associated with Coexistence of Elevated Alanine Aminotransferase and the Metabolic Syndrome in the General Population. Metabolic Syndrome and Related Disorders, 2013, 11, 377-384.	0.5	3
81	Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at theABCG5/8lithogenic locus. Hepatology, 2013, 57, 2407-2417.	3.6	74
82	Diagnosing Fatty Liver Disease: A Comparative Evaluation of Metabolic Markers, Phenotypes, Genotypes and Established Biomarkers. PLoS ONE, 2013, 8, e76813.	1.1	8
83	Copy number variation in patients with cervical artery dissection. European Journal of Human Genetics, 2012, 20, 1295-1299.	1.4	29
84	Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome. Forensic Science International: Genetics, 2012, 6, 778-784.	1.6	60
85	How to distinguish genetically between an alleged father and his monozygotic twin: A thought experiment. Forensic Science International: Genetics, 2012, 6, e129-e130.	1.6	14
86	Genome-wide search for novel human uORFs and N-terminal protein extensions using ribosomal footprinting. Genome Research, 2012, 22, 2208-2218.	2.4	198
87	SFRS10â€”A Splicing Factor Gene Reduced in Human Obesity?. Cell Metabolism, 2012, 15, 265-266.	7.2	11
88	â€˜Sifting the significance from the dataâ€™ - the impact of high-throughput genomic technologies on human genetics and health care. Human Genomics, 2012, 6, 11.	1.4	5
89	Association studies of the copy-number variable ÃŸ-defensin cluster on 8p23.1 in adenocarcinoma and chronic pancreatitis. BMC Research Notes, 2012, 5, 629.	0.6	12
90	Pipeline for Large-Scale Microdroplet Bisulfite PCR-Based Sequencing Allows the Tracking of Hepitype Evolution in Tumors. PLoS ONE, 2011, 6, e21332.	1.1	8

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91	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
92	Genetic testing and common disorders in a public health framework: how to assess relevance and possibilities. European Journal of Human Genetics, 2011, 19, S6-S44.	1.4	75
93	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. Mechanisms of Ageing and Development, 2011, 132, 324-330.	2.2	184
94	Technology-specific error signatures in the 1000 Genomes Project data. Human Genetics, 2011, 130, 505-516.	1.8	37
95	Biobanking and international interoperability: samples. Human Genetics, 2011, 130, 369-376.	1.8	34
96	Rauchen und Lungenkrebs. Medizinische Genetik, 2011, 23, 400-406.	0.1	1
97	Genetic variation in the PNPLA3 gene is associated with alcoholic liver injury in caucasians. Hepatology, 2011, 53, 86-95.	3.6	252
98	Statistical inference of allelic imbalance from transcriptome data. Human Mutation, 2011, 32, 98-106.	1.1	33
99	Single base-pair substitutions at the translation initiation sites of human genes as a cause of inherited disease. Human Mutation, 2011, 32, 1137-1143.	1.1	32
100	Empirical Evaluation Reveals Best Fit of a Logistic Mutation Model for Human Y-Chromosomal Microsatellites. Genetics, 2011, 189, 1403-1411.	1.2	11
101	Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. Human Molecular Genetics, 2011, 20, 1660-1671.	1.4	47
102	Association of TLR7 Variants with AIDS-Like Disease and AIDS Vaccine Efficacy in Rhesus Macaques. PLoS ONE, 2011, 6, e25474.	1.1	7
103	Psychomotor developmental delay and epilepsy in an offspring of fatherâ€“daughter incest: quantification of the causality probability. International Journal of Legal Medicine, 2010, 124, 449-450.	1.2	8
104	Potentials and limits of pairwise kinship analysis using autosomal short tandem repeat loci. International Journal of Legal Medicine, 2010, 124, 205-215.	1.2	48
105	Heritability of chronic venous disease. Human Genetics, 2010, 127, 669-674.	1.8	67
106	How obedience of marriage rules may counteract genetic drift. Journal of Community Genetics, 2010, 1, 23-28.	0.5	5
107	Biobanken. Medizinische Genetik, 2010, 22, 229-234.	0.1	1
108	Genes, mutations, and human inherited disease at the dawn of the age of personalized genomics. Human Mutation, 2010, 31, 631-655.	1.1	161

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109	Triangulation of the human, chimpanzee, and Neanderthal genome sequences identifies potentially compensated mutations. Human Mutation, 2010, 31, 1286-1293.	1.1	12
110	A Markov chain description of the stepwise mutation model: Local and global behaviour of the allele process. Journal of Theoretical Biology, 2010, 266, 336-342.	0.8	9
111	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2with serum creatinine level. BMC Medical Genetics, 2010, 11, 41.	2.1	48
112	Is the NIH policy for sharing GWAS data running the risk of being counterproductive?. Investigative Genetics, 2010, 1, 3.	3.3	4
113	Legal and ethical consequences of international biobanking from a national perspective: the German BMB-EUCoop project. European Journal of Human Genetics, 2010, 18, 522-525.	1.4	16
114	Genome-wide association study identifies two susceptibility loci for nonsyndromic cleft lip with or without cleft palate. Nature Genetics, 2010, 42, 24-26.	9.4	379
115	Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294.	9.4	177
116	Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. Human Molecular Genetics, 2010, 19, 2927-2935.	1.4	146
117	Genome-wide association study for colorectal cancer identifies risk polymorphisms in German familial cases and implicates MAPK signalling pathways in disease susceptibility. Carcinogenesis, 2010, 31, 1612-1619.	1.3	57
118	Loci From a Genome-Wide Analysis of Bilirubin Levels Are Associated With Gallstone Risk and Composition. Gastroenterology, 2010, 139, 1942-1951.e2.	0.6	96
119	Clinical Validity and Utility of Genetic Testing in Common Multifactorial Diseases. , 2010, , 157-164.		0
120	Genetic Structure of Europeans: A View from the Northâ€“East. PLoS ONE, 2009, 4, e5472.	1.1	279
121	A functional EXO1 promoter variant is associated with prolonged life expectancy in centenarians. Mechanisms of Ageing and Development, 2009, 130, 691-699.	2.2	43
122	A gene conversion hotspot in the human growth hormone (GH1) gene promoter. Human Mutation, 2009, 30, 239-247.	1.1	13
123	Systematic evaluation of the effect of common SNPs on pre-mRNA splicing. Human Mutation, 2009, 30, 625-632.	1.1	28
124	Age-related macular degeneration and functional promoter and coding variants of the apolipoprotein E gene. Human Mutation, 2009, 30, 1048-1053.	1.1	36
125	Investigation of the colorectal cancer susceptibility region on chromosome 8q24.21 in a large German caseâ€control sample. International Journal of Cancer, 2009, 124, 75-80.	2.3	44
126	A comprehensive evaluation of SNP genotype imputation. Human Genetics, 2009, 125, 163-171.	1.8	139

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127	Investigation of innate immunity genes CARD4, CARD8 and CARD15 as germline susceptibility factors for colorectal cancer. BMC Gastroenterology, 2009, 9, 79.	0.8	39
128	An evaluation of the genetic-matched pair study design using genome-wide SNP data from the European population. European Journal of Human Genetics, 2009, 17, 967-975.	1.4	8
129	X Chromosomal Variation Is Associated with Slow Progression to AIDS in HIV-1-Infected Women. American Journal of Human Genetics, 2009, 85, 228-239.	2.6	41
130	Association of HTRA1 and ARMS2 gene variation with drusen formation in rhesus macaques. Experimental Eye Research, 2009, 88, 479-482.	1.2	25
131	A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Human Molecular Genetics, 2009, 18, 3516-3524.	1.4	76
132	EinfÃ¼hrung â€žPopulationsgenetikâ€œ. Medizinische Genetik, 2008, 20, 273-275.	0.1	0
133	Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. Nature Genetics, 2008, 40, 1103-1106.	9.4	239
134	On the Use of General Control Samples for Genome-wide Association Studies: Genetic Matching Highlights Causal Variants. American Journal of Human Genetics, 2008, 82, 453-463.	2.6	120
135	An Illicit Love Affair During the Third Reich: Who is My Grandfather?. Journal of Forensic Sciences, 2008, 53, 377-379.	0.9	2
136	Hypotheses in genome-wide association scans. European Journal of Human Genetics, 2008, 16, 1174-1175.	1.4	1
137	Replication of signals from recent studies of Crohn's disease identifies previously unknown disease loci for ulcerative colitis. Nature Genetics, 2008, 40, 713-715.	9.4	333
138	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323.	9.4	534
139	Increased heritability of gallstone disease in early onset cases. Liver International, 2008, 28, 895-897.	1.9	2
140	Chromosomal evolution of the PKD1 gene family in primates. BMC Evolutionary Biology, 2008, 8, 263.	3.2	10
141	Correlation between Genetic and Geographic Structure in Europe. Current Biology, 2008, 18, 1241-1248.	1.8	449
142	Genome-Wide Association Analysis in Sarcoidosis and Crohn's Disease Unravels a Common Susceptibility Locus on 10p12.2. Gastroenterology, 2008, 135, 1207-1215.	0.6	85
143	Plastin 3 Is a Protective Modifier of Autosomal Recessive Spinal Muscular Atrophy. Science, 2008, 320, 524-527.	6.0	434
144	Growth hormone (GH1) gene variation and the growth hormone receptor (GHR) exon 3 deletion polymorphism in a West-African population. Molecular and Cellular Endocrinology, 2008, 296, 18-25.	1.6	16

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145	Genetic Variants of the Copy Number Polymorphic β-Defensin Locus Are Associated with Sporadic Prostate Cancer. Tumor Biology, 2008, 29, 83-92.	0.8	24
146	Familial influences and obesity-associated metabolic risk factors contribute to the variation in resting energy expenditure: the Kiel Obesity Prevention Study. American Journal of Clinical Nutrition, 2008, 87, 1695-1701.	2.2	46
147	An Illicit Love Affair During the Third Reich: Who is My Grandfather?. Journal of Forensic Sciences, 2008, 53, 080219072231020-???.	0.9	0
148	A common haplotype of the annexin A5 (ANXA5) gene promoter is associated with recurrent pregnancy loss. Human Molecular Genetics, 2007, 16, 573-578.	1.4	107
149	Comparative Assessment of the Association Information Captured by SNP Tagging. Human Heredity, 2007, 64, 27-34.	0.4	3
150	Efficacy assessment of SNP sets for genome-wide disease association studies. Nucleic Acids Research, 2007, 35, e113-e113.	6.5	15
151	Kinship testing with X-chromosomal markers: Mathematical and statistical issues. Forensic Science International: Genetics, 2007, 1, 111-114.	1.6	49
152	Relating two deep-rooted pedigrees from Central Germany by high-resolution Y-STR haplotyping. Forensic Science International: Genetics, 2007, 1, 125-128.	1.6	39
153	A genome-wide association scan identifies the hepatic cholesterol transporter ABCG8 as a susceptibility factor for human gallstone disease. Nature Genetics, 2007, 39, 995-999.	9.4	306
154	On the Testing Load Incurred by Cascade Genetic Carrier Screening for Mendelian Disorders: A Brief Report. Genetic Testing and Molecular Biomarkers, 2007, 11, 417-420.	1.7	7
155	On the length distribution of external branches in coalescence trees: Genetic diversity within species. Theoretical Population Biology, 2007, 72, 245-252.	0.5	27
156	Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. PLoS ONE, 2007, 2, e691.	1.1	123
157	Juristische Grundlagen von Biomaterialbanken â€“ Mehr Rechtssicherheit fÃ¼r Betreiber und Spender in Deutschland (The Legal Basis of Biobanks â€“ Improved Juridical Assurance for Operators and Donors in) Tj ETQq1 1 0.784314 rgBT /Ov		
158	Single base-pair substitutions in exon-intron junctions of human genes: nature, distribution, and consequences for mRNA splicing. Human Mutation, 2007, 28, 150-158.	1.1	324
159	Diversity of cystathionine Î²-synthase haplotypes bearing the most common homocystinuria mutation c.833T>C: a possible role for gene conversion. Human Mutation, 2007, 28, 255-264.	1.1	20
160	Genetic investigation of DNA-repair pathway genesPMS2,MLH1,MSH2,MSH6,MUTYH,OGG1 andMTH1 in sporadic colon cancer. International Journal of Cancer, 2007, 121, 555-558.	2.3	42
161	A genome-wide association scan of nonsynonymous SNPs identifies a susceptibility variant for Crohn disease in ATG16L1. Nature Genetics, 2007, 39, 207-211.	9.4	1,712
162	A legal framework for biobanking: the German experience. European Journal of Human Genetics, 2007, 15, 528-532.	1.4	17

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163	IMPG1 gene variation in rhesus macular drusen. Veterinary Ophthalmology, 2007, 10, 274-277.	0.6	4
164	Investigation of the Lith6 candidate genes APOBEC1 and PPARG in human gallstone disease. Liver International, 2007, 27, 910-919.	1.9	6
165	Biobanken im Spannungsfeld zwischen Forschung und Gesellschaft (Biobanks: Research Tools in the) Tj ETQq1 1 0.784314 rgBT /Ove	0.6	0
166	PopGen â€“ BevÃ¶lkerungsbasierte Rekrutierung von Patienten und Kontrollen fÃ¼r die Untersuchung komplexer Genotyp-PhÃnotyp-Beziehungen (PopGen â€“ Population-based Recruitment of Patients and) Tj ETQq0 0 0 rgBT /Overlock 10 2007, 49, 374-380.	0.6	0
167	PopGen: Population-Based Recruitment of Patients and Controls for the Analysis of Complex Genotype-Phenotype Relationships. Public Health Genomics, 2006, 9, 55-61.	0.6	265
168	Hereditary hemorrhagic telangiectasia is caused byÂtheÂQ490X mutation ofÂtheÂACVRL1 gene inÂaÂlarge Arab family: support ofÂhomozygous lethality. European Journal of Medical Genetics, 2006, 49, 323-330.	0.7	12
169	Predictors of gallstone composition in 1025 symptomatic gallstones from Northern Germany. BMC Gastroenterology, 2006, 6, 36.	0.8	74
170	Y-chromosomal STR haplotype analysis reveals surname-associated strata in the East-German population. European Journal of Human Genetics, 2006, 14, 577-582.	1.4	23
171	Genetic variation at the growth hormone (GH1) and growth hormone receptor (GHR) loci as a risk factor for hypertension and stroke. Human Genetics, 2006, 119, 527-540.	1.8	29
172	Paternal kin bias in the agonistic interventions of adult female rhesus macaques (Macaca mulatta). Behavioral Ecology and Sociobiology, 2006, 61, 205-214.	0.6	62
173	Allelic variation in the CNDP1 gene and its lack of association with longevity and coronary heart disease. Mechanisms of Ageing and Development, 2006, 127, 817-820.	2.2	9
174	GENOMIZER: an integrated analysis system for genome-wide association data. Human Mutation, 2006, 27, 583-588.	1.1	24
175	SNP-Based Analysis of Genetic Substructure in the German Population. Human Heredity, 2006, 62, 20-29.	0.4	121
176	Genetic Influence on Reproductive Behavior in Female Rhesus Macaques. Twin Research and Human Genetics, 2005, 8, 551-552.	0.3	1
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