# Michael Krawczak

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 286 papers | 26,258 citations | 9786 73 h-index | 6996 154 g-index |
| 300 all docs | 300 docs citations | 300 times ranked | 34161 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. | 2.4 | 4 |
| 2 | Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. Gut Microbes, 2022, 14, 2024415. | 9.8 | 5 |
| 3 | PanelDesign: Integrating Epidemiological Information into the Design of Diagnostic NGS Gene Panels. Genes, 2022, 13, 684. | 2.4 | 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. | 7.1 | 66 |
| 5 | The germlines of male monozygotic (MZ) twins: Very similar, but not identical. Forensic Science International: Genetics, 2021, 50, 102408. | 3.1 | 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. | 2.8 | 26 |
| 7 | The copy number variation and stroke (CaNVAS) risk and outcome study. PLoS ONE, 2021, 16, e0248791. | 2.5 | 2 |
| 8 | Genotype imputation in case-only studies of gene-environment interaction: validity and power. Human Genetics, 2021, 140, 1217-1228. | 3.8 | 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. | 2.8 | 6 |
| 10 | Validity and Prognostic Value of a Polygenic Risk Score for Parkinsonâ€™s Disease. Genes, 2021, 12, 1859. | 2.4 | 15 |
| 11 | Secondary research use of personal medical data: patient attitudes towards data donation. BMC Medical Ethics, 2021, 22, 164. | 2.4 | 18 |
| 12 | Case-only analysis of geneâ€“gene interactions in inflammatory bowel disease. Scandinavian Journal of Gastroenterology, 2020, 55, 897-906. | 1.5 | 2 |
| 13 | Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. Movement Disorders, 2020, 35, 1245-1248. | 3.9 | 37 |
| 14 | Private variants in PRKN are associated with late-onset Parkinson's disease. Parkinsonism and Related Disorders, 2020, 75, 24-26. | 2.2 | 4 |
| 15 | Role of rhesus macaque IFITM3(2) in simian immunodeficiency virus infection of macaques. PLoS ONE, 2019, 14, e0224082. | 2.5 | 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. | 4.1 | 1 |
| 17 | Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. Gut, 2019, 68, 854-865. | 12.1 | 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. | 2.8 | 48 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Genetic Imbalance Is Associated With Functional Outcome After Ischemic Stroke. Stroke, 2019, 50, 298-304. | 2.0 | 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. | 1.2 | 13 |
| 21 | Does big data require a methodological change in medical research?. BMC Medical Research Methodology, 2019, 19, 125. | 3.1 | 17 |
| 22 | Linking pre-existing biorepositories for medical research: the PopGen 2.0 Network. Journal of Community Genetics, 2019, 10, 523-530. | 1.2 | 10 |
| 23 | VarWatchâ€"A stand-alone software tool for variant matching. PLoS ONE, 2019, 14, e0215618. | 2.5 | 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. | 3.8 | 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. | 3.4 | 0 |
| 26 | Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. Nature Communications, 2018, 9, 327. | 12.8 | 94 |
| 27 | Phenotypes of organ involvement in sarcoidosis. European Respiratory Journal, 2018, 51, 1700991. | 6.7 | 146 |
| 28 | Biobanks in the Era of Digital Medicine. Clinical Pharmacology and Therapeutics, 2018, 103, 761-762. | 4.7 | 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. | 2.4 | 45 |
| 30 | Predictive values in Forensic DNA Phenotyping are not necessarily prevalence-dependent. Forensic Science International: Genetics, 2018, 33, e7-e8. | 3.1 | 10 |
| 31 | Distinguishing genetically between the germlines of male monozygotic twins. PLoS Genetics, 2018, 14, e1007756. | 3.5 | 7 |
| 32 | Match probabilities for Y-chromosomal profiles: A paradigm shift. Forensic Science International: Genetics, 2018, 37, 200-203. | 3.1 | 8 |
| 33 | Epigenomic map of human liver reveals principles of zonated morphogenic and metabolic control. Nature Communications, 2018, 9, 4150. | 12.8 | 65 |
| 34 | Low-Frequency Blood Group Antigens in Switzerland. Transfusion Medicine and Hemotherapy, 2018, 45, 239-250. | 1.6 | 8 |
| 35 | The case of GWAS of obesity: does body weight control play by the rules?. International Journal of Obesity, 2018, 42, 1395-1405. | 3.4 | 45 |
| 36 | Genetic Profiles of Clinical Features in Sarcoidosis. , 2018, , . | | 1 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | IMHOTEPâ€"a composite score integrating popular tools for predicting the functional consequences of non-synonymous sequence variants. Nucleic Acids Research, 2017, 45, gkw886. | 14.5 | 10 |
| 38 | Uncoupling of mucosal gene regulation, mRNA splicing and adherent microbiota signatures in inflammatory bowel disease. Gut, 2017, 66, 2087-2097. | 12.1 | 81 |
| 39 | Likelihood ratio and posterior odds in forensic genetics: Two sides of the same coin. Forensic Science International: Genetics, 2017, 28, 203-210. | 3.1 | 12 |
| 40 | Genetic Factors Interact With Tobacco Smoke to Modify Risk for Inflammatory Bowel Disease in Humans and Mice. Gastroenterology, 2017, 153, 550-565. | 1.3 | 68 |
| 41 | Insights into early pig domestication provided by ancient DNA analysis. Scientific Reports, 2017, 7, 44550. | 3.3 | 19 |
| 42 | Increased Tryptophan Metabolism Is Associated With Activity of Inflammatory Bowel Diseases. Gastroenterology, 2017, 153, 1504-1516.e2. | 1.3 | 338 |
| 43 | Vector Order Determines Protection against Pathogenic Simian Immunodeficiency Virus Infection in a Triple-Component Vaccine by Balancing CD4 <sup>+</sup> and CD8 <sup>+</sup> T-Cell Responses. Journal of Virology, 2017, 91, . | 3.4 | 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. | 2.5 | 7 |
| 46 | Prospective evaluation of a patented DNA test for canine hip dysplasia (CHD). PLoS ONE, 2017, 12, e0182093. | 2.5 | 6 |
| 47 | Genetic Imbalance in Patients with Cervical Artery Dissection. Current Genomics, 2017, 18, 206-213. | 1.6 | 28 |
| 48 | The Slavic NBN Founder Mutation: A Role for Reproductive Fitness?. PLoS ONE, 2016, 11, e0167984. | 2.5 | 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. | 3.3 | 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. | 1.7 | 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. | 3.1 | 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. | 6.5 | 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. | 2.8 | 9 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Family-Based Benchmarking of Copy Number Variation Detection Software. PLoS ONE, 2015, 10, e0133465. | 2.5 | 9 |
| 56 | The role of linkage disequilibrium in case-only studies of geneâ€“environment interactions. Human Genetics, 2015, 134, 89-96. | 3.8 | 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. | 3.4 | 30 |
| 58 | Allowing for population stratification in case-only studies of geneâ€“environment interaction, using genomic control. Human Genetics, 2015, 134, 1117-1125. | 3.8 | 2 |
| 59 | No shortcut solution to the problem of Y-STR match probability calculation. Forensic Science International: Genetics, 2015, 15, 69-75. | 3.1 | 23 |
| 60 | Mutations Causing Complex Disease May under Certain Circumstances Be Protective in an Epidemiological Sense. PLoS ONE, 2015, 10, e0132150. | 2.5 | 4 |
| 61 | A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. European Heart Journal, 2014, 35, 1069-1077. | 2.2 | 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. | 2.8 | 31 |
| 63 | Molecular genetic epidemiology of human diseases: from patterns to predictions. Human Genetics, 2014, 133, 425-430. | 3.8 | 10 |
| 64 | Causality of incest: a reply to ten Kate. International Journal of Legal Medicine, 2014, 128, 747-747. | 2.2 | 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. | 2.9 | 50 |
| 66 | A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23. | 3.1 | 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. | 2.8 | 6 |
| 69 | Recurrence of gallstones after cholecystectomy is associated with ABCG5/8 genotype. Journal of Gastroenterology, 2013, 48, 391-396. | 5.1 | 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. | 16.2 | 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. | 3.8 | 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. | 2.8 | 64 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347. | 1.3 | 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. | 3.1 | 27 |
| 75 | Decision-making in familial database searching: KI alone or not alone?. Forensic Science International: Genetics, 2013, 7, 52-54. | 3.1 | 24 |
| 76 | Genome-wide investigation of geneâ€“environment interactions in colorectal cancer. Human Genetics, 2013, 132, 219-231. | 3.8 | 38 |
| 77 | Estimating trace-suspect match probabilities for singleton Y-STR haplotypes using coalescent theory. Forensic Science International: Genetics, 2013, 7, 264-271. | 3.1 | 35 |
| 78 | Genetic investigation of FOXO3A requires special attention due to sequence homology with FOXO3B. European Journal of Human Genetics, 2013, 21, 240-242. | 2.8 | 18 |
| 79 | Continent-Wide Decoupling of Y-Chromosomal Genetic Variation from Language and Geography in Native South Americans. PLoS Genetics, 2013, 9, e1003460. | 3.5 | 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. | 1.3 | 3 |
| 81 | Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at theABCG5/8lithogenic locus. Hepatology, 2013, 57, 2407-2417. | 7.3 | 74 |
| 82 | Diagnosing Fatty Liver Disease: A Comparative Evaluation of Metabolic Markers, Phenotypes, Genotypes and Established Biomarkers. PLoS ONE, 2013, 8, e76813. | 2.5 | 8 |
| 83 | Copy number variation in patients with cervical artery dissection. European Journal of Human Genetics, 2012, 20, 1295-1299. | 2.8 | 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. | 3.1 | 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. | 3.1 | 14 |
| 86 | Genome-wide search for novel human uORFs and N-terminal protein extensions using ribosomal footprinting. Genome Research, 2012, 22, 2208-2218. | 5.5 | 198 |
| 87 | SFRS10â€”A Splicing Factor Gene Reduced in Human Obesity?. Cell Metabolism, 2012, 15, 265-266. | 16.2 | 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. | 2.9 | 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. | 1.4 | 12 |
| 90 | Pipeline for Large-Scale Microdroplet Bisulfite PCR-Based Sequencing Allows the Tracking of Hepitype Evolution in Tumors. PLoS ONE, 2011, 6, e21332. | 2.5 | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 91 | Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435. | 21.4 | 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. | 2.8 | 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. | 4.6 | 184 |
| 94 | Technology-specific error signatures in the 1000 Genomes Project data. Human Genetics, 2011, 130, 505-516. | 3.8 | 37 |
| 95 | Biobanking and international interoperability: samples. Human Genetics, 2011, 130, 369-376. | 3.8 | 34 |
| 96 | Rauchen und Lungenkrebs. Medizinische Genetik, 2011, 23, 400-406. | 0.2 | 1 |
| 97 | Genetic variation in the PNPLA3 gene is associated with alcoholic liver injury in caucasians. Hepatology, 2011, 53, 86-95. | 7.3 | 252 |
| 98 | Statistical inference of allelic imbalance from transcriptome data. Human Mutation, 2011, 32, 98-106. | 2.5 | 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. | 2.5 | 32 |
| 100 | Empirical Evaluation Reveals Best Fit of a Logistic Mutation Model for Human Y-Chromosomal Microsatellites. Genetics, 2011, 189, 1403-1411. | 2.9 | 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. | 2.9 | 47 |
| 102 | Association of TLR7 Variants with AIDS-Like Disease and AIDS Vaccine Efficacy in Rhesus Macaques. PLoS ONE, 2011, 6, e25474. | 2.5 | 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. | 2.2 | 8 |
| 104 | Potentials and limits of pairwise kinship analysis using autosomal short tandem repeat loci. International Journal of Legal Medicine, 2010, 124, 205-215. | 2.2 | 48 |
| 105 | Heritability of chronic venous disease. Human Genetics, 2010, 127, 669-674. | 3.8 | 67 |
| 106 | How obedience of marriage rules may counteract genetic drift. Journal of Community Genetics, 2010, 1, 23-28. | 1.2 | 5 |
| 107 | Biobanken. Medizinische Genetik, 2010, 22, 229-234. | 0.2 | 1 |
| 108 | Genes, mutations, and human inherited disease at the dawn of the age of personalized genomics. Human Mutation, 2010, 31, 631-655. | 2.5 | 161 |

| # | Article | IF | Citations |
|---|---|---|---|
| 109 | Triangulation of the human, chimpanzee, and Neanderthal genome sequences identifies potentially compensated mutations. Human Mutation, 2010, 31, 1286-1293. | 2.5 | 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. | 1.7 | 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. | 2.8 | 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. | 21.4 | 379 |
| 115 | Genome-wide association study for ulcerative colitis identifies risk loci at 7q22 and 22q13 (IL17REL). Nature Genetics, 2010, 42, 292-294. | 21.4 | 177 |
| 116 | Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. Human Molecular Genetics, 2010, 19, 2927-2935. | 2.9 | 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. | 2.8 | 57 |
| 118 | Loci From a Genome-Wide Analysis of Bilirubin Levels Are Associated With Gallstone Risk and Composition. Gastroenterology, 2010, 139, 1942-1951.e2. | 1.3 | 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. | 2.5 | 279 |
| 121 | A functional EXO1 promoter variant is associated with prolonged life expectancy in centenarians. Mechanisms of Ageing and Development, 2009, 130, 691-699. | 4.6 | 43 |
| 122 | A gene conversion hotspot in the human growth hormone (GH1) gene promoter. Human Mutation, 2009, 30, 239-247. | 2.5 | 13 |
| 123 | Systematic evaluation of the effect of common SNPs on pre-mRNA splicing. Human Mutation, 2009, 30, 625-632. | 2.5 | 28 |
| 124 | Age-related macular degeneration and functional promoter and coding variants of the apolipoprotein E gene. Human Mutation, 2009, 30, 1048-1053. | 2.5 | 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. | 5.1 | 44 |
| 126 | A comprehensive evaluation of SNP genotype imputation. Human Genetics, 2009, 125, 163-171. | 3.8 | 139 |

| # | Article | IF | Citations |
|---|---|---|---|
| 127 | Investigation of innate immunity genes CARD4, CARD8 and CARD15 as germline susceptibility factors for colorectal cancer. BMC Gastroenterology, 2009, 9, 79. | 2.0 | 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. | 2.8 | 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. | 6.2 | 41 |
| 130 | Association of HTRA1 and ARMS2 gene variation with drusen formation in rhesus macaques. Experimental Eye Research, 2009, 88, 479-482. | 2.6 | 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. | 2.9 | 76 |
| 132 | EinfÃ¼hrung â€žPopulationsgenetikâ€œ. Medizinische Genetik, 2008, 20, 273-275. | 0.2 | 0 |
| 133 | Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. Nature Genetics, 2008, 40, 1103-1106. | 21.4 | 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. | 6.2 | 120 |
| 135 | An Illicit Love Affair During the Third Reich: Who is My Grandfather?. Journal of Forensic Sciences, 2008, 53, 377-379. | 1.6 | 2 |
| 136 | Hypotheses in genome-wide association scans. European Journal of Human Genetics, 2008, 16, 1174-1175. | 2.8 | 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. | 21.4 | 333 |
| 138 | Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. Nature Genetics, 2008, 40, 1319-1323. | 21.4 | 534 |
| 139 | Increased heritability of gallstone disease in early onset cases. Liver International, 2008, 28, 895-897. | 3.9 | 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. | 3.9 | 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. | 1.3 | 85 |
| 143 | Plastin 3 Is a Protective Modifier of Autosomal Recessive Spinal Muscular Atrophy. Science, 2008, 320, 524-527. | 12.6 | 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. | 3.2 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 145 | Genetic Variants of the Copy Number Polymorphic β-Defensin Locus Are Associated with Sporadic Prostate Cancer. Tumor Biology, 2008, 29, 83-92. | 1.8 | 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. | 4.7 | 46 |
| 147 | An Illicit Love Affair During the Third Reich: Who is My Grandfather?. Journal of Forensic Sciences, 2008, 53, 080219072231020-???. | 1.6 | 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. | 2.9 | 107 |
| 149 | Comparative Assessment of the Association Information Captured by SNP Tagging. Human Heredity, 2007, 64, 27-34. | 0.8 | 3 |
| 150 | Efficacy assessment of SNP sets for genome-wide disease association studies. Nucleic Acids Research, 2007, 35, e113-e113. | 14.5 | 15 |
| 151 | Kinship testing with X-chromosomal markers: Mathematical and statistical issues. Forensic Science International: Genetics, 2007, 1, 111-114. | 3.1 | 49 |
| 152 | Relating two deep-rooted pedigrees from Central Germany by high-resolution Y-STR haplotyping. Forensic Science International: Genetics, 2007, 1, 125-128. | 3.1 | 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. | 21.4 | 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. | 1.1 | 27 |
| 156 | Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. PLoS ONE, 2007, 2, e691. | 2.5 | 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. | 2.5 | 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. | 2.5 | 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. | 5.1 | 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. | 21.4 | 1,712 |
| 162 | A legal framework for biobanking: the German experience. European Journal of Human Genetics, 2007, 15, 528-532. | 2.8 | 17 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | IMPG1 gene variation in rhesus macular drusen. Veterinary Ophthalmology, 2007, 10, 274-277. | 1.0 | 4 |
| 164 | Investigation of the Lith6 candidate genes APOBEC1 and PPARG in human gallstone disease. Liver International, 2007, 27, 910-919. | 3.9 | 6 |
| 165 | Biobanken im Spannungsfeld zwischen Forschung und Gesellschaft (Biobanks: Research Tools in the) Tj ETQq1 1 0.784314 rgBT /Ove | 0.9 | 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. | 0.9 | 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. | 1.0 | 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. | 1.3 | 12 |
| 169 | Predictors of gallstone composition in 1025 symptomatic gallstones from Northern Germany. BMC Gastroenterology, 2006, 6, 36. | 2.0 | 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. | 2.8 | 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. | 3.8 | 29 |
| 172 | Paternal kin bias in the agonistic interventions of adult female rhesus macaques (Macaca mulatta). Behavioral Ecology and Sociobiology, 2006, 61, 205-214. | 1.4 | 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. | 4.6 | 9 |
| 174 | GENOMIZER: an integrated analysis system for genome-wide association data. Human Mutation, 2006, 27, 583-588. | 2.5 | 24 |
| 175 | SNP-Based Analysis of Genetic Substructure in the German Population. Human Heredity, 2006, 62, 20-29. | 0.8 | 121 |
| 176 | Genetic Influence on Reproductive Behavior in Female Rhesus Macaques. Twin Research and Human Genetics, 2005, 8, 551-552. | 0.6 | 1 |
| 177 | Forensic interpretation of Y-chromosomal DNA mixtures. Forensic Science International, 2005, 152, 209-213. | 2.2 | 25 |
| 178 | Sarcoidosis is associated with a truncating splice site mutation in BTNL2. Nature Genetics, 2005, 37, 357-364. | 21.4 | 451 |
| 179 | Genetics of Crohn disease, an archetypal inflammatory barrier disease. Nature Reviews Genetics, 2005, 6, 376-388. | 16.3 | 290 |
| 180 | Microdeletions and microinsertions causing human genetic disease: common mechanisms of mutagenesis and the role of local DNA sequence complexity. Human Mutation, 2005, 26, 205-213. | 2.5 | 136 |

| # | Article | IF | Citations |
|---|---|---|---|
| 181 | Y-chromosomal STR haplotypes and their applications to forensic and population studies in east Asia. International Journal of Legal Medicine, 2005, 119, 195-201. | 2.2 | 60 |
| 182 | Haplotyping of STR cluster DXS6801â€“DXS6809â€“DXS6789 on Xq21 provides a powerful tool for kinship testing. International Journal of Legal Medicine, 2005, 119, 363-369. | 2.2 | 94 |
| 183 | Signature of recent historical events in the European Y-chromosomal STR haplotype distribution. Human Genetics, 2005, 116, 279-291. | 3.8 | 168 |
| 184 | Male Reproductive Timing in Rhesus Macaques Is Influenced by the 5HTTLPR Promoter Polymorphism of the Serotonin Transporter Gene1. Biology of Reproduction, 2005, 72, 1109-1113. | 2.7 | 33 |
| 185 | Mapping of a macular drusen susceptibility locus in rhesus macaques to the homologue of human chromosome 6q14-15. Experimental Eye Research, 2005, 81, 401-406. | 2.6 | 6 |
| 186 | No association between microsomal triglyceride transfer protein (MTP) haplotype and longevity in humans. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7906-7909. | 7.1 | 89 |
| 187 | A longitudinal analysis of reproductive skew in male rhesus macaques. Proceedings of the Royal Society B: Biological Sciences, 2004, 271, 819-826. | 2.6 | 169 |
| 188 | Patterns of linkage disequilibrium in the MHC region on human chromosome 6p. Human Genetics, 2004, 114, 377-385. | 3.8 | 92 |
| 189 | Gross rearrangement breakpoint database (GRaBD?). Human Mutation, 2004, 23, 219-221. | 2.5 | 24 |
| 190 | Three different pathological lesions in the NF1 gene originating de novo in a family with neurofibromatosis type 1. Human Genetics, 2003, 112, 12-17. | 3.8 | 24 |
| 191 | A longitudinal study of age-specific reproductive output and body condition among male rhesus macaques, Macaca mulatta. Die Naturwissenschaften, 2003, 90, 309-312. | 1.6 | 88 |
| 192 | Association of inflammatory bowel disease with indicators for childhood antigen and infection exposure. International Journal of Colorectal Disease, 2003, 18, 413-417. | 2.2 | 50 |
| 193 | Bimodal allele frequency distribution at Y-STR loci DYS392 and DYS438: no evidence for a deviation from the stepwise mutation model. International Journal of Legal Medicine, 2003, 117, 287-290. | 2.2 | 6 |
| 194 | Entropy-based SNP selection for genetic association studies. Human Genetics, 2003, 114, 36-43. | 3.8 | 74 |
| 195 | Meta-analysis of indels causing human genetic disease: mechanisms of mutagenesis and the role of local DNA sequence complexity. Human Mutation, 2003, 21, 28-44. | 2.5 | 112 |
| 196 | Human growth hormone 1 (GH1) gene expression: Complex haplotype-dependent influence of polymorphic variation in the proximal promoter and locus control region. Human Mutation, 2003, 21, 408-423. | 2.5 | 99 |
| 197 | Novel mutations of the growth hormone 1 (GH1) gene disclosed by modulation of the clinical selection criteria for individuals with short stature. Human Mutation, 2003, 21, 424-440. | 2.5 | 106 |
| 198 | Human Gene Mutation Database (HGMD<sup>Â®</sup>): 2003 update. Human Mutation, 2003, 21, 577-581. | 2.5 | 1,571 |

| # | Article | IF | Citations |
|---|---|---|---|
| 199 | Translocation and gross deletion breakpoints in human inherited disease and cancer II: Potential involvement of repetitive sequence elements in secondary structure formation between DNA ends. Human Mutation, 2003, 22, 245-251. | 2.5 | 98 |
| 200 | Translocation and gross deletion breakpoints in human inherited disease and cancer I: Nucleotide composition and recombination-associated motifs. Human Mutation, 2003, 22, 229-244. | 2.5 | 214 |
| 201 | Asian online Y-STR Haplotype Reference Database. Legal Medicine, 2003, 5, S160-S163. | 1.3 | 42 |
| 202 | Haplotype structure and association to Crohn's disease of CARD15 mutations in two ethnically divergent populations. European Journal of Human Genetics, 2003, 11, 6-16. | 2.8 | 216 |
| 203 | Haplotype structure analysis in the HLA region and implications for association mapping in inflammatory bowel disease. Gastroenterology, 2003, 124, A370. | 1.3 | 0 |
| 204 | Evidence for a NOD2-independent susceptibility locus for inflammatory bowel disease on chromosome 16p. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 321-326. | 7.1 | 106 |
| 205 | Affiliation and aggression among adult female rhesus macaques: a genetic analysis of paternal cohorts. Behaviour, 2002, 139, 371-391. | 0.8 | 64 |
| 206 | THE EVOLUTION OF THE VERTEBRATE Î²-GLOBIN GENE PROMOTER. Evolution; International Journal of Organic Evolution, 2002, 56, 224. | 2.3 | 2 |
| 207 | MHC Class I Alleles Influence Set-Point Viral Load and Survival Time in Simian Immunodeficiency Virus-Infected Rhesus Monkeys. Journal of Immunology, 2002, 169, 3438-3446. | 0.8 | 142 |
| 208 | Association of NOD2 (CARD 15) genotype with clinical course of Crohn's disease: a cohort study. Lancet, The, 2002, 359, 1661-1665. | 13.7 | 397 |
| 209 | Genotypeâ€“phenotype correlations in X-linked myotubular myopathy. Neuromuscular Disorders, 2002, 12, 939-946. | 0.6 | 122 |
| 210 | Schizophrenia and functional polymorphisms in the MAOA and COMT genes: No evidence for association or epistasis. American Journal of Medical Genetics Part A, 2002, 114, 491-496. | 2.4 | 71 |
| 211 | Multiple sirehood in free-ranging twin rhesus macaques (Macaca mulatta). American Journal of Primatology, 2002, 57, 31-34. | 1.7 | 27 |
| 212 | Assessing the relative importance of the biophysical properties of amino acid substitutions associated with human genetic disease. Human Mutation, 2002, 20, 98-109. | 2.5 | 39 |
| 213 | A major marker for normal tension glaucoma: association with polymorphisms in the OPA1 gene. Human Genetics, 2002, 110, 52-56. | 3.8 | 123 |
| 214 | Proposed guidelines for papers describing DNA polymorphism-disease associations. Human Genetics, 2002, 110, 207-208. | 3.8 | 114 |
| 215 | THE EVOLUTION OF THE VERTEBRATE ?-GLOBIN GENE PROMOTER. Evolution; International Journal of Organic Evolution, 2002, 56, 224-232. | 2.3 | 7 |
| 216 | An Extensive Analysis of Y-Chromosomal Microsatellite Haplotypes in Globally Dispersed Human Populations. American Journal of Human Genetics, 2001, 68, 990-1018. | 6.2 | 186 |

| # | Article | IF | Citations |
|---|---|---|---|
| 217 | Estimating the Efficacy and Efficiency of Cascade Genetic Screening. American Journal of Human Genetics, 2001, 69, 361-370. | 6.2 | 62 |
| 218 | Association between insertion mutation in NOD2 gene and Crohn's disease in German and British populations. Lancet, The, 2001, 357, 1925-1928. | 13.7 | 1,071 |
| 219 | Correcting for multiple testing in genetic association studies: the legend lives on. Human Genetics, 2001, 109, 566-567. | 3.8 | 10 |
| 220 | ASP â€“ a simulation-based power calculator for genetic linkage studies of qualitative traits, using sib-pairs. Human Genetics, 2001, 109, 675-677. | 3.8 | 9 |
| 221 | The Frequency of Inherited Disorders Database. Human Genetics, 2001, 108, 72-74. | 3.8 | 6 |
| 222 | Human type I hair keratin pseudogene ? hHaA has functional orthologs in the chimpanzee and gorilla: evidence for recent inactivation of the human gene after the Pan-Homo divergence. Human Genetics, 2001, 108, 37-42. | 3.8 | 87 |
| 223 | Increased reproductive success of MHC class II heterozygous males among free-ranging rhesus macaques. Human Genetics, 2001, 108, 249-254. | 3.8 | 79 |
| 224 | Forensic evaluation of Y-STR haplotype matches: a comment. Forensic Science International, 2001, 118, 114-115. | 2.2 | 33 |
| 225 | Population genetics of Y-chromosomal microsatellites in Baltic males. Forensic Science International, 2001, 118, 153-157. | 2.2 | 31 |
| 226 | The Frequency of Inherited Disorders Database: Prevalence of Huntington Disease. Public Health Genomics, 2001, 4, 148-157. | 1.0 | 13 |
| 227 | Human Gene Mutation Database?A biomedical information and research resource. Human Mutation, 2000, 15, 45-51. | 2.5 | 241 |
| 228 | Location of mutations within the PKD2 gene influences clinical outcome. Kidney International, 2000, 57, 1444-1451. | 5.2 | 70 |
| 229 | Natal dispersal in rhesus macaques is related to serotonin transporter gene promoter variation. Behavior Genetics, 2000, 30, 295-301. | 2.1 | 91 |
| 230 | Genetic association studies of bronchial asthma â€“ a need for Bonferroni correction?. Human Genetics, 2000, 107, 197-197. | 3.8 | 49 |
| 231 | Changes in primary DNA sequence complexity influence the phenotypic consequences of mutations in human gene regulatory regions. Human Genetics, 2000, 107, 362-365. | 3.8 | 16 |
| 232 | Homozygosity for a Conserved Mhc Class II DQ-DRB Haplotype Is Associated with Rapid Disease Progression in Simian Immunodeficiency Virusâ€"Infected Macaques: Results from a Prospective Study. Journal of Infectious Diseases, 2000, 182, 716-724. | 4.0 | 49 |
| 233 | Promoter shuffling has occurred during the evolution of the vertebrate growth hormone gene. Gene, 2000, 254, 9-18. | 2.2 | 19 |
| 234 | Characteristics and Frequency of Germline Mutations at Microsatellite Loci from the Human Y Chromosome, as Revealed by Direct Observation in Father/Son Pairs. American Journal of Human Genetics, 2000, 66, 1580-1588. | 6.2 | 334 |

| # | Article | IF | Citations |
|---|---|---|---|
| 235 | Disease-causing mutations in the human genome. European Journal of Pediatrics, 2000, 159, S173-S178. | 2.7 | 64 |
| 236 | Informativity assessment for biallelic single nucleotide polymorphisms. Electrophoresis, 1999, 20, 1676-1681. | 2.4 | 91 |
| 237 | DNA sequence polymorphisms in genes involved in the regulation of dopamine and serotonin metabolism in rhesus macaques. Electrophoresis, 1999, 20, 1771-1777. | 2.4 | 11 |
| 238 | Evolution of the proximal promoter region of the mammalian growth hormone gene. Gene, 1999, 237, 143-151. | 2.2 | 34 |
| 239 | Informativity assessment for biallelic single nucleotide polymorphisms. Electrophoresis, 1999, 20, 1676-1681. | 2.4 | 1 |
| 240 | Statistical Inference from DNA Evidence. , 1999, , 229-244. | | 5 |
| 241 | Variation of site-specific methylation patterns in the factor VIII ( F8C ) gene in human sperm DNA. Human Genetics, 1998, 103, 228-233. | 3.8 | 7 |
| 242 | Neighboring-Nucleotide Effects on the Rates of Germ-Line Single-Base-Pair Substitution in Human Genes. American Journal of Human Genetics, 1998, 63, 474-488. | 6.2 | 291 |
| 243 | p53 mutations, benzo[a]pyrene and lung cancer. Mutagenesis, 1998, 13, 319-320. | 2.6 | 26 |
| 244 | De Novo Rearrangements Found in 2% of Index Patients with Spinal Muscular Atrophy: Mutational Mechanisms, Parental Origin, Mutation Rate, and Implications for Genetic Counseling. American Journal of Human Genetics, 1997, 61, 1102-1111. | 6.2 | 155 |
| 245 | Meiotic Microdeletion Breakpoints in the BRCA1 Gene Are Significantly Associated with Symmetric DNA-Sequence Elements. American Journal of Human Genetics, 1997, 61, 1454-1456. | 6.2 | 16 |
| 246 | Possible association of the allele status of the CS.7/ Hha I polymorphism 5â€² of the CFTR gene with postnatal female survival. Human Genetics, 1997, 99, 565-572. | 3.8 | 15 |
| 247 | Characterization and significance of nine novel mutations in exon 16 of the neurofibromatosis type 1 (NF1) gene. Human Genetics, 1997, 99, 674-676. | 3.8 | 26 |
| 248 | A paternity case with apparently conflicting multilocus and single-locus DNA typing results. Electrophoresis, 1997, 18, 1598-1601. | 2.4 | 3 |
| 249 | Applications of microsatelliteâ€based Y chromosome haplotyping. Electrophoresis, 1997, 18, 1602-1607. | 2.4 | 63 |
| 250 | Human Gene Mutation Database. Human Genetics, 1996, 98, 629-629. | 3.8 | 46 |
| 251 | Single base-pair substitutions in pathology and evolution: Two sides to the same coin. Human Mutation, 1996, 8, 23-31. | 2.5 | 23 |
| 252 | Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations [published erratum appears in Hum Mol Genet 1997 May;6(5):828]. Human Molecular Genetics, 1996, 5, 1029-1033. | 2.9 | 173 |

| # | Article | IF | Citations |
|---|---|---|---|
| 253 | An informativity index for multilocus DNA fingerprints. Electrophoresis, 1995, 16, 16-21. | 2.4 | 16 |
| 254 | Somatic spectrum of cancer-associated single basepair substitutions in the TP53 gene is determined mainly by endogenous mechanisms of mutation and by selection. Human Mutation, 1995, 5, 48-57. | 2.5 | 56 |
| 255 | The mutational demography of protein C deficiency. Human Genetics, 1995, 96, 142-146. | 3.8 | 10 |
| 256 | A novel missense mutation (Thr176?Ile) at the putative hinge of the neo N-terminus of activated protein C. Human Genetics, 1995, 95, 447-50. | 3.8 | 2 |
| 257 | Core database. Nature, 1995, 374, 402-402. | 27.8 | 8 |
| 258 | Recurrent nasal polyps as a monosymptomatic form of cystic fibrosis associated with a novel in-frame deletion (591del18) in the CFTR gene. Human Molecular Genetics, 1995, 4, 1463-1464. | 2.9 | 21 |
| 259 | Determinants of the factor IX mutational spectrum in haemophilia B: an analysis of missense mutations using a multi-domain molecular model of the activated protein. Human Genetics, 1994, 94, 594-608. | 3.8 | 20 |
| 260 | A 32-bp deletion (2991del32) in the cystic fibrosis gene associated with CFTR mRNA reduction. Human Mutation, 1994, 4, 65-70. | 2.5 | 10 |
| 261 | Multilocus DNA fingerprinting: The independence problem in quantitative paternity testing. Electrophoresis, 1994, 15, 165-169. | 2.4 | 4 |
| 262 | 2. A Multilocus DNA Fingerprint with Built-in Security Devices. Medicine, Science and the Law, 1994, 34, 256-262. | 1.0 | 1 |
| 263 | Paternity testing with oligonucleotide multilocus probe (CAC)5/(GTG)5: A multicenter study. Forensic Science International, 1993, 59, 101-117. | 2.2 | 12 |
| 264 | Power and limits of DNA-profiling in primate populations: Paternity assessment in rhesus macaques from Cayo Santiago. Primates, 1993, 34, 395-402. | 1.1 | 13 |
| 265 | The mutational spectrum of single base-pair substitutions in mRNA splice junctions of human genes: Causes and consequences. Human Genetics, 1992, 90, 41-54. | 3.8 | 1,182 |
| 266 | Intra- and extragenic marker haplotypes of CFTR mutations in cystic fibrosis families. Human Genetics, 1992, 88, 417-425. | 3.8 | 73 |
| 267 | A genetic factor model for the statistical analysis of multilocus DNA fingerprints. Electrophoresis, 1992, 13, 10-17. | 2.4 | 30 |
| 268 | The Decision Theory of Paternity Disputes: Optimization Considerations Applied to Multilocus DNA Fingerprinting. Journal of Forensic Sciences, 1992, 37, 1525-1533. | 1.6 | 8 |
| 269 | Genetic influences in the formation of nasal polyps. Lancet, The, 1991, 337, 974. | 13.7 | 35 |
| 270 | Genetic analysis of susceptibility to diabetes mellitus in F2-hybrids between diabetes-prone BB and various MHC-recombinant congenic rat strains. Journal of Autoimmunity, 1991, 4, 543-551. | 6.5 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 271 | Gene deletions causing human genetic disease: mechanisms of mutagenesis and the role of the local DNA sequence environment. Human Genetics, 1991, 86, 425-41. | 3.8 | 438 |
| 272 | Mechanisms of insertional mutagenesis in human genes causing genetic disease. Human Genetics, 1991, 87, 409-15. | 3.8 | 119 |
| 273 | Discrimination between recurrent mutation and identity by descent: application to point mutations in exon 11 of the cystic fibrosis (CFTR) gene. Human Genetics, 1991, 87, 457-61. | 3.8 | 25 |
| 274 | DNA-fingerprinting: a short note on mutation rates. Human Genetics, 1991, 87, 632-3. | 3.8 | 11 |
| 275 | Genotype-Phenotype Correlations in Cystic Fibrosis Patients. Advances in Experimental Medicine and Biology, 1991, 290, 97-103. | 1.6 | 5 |
| 276 | Frequency of the Î”F508 mutation and flanking marker haplotypes at the CF locus from 167 Czech families. Human Genetics, 1990, 85, 417-418. | 3.8 | 9 |
| 277 | Distribution patterns of the Î”F508 mutation in the CFTR gene on CF-linked marker haplotypes in the German population. Human Genetics, 1990, 85, 421-422. | 3.8 | 17 |
| 278 | The mutational spectrum of single base-pair substitutions causing human genetic disease: patterns and predictions. Human Genetics, 1990, 85, 55-74. | 3.8 | 358 |
| 279 | The effect of replication errors on the mismatch analysis of PCR-amplified DNA. Nucleic Acids Research, 1990, 18, 973-978. | 14.5 | 47 |
| 280 | Genotype analysis of cystic fibrosis patients in relation to pancreatic sufficiency. Lancet, The, 1990, 335, 738-739. | 13.7 | 28 |
| 281 | Polymerase chain reaction: replication errors and reliability of gene diagnosis. Nucleic Acids Research, 1989, 17, 2197-2201. | 14.5 | 107 |
| 282 | A search for restriction fragment length polymorphism on the human Y chromosome. Human Genetics, 1989, 84, 86-88. | 3.8 | 67 |
| 283 | Cytosine methylation and the fate of CpG dinucleotides in vertebrate genomes. Human Genetics, 1989, 83, 181-188. | 3.8 | 303 |
| 284 | Human gene cloning: the storm before the lull?. Nature, 1986, 322, 119-119. | 27.8 | 8 |
| 285 | On upcrossing inequalities for subadditive superstationary processes. Ergodic Theory and Dynamical Systems, 1985, 5, 409-416. | 0.6 | 1 |
| 286 | Carrier detection probabilities for autosomal recessive variants in unrelated and consanguineous couples â€" an evaluation of the 86 genes of the ACMG â€˜Tier 3â€™ panel. Journal of Community Genetics, 0, , . | 1.2 | 0 |