Michael Nothnagel

List of Publications by Year in Descending Order

126 papers	6,824 citations	41 h-index	81 g-index
134 ext. papers	7,962 ext. citations	8.1 avg, IF	4.83 L-index

#	Paper	IF	Citations
126	Exome sequencing utility in defining the genetic landscape of hearing loss and novel-gene discovery in Iran. *Clinical Genetics*, **2021**, 100, 59-78	4	1
125	Analysis of single nucleotide polymorphisms in chronic beryllium disease. *Respiratory Research*, **2021**, 22, 107	7.3	
124	What Makes a Hot-Spring Habitat Hot for the Hot-Spring Snake: Distributional Data and Niche Modelling for the Genus Thermophis (Serpentes, Colubridae). *Diversity*, **2021**, 13, 325	2.5	
123	Evaluation of supervised machine-learning methods for predicting appearance traits from DNA. *Forensic Science International: Genetics*, **2021**, 53, 102507	4.3	3
122	The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. *Forensic Science International: Genetics*, **2021**, 50, 102395	4.3	1
121	A Y-chromosomal survey of Ecuador's multi-ethnic population reveals new insights into the tri-partite population structure and supports an early Holocene age of the rare Native American founder lineage C3-MPB373. *Forensic Science International: Genetics*, **2021**, 51, 102427	4.3	0
120	Testing the impact of trait prevalence priors in Bayesian-based genetic prediction modeling of human appearance traits. *Forensic Science International: Genetics*, **2021**, 50, 102412	4.3	0
119	Distinct gene-set burden patterns underlie common generalized and focal epilepsies. *EBioMedicine*, **2021**, 72, 103588	8.8	0
118	Expanding the genetic architecture of nicotine dependence and its shared genetics with multiple traits. *Nature Communications*, **2020**, 11, 5562	17.4	25
117	The exhaustive genomic scan approach, with an application to rare-variant association analysis. *European Journal of Human Genetics*, **2020**, 28, 1283-1291	5.3	0
116	Towards a fine-scale picture of European genetic diversity. *European Journal of Human Genetics*, **2020**, 28, 851-852	5.3	
115	Special issue on 'Genetic epidemiology of complex diseases: impact of population history and modelling assumptions'. *Human Genetics*, **2020**, 139, 1-3	6.3	0
114	Distinct genetic variation and heterogeneity of the Iranian population. *PLoS Genetics*, **2019**, 15, e1008385		18
113	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,	2.8	11
112	Heterozygous carriage of the alpha1-antitrypsin Pi*Z variant increases the risk to develop liver cirrhosis. *Gut*, **2019**, 68, 1099-1107	19.2	62
111	A Rare Variant Nonparametric Linkage Method for Nuclear and Extended Pedigrees with Application to Late-Onset Alzheimer Disease via WGS Data. *American Journal of Human Genetics*, **2019**, 105, 822-835	11	8
110	True colors: A literature review on the spatial distribution of eye and hair pigmentation. *Forensic Science International: Genetics*, **2019**, 39, 109-118	4.3	15

109	Unsupported claim of significant discrimination between monozygotic twins from multiple pairs based on three age-related DNA methylation markers. *Forensic Science International: Genetics*, **2019**, 39, e1-e2	4.3	1
108	Pathway-induced allelic spectra of diseases in the presence of strong genetic effects. *Human Genetics*, **2018**, 137, 215-230	6.3	1
107	Exome-wide analysis of mutational burden in patients with typical and atypical Rolandic epilepsy. *European Journal of Human Genetics*, **2018**, 26, 258-264	5.3	12
106	Clinical and experimental evidence suggest a link between KIF7 and C5orf42-related ciliopathies through Sonic Hedgehog signaling. *European Journal of Human Genetics*, **2018**, 26, 197-209	5.3	13
105	Ancient DNA study reveals HLA susceptibility locus for leprosy in medieval Europeans. *Nature Communications*, **2018**, 9, 1569	17.4	41
104	Rare coding variants in genes encoding GABA receptors in genetic generalised epilepsies: an exome-based case-control study. *Lancet Neurology, The*, **2018**, 17, 699-708	24.1	44
103	Performance of in silico prediction tools for the classification of rare BRCA1/2 missense variants in clinical diagnostics. *BMC Medical Genomics*, **2018**, 11, 35	3.7	44
102	Guideline-based and bioinformatic reassessment of lesion-associated gene and variant pathogenicity in focal human epilepsies. *Epilepsia*, **2018**, 59, 2145-2152	6.4	6
101	Evaluation of potential effects of Plastin 3 overexpression and low-dose SMN-antisense oligonucleotides on putative biomarkers in spinal muscular atrophy mice. *PLoS ONE*, **2018**, 13, e0203398	3.7	8
100	Securing the use of existing sample collections for future human genetic research. *European Journal of Human Genetics*, **2017**, 25, 522-529	5.3	
99	Revisiting the male genetic landscape of China: a multi-center study of almost 38,000 Y-STR haplotypes. *Human Genetics*, **2017**, 136, 485-497	6.3	51
98	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. *Nature Communications*, **2017**, 8, 14694	17.4	36
97	Serum metabolomic profiling highlights pathways associated with liver fat content in a general population sample. *European Journal of Clinical Nutrition*, **2017**, 71, 995-1001	5.2	13
96	A Genome-wide Association Study of Dupuytren Disease Reveals 17 Additional Variants Implicated in Fibrosis. *American Journal of Human Genetics*, **2017**, 101, 417-427	11	35
95	Identification and characterization of two functional variants in the human longevity gene FOXO3. *Nature Communications*, **2017**, 8, 2063	17.4	46
94	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	4.3	13
93	Increased Probability of Co-Occurrence of Two Rare Diseases in Consanguineous Families and Resolution of a Complex Phenotype by Next Generation Sequencing. *PLoS ONE*, **2016**, 11, e0146040	3.7	22
92	Evaluation of Presumably Disease Causing SCN1A Variants in a Cohort of Common Epilepsy Syndromes. *PLoS ONE*, **2016**, 11, e0150426	3.7	10

91	A Critical Evaluation of Analytic Aspects of Gene Expression Profiling in Lymphoid Leukemias with Broad Applications to Cancer Genomics. *AIMS Medical Science*, **2016**, 3, 248-271	0.4	1
90	Meta-Analysis of Genome-Wide Association Studies and Network Analysis-Based Integration with Gene Expression Data Identify New Suggestive Loci and Unravel a Wnt-Centric Network Associated with Dupuytren's Disease. *PLoS ONE*, **2016**, 11, e0158101	3.7	16
89	The Slavic NBN Founder Mutation: A Role for Reproductive Fitness?. *PLoS ONE*, **2016**, 11, e0167984	3.7	10
88	Benign infantile seizures and paroxysmal dyskinesia caused by an SCN8A mutation. *Annals of Neurology*, **2016**, 79, 428-36	9.4	124
87	De novo loss- or gain-of-function mutations in KCNA2 cause epileptic encephalopathy. *Nature Genetics*, **2015**, 47, 393-399	36.3	162
86	A genome-wide association study confirms PNPLA3 and identifies TM6SF2 and MBOAT7 as risk loci for alcohol-related cirrhosis. *Nature Genetics*, **2015**, 47, 1443-8	36.3	303
85	Rare variants in γaminobutyric acid type A receptor genes in rolandic epilepsy and related syndromes. *Annals of Neurology*, **2015**, 77, 972-86	9.4	40
84	Family-Based Benchmarking of Copy Number Variation Detection Software. *PLoS ONE*, **2015**, 10, e0133465	3.7	7
83	CoNCoS: copy number estimation in cancer with controlled support. *Journal of Bioinformatics and Computational Biology*, **2015**, 13, 1550027	1	1
82	Shannon's equivocation for forensic Y-STR marker selection. *Forensic Science International: Genetics*, **2015**, 16, 216-225	4.3	14
81	Mutations Causing Complex Disease May under Certain Circumstances Be Protective in an Epidemiological Sense. *PLoS ONE*, **2015**, 10, e0132150	3.7	3
80	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, 3883-90	5.6	36
79	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. *Forensic Science International: Genetics*, **2014**, 12, 12-23	4.3	171
78	Effects of Pleistocene climatic fluctuations on the phylogeography, demography and population structure of a high-elevation snake species, Thermophisbaileyi, on the Tibetan Plateau. *Journal of Biogeography*, **2014**, 41, 2162-2172	4.1	11
77	Prognostic relevance of gastric cancer staging by endoscopic ultrasound. *Surgical Endoscopy and Other Interventional Techniques*, **2013**, 27, 1124-9	5.2	17
76	Association between variants of PRDM1 and NDP52 and Crohn's disease, based on exome sequencing and functional studies. *Gastroenterology*, **2013**, 145, 339-47	13.3	125
75	Mutations in GRIN2A cause idiopathic focal epilepsy with rolandic spikes. *Nature Genetics*, **2013**, 45, 1067-72	36.3	301
74	Genome-wide investigation of gene-environment interactions in colorectal cancer. *Human Genetics*, **2013**, 132, 219-31	6.3	32

73	Haplotypes of IL-12Rβ1 impact on the clinical phenotype of hidradenitis suppurativa. *Cytokine*, **2013**, 62, 297-301	4	20
72	Genome-wide association analysis reveals 12q13.3-q14.1 as new risk locus for sarcoidosis. *European Respiratory Journal*, **2013**, 41, 888-900	13.6	26
71	Continent-wide decoupling of Y-chromosomal genetic variation from language and geography in native South Americans. *PLoS Genetics*, **2013**, 9, e1003460	6	75
70	Validation of reported genetic risk factors for periodontitis in a large-scale replication study. *Journal of Clinical Periodontology*, **2013**, 40, 563-72	7.7	68
69	Genetic and functional identification of the likely causative variant for cholesterol gallstone disease at the ABCG5/8 lithogenic locus. *Hepatology*, **2013**, 57, 2407-17	11.2	61
68	Metabolic signature of electrosurgical liver dissection. *PLoS ONE*, **2013**, 8, e72022	3.7	2
67	Diagnosing fatty liver disease: a comparative evaluation of metabolic markers, phenotypes, genotypes and established biomarkers. *PLoS ONE*, **2013**, 8, e76813	3.7	8
66	A case-only study of gene-environment interaction between genetic susceptibility variants in NOD2 and cigarette smoking in Crohn's disease aetiology. *BMC Medical Genetics*, **2012**, 13, 14	2.1	17
65	Collaborative genetic mapping of 12 forensic short tandem repeat (STR) loci on the human X chromosome. *Forensic Science International: Genetics*, **2012**, 6, 778-84	4.3	49
64	Genome-wide search for novel human uORFs and N-terminal protein extensions using ribosomal footprinting. *Genome Research*, **2012**, 22, 2208-18	9.7	150
63	SFRS10--a splicing factor gene reduced in human obesity?. *Cell Metabolism*, **2012**, 15, 265-6; author reply 267-9	24.6	9
62	Association studies of the copy-number variable β-defensin cluster on 8p23.1 in adenocarcinoma and chronic pancreatitis. *BMC Research Notes*, **2012**, 5, 629	2.3	12
61	Combined analysis of genome-wide association studies for Crohn disease and psoriasis identifies seven shared susceptibility loci. *American Journal of Human Genetics*, **2012**, 90, 636-47	11	224
60	Polymorphisms in the glial glutamate transporter SLC1A2 are associated with essential tremor. *Neurology*, **2012**, 79, 243-8	6.5	94
59	The effect of FABP2 promoter haplotype on response to a diet with medium-chain triacylglycerols. *Genes and Nutrition*, **2012**, 7, 437-45	4.3	3
58	Common genetic risk variants of TLR2 are not associated with periodontitis in large European case-control populations. *Journal of Clinical Periodontology*, **2012**, 39, 315-22	7.7	8
57	Schizophrenia risk polymorphisms in the TCF4 gene interact with smoking in the modulation of auditory sensory gating. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 6271-6	11.5	45
56	A novel sarcoidosis risk locus for Europeans on chromosome 11q13.1. *American Journal of Respiratory and Critical Care Medicine*, **2012**, 186, 877-85	10.2	34

55	CDKN2BAS is associated with periodontitis in different European populations and is activated by bacterial infection. *Journal of Medical Genetics*, **2011**, 48, 38-47	5.8	57
54	Pipeline for large-scale microdroplet bisulfite PCR-based sequencing allows the tracking of hepitype evolution in tumors. *PLoS ONE*, **2011**, 6, e21332	3.7	8
53	GABA(A) receptor- and GABA transporter polymorphisms and risk for essential tremor. *European Journal of Neurology*, **2011**, 18, 1098-100	6	24
52	A genome-wide association study confirms APOE as the major gene influencing survival in long-lived individuals. *Mechanisms of Ageing and Development*, **2011**, 132, 324-30	5.6	162
51	Technology-specific error signatures in the 1000 Genomes Project data. *Human Genetics*, **2011**, 130, 505-16	4.9	36
50	Statistical inference of allelic imbalance from transcriptome data. *Human Mutation*, **2011**, 32, 98-106	4.7	18
49	A genome-wide association study reveals evidence of association with sarcoidosis at 6p12.1. *European Respiratory Journal*, **2011**, 38, 1127-35	13.6	40
48	Association of inflammatory bowel disease risk loci with sarcoidosis, and its acute and chronic subphenotypes. *European Respiratory Journal*, **2011**, 37, 610-6	13.6	40
47	Wnt signaling and Dupuytren's disease. *New England Journal of Medicine*, **2011**, 365, 307-17	59.2	153
46	Depletion of potential A2M risk haplotype for Alzheimer's disease in long-lived individuals. *European Journal of Human Genetics*, **2010**, 18, 59-61	5.3	8
45	A 3' UTR transition within DEFB1 is associated with chronic and aggressive periodontitis. *Genes and Immunity*, **2010**, 11, 45-54	4.4	56
44	Association of postprandial and fasting triglycerides with traits of the metabolic syndrome in the Metabolic Intervention Cohort Kiel. *European Journal of Endocrinology*, **2010**, 162, 719-27	6.5	11
43	Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. *Human Molecular Genetics*, **2010**, 19, 2927-35	5.6	99
42	A genome-wide association study identifies GLT6D1 as a susceptibility locus for periodontitis. *Human Molecular Genetics*, **2010**, 19, 553-62	5.6	150
41	A genome-wide linkage analysis in 181 German sarcoidosis families using clustered biallelic markers. *Chest*, **2010**, 138, 151-7	5.3	17
40	Genome-wide association analysis in primary sclerosing cholangitis. *Gastroenterology*, **2010**, 138, 1102-11	13.3	255
39	Loci from a genome-wide analysis of bilirubin levels are associated with gallstone risk and composition. *Gastroenterology*, **2010**, 139, 1942-1951.e2	13.3	74
38	COX-2 is associated with periodontitis in Europeans. *Journal of Dental Research*, **2010**, 89, 384-8	8.1	38

37	Potentials and limits of pairwise kinship analysis using autosomal short tandem repeat loci. *International Journal of Legal Medicine*, **2010**, 124, 205-15	3.1	41
36	LINGO1 is not associated with Parkinson's disease in German patients. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1173-8	3.5	6
35	LINGO1 polymorphisms are associated with essential tremor in Europeans. *Movement Disorders*, **2010**, 25, 717-23	7	44
34	Identification of a shared genetic susceptibility locus for coronary heart disease and periodontitis. *PLoS Genetics*, **2009**, 5, e1000378	6	162
33	NOD1 gene polymorphisms in relation to aggressive periodontitis. *Innate Immunity*, **2009**, 15, 225-32	2.7	4
32	Variation in genes of the epidermal differentiation complex in German atopic dermatitis patients. *International Journal of Immunogenetics*, **2009**, 36, 217-22	2.3	12
31	A comprehensive evaluation of SNP genotype imputation. *Human Genetics*, **2009**, 125, 163-71	6.3	123
30	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, 967-75	5.3	7
29	15q13.3 microdeletions increase risk of idiopathic generalized epilepsy. *Nature Genetics*, **2009**, 41, 160-2	36.3	454
28	X chromosomal variation is associated with slow progression to AIDS in HIV-1-infected women. *American Journal of Human Genetics*, **2009**, 85, 228-39	11	39
27	Current software for genotype imputation. *Human Genomics*, **2009**, 3, 371-80	6.8	18
26	Hypotheses in genome-wide association scans. *European Journal of Human Genetics*, **2008**, 16, 1174-5; author reply 1175	5.3	1
25	Sequence variants in IL10, ARPC2 and multiple other loci contribute to ulcerative colitis susceptibility. *Nature Genetics*, **2008**, 40, 1319-23	36.3	468
24	Correlation between genetic and geographic structure in Europe. *Current Biology*, **2008**, 18, 1241-8	6.3	382
23	Genome-wide association analysis in sarcoidosis and Crohn's disease unravels a common susceptibility locus on 10p12.2. *Gastroenterology*, **2008**, 135, 1207-15	13.3	66
22	s-ICAM-1 and s-VCAM-1 in healthy men are strongly associated with traits of the metabolic syndrome, becoming evident in the postprandial response to a lipid-rich meal. *Lipids in Health and Disease*, **2008**, 7, 32	4.4	25
21	Polymorphisms in the interleukin-1 (IL1) gene cluster are not associated with aggressive periodontitis in a large Caucasian population. *Genomics*, **2008**, 92, 309-15	4.3	40
20	Female-specific association of C-C chemokine receptor 5 gene polymorphisms with LEgren's syndrome. *Journal of Molecular Medicine*, **2008**, 86, 553-61	5.5	12

19	The Wegener's granulomatosis quantitative trait locus on chromosome 6p21.3 as characterised by tagSNP genotyping. *Annals of the Rheumatic Diseases*, **2008**, 67, 972-9	2.4	59
18	Postprandial plasma adiponectin decreases after glucose and high fat meal and is independently associated with postprandial triacylglycerols but not with -- 11388 promoter polymorphism. *British Journal of Nutrition*, **2008**, 99, 76-82	3.6	22
17	Genome-wide association study identifies ANXA11 as a new susceptibility locus for sarcoidosis. *Nature Genetics*, **2008**, 40, 1103-6	36.3	175
16	The association of fatty acid-binding protein 2 A54T polymorphism with postprandial lipemia depends on promoter variability. *Metabolism: Clinical and Experimental*, **2007**, 56, 723-31	12.7	22
15	Role of NOD2/CARD15 in coronary heart disease. *BMC Genetics*, **2007**, 8, 76	2.6	11
14	Association of toll-interacting protein gene polymorphisms with atopic dermatitis. *BMC Dermatology*, **2007**, 7, 3	2.1	30
13	Polymorphisms in NACHT-LRR (NLR) genes in atopic dermatitis. *Experimental Dermatology*, **2007**, 16, 692-8	4	94
12	Role of the toll-like receptor 4 polymorphism Asp299Gly in longevity and myocardial infarction in German men. *Mechanisms of Ageing and Development*, **2007**, 128, 409-11	5.6	28
11	Modellvorstellungen zur Genetik multifaktorieller Krankheiten. *Medizinische Genetik*, **2007**, 19, 295-299	0.5	
10	Comparative assessment of the association information captured by SNP tagging. *Human Heredity*, **2007**, 64, 27-34	1.1	3
9	Efficacy assessment of SNP sets for genome-wide disease association studies. *Nucleic Acids Research*, **2007**, 35, e113	20.1	10
8	The minor allele of the PPARgamma2 pro12Ala polymorphism is associated with lower postprandial TAG and insulin levels in non-obese healthy men. *British Journal of Nutrition*, **2007**, 97, 847-54	3.6	17
7	Association screen for atopic dermatitis candidate gene regions using microsatellite markers in pooled DNA samples. *International Journal of Immunogenetics*, **2006**, 33, 401-9	2.3	10
6	The effect of single-nucleotide polymorphism marker selection on patterns of haplotype blocks and haplotype frequency estimates. *American Journal of Human Genetics*, **2005**, 77, 988-98	11	51
5	Entropy as a measure for linkage disequilibrium over multilocus haplotype blocks. *Human Heredity*, **2002**, 54, 186-98	1.1	68
4	Power and sample size calculations for case-control genetic association tests when errors are present: application to single nucleotide polymorphisms. *Human Heredity*, **2002**, 54, 22-33	1.1	242
3	Statistical gene mapping of traits in humans--hypertension as a complex trait: is it amenable to genetic analysis?. *Seminars in Nephrology*, **2002**, 22, 105-14	4.8	2
2	Approaches to the genetics of cardiovascular disease through genetic field work. *Kidney International*, **1998**, 53, 1449-54	9.9	5

List of Publications

1	Expanding the Genetic Architecture of Nicotine Dependence and its Shared Genetics with Multiple Traits: Findings from the Nicotine Dependence GenOmics (iNDiGO) Consortium	3