# Per Hoffmann

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5541620/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 234 papers | 27,250 citations | 18482 62 h-index | 8396 147 g-index |
| 249 all docs | 249 docs citations | 249 times ranked | 36674 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Elucidation of the genetic causes of bicuspid aortic valve disease. Cardiovascular Research, 2023, 119, 857-866. | 3.8 | 11 |
| 2 | Effects of copy number variations on brain structure and risk for psychiatric illness: Largeâ€scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328. | 3.6 | 30 |
| 3 | Blood copper and risk of cardiometabolic diseases: a Mendelian randomization study. Human Molecular Genetics, 2022, 31, 783-791. | 2.9 | 12 |
| 4 | Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327. | 1.3 | 114 |
| 5 | Genome-wide Association Study of Postoperative Cognitive Dysfunction in Older Surgical Patients. Journal of Neurosurgical Anesthesiology, 2022, 34, 248-250. | 1.2 | 3 |
| 6 | Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. Molecular Psychiatry, 2022, 27, 1111-1119. | 7.9 | 24 |
| 7 | Epigenome-wide association study of alcohol use disorder in five brain regions. Neuropsychopharmacology, 2022, 47, 832-839. | 5.4 | 16 |
| 8 | Using polygenic scores and clinical data for bipolar disorder patient stratification and lithium response prediction: machine learning approach. British Journal of Psychiatry, 2022, 220, 219-228. | 2.8 | 11 |
| 9 | Dihydroceramide- and ceramide-profiling provides insights into human cardiometabolic disease etiology. Nature Communications, 2022, 13, 936. | 12.8 | 28 |
| 10 | Epigenome-Wide Analysis of DNA Methylation in Parkinsonâ€™s Disease Cortex. Life, 2022, 12, 502. | 2.4 | 14 |
| 11 | A genetic risk score of alleles related to MGUS interacts with socioeconomic position in a population-based cohort. Scientific Reports, 2022, 12, 4409. | 3.3 | 0 |
| 12 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508. | 27.8 | 929 |
| 13 | New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436. | 21.4 | 700 |
| 14 | Genome-wide meta-analysis of monoclonal gammopathy of undetermined significance (MGUS) identifies risk loci impacting IRF-6. Blood Cancer Journal, 2022, 12, 60. | 6.2 | 2 |
| 15 | Multi-omics signatures of alcohol use disorder in the dorsal and ventral striatum. Translational Psychiatry, 2022, 12, 190. | 4.8 | 11 |
| 16 | Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190. | 7.9 | 58 |
| 17 | Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. Molecular Psychiatry, 2021, 26, 3004-3017. | 7.9 | 56 |
| 18 | Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. Molecular Psychiatry, 2021, 26, 2457-2470. | 7.9 | 44 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Shared genetic risk between eating disorderâ€•and substanceâ€•useâ€•related phenotypes: Evidence from genomeâ€•wide association studies. Addiction Biology, 2021, 26, e12880. | 2.6 | 28 |
| 20 | Integrative genomic analysis of pediatric T-cell lymphoblastic lymphoma reveals candidates of clinical significance. Blood, 2021, 137, 2347-2359. | 1.4 | 31 |
| 21 | Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. Movement Disorders, 2021, 36, 449-459. | 3.9 | 16 |
| 22 | Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. Molecular Psychiatry, 2021, 26, 1286-1298. | 7.9 | 33 |
| 23 | Exome-Wide Association Study Identifies FN3KRP and PGP as New Candidate Longevity Genes. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 786-795. | 3.6 | 14 |
| 24 | Clinical and genetic differences between bipolar disorder type 1 and 2 in multiplex families. Translational Psychiatry, 2021, 11, 31. | 4.8 | 22 |
| 25 | 1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182. | 4.8 | 24 |
| 26 | Generation of integration-free induced pluripotent stem cell lines from four pediatric ADHD patients. Stem Cell Research, 2021, 53, 102268. | 0.7 | 7 |
| 27 | Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829. | 21.4 | 629 |
| 28 | DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. DNA Repair, 2021, 101, 103079. | 2.8 | 3 |
| 29 | Pharmacogenetic association of diabetes-associated genetic risk score with rapid progression of coronary artery calcification following treatment with HMG-CoA-reductase inhibitors â€"results of the Heinz Nixdorf Recall Study. Naunyn-Schmiedeberg's Archives of Pharmacology, 2021, 394, 1713-1725. | 3.0 | 4 |
| 30 | Generation of integration-free induced pluripotent stem cells from healthy individuals. Stem Cell Research, 2021, 53, 102269. | 0.7 | 6 |
| 31 | Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417. | 12.8 | 140 |
| 32 | DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. Frontiers in Genetics, 2021, 12, 691947. | 2.3 | 3 |
| 33 | LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562. | 17.5 | 46 |
| 34 | Search for AL amyloidosis risk factors using Mendelian randomization. Blood Advances, 2021, 5, 2725-2731. | 5.2 | 5 |
| 35 | Differential <scp>DNA</scp> methylation and <scp>mRNA</scp> transcription in gingival tissues in periodontal health and disease. Journal of Clinical Periodontology, 2021, 48, 1152-1164. | 4.9 | 21 |
| 36 | Identification of pleiotropy at the gene level between psychiatric disorders and related traits. Translational Psychiatry, 2021, 11, 410. | 4.8 | 7 |

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|---|---|---|---|
| 37 | Interaction of Alzheimerâ€™s Disease-Associated Genetic Risk with Indicators of Socioeconomic Position on Mild Cognitive Impairment in the Heinz Nixdorf Recall Study. Journal of Alzheimer's Disease, 2021, 82, 1715-1725. | 2.6 | 6 |
| 38 | HLA-DRB1 and HLA-DQB1 genetic diversity modulates response to lithium in bipolar affective disorders. Scientific Reports, 2021, 11, 17823. | 3.3 | 10 |
| 39 | Association between genetic variants of the cholinergic system and postoperative delirium and cognitive dysfunction in elderly patients. BMC Medical Genomics, 2021, 14, 248. | 1.5 | 8 |
| 40 | Combining schizophrenia and depression polygenic risk scores improves the genetic prediction of lithium response in bipolar disorder patients. Translational Psychiatry, 2021, 11, 606. | 4.8 | 25 |
| 41 | Polygenic risk scores across the extended psychosis spectrum. Translational Psychiatry, 2021, 11, 600. | 4.8 | 11 |
| 42 | Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602. | 7.9 | 49 |
| 43 | Identification of ADHD risk genes in extended pedigrees by combining linkage analysis and whole-exome sequencing. Molecular Psychiatry, 2020, 25, 2047-2057. | 7.9 | 17 |
| 44 | Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. Journal of Allergy and Clinical Immunology, 2020, 145, 1208-1218. | 2.9 | 29 |
| 45 | Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420. | 11.0 | 54 |
| 46 | Eight novel loci implicate shared genetic etiology in multiple myeloma, AL amyloidosis, and monoclonal gammopathy of unknown significance. Leukemia, 2020, 34, 1187-1191. | 7.2 | 13 |
| 47 | Genome-wide study on uveal melanoma patients finds association to DNA repair gene TDP1. Melanoma Research, 2020, 30, 166-172. | 1.2 | 6 |
| 48 | Genotype-phenotype feasibility studies on khat abuse, traumatic experiences and psychosis in Ethiopia. Psychiatric Genetics, 2020, 30, 34-38. | 1.1 | 1 |
| 49 | Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796. | 12.8 | 61 |
| 50 | Infection fatality rate of SARS-CoV2 in a super-spreading event in Germany. Nature Communications, 2020, 11, 5829. | 12.8 | 207 |
| 51 | Desaturase Activity and the Risk of Type 2 Diabetes and Coronary Artery Disease: A Mendelian Randomization Study. Nutrients, 2020, 12, 2261. | 4.1 | 16 |
| 52 | Risk prediction for coronary heart disease by a genetic risk score - results from the Heinz Nixdorf Recall study. BMC Medical Genetics, 2020, 21, 178. | 2.1 | 11 |
| 53 | Gene expression is stable in a complete CIB1 knockout keratinocyte model. Scientific Reports, 2020, 10, 14952. | 3.3 | 2 |
| 54 | Mendelian Randomization Study on Amino Acid Metabolism Suggests Tyrosine as Causal Trait for Type 2 Diabetes. Nutrients, 2020, 12, 3890. | 4.1 | 8 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Impact of genetic polymorphisms in kinetochore and spindle assembly genes on chromosomal aberration frequency in healthy humans. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2020, 858-860, 503253. | 1.7 | 2 |
| 56 | Genetic risk scores for coronary artery disease and its traditional risk factors: Their role in the progression of coronary artery calcificationâ€"Results of the Heinz Nixdorf Recall study. PLoS ONE, 2020, 15, e0232735. | 2.5 | 7 |
| 57 | Replication of a hippocampus specific effect of the tescalcin regulating variant rs7294919 on gray matter structure. European Neuropsychopharmacology, 2020, 36, 10-17. | 0.7 | 2 |
| 58 | Translation of mouse model to human gives insights into periodontitis etiology. Scientific Reports, 2020, 10, 4892. | 3.3 | 12 |
| 59 | The genetic architecture of the human cerebral cortex. Science, 2020, 367, . | 12.6 | 450 |
| 60 | Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. Translational Psychiatry, 2020, 10, 57. | 4.8 | 23 |
| 61 | Association between lipoprotein(a) (Lp(a)) levels and Lp(a) genetic variants with coronary artery calcification. BMC Medical Genetics, 2020, 21, 62. | 2.1 | 23 |
| 62 | Insights into the genomics of affective disorders. Medizinische Genetik, 2020, 32, 9-18. | 0.2 | 2 |
| 63 | Brain imaging genomics: influences of genomic variability on the structure and function of the human brain. Medizinische Genetik, 2020, 32, 47-56. | 0.2 | 3 |
| 64 | Investigating polygenic burden in age at disease onset in bipolar disorder: Findings from an international multicentric study. Bipolar Disorders, 2019, 21, 68-75. | 1.9 | 20 |
| 65 | Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37. | 2.9 | 14 |
| 66 | Distinct pathways associated with chromosomal aberration frequency in a cohort exposed to genotoxic compounds compared to general population. Mutagenesis, 2019, 34, 323-330. | 2.6 | 6 |
| 67 | Mendelian randomization provides support for obesity as a risk factor for meningioma. Scientific Reports, 2019, 9, 309. | 3.3 | 21 |
| 68 | Transethnic meta-analysis of rare coding variants in PLCG2, ABI3, and TREM2 supports their general contribution to Alzheimerâ€™s disease. Translational Psychiatry, 2019, 9, 55. | 4.8 | 32 |
| 69 | Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803. | 21.4 | 1,191 |
| 70 | No evidence for a BRD 2 promoter hypermethylation inÂblood leukocytes of Europeans with juvenile myoclonicÂepilepsy. Epilepsia, 2019, 60, e31-e36. | 5.1 | 4 |
| 71 | Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821. | 7.2 | 14 |
| 72 | Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77. | 4.8 | 82 |

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|---|---|---|---|
| 73 | Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates Aî², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430. | 21.4 | 1,962 |
| 74 | Alzheimerâ€™s disease-associated (hydroxy)methylomic changes in the brain and blood. Clinical Epigenetics, 2019, 11, 164. | 4.1 | 88 |
| 75 | Methylomic profiling in trisomy 21 identifies cognition- and Alzheimerâ€™s disease-related dysregulation. Clinical Epigenetics, 2019, 11, 195. | 4.1 | 14 |
| 76 | Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11. | 28.9 | 935 |
| 77 | Meta-analysis of genome-wide association studies of aggressive and chronic periodontitis identifies two novel risk loci. European Journal of Human Genetics, 2019, 27, 102-113. | 2.8 | 58 |
| 78 | Compound heterozygous SZT2 mutations in two siblings with early-onset epilepsy, intellectual disability and macrocephaly. Seizure: the Journal of the British Epilepsy Association, 2019, 66, 81-85. | 2.0 | 14 |
| 79 | Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1. | 6.2 | 40 |
| 80 | Genetic variation associated with chromosomal aberration frequency: A genomeâ€wide association study. Environmental and Molecular Mutagenesis, 2019, 60, 17-28. | 2.2 | 9 |
| 81 | Association of Polygenic Score for Schizophrenia and HLA Antigen and Inflammation Genes With Response to Lithium in Bipolar Affective Disorder. JAMA Psychiatry, 2018, 75, 65-74. | 11.0 | 102 |
| 82 | Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340. | 12.8 | 58 |
| 83 | Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681. | 21.4 | 2,224 |
| 84 | Primary Osteoporosis Is Not Reflected by Disease-Specific DNA Methylation or Accelerated Epigenetic Age in Blood. Journal of Bone and Mineral Research, 2018, 33, 356-361. | 2.8 | 33 |
| 85 | Gene set enrichment analysis and expression pattern exploration implicate an involvement of neurodevelopmental processes in bipolar disorder. Journal of Affective Disorders, 2018, 228, 20-25. | 4.1 | 14 |
| 86 | Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669. | 14.8 | 490 |
| 87 | Generation of human induced pluripotent stem cell lines (hiPSC) from one bipolar disorder patient carrier of a DGKH risk haplotype and one non-risk-variant-carrier bipolar disorder patient. Stem Cell Research, 2018, 32, 104-109. | 0.7 | 7 |
| 88 | The severity of human periâ€implantitis lesions correlates with the level of submucosal microbial dysbiosis. Journal of Clinical Periodontology, 2018, 45, 1498-1509. | 4.9 | 60 |
| 89 | Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707. | 12.8 | 86 |
| 90 | Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052. | 1.4 | 17 |

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|---|---|---|---|
| 91 | Enrichment of B cell receptor signaling and epidermal growth factor receptor pathways in monoclonal gammopathy of undetermined significance: a genome-wide genetic interaction study. Molecular Medicine, 2018, 24, 30. | 4.4 | 9 |
| 92 | Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. Scientific Reports, 2018, 8, 13678. | 3.3 | 35 |
| 93 | Satisfying your neuro-oncologist: a fast approach to routine molecular glioma diagnostics. Neuro-Oncology, 2018, 20, 1682-1683. | 1.2 | 8 |
| 94 | Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194. | 6.2 | 119 |
| 95 | Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493. | 1.2 | 23 |
| 96 | Copy number variation analysis and targeted NGS in 77 families with suspected Lynch syndrome reveals novel potential causative genes. International Journal of Cancer, 2018, 143, 2800-2813. | 5.1 | 11 |
| 97 | Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16. | 28.9 | 623 |
| 98 | Shared genetic etiology between alcohol dependence and major depressive disorder. Psychiatric Genetics, 2018, 28, 66-70. | 1.1 | 19 |
| 99 | Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071. | 3.3 | 31 |
| 100 | Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836. | 2.8 | 214 |
| 101 | A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. Human Molecular Genetics, 2017, 26, 2577-2588. | 2.9 | 87 |
| 102 | The PF4/PPBP/CXCL5 Gene Cluster Is Associated with Periodontitis. Journal of Dental Research, 2017, 96, 945-952. | 5.2 | 29 |
| 103 | Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382. | 12.8 | 251 |
| 104 | Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79. | 2.2 | 16 |
| 105 | Genome-Wide Analysis of Periodontal and Peri-Implant Cells and Tissues. Methods in Molecular Biology, 2017, 1537, 307-326. | 0.9 | 4 |
| 106 | Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384. | 21.4 | 783 |
| 107 | Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. Scientific Reports, 2017, 7, 6037. | 3.3 | 12 |
| 108 | Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892. | 12.8 | 40 |

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|---|---|---|---|
| 109 | Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511. | 12.8 | 60 |
| 110 | Association between neuropeptide Y receptor Y2 promoter variant rs6857715 and major depressive disorder. Psychiatric Genetics, 2017, 27, 34-37. | 1.1 | 13 |
| 111 | Human Platelet Lysate versus Fetal Calf Serum: These Supplements Do Not Select for Different Mesenchymal Stromal Cells. Scientific Reports, 2017, 7, 5132. | 3.3 | 60 |
| 112 | Genome-wide association study of clinical parameters in immunoglobulin light chain amyloidosis in three patient cohorts. Haematologica, 2017, 102, e411-e414. | 3.5 | 7 |
| 113 | Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35. | 21.4 | 838 |
| 114 | Analysis of the joint effect of SNPs to identify independent loci and allelic heterogeneity in schizophrenia GWAS data. Translational Psychiatry, 2017, 7, 1289. | 4.8 | 4 |
| 115 | Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. Genes, 2017, 8, 183. | 2.4 | 11 |
| 116 | Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595. | 2.5 | 77 |
| 117 | Exome sequencing characterizes the somatic mutation spectrum of early serrated lesions in a patient with serrated polyposis syndrome (SPS). Hereditary Cancer in Clinical Practice, 2017, 15, 22. | 1.5 | 6 |
| 118 | Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. Epigenetics and Chromatin, 2017, 10, 37. | 3.9 | 20 |
| 119 | Copy number variations in 375 patients with oesophageal atresia and/or tracheoesophageal fistula. European Journal of Human Genetics, 2016, 24, 1715-1723. | 2.8 | 27 |
| 120 | Immunochip analysis identifies association of the  <scp>RAD</scp> 50/ <scp>IL</scp> 13  region with human longevity. Aging Cell, 2016, 15, 585-588. | 6.7 | 20 |
| 121 | Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050. | 12.8 | 146 |
| 122 | A statistical model for the analysis of beta values in DNA methylation studies. BMC Bioinformatics, 2016, 17, 480. | 2.6 | 62 |
| 123 | Genome-wide association study of 40,000 individuals identifies two novel loci associated with bipolar disorder. Human Molecular Genetics, 2016, 25, 3383-3394. | 2.9 | 182 |
| 124 | Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis. Familial Cancer, 2016, 15, 281-288. | 1.9 | 40 |
| 125 | Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. Lancet, The, 2016, 387, 1085-1093. | 13.7 | 306 |
| 126 | Low-levelAPCmutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases. Journal of Medical Genetics, 2016, 53, 172-179. | 3.2 | 51 |

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|---|---|---|---|
| 127 | Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290. | 12.8 | 31 |
| 128 | Association of the OPRM1 Variant rs1799971 (A118G) with Non-Specific Liability to Substance Dependence in a Collaborative de novo Meta-Analysis of European-Ancestry Cohorts. Behavior Genetics, 2016, 46, 151-169. | 2.1 | 98 |
| 129 | Evidence of Inbreeding in Hodgkin Lymphoma. PLoS ONE, 2016, 11, e0154259. | 2.5 | 8 |
| 130 | Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467. | 3.3 | 4 |
| 131 | The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065. | 3.3 | 24 |
| 132 | The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. Haematologica, 2015, 100, e110-e113. | 3.5 | 27 |
| 133 | Extending the phenotypic spectrum of <scp>RBFOX</scp>1 deletions: Sporadic focal epilepsy. Epilepsia, 2015, 56, e129-33. | 5.1 | 38 |
| 134 | DNA methylation signature in peripheral blood reveals distinct characteristics of human X chromosome numerical aberrations. Clinical Epigenetics, 2015, 7, 76. | 4.1 | 59 |
| 135 | Investigation of the role of TCF4 rare sequence variants in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 354-362. | 1.7 | 12 |
| 136 | Novel genetic variants in differentiated thyroid cancer and assessment of the cumulative risk. Scientific Reports, 2015, 5, 8922. | 3.3 | 23 |
| 137 | Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. Circulation: Cardiovascular Genetics, 2015, 8, 327-333. | 5.1 | 17 |
| 138 | Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897. | 12.8 | 173 |
| 139 | Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. Nature Communications, 2015, 6, 6031. | 12.8 | 158 |
| 140 | Destabilization of the human epigenome: consequences of foreign DNA insertions. Epigenomics, 2015, 7, 745-755. | 2.1 | 15 |
| 141 | XRCC5 as a Risk Gene for Alcohol Dependence: Evidence from a Genome-Wide Gene-Set-Based Analysis and Follow-up Studies in Drosophila and Humans. Neuropsychopharmacology, 2015, 40, 361-371. | 5.4 | 12 |
| 142 | Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. American Journal of Human Genetics, 2015, 97, 816-836. | 6.2 | 245 |
| 143 | Frequency and phenotypic spectrum of germline mutations in <scp>POLE</scp> and seven other polymerase genes in 266 patients with colorectal adenomas and carcinomas. International Journal of Cancer, 2015, 137, 320-331. | 5.1 | 121 |
| 144 | Molecular Characterization of F8 Secreting Cell. Blood, 2015, 126, 4671-4671. | 1.4 | 0 |

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|---|---|---|---|
| 145 | Systematic Pathway Enrichment Analysis of a Genome-Wide Association Study on Breast Cancer Survival Reveals an Influence of Genes Involved in Cell Adhesion and Calcium Signaling on the Patientsâ€™ Clinical Outcome. PLoS ONE, 2014, 9, e98229. | 2.5 | 16 |
| 146 | 16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080. | 2.9 | 61 |
| 147 | SUCLG2 identified as both a determinator of CSF AÎ²1â€“42 levels and an attenuator of cognitive decline in Alzheimer's disease. Human Molecular Genetics, 2014, 23, 6644-6658. | 2.9 | 45 |
| 148 | Genome-wide analysis of rare copy number variations reveals PARK2 as a candidate gene for attention-deficit/hyperactivity disorder. Molecular Psychiatry, 2014, 19, 115-121. | 7.9 | 76 |
| 149 | Investigation of the involvement of MIR185 and its target genes in the development of schizophrenia. Journal of Psychiatry and Neuroscience, 2014, 39, 386-396. | 2.4 | 23 |
| 150 | Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within Gremlinâ€1, a component of the bone morphogenetic protein 4 pathway. Birth Defects Research Part A: Clinical and Molecular Teratology, 2014, 100, 493-498. | 1.6 | 24 |
| 151 | Complete homozygous deletion of <scp>CTSC</scp> in an <scp>I</scp>ranian family with <scp>P</scp>apillonâ€“<scp>L</scp>efÃ¨vre syndrome. International Journal of Dermatology, 2014, 53, 885-887. | 1.0 | 9 |
| 152 | A common microdeletion affecting a hippocampusâ€•and amygdalaâ€specific isoform of tryptophan hydroxylase 2 is not associated with affective disorders. Bipolar Disorders, 2014, 16, 764-768. | 1.9 | 2 |
| 153 | Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. European Journal of Human Genetics, 2014, 22, 675-680. | 2.8 | 59 |
| 154 | Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339. | 12.8 | 294 |
| 155 | Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186. | 21.4 | 1,818 |
| 156 | Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904. | 21.4 | 104 |
| 157 | Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836. | 21.4 | 281 |
| 158 | Hippo Signaling Mediates Proliferation, Invasiveness, and Metastatic Potential of Clear Cell Renal Cell Carcinoma. Translational Oncology, 2014, 7, 309-321. | 3.7 | 63 |
| 159 | Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. Blood, 2014, 123, 2513-2517. | 1.4 | 32 |
| 160 | Risk loci for coronary artery calcification replicated at 9p21 and 6q24 in the Heinz Nixdorf Recall Study. BMC Medical Genetics, 2013, 14, 23. | 2.1 | 32 |
| 161 | Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225. | 21.4 | 143 |
| 162 | The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525. | 21.4 | 91 |

| # | Article | IF | Citations |
|---|---|---|---|
| 163 | Levetiracetam resistance: Synaptic signatures & corresponding promoter SNPs in epileptic hippocampi. Neurobiology of Disease, 2013, 60, 115-125. | 4.4 | 19 |
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