

Per Hoffmann

List of Publications by Year in descending order

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Version: 2024-02-01

234
papers

27,250
citations

18436

62
h-index

8370

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. <i>Cardiovascular Research</i> , 2023, 119, 857-866.	1.8	11
2	Effects of copy number variations on brain structure and risk for psychiatric illness: Large-scale studies from the ENIGMA working groups on CNVs. <i>Human Brain Mapping</i> , 2022, 43, 300-328.	1.9	30
3	Blood copper and risk of cardiometabolic diseases: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2022, 31, 783-791.	1.4	12
4	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. <i>Biological Psychiatry</i> , 2022, 91, 313-327.	0.7	114
5	Genome-wide Association Study of Postoperative Cognitive Dysfunction in Older Surgical Patients. <i>Journal of Neurosurgical Anesthesiology</i> , 2022, 34, 248-250.	0.6	3
6	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. <i>Molecular Psychiatry</i> , 2022, 27, 1111-1119.	4.1	24
7	Epigenome-wide association study of alcohol use disorder in five brain regions. <i>Neuropsychopharmacology</i> , 2022, 47, 832-839.	2.8	16
8	Using polygenic scores and clinical data for bipolar disorder patient stratification and lithium response prediction: machine learning approach. <i>British Journal of Psychiatry</i> , 2022, 220, 219-228.	1.7	11
9	Dihydroceramide- and ceramide-profiling provides insights into human cardiometabolic disease etiology. <i>Nature Communications</i> , 2022, 13, 936.	5.8	28
10	Epigenome-Wide Analysis of DNA Methylation in Parkinson's Disease Cortex. <i>Life</i> , 2022, 12, 502.	1.1	14
11	A genetic risk score of alleles related to MGUS interacts with socioeconomic position in a population-based cohort. <i>Scientific Reports</i> , 2022, 12, 4409.	1.6	0
12	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
13	New insights into the genetic etiology of Alzheimer's disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	9.4	700
14	Genome-wide meta-analysis of monoclonal gammopathy of undetermined significance (MGUS) identifies risk loci impacting IRF-6. <i>Blood Cancer Journal</i> , 2022, 12, 60.	2.8	2
15	Multi-omics signatures of alcohol use disorder in the dorsal and ventral striatum. <i>Translational Psychiatry</i> , 2022, 12, 190.	2.4	11
16	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. <i>Molecular Psychiatry</i> , 2021, 26, 4179-4190.	4.1	58
17	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. <i>Molecular Psychiatry</i> , 2021, 26, 3004-3017.	4.1	56
18	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 2457-2470.	4.1	44

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19	Shared genetic risk between eating disorder and substance use-related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	1.4	28
20	Integrative genomic analysis of pediatric T-cell lymphoblastic lymphoma reveals candidates of clinical significance. <i>Blood</i> , 2021, 137, 2347-2359.	0.6	31
21	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. <i>Movement Disorders</i> , 2021, 36, 449-459.	2.2	16
22	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 1286-1298.	4.1	33
23	Exome-Wide Association Study Identifies <i>FN3KRP</i> and <i>PGP</i> as New Candidate Longevity Genes. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2021, 76, 786-795.	1.7	14
24	Clinical and genetic differences between bipolar disorder type 1 and 2 in multiplex families. <i>Translational Psychiatry</i> , 2021, 11, 31.	2.4	22
25	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. <i>Translational Psychiatry</i> , 2021, 11, 182.	2.4	24
26	Generation of integration-free induced pluripotent stem cell lines from four pediatric ADHD patients. <i>Stem Cell Research</i> , 2021, 53, 102268.	0.3	7
27	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	9.4	629
28	DNA repair gene polymorphisms and chromosomal aberrations in healthy, nonsmoking population. <i>DNA Repair</i> , 2021, 101, 103079.	1.3	3
29	Pharmacogenetic association of diabetes-associated genetic risk score with rapid progression of coronary artery calcification following treatment with HMG-CoA-reductase inhibitors – results of the Heinz Nixdorf Recall Study. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2021, 394, 1713-1725.	1.4	4
30	Generation of integration-free induced pluripotent stem cells from healthy individuals. <i>Stem Cell Research</i> , 2021, 53, 102269.	0.3	6
31	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. <i>Nature Communications</i> , 2021, 12, 3417.	5.8	140
32	DNA Repair Gene Polymorphisms and Chromosomal Aberrations in Exposed Populations. <i>Frontiers in Genetics</i> , 2021, 12, 691947.	1.1	3
33	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. <i>Nature Biotechnology</i> , 2021, 39, 1556-1562.	9.4	46
34	Search for AL amyloidosis risk factors using Mendelian randomization. <i>Blood Advances</i> , 2021, 5, 2725-2731.	2.5	5
35	Differential DNA methylation and mRNA transcription in gingival tissues in periodontal health and disease. <i>Journal of Clinical Periodontology</i> , 2021, 48, 1152-1164.	2.3	21
36	Identification of pleiotropy at the gene level between psychiatric disorders and related traits. <i>Translational Psychiatry</i> , 2021, 11, 410.	2.4	7

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37	Interaction of Alzheimer's Disease-Associated Genetic Risk with Indicators of Socioeconomic Position on Mild Cognitive Impairment in the Heinz Nixdorf Recall Study. <i>Journal of Alzheimer's Disease</i> , 2021, 82, 1715-1725.	1.2	6
38	HLA-DRB1 and HLA-DQB1 genetic diversity modulates response to lithium in bipolar affective disorders. <i>Scientific Reports</i> , 2021, 11, 17823.	1.6	10
39	Association between genetic variants of the cholinergic system and postoperative delirium and cognitive dysfunction in elderly patients. <i>BMC Medical Genomics</i> , 2021, 14, 248.	0.7	8
40	Combining schizophrenia and depression polygenic risk scores improves the genetic prediction of lithium response in bipolar disorder patients. <i>Translational Psychiatry</i> , 2021, 11, 606.	2.4	25
41	Polygenic risk scores across the extended psychosis spectrum. <i>Translational Psychiatry</i> , 2021, 11, 600.	2.4	11
42	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. <i>Molecular Psychiatry</i> , 2020, 25, 584-602.	4.1	49
43	Identification of ADHD risk genes in extended pedigrees by combining linkage analysis and whole-exome sequencing. <i>Molecular Psychiatry</i> , 2020, 25, 2047-2057.	4.1	17
44	Protein-coding variants contribute to the risk of atopic dermatitis and skin-specific gene expression. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 1208-1218.	1.5	29
45	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. <i>JAMA Psychiatry</i> , 2020, 77, 420.	6.0	54
46	Eight novel loci implicate shared genetic etiology in multiple myeloma, AL amyloidosis, and monoclonal gammopathy of unknown significance. <i>Leukemia</i> , 2020, 34, 1187-1191.	3.3	13
47	Genome-wide study on uveal melanoma patients finds association to DNA repair gene TDP1. <i>Melanoma Research</i> , 2020, 30, 166-172.	0.6	6
48	Genotype-phenotype feasibility studies on khat abuse, traumatic experiences and psychosis in Ethiopia. <i>Psychiatric Genetics</i> , 2020, 30, 34-38.	0.6	1
49	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61
50	Infection fatality rate of SARS-CoV2 in a super-spreading event in Germany. <i>Nature Communications</i> , 2020, 11, 5829.	5.8	207
51	Desaturase Activity and the Risk of Type 2 Diabetes and Coronary Artery Disease: A Mendelian Randomization Study. <i>Nutrients</i> , 2020, 12, 2261.	1.7	16
52	Risk prediction for coronary heart disease by a genetic risk score - results from the Heinz Nixdorf Recall study. <i>BMC Medical Genetics</i> , 2020, 21, 178.	2.1	11
53	Gene expression is stable in a complete CIB1 knockout keratinocyte model. <i>Scientific Reports</i> , 2020, 10, 14952.	1.6	2
54	Mendelian Randomization Study on Amino Acid Metabolism Suggests Tyrosine as Causal Trait for Type 2 Diabetes. <i>Nutrients</i> , 2020, 12, 3890.	1.7	8

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55	Impact of genetic polymorphisms in kinetochore and spindle assembly genes on chromosomal aberration frequency in healthy humans. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2020, 858-860, 503253.	0.9	2
56	Genetic risk scores for coronary artery disease and its traditional risk factors: Their role in the progression of coronary artery calcification—Results of the Heinz Nixdorf Recall study. <i>PLoS ONE</i> , 2020, 15, e0232735.	1.1	7
57	Replication of a hippocampus specific effect of the tescalcin regulating variant rs7294919 on gray matter structure. <i>European Neuropsychopharmacology</i> , 2020, 36, 10-17.	0.3	2
58	Translation of mouse model to human gives insights into periodontitis etiology. <i>Scientific Reports</i> , 2020, 10, 4892.	1.6	12
59	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	6.0	450
60	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. <i>Translational Psychiatry</i> , 2020, 10, 57.	2.4	23
61	Association between lipoprotein(a) (Lp(a)) levels and Lp(a) genetic variants with coronary artery calcification. <i>BMC Medical Genetics</i> , 2020, 21, 62.	2.1	23
62	Insights into the genomics of affective disorders. <i>Medizinische Genetik</i> , 2020, 32, 9-18.	0.1	2
63	Brain imaging genomics: influences of genomic variability on the structure and function of the human brain. <i>Medizinische Genetik</i> , 2020, 32, 47-56.	0.1	3
64	Investigating polygenic burden in age at disease onset in bipolar disorder: Findings from an international multicentric study. <i>Bipolar Disorders</i> , 2019, 21, 68-75.	1.1	20
65	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. <i>Human Genomics</i> , 2019, 13, 37.	1.4	14
66	Distinct pathways associated with chromosomal aberration frequency in a cohort exposed to genotoxic compounds compared to general population. <i>Mutagenesis</i> , 2019, 34, 323-330.	1.0	6
67	Mendelian randomization provides support for obesity as a risk factor for meningioma. <i>Scientific Reports</i> , 2019, 9, 309.	1.6	21
68	Transethnic meta-analysis of rare coding variants in PLCG2, ABI3, and TREM2 supports their general contribution to Alzheimer's disease. <i>Translational Psychiatry</i> , 2019, 9, 55.	2.4	32
69	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	9.4	1,191
70	No evidence for a BRD 2 promoter hypermethylation in blood leukocytes of Europeans with juvenile myoclonic epilepsy. <i>Epilepsia</i> , 2019, 60, e31-e36.	2.6	4
71	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. <i>Leukemia</i> , 2019, 33, 1817-1821.	3.3	14
72	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. <i>Translational Psychiatry</i> , 2019, 9, 77.	2.4	82

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73	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β , tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	9.4	1,962
74	Alzheimer's disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019, 11, 164.	1.8	88
75	Methylomic profiling in trisomy 21 identifies cognition- and Alzheimer's disease-related dysregulation. <i>Clinical Epigenetics</i> , 2019, 11, 195.	1.8	14
76	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	13.5	935
77	Meta-analysis of genome-wide association studies of aggressive and chronic periodontitis identifies two novel risk loci. <i>European Journal of Human Genetics</i> , 2019, 27, 102-113.	1.4	58
78	Compound heterozygous SZT2 mutations in two siblings with early-onset epilepsy, intellectual disability and macrocephaly. <i>Seizure: the Journal of the British Epilepsy Association</i> , 2019, 66, 81-85.	0.9	14
79	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , 2019, 9, 1.	2.8	40
80	Genetic variation associated with chromosomal aberration frequency: A genome-wide association study. <i>Environmental and Molecular Mutagenesis</i> , 2019, 60, 17-28.	0.9	9
81	Association of Polygenic Score for Schizophrenia and HLA Antigen and Inflammation Genes With Response to Lithium in Bipolar Affective Disorder. <i>JAMA Psychiatry</i> , 2018, 75, 65-74.	6.0	102
82	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. <i>Nature Communications</i> , 2018, 9, 1340.	5.8	58
83	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
84	Primary Osteoporosis Is Not Reflected by Disease-Specific DNA Methylation or Accelerated Epigenetic Age in Blood. <i>Journal of Bone and Mineral Research</i> , 2018, 33, 356-361.	3.1	33
85	Gene set enrichment analysis and expression pattern exploration implicate an involvement of neurodevelopmental processes in bipolar disorder. <i>Journal of Affective Disorders</i> , 2018, 228, 20-25.	2.0	14
86	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. <i>Nature Neuroscience</i> , 2018, 21, 1656-1669.	7.1	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. <i>Stem Cell Research</i> , 2018, 32, 104-109.	0.3	7
88	The severity of human peri-implantitis lesions correlates with the level of submucosal microbial dysbiosis. <i>Journal of Clinical Periodontology</i> , 2018, 45, 1498-1509.	2.3	60
89	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3707.	5.8	86
90	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. <i>Blood</i> , 2018, 132, 2040-2052.	0.6	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. <i>Molecular Medicine</i> , 2018, 24, 30.	1.9	9
92	Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. <i>Scientific Reports</i> , 2018, 8, 13678.	1.6	35
93	Satisfying your neuro-oncologist: a fast approach to routine molecular glioma diagnostics. <i>Neuro-Oncology</i> , 2018, 20, 1682-1683.	0.6	8
94	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018, 102, 1185-1194.	2.6	119
95	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. <i>Neuro-Oncology</i> , 2018, 20, 1485-1493.	0.6	23
96	Copy number variation analysis and targeted NGS in 77 families with suspected Lynch syndrome reveals novel potential causative genes. <i>International Journal of Cancer</i> , 2018, 143, 2800-2813.	2.3	11
97	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.	13.5	623
98	Shared genetic etiology between alcohol dependence and major depressive disorder. <i>Psychiatric Genetics</i> , 2018, 28, 66-70.	0.6	19
99	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. <i>Scientific Reports</i> , 2017, 7, 41071.	1.6	31
100	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	1.2	214
101	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. <i>Human Molecular Genetics</i> , 2017, 26, 2577-2588.	1.4	87
102	The <i>PF4/PPBP/CXCL5</i> Gene Cluster Is Associated with Periodontitis. <i>Journal of Dental Research</i> , 2017, 96, 945-952.	2.5	29
103	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. <i>Nature Communications</i> , 2017, 8, 15382.	5.8	251
104	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). <i>European Journal of Haematology</i> , 2017, 99, 70-79.	1.1	16
105	Genome-Wide Analysis of Periodontal and Peri-Implant Cells and Tissues. <i>Methods in Molecular Biology</i> , 2017, 1537, 307-326.	0.4	4
106	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	9.4	783
107	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017, 7, 6037.	1.6	12
108	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. <i>Nature Communications</i> , 2017, 8, 1892.	5.8	40

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109	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. <i>Nature Communications</i> , 2017, 8, 1511.	5.8	60
110	Association between neuropeptide Y receptor Y2 promoter variant rs6857715 and major depressive disorder. <i>Psychiatric Genetics</i> , 2017, 27, 34-37.	0.6	13
111	Human Platelet Lysate versus Fetal Calf Serum: These Supplements Do Not Select for Different Mesenchymal Stromal Cells. <i>Scientific Reports</i> , 2017, 7, 5132.	1.6	60
112	Genome-wide association study of clinical parameters in immunoglobulin light chain amyloidosis in three patient cohorts. <i>Haematologica</i> , 2017, 102, e411-e414.	1.7	7
113	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
114	Analysis of the joint effect of SNPs to identify independent loci and allelic heterogeneity in schizophrenia GWAS data. <i>Translational Psychiatry</i> , 2017, 7, 1289.	2.4	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. <i>Genes</i> , 2017, 8, 183.	1.0	11
116	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. <i>PLoS ONE</i> , 2017, 12, e0171595.	1.1	77
117	Exome sequencing characterizes the somatic mutation spectrum of early serrated lesions in a patient with serrated polyposis syndrome (SPS). <i>Hereditary Cancer in Clinical Practice</i> , 2017, 15, 22.	0.6	6
118	Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. <i>Epigenetics and Chromatin</i> , 2017, 10, 37.	1.8	20
119	Copy number variations in 375 patients with oesophageal atresia and/or tracheoesophageal fistula. <i>European Journal of Human Genetics</i> , 2016, 24, 1715-1723.	1.4	27
120	ImmunoChIP analysis identifies association of the <i>RAD50</i> region with human longevity. <i>Aging Cell</i> , 2016, 15, 585-588.	3.0	20
121	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , 2016, 7, 12050.	5.8	146
122	A statistical model for the analysis of beta values in DNA methylation studies. <i>BMC Bioinformatics</i> , 2016, 17, 480.	1.2	62
123	Genome-wide association study of 40,000 individuals identifies two novel loci associated with bipolar disorder. <i>Human Molecular Genetics</i> , 2016, 25, 3383-3394.	1.4	182
124	Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis. <i>Familial Cancer</i> , 2016, 15, 281-288.	0.9	40
125	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. <i>Lancet</i> , 2016, 387, 1085-1093.	6.3	306
126	Low-level <i>APC</i> mutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases. <i>Journal of Medical Genetics</i> , 2016, 53, 172-179.	1.5	51

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127	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. <i>Nature Communications</i> , 2016, 7, 10290.	5.8	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. <i>Behavior Genetics</i> , 2016, 46, 151-169.	1.4	98
129	Evidence of Inbreeding in Hodgkin Lymphoma. <i>PLoS ONE</i> , 2016, 11, e0154259.	1.1	8
130	Inbreeding and homozygosity in breast cancer survival. <i>Scientific Reports</i> , 2015, 5, 16467.	1.6	4
131	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. <i>Scientific Reports</i> , 2015, 5, 15065.	1.6	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. <i>Haematologica</i> , 2015, 100, e110-e113.	1.7	27
133	Extending the phenotypic spectrum of <i>RBFOX1</i> deletions: Sporadic focal epilepsy. <i>Epilepsia</i> , 2015, 56, e129-33.	2.6	38
134	DNA methylation signature in peripheral blood reveals distinct characteristics of human X chromosome numerical aberrations. <i>Clinical Epigenetics</i> , 2015, 7, 76.	1.8	59
135	Investigation of the role of <i>TCF4</i> rare sequence variants in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 354-362.	1.1	12
136	Novel genetic variants in differentiated thyroid cancer and assessment of the cumulative risk. <i>Scientific Reports</i> , 2015, 5, 8922.	1.6	23
137	Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 327-333.	5.1	17
138	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173
139	Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. <i>Nature Communications</i> , 2015, 6, 6031.	5.8	158
140	Destabilization of the human epigenome: consequences of foreign DNA insertions. <i>Epigenomics</i> , 2015, 7, 745-755.	1.0	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. <i>Neuropsychopharmacology</i> , 2015, 40, 361-371.	2.8	12
142	Genome-wide Association Analysis of Psoriatic Arthritis and Cutaneous Psoriasis Reveals Differences in Their Genetic Architecture. <i>American Journal of Human Genetics</i> , 2015, 97, 816-836.	2.6	245
143	Frequency and phenotypic spectrum of germline mutations in <i>POLE</i> and seven other polymerase genes in 266 patients with colorectal adenomas and carcinomas. <i>International Journal of Cancer</i> , 2015, 137, 320-331.	2.3	121
144	Molecular Characterization of F8 Secreting Cell. <i>Blood</i> , 2015, 126, 4671-4671.	0.6	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 Patients' Clinical Outcome. PLoS ONE, 2014, 9, e98229.	1.1	16
146	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080.	1.4	61
147	SUCLG2 identified as both a determinant of CSF A β 42 levels and an attenuator of cognitive decline in Alzheimer's disease. Human Molecular Genetics, 2014, 23, 6644-6658.	1.4	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.	4.1	76
149	Investigation of the involvement of <i>MIR185</i> and its target genes in the development of schizophrenia. Journal of Psychiatry and Neuroscience, 2014, 39, 386-396.	1.4	23
150	Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within <i>Gremlin1</i> , 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 <i>CTSC</i> in an Iranian family with Pilonidal cyst syndrome. International Journal of Dermatology, 2014, 53, 885-887.	0.5	9
152	A common microdeletion affecting a hippocampus- and amygdala-specific isoform of tryptophan hydroxylase 2 is not associated with affective disorders. Bipolar Disorders, 2014, 16, 764-768.	1.1	2
153	Genetic analysis of dyslexia candidate genes in the European cross-linguistic NeuroDys cohort. European Journal of Human Genetics, 2014, 22, 675-680.	1.4	59
154	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	5.8	294
155	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
156	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	9.4	104
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