Per Hoffmann

List of Publications by Year
in descending order

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	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
2	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.	9.4	1,962
3	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
4	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
5	Identification of loci associated with schizophrenia by genome-wide association and follow-up. Nature Genetics, 2008, 40, 1053-1055.	9.4	977
6	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
7	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
8	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. Nature Genetics, 2012, 44, 1341-1348.	9.4	848
9	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
10	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
11	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	9.4	700
12	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.	9.4	629
13	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
14	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	7.1	490
15	Direct Conversion of Fibroblasts into Stably Expandable Neural Stem Cells. Cell Stem Cell, 2012, 10, 473-479.	5.2	473
16	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	6.0	450
17	Disruption of the neurexin 1 gene is associated with schizophrenia. Human Molecular Genetics, 2009, 18, 988-996.	1.4	424
18	Key susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24. Nature Genetics, 2009, 41, 473-477.	9.4	415

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19	Genome-wide association study identifies two susceptibility loci for nonsyndromic cleft lip with or without cleft palate. Nature Genetics, 2010, 42, 24-26.	9.4	379
20	Genome-wide meta-analyses of nonsyndromic cleft lip with or without cleft palate identify six new risk loci. Nature Genetics, 2012, 44, 968-971.	9.4	311
21	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. Lancet, The, 2016, 387, 1085-1093.	6.3	306
22	Genome-wide association study reveals two new risk loci for bipolar disorder. Nature Communications, 2014, 5, 3339.	5.8	294
23	Excitation-induced ataxin-3 aggregation in neurons from patients with Machadoâ€“Joseph disease. Nature, 2011, 480, 543-546.	13.7	282
24	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
25	Large scale meta-analysis characterizes genetic architecture for common psoriasis associated variants. Nature Communications, 2017, 8, 15382.	5.8	251
26	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.	2.6	245
27	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
28	Infection fatality rate of SARS-CoV2 in a super-spreading event in Germany. Nature Communications, 2020, 11, 5829.	5.8	207
29	Genome-wide association study of 40,000 individuals identifies two novel loci associated with bipolar disorder. Human Molecular Genetics, 2016, 25, 3383-3394.	1.4	182
30	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
31	High-density genotyping study identifies four new susceptibility loci for atopic dermatitis. Nature Genetics, 2013, 45, 808-812.	9.4	167
32	Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. Nature Communications, 2015, 6, 6031.	5.8	158
33	Genomeâ€wide significant association between alcohol dependence and a variant in the ADH gene cluster. Addiction Biology, 2012, 17, 171-180.	1.4	154
34	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	5.8	146
35	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	9.4	143
36	Common variants in Alzheimerâ€™s disease and risk stratification by polygenic risk scores. Nature Communications, 2021, 12, 3417.	5.8	140

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37	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	9.4	137
38	Characterization of a Family with Rare Deletions in CNTNAP5 and DOCK4 Suggests Novel Risk Loci for Autism and Dyslexia. Biological Psychiatry, 2010, 68, 320-328.	0.7	131
39	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.	2.3	121
40	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
41	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	0.7	114
42	Genetics of dyslexia: the evolving landscape. Journal of Medical Genetics, 2007, 44, 289-297.	1.5	107
43	Association between genetic variation in a region on chromosome 11 and schizophrenia in large samples from Europe. Molecular Psychiatry, 2012, 17, 906-917.	4.1	105
44	Common variants in the HLA-DQ region confer susceptibility to idiopathic achalasia. Nature Genetics, 2014, 46, 901-904.	9.4	104
45	A locus on 2p12 containing the co-regulated MRPL19 and C2ORF3 genes is associated to dyslexia. Human Molecular Genetics, 2007, 16, 667-677.	1.4	102
46	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.	6.0	102
47	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.	1.4	98
48	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	9.4	91
49	First genome-wide association scan on neurophysiological endophenotypes points to trans-regulation effects on SLC2A3 in dyslexic children. Molecular Psychiatry, 2011, 16, 97-107.	4.1	88
50	Alzheimerâ€™s disease-associated (hydroxy)methylomic changes in the brain and blood. Clinical Epigenetics, 2019, 11, 164.	1.8	88
51	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. Human Molecular Genetics, 2017, 26, 2577-2588.	1.4	87
52	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
53	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. Translational Psychiatry, 2019, 9, 77.	2.4	82
54	The DISC locus and schizophrenia: evidence from an association study in a central European sample and from a meta-analysis across different European populations. Human Molecular Genetics, 2009, 18, 2719-2727.	1.4	78

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55	Common obesity risk alleles in childhood attentionâ€deficit/hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 295-305.	1.1	77
56	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. PLoS ONE, 2017, 12, e0171595.	1.1	77
57	Genomeâ€wide association study in German patients with attention deficit/hyperactivity disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 888-897.	1.1	76
58	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
59	TLR4, ATF-3 and IL8 inflammation mediator expression correlates with seizure frequency in human epileptic brain tissue. Seizure: the Journal of the British Epilepsy Association, 2013, 22, 675-678.	0.9	74
60	Association between schizophrenia and common variation in neurocan (NCAN), a genetic risk factor for bipolar disorder. Schizophrenia Research, 2012, 138, 69-73.	1.1	70
61	Analysis of 10 independent samples provides evidence for association between schizophrenia and a SNP flanking fibroblast growth factor receptor 2. Molecular Psychiatry, 2009, 14, 30-36.	4.1	66
62	Î±CaMKII Autophosphorylation Controls the Establishment of Alcohol Drinking Behavior. Neuropsychopharmacology, 2013, 38, 1636-1647.	2.8	63
63	Hippo Signaling Mediates Proliferation, Invasiveness, and Metastatic Potential of Clear Cell Renal Cell Carcinoma. Translational Oncology, 2014, 7, 309-321.	1.7	63
64	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkinâ€™s lymphoma. Nature Communications, 2013, 4, 2549.	5.8	62
65	A statistical model for the analysis of beta values in DNA methylation studies. BMC Bioinformatics, 2016, 17, 480.	1.2	62
66	16p11.2 600 kb Duplications confer risk for typical and atypical Rolandic epilepsy. Human Molecular Genetics, 2014, 23, 6069-6080.	1.4	61
67	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	5.8	61
68	The Aromatase Gene CYP19A1: Several Genetic and Functional Lines of Evidence Supporting a Role in Reading, Speech and Language. Behavior Genetics, 2012, 42, 509-527.	1.4	60
69	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. Nature Communications, 2017, 8, 1511.	5.8	60
70	Human Platelet Lysate versus Fetal Calf Serum: These Supplements Do Not Select for Different Mesenchymal Stromal Cells. Scientific Reports, 2017, 7, 5132.	1.6	60
71	The severity of human periâ€implantitis lesions correlates with the level of submucosal microbial dysbiosis. Journal of Clinical Periodontology, 2018, 45, 1498-1509.	2.3	60
72	Supporting evidence for LRRTM1 imprinting effects in schizophrenia. Molecular Psychiatry, 2009, 14, 743-745.	4.1	59

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73	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
74	DNA methylation signature in peripheral blood reveals distinct characteristics of human X chromosome numerical aberrations. Clinical Epigenetics, 2015, 7, 76.	1.8	59
75	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	5.8	58
76	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. Molecular Psychiatry, 2021, 26, 4179-4190.	4.1	58
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.	1.4	58
78	Deep intronicAPCmutations explain a substantial proportion of patients with familial or early-onset adenomatous polyposis. Human Mutation, 2012, 33, 1045-1050.	1.1	57
79	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. Molecular Psychiatry, 2021, 26, 3004-3017.	4.1	56
80	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
81	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.	1.5	51
82	Genetic risk factors for nonsyndromic cleft lip with or without cleft palate in a Mesoamerican population: Evidence for IRF6 and variants at 8q24 and 10q25. Birth Defects Research Part A: Clinical and Molecular Teratology, 2010, 88, 535-537.	1.6	50
83	Common variation at 10p12.31 near MLLT10 influences meningioma risk. Nature Genetics, 2011, 43, 825-827.	9.4	49
84	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
85	Investigation of the DCDC2 intron 2 deletion/compound short tandem repeat polymorphism in a large German dyslexia sample. Psychiatric Genetics, 2008, 18, 310-312.	0.6	46
86	IRF6 gene variants in Central European patients with nonâ€syndromic cleft lip with or without cleft palate. European Journal of Oral Sciences, 2009, 117, 766-769.	0.7	46
87	LAMP-Seq enables sensitive, multiplexed COVID-19 diagnostics using molecular barcoding. Nature Biotechnology, 2021, 39, 1556-1562.	9.4	46
88	Microduplications at 22q11.21 are associated with non-syndromic classic bladder exstrophy. European Journal of Medical Genetics, 2010, 53, 55-60.	0.7	45
89	Association of a Rare Variant with Mismatch Negativity in a Region Between KIAA0319 and DCDC2 in Dyslexia. Behavior Genetics, 2011, 41, 110-119.	1.4	45
90	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.	1.4	45

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91	Imaging genetics of FOXP2 in dyslexia. European Journal of Human Genetics, 2012, 20, 224-229.	1.4	44
92	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. Molecular Psychiatry, 2021, 26, 2457-2470.	4.1	44
93	Investigation of interaction between DCDC2 and KIAA0319 in a large German dyslexia sample. Journal of Neural Transmission, 2008, 115, 1587-1589.	1.4	41
94	Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis. Familial Cancer, 2016, 15, 281-288.	0.9	40
95	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	40
96	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	2.8	40
97	Patient-derived dendritic cells transduced with an a-fetoprotein-encoding adenovirus and co-cultured with autologous cytokine-induced lymphocytes induce a specific and strong immune response against hepatocellular carcinoma cells. Liver International, 2006, 26, 369-379.	1.9	39
98	Extending the phenotypic spectrum of <scp>RBFOX</scp>1 deletions: Sporadic focal epilepsy. Epilepsia, 2015, 56, e129-33.	2.6	38
99	Variation in GRIN2B contributes to weak performance in verbal shortâ€term memory in children with dyslexia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 503-511.	1.1	37
100	Familial occurrence of the VATER/VACTERL association. Pediatric Surgery International, 2012, 28, 725-729.	0.6	36
101	Stimulation of MMP-1 and CCL2 by NAMPT in PDL Cells. Mediators of Inflammation, 2013, 2013, 1-12.	1.4	36
102	Replication of novel susceptibility locus for nonsyndromic cleft lip with or without cleft palate on chromosome 8q24 in Estonian and Lithuanian patients. American Journal of Medical Genetics, Part A, 2009, 149A, 2551-2553.	0.7	35
103	Association between copy number variants in 16p11.2 and major depressive disorder in a German caseâ€“control sample. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 263-273.	1.1	35
104	Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. Scientific Reports, 2018, 8, 13678.	1.6	35
105	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.	3.1	33
106	Bipolar multiplex families have an increased burden of common risk variants for psychiatric disorders. Molecular Psychiatry, 2021, 26, 1286-1298.	4.1	33
107	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
108	Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. Blood, 2014, 123, 2513-2517.	0.6	32

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109	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.	2.4	32
110	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290.	5.8	31
111	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	1.6	31
112	Integrative genomic analysis of pediatric T-cell lymphoblastic lymphoma reveals candidates of clinical significance. Blood, 2021, 137, 2347-2359.	0.6	31
113	Single nucleotide polymorphisms in the 20q13 amplicon genes in relation to breast cancer risk and clinical outcome. Breast Cancer Research and Treatment, 2011, 130, 905-916.	1.1	30
114	Activation of Invariant NK T Cells in Periodontitis Lesions. Journal of Immunology, 2013, 190, 2282-2291.	0.4	30
115	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.	1.9	30
116	The PF4/PPBP/CXCL5 Gene Cluster Is Associated with Periodontitis. Journal of Dental Research, 2017, 96, 945-952.	2.5	29
117	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.	1.5	29
118	A common variant in Myosin-18B contributes to mathematical abilities in children with dyslexia and intraparietal sulcus variability in adults. Translational Psychiatry, 2013, 3, e229-e229.	2.4	28
119	Shared genetic risk between eating disorderâ€•and substanceâ€useâ€related phenotypes: Evidence from genomeâ€wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
120	Dihydroceramide- and ceramide-profiling provides insights into human cardiometabolic disease etiology. Nature Communications, 2022, 13, 936.	5.8	28
121	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.	1.7	27
122	Copy number variations in 375 patients with oesophageal atresia and/or tracheoesophageal fistula. European Journal of Human Genetics, 2016, 24, 1715-1723.	1.4	27
123	Mapping for dyslexia and related cognitive trait loci provides strong evidence for further risk genes on chromosome 6p21. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2011, 156, 36-43.	1.1	26
124	VATER/VACTERL association. Clinical Dysmorphology, 2012, 21, 191-195.	0.1	26
125	Altered Expression of TGF-Î² Receptors in Hepatocellular Carcinoma â€“ Effects of a Constitutively Active TGF-Î² Type I Receptor Mutant. Digestion, 2005, 71, 78-91.	1.2	25
126	Combining schizophrenia and depression polygenic risk scores improves the genetic prediction of lithium response in bipolar disorder patients. Translational Psychiatry, 2021, 11, 606.	2.4	25

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127	Copy Number Variants in German Patients with Schizophrenia. PLoS ONE, 2013, 8, e64035.	1.1	24
128	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
129	The 9p21.3 risk of childhood acute lymphoblastic leukaemia is explained by a rare high-impact variant in CDKN2A. Scientific Reports, 2015, 5, 15065.	1.6	24
130	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
131	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. Molecular Psychiatry, 2022, 27, 1111-1119.	4.1	24
132	Genetics and Neuroscience in Dyslexia: Perspectives for Education and Remediation. Mind, Brain, and Education, 2007, 1, 162-172.	0.9	23
133	Investigation of the involvement of MIR185 and its target genes in the development of schizophrenia. Journal of Psychiatry and Neuroscience, 2014, 39, 386-396.	1.4	23
134	Novel genetic variants in differentiated thyroid cancer and assessment of the cumulative risk. Scientific Reports, 2015, 5, 8922.	1.6	23
135	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493.	0.6	23
136	Whole-exome sequencing of 81 individuals from 27 multiply affected bipolar disorder families. Translational Psychiatry, 2020, 10, 57.	2.4	23
137	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
138	Clinical and genetic differences between bipolar disorder type 1 and 2 in multiplex families. Translational Psychiatry, 2021, 11, 31.	2.4	22
139	Mendelian randomization provides support for obesity as a risk factor for meningioma. Scientific Reports, 2019, 9, 309.	1.6	21
140	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.	2.3	21
141	De novo duplication of 18p11.21â€“18q12.1 in a female with anorectal malformation. American Journal of Medical Genetics, Part A, 2011, 155, 445-449.	0.7	20
142	Immunochip analysis identifies association of the <scp>RAD</scp> 50/ <scp>IL</scp> 13 region with human longevity. Aging Cell, 2016, 15, 585-588.	3.0	20
143	Regions of common inter-individual DNA methylation differences in human monocytes: genetic basis and potential function. Epigenetics and Chromatin, 2017, 10, 37.	1.8	20
144	Investigating polygenic burden in age at disease onset in bipolar disorder: Findings from an international multicentric study. Bipolar Disorders, 2019, 21, 68-75.	1.1	20

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145	Susceptibility locus for nonâ€syndromic cleft lip with or without cleft palate on chromosome 10q25 confers risk in Estonian patients. European Journal of Oral Sciences, 2010, 118, 317-319.	0.7	19
146	Levetiracetam resistance: Synaptic signatures & corresponding promoter SNPs in epileptic hippocampi. Neurobiology of Disease, 2013, 60, 115-125.	2.1	19
147	Shared genetic etiology between alcohol dependence and major depressive disorder. Psychiatric Genetics, 2018, 28, 66-70.	0.6	19
148	Isolated bladder exstrophy associated with a de novo 0.9 Mb microduplication on chromosome 19p13.12. Birth Defects Research Part A: Clinical and Molecular Teratology, 2013, 97, 133-139.	1.6	18
149	Promoter Variants Determine Î³-Aminobutyric Acid Homeostasis-Related Gene Transcription in Human Epileptic Hippocampi. Journal of Neuropathology and Experimental Neurology, 2011, 70, 1080-1088.	0.9	17
150	Evidence for the involvement of ZNF804A in cognitive processes of relevance to reading and spelling. Translational Psychiatry, 2012, 2, e136-e136.	2.4	17
151	Rs6295 promoter variants of the serotonin type 1A receptor are differentially activated by c-Jun in vitro and correlate to transcript levels in human epileptic brain tissue. Brain Research, 2013, 1499, 136-144.	1.1	17
152	Serum Lipid Levels, Body Mass Index, and Their Role in Coronary Artery Calcification. Circulation: Cardiovascular Genetics, 2015, 8, 327-333.	5.1	17
153	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	0.6	17
154	Identification of ADHD risk genes in extended pedigrees by combining linkage analysis and whole-exome sequencing. Molecular Psychiatry, 2020, 25, 2047-2057.	4.1	17
155	Autosomal-dominant non-syndromic anal atresia: sequencing of candidate genes, array-based molecular karyotyping, and review of the literature. European Journal of Pediatrics, 2011, 170, 741-746.	1.3	16
156	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.	1.1	16
157	Genomewide association study on monoclonal gammopathy of unknown significance (MGUS). European Journal of Haematology, 2017, 99, 70-79.	1.1	16
158	Desaturase Activity and the Risk of Type 2 Diabetes and Coronary Artery Disease: A Mendelian Randomization Study. Nutrients, 2020, 12, 2261.	1.7	16
159	Shared Genetics of Multiple System Atrophy and Inflammatory Bowel Disease. Movement Disorders, 2021, 36, 449-459.	2.2	16
160	Epigenome-wide association study of alcohol use disorder in five brain regions. Neuropsychopharmacology, 2022, 47, 832-839.	2.8	16
161	Hammerhead ribozymes with cleavage site specificity for NUH and NCH display significant anti-hepatitis C viral effect in vitro and in recombinant HepG2 and CCL13 cells. Journal of Hepatology, 2006, 44, 1017-1025.	1.8	15
162	Destabilization of the human epigenome: consequences of foreign DNA insertions. Epigenomics, 2015, 7, 745-755.	1.0	15

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163	Resequencing of VAX1 in patients with nonsyndromic cleft lip with or without cleft palate. Birth Defects Research Part A: Clinical and Molecular Teratology, 2012, 94, 925-933.	1.6	14
164	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.	2.0	14
165	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	1.4	14
166	Genome-wide association study of monoclonal gammopathy of unknown significance (MGUS): comparison with multiple myeloma. Leukemia, 2019, 33, 1817-1821.	3.3	14
167	Methylomic profiling in trisomy 21 identifies cognition- and Alzheimerâ€™s disease-related dysregulation. Clinical Epigenetics, 2019, 11, 195.	1.8	14
168	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.	0.9	14
169	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.	1.7	14
170	Epigenome-Wide Analysis of DNA Methylation in Parkinsonâ€™s Disease Cortex. Life, 2022, 12, 502.	1.1	14
171	Genetic variation at the synaptic vesicle gene SV2A is associated with schizophrenia. Schizophrenia Research, 2012, 141, 262-265.	1.1	13
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