# Peter A Holmans

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 306 papers | 61,525 citations | 94 h-index | 247 g-index |
| 356 ext. papers | 73,577 ext. citations | 11.5 avg, IF | 8.59 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 306 | Genetic modifiers of Huntington disease differentially influence motor and cognitive domains.. *American Journal of Human Genetics*, **2022**, | 11 | 2 |
| 305 | Exome sequencing of individuals with Huntington's disease implicates FAN1 nuclease activity in slowing CAG expansion and disease onset.. *Nature Neuroscience*, **2022**, | 25.5 | 3 |
| 304 | Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**, | 50.4 | 35 |
| 303 | New insights into the genetic etiology of Alzheimer's disease and related dementias.. *Nature Genetics*, **2022**, | 36.3 | 27 |
| 302 | Rare genetic modifiers of Huntington's disease reveal novel pathological mechanisms. *Journal of Neurology, Neurosurgery and Psychiatry*, **2022**, 93, A4.3-A5 | 5.5 | |
| 301 | Genetic risk for schizophrenia is associated with altered visually-induced gamma band activity: evidence from a population sample stratified polygenic risk. *Translational Psychiatry*, **2021**, 11, 592 | 8.6 | 0 |
| 300 | Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. *Molecular Psychiatry*, **2021**, 26, 4496-4510 | 15.1 | 39 |
| 299 | Genetic association of FMRP targets with psychiatric disorders. *Molecular Psychiatry*, **2021**, 26, 2977-2990 | 15.1 | 7 |
| 298 | Timing and Impact of Psychiatric, Cognitive, and Motor Abnormalities in Huntington Disease. *Neurology*, **2021**, 96, e2395-e2406 | 6.5 | 11 |
| 297 | Risk Factors, Clinical Features, and Polygenic Risk Scores in Schizophrenia and Schizoaffective Disorder Depressive-Type. *Schizophrenia Bulletin*, **2021**, 47, 1375-1384 | 1.3 | 0 |
| 296 | Defining functional variants associated with Alzheimer's disease in the induced immune response. *Brain Communications*, **2021**, 3, fcab083 | 4.5 | 3 |
| 295 | 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 | 36.3 | 83 |
| 294 | Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. *Nature Communications*, **2021**, 12, 3417 | 17.4 | 23 |
| 293 | Association Analysis of Chromosome X to Identify Genetic Modifiers of Huntington's Disease. *Journal of Huntington's Disease*, **2021**, 10, 367-375 | 1.9 | 1 |
| 292 | Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. *Molecular Psychiatry*, **2021**, | 15.1 | 5 |
| 291 | Modest changes in Spi1 dosage reveal the potential for altered microglial function as seen in Alzheimer's disease. *Scientific Reports*, **2021**, 11, 14935 | 4.9 | 4 |
| 290 | A polygenic resilience score moderates the genetic risk for schizophrenia. *Molecular Psychiatry*, **2021**, 26, 800-815 | 15.1 | 15 |

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| 289 | Huntington's Disease Pathogenesis: Two Sequential Components. *Journal of Huntington's Disease*, **2021**, 10, 35-51 | 1.9 | 16 |
| 288 | What is the Pathogenic CAG Expansion Length in Huntington's Disease?. *Journal of Huntington's Disease*, **2021**, 10, 175-202 | 1.9 | 7 |
| 287 | Rare Copy Number Variants Are Associated With Poorer Cognition in Schizophrenia. *Biological Psychiatry*, **2021**, 90, 28-34 | 7.9 | 5 |
| 286 | Associations Between Schizophrenia Polygenic Liability, Symptom Dimensions, and Cognitive Ability in Schizophrenia. *JAMA Psychiatry*, **2021**, 78, 1143-1151 | 14.5 | 4 |
| 285 | Cognitive Decline in Alzheimer's Disease Is Not Associated with APOE. *Journal of Alzheimer's Disease*, **2021**, 84, 141-149 | 4.3 | 1 |
| 284 | Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. *Biological Psychiatry*, **2021**, 90, 399-408 | 7.9 | 3 |
| 283 | Schizophrenia, autism spectrum disorders and developmental disorders share specific disruptive coding mutations. *Nature Communications*, **2021**, 12, 5353 | 17.4 | 8 |
| 282 | A genetic exploration of cognitive decline in Alzheimer's disease.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e053063 | 1.2 | |
| 281 | The Relationship Between Polygenic Risk Scores and Cognition in Schizophrenia. *Schizophrenia Bulletin*, **2020**, 46, 336-344 | 1.3 | 38 |
| 280 | Genome-wide association study of progression in Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, e040950 | 1.2 | |
| 279 | Genome-wide meta-analysis of late-onset Alzheimer disease using rare variant imputation in 65,602 subjects identifies risk loci with roles in memory, neurodevelopment, and cardiometabolic traits: The international genomics of Alzheimer project (IGAP). *Alzheimer's and Dementia*, **2020**, 16, e044193 | 1.2 | 0 |
| 278 | Examining pathways between genetic liability for schizophrenia and patterns of tobacco and cannabis use in adolescence. *Psychological Medicine*, **2020**, 1-8 | 6.9 | 2 |
| 277 | Reply: The repeat variant in MSH3 is not a genetic modifier for spinocerebellar ataxia type 3 and Friedreich's ataxia. *Brain*, **2020**, 143, e26 | 11.2 | 1 |
| 276 | Genetic and Functional Analyses Point to FAN1 as the Source of Multiple Huntington Disease Modifier Effects. *American Journal of Human Genetics*, **2020**, 107, 96-110 | 11 | 21 |
| 275 | De novo mutations identified by exome sequencing implicate rare missense variants in SLC6A1 in schizophrenia. *Nature Neuroscience*, **2020**, 23, 179-184 | 25.5 | 47 |
| 274 | Characterization of Single Gene Copy Number Variants in Schizophrenia. *Biological Psychiatry*, **2020**, 87, 736-744 | 7.9 | 8 |
| 273 | The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. *Biological Psychiatry*, **2020**, 88, 169-184 | 7.9 | 57 |
| 272 | A transcriptome-wide association study implicates specific pre- and post-synaptic abnormalities in schizophrenia. *Human Molecular Genetics*, **2020**, 29, 159-167 | 5.6 | 27 |

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| 271 | Genetic Risk Underlying Psychiatric and Cognitive Symptoms in Huntington's Disease. *Biological Psychiatry*, **2020**, 87, 857-865 | 7.9 | 13 |
| 270 | A Population-Based Cohort Study Examining the Incidence and Impact of Psychotic Experiences From Childhood to Adulthood, and Prediction of Psychotic Disorder. *American Journal of Psychiatry*, **2020**, 177, 308-317 | 11.9 | 46 |
| 269 | Association of Genetic Liability to Psychotic Experiences With Neuropsychotic Disorders and Traits. *JAMA Psychiatry*, **2019**, 76, 1256-1265 | 14.5 | 58 |
| 268 | MSH3 modifies somatic instability and disease severity in Huntington's and myotonic dystrophy type 1. *Brain*, **2019**, | 11.2 | 57 |
| 267 | Genotype-phenotype associations in children with copy number variants associated with high neuropsychiatric risk in the UK (IMAGINE-ID): a case-control cohort study. *Lancet Psychiatry,the*, **2019**, 6, 493-505 | 23.3 | 41 |
| 266 | Novel Insight Into the Etiology of Autism Spectrum Disorder Gained by Integrating Expression Data With Genome-wide Association Statistics. *Biological Psychiatry*, **2019**, 86, 265-273 | 7.9 | 26 |
| 265 | Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803 | 36.3 | 662 |
| 264 | Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 223-231 | 3.5 | 2 |
| 263 | Dynamic expression of genes associated with schizophrenia and bipolar disorder across development. *Translational Psychiatry*, **2019**, 9, 74 | 8.6 | 18 |
| 262 | CAG Repeat Not Polyglutamine Length Determines Timing of Huntington's Disease Onset. *Cell*, **2019**, 178, 887-900.e14 | 56.2 | 155 |
| 261 | Gene-based analysis in HRC imputed genome wide association data identifies three novel genes for Alzheimer's disease. *PLoS ONE*, **2019**, 14, e0218111 | 3.7 | 12 |
| 260 | A genetic association study of glutamine-encoding DNA sequence structures, somatic CAG expansion, and DNA repair gene variants, with Huntington disease clinical outcomes. *EBioMedicine*, **2019**, 48, 568-580 | 8.8 | 63 |
| 259 | Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2019**, 18, 1091-1102 | 24.1 | 562 |
| 258 | Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430 | 36.3 | 917 |
| 257 | Comparative genetic architectures of schizophrenia in East Asian and European populations. *Nature Genetics*, **2019**, 51, 1670-1678 | 36.3 | 185 |
| 256 | Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell*, **2019**, 179, 1469-1482.e11 | 56.2 | 402 |
| 255 | Targeted Sequencing of 10,198 Samples Confirms Abnormalities in Neuronal Activity and Implicates Voltage-Gated Sodium Channels in Schizophrenia Pathogenesis. *Biological Psychiatry*, **2019**, 85, 554-562 | 7.9 | 21 |
| 254 | FAN1 modifies Huntington's disease progression by stabilizing the expanded HTT CAG repeat. *Human Molecular Genetics*, **2019**, 28, 650-661 | 5.6 | 56 |

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| 253 | Predictive modeling of schizophrenia from genomic data: Comparison of polygenic risk score with kernel support vector machines approach. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 80-85 | 3.5 | 15 |
| 252 | Structural and Functional Neuroimaging of Polygenic Risk for Schizophrenia: A Recall-by-Genotype-Based Approach. *Schizophrenia Bulletin*, **2019**, 45, 405-414 | 1.3 | 17 |
| 251 | Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. *Nature Genetics*, **2018**, 50, 381-389 | 36.3 | 787 |
| 250 | Disentangling the biological pathways involved in early features of Alzheimer's disease in the Rotterdam Study. *Alzheimer's and Dementia*, **2018**, 14, 848-857 | 1.2 | 23 |
| 249 | POLARIS: Polygenic LD-adjusted risk score approach for set-based analysis of GWAS data. *Genetic Epidemiology*, **2018**, 42, 366-377 | 2.6 | 16 |
| 248 | Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360, | 33.3 | 666 |
| 247 | Association of Elevated Urinary miR-126, miR-155, and miR-29b with Diabetic Kidney Disease. *American Journal of Pathology*, **2018**, 188, 1982-1992 | 5.8 | 44 |
| 246 | Investigating the genetic architecture of general and specific psychopathology in adolescence. *Translational Psychiatry*, **2018**, 8, 145 | 8.6 | 31 |
| 245 | Population-specific genetic modification of Huntington's disease in Venezuela. *PLoS Genetics*, **2018**, 14, e1007274 | 6 | 18 |
| 244 | Association Between Schizophrenia-Related Polygenic Liability and the Occurrence and Level of Mood-Incongruent Psychotic Symptoms in Bipolar Disorder. *JAMA Psychiatry*, **2018**, 75, 28-35 | 14.5 | 66 |
| 243 | A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053 | 7.9 | 93 |
| 242 | Brain Regions Showing White Matter Loss in Huntington's Disease Are Enriched for Synaptic and Metabolic Genes. *Biological Psychiatry*, **2018**, 83, 456-465 | 7.9 | 54 |
| 241 | P1-152: GENE-BASED ANALYSIS IN HRC IMPUTED GERAD GWAS **2018**, 14, P335-P335 | | |
| 240 | Using Genomic Data to Find Disease-Modifying Loci in Huntington's Disease (HD). *Methods in Molecular Biology*, **2018**, 1780, 443-461 | 1.4 | 1 |
| 239 | Identification of genetic variants associated with Huntington's disease progression: a genome-wide association study. *Lancet Neurology, The*, **2017**, 16, 701-711 | 24.1 | 161 |
| 238 | Huntington's disease blood and brain show a common gene expression pattern and share an immune signature with Alzheimer's disease. *Scientific Reports*, **2017**, 7, 44849 | 4.9 | 31 |
| 237 | Haplotype-based stratification of Huntington's disease. *European Journal of Human Genetics*, **2017**, 25, 1202-1209 | 5.3 | 14 |
| 236 | Treating the placenta to prevent adverse effects of gestational hypoxia on fetal brain development. *Scientific Reports*, **2017**, 7, 9079 | 4.9 | 57 |

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| 235 | Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 724-731 | 3.5 | 16 |
| 234 | Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384 | 36.3 | 508 |
| 233 | Genetic modifiers of Mendelian disease: Huntington's disease and the trinucleotide repeat disorders. *Human Molecular Genetics*, **2017**, 26, R83-R90 | 5.6 | 37 |
| 232 | Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35 | 36.3 | 530 |
| 231 | [P1139]: PATHWAY-SPECIFIC GENETIC RISK SCORE ASSOCIATED WITH ALZHEIMER's DISEASE AND WHITE MATTER LESIONS IN COGNITIVELY NORMAL SUBJECTS **2017**, 13, P295-P296 | | |
| 230 | [P2110]: NOVEL APPROACH TO GENE-BASED ANALYSIS OF ALZHEIMER's DISEASE INFORMED BY GENETICS OF PSYCHIATRIC DISORDERS **2017**, 13, P649-P649 | | |
| 229 | A modifier of Huntington's disease onset at the MLH1 locus. *Human Molecular Genetics*, **2017**, 26, 3859-3867 | 5.6 | 59 |
| 228 | Analysis of Intellectual Disability Copy Number Variants for Association With Schizophrenia. *JAMA Psychiatry*, **2016**, 73, 963-969 | 14.5 | 75 |
| 227 | B13 Integrating gene expression changes in human huntington's disease brain with those in mouse models of disease. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A13.2-A13 | 5.5 | |
| 226 | B15 Innate transcriptional dysregulation is associated with proinflammatory pathway activation in huntington's disease myeloid cells. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A14.1-A14 | 5.5 | |
| 225 | Pathogenic copy number variants and SCN1A mutations in patients with intellectual disability and childhood-onset epilepsy. *BMC Medical Genetics*, **2016**, 17, 34 | 2.1 | 16 |
| 224 | RNA-Seq of Huntington's disease patient myeloid cells reveals innate transcriptional dysregulation associated with proinflammatory pathway activation. *Human Molecular Genetics*, **2016**, 25, 2893-2904 | 5.6 | 33 |
| 223 | The HTT CAG-Expansion Mutation Determines Age at Death but Not Disease Duration in Huntington Disease. *American Journal of Human Genetics*, **2016**, 98, 287-98 | 11 | 92 |
| 222 | A potential endophenotype for Alzheimer's disease: cerebrospinal fluid clusterin. *Neurobiology of Aging*, **2016**, 37, 208.e1-208.e9 | 5.6 | 29 |
| 221 | Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. *Nature Neuroscience*, **2016**, 19, 571-7 | 25.5 | 284 |
| 220 | Phenotypic Manifestation of Genetic Risk for Schizophrenia During Adolescence in the General Population. *JAMA Psychiatry*, **2016**, 73, 221-8 | 14.5 | 145 |
| 219 | B17 Blood transcriptome replicates dysregulation found in human huntington's disease brain and shares an immune signature with alzheimer's disease. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A15.1-A15 | 5.5 | |
| 218 | B12 Characterising gene expression changes in mouse lines with varying repeat lengths in HTT. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A13.1-A13 | 5.5 | |

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| 217 | B48 DNA repair pathways as a common genetic mechanism modulating the age at onset in polyglutamine diseases. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A26.1-A26 | 5.5 | |
| 216 | B49 Genetic modifiers of huntington's disease progression. *Journal of Neurology, Neurosurgery and Psychiatry*, **2016**, 87, A26.2-A27 | 5.5 | |
| 215 | Gender differences in CNV burden do not confound schizophrenia CNV associations. *Scientific Reports*, **2016**, 6, 25986 | 4.9 | 6 |
| 214 | P2-082: Comparison of Gene-Based Methods to Identify Novel Alzheimer's Disease Associated Genes **2016**, 12, P640-P640 | | |
| 213 | Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. *Annals of Neurology*, **2016**, 79, 739-747 | 9.4 | 42 |
| 212 | DNA repair pathways underlie a common genetic mechanism modulating onset in polyglutamine diseases. *Annals of Neurology*, **2016**, 79, 983-90 | 9.4 | 135 |
| 211 | Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience*, **2015**, 18, 199-209 | 25.5 | 572 |
| 210 | Identification of Genetic Factors that Modify Clinical Onset of Huntington's Disease. *Cell*, **2015**, 162, 516-26 | 32 | 378 |
| 209 | No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. *European Journal of Human Genetics*, **2015**, 23, 555-7 | 5.3 | 17 |
| 208 | Common polygenic variation enhances risk prediction for Alzheimer's disease. *Brain*, **2015**, 138, 3673-84 | 11.2 | 227 |
| 207 | A systematic screening to identify de novo mutations causing sporadic early-onset Parkinson's disease. *Human Molecular Genetics*, **2015**, 24, 6711-20 | 5.6 | 26 |
| 206 | New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. *International Journal of Epidemiology*, **2015**, 44, 1706-21 | 7.8 | 43 |
| 205 | Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimer's and Dementia*, **2015**, 11, 658-71 | 1.2 | 146 |
| 204 | O4-05-06: A potential endophenotype for Alzheimer's disease: Cerebrospinal fluid clusterin **2015**, 11, P280-P280 | | |
| 203 | The Genetic Modifiers of Motor Onset Age (GeM MOA) Website: Genome-wide Association Analysis for Genetic Modifiers of Huntington's Disease. *Journal of Huntington's Disease*, **2015**, 4, 279-84 | 1.9 | 20 |
| 202 | Similar striatal gene expression profiles in the striatum of the YAC128 and HdhQ150 mouse models of Huntington's disease are not reflected in mutant Huntingtin inclusion prevalence. *BMC Genomics*, **2015**, 16, 1079 | 4.5 | 5 |
| 201 | Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. *Neuron*, **2015**, 86, 1203-14 | 13.9 | 119 |
| 200 | De novo mutations in schizophrenia implicate synaptic networks. *Nature*, **2014**, 506, 179-84 | 50.4 | 1163 |

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| 199 | Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. *Molecular Psychiatry*, **2014**, 19, 1017-1024 | 15.1 | 258 |
| 198 | Biological insights from 108 schizophrenia-associated genetic loci. *Nature*, **2014**, 511, 421-7 | 50.4 | 5249 |
| 197 | Replication of brain function effects of a genome-wide supported psychiatric risk variant in the CACNA1C gene and new multi-locus effects. *NeuroImage*, **2014**, 94, 147-154 | 7.9 | 28 |
| 196 | Pathway analyses implicate glial cells in schizophrenia. *PLoS ONE*, **2014**, 9, e89441 | 3.7 | 45 |
| 195 | Identifying gene-environment interactions in schizophrenia: contemporary challenges for integrated, large-scale investigations. *Schizophrenia Bulletin*, **2014**, 40, 729-36 | 1.3 | 186 |
| 194 | Scientific rigor and the art of motorcycle maintenance. *Nature Biotechnology*, **2014**, 32, 871-3 | 44.5 | 26 |
| 193 | A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. *Human Molecular Genetics*, **2014**, 23, 562-562 | 5.6 | 3 |
| 192 | De novo CNVs in bipolar affective disorder and schizophrenia. *Human Molecular Genetics*, **2014**, 23, 6677-88 | 5.6 | 57 |
| 191 | Biological overlap of attention-deficit/hyperactivity disorder and autism spectrum disorder: evidence from copy number variants. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2014**, 53, 761-70.e26 | 7.2 | 74 |
| 190 | Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS ONE*, **2014**, 9, e94661 | 3.7 | 90 |
| 189 | Analysis of genome-wide association studies of Alzheimer disease and of Parkinson disease to determine if these 2 diseases share a common genetic risk. *JAMA Neurology*, **2013**, 70, 1268-76 | 17.2 | 46 |
| 188 | Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9 | 36.3 | 1153 |
| 187 | Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8 | 36.3 | 2714 |
| 186 | Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94 | 36.3 | 1628 |
| 185 | Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. *Lancet, The*, **2013**, 381, 1371-1379 | 40 | 2112 |
| 184 | Replication of bipolar disorder susceptibility alleles and identification of two novel genome-wide significant associations in a new bipolar disorder case-control sample. *Molecular Psychiatry*, **2013**, 18, 1302-7 | 15.1 | 110 |
| 183 | Genome-wide significant associations in schizophrenia to ITIH3/4, CACNA1C and SDCCAG8, and extensive replication of associations reported by the Schizophrenia PGC. *Molecular Psychiatry*, **2013**, 18, 708-12 | 15.1 | 184 |
| 182 | High loading of polygenic risk for ADHD in children with comorbid aggression. *American Journal of Psychiatry*, **2013**, 170, 909-16 | 11.9 | 110 |

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|---|---|---|---|
| 181 | A pathway-based analysis provides additional support for an immune-related genetic susceptibility to Parkinson's disease. *Human Molecular Genetics*, **2013**, 22, 1039-49 | 5.6 | 96 |
| 180 | Shared polygenic contribution between childhood attention-deficit hyperactivity disorder and adult schizophrenia. *British Journal of Psychiatry*, **2013**, 203, 107-11 | 5.4 | 78 |
| 179 | A genome-wide study shows a limited contribution of rare copy number variants to Alzheimer's disease risk. *Human Molecular Genetics*, **2013**, 22, 816-24 | 5.6 | 26 |
| 178 | Genome-wide association study of clinical dimensions of schizophrenia: polygenic effect on disorganized symptoms. *American Journal of Psychiatry*, **2012**, 169, 1309-17 | 11.9 | 93 |
| 177 | Genome-wide association study of multiplex schizophrenia pedigrees. *American Journal of Psychiatry*, **2012**, 169, 963-73 | 11.9 | 50 |
| 176 | De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. *Molecular Psychiatry*, **2012**, 17, 142-53 | 15.1 | 611 |
| 175 | Genome-wide association study of Alzheimer's disease with psychotic symptoms. *Molecular Psychiatry*, **2012**, 17, 1316-27 | 15.1 | 90 |
| 174 | Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. *Molecular Psychiatry*, **2012**, 17, 193-201 | 15.1 | 104 |
| 173 | Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. *Human Molecular Genetics*, **2012**, 21, 4996-5009 | 5.6 | 145 |
| 172 | Genetic predictors of response to serotonergic and noradrenergic antidepressants in major depressive disorder: a genome-wide analysis of individual-level data and a meta-analysis. *PLoS Medicine*, **2012**, 9, e1001326 | 11.6 | 94 |
| 171 | Permutation-based approaches do not adequately allow for linkage disequilibrium in gene-wide multi-locus association analysis. *European Journal of Human Genetics*, **2012**, 20, 890-6 | 5.3 | 17 |
| 170 | Investigating the contribution of common genetic variants to the risk and pathogenesis of ADHD. *American Journal of Psychiatry*, **2012**, 169, 186-94 | 11.9 | 147 |
| 169 | Genome-wide analysis of copy number variants in attention deficit hyperactivity disorder: the role of rare variants and duplications at 15q13.3. *American Journal of Psychiatry*, **2012**, 169, 195-204 | 11.9 | 195 |
| 168 | Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. *Molecular Psychiatry*, **2012**, 17, 996-1006 | 15.1 | 123 |
| 167 | Genome-wide association of mood-incongruent psychotic bipolar disorder. *Translational Psychiatry*, **2012**, 2, e180 | 8.6 | 51 |
| 166 | The role of variation at APP, PSEN1, PSEN2, and MAPT in late onset Alzheimer's disease. *Journal of Alzheimer's Disease*, **2012**, 28, 377-87 | 4.3 | 47 |
| 165 | Cooperative genome-wide analysis shows increased homozygosity in early onset Parkinson's disease. *PLoS ONE*, **2012**, 7, e28787 | 3.7 | 18 |
| 164 | An examination of single nucleotide polymorphism selection prioritization strategies for tests of gene-gene interaction. *Biological Psychiatry*, **2011**, 70, 198-203 | 7.9 | 10 |

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|---|---|---|---|
| 163 | Genome-wide association study identifies five new schizophrenia loci. *Nature Genetics*, **2011**, 43, 969-76 | 36.3 | 1508 |
| 162 | ACSL6 is associated with the number of cigarettes smoked and its expression is altered by chronic nicotine exposure. *PLoS ONE*, **2011**, 6, e28790 | 3.7 | 8 |
| 161 | Genomewide association analysis of symptoms of alcohol dependence in the molecular genetics of schizophrenia (MGS2) control sample. *Alcoholism: Clinical and Experimental Research*, **2011**, 35, 963-75 | 3.7 | 104 |
| 160 | Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. *Nature Genetics*, **2011**, 43, 429-35 | 36.3 | 1421 |
| 159 | Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. *Molecular Psychiatry*, **2011**, 16, 2-4 | 15.1 | 130 |
| 158 | Genome-wide association study of recurrent early-onset major depressive disorder. *Molecular Psychiatry*, **2011**, 16, 193-201 | 15.1 | 206 |
| 157 | Novel loci for major depression identified by genome-wide association study of Sequenced Treatment Alternatives to Relieve Depression and meta-analysis of three studies. *Molecular Psychiatry*, **2011**, 16, 202-15 | 15.1 | 209 |
| 156 | Fine mapping of ZNF804A and genome-wide significant evidence for its involvement in schizophrenia and bipolar disorder. *Molecular Psychiatry*, **2011**, 16, 429-41 | 15.1 | 221 |
| 155 | Genetic risk sum score comprised of common polygenic variation is associated with body mass index. *Human Genetics*, **2011**, 129, 221-30 | 6.3 | 51 |
| 154 | No evidence that extended tracts of homozygosity are associated with Alzheimer's disease. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 764-71 | 3.5 | 15 |
| 153 | Phenotype evaluation and genomewide linkage study of clinical variables in schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 929-40 | 3.5 | 13 |
| 152 | Evaluation of an approximation method for assessment of overall significance of multiple-dependent tests in a genomewide association study. *Genetic Epidemiology*, **2011**, 35, 861-6 | 2.6 | 39 |
| 151 | The Machado-Joseph disease-associated mutant form of ataxin-3 regulates parkin ubiquitination and stability. *Human Molecular Genetics*, **2011**, 20, 141-54 | 5.6 | 217 |
| 150 | Clinical and cognitive characteristics of children with attention-deficit hyperactivity disorder, with and without copy number variants. *British Journal of Psychiatry*, **2011**, 199, 398-403 | 5.4 | 23 |
| 149 | Copy number variants in schizophrenia: confirmation of five previous findings and new evidence for 3q29 microdeletions and VIPR2 duplications. *American Journal of Psychiatry*, **2011**, 168, 302-16 | 11.9 | 344 |
| 148 | Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. *Nature Genetics*, **2011**, 43, 977-83 | 36.3 | 1094 |
| 147 | Strong genetic evidence for a selective influence of GABAA receptors on a component of the bipolar disorder phenotype. *Molecular Psychiatry*, **2010**, 15, 146-53 | 15.1 | 94 |
| 146 | The bipolar disorder risk allele at CACNA1C also confers risk of recurrent major depression and of schizophrenia. *Molecular Psychiatry*, **2010**, 15, 1016-22 | 15.1 | 389 |

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| 145 | Evidence for rare and common genetic risk variants for schizophrenia at protein kinase C, alpha. *Molecular Psychiatry*, **2010**, 15, 1101-11 | 15.1 | 28 |
| 144 | Genetic evidence implicates the immune system and cholesterol metabolism in the aetiology of Alzheimer's disease. *PLoS ONE*, **2010**, 5, e13950 | 3.7 | 276 |
| 143 | Genetic differences between five European populations. *Human Heredity*, **2010**, 70, 141-9 | 1.1 | 24 |
| 142 | Meta-analysis of genome-wide association studies of attention-deficit/hyperactivity disorder. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2010**, 49, 884-97 | 7.2 | 357 |
| 141 | Case-control genome-wide association study of attention-deficit/hyperactivity disorder. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2010**, 49, 906-20 | 7.2 | 131 |
| 140 | Rare chromosomal deletions and duplications in attention-deficit hyperactivity disorder: a genome-wide analysis. *Lancet, The*, **2010**, 376, 1401-8 | 40 | 399 |
| 139 | Statistical methods for pathway analysis of genome-wide data for association with complex genetic traits. *Advances in Genetics*, **2010**, 72, 141-79 | 3.3 | 74 |
| 138 | Rare copy number variants: a point of rarity in genetic risk for bipolar disorder and schizophrenia. *Archives of General Psychiatry*, **2010**, 67, 318-27 | | 154 |
| 137 | Variation at the GABAA receptor gene, Rho 1 (GABRR1) associated with susceptibility to bipolar schizoaffective disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1347-9 | 3.5 | 14 |
| 136 | No evidence that rare coding variants in ZNF804A confer risk of schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1411-6 | 3.5 | 18 |
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| 133 | Genome-wide linkage and follow-up association study of postpartum mood symptoms. *American Journal of Psychiatry*, **2009**, 166, 1229-37 | 11.9 | 68 |
| 132 | Genetic utility of broadly defined bipolar schizoaffective disorder as a diagnostic concept. *British Journal of Psychiatry*, **2009**, 195, 23-9 | 5.4 | 76 |
| 131 | Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *American Journal of Psychiatry*, **2009**, 166, 540-56 | 11.9 | 355 |
| 130 | Molecular genetic contribution to the developmental course of attention-deficit hyperactivity disorder. *European Child and Adolescent Psychiatry*, **2009**, 18, 26-32 | 5.5 | 31 |
| 129 | Gene-wide analyses of genome-wide association data sets: evidence for multiple common risk alleles for schizophrenia and bipolar disorder and for overlap in genetic risk. *Molecular Psychiatry*, **2009**, 14, 252-60 | 15.1 | 296 |
| 128 | Meta-analysis of 32 genome-wide linkage studies of schizophrenia. *Molecular Psychiatry*, **2009**, 14, 774-85 | 15.1 | 202 |

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| 127 | Genomewide linkage scan of schizophrenia in a large multicenter pedigree sample using single nucleotide polymorphisms. *Molecular Psychiatry*, **2009**, 14, 786-95 | 15.1 | 54 |
| 126 | Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature*, **2009**, 460, 748-52 | 50.4 | 3568 |
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| 122 | Analysis of 10 independent samples provides evidence for association between schizophrenia and a SNP flanking fibroblast growth factor receptor 2. *Molecular Psychiatry*, **2009**, 14, 30-6 | 15.1 | 62 |
| 121 | Genetic control of human brain transcript expression in Alzheimer disease. *American Journal of Human Genetics*, **2009**, 84, 445-58 | 11 | 229 |
| 120 | Gene ontology analysis of GWA study data sets provides insights into the biology of bipolar disorder. *American Journal of Human Genetics*, **2009**, 85, 13-24 | 11 | 333 |
| 119 | Rare chromosomal deletions and duplications increase risk of schizophrenia. *Nature*, **2008**, 455, 237-41 | 50.4 | 1251 |
| 118 | Identification of loci associated with schizophrenia by genome-wide association and follow-up. *Nature Genetics*, **2008**, 40, 1053-5 | 36.3 | 877 |
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| 114 | Evidence that common variation in NEDD9 is associated with susceptibility to late-onset Alzheimer's and Parkinson's disease. *Human Molecular Genetics*, **2008**, 17, 759-67 | 5.6 | 35 |
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| 103 | Linkage analyses of rheumatoid arthritis and related quantitative phenotypes: the GAW15 experience. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S86-95 | 2.6 | 1 |
| 102 | Multiple testing in the genomics era: findings from Genetic Analysis Workshop 15, Group 15. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S124-31 | 2.6 | 11 |
| 101 | Effects of low birth weight, maternal smoking in pregnancy and social class on the phenotypic manifestation of Attention Deficit Hyperactivity Disorder and associated antisocial behaviour: investigation in a clinical sample. *BMC Psychiatry*, **2007**, 7, 26 | 4.2 | 72 |
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| 99 | Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*, **2007**, 447, 661-78 | 50.4 | 7801 |
| 98 | Genome-wide linkage analysis of 723 affected relative pairs with late-onset Alzheimer's disease. *Human Molecular Genetics*, **2007**, 16, 2703-12 | 5.6 | 44 |
| 97 | Conservation of regional gene expression in mouse and human brain. *PLoS Genetics*, **2007**, 3, e59 | 6 | 78 |
| 96 | Promoting Measured Genes and Measured Environments: On the Importance of Careful Statistical Analyses and Biological RelevanceReply. *Archives of General Psychiatry*, **2007**, 64, 378 | | 1 |
| 95 | Genetics of recurrent early-onset major depression (GenRED): significant linkage on chromosome 15q25-q26 after fine mapping with single nucleotide polymorphism markers. *American Journal of Psychiatry*, **2007**, 164, 259-64 | 11.9 | 43 |
| 94 | Evidence for novel susceptibility genes for late-onset Alzheimer's disease from a genome-wide association study of putative functional variants. *Human Molecular Genetics*, **2007**, 16, 865-73 | 5.6 | 221 |
| 93 | Expression profiling of Huntington's disease models suggests that brain-derived neurotrophic factor depletion plays a major role in striatal degeneration. *Journal of Neuroscience*, **2007**, 27, 11758-68 | 6.6 | 183 |
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| 89 | Effects of differential genotyping error rate on the type I error probability of case-control studies. *Human Heredity*, **2006**, 61, 55-64 | 1.1 | 78 |
| 88 | Convergent evidence that oligodendrocyte lineage transcription factor 2 (OLIG2) and interacting genes influence susceptibility to schizophrenia. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 12469-74 | 11.5 | 101 |
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| 86 | A scan of chromosome 10 identifies a novel locus showing strong association with late-onset Alzheimer disease. *American Journal of Human Genetics*, **2006**, 78, 78-88 | 11 | 137 |
| 85 | Reply to Bertram et al.. *American Journal of Human Genetics*, **2006**, 79, 183-184 | 11 | 4 |
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| 83 | Genome wide significant linkage in schizophrenia conditioning on occurrence of depressive episodes. *Journal of Medical Genetics*, **2006**, 43, 563-7 | 5.8 | 15 |
| 82 | Effect of genotyping error on type-I error rate of affected sib pair studies with genotyped parents. *Human Heredity*, **2005**, 59, 157-64 | 1.1 | 9 |
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| 80 | Design of case-controls studies with unscreened controls. *Annals of Human Genetics*, **2005**, 69, 566-76 | 2.2 | 91 |
| 79 | Stage 2 of the Wellcome Trust UK-Irish bipolar affective disorder sibling-pair genome screen: evidence for linkage on chromosomes 6q16-q21, 4q12-q21, 9p21, 10p14-p12 and 18q22. *Molecular Psychiatry*, **2005**, 10, 831-41 | 15.1 | 52 |
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| 76 | Genome screen for loci influencing age at onset and rate of decline in late onset Alzheimer's disease. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2005**, 135B, 24-32 | 3.5 | 56 |
| 75 | Association studies between risk for late-onset Alzheimer's disease and variants in insulin degrading enzyme. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2005**, 136B, 62-8 | 3.5 | 30 |
| 74 | Covariate linkage analysis of GAW14 simulated data incorporating subclinical phenotype, sex, population, parent-of-origin, and interaction. *BMC Genetics*, **2005**, 6 Suppl 1, S45 | 2.6 | 8 |

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| 73 | The effect of linkage disequilibrium on linkage analysis of incomplete pedigrees. *BMC Genetics*, **2005**, 6 Suppl 1, S6 | 2.6 | 22 |
| 72 | Genomewide linkage scan in schizoaffective disorder: significant evidence for linkage at 1q42 close to DISC1, and suggestive evidence at 22q11 and 19p13. *Archives of General Psychiatry*, **2005**, 62, 1081-8 | | 164 |
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| 69 | Alpha-T-catenin is expressed in human brain and interacts with the Wnt signaling pathway but is not responsible for linkage to chromosome 10 in Alzheimer's disease. *NeuroMolecular Medicine*, **2004**, 5, 133-46 | 4.6 | 38 |
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| 67 | Bayesian trio models for association in the presence of genotyping errors. *Genetic Epidemiology*, **2004**, 26, 70-80 | 2.6 | 21 |
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| 65 | Genomewide significant linkage to recurrent, early-onset major depressive disorder on chromosome 15q. *American Journal of Human Genetics*, **2004**, 74, 1154-67 | 11 | 102 |
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| 60 | A systematic genomewide linkage study in 353 sib pairs with schizophrenia. *American Journal of Human Genetics*, **2003**, 73, 1355-67 | 11 | 111 |
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| 54 | Detecting gene-gene interactions using affected sib pair analysis with covariates. *Human Heredity*, **2002**, 53, 92-102 | 1.1 | 37 |
| 53 | A genomewide linkage study of age at onset in schizophrenia. *American Journal of Medical Genetics Part A*, **2001**, 105, 439-45 | | 55 |
| 52 | Likelihood-ratio affected sib-pair tests applied to multiply affected sibships: issues of power and type I error rate. *Genetic Epidemiology*, **2001**, 20, 44-56 | 2.6 | 11 |
| 51 | Detailed genotyping demonstrates association between the slow acetylator genotype for N-acetyltransferase 2 (NAT2) and familial Parkinson's disease. *Movement Disorders*, **2000**, 15, 30-5 | 7 | 32 |
| 50 | Clustering methods applied to allele sharing data. *Genetic Epidemiology*, **2000**, 19 Suppl 1, S57-63 | 2.6 | 7 |
| 49 | Multicenter linkage study of schizophrenia candidate regions on chromosomes 5q, 6q, 10p, and 13q: schizophrenia linkage collaborative group III. *American Journal of Human Genetics*, **2000**, 67, 652-63 | 11 | 182 |
| 48 | Susceptibility locus for Alzheimer's disease on chromosome 10. *Science*, **2000**, 290, 2304-5 | 33.3 | 345 |
| 47 | A two-stage genome scan for schizophrenia susceptibility genes in 196 affected sibling pairs. *Human Molecular Genetics*, **1999**, 8, 1729-39 | 5.6 | 122 |
| 46 | A full genome scan for late onset Alzheimer's disease. *Human Molecular Genetics*, **1999**, 8, 237-45 | 5.6 | 279 |
| 45 | Familial phenotype differences in PKD11. *Kidney International*, **1999**, 56, 34-40 | 9.9 | 44 |
| 44 | Variation in DCP1, encoding ACE, is associated with susceptibility to Alzheimer disease. *Nature Genetics*, **1999**, 21, 71-2 | 36.3 | 236 |
| 43 | Alpha-2 macroglobulin gene and Alzheimer disease. *Nature Genetics*, **1999**, 22, 17-9; author reply 21-2 | 36.3 | 88 |
| 42 | Autosome search for schizophrenia susceptibility genes in multiply affected families. *Molecular Psychiatry*, **1999**, 4, 353-9 | 15.1 | 19 |
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| 38 | A meta-analysis and transmission disequilibrium study of association between the dopamine D3 receptor gene and schizophrenia. *Molecular Psychiatry*, **1998**, 3, 141-9 | 15.1 | 143 |

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| 37 | Dopa-responsive dystonia: a clinical and molecular genetic study. *Annals of Neurology*, **1998**, 44, 649-56 | 9.4 | 143 |
| 36 | Efficient strategies for genome scanning with affected sib pairs. *American Journal of Human Genetics*, **1998**, 62, 204-7 | 11 | 2 |
| 35 | Reply to Curtis. *American Journal of Human Genetics*, **1998**, 62, 205-207 | 11 | |
| 34 | A simple method for analyzing microsatellite allele image patterns generated from DNA pools and its application to allelic association studies. *American Journal of Human Genetics*, **1998**, 62, 1189-97 | 11 | 105 |
| 33 | The butyrylcholinesterase K variant and susceptibility to Alzheimer's disease. *Journal of Medical Genetics*, **1998**, 35, 1034-5 | 5.8 | 23 |
| 32 | Genetic studies on chromosome 12 in late-onset Alzheimer disease. *JAMA - Journal of the American Medical Association*, **1998**, 280, 619-22 | 27.4 | 68 |
| 31 | Factor-derived subsyndromes of schizophrenia and familial morbid risks. *Schizophrenia Research*, **1997**, 23, 231-8 | 3.6 | 50 |
| 30 | Association of slow acetylator genotype for N-acetyltransferase 2 with familial Parkinson's disease. *Lancet, The*, **1997**, 350, 1136-9 | 40 | 110 |
| 29 | Association studies of bipolar disorder at the human serotonin transporter gene (hSERT; 5HTT). *Molecular Psychiatry*, **1997**, 2, 398-402 | 15.1 | 140 |
| 28 | Association of the angiotensin I converting enzyme gene deletion polymorphism with early onset of ESRF in PKD1 adult polycystic kidney disease. *Kidney International*, **1997**, 52, 607-13 | 9.9 | 63 |
| 27 | Linkage study of chromosome 6p in sib-pairs with schizophrenia. *American Journal of Medical Genetics Part A*, **1997**, 74, 319-23 | | 12 |
| 26 | Association between a PS-1 intronic polymorphism and late onset Alzheimer's disease. *NeuroReport* , **1996**, 7, 2155-8 | 1.7 | 23 |
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| 24 | Additional support for schizophrenia linkage on chromosomes 6 and 8: a multicenter study. Schizophrenia Linkage Collaborative Group for Chromosomes 3, 6 and 8. *American Journal of Medical Genetics Part A*, **1996**, 67, 580-94 | | 147 |
| 23 | Susceptibility to multiple sclerosis and the immunoglobulin heavy chain variable region. *Journal of Neurology*, **1995**, 242, 677-82 | 5.5 | 30 |
| 22 | Partial characterization and assignment of the gene for protoporphyrinogen oxidase and variegate porphyria to human chromosome 1q23. *Human Molecular Genetics*, **1995**, 4, 2387-90 | 5.6 | 58 |
| 21 | Multiple sclerosis and the HLA-D region: linkage and association studies. *Journal of Neuroimmunology*, **1995**, 58, 183-90 | 3.5 | 58 |
| 20 | Genome scan for association and linkage. *Genetic Epidemiology*, **1995**, 12, 613-8 | 2.6 | 2 |

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| 19 | No linkage or association between multiple sclerosis and the myelin basic protein gene in affected sibling pairs. *Journal of Neurology, Neurosurgery and Psychiatry*, **1994**, 57, 1191-4 | 5.5 | 23 |
| 18 | No linkage between multiple sclerosis and the T cell receptor alpha chain locus. *Journal of the Neurological Sciences*, **1994**, 124, 32-7 | 3.2 | 11 |
| 17 | Characterization of single gene copy number variants in schizophrenia | | 1 |
| 16 | Genome-Wide Association Identifies the First Risk Loci for Psychosis in Alzheimer Disease | | 1 |
| 15 | Common schizophrenia alleles are enriched in mutation-intolerant genes and maintained by background selection | | 20 |
| 14 | Genome-wide association study identifies 30 Loci Associated with Bipolar Disorder | | 28 |
| 13 | The timing and impact of psychiatric, cognitive and motor abnormalities in Huntington's disease | | 1 |
| 12 | Schizophrenia, autism spectrum disorders and developmental disorders share specific disruptive coding mutations | | 1 |
| 11 | Genome-wide association study of over 40,000 bipolar disorder cases provides new insights into the underlying biology | | 11 |
| 10 | New insights on the genetic etiology of Alzheimer's and related dementia | | 25 |
| 9 | Association between schizophrenia and both loss of function and missense mutations in paralog conserved sites of voltage-gated sodium channels | | 2 |
| 8 | Gene-Based Analysis in HRC Imputed Genome Wide Association Data Identifies Three Novel Genes For Alzheimer's Disease | | 1 |
| 7 | A Transcriptome Wide Association Study implicates specific pre- and post-synaptic abnormalities in Schizophrenia | | 1 |
| 6 | Comparative genetic architectures of schizophrenia in East Asian and European populations | | 8 |
| 5 | Huntington's disease onset is determined by length of uninterrupted CAG, not encoded polyglutamine, and is modified by DNA maintenance mechanisms | | 2 |
| 4 | Analyses of rare and common alleles in parent-proband trios implicate rare missense variants in SLC6A1 in schizophrenia and confirm the involvement of loss of function intolerant and neurodevelopmental disorder genes | | 2 |
| 3 | Genetic risk underlying psychiatric and cognitive symptoms in Huntington's Disease | | 1 |
| 2 | Genome-Wide Meta-Analysis of Late-Onset Alzheimer's Disease Using Rare Variant Imputation in 65,602 Subjects Identifies Novel Rare Variant Locus NCK2: The International Genomics of Alzheimer's Project (IGAP) | | 2 |

# List of Publications

1 The impact of genetic risk for Alzheimer's disease on the structural brain networks of young adults 1