# Yanling Liu

## List of Publications by Citations



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|---|---|---|---|
| 160 papers | 12,664 citations | 51 h-index | 112 g-index |
| 191 ext. papers | 15,905 ext. citations | 10 avg, IF | 6.56 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 160 | Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94 | 36.3 | 1628 |
| 159 | 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 |
| 158 | Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803 | 36.3 | 662 |
| 157 | Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience*, **2015**, 18, 199-209 | 25.5 | 572 |
| 156 | Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. *Science*, **2018**, 359, 693-697 | 33.3 | 547 |
| 155 | Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362, | 33.3 | 434 |
| 154 | Mutations in the gene encoding gap junction protein beta-3 associated with autosomal dominant hearing impairment. *Nature Genetics*, **1998**, 20, 370-3 | 36.3 | 376 |
| 153 | Genetic control of individual differences in gene-specific methylation in human brain. *American Journal of Human Genetics*, **2010**, 86, 411-9 | 11 | 329 |
| 152 | Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362, | 33.3 | 319 |
| 151 | Removing batch effects in analysis of expression microarray data: an evaluation of six batch adjustment methods. *PLoS ONE*, **2011**, 6, e17238 | 3.7 | 303 |
| 150 | Genome-wide association study of bipolar disorder in European American and African American individuals. *Molecular Psychiatry*, **2009**, 14, 755-63 | 15.1 | 287 |
| 149 | Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362, | 33.3 | 277 |
| 148 | Genome-wide association study of obsessive-compulsive disorder. *Molecular Psychiatry*, **2013**, 18, 788-98 | 15.1 | 244 |
| 147 | Polymorphisms at the G72/G30 gene locus, on 13q33, are associated with bipolar disorder in two independent pedigree series. *American Journal of Human Genetics*, **2003**, 72, 1131-40 | 11 | 228 |
| 146 | The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12 | 25.5 | 226 |
| 145 | Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics*, **2013**, 9, e1003864 | 6 | 189 |
| 144 | De novo genic mutations among a Chinese autism spectrum disorder cohort. *Nature Communications*, **2016**, 7, 13316 | 17.4 | 183 |

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| 143 | Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *American Journal of Human Genetics*, **2015**, 96, 283-94 | 11 | 161 |
| 142 | After GWAS: searching for genetic risk for schizophrenia and bipolar disorder. *American Journal of Psychiatry*, **2011**, 168, 253-6 | 11.9 | 159 |
| 141 | Clock genes may influence bipolar disorder susceptibility and dysfunctional circadian rhythm. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1047-55 | 3.5 | 159 |
| 140 | Genome-wide association study meta-analysis of European and Asian-ancestry samples identifies three novel loci associated with bipolar disorder. *Molecular Psychiatry*, **2013**, 18, 195-205 | 15.1 | 155 |
| 139 | Genetic associations with schizophrenia: meta-analyses of 12 candidate genes. *Schizophrenia Research*, **2008**, 104, 96-107 | 3.6 | 145 |
| 138 | Frequency of SCA1, SCA2, SCA3/MJD, SCA6, SCA7, and DRPLA CAG trinucleotide repeat expansion in patients with hereditary spinocerebellar ataxia from Chinese kindreds. *Archives of Neurology*, **2000**, 57, 540-4 | | 144 |
| 137 | Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362, | 33.3 | 142 |
| 136 | Genome-wide association study of Tourette‘s syndrome. *Molecular Psychiatry*, **2013**, 18, 721-8 | 15.1 | 138 |
| 135 | Enrichment of cis-regulatory gene expression SNPs and methylation quantitative trait loci among bipolar disorder susceptibility variants. *Molecular Psychiatry*, **2013**, 18, 340-6 | 15.1 | 134 |
| 134 | Mood disorder susceptibility gene CACNA1C modifies mood-related behaviors in mice and interacts with sex to influence behavior in mice and diagnosis in humans. *Biological Psychiatry*, **2010**, 68, 801-10 | 7.9 | 131 |
| 133 | Genome-wide association study of 40,000 individuals identifies two novel loci associated with bipolar disorder. *Human Molecular Genetics*, **2016**, 25, 3383-3394 | 5.6 | 125 |
| 132 | Singleton deletions throughout the genome increase risk of bipolar disorder. *Molecular Psychiatry*, **2009**, 14, 376-80 | 15.1 | 121 |
| 131 | Inflammation-related biomarkers in major psychiatric disorders: a cross-disorder assessment of reproducibility and specificity in 43 meta-analyses. *Translational Psychiatry*, **2019**, 9, 233 | 8.6 | 112 |
| 130 | Rare variants in neuronal excitability genes influence risk for bipolar disorder. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 3576-81 | 11.5 | 112 |
| 129 | Genes with de novo mutations are shared by four neuropsychiatric disorders discovered from NPdenovo database. *Molecular Psychiatry*, **2016**, 21, 290-7 | 15.1 | 109 |
| 128 | Two gene co-expression modules differentiate psychotics and controls. *Molecular Psychiatry*, **2013**, 18, 1308-14 | 15.1 | 107 |
| 127 | Cross-disorder genome-wide analyses suggest a complex genetic relationship between Tourette‘s syndrome and OCD. *American Journal of Psychiatry*, **2015**, 172, 82-93 | 11.9 | 101 |
| 126 | Transcriptome sequencing and genome-wide association analyses reveal lysosomal function and actin cytoskeleton remodeling in schizophrenia and bipolar disorder. *Molecular Psychiatry*, **2015**, 20, 563-572 | 15.1 | 96 |

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| 125 | Genome-wide association study implicates NDST3 in schizophrenia and bipolar disorder. *Nature Communications*, **2013**, 4, 2739 | 17.4 | 88 |
| 124 | Maternal preconception body mass index and offspring cord blood DNA methylation: exploration of early life origins of disease. *Environmental and Molecular Mutagenesis*, **2014**, 55, 223-30 | 3.2 | 86 |
| 123 | Allelic association of G72/G30 with schizophrenia and bipolar disorder: a comprehensive meta-analysis. *Schizophrenia Research*, **2008**, 98, 89-97 | 3.6 | 86 |
| 122 | A rare mutation of CACNA1C in a patient with bipolar disorder, and decreased gene expression associated with a bipolar-associated common SNP of CACNA1C in brain. *Molecular Psychiatry*, **2014**, 19, 890-4 | 15.1 | 75 |
| 121 | Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. *Nature Communications*, **2018**, 9, 3121 | 17.4 | 74 |
| 120 | Correlation between DNA methylation and gene expression in the brains of patients with bipolar disorder and schizophrenia. *Bipolar Disorders*, **2014**, 16, 790-9 | 3.8 | 71 |
| 119 | Genome-wide linkage and follow-up association study of postpartum mood symptoms. *American Journal of Psychiatry*, **2009**, 166, 1229-37 | 11.9 | 68 |
| 118 | SLC39A5 mutations interfering with the BMP/TGF-□pathway in non-syndromic high myopia. *Journal of Medical Genetics*, **2014**, 51, 518-25 | 5.8 | 66 |
| 117 | A Bayesian framework that integrates multi-omics data and gene networks predicts risk genes from schizophrenia GWAS data. *Nature Neuroscience*, **2019**, 22, 691-699 | 25.5 | 62 |
| 116 | Whole-genome association mapping of gene expression in the human prefrontal cortex. *Molecular Psychiatry*, **2010**, 15, 779-84 | 15.1 | 60 |
| 115 | Inherited and multiple de novo mutations in autism/developmental delay risk genes suggest a multifactorial model. *Molecular Autism*, **2018**, 9, 64 | 6.5 | 58 |
| 114 | A network-based approach to prioritize results from genome-wide association studies. *PLoS ONE*, **2011**, 6, e24220 | 3.7 | 57 |
| 113 | Accuracy of CNV Detection from GWAS Data. *PLoS ONE*, **2011**, 6, e14511 | 3.7 | 57 |
| 112 | Genetic imaging of the association of oxytocin receptor gene (OXTR) polymorphisms with positive maternal parenting. *Frontiers in Behavioral Neuroscience*, **2014**, 8, 21 | 3.5 | 54 |
| 111 | Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. *Molecular Psychiatry*, **2017**, 22, 1282-1290 | 15.1 | 53 |
| 110 | Genome-wide association of bipolar disorder suggests an enrichment of replicable associations in regions near genes. *PLoS Genetics*, **2011**, 7, e1002134 | 6 | 53 |
| 109 | Cerebellar telomere length and psychiatric disorders. *Behavior Genetics*, **2010**, 40, 250-4 | 3.2 | 51 |
| 108 | The transcription factor POU3F2 regulates a gene coexpression network in brain tissue from patients with psychiatric disorders. *Science Translational Medicine*, **2018**, 10, | 17.5 | 46 |

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| 107 | Intronic pentanucleotide TTTCA repeat insertion in the SAMD12 gene causes familial cortical myoclonic tremor with epilepsy type 1. *Brain*, **2018**, 141, 2280-2288 | 11.2 | 45 |
| 106 | Mutations of P4HA2 encoding prolyl 4-hydroxylase 2 are associated with nonsyndromic high myopia. *Genetics in Medicine*, **2015**, 17, 300-6 | 8.1 | 44 |
| 105 | The long noncoding RNA may regulate expression of several schizophrenia-related genes. *Science Translational Medicine*, **2018**, 10, | 17.5 | 42 |
| 104 | A decade in psychiatric GWAS research. *Molecular Psychiatry*, **2019**, 24, 378-389 | 15.1 | 40 |
| 103 | Genome-wide association analysis of age at onset and psychotic symptoms in bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 370-8 | 3.5 | 39 |
| 102 | Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. *Scientific Reports*, **2016**, 6, 18909 | 4.9 | 39 |
| 101 | Genome-wide association study of personality traits in bipolar patients. *Psychiatric Genetics*, **2011**, 21, 190-4 | 2.9 | 36 |
| 100 | A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. *Nature Genetics*, **2020**, 52, 1239-1246 | 36.3 | 35 |
| 99 | Fine mapping supports previous linkage evidence for a bipolar disorder susceptibility locus on 13q32. *American Journal of Medical Genetics Part A*, **2001**, 105, 375-80 | | 32 |
| 98 | Genome-wide copy number variation analysis in a Chinese autism spectrum disorder cohort. *Scientific Reports*, **2017**, 7, 44155 | 4.9 | 30 |
| 97 | Whole-genome sequencing of monozygotic twins discordant for schizophrenia indicates multiple genetic risk factors for schizophrenia. *Journal of Genetics and Genomics*, **2017**, 44, 295-306 | 4 | 30 |
| 96 | Revealing the brain's molecular architecture. *Science*, **2018**, 362, 1262-1263 | 33.3 | 29 |
| 95 | Genome-wide association study identifies 30 Loci Associated with Bipolar Disorder | | 28 |
| 94 | Loci nominally associated with autism from genome-wide analysis show enrichment of brain expression quantitative trait loci but not lymphoblastoid cell line expression quantitative trait loci. *Molecular Autism*, **2012**, 3, 3 | 6.5 | 27 |
| 93 | No evidence for association between 19 cholinergic genes and bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2007**, 144B, 715-23 | 3.5 | 26 |
| 92 | Genetic tests of biologic systems in affective disorders. *Molecular Psychiatry*, **2005**, 10, 719-40 | 15.1 | 26 |
| 91 | Genetics and epigenetics of circadian rhythms and their potential roles in neuropsychiatric disorders. *Neuroscience Bulletin*, **2015**, 31, 141-59 | 4.3 | 25 |
| 90 | Sequence variation in DOCK9 and heterogeneity in bipolar disorder. *Psychiatric Genetics*, **2007**, 17, 274-86 | 2.9 | 25 |

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| 89 | Genome-wide linkage analysis of 972 bipolar pedigrees using single-nucleotide polymorphisms. *Molecular Psychiatry*, **2012**, 17, 818-26 | 15.1 | 24 |
| 88 | Brain expression quantitative trait locus mapping informs genetic studies of psychiatric diseases. *Neuroscience Bulletin*, **2011**, 27, 123-33 | 4.3 | 23 |
| 87 | Neurotransmission and bipolar disorder: a systematic family-based association study. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1270-7 | 3.5 | 22 |
| 86 | A comparative study of the genetic components of three subcategories of autism spectrum disorder. *Molecular Psychiatry*, **2019**, 24, 1720-1731 | 15.1 | 18 |
| 85 | Data mining approaches for genome-wide association of mood disorders. *Psychiatric Genetics*, **2012**, 22, 55-61 | 2.9 | 18 |
| 84 | An evaluation of the assembly of an approximately 15-Mb region on human chromosome 13q32-q33 linked to bipolar disorder and schizophrenia. *Genomics*, **2002**, 79, 635-56 | 4.3 | 18 |
| 83 | DNA Methylation and Psychiatric Disorders. *Progress in Molecular Biology and Translational Science*, **2018**, 157, 175-232 | 4 | 17 |
| 82 | Expression of the G72/G30 gene in transgenic mice induces behavioral changes. *Molecular Psychiatry*, **2014**, 19, 175-83 | 15.1 | 17 |
| 81 | SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015, | 5 | 17 |
| 80 | Sex-differential DNA methylation and associated regulation networks in human brain implicated in the sex-biased risks of psychiatric disorders. *Molecular Psychiatry*, **2021**, 26, 835-848 | 15.1 | 17 |
| 79 | Ethnic disparities in the perception of ethical risks from psychiatric genetic studies. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2011**, 156B, 569-80 | 3.5 | 16 |
| 78 | Protein disulfide isomerases are promising targets for predicting the survival and tumor progression in glioma patients. *Aging*, **2020**, 12, 2347-2372 | 5.6 | 16 |
| 77 | Three dysconnectivity patterns in treatment-resistant schizophrenia patients and their unaffected siblings. *NeuroImage: Clinical*, **2015**, 8, 95-103 | 5.3 | 15 |
| 76 | Positional effects revealed in Illumina methylation array and the impact on analysis. *Epigenomics*, **2018**, 10, 643-659 | 4.4 | 14 |
| 75 | Molecular network analysis enhances understanding of the biology of mental disorders. *BioEssays*, **2014**, 36, 606-16 | 4.1 | 13 |
| 74 | Preliminary genetic imaging study of the association between estrogen receptor-gene polymorphisms and harsh human maternal parenting. *Neuroscience Letters*, **2012**, 525, 17-22 | 3.3 | 13 |
| 73 | Genome wide association study identifies variants in NBEA associated with migraine in bipolar disorder. *Journal of Affective Disorders*, **2015**, 172, 453-61 | 6.6 | 12 |
| 72 | Genome-wide significant association between a negative mood delusions dimension in bipolar disorder and genetic variation on chromosome 3q26.1. *Translational Psychiatry*, **2012**, 2, e165 | 8.6 | 12 |

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| 71 | PDLIM5 and susceptibility to bipolar disorder: a family-based association study and meta-analysis. *Psychiatric Genetics*, **2008**, 18, 116-21 | 2.9 | 11 |
| 70 | Integration of multi-omics data for integrative gene regulatory network inference. *International Journal of Data Mining and Bioinformatics*, **2017**, 18, 223-239 | 0.5 | 11 |
| 69 | Impact of a cis-associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. *British Journal of Psychiatry*, **2016**, 208, 128-37 | 5.4 | 10 |
| 68 | Evidence for association of bipolar disorder to haplotypes in the 22q12.3 region near the genes stargazin, IFT27 and parvalbumin. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 941-50 | 3.5 | 10 |
| 67 | Database of genetic studies of bipolar disorder. *Psychiatric Genetics*, **2011**, 21, 57-68 | 2.9 | 10 |
| 66 | Common and rare variants of DAOA in bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 960-6 | 3.5 | 10 |
| 65 | Intronic (TTTGA) insertion in SAMD12 also causes familial cortical myoclonic tremor with epilepsy. *Movement Disorders*, **2019**, 34, 1571-1576 | 7 | 9 |
| 64 | Multiblock discriminant analysis for integrative genomic study. *BioMed Research International*, **2015** , 2015, 783592 | 3 | 8 |
| 63 | eQTL epistasis: detecting epistatic effects and inferring hierarchical relationships of genes in biological pathways. *Bioinformatics*, **2015**, 31, 656-64 | 7.2 | 8 |
| 62 | Genetic association of bipolar disorder with the (3) nicotinic receptor subunit gene. *Psychiatric Genetics*, **2011**, 21, 77-84 | 2.9 | 8 |
| 61 | Further evidence for an association of G72/G30 with schizophrenia in Chinese. *Schizophrenia Research*, **2009**, 107, 324-6 | 3.6 | 8 |
| 60 | New ZNF644 mutations identified in patients with high myopia. *Molecular Vision*, **2014**, 20, 939-46 | 2.3 | 8 |
| 59 | Drug Response-Related DNA Methylation Changes in Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. *Frontiers in Neuroscience*, **2021**, 15, 674273 | 5.1 | 8 |
| 58 | NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis. *Translational Psychiatry*, **2019**, 9, 230 | 8.6 | 7 |
| 57 | GWAS significance thresholds for deep phenotyping studies can depend upon minor allele frequencies and sample size. *Molecular Psychiatry*, **2021**, 26, 2048-2055 | 15.1 | 7 |
| 56 | Genetic analysis of deep phenotyping projects in common disorders. *Schizophrenia Research*, **2018**, 195, 51-57 | 3.6 | 7 |
| 55 | No association of trace amine receptor genes with bipolar disorder. *Molecular Psychiatry*, **2007**, 12, 979-81 | 15.1 | 7 |
| 54 | Polygenic risk for anxiety influences anxiety comorbidity and suicidal behavior in bipolar disorder. *Translational Psychiatry*, **2020**, 10, 298 | 8.6 | 7 |

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| 53 | Electrospun polycaprolactone/hydroxyapatite/ZnO films as potential biomaterials for application in bone-tendon interface repair. *Colloids and Surfaces B: Biointerfaces*, **2021**, 204, 111825 | 6 | 7 |
| 52 | Shared Molecular Neuropathology Across Major Psychiatric Disorders Parallels Polygenic Overlap. *Focus (American Psychiatric Publishing)*, **2019**, 17, 66-72 | 1.1 | 6 |
| 51 | BrainEXP: a database featuring with spatiotemporal expression variations and co-expression organizations in human brains. *Bioinformatics*, **2019**, 35, 172-174 | 7.2 | 6 |
| 50 | BDNF expression in lymphoblastoid cell lines carrying BDNF SNPs associated with bipolar disorder. *Psychiatric Genetics*, **2012**, 22, 253-5 | 2.9 | 6 |
| 49 | MutScreener: primer design tool for PCR-direct sequencing. *Nucleic Acids Research*, **2006**, 34, W660-4 | 20.1 | 6 |
| 48 | Frequency Finder: a multi-source web application for collection of public allele frequencies of SNP markers. *Bioinformatics*, **2004**, 20, 439-43 | 7.2 | 6 |
| 47 | Mutation screening of two candidate genes from 13q32 in families affected with Bipolar disorder: human peptide transporter (SLC15A1) and human glypican5 (GPC5). *BMC Genomics*, **2002**, 3, 30 | 4.5 | 6 |
| 46 | Rare inherited missense variants of POGZ associate with autism risk and disrupt neuronal development. *Journal of Genetics and Genomics*, **2019**, 46, 247-257 | 4 | 5 |
| 45 | Inference of SNP-gene regulatory networks by integrating gene expressions and genetic perturbations. *BioMed Research International*, **2014**, 2014, 629697 | 3 | 5 |
| 44 | Integration of DNA Methylation, Copy Number Variation, and Gene Expression for Gene Regulatory Network Inference and Application to Psychiatric Disorders **2014**, | | 5 |
| 43 | Evaluation of Chromatin Accessibility in Prefrontal Cortex of Schizophrenia Cases and Controls | | 5 |
| 42 | Transcription factor POU3F2 regulates TRIM8 expression contributing to cellular functions implicated in schizophrenia. *Molecular Psychiatry*, **2021**, 26, 3444-3460 | 15.1 | 5 |
| 41 | Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. *European Neuropsychopharmacology*, **2019**, 29, 156-170 | 1.2 | 5 |
| 40 | Serious Workplace Violence Against Healthcare Providers in China Between 2004 and 2018. *Frontiers in Public Health*, **2020**, 8, 574765 | 6 | 5 |
| 39 | Integrative approach for inference of gene regulatory networks using lasso-based random featuring and application to psychiatric disorders. *BMC Medical Genomics*, **2016**, 9 Suppl 2, 50 | 3.7 | 4 |
| 38 | DNannotator: Annotation software tool kit for regional genomic sequences. *Nucleic Acids Research*, **2003**, 31, 3729-35 | 20.1 | 4 |
| 37 | csuWGCNA: a combination of signed and unsigned WGCNA to capture negative correlations | | 4 |
| 36 | Review of multi-omics data resources and integrative analysis for human brain disorders. *Briefings in Functional Genomics*, **2021**, 20, 223-234 | 4.9 | 4 |

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| 35 | Detecting significant genotype-phenotype association rules in bipolar disorder: market research meets complex genetics. *International Journal of Bipolar Disorders*, **2018**, 6, 24 | 5.4 | 4 |
| 34 | DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data. *PLoS Computational Biology*, **2020**, 16, e1007522 | 5 | 3 |
| 33 | Sparse generalized canonical correlation analysis for biological model integration: a genetic study of psychiatric disorders. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2013**, 2013, 1490-3 | 0.9 | 3 |
| 32 | Integrative analyses prioritize GNL3 as a risk gene for bipolar disorder. *Molecular Psychiatry*, **2020**, 25, 2672-2684 | 15.1 | 3 |
| 31 | Absence of coding somatic single nucleotide variants within well-known candidate genes in late-onset sporadic Alzheimer's Disease based on the analysis of multi-omics data. *Neurobiology of Aging*, **2021**, 108, 207-209 | 5.6 | 3 |
| 30 | Multi-block and Multi-task Learning for Integrative Genomic Study **2014**, | | 2 |
| 29 | eQTL Mapping Study via Regularized Sparse Canonical Correlation Analysis **2013**, | | 2 |
| 28 | Linkage disequilibrium analysis in the LOC93081-KDELC1-BIVM region on 13q in bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2005**, 133B, 12-7 | 3.5 | 2 |
| 27 | Common variants ofNRXN1, LRP1BandRORAare associated with increased ventricular volumes in psychosis - GWAS findings from the B-SNIP deep phenotyping study | | 2 |
| 26 | Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968 | 17.4 | 2 |
| 25 | SLC39A5 dysfunction impairs extracellular matrix synthesis in high myopia pathogenesis. *Journal of Cellular and Molecular Medicine*, **2021**, 25, 8432-8441 | 5.6 | 2 |
| 24 | Integrative Gene Regulatory Network inference using multi-omics data **2016**, | | 2 |
| 23 | Cell group analysis reveals changes in upper-layer neurons associated with schizophrenia | | 1 |
| 22 | Help-seeking behavior of individuals with schizophrenia in the general population of Hunan, China. *Scientific Reports*, **2021**, 11, 23012 | 4.9 | 1 |
| 21 | Children and AdolescentsTPsychological Well-Being Became Worse in Heavily Hit Chinese Provinces during the COVID-19 Epidemic. *Journal of Psychiatry and Brain Science*, **2021**, 6, | 1.7 | 1 |
| 20 | Spatiotemporal specificity of correlated DNA methylation and gene expression pairs across different human tissues and stages of brain development. *Epigenetics*, **2021**, 1-18 | 5.7 | 1 |
| 19 | Risperidone-induced changes in DNA methylation from peripheral blood in first-episode schizophrenia parallel neuroimaging and cognitive phenotype | | 1 |
| 18 | Agonal factors distort gene-expression patterns in human postmortem brains | | 1 |

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| 17 | Distinct transcriptomic signature of mRNA and microRNA in ulcerative colitis and irritable bowel syndrome | | 1 |
| 16 | Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. *Neuropsychopharmacology*, **2021**, 46, 1788-1801 | 8.7 | 1 |
| 15 | swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution | | 1 |
| 14 | QTL Mapping of Molecular Traits for Studies of Human Complex Diseases. *Translational Bioinformatics*, **2012**, 61-82 | | 0 |
| 13 | Agonal Factors Distort Gene-Expression Patterns in Human Postmortem Brains. *Frontiers in Neuroscience*, **2021**, 15, 614142 | 5.1 | 0 |
| 12 | Human forebrain organoids reveal connections between valproic acid exposure and autism risk.. *Translational Psychiatry*, **2022**, 12, 130 | 8.6 | 0 |
| 11 | Asymmetric independence modeling identifies novel gene-environment interactions. *Scientific Reports*, **2019**, 9, 2455 | 4.9 | |
| 10 | DNannotator4nnotation Software Tool Kit for Regional Genomic Sequences **2004**, 364-369 | | |
| 9 | SMAP is a pipeline for sample matching in proteogenomics.. *Nature Communications*, **2022**, 13, 744 | 17.4 | |
| 8 | QTL Mapping of Molecular Traits for Studies of Human Complex Diseases. *Translational Bioinformatics*, **2018**, 59-80 | | |
| 7 | Cross-Disorder Analysis of De Novo Mutations in Neuropsychiatric Disorders. *Journal of Autism and Developmental Disorders*, **2021**, 1 | 4.6 | |
| 6 | DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522 | | |
| 5 | DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522 | | |
| 4 | DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522 | | |
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