Yanling Liu

List of Publications by Year in Descending Order

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	SMAP is a pipeline for sample matching in proteogenomics.. *Nature Communications*, **2022**, 13, 744	17.4	
159	Human forebrain organoids reveal connections between valproic acid exposure and autism risk.. *Translational Psychiatry*, **2022**, 12, 130	8.6	0
158	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
157	Help-seeking behavior of individuals with schizophrenia in the general population of Hunan, China. *Scientific Reports*, **2021**, 11, 23012	4.9	1
156	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
155	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
154	Transcription factor POU3F2 regulates TRIM8 expression contributing to cellular functions implicated in schizophrenia. *Molecular Psychiatry*, **2021**, 26, 3444-3460	15.1	5
153	Agonal Factors Distort Gene-Expression Patterns in Human Postmortem Brains. *Frontiers in Neuroscience*, **2021**, 15, 614142	5.1	0
152	Review of multi-omics data resources and integrative analysis for human brain disorders. *Briefings in Functional Genomics*, **2021**, 20, 223-234	4.9	4
151	Drug Response-Related DNA Methylation Changes in Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. *Frontiers in Neuroscience*, **2021**, 15, 674273	5.1	8
150	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. *Neuropsychopharmacology*, **2021**, 46, 1788-1801	8.7	1
149	Cross-Disorder Analysis of De Novo Mutations in Neuropsychiatric Disorders. *Journal of Autism and Developmental Disorders*, **2021**, 1	4.6	
148	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
147	SLC39A5 dysfunction impairs extracellular matrix synthesis in high myopia pathogenesis. *Journal of Cellular and Molecular Medicine*, **2021**, 25, 8432-8441	5.6	2
146	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
145	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
144	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

143	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
142	Protein disulfide isomerases are promising targets for predicting the survival and tumor progression in glioma patients. *Aging*, **2020**, 12, 2347-2372	5.6	16
141	A unified framework for joint-tissue transcriptome-wide association and Mendelian randomization analysis. *Nature Genetics*, **2020**, 52, 1239-1246	36.3	35
140	Polygenic risk for anxiety influences anxiety comorbidity and suicidal behavior in bipolar disorder. *Translational Psychiatry*, **2020**, 10, 298	8.6	7
139	Integrative analyses prioritize GNL3 as a risk gene for bipolar disorder. *Molecular Psychiatry*, **2020**, 25, 2672-2684	15.1	3
138	Serious Workplace Violence Against Healthcare Providers in China Between 2004 and 2018. *Frontiers in Public Health*, **2020**, 8, 574765	6	5
137	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
136	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
135	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
134	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
133	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
132	DRAMS: A tool to detect and re-align mixed-up samples for integrative studies of multi-omics data **2020**, 16, e1007522		
131	Intronic (TTTGA) insertion in SAMD12 also causes familial cortical myoclonic tremor with epilepsy. *Movement Disorders*, **2019**, 34, 1571-1576	7	9
130	NRXN1 is associated with enlargement of the temporal horns of the lateral ventricles in psychosis. *Translational Psychiatry*, **2019**, 9, 230	8.6	7
129	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
128	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
127	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
126	Shared Molecular Neuropathology Across Major Psychiatric Disorders Parallels Polygenic Overlap. *Focus (American Psychiatric Publishing)*, **2019**, 17, 66-72	1.1	6

125	Asymmetric independence modeling identifies novel gene-environment interactions. *Scientific Reports*, **2019**, 9, 2455	4.9	
124	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
123	A comparative study of the genetic components of three subcategories of autism spectrum disorder. *Molecular Psychiatry*, **2019**, 24, 1720-1731	15.1	18
122	A decade in psychiatric GWAS research. *Molecular Psychiatry*, **2019**, 24, 378-389	15.1	40
121	BrainEXP: a database featuring with spatiotemporal expression variations and co-expression organizations in human brains. *Bioinformatics*, **2019**, 35, 172-174	7.2	6
120	Efficient region-based test strategy uncovers genetic risk factors for functional outcome in bipolar disorder. *European Neuropsychopharmacology*, **2019**, 29, 156-170	1.2	5
119	Positional effects revealed in Illumina methylation array and the impact on analysis. *Epigenomics*, **2018**, 10, 643-659	4.4	14
118	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. *Science*, **2018**, 359, 693-697	33.3	547
117	DNA Methylation and Psychiatric Disorders. *Progress in Molecular Biology and Translational Science*, **2018**, 157, 175-232	4	17
116	Genetic analysis of deep phenotyping projects in common disorders. *Schizophrenia Research*, **2018**, 195, 51-57	3.6	7
115	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
114	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. *Nature Communications*, **2018**, 9, 3121	17.4	74
113	QTL Mapping of Molecular Traits for Studies of Human Complex Diseases. *Translational Bioinformatics*, **2018**, 59-80		
112	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
111	Inherited and multiple de novo mutations in autism/developmental delay risk genes suggest a multifactorial model. *Molecular Autism*, **2018**, 9, 64	6.5	58
110	Revealing the brain's molecular architecture. *Science*, **2018**, 362, 1262-1263	33.3	29
109	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
108	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277

107	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
106	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
105	The long noncoding RNA may regulate expression of several schizophrenia-related genes. *Science Translational Medicine*, **2018**, 10,	17.5	42
104	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
103	Genome-wide copy number variation analysis in a Chinese autism spectrum disorder cohort. *Scientific Reports*, **2017**, 7, 44155	4.9	30
102	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
101	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
100	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
99	Genes with de novo mutations are shared by four neuropsychiatric disorders discovered from NPdenovo database. *Molecular Psychiatry*, **2016**, 21, 290-7	15.1	109
98	De novo genic mutations among a Chinese autism spectrum disorder cohort. *Nature Communications*, **2016**, 7, 13316	17.4	183
97	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
96	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
95	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
94	Integrative Gene Regulatory Network inference using multi-omics data **2016**,		2
93	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. *Scientific Reports*, **2016**, 6, 18909	4.9	39
92	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. *Nature Neuroscience*, **2015**, 18, 199-209	25.5	572
91	Mutations of P4HA2 encoding prolyl 4-hydroxylase 2 are associated with nonsyndromic high myopia. *Genetics in Medicine*, **2015**, 17, 300-6	8.1	44
90	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

89	Three dysconnectivity patterns in treatment-resistant schizophrenia patients and their unaffected siblings. *NeuroImage: Clinical*, **2015**, 8, 95-103	5.3	15
88	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
87	SCAN database: facilitating integrative analyses of cytosine modification and expression QTL. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	17
86	Multiblock discriminant analysis for integrative genomic study. *BioMed Research International*, **2015** , 2015, 783592	3	8
85	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
84	Genetics and epigenetics of circadian rhythms and their potential roles in neuropsychiatric disorders. *Neuroscience Bulletin*, **2015**, 31, 141-59	4.3	25
83	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
82	eQTL epistasis: detecting epistatic effects and inferring hierarchical relationships of genes in biological pathways. *Bioinformatics*, **2015**, 31, 656-64	7.2	8
81	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
80	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
79	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
78	Expression of the G72/G30 gene in transgenic mice induces behavioral changes. *Molecular Psychiatry*, **2014**, 19, 175-83	15.1	17
77	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
76	Inference of SNP-gene regulatory networks by integrating gene expressions and genetic perturbations. *BioMed Research International*, **2014**, 2014, 629697	3	5
75	Multi-block and Multi-task Learning for Integrative Genomic Study **2014**,		2
74	Integration of DNA Methylation, Copy Number Variation, and Gene Expression for Gene Regulatory Network Inference and Application to Psychiatric Disorders **2014**,		5
73	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
72	Molecular network analysis enhances understanding of the biology of mental disorders. *BioEssays*, **2014**, 36, 606-16	4.1	13

71	SLC39A5 mutations interfering with the BMP/TGF-β pathway in non-syndromic high myopia. *Journal of Medical Genetics*, **2014**, 51, 518-25	5.8	66
70	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
69	New ZNF644 mutations identified in patients with high myopia. *Molecular Vision*, **2014**, 20, 939-46	2.3	8
68	Genome-wide association study of Tourette's syndrome. *Molecular Psychiatry*, **2013**, 18, 721-8	15.1	138
67	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94	36.3	1628
66	Two gene co-expression modules differentiate psychotics and controls. *Molecular Psychiatry*, **2013**, 18, 1308-14	15.1	107
65	Genome-wide association study of obsessive-compulsive disorder. *Molecular Psychiatry*, **2013**, 18, 788-98	15.1	244
64	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
63	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
62	eQTL Mapping Study via Regularized Sparse Canonical Correlation Analysis **2013**,		2
61	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. *PLoS Genetics*, **2013**, 9, e1003864	6	189
60	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
59	Genome-wide association study implicates NDST3 in schizophrenia and bipolar disorder. *Nature Communications*, **2013**, 4, 2739	17.4	88
58	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
57	Preliminary genetic imaging study of the association between estrogen receptor-β gene polymorphisms and harsh human maternal parenting. *Neuroscience Letters*, **2012**, 525, 17-22	3.3	13
56	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
55	BDNF expression in lymphoblastoid cell lines carrying BDNF SNPs associated with bipolar disorder. *Psychiatric Genetics*, **2012**, 22, 253-5	2.9	6
54	Data mining approaches for genome-wide association of mood disorders. *Psychiatric Genetics*, **2012**, 22, 55-61	2.9	18

53	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
52	Genome-wide linkage analysis of 972 bipolar pedigrees using single-nucleotide polymorphisms. *Molecular Psychiatry*, **2012**, 17, 818-26	15.1	24
51	QTL Mapping of Molecular Traits for Studies of Human Complex Diseases. *Translational Bioinformatics*, **2012**, 61-82		0
50	A network-based approach to prioritize results from genome-wide association studies. *PLoS ONE*, **2011**, 6, e24220	3.7	57
49	Accuracy of CNV Detection from GWAS Data. *PLoS ONE*, **2011**, 6, e14511	3.7	57
48	Genome-wide association study of personality traits in bipolar patients. *Psychiatric Genetics*, **2011**, 21, 190-4	2.9	36
47	Genetic association of bipolar disorder with the (β3) nicotinic receptor subunit gene. *Psychiatric Genetics*, **2011**, 21, 77-84	2.9	8
46	Database of genetic studies of bipolar disorder. *Psychiatric Genetics*, **2011**, 21, 57-68	2.9	10
45	Brain expression quantitative trait locus mapping informs genetic studies of psychiatric diseases. *Neuroscience Bulletin*, **2011**, 27, 123-33	4.3	23
44	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
43	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
42	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
41	After GWAS: searching for genetic risk for schizophrenia and bipolar disorder. *American Journal of Psychiatry*, **2011**, 168, 253-6	11.9	159
40	Genome-wide association of bipolar disorder suggests an enrichment of replicable associations in regions near genes. *PLoS Genetics*, **2011**, 7, e1002134	6	53
39	Removing batch effects in analysis of expression microarray data: an evaluation of six batch adjustment methods. *PLoS ONE*, **2011**, 6, e17238	3.7	303
38	Whole-genome association mapping of gene expression in the human prefrontal cortex. *Molecular Psychiatry*, **2010**, 15, 779-84	15.1	60
37	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
36	Genetic control of individual differences in gene-specific methylation in human brain. *American Journal of Human Genetics*, **2010**, 86, 411-9	11	329

35	Cerebellar telomere length and psychiatric disorders. *Behavior Genetics*, **2010**, 40, 250-4	3.2	51
34	Genome-wide linkage and follow-up association study of postpartum mood symptoms. *American Journal of Psychiatry*, **2009**, 166, 1229-37	11.9	68
33	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
32	Singleton deletions throughout the genome increase risk of bipolar disorder. *Molecular Psychiatry*, **2009**, 14, 376-80	15.1	121
31	Genome-wide association study of bipolar disorder in European American and African American individuals. *Molecular Psychiatry*, **2009**, 14, 755-63	15.1	287
30	Further evidence for an association of G72/G30 with schizophrenia in Chinese. *Schizophrenia Research*, **2009**, 107, 324-6	3.6	8
29	Allelic association of G72/G30 with schizophrenia and bipolar disorder: a comprehensive meta-analysis. *Schizophrenia Research*, **2008**, 98, 89-97	3.6	86
28	Genetic associations with schizophrenia: meta-analyses of 12 candidate genes. *Schizophrenia Research*, **2008**, 104, 96-107	3.6	145
27	PDLIM5 and susceptibility to bipolar disorder: a family-based association study and meta-analysis. *Psychiatric Genetics*, **2008**, 18, 116-21	2.9	11
26	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
25	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
24	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
23	No association of trace amine receptor genes with bipolar disorder. *Molecular Psychiatry*, **2007**, 12, 979-81	15.1	7
22	Sequence variation in DOCK9 and heterogeneity in bipolar disorder. *Psychiatric Genetics*, **2007**, 17, 274-86	2.9	25
21	MutScreener: primer design tool for PCR-direct sequencing. *Nucleic Acids Research*, **2006**, 34, W660-4	20.1	6
20	Genetic tests of biologic systems in affective disorders. *Molecular Psychiatry*, **2005**, 10, 719-40	15.1	26
19	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
18	Frequency Finder: a multi-source web application for collection of public allele frequencies of SNP markers. *Bioinformatics*, **2004**, 20, 439-43	7.2	6

17	DNannotatorAnnotation Software Tool Kit for Regional Genomic Sequences **2004**, 364-369		
16	DNannotator: Annotation software tool kit for regional genomic sequences. *Nucleic Acids Research*, **2003**, 31, 3729-35	20.1	4
15	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
14	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
13	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
12	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
11	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
10	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
9	Cell group analysis reveals changes in upper-layer neurons associated with schizophrenia		1
8	Risperidone-induced changes in DNA methylation from peripheral blood in first-episode schizophrenia parallel neuroimaging and cognitive phenotype		1
7	Evaluation of Chromatin Accessibility in Prefrontal Cortex of Schizophrenia Cases and Controls		5
6	Genome-wide association study identifies 30 Loci Associated with Bipolar Disorder		28
5	Common variants ofNRXN1, LRP1BandRORAare associated with increased ventricular volumes in psychosis - GWAS findings from the B-SNIP deep phenotyping study		2
4	Agonal factors distort gene-expression patterns in human postmortem brains		1
3	csuWGCNA: a combination of signed and unsigned WGCNA to capture negative correlations		4
2	Distinct transcriptomic signature of mRNA and microRNA in ulcerative colitis and irritable bowel syndrome		1
1	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution		1