

# Schahram Akbarian

## List of Publications by Year in descending order

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Version: 2024-02-01

192  
papers

21,083  
citations

13332

70  
h-index

12940

136  
g-index

214  
all docs

214  
docs citations

214  
times ranked

26838  
citing authors

#	ARTICLE	IF	CITATIONS
1	Induction of dopaminergic neurons for neuronal subtype-specific modeling of psychiatric disease risk. <i>Molecular Psychiatry</i> , 2023, 28, 1970-1982.	4.1	13
2	Towards DSM 10: A bio-classification of developmental schizophrenia?. <i>Schizophrenia Research</i> , 2022, 242, 4-6.	1.1	4
3	Targeting histone demethylase LSD1 for treatment of deficits in autism mouse models. <i>Molecular Psychiatry</i> , 2022, 27, 3355-3366.	4.1	9
4	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. <i>Nature Neuroscience</i> , 2022, 25, 474-483.	7.1	25
5	Convergence of case-specific epigenetic alterations identify a confluence of genetic vulnerabilities tied to opioid overdose. <i>Molecular Psychiatry</i> , 2022, 27, 2158-2170.	4.1	9
6	PPARdelta activation induces metabolic and contractile maturation of human pluripotent stem cell-derived cardiomyocytes. <i>Cell Stem Cell</i> , 2022, 29, 559-576.e7.	5.2	34
7	Chromatin architecture in addiction circuitry identifies risk genes and potential biological mechanisms underlying cigarette smoking and alcohol use traits. <i>Molecular Psychiatry</i> , 2022, 27, 3085-3094.	4.1	13
8	Cylindromatosis drives synapse pruning and weakening by promoting macroautophagy through Akt-mTOR signaling. <i>Molecular Psychiatry</i> , 2022, 27, 2414-2424.	4.1	14
9	RTL1/PEG11 imprinted in human and mouse brain mediates anxiety-like and social behaviors and regulates neuronal excitability in the locus coeruleus. <i>Human Molecular Genetics</i> , 2022, 31, 3161-3180.	1.4	14
10	The tRNA regulome in neurodevelopmental and neuropsychiatric disease. <i>Molecular Psychiatry</i> , 2022, 27, 3204-3213.	4.1	9
11	Parsing the Functional Impact of Noncoding Genetic Variants in the Brain Epigenome. <i>Biological Psychiatry</i> , 2021, 89, 65-75.	0.7	8
12	Functional genomics of psychiatric disease risk using genome engineering. , 2021, , 711-734.		0
13	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. <i>Nature Neuroscience</i> , 2021, 24, 176-185.	7.1	73
14	Common Genetic Variation in Humans Impacts In Vitro Susceptibility to SARS-CoV-2 Infection. <i>Stem Cell Reports</i> , 2021, 16, 505-518.	2.3	39
15	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021, 22, 92.	3.8	26
16	Isolation of Adult Human Astrocyte Populations from Fresh-Frozen Cortex Using Fluorescence-Activated Nuclei Sorting. <i>Journal of Visualized Experiments</i> , 2021, , .	0.2	4
17	Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 664912.	1.4	12
18	An Adolescent Sensitive Period for Social Dominance Hierarchy Plasticity Is Regulated by Cortical Plasticity Modulators in Mice. <i>Frontiers in Neural Circuits</i> , 2021, 15, 676308.	1.4	5

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19	Integration of evidence across human and model organism studies: A meeting report. <i>Genes, Brain and Behavior</i> , 2021, 20, e12738.	1.1	12
20	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	5.8	48
21	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. <i>Genome Medicine</i> , 2021, 13, 118.	3.6	81
22	Neuronal Nsun2 deficiency produces tRNA epitranscriptomic alterations and proteomic shifts impacting synaptic signaling and behavior. <i>Nature Communications</i> , 2021, 12, 4913.	5.8	42
23	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021, 24, 186-196.	7.1	22
24	Neuron-specific chromosomal megadomain organization is adaptive to recent retrotransposon expansions. <i>Nature Communications</i> , 2021, 12, 7243.	5.8	10
25	Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. <i>Molecular Psychiatry</i> , 2020, 25, 2952-2969.	4.1	66
26	CRISPR-based functional evaluation of schizophrenia risk variants. <i>Schizophrenia Research</i> , 2020, 217, 26-36.	1.1	10
27	Special volume: The genomics and epigenomics of schizophrenia. <i>Schizophrenia Research</i> , 2020, 217, 1-3.	1.1	3
28	S189. PREFRONTAL PARVALBUMIN INTERNEURONS REQUIRE JUVENILE SOCIAL EXPERIENCE TO ESTABLISH ADULT SOCIAL BEHAVIOR. <i>Schizophrenia Bulletin</i> , 2020, 46, S110-S110.	2.3	0
29	Epigenetic Clocks in Schizophrenia: Promising Biomarkers, Foggy Clockwork. <i>Biological Psychiatry</i> , 2020, 88, 210-211.	0.7	1
30	Large-Scale Integrative Brain Transcriptome and Epigenome Imputation for PTSD Identifies Implicated Genes and Pathways. <i>Biological Psychiatry</i> , 2020, 87, S52.	0.7	0
31	NSUN2-Mediated tRNA Methylation: A Novel Neurobiological Mechanism for Memory and Emotion. <i>Biological Psychiatry</i> , 2020, 87, S57.	0.7	0
32	Genotype-phenotype correlation at codon 1740 of <i>SETD2</i> . <i>American Journal of Medical Genetics, Part A</i> , 2020, 182, 2037-2048.	0.7	14
33	A prefrontal-paraventricular thalamus circuit requires juvenile social experience to regulate adult sociability in mice. <i>Nature Neuroscience</i> , 2020, 23, 1240-1252.	7.1	95
34	Publicly Available hiPSC Lines with Extreme Polygenic Risk Scores for Modeling Schizophrenia. <i>Complex Psychiatry</i> , 2020, 6, 68-82.	1.3	18
35	A computational tool (H-MAGMA) for improved prediction of brain-disorder risk genes by incorporating brain chromatin interaction profiles. <i>Nature Neuroscience</i> , 2020, 23, 583-593.	7.1	194
36	Prefrontal parvalbumin interneurons require juvenile social experience to establish adult social behavior. <i>Nature Communications</i> , 2020, 11, 1003.	5.8	95

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37	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. <i>Genome Medicine</i> , 2020, 12, 19.	3.6	31
38	Investigation of Schizophrenia with Human Induced Pluripotent Stem Cells. <i>Advances in Neurobiology</i> , 2020, 25, 155-206.	1.3	11
39	Chromatin profiling of cortical neurons identifies individual epigenetic signatures in schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 256.	2.4	18
40	O1.3. DIFFERENTIAL HISTONE MODIFICATIONS IN 250 SCHIZOPHRENIA CASES AND 330 CONTROLS. <i>Schizophrenia Bulletin</i> , 2019, 45, S159-S160.	2.3	0
41	In vivo epigenetic editing of <i>Sema6a</i> promoter reverses transcallosal dysconnectivity caused by <i>C11orf46/Arl14ep</i> risk gene. <i>Nature Communications</i> , 2019, 10, 4112.	5.8	34
42	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. <i>Scientific Data</i> , 2019, 6, 180.	2.4	149
43	Metabolome signature of autism in the human prefrontal cortex. <i>Communications Biology</i> , 2019, 2, 234.	2.0	42
44	Spatial genome exploration in the context of cognitive and neurological disease. <i>Current Opinion in Neurobiology</i> , 2019, 59, 112-119.	2.0	12
45	Epigenetic genetic chromatin footprinting identifies novel and subject specific genes active in prefrontal cortex neurons. <i>FASEB Journal</i> , 2019, 33, 8161-8173.	0.2	12
46	Use of the epigenetic toolbox to contextualize common variants associated with schizophrenia risk. <i>Dialogues in Clinical Neuroscience</i> , 2019, 21, 407-416.	1.8	3
47	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	6.0	851
48	Allele-specific expression in a family quartet with autism reveals mono-to-biallelic switch and novel transcriptional processes of autism susceptibility genes. <i>Scientific Reports</i> , 2018, 8, 4277.	1.6	35
49	MEF2C transcription factor is associated with the genetic and epigenetic risk architecture of schizophrenia and improves cognition in mice. <i>Molecular Psychiatry</i> , 2018, 23, 123-132.	4.1	70
50	O4.1. GENETIC VULNERABILITY TO DUSP22 PROMOTOR HYPERMETHYLATION IS INVOLVED IN THE RELATION BETWEEN IN UTERO FAMINE EXPOSURE AND SCHIZOPHRENIA. <i>Schizophrenia Bulletin</i> , 2018, 44, S82-S82.	2.3	0
51	Revealing the brain's molecular architecture. <i>Science</i> , 2018, 362, 1262-1263.	6.0	45
52	Neuron-specific signatures in the chromosomal connectome associated with schizophrenia risk. <i>Science</i> , 2018, 362, .	6.0	162
53	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	6.0	516
54	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	6.0	805

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55	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
56	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	2.6	128
57	Chromosomal Conformations and Epigenomic Regulation in Schizophrenia. <i>Progress in Molecular Biology and Translational Science</i> , 2018, 157, 21-40.	0.9	16
58	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 3121.	5.8	141
59	Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. <i>Nature Neuroscience</i> , 2018, 21, 1126-1136.	7.1	112
60	Modeling Neuropsychiatric and Neurodegenerative Diseases With Induced Pluripotent Stem Cells. <i>Frontiers in Pediatrics</i> , 2018, 6, 82.	0.9	16
61	Genetic vulnerability to DUSP22 promoter hypermethylation is involved in the relation between in utero famine exposure and schizophrenia. <i>NPJ Schizophrenia</i> , 2018, 4, 16.	2.0	34
62	Activity-Induced Regulation of Synaptic Strength through the Chromatin Reader L3mbtl1. <i>Cell Reports</i> , 2018, 23, 3209-3222.	2.9	29
63	Practical Guidelines for High-Resolution Epigenomic Profiling of Nucleosomal Histones in Postmortem Human Brain Tissue. <i>Biological Psychiatry</i> , 2017, 81, 162-170.	0.7	48
64	Cocaine-Induced Chromatin Modifications Associate With Increased Expression and Three-Dimensional Looping of <i>Auts2</i> . <i>Biological Psychiatry</i> , 2017, 82, 794-805.	0.7	47
65	Phf8 loss confers resistance to depression-like and anxiety-like behaviors in mice. <i>Nature Communications</i> , 2017, 8, 15142.	5.8	35
66	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017, 356, .	6.0	206
67	Application of CRISPR/Cas9 to the study of brain development and neuropsychiatric disease. <i>Molecular and Cellular Neurosciences</i> , 2017, 82, 157-166.	1.0	25
68	Gene Regulation As A Function of Epigenetic Marks (H3K4ME3, H3K27AC) And Cell Types (Neuronal And) Tj ETQq0,0,0 rgBT (Overlock 1	0.3	0
69	The epigenomics of schizophrenia, in the mouse. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 631-640.	1.1	12
70	Evaluating Synthetic Activation and Repression of Neuropsychiatric-Related Genes in hiPSC-Derived NPCs, Neurons, and Astrocytes. <i>Stem Cell Reports</i> , 2017, 9, 615-628.	2.3	76
71	Antipsychotic-induced Hdac2 transcription via NF- $\kappa$ B leads to synaptic and cognitive side effects. <i>Nature Neuroscience</i> , 2017, 20, 1247-1259.	7.1	79
72	The methyltransferase SETDB1 regulates a large neuron-specific topological chromatin domain. <i>Nature Genetics</i> , 2017, 49, 1239-1250.	9.4	133

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73	Consensus paper of the WFSBP Task Force on Biological Markers: Criteria for biomarkers and endophenotypes of schizophrenia, part III: Molecular mechanisms. World Journal of Biological Psychiatry, 2017, 18, 330-356.	1.3	33
74	Epigenetic Approaches to Define the Molecular and Genetic Risk Architectures of Schizophrenia. , 2016, , 61-82.		1
75	Disruption of an Evolutionarily Novel Synaptic Expression Pattern in Autism. PLoS Biology, 2016, 14, e1002558.	2.6	73
76	Insulin-like Growth Factor 1 for Healthy Spines and Healthy Minds?. Biological Psychiatry, 2016, 80, 260-262.	0.7	0
77	Spatial genome organization and cognition. Nature Reviews Neuroscience, 2016, 17, 681-691.	4.9	69
78	Neuronal Deletion of Kmt2a/Mll1 Histone Methyltransferase in Ventral Striatum is Associated with Defective Spike-Timing-Dependent Striatal Synaptic Plasticity, Altered Response to Dopaminergic Drugs, and Increased Anxiety. Neuropsychopharmacology, 2016, 41, 3103-3113.	2.8	40
79	Constance E. Lieber, Theodore R. Stanley, and the Enduring Impact of Philanthropy on Psychiatry Research. Biological Psychiatry, 2016, 80, 84-86.	0.7	2
80	Longitudinal assessment of neuronal 3D genomes in mouse prefrontal cortex. Nature Communications, 2016, 7, 12743.	5.8	16
81	DNA Methylation Signatures of Early Childhood Malnutrition Associated With Impairments in Attention and Cognition. Biological Psychiatry, 2016, 80, 765-774.	0.7	124
82	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	1.1	22
83	NeuN+ neuronal nuclei in non-human primate prefrontal cortex and subcortical white matter after clozapine exposure. Schizophrenia Research, 2016, 170, 235-244.	1.1	20
84	Back to the past in schizophrenia genomics. Nature Neuroscience, 2016, 19, 1-2.	7.1	49
85	Pharmacological modulation of astrocytes and the role of cell type-specific histone modifications for the treatment of mood disorders. Current Opinion in Pharmacology, 2016, 26, 61-66.	1.7	10
86	Epigenetic Basis of Mental Illness. Neuroscientist, 2016, 22, 447-463.	2.6	236
87	Chemogenetic Inactivation of Dorsal Anterior Cingulate Cortex Neurons Disrupts Attentional Behavior in Mouse. Neuropsychopharmacology, 2016, 41, 1014-1023.	2.8	82
88	Bioinformatic analyses and conceptual synthesis of evidence linking <i>ZNF804A</i> to risk for schizophrenia and bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 14-35.	1.1	19
89	Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. Frontiers in Genetics, 2015, 6, 190.	1.1	0
90	RNA Sequence Analysis of Human Huntington Disease Brain Reveals an Extensive Increase in Inflammatory and Developmental Gene Expression. PLoS ONE, 2015, 10, e0143563.	1.1	150

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91	Prefrontal Cortex and Social Cognition in Mouse and Man. <i>Frontiers in Psychology</i> , 2015, 6, 1805.	1.1	354
92	Epigenetics and sex differences in the brain: A genome-wide comparison of histone-3 lysine-4 trimethylation (H3K4me3) in male and female mice. <i>Experimental Neurology</i> , 2015, 268, 21-29.	2.0	73
93	Critical Role of Histone Turnover in Neuronal Transcription and Plasticity. <i>Neuron</i> , 2015, 87, 77-94.	3.8	257
94	Interneuron epigenomes during the critical period of cortical plasticity: Implications for schizophrenia. <i>Neurobiology of Learning and Memory</i> , 2015, 124, 104-110.	1.0	36
95	miR-10b-5p expression in Huntington's disease brain relates to age of onset and the extent of striatal involvement. <i>BMC Medical Genomics</i> , 2015, 8, 10.	0.7	114
96	Transcriptional regulation of GAD1 GABA synthesis gene in the prefrontal cortex of subjects with schizophrenia. <i>Schizophrenia Research</i> , 2015, 167, 28-34.	1.1	50
97	Neuronal Kmt2a/Mll1 Histone Methyltransferase Is Essential for Prefrontal Synaptic Plasticity and Working Memory. <i>Journal of Neuroscience</i> , 2015, 35, 5097-5108.	1.7	126
98	DNA methylation levels of $\beta$ -synuclein intron 1 in the aging brain. <i>Neurobiology of Aging</i> , 2015, 36, 3334.e7-3334.e11.	1.5	23
99	Deciphering H3K4me3 broad domains associated with gene-regulatory networks and conserved epigenomic landscapes in the human brain. <i>Translational Psychiatry</i> , 2015, 5, e679-e679.	2.4	57
100	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	7.1	371
101	<i>CHRNA7</i> and <i>CHRFAM7A</i> : Psychosis and Smoking? Blame the Neighbors!. <i>American Journal of Psychiatry</i> , 2015, 172, 1054-1056.	4.0	6
102	Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. <i>Human Molecular Genetics</i> , 2015, 24, 1441-1456.	1.4	67
103	Cognition and Mood-Related Behaviors in <i>L3mbtl1</i> Null Mutant Mice. <i>PLoS ONE</i> , 2015, 10, e0121252.	1.1	3
104	The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. <i>PLoS ONE</i> , 2015, 10, e0144398.	1.1	47
105	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	2.9	225
106	MicroRNAs Located in the Hox Gene Clusters Are Implicated in Huntington's Disease Pathogenesis. <i>PLoS Genetics</i> , 2014, 10, e1004188.	1.5	97
107	Alterations in microRNA-124 and AMPA receptors contribute to social behavioral deficits in frontotemporal dementia. <i>Nature Medicine</i> , 2014, 20, 1444-1451.	15.2	165
108	Conserved Higher-Order Chromatin Regulates NMDA Receptor Gene Expression and Cognition. <i>Neuron</i> , 2014, 84, 997-1008.	3.8	76

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109	The Future of Neuroepigenetics in the Human Brain. <i>Progress in Molecular Biology and Translational Science</i> , 2014, 128, 199-228.	0.9	14
110	Chromatin-bound RNA and the neurobiology of psychiatric disease. <i>Neuroscience</i> , 2014, 264, 131-141.	1.1	8
111	Neuroinflammation and $\alpha$ -synuclein accumulation in response to glucocerebrosidase deficiency are accompanied by synaptic dysfunction. <i>Molecular Genetics and Metabolism</i> , 2014, 111, 152-162.	0.5	94
112	The Genome in Three Dimensions: A New Frontier in Human Brain Research. <i>Biological Psychiatry</i> , 2014, 75, 961-969.	0.7	51
113	Analytical tools and current challenges in the modern era of neuroepigenomics. <i>Nature Neuroscience</i> , 2014, 17, 1476-1490.	7.1	100
114	Regulation of histone H3K4 methylation in brain development and disease. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130514.	1.8	113
115	A Unique Set of Centrosome Proteins Requires Pericentrin for Spindle-Pole Localization and Spindle Orientation. <i>Current Biology</i> , 2014, 24, 2327-2334.	1.8	77
116	Epigenetic Dysregulation in the Schizophrenic Brain. <i>Current Behavioral Neuroscience Reports</i> , 2014, 1, 86-93.	0.6	3
117	Epigenetic mechanisms in schizophrenia. <i>Dialogues in Clinical Neuroscience</i> , 2014, 16, 405-417.	1.8	74
118	Epigenetics in the Human Brain. <i>Neuropsychopharmacology</i> , 2013, 38, 183-197.	2.8	65
119	Epigenetic Mechanisms in Psychiatry. <i>Neuropsychopharmacology</i> , 2013, 38, 1-2.	2.8	34
120	Prefrontal Cortical Dysfunction After Overexpression of Histone Deacetylase 1. <i>Biological Psychiatry</i> , 2013, 74, 696-705.	0.7	48
121	Epigenetic dysregulation in schizophrenia: molecular and clinical aspects of histone deacetylase inhibitors. <i>European Archives of Psychiatry and Clinical Neuroscience</i> , 2013, 263, 273-284.	1.8	44
122	Epigenetic Determinants of Healthy and Diseased Brain Aging and Cognition. <i>JAMA Neurology</i> , 2013, 70, 711.	4.5	72
123	The Neuroepigenetics of Suicide. <i>American Journal of Psychiatry</i> , 2013, 170, 462-465.	4.0	6
124	Coordinated Cell Type-Specific Epigenetic Remodeling in Prefrontal Cortex Begins before Birth and Continues into Early Adulthood. <i>PLoS Genetics</i> , 2013, 9, e1003433.	1.5	68
125	Conserved Chromosome 2q31 Conformations Are Associated with Transcriptional Regulation of GAD1 GABA Synthesis Enzyme and Altered in Prefrontal Cortex of Subjects with Schizophrenia. <i>Journal of Neuroscience</i> , 2013, 33, 11839-11851.	1.7	60
126	Genetic and acute CPEB1 depletion ameliorate fragile X pathophysiology. <i>Nature Medicine</i> , 2013, 19, 1473-1477.	15.2	115

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127	Exploring the epigenetics of cocaine resistance. <i>Nature Medicine</i> , 2013, 19, 136-137.	15.2	3
128	The histone deacetylase inhibitor, sodium butyrate, alleviates cognitive deficits in pre-motor stage PD. <i>Neuropharmacology</i> , 2012, 62, 2409-2412.	2.0	69
129	Epigenetic Signatures of Autism. <i>Archives of General Psychiatry</i> , 2012, 69, 314.	13.8	174
130	The Polycomb Group Protein L3mbtl2 Assembles an Atypical PRC1-Family Complex that Is Essential in Pluripotent Stem Cells and Early Development. <i>Cell Stem Cell</i> , 2012, 11, 319-332.	5.2	118
131	Maternal immune activation alters behavior in adult offspring, with subtle changes in the cortical transcriptome and epigenome. <i>Schizophrenia Research</i> , 2012, 140, 175-184.	1.1	89
132	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. <i>PLoS Biology</i> , 2012, 10, e1001427.	2.6	113
133	Gender-Specific Reduction of Estrogen-Sensitive Small RNA, miR-30b, in Subjects With Schizophrenia. <i>Schizophrenia Bulletin</i> , 2012, 38, 433-443.	2.3	69
134	Epigenetic mechanisms in neurological disease. <i>Nature Medicine</i> , 2012, 18, 1194-1204.	15.2	394
135	Epigenetic and post-transcriptional dysregulation of gene expression in schizophrenia and related disease. <i>Neurobiology of Disease</i> , 2012, 46, 255-262.	2.1	41
136	Balancing histone methylation activities in psychiatric disorders. <i>Trends in Molecular Medicine</i> , 2011, 17, 372-379.	3.5	100
137	White matter neuron alterations in schizophrenia and related disorders. <i>International Journal of Developmental Neuroscience</i> , 2011, 29, 325-334.	0.7	66
138	Setdb1-mediated histone H3K9 hypermethylation in neurons worsens the neurological phenotype of Mecp2-deficient mice. <i>Neuropharmacology</i> , 2011, 60, 1088-1097.	2.0	14
139	<i>RPP25</i> is developmentally regulated in prefrontal cortex and expressed at decreased levels in autism spectrum disorder. <i>Autism Research</i> , 2010, 3, 153-161.	2.1	24
140	Keep the 'phospho' on MAPK, be happy. <i>Nature Medicine</i> , 2010, 16, 1187-1188.	15.2	8
141	The C-Terminal TDP-43 Fragments Have a High Aggregation Propensity and Harm Neurons by a Dominant-Negative Mechanism. <i>PLoS ONE</i> , 2010, 5, e15878.	1.1	164
142	Chromatin Protein L3MBTL1 Is Dispensable for Development and Tumor Suppression in Mice. <i>Journal of Biological Chemistry</i> , 2010, 285, 27767-27775.	1.6	24
143	A simple method for improving the specificity of anti-methyl histone antibodies. <i>Epigenetics</i> , 2010, 5, 392-395.	1.3	7
144	Epigenetics of Schizophrenia. <i>Current Topics in Behavioral Neurosciences</i> , 2010, 4, 611-628.	0.8	54

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145	Developmental regulation and individual differences of neuronal H3K4me3 epigenomes in the prefrontal cortex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8824-8829.	3.3	218
146	The molecular pathology of schizophreniaâ€”Focus on histone and DNA modifications. <i>Brain Research Bulletin</i> , 2010, 83, 103-107.	1.4	37
147	Setdb1 Histone Methyltransferase Regulates Mood-Related Behaviors and Expression of the NMDA Receptor Subunit NR2B. <i>Journal of Neuroscience</i> , 2010, 30, 7152-7167.	1.7	104
148	Cocaine-induced metabolic activation in cortico-limbic circuitry is increased after exposure to the histone deacetylase inhibitor, sodium butyrate. <i>Neuroscience Letters</i> , 2009, 465, 267-271.	1.0	19
149	Epigenetic Regulation in Human Brainâ€”Focus on Histone Lysine Methylation. <i>Biological Psychiatry</i> , 2009, 65, 198-203.	0.7	206
150	Molecular Determinants of Dysregulated GABAergic Gene Expression in the Prefrontal Cortex of Subjects with Schizophrenia. <i>Biological Psychiatry</i> , 2009, 65, 1006-1014.	0.7	246
151	Cingulate White Matter Neurons in Schizophrenia and Bipolar Disorder. <i>Biological Psychiatry</i> , 2009, 66, 486-493.	0.7	67
152	A Chromatin Assay for Human Brain Tissue. <i>Journal of Visualized Experiments</i> , 2008, , .	0.2	14
153	Isolation of neuronal chromatin from brain tissue. <i>BMC Neuroscience</i> , 2008, 9, 42.	0.8	176
154	Approaching the Molecular Pathology of Suicide. <i>Biological Psychiatry</i> , 2008, 64, 643-644.	0.7	8
155	Epigenetics in the Nervous System: Figure 1.. <i>Journal of Neuroscience</i> , 2008, 28, 11753-11759.	1.7	200
156	Drug-Induced Activation of Dopamine D1 Receptor Signaling and Inhibition of Class I/II Histone Deacetylase Induce Chromatin Remodeling in Reward Circuitry and Modulate Cocaine-Related Behaviors. <i>Neuropsychopharmacology</i> , 2008, 33, 2981-2992.	2.8	125
157	DNA methylation changes in schizophrenia and bipolar disorder. <i>Epigenetics</i> , 2008, 3, 55-58.	1.3	76
158	A set of differentially expressed miRNAs, including miR-30a-5p, act as post-transcriptional inhibitors of BDNF in prefrontal cortex. <i>Human Molecular Genetics</i> , 2008, 17, 3030-3042.	1.4	239
159	Restoring GABAergic Signaling and Neuronal Synchrony in Schizophrenia. <i>American Journal of Psychiatry</i> , 2008, 165, 1507-1509.	4.0	9
160	Neuronal Nuclei Isolation from Human Postmortem Brain Tissue. <i>Journal of Visualized Experiments</i> , 2008, , .	0.2	103
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