Peng Jin

List of Publications by Year
in descending order

211	22,703	14644 66	9090 144
papers	citations	h-index	g-index

225	225	225	27273
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Disease category-specific annotation of variants using an ensemble learning framework. Briefings in Bioinformatics, 2022, 23, .	3.2	7
2	The Phenotypes and Mechanisms of NOTCH2NLC-Related GGC Repeat Expansion Disorders: a Comprehensive Review. Molecular Neurobiology, 2022, 59, 523-534.	1.9	27
3	Stephen T. Warren, Ph.D. (1953â€“2021): A remembrance. American Journal of Human Genetics, 2022, 109, 3-11.	2.6	2
4	Cell-free DNA methylation as a potential biomarker in brain disorders. Epigenomics, 2022, 14, 369-374.	1.0	4
5	Brain microRNAs are associated with variation in cognitive trajectory in advanced age. Translational Psychiatry, 2022, 12, 47.	2.4	7
6	LRcell: detecting the source of differential expression at the subâ€“cell-type level from bulk RNA-seq data. Briefings in Bioinformatics, 2022, 23, .	3.2	4
7	Reducing the Excess Activin Signaling Rescues Muscle Degeneration in Myotonic Dystrophy Type 2 Drosophila Model. Journal of Personalized Medicine, 2022, 12, 385.	1.1	3
8	Dysregulated mitochondrial and cytosolic tRNA m1A methylation in Alzheimerâ€™s disease. Human Molecular Genetics, 2022, 31, 1673-1680.	1.4	23
9	PDZRN4 suppresses tumorigenesis and androgen therapy-resistance in prostate cancer. Journal of Cancer, 2022, 13, 2293-2300.	1.2	2
10	Epitranscriptomic dynamics in brain development and disease. Molecular Psychiatry, 2022, 27, 3633-3646.	4.1	10
11	Across Dimensions: Developing 2D and 3D Human iPSC-Based Models of Fragile X Syndrome. Cells, 2022, 11, 1725.	1.8	3
12	Identification of PSMB5 as a genetic modifier of fragile Xâ€“associated tremor/ataxia syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	7
13	Altered hydroxymethylome in the substantia nigra of Parkinsonâ€™s disease. Human Molecular Genetics, 2022, 31, 3494-3503.	1.4	7
14	Important Correlates of Purpose in Life Identified Through a Machine Learning Approach. American Journal of Geriatric Psychiatry, 2021, 29, 488-498.	0.6	19
15	Stem cell epigenetics in medical therapy. , 2021, , 873-884.		0
16	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. Nature Communications, 2021, 12, 795.	5.8	22
17	Downregulation of TOP2 modulates neurodegeneration caused by GGGGCC expanded repeats. Human Molecular Genetics, 2021, 30, 893-901.	1.4	4
18	Detecting m6A methylation regions from Methylated RNA Immunoprecipitation Sequencing. Bioinformatics, 2021, 37, 2818-2824.	1.8	10

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19	Targeting the ALS/FTD-associated A-DNA kink with anthracene-based metal complex causes DNA backbone straightening and groove contraction. Nucleic Acids Research, 2021, 49, 9526-9538.	6.5	5
20	Ectopic expression of CGG-repeats alters ovarian response to gonadotropins and leads to infertility in a murine FMR1 premutation model. Human Molecular Genetics, 2021, 30, 923-938.	1.4	4
21	Ten-eleven translocation protein 1 modulates medulloblastoma progression. Genome Biology, 2021, 22, 125.	3.8	3
22	A Partial Picture of the Single-Cell Transcriptomics of Human IgA Nephropathy. Frontiers in Immunology, 2021, 12, 645988.	2.2	31
23	Single-cell analysis of angiotensin-converting enzyme II expression in human kidneys and bladders reveals a potential route of 2019 novel coronavirus infection. Chinese Medical Journal, 2021, 134, 935-943.	0.9	28
24	Cell-type-specific profiling of human cellular models of fragile X syndrome reveal PI3K-dependent defects in translation and neurogenesis. Cell Reports, 2021, 35, 108991.	2.9	36
25	Therapeutic Development for CGG Repeat Expansion-Associated Neurodegeneration. Frontiers in Cellular Neuroscience, 2021, 15, 655568.	1.8	12
26	Single-Cell Profiling Reveals Transcriptional Signatures and Cell-Cell Crosstalk in Anti-PLA2R Positive Idiopathic Membranous Nephropathy Patients. Frontiers in Immunology, 2021, 12, 683330.	2.2	23
27	Ten-eleven translocation 2 modulates allergic inflammation by 5-hydroxymethylcytosine remodeling of immunologic pathways. Human Molecular Genetics, 2021, 30, 1985-1995.	1.4	2
28	A Porcine Congenital Single-Sided Deafness Model, Its Population Statistics and Degenerative Changes. Frontiers in Cell and Developmental Biology, 2021, 9, 672216.	1.8	0
29	A machine learning approach to brain epigenetic analysis reveals kinases associated with Alzheimerâ€™s disease. Nature Communications, 2021, 12, 4472.	5.8	28
30	Stress modulates Ahi1-dependent nuclear localization of ten-eleven translocation protein 2. Human Molecular Genetics, 2021, 30, 2149-2160.	1.4	10
31	A human forebrain organoid model of fragile X syndrome exhibits altered neurogenesis and highlights new treatment strategies. Nature Neuroscience, 2021, 24, 1377-1391.	7.1	80
32	Remembering Stephen T. Warren, a pillar of neurogenetics (1953â€“2021). Nature Neuroscience, 2021, 24, 1340-1341.	7.1	0
33	Identifying susceptibility genes for primary ovarian insufficiency on the high-risk genetic background of a fragile X premutation. Fertility and Sterility, 2021, 116, 843-854.	0.5	5
34	N6-methyladenosine dynamics in neurodevelopment and aging, and its potential role in Alzheimerâ€™s disease. Genome Biology, 2021, 22, 17.	3.8	131
35	Activation of GPR39 with TC-G 1008Âattenuates neuroinflammation via SIRT1/PGC-1Î±/Nrf2 pathway post-neonatal hypoxicâ€“ischemic injury in rats. Journal of Neuroinflammation, 2021, 18, 226.	3.1	20
36	Risk factors for urinary tract infection in kidney transplantation from brain death donor and its role in graft function.. Journal of Central South University (Medical Sciences), 2021, 46, 1220-1226.	0.1	0

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37	A comprehensive review of computational prediction of genome-wide features. Briefings in Bioinformatics, 2020, 21, 120-134.	3.2	12
38	Age-related DNA hydroxymethylation is enriched for gene expression and immune system processes in human peripheral blood. Epigenetics, 2020, 15, 294-306.	1.3	8
39	Regulatory annotation of genomic intervals based on tissue-specific expression QTLs. Bioinformatics, 2020, 36, 690-697.	1.8	9
40	Ethnicity-specific and overlapping alterations of brain hydroxymethylome in Alzheimerâ€™s disease. Human Molecular Genetics, 2020, 29, 149-158.	1.4	11
41	Neuropeptides Modulate Local Astrocytes to Regulate Adult Hippocampal Neural Stem Cells. Neuron, 2020, 108, 349-366.e6.	3.8	42
42	Neddylation activity modulates the neurodegeneration associated with fragile X associated tremor/ataxia syndrome (FXTAS) through regulating Sima. Neurobiology of Disease, 2020, 143, 105013.	2.1	4
43	Metabolic Alterations in FMR1 Premutation Carriers. Frontiers in Molecular Biosciences, 2020, 7, 571092.	1.6	2
44	Integrated analysis of a compendium of RNA-Seq datasets for splicing factors. Scientific Data, 2020, 7, 178.	2.4	2
45	Robust partial reference-free cell composition estimation from tissue expression. Bioinformatics, 2020, 36, 3431-3438.	1.8	12
46	Dynamic N6-methyladenosine RNA methylation in brain and diseases. Epigenomics, 2020, 12, 371-380.	1.0	17
47	Proteomic and lipidomic analysis of exosomes derived from ovarian cancer cells and ovarian surface epithelial cells. Journal of Ovarian Research, 2020, 13, 9.	1.3	57
48	Development of Chinese genetic reference panel for Fragile X Syndrome and its application to the screen of 10,000 Chinese pregnant women and women planning pregnancy. Molecular Genetics & Genomic Medicine, 2020, 8, e1236.	0.6	7
49	Characterization of hazard infiltrating immune cells and relative risk genes in bladder urothelial carcinoma. American Journal of Translational Research (discontinued), 2020, 12, 7510-7527.	0.0	2
50	Assessment of hazard immune-related genes and tumor immune infiltrations in renal cell carcinoma. American Journal of Translational Research (discontinued), 2020, 12, 7096-7113.	0.0	2
51	Reversing Behavioral, Neuroanatomical, and Germline Influences of Intergenerational Stress. Biological Psychiatry, 2019, 85, 248-256.	0.7	23
52	The Taiman Transcriptional Coactivator Engages Toll Signals to Promote Apoptosis and Intertissue Invasion in Drosophila. Current Biology, 2019, 29, 2790-2800.e4.	1.8	12
53	Dysfunction of Habituation Learning: A Novel Pathogenic Paradigm of Intellectual Disability and Autism Spectrum Disorder. Biological Psychiatry, 2019, 86, 253-254.	0.7	2
54	Progress in the genetic analysis of Parkinsonâ€™s disease. Human Molecular Genetics, 2019, 28, R241-R253.	1.4	25

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55	Altered 5-Hydroxymethylcytosine Landscape in Primary Gastric Adenocarcinoma. DNA and Cell Biology, 2019, 38, 1460-1469.	0.9	4
56	Expansion of Human-Specific GGC Repeat in Neuronal Intranuclear Inclusion Disease-Related Disorders. American Journal of Human Genetics, 2019, 105, 166-176.	2.6	212
57	Amyotrophic Lateral Sclerosis-associated GGGGCC repeat expansion promotes Tau phosphorylation and toxicity. Neurobiology of Disease, 2019, 130, 104493.	2.1	8
58	Rare variants in MYH15 modify amyotrophic lateral sclerosis risk. Human Molecular Genetics, 2019, 28, 2309-2318.	1.4	4
59	Application of Drosophila Model Toward Understanding the Molecular Basis of Fragile X Syndrome. Methods in Molecular Biology, 2019, 1942, 141-153.	0.4	0
60	Dissecting differential signals in high-throughput data from complex tissues. Bioinformatics, 2019, 35, 3898-3905.	1.8	35
61	Metabolic pathways modulate the neuronal toxicity associated with fragile X-associated tremor/ataxia syndrome. Human Molecular Genetics, 2019, 28, 980-991.	1.4	10
62	Disease prediction by cell-free DNA methylation. Briefings in Bioinformatics, 2019, 20, 585-597.	3.2	35
63	Developing DNA methylation-based diagnostic biomarkers. Journal of Genetics and Genomics, 2018, 45, 87-97.	1.7	41
64	Epitranscriptomic m6A Regulation of Axon Regeneration in the Adult Mammalian Nervous System. Neuron, 2018, 97, 313-325.e6.	3.8	292
65	A unique epigenomic landscape defines the characteristics and differentiation potentials of glioma stem cells. Genome Biology, 2018, 19, 51.	3.8	1
66	Medical genetics: Towards precision medicine. Journal of Genetics and Genomics, 2018, 45, 55-56.	1.7	2
67	Partial loss of psychiatric risk gene Mir137 in mice causes repetitive behavior and impairs sociability and learning via increased Pde10a. Nature Neuroscience, 2018, 21, 1689-1703.	7.1	127
68	Ten-Eleven Translocation Proteins Modulate the Response to Environmental Stress in Mice. Cell Reports, 2018, 25, 3194-3203.e4.	2.9	46
69	5-Hydroxymethylcytosine alterations in the human postmortem brains of autism spectrum disorder. Human Molecular Genetics, 2018, 27, 2955-2964.	1.4	28
70	Optimized distributed systems achieve significant performance improvement on sorted merging of massive VCF files. GigaScience, 2018, 7, .	3.3	4
71	Active N6-Methyladenine Demethylation by DMAD Regulates Gene Expression by Coordinating with Polycomb Protein in Neurons. Molecular Cell, 2018, 71, 848-857.e6.	4.5	71
72	Piperine ameliorates SCA17 neuropathology by reducing ER stress. Molecular Neurodegeneration, 2018, 13, 4.	4.4	29

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73	Fragile X mental retardation protein modulates the stability of its m6A-marked messenger RNA targets. Human Molecular Genetics, 2018, 27, 3936-3950.	1.4	129
74	A genomeâ€wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. Alzheimer's and Dementia, 2017, 13, 674-688.	0.4	83
75	Fat mass and obesity-associated (FTO) protein regulates adult neurogenesis. Human Molecular Genetics, 2017, 26, 2398-2411.	1.4	221
76	Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. Nature Communications, 2017, 8, 15102.	5.8	88
77	Temporal Control of Mammalian Cortical Neurogenesis by m6A Methylation. Cell, 2017, 171, 877-889.e17.	13.5	567
78	DNA N6-methyladenine is dynamically regulated in the mouse brain following environmental stress. Nature Communications, 2017, 8, 1122.	5.8	182
79	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. Cell Stem Cell, 2017, 21, 349-358.e6.	5.2	163
80	Zika virus directly infects peripheral neurons and induces cell death. Nature Neuroscience, 2017, 20, 1209-1212.	7.1	85
81	Essential role of microRNA-650 in the regulation of B-cell CLL/lymphoma 11B gene expression following transplantation: A novel mechanism behind the acute rejection of renal allografts. International Journal of Molecular Medicine, 2017, 40, 1840-1850.	1.8	9
82	Ten-eleven translocation 2 interacts with forkhead box O3 and regulates adult neurogenesis. Nature Communications, 2017, 8, 15903.	5.8	82
83	Fragile X-Associated Tremor/Ataxia Syndrome: From Molecular Pathogenesis to Development of Therapeutics. Frontiers in Cellular Neuroscience, 2017, 11, 128.	1.8	49
84	Animal Models of Fragile X Syndrome. , 2017, , 123-147.		3
85	CRISPR/Cas9-mediated gene editing ameliorates neurotoxicity in mouse model of Huntingtonâ€™s disease. Journal of Clinical Investigation, 2017, 127, 2719-2724.	3.9	282
86	Global and Site-Specific Changes in 5-Methylcytosine and 5-Hydroxymethylcytosine after Extended Post-mortem Interval. Frontiers in Genetics, 2016, 7, 120.	1.1	5
87	The Drosophila Helicase MLE Targets Hairpin Structures in Genomic Transcripts. PLoS Genetics, 2016, 12, e1005761.	1.5	13
88	Zika Virus Infects Human Cortical Neural Progenitors and Attenuates Their Growth. Cell Stem Cell, 2016, 18, 587-590.	5.2	1,125
89	Brain-Region-Specific Organoids Using Mini-bioreactors for Modeling ZIKV Exposure. Cell, 2016, 165, 1238-1254.	13.5	1,680
90	5-Hydroxymethylation-associated epigenetic modifiers of Alzheimerâ€™s disease modulate Tau-induced neurotoxicity. Human Molecular Genetics, 2016, 25, ddw109.	1.4	53

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91	Sex-specific hippocampal 5-hydroxymethylcytosine is disrupted in response to acute stress. Neurobiology of Disease, 2016, 96, 54-66.	2.1	24
92	Structural dynamics control the MicroRNA maturation pathway. Nucleic Acids Research, 2016, 44, gkw793.	6.5	17
93	Molecular signatures associated with ZIKV exposure in human cortical neural progenitors. Nucleic Acids Research, 2016, 44, 8610-8620.	6.5	155
94	Distinctive Klf4 mutants determine preference for DNA methylation status. Nucleic Acids Research, 2016, 44, gkw774.	6.5	19
95	Histone deacetylase 3 associates with MeCP2 to regulate FOXO and social behavior. Nature Neuroscience, 2016, 19, 1497-1505.	7.1	88
96	Genome-wide alteration of 5-hydroxymenthylcytosine in a mouse model of Alzheimerâ€™s disease. BMC Genomics, 2016, 17, 381.	1.2	48
97	DIVAN: accurate identification of non-coding disease-specific risk variants using multi-omics profiles. Genome Biology, 2016, 17, 252.	3.8	67
98	Epigenetic mechanisms in neurogenesis. Nature Reviews Neuroscience, 2016, 17, 537-549.	4.9	299
99	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. Molecular Cell, 2016, 61, 153-160.	4.5	74
100	5-Hydroxymethylcytosine-mediated alteration of transposon activity associated with the exposure to adversein uteroenvironments in human. Human Molecular Genetics, 2016, 25, 2208-2219.	1.4	25
101	DNA methylation dynamics in neurogenesis. Epigenomics, 2016, 8, 401-414.	1.0	52
102	Genome-wide alterations in hippocampal 5-hydroxymethylcytosine links plasticity genes to acute stress. Neurobiology of Disease, 2016, 86, 99-108.	2.1	48
103	Structural basis of nucleic-acid recognition and double-strand unwinding by the essential neuronal protein Pur-alpha. ELife, 2016, 5, .	2.8	35
104	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo. Nucleic Acids Research, 2015, 43, 2757-2766.	6.5	46
105	High-Throughput Sequencing-Based Mapping of Cytosine Modifications. , 2015, , 39-53.		5
106	DICER1 and microRNA regulation in post-traumatic stress disorder with comorbid depression. Nature Communications, 2015, 6, 10106.	5.8	81
107	Gossypol Acetic Acid Prevents Oxidative Stress-Induced Retinal Pigment Epithelial Necrosis by Regulating the FoxO3/Sestrin2 Pathway. Molecular and Cellular Biology, 2015, 35, 1952-1963.	1.1	23
108	Glutamate Dehydrogenase 1 Signals through Antioxidant Glutathione Peroxidase 1 to Regulate Redox Homeostasis and Tumor Growth. Cancer Cell, 2015, 27, 257-270.	7.7	269

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109	Altering 5-hydroxymethylcytosine modification impacts ischemic brain injury. Human Molecular Genetics, 2015, 24, 5855-5866.	1.4	57
110	The Ecdysone Receptor Coactivator Taiman Links Yorkie to Transcriptional Control of Germline Stem Cell Factors in Somatic Tissue. Developmental Cell, 2015, 34, 168-180.	3.1	56
111	DNA methylation and hydroxymethylation in stem cells. Cell Biochemistry and Function, 2015, 33, 161-173.	1.4	43
112	Role of Tet1 and 5-hydroxymethylcytosine in cocaine action. Nature Neuroscience, 2015, 18, 536-544.	7.1	160
113	Small Molecules Efficiently Reprogram Human Astroglial Cells into Functional Neurons. Cell Stem Cell, 2015, 17, 735-747.	5.2	250
114	Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates. Nucleic Acids Research, 2015, 43, gkv715.	6.5	203
115	Combined Loss of Tet1 and Tet2 Promotes B Cell, but Not Myeloid Malignancies, in Mice. Cell Reports, 2015, 13, 1692-1704.	2.9	83
116	5-Hydroxymethylcytosine: A new player in brain disorders?. Experimental Neurology, 2015, 268, 3-9.	2.0	72
117	Small-Molecule Screening Using Drosophila Models of Human Neurological Disorders. Methods in Molecular Biology, 2015, 1263, 127-138.	0.4	4
118	Combined Loss of Tet1 and Tet2 Promotes B-Cell, but Not Myeloid Malignancies in Mice. Blood, 2015, 126, 3650-3650.	0.6	0
119	CGG repeats in RNA modulate expression of TDP-43 in mouse and fly models of fragile X tremor ataxia syndrome. Human Molecular Genetics, 2014, 23, 5906-5915.	1.4	21
120	Towards Understanding RNA-Mediated Neurological Disorders. Journal of Genetics and Genomics, 2014, 41, 473-484.	1.7	14
121	Cell cycle-linked MeCP2 phosphorylation modulates adult neurogenesis involving the Notch signalling pathway. Nature Communications, 2014, 5, 5601.	5.8	57
122	Integrating DNA methylation dynamics into a framework for understanding epigenetic codes. BioEssays, 2014, 36, 107-117.	1.2	37
123	A feed-forward mechanism involving Drosophila fragile X mental retardation protein triggers a replication stress-induced DNA damage response. Human Molecular Genetics, 2014, 23, 5188-5196.	1.4	26
124	Genome-wide alteration of 5-hydroxymethylcytosine in a mouse model of fragile X-associated tremor/ataxia syndrome. Human Molecular Genetics, 2014, 23, 1095-1107.	1.4	52
125	Cytosine modifications in neurodevelopment and diseases. Cellular and Molecular Life Sciences, 2014, 71, 405-418.	2.4	34
126	shRNA-mediated GSTP1 gene silencing enhances androgen-independent cell line DU145 chemosensitivity. International Urology and Nephrology, 2014, 46, 1115-1121.	0.6	4

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127	Genome-wide antagonism between 5-hydroxymethylcytosine and DNA methylation in the adult mouse brain. Frontiers in Biology, 2014, 9, 66-74.	0.7	26
128	Fat mass and obesity-associated (FTO) protein interacts with CaMKII and modulates the activity of CREB signaling pathway. Human Molecular Genetics, 2014, 23, 3299-3306.	1.4	43
129	AGO3 Slicer activity regulates mitochondriaâ€“nuage localization of Armitage and piRNA amplification. Journal of Cell Biology, 2014, 206, 217-230.	2.3	50
130	Use of model systems to understand the etiology of fragile X-associated primary ovarian insufficiency (FXPOI). Journal of Neurodevelopmental Disorders, 2014, 6, 26.	1.5	55
131	Environmental enrichment modulates 5-hydroxymethylcytosine dynamics in hippocampus. Genomics, 2014, 104, 376-382.	1.3	57
132	Coordination of Engineered Factors with TET1/2 Promotes Early-Stage Epigenetic Modification during Somatic Cell Reprogramming. Stem Cell Reports, 2014, 2, 253-261.	2.3	25
133	Unlocking epigenetic codes in neurogenesis. Genes and Development, 2014, 28, 1253-1271.	2.7	79
134	U1 small nuclear ribonucleoprotein complex and RNA splicing alterations in Alzheimerâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16562-16567.	3.3	268
135	Cell-Cycle Control of Developmentally Regulated Transcription Factors Accounts for Heterogeneity in Human Pluripotent Cells. Stem Cell Reports, 2013, 1, 532-544.	2.3	129
136	Probing the microRNA pathway with small molecules. Bioorganic and Medicinal Chemistry, 2013, 21, 6119-6123.	1.4	4
137	Tet-mediated covalent labelling of 5-methylcytosine for its genome-wide detection and sequencing. Nature Communications, 2013, 4, 1517.	5.8	48
138	Genome-wide Profiling of 5-Formylcytosine Reveals Its Roles in Epigenetic Priming. Cell, 2013, 153, 678-691.	13.5	502
139	Chemical Modification-Assisted Bisulfite Sequencing (CAB-Seq) for 5-Carboxylcytosine Detection in DNA. Journal of the American Chemical Society, 2013, 135, 9315-9317.	6.6	116
140	Subtelomeric hotspots of aberrant 5-hydroxymethylcytosine-mediated epigenetic modifications during reprogramming to pluripotency. Nature Cell Biology, 2013, 15, 700-711.	4.6	87
141	Toward pluripotency by reprogramming: mechanisms and application. Protein and Cell, 2013, 4, 820-832.	4.8	21
142	Expanded GGGGCC repeat RNA associated with amyotrophic lateral sclerosis and frontotemporal dementia causes neurodegeneration. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7778-7783.	3.3	306
143	TET1 plays an essential oncogenic role in MLL -rearranged leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11994-11999.	3.3	185
144	MicroRNA-277 Modulates the Neurodegeneration Caused by Fragile X Premutation rCGG Repeats. PLoS Genetics, 2012, 8, e1002681.	1.5	50

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145	Retrotransposon activation contributes to fragile X premutation rCGG-mediated neurodegeneration. Human Molecular Genetics, 2012, 21, 57-65.	1.4	69
146	Selective Capture of 5-hydroxymethylcytosine from Genomic DNA. Journal of Visualized Experiments, 2012, , .	0.2	3
147	Tet-assisted bisulfite sequencing of 5-hydroxymethylcytosine. Nature Protocols, 2012, 7, 2159-2170.	5.5	236
148	Chemical screen reveals small molecules suppressing fragile X premutation rCGG repeat-mediated neurodegeneration in Drosophila. Human Molecular Genetics, 2012, 21, 2068-2075.	1.4	42
149	Epigenetics-Based Therapeutics for Neurodegenerative Disorders. Current Geriatrics Reports, 2012, 1, 229-236.	1.1	36
150	Fragile X premutation RNA is sufficient to cause primary ovarian insufficiency in mice. Human Molecular Genetics, 2012, 21, 5039-5047.	1.4	78
151	Genome-wide DNA hydroxymethylation changes are associated with neurodevelopmental genes in the developing human cerebellum. Human Molecular Genetics, 2012, 21, 5500-5510.	1.4	157
152	Base-Resolution Analysis of 5-Hydroxymethylcytosine in the Mammalian Genome. Cell, 2012, 149, 1368-1380.	13.5	912
153	Iron Homeostasis Regulates the Activity of the MicroRNA Pathway through Poly(C)-Binding Protein 2. Cell Metabolism, 2012, 15, 895-904.	7.2	55
154	Circadian Rhythm-Dependent Alterations of Gene Expression in Drosophila Brain Lacking Fragile X Mental Retardation Protein. PLoS ONE, 2012, 7, e37937.	1.1	19
155	Dynamics of DNA Methylation in Aging and Alzheimer's Disease. DNA and Cell Biology, 2012, 31, S-42-S-48.	0.9	84
156	Role of noncoding RNAs in trinucleotide repeat neurodegenerative disorders. Experimental Neurology, 2012, 235, 469-475.	2.0	17
157	RNA-mediated neurodegeneration in fragile X-associated tremor/ataxia syndrome. Brain Research, 2012, 1462, 112-117.	1.1	35
158	Fragile X Mental Retardation Protein and Stem Cells. Results and Problems in Cell Differentiation, 2012, 54, 157-164.	0.2	1
159	5-Hydroxymethylcytosine (5-hmC) Specific Enrichment. Bio-protocol, 2012, 2, .	0.2	2
160	Ablation of Fmrp in adult neural stem cells disrupts hippocampus-dependent learning. Nature Medicine, 2011, 17, 559-565.	15.2	205
161	5-hmCâ€“mediated epigenetic dynamics during postnatal neurodevelopment and aging. Nature Neuroscience, 2011, 14, 1607-1616.	7.1	746
162	RNA-Binding Protein FXR2 Regulates Adult Hippocampal Neurogenesis by Reducing Noggin Expression. Neuron, 2011, 70, 924-938.	3.8	78

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163	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. Nature Biotechnology, 2011, 29, 68-72.	9.4	955
164	Nuclear Accumulation of Stress Response mRNAs Contributes to the Neurodegeneration Caused by Fragile X Premutation rCGG Repeats. PLoS Genetics, 2011, 7, e1002102.	1.5	56
165	Integrating 5-Hydroxymethylcytosine into the Epigenomic Landscape of Human Embryonic Stem Cells. PLoS Genetics, 2011, 7, e1002154.	1.5	250
166	Small RNA-Mediated Gene Regulation in Neurodevelopmental Disorders. Current Psychiatry Reports, 2010, 12, 154-161.	2.1	11
167	Emergence of Chemical Biology Approaches to the RNAi/miRNA Pathway. Chemistry and Biology, 2010, 17, 584-589.	6.2	27
168	MicroRNA miR-137 Regulates Neuronal Maturation by Targeting Ubiquitin Ligase Mind Bomb-1. Stem Cells, 2010, 28, 1060-1070.	1.4	349
169	Roles of small regulatory RNAs in determining neuronal identity. Nature Reviews Neuroscience, 2010, 11, 329-338.	4.9	168
170	Cross talk between microRNA and epigenetic regulation in adult neurogenesis. Journal of Cell Biology, 2010, 189, 127-141.	2.3	445
171	Fragile X Mental Retardation Protein Regulates Proliferation and Differentiation of Adult Neural Stem/Progenitor Cells. PLoS Genetics, 2010, 6, e1000898.	1.5	211
172	Epigenetic Regulation of miR-184 by MBD1 Governs Neural Stem Cell Proliferation and Differentiation. Cell Stem Cell, 2010, 6, 433-444.	5.2	287
173	Animal Models for FXTAS. , 2010, , 123-136.		1
174	Small regulatory RNAs in neurodevelopmental disorders. Human Molecular Genetics, 2009, 18, R18-R26.	1.4	47
175	The Bantam microRNA Is Associated with Drosophila Fragile X Mental Retardation Protein and Regulates the Fate of Germline Stem Cells. PLoS Genetics, 2009, 5, e1000444.	1.5	103
176	Macro Role(s) of MicroRNAs in Fragile X Syndrome?. NeuroMolecular Medicine, 2009, 11, 200-207.	1.8	14
177	RNA-mediated pathogenesis in fragile X-associated disorders. Neuroscience Letters, 2009, 466, 103-108.	1.0	18
178	A small molecule enhances RNA interference and promotes microRNA processing. Nature Biotechnology, 2008, 26, 933-940.	9.4	230
179	Identification of small molecules rescuing fragile X syndrome phenotypes in Drosophila. Nature Chemical Biology, 2008, 4, 256-263.	3.9	248
180	The microRNA pathway and fragile X mental retardation protein. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2008, 1779, 702-705.	0.9	43

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181	FXTAS: a bad RNA and a hope for a cure. Expert Opinion on Biological Therapy, 2008, 8, 249-253.	1.4	8
182	Epigenetic Regulation of miRNA in Stem Cells. , 2008, , 187-204.		0
183	The loss of methyl-CpG binding protein 1 leads to autism-like behavioral deficits. Human Molecular Genetics, 2008, 17, 2047-2057.	1.4	89
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