Zhongsheng Sun

List of Publications by Year
in descending order

107 papers	7,299 citations	94269 37 h-index	58464 82 g-index
112 all docs	112 docs citations	112 times ranked	10125 citing authors

#	Article	IF	Citations
1	The p21-activated kinases in neural cytoskeletal remodeling and related neurological disorders. Protein and Cell, 2022, 13, 6-25.	4.8	25
2	Cross-Disorder Analysis of De Novo Mutations in Neuropsychiatric Disorders. Journal of Autism and Developmental Disorders, 2022, 52, 1299-1313.	1.7	3
3	Prenatal witness stress induces intergenerational anxiety-like behaviors and altered gene expression profiles in male mice. Neuropharmacology, 2022, 202, 108857.	2.0	3
4	Comprehensive evaluation of computational methods for predicting cancer driver genes. Briefings in Bioinformatics, 2022, 23, .	3.2	19
5	Putative complement control protein CSMD3 dysfunction impairs synaptogenesis and induces neurodevelopmental disorders. Brain, Behavior, and Immunity, 2022, 102, 237-250.	2.0	12
6	Transcriptomic signatures associated with autoimmune thyroiditis in papillary thyroid carcinoma and cancer immunotherapy-induced thyroid dysfunction. Computational and Structural Biotechnology Journal, 2022, 20, 2391-2401.	1.9	0
7	Comprehensive characterization of posttranscriptional impairment-related 3â€²-UTR mutations in 2413 whole genomes of cancer patients. Npj Genomic Medicine, 2022, 7, .	1.7	7
8	Integrative analysis prioritised oxytocin-related biomarkers associated with the aetiology of autism spectrum disorder. EBioMedicine, 2022, 81, 104091.	2.7	7
9	Pan-cancer analyses of synonymous mutations based on tissue-specific codon optimality. Computational and Structural Biotechnology Journal, 2022, 20, 3567-3580.	1.9	0
10	OncoVar: an integrated database and analysis platform for oncogenic driver variants in cancers. Nucleic Acids Research, 2021, 49, D1289-D1301.	6.5	64
11	Restricted Feeding Resets Endogenous Circadian Rhythm in Female Mice Under Constant Darkness. Neuroscience Bulletin, 2021, 37, 1005-1009.	1.5	3
12	Targeted sequencing and integrative analysis of 3,195 Chinese patients with neurodevelopmental disorders prioritized 26 novel candidate genes. Journal of Genetics and Genomics, 2021, 48, 312-323.	1.7	11
13	Targeted sequencing and integrative analysis to prioritize candidate genes in neurodevelopmental disorders. Molecular Neurobiology, 2021, 58, 3863-3873.	1.9	5
14	A new approach to decode DNA methylome and genomic variants simultaneously from double strand bisulfite sequencing. Briefings in Bioinformatics, 2021, 22, .	3.2	5
15	Mapping of de novo mutations in primary biliary cholangitis to a disease-specific co-expression network underlying homeostasis and metabolism. Journal of Genetics and Genomics, 2021, , .	1.7	1
16	Co-expression Network of mRNAs and lncRNAs Regulated by Stress-Linked Behavioral Assays. Psychopharmacology, 2020, 237, 571-582.	1.5	9
17	Functional relationships between recessive inherited genes and genes with de novo variants in autism spectrum disorder. Molecular Autism, 2020, 11, 75.	2.6	5
18	Inter- and intratumor DNA methylation heterogeneity associated with lymph node metastasis and prognosis of esophageal squamous cell carcinoma. Theranostics, 2020, 10, 3035-3048.	4.6	21

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19	The Relationships Between Stress, Mental Disorders, and Epigenetic Regulation of BDNF. International Journal of Molecular Sciences, 2020, 21, 1375.	1.8	53
20	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. Translational Psychiatry, 2020, 10, 4.	2.4	84
21	Prevalence and architecture of posttranscriptionally impaired synonymous mutations in 8,320 genomes across 22 cancer types. Nucleic Acids Research, 2020, 48, 1192-1205.	6.5	31
22	AI-Driver: an ensemble method for identifying driver mutations in personal cancer genomes. NAR Genomics and Bioinformatics, 2020, 2, lqaa084.	1.5	19
23	Low intratumor heterogeneity correlates with increased response to PD-1 blockade in renal cell carcinoma. Therapeutic Advances in Medical Oncology, 2020, 12, 175883592097711.	1.4	20
24	A comparative study of the genetic components of three subcategories of autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1720-1731.	4.1	22
25	Androgen deprivation drives variation of androgen receptor trinucleotide repeats. Acta Biochimica Et Biophysica Sinica, 2019, 51, 972-975.	0.9	0
26	OncoBase: a platform for decoding regulatory somatic mutations in human cancers. Nucleic Acids Research, 2019, 47, D1044-D1055.	6.5	33
27	The biological basis of sexual orientation: How hormonal, genetic, and environmental factors influence to whom we are sexually attracted. Frontiers in Neuroendocrinology, 2019, 55, 100798.	2.5	19
28	A 17 gene panel for nonâ€smallâ€cell lung cancer prognosis identified through integrative epigenomicâ€transcriptomic analyses of hypoxiaâ€induced epithelialâ€“mesenchymal transition. Molecular Oncology, 2019, 13, 1490-1502.	2.1	25
29	Presence of the pregnant partner regulates microRNA-30a and BDNF levels and protects male mice from social defeat-induced abnormal behaviors. Neuropharmacology, 2019, 159, 107589.	2.0	15
30	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	6.5	148
31	Screening for possible oligogenic pathogenesis in Chinese sporadic ALS patients. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2018, 19, 419-425.	1.1	16
32	CirGRDB: a database for the genome-wide deciphering circadian genes and regulators. Nucleic Acids Research, 2018, 46, D64-D70.	6.5	29
33	Anxiety-Related Behaviours Associated with microRNA-206-3p and BDNF Expression in Pregnant Female Mice Following Psychological Social Stress. Molecular Neurobiology, 2018, 55, 1097-1111.	1.9	37
34	CRISPR Editing in Biological and Biomedical Investigation. Journal of Cellular Biochemistry, 2018, 119, 52-61.	1.2	17
35	EpiDenovo: a platform for linking regulatory de novo mutations to developmental epigenetics and diseases. Nucleic Acids Research, 2018, 46, D92-D99.	6.5	17
36	Genetic landscape of papillary thyroid carcinoma in the Chinese population. Journal of Pathology, 2018, 244, 215-226.	2.1	90

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37	Targeted deletion of Insm2 in mice result in reduced insulin secretion and glucose intolerance. Journal of Translational Medicine, 2018, 16, 297.	1.8	8
38	Genomic landscapes of Chinese sporadic autism spectrum disorders revealed by whole-genome sequencing. Journal of Genetics and Genomics, 2018, 45, 527-538.	1.7	33
39	Identification and characterization of novel fusion genes in prostate cancer by targeted RNA capture and next-generation sequencing. Acta Biochimica Et Biophysica Sinica, 2018, 50, 1166-1172.	0.9	10
40	Performance evaluation of pathogenicity-computation methods for missense variants. Nucleic Acids Research, 2018, 46, 7793-7804.	6.5	168
41	A Statistical Framework for Mapping Risk Genes from De Novo Mutations in Whole-Genome-Sequencing Studies. American Journal of Human Genetics, 2018, 102, 1031-1047.	2.6	26
42	Altered expressions of memory genes in food-entrained circadian rhythm. Acta Biochimica Et Biophysica Sinica, 2018, 50, 1068-1071.	0.9	1
43	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. Cell Reports, 2018, 24, 2029-2041.	2.9	64
44	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. Theranostics, 2018, 8, 4345-4358.	4.6	63
45	Identification of Novel Compound Mutations in PLA2G6-Associated Neurodegeneration Patient with Characteristic MRI Imaging. Molecular Neurobiology, 2017, 54, 4636-4643.	1.9	13
46	Lamarck rises from his grave: parental environmentâ€induced epigenetic inheritance in model organisms and humans. Biological Reviews, 2017, 92, 2084-2111.	4.7	123
47	Vitamin Dâ€related genes are subjected to significant de novo mutation burdens in autism spectrum disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 568-577.	1.1	20
48	A genome-wide association study identifies six novel risk loci for primary biliary cholangitis. Nature Communications, 2017, 8, 14828.	5.8	102
49	Population Genomics Reveals Speciation and Introgression between Brown Norway Rats and Their Sibling Species. Molecular Biology and Evolution, 2017, 34, 2214-2228.	3.5	47
50	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. Molecular Psychiatry, 2017, 22, 1282-1290.	4.1	95
51	TET1 modulates H4K16 acetylation by controlling auto-acetylation of hMOF to affect gene regulation and DNA repair function. Nucleic Acids Research, 2017, 45, 672-684.	6.5	56
52	mirVAFC: A Web Server for Prioritizations of Pathogenic Sequence Variants from Exome Sequencing Data via Classifications. Human Mutation, 2017, 38, 25-33.	1.1	3
53	Acetylation of hMOF Modulates H4K16ac to Regulate DNA Repair Genes in Response to Oxidative Stress. International Journal of Biological Sciences, 2017, 13, 923-934.	2.6	17
54	Epigenetic Activation of ASCT2 in the Hippocampus Contributes to Depression-Like Behavior by Regulating D-Serine in Mice. Frontiers in Molecular Neuroscience, 2017, 10, 139.	1.4	18

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55	S-adenosyl-methionine (SAM) alters the transcriptome and methylome and specifically blocks growth and invasiveness of liver cancer cells. Oncotarget, 2017, 8, 111866-111881.	0.8	38
56	Genomeâ€wide identification of differential methylation between primary and recurrent hepatocellular carcinomas. Molecular Carcinogenesis, 2016, 55, 1163-1174.	1.3	15
57	Whole-Genome Sequencing Reveals Genetic Variation in the Asian House Rat. G3: Genes, Genomes, Genetics, 2016, 6, 1969-1977.	0.8	8
58	Demethylation of c-MYB binding site mediates upregulation of Bdnf IV in cocaine-conditioned place preference. Scientific Reports, 2016, 6, 22087.	1.6	13
59	A novel 10-base pair insertion mutation in exon 5 of the SOD1 gene in a Chinese family with amyotrophic lateral sclerosis. Neurobiology of Aging, 2016, 45, 212.e1-212.e4.	1.5	3
60	Mutations in WNT10B Are Identified in Individuals with Oligodontia. American Journal of Human Genetics, 2016, 99, 195-201.	2.6	91
61	Recent Progress in CRISPR/Cas9 Technology. Journal of Genetics and Genomics, 2016, 43, 63-75.	1.7	94
62	RBP-Var: a database of functional variants involved in regulation mediated by RNA-binding proteins. Nucleic Acids Research, 2016, 44, D154-D163.	6.5	52
63	Chronic exposure to air pollution particles increases the risk of obesity and metabolic syndrome: findings from a natural experiment in Beijing. FASEB Journal, 2016, 30, 2115-2122.	0.2	181
64	Genes with de novo mutations are shared by four neuropsychiatric disorders discovered from NPdenovo database. Molecular Psychiatry, 2016, 21, 290-297.	4.1	167
65	Wide mutation spectrum and frequent variant Ala27Thr of FBN1 identified in a large cohort of Chinese patients with sporadic TAAD. Scientific Reports, 2015, 5, 13115.	1.6	15
66	Investigation of Pathogenic Genes in Chinese sporadic Hypertrophic Cardiomyopathy Patients by Whole Exome Sequencing. Scientific Reports, 2015, 5, 16609.	1.6	39
67	EpilepsyGene: a genetic resource for genes and mutations related to epilepsy. Nucleic Acids Research, 2015, 43, D893-D899.	6.5	71
68	Sex-related difference in food-anticipatory activity of mice. Hormones and Behavior, 2015, 70, 38-46.	1.0	23
69	Lysosomal storage disease in the brain: mutations of the Î²-mannosidase gene identified in autosomal dominant nystagmus. Genetics in Medicine, 2015, 17, 971-979.	1.1	26
70	mirTrios: an integrated pipeline for detection of de novo and rare inherited mutations from trios-based next-generation sequencing. Journal of Medical Genetics, 2015, 52, 275-281.	1.5	35
71	Q-RRBS: a quantitative reduced representation bisulfite sequencing method for single-cell methylome analyses. Epigenetics, 2015, 10, 775-783.	1.3	23
72	Dysplastic spondylolysis is caused by mutations in the diastrophic dysplasia sulfate transporter gene. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8064-8069.	3.3	39

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73	MBRidge: an accurate and cost-effective method for profiling DNA methylome at single-base resolution. Journal of Molecular Cell Biology, 2015, 7, 299-313.	1.5	5
74	Clock-controlled StARâ€™s expression and corticosterone production contribute to the endotoxemia immune response. Chronobiology International, 2015, 32, 358-367.	0.9	9
75	A Bayesian Framework to Identify Methylcytosines from High-Throughput Bisulfite Sequencing Data. PLoS Computational Biology, 2014, 10, e1003853.	1.5	4
76	Comparative RNA-seq analysis reveals potential mechanisms mediating the conversion to androgen independence in an LNCaP progression cell model. Cancer Letters, 2014, 342, 130-138.	3.2	16
77	RSPO2â€“LGR5 signaling has tumour-suppressive activity in colorectal cancer. Nature Communications, 2014, 5, 3149.	5.8	101
78	Ras-induced Epigenetic Inactivation of the RRAD (Ras-related Associated with Diabetes) Gene Promotes Glucose Uptake in a Human Ovarian Cancer Model. Journal of Biological Chemistry, 2014, 289, 14225-14238.	1.6	37
79	Single-Cell Sequencing Technologies: Current and Future. Journal of Genetics and Genomics, 2014, 41, 513-528.	1.7	74
80	Identification of a novel missense (C7W) mutation of SOD1 in a large familial amyotrophic lateral sclerosis pedigree. Neurobiology of Aging, 2014, 35, 725.e11-725.e15.	1.5	6
81	New mutation in the SOD1 (copper/zinc superoxide dismutase-1) gene in a Chinese amyotrophic lateral sclerosis (ALS) patient. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2013, 14, 635-637.	1.1	2
82	RRBS-Analyser: A Comprehensive Web Server for Reduced Representation Bisulfite Sequencing Data Analysis. Human Mutation, 2013, 34, 1606-1610.	1.1	60
83	Genome-wide identification and divergent transcriptional expression of StAR-related lipid transfer (START) genes in teleosts. Gene, 2013, 519, 18-25.	1.0	4
84	mirTools 2.0 for non-coding RNA discovery, profiling, and functional annotation based on high-throughput sequencing. RNA Biology, 2013, 10, 1087-1092.	1.5	84
85	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. Genomics, 2012, 99, 178-182.	1.3	43
86	Mutations ofANK3identified by exome sequencing are associated with autism susceptibility. Human Mutation, 2012, 33, 1635-1638.	1.1	107
87	Exome-assistant: a rapid and easy detection of disease-related genes and genetic variations from exome sequencing. BMC Genomics, 2012, 13, 692.	1.2	11
88	Identification of a novel Cys146X mutation of SOD1 in familial amyotrophic lateral sclerosis by whole-exome sequencing. Genetics in Medicine, 2012, 14, 823-826.	1.1	24
89	Reversal of Cocaine-Conditioned Place Preference through Methyl Supplementation in Mice: Altering Global DNA Methylation in the Prefrontal Cortex. PLoS ONE, 2012, 7, e33435.	1.1	82
90	Regulation of Peripheral Clock to Oscillation of Substance P Contributes to Circadian Inflammatory Pain. Anesthesiology, 2012, 117, 149-160.	1.3	45

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91	Deficiency of Antinociception and Excessive Grooming Induced by Acute Immobilization Stress in Per1 Mutant Mice. PLoS ONE, 2011, 6, e16212.	1.1	20
92	Systematic evaluation of genome-wide methylated DNA enrichment using a CpG island array. BMC Genomics, 2011, 12, 10.	1.2	13
93	Evolutionary Mode and Functional Divergence of Vertebrate NMDA Receptor Subunit 2 Genes. PLoS ONE, 2010, 5, e13342.	1.1	18
94	mirTools: microRNA profiling and discovery based on high-throughput sequencing. Nucleic Acids Research, 2010, 38, W392-W397.	6.5	120
95	MagicViewer: integrated solution for next-generation sequencing data visualization and genetic variation detection and annotation. Nucleic Acids Research, 2010, 38, W732-W736.	6.5	45
96	EXPRESSION PROFILING REVEALS A POSITIVE REGULATION BYMPER2ON CIRCADIAN RHYTHM OF CYTOTOXICITY RECEPTORS:LY49CANDNKG2D. Chronobiology International, 2009, 26, 1514-1544.	0.9	13
97	The APP-interacting protein FE65 is required for hippocampus-dependent learning and long-term potentiation. Learning and Memory, 2009, 16, 537-544.	0.5	32
98	Converging signal on ERK1/2 activity regulates group I mGluR-mediated Arc transcription. Neuroscience Letters, 2009, 460, 36-40.	1.0	17
99	The Circadian Clock Period 2 Gene Regulates Gamma Interferon Production of NK Cells in Host Response to Lipopolysaccharide-Induced Endotoxic Shock. Infection and Immunity, 2007, 75, 4186-4186.	1.0	2
100	MethyCancer: the database of human DNA methylation and cancer. Nucleic Acids Research, 2007, 36, D836-D841.	6.5	127
101	Proteomic Analysis of Rat Prefrontal Cortex in Three Phases of Morphine-Induced Conditioned Place Preference. Journal of Proteome Research, 2007, 6, 2239-2247.	1.8	31
102	The Circadian Clock Period 2 Gene Regulates Gamma Interferon Production of NK Cells in Host Response to Lipopolysaccharide-Induced Endotoxic Shock. Infection and Immunity, 2006, 74, 4750-4756.	1.0	209
103	Nonredundant Roles of the mPer1 and mPer2 Genes in the Mammalian Circadian Clock. Cell, 2001, 105, 683-694.	13.5	802
104	mPer1 and mPer2 Are Essential for Normal Resetting of the Circadian Clock. Journal of Biological Rhythms, 2001, 16, 100-104.	1.4	337
105	The mPer2 gene encodes a functional component of the mammalian circadian clock. Nature, 1999, 400, 169-173.	13.7	618
106	RIGUI, a Putative Mammalian Ortholog of the Drosophila period Gene. Cell, 1997, 90, 1003-1011.	13.5	648
107	A Differential Response of Two Putative Mammalian Circadian Regulators, mper1and mper2, to Light. Cell, 1997, 91, 1055-1064.	13.5	813