Feng Zhang

List of Publications by Year
in descending order

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Version: 2024-02-01

337 papers	15,217 citations	36303 51 h-index	26613 107 g-index
343 all docs	343 docs citations	343 times ranked	23238 citing authors

#	Article	IF	Citations
1	Identifying Candidate Genes Associated with Sporadic Amyotrophic Lateral Sclerosis via Integrative Analysis of Transcriptome-Wide Association Study and Messenger RNA Expression Profile. Cellular and Molecular Neurobiology, 2023, 43, 327-338.	3.3	1
2	Evaluating the interactive effects of dietary habits and human gut microbiome on the risks of depression and anxiety. Psychological Medicine, 2023, 53, 3047-3055.	4.5	7
3	Haploinsufficiency in non-homologous end joining factor 1 induces ovarian dysfunction in humans and mice. Journal of Medical Genetics, 2022, 59, 579-588.	3.2	3
4	The first human induced pluripotent stem cell line of Kashinâ€“Beck disease reveals involvement of heparan sulfate proteoglycan biosynthesis and PPAR pathway. FEBS Journal, 2022, 289, 279-293.	4.7	3
5	Homozygous mutations in CCDC34 cause male infertility with oligoasthenoteratozoospermia in humans and mice. Journal of Medical Genetics, 2022, 59, 710-718.	3.2	20
6	A multi-environments-gene interaction study of anxiety, depression and self-harm in the UK Biobank cohort. Journal of Psychiatric Research, 2022, 147, 59-66.	3.1	8
7	Genome-Wide Association Study and Genetic Correlation Scan Provide Insights into Its Genetic Architecture of Sleep Health Score in the UK Biobank Cohort. Nature and Science of Sleep, 2022, Volume 14, 1-12.	2.7	6
8	Associations between genetic loci, environment factors and mental disorders: a genome-wide survival analysis using the UK Biobank data. Translational Psychiatry, 2022, 12, 17.	4.8	2
9	An integrative analysis of DNA methylation and transcriptome showed the dysfunction of MAPK pathway was involved in the damage of human chondrocyte induced by T-2 toxin. BMC Molecular and Cell Biology, 2022, 23, 4.	2.0	6
10	Homozygous mutation in SLO3 leads to severe asthenoteratozoospermia due to acrosome hypoplasia and mitochondrial sheath malformations. Reproductive Biology and Endocrinology, 2022, 20, 5.	3.3	11
11	Assessing the joint effects of brain aging and gut microbiota on the risks of psychiatric disorders. Brain Imaging and Behavior, 2022, 16, 1504-1515.	2.1	7
12	A largeâ€scale genetic correlation scan between rheumatoid arthritis and human blood metabolites. Annals of Human Genetics, 2022, , .	0.8	2
13	Chromosome-Level Genome Assembly of Anthidium xuezhongi Niu & Zhu, 2020 (Hymenoptera: Apoidea:) Tj ETQq1 1 0.784314 rgBT /O	2.5	1
14	Dissecting the association between psychiatric disorders and neurological proteins: a genetic correlation and two-sample bidirectional Mendelian randomization study. Acta Neuropsychiatrica, 2022, 34, 311-317.	2.1	2
15	Evaluating the Effects of Diet-Gut Microbiota Interactions on Sleep Traits Using the UK Biobank Cohort. Nutrients, 2022, 14, 1134.	4.1	5
16	An atlas of genetic correlations between gestational age and common psychiatric disorders. Autism Research, 2022, 15, 1008-1017.	3.8	5
17	Exome-wide screening identifies novel rare risk variants for major depression disorder. Molecular Psychiatry, 2022, 27, 3069-3074.	7.9	15
18	The associations between sleep behaviors, lifestyle factors, genetic risk and mental disorders: A cohort study of 402 290 UK Biobank participants. Psychiatry Research, 2022, 311, 114488.	3.3	6

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19	Associations between electronic devices use and common mental traits: A geneâ€“environment interaction model using the UK Biobank data. Addiction Biology, 2022, 27, e13111.	2.6	3
20	A large-scale genetic correlation scan between rheumatoid arthritis and human plasma protein. Bone and Joint Research, 2022, 11, 134-142.	3.6	6
21	The Causal Relationships Between Sleep-related Phenotypes and Body Composition: A Mendelian Randomized Study. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e3463-e3473.	3.6	6
22	Large-scale genetic correlation scanning and causal association between deep vein thrombosis and human blood metabolites. Scientific Reports, 2022, 12, 7888.	3.3	0
23	Identification of Human Brain Proteins for Bitter-Sweet Taste Perception: A Joint Proteome-Wide and Transcriptome-Wide Association Study. Nutrients, 2022, 14, 2177.	4.1	4
24	Genome-wide association studies in non-anxiety individuals identified novel risk loci for depression. European Psychiatry, 2022, 65, .	0.2	1
25	Genetic Correlation Analysis and Transcriptome-wide Association Study Suggest the Overlapped Genetic Mechanism between Gout and Attention-deficit Hyperactivity Disorder. Canadian Journal of Psychiatry, 2021, 66, 1077-1084.	1.9	3
26	Diagnostic yield and clinical impact of exome sequencing in early-onset scoliosis (EOS). Journal of Medical Genetics, 2021, 58, 41-47.	3.2	40
27	Profiling of selenium and other trace elements in breads from rice and maize cultivated in a seleniferous area of Punjab (India). Journal of Food Science and Technology, 2021, 58, 825-833.	2.8	3
28	A heterozygous hypomorphic mutation of Fanca causes impaired follicle development and subfertility in female mice. Molecular Genetics and Genomics, 2021, 296, 103-112.	2.1	9
29	Novel lossâ€ofâ€function variants in <scp>DNAH17</scp> cause multiple morphological abnormalities of the sperm flagella in humans and mice. Clinical Genetics, 2021, 99, 176-186.	2.0	26
30	Integrated transcriptomic and proteomic analysis indicated that neurotoxicity of rats with chronic fluorosis may be in mechanism involved in the changed cholinergic pathway and oxidative stress. Journal of Trace Elements in Medicine and Biology, 2021, 64, 126688.	3.0	12
31	Long-term antibiotic use during early life and risks to mental traits: an observational study and geneâ€“environment-wide interaction study in UK Biobank cohort. Neuropsychopharmacology, 2021, 46, 1086-1092.	5.4	12
32	Whole exome sequencing and trio analysis to broaden the variant spectrum of genes in idiopathic hypogonadotropic hypogonadism. Asian Journal of Andrology, 2021, 23, 288.	1.6	5
33	Transcriptome-wide association study identifies susceptibility genes for rheumatoid arthritis. Arthritis Research and Therapy, 2021, 23, 38.	3.5	21
34	Evaluating the genetic effects of sex hormone traits on the development of mental traits: a polygenic score analysis and gene-environment-wide interaction study in UK Biobank cohort. Molecular Brain, 2021, 14, 3.	2.6	6
35	Deleterious variants in X-linked CFAP47 induce asthenoteratozoospermia and primary male infertility. American Journal of Human Genetics, 2021, 108, 309-323.	6.2	74
36	Integrative Analysis of MicroRNA and mRNA Sequencing Data Identifies Novel Candidate Genes and Pathways for Developmental Dysplasia of Hip. Cartilage, 2021, 13, 1618S-1626S.	2.7	2

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37	Perturbations of genes essential for MÃ¼llerian duct and WÃ¶lffian duct development in Mayer-Rokitansky-KÃ¼ster-Hauser syndrome. American Journal of Human Genetics, 2021, 108, 337-345.	6.2	41
38	Genome-Wide Differentially Methylated Region Analysis to Reveal Epigenetic Differences of Articular Cartilage in Kashinâ€“Beck Disease and Osteoarthritis. Frontiers in Cell and Developmental Biology, 2021, 9, 636291.	3.7	8
39	A chromosome-level genome of the spider Trichonephila antipodiana reveals the genetic basis of its polyphagy and evidence of an ancient whole-genome duplication event. GigaScience, 2021, 10, .	6.4	187
40	A mitogenomic phylogeny of the Entomobryoidea (Collembola): A comparative perspective. Zoologica Scripta, 2021, 50, 658-666.	1.7	5
41	Dietary Habit Is Associated with Depression and Intelligence: An Observational and Genome-Wide Environmental Interaction Analysis in the UK Biobank Cohort. Nutrients, 2021, 13, 1150.	4.1	4
42	Genome-wide CRISPR screens reveal synthetic lethal interaction between CREBBP and EP300 in diffuse large B-cell lymphoma. Cell Death and Disease, 2021, 12, 419.	6.3	21
43	Sex specific effect of gut microbiota on the risk of psychiatric disorders: A Mendelian randomisation study and PRS analysis using UK Biobank cohort. World Journal of Biological Psychiatry, 2021, 22, 495-504.	2.6	2
44	Socioeconomic Deprivation Index Is Associated With Psychiatric Disorders: An Observational and Genome-wide Gene-by-Environment Interaction Analysis in the UK Biobank Cohort. Biological Psychiatry, 2021, 89, 888-895.	1.3	51
45	Novel bi-allelic variants in DNAH2 cause severe asthenoteratozoospermia with multiple morphological abnormalities of the flagella. Reproductive BioMedicine Online, 2021, 42, 963-972.	2.4	19
46	Evaluate the effects of serum urate level on bone mineral density: a genome-wide geneâ€“environment interaction analysis in UK Biobank cohort. Endocrine, 2021, 73, 702-711.	2.3	6
47	Joint Genome-Wide Association Analyses Identified 49 Novel Loci For Age at Natural Menopause. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 2574-2591.	3.6	6
48	Temporal transcriptomic landscape of postnatal mouse ovaries reveals dynamic gene signatures associated with ovarian aging. Human Molecular Genetics, 2021, 30, 1941-1954.	2.9	8
49	Loss of DRC1 function leads to multiple morphological abnormalities of the sperm flagella and male infertility in human and mouse. Human Molecular Genetics, 2021, 30, 1996-2011.	2.9	26
50	Evaluating the associations of adult heel BMD with birth weight and growth parameters at age 10 in UK biobank cohort. Bone, 2021, 152, 116038.	2.9	2
51	Novel Mutations in X-Linked, USP26-Induced Asthenoteratozoospermia and Male Infertility. Cells, 2021, 10, 1594.	4.1	6
52	CFAP65 is required in the acrosome biogenesis and mitochondrial sheath assembly during spermiogenesis. Human Molecular Genetics, 2021, 30, 2240-2254.	2.9	18
53	Bi-allelic truncating variants in CFAP206 cause male infertility in human and mouse. Human Genetics, 2021, 140, 1367-1377.	3.8	23
54	Genome mapping coupled with CRISPR gene editing reveals a P450 gene confers avermectin resistance in the beet armyworm. PLoS Genetics, 2021, 17, e1009680.	3.5	44

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55	Ongoing global and regional adaptive evolution of SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	196
56	Traumatic events during childhood and its risks to substance use in adulthood: an observational and genome-wide by environment interaction study in UK Biobank. Translational Psychiatry, 2021, 11, 431.	4.8	7
57	Bi-allelic mutations of DNAH10 cause primary male infertility with asthenoteratozoospermia in humans and mice. American Journal of Human Genetics, 2021, 108, 1466-1477.	6.2	50
58	Maternal smoking during pregnancy and risks to depression and anxiety in offspring: An observational study and genome-wide gene-environment interaction analysis in UK biobank cohort. Journal of Psychiatric Research, 2021, 140, 149-158.	3.1	11
59	First record of Seira dowlingi (Wray, 1953) (Collembola, Entomobryidae, Seirinae) from China and mitogenome comparison with the New World specimens. Zootaxa, 2021, 5020, 191-196.	0.5	4
60	Genetic association scan of 32 osteoarthritis susceptibility genes identified TP63 associated with an endemic osteoarthritis, Kashin-Beck disease. Bone, 2021, 150, 115997.	2.9	7
61	Vitamin D and the Risks of Depression and Anxiety: An Observational Analysis and Genome-Wide Environment Interaction Study. Nutrients, 2021, 13, 3343.	4.1	11
62	Assessing the effect of interaction between C-reactive protein and gut microbiome on the risks of anxiety and depression. Molecular Brain, 2021, 14, 133.	2.6	16
63	Insomnia affects the levels of plasma bilirubin and protein metabolism: an observational study and GWGEIS in UK Biobank cohort. Sleep Medicine, 2021, 85, 184-190.	1.6	2
64	A recurrent rare intronic variant in CAPN3 alters mRNA splicing and causes autosomal recessive limbâ€girdle muscular dystrophyâ€1 in three Pakistani pedigrees. American Journal of Medical Genetics, Part A, 2021, , .	1.2	0
65	Familial Translocation t(2;4) (q37.3;p16.3), Resulting in a Partial Trisomy of 2q (or 4p) and a Partial Monosomy of 4p (or 2q), Causes Dysplasia. Frontiers in Genetics, 2021, 12, 741607.	2.3	0
66	Gut microbiota is associated with bone mineral density. Bone and Joint Research, 2021, 10, 734-741.	3.6	15
67	Genetic Variants and Protein Alterations of Selenium- and T-2 Toxin-Responsive Genes Are Associated With Chondrocytic Damage in Endemic Osteoarthropathy. Frontiers in Genetics, 2021, 12, 773534.	2.3	2
68	Transcriptome-wide association study identified candidate genes associated with gut microbiota. Gut Pathogens, 2021, 13, 74.	3.4	6
69	Identifying psychiatric disorder-associated gut microbiota using microbiota-related gene set enrichment analysis. Briefings in Bioinformatics, 2020, 21, 1016-1022.	6.5	63
70	Homozygous mutations inSPEF2induce multiple morphological abnormalities of the sperm flagella and male infertility. Journal of Medical Genetics, 2020, 57, 31-37.	3.2	57
71	Biallelic mutations inCFAP65cause male infertility with multiple morphological abnormalities of the sperm flagella in humans and mice. Journal of Medical Genetics, 2020, 57, 89-95.	3.2	55
72	Joint utilization of genetic analysis and semi-cloning technology reveals a digenic etiology of MÃ¼llerian anomalies. Cell Research, 2020, 30, 91-94.	12.0	10

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73	Integrating genome-wide association study and methylation functional annotation data identified candidate genes and pathways for schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2020, 96, 109736.	4.8	7
74	Xq22 deletions and correlation with distinct neurological disease traits in females: Further evidence for a contiguous gene syndrome. Human Mutation, 2020, 41, 150-168.	2.5	15
75	Integrative analysis of genomeâ€wide association study and expression quantitative trait loci datasets identified various immune cellâ€related pathways for rheumatoid arthritis. Annals of Human Genetics, 2020, 84, 72-79.	0.8	8
76	The Nuclear Matrix Protein SAFB Cooperates with Major Satellite RNAs to Stabilize Heterochromatin Architecture Partially through Phase Separation. Molecular Cell, 2020, 77, 368-383.e7.	9.7	104
77	TBX6 missense variants expand the mutational spectrum in a nonâ€Mendelian inheritance disease. Human Mutation, 2020, 41, 182-195.	2.5	27
78	MircroRNA-10b Promotes Human Embryonic Stem Cell-Derived Cardiomyocyte Proliferation via Novel Target Gene LATS1. Molecular Therapy - Nucleic Acids, 2020, 19, 437-445.	5.1	14
79	Evaluating the Correlations Between Osteoporosis and Lifestyle-Related Factors Using Transcriptome-Wide Association Study. Calcified Tissue International, 2020, 106, 256-263.	3.1	10
80	The molecular mechanism study of COMP involved in the articular cartilage damage of Kashin-Beck disease. Bone and Joint Research, 2020, 9, 578-586.	3.6	6
81	Assessing the genetic relationships between osteoarthritis and human plasma proteins: a large scale genetic correlation scan. Annals of Translational Medicine, 2020, 8, 677-677.	1.7	6
82	Integrative Genomic Enrichment Analysis Identified the Brain Regions and Development Stages Related to Anorexia Nervosa and Obsessive-Compulsive Disorder. Cerebral Cortex, 2020, 30, 6481-6489.	2.9	6
83	An integrative analysis of genome-wide association study and regulatory SNP annotation datasets identified candidate genes for bipolar disorder. International Journal of Bipolar Disorders, 2020, 8, 6.	2.2	5
84	CGSEA: A Flexible Tool for Evaluating the Associations of Chemicals with Complex Diseases. G3: Genes, Genomes, Genetics, 2020, 10, 945-949.	1.8	5
85	Genome-Wide Association Analysis Identified ANXA1 Associated with Shoulder Impingement Syndrome in UK Biobank Samples. G3: Genes, Genomes, Genetics, 2020, 10, 3279-3284.	1.8	5
86	Evaluating the effect of birth weight on brain volumes and depression: An observational and genetic study using UK Biobank cohort. European Psychiatry, 2020, 63, e73.	0.2	7
87	Rationally Designed APOBEC3B Cytosine Base Editors with Improved Specificity. Molecular Cell, 2020, 79, 728-740.e6.	9.7	104
88	Rare deleterious BUB1B variants induce premature ovarian insufficiency and early menopause. Human Molecular Genetics, 2020, 29, 2698-2707.	2.9	13
89	Bi-allelic Loss-of-function Variants in CFAP58 Cause Flagellar Axoneme and Mitochondrial Sheath Defects and Asthenoteratozoospermia in Humans and Mice. American Journal of Human Genetics, 2020, 107, 514-526.	6.2	71
90	Molecular structure and evolution mechanism of two populations of double minutes in human colorectal cancer cells. Journal of Cellular and Molecular Medicine, 2020, 24, 14205-14216.	3.6	9

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91	A DNAH17 missense variant causes flagella destabilization and asthenozoospermia. Journal of Experimental Medicine, 2020, 217, .	8.5	88
92	Human Pluripotent Stem Cell-Derived Neural Cells and Brain Organoids Reveal SARS-CoV-2 Neurotropism Predominates in Choroid Plexus Epithelium. Cell Stem Cell, 2020, 27, 937-950.e9.	11.1	314
93	Disruption in ACTL7A causes acrosomal ultrastructural defects in human and mouse sperm as a novel male factor inducing early embryonic arrest. Science Advances, 2020, 6, eaaz4796.	10.3	50
94	Bi-allelic SHOC1 loss-of-function mutations cause meiotic arrest and non-obstructive azoospermia. Journal of Medical Genetics, 2020, 58, jmedgenet-2020-107042.	3.2	20
95	The integrative analysis of DNA methylation and mRNA expression profiles confirmed the role of selenocompound metabolism pathway in Kashin-Beck disease. Cell Cycle, 2020, 19, 2351-2366.	2.6	3
96	The First Draft Genome of the Plasterer Bee Colletes gigas (Hymenoptera: Colletidae: Colletes). Genome Biology and Evolution, 2020, 12, 860-866.	2.5	12
97	Homology of labial chaetae in Entomobryoidea (Collembola). Zootaxa, 2020, 4766, zootaxa.4766.3.8.	0.5	6
98	Comparing GWAS and Brain Structure-Specific Gene Expression Profiles Identifies Psychiatric Disorder-Related Brain Structures at Different Developmental Stages. Neuroscience Bulletin, 2020, 36, 1046-1050.	2.9	1
99	Association between herpes simplex virus 1 exposure and the risk of depression in UK Biobank. Clinical and Translational Medicine, 2020, 10, e108.	4.0	13
100	Integration of transcriptome-wide association study and messenger RNA expression profile to identify genes associated with osteoarthritis. Bone and Joint Research, 2020, 9, 130-138.	3.6	18
101	Identifying insomnia-related chemicals through integrative analysis of genome-wide association studies and chemicalâ€“genes interaction information. Sleep, 2020, 43, .	1.1	1
102	Bi-allelic DNAH8 Variants Lead to Multiple Morphological Abnormalities of the Sperm Flagella and Primary Male Infertility. American Journal of Human Genetics, 2020, 107, 330-341.	6.2	111
103	A transâ€ethnic twoâ€stage polygenetic scoring analysis detects genetic correlation between osteoporosis and schizophrenia. Clinical and Translational Medicine, 2020, 9, 21.	4.0	2
104	DVL mutations identified from human neural tube defects and Dandy-Walker malformation obstruct the Wnt signaling pathway. Journal of Genetics and Genomics, 2020, 47, 301-310.	3.9	6
105	Streamlining universal singleâ€copy orthologue and ultraconserved element design: A case study in Collembola. Molecular Ecology Resources, 2020, 20, 706-717.	4.8	10
106	Evaluating the Genetic Correlations Between Left-Handedness and Mental Disorder Using Linkage Disequilibrium Score Regression and Transcriptome-Wide Association Study. Biochemical Genetics, 2020, 58, 348-358.	1.7	3
107	An atlas of genetic correlations between psychiatric disorders and human blood plasma proteome. European Psychiatry, 2020, 63, e17.	0.2	10
108	A genome-wide multiphenotypic association analysis identified common candidate genes for subjective well-being, depressive symptoms and neuroticism. Journal of Psychiatric Research, 2020, 124, 22-28.	3.1	5

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109	Assessing the Relationship Between Gut Microbiota and Bone Mineral Density. Frontiers in Genetics, 2020, 11, 6.	2.3	33
110	A Large-Scale Genetic Correlation Scan Between Intelligence and Brain Imaging Phenotypes. Cerebral Cortex, 2020, 30, 4197-4203.	2.9	5
111	Patients with severe asthenoteratospermia carrying SPAG6 or RSPH3 mutations have a positive pregnancy outcome following intracytoplasmic sperm injection. Journal of Assisted Reproduction and Genetics, 2020, 37, 829-840.	2.5	30
112	A large-scale genetic correlation scan identified the plasma proteins associated with brain function related traits. Brain Research Bulletin, 2020, 158, 84-89.	3.0	2
113	Phylogeny of Neotropical Seirinae (Collembola, Entomobryidae) based on mitochondrial genomes. Zoologica Scripta, 2020, 49, 329-339.	1.7	11
114	A novel homozygous mutation in WDR19 induces disorganization of microtubules in sperm flagella and nonsyndromic asthenoteratospermia. Journal of Assisted Reproduction and Genetics, 2020, 37, 1431-1439.	2.5	35
115	Rare mutations in the autophagyâ€regulating gene AMBRA1 contribute to human neural tube defects. Human Mutation, 2020, 41, 1383-1393.	2.5	15
116	Identifying 5 Common Psychiatric Disorders Associated Chemicals Through Integrative Analysis of Genome-Wide Association Study and Chemical-Gene Interaction Datasets. Schizophrenia Bulletin, 2020, 46, 1182-1190.	4.3	7
117	A novel hemizygous loss-of-function mutation in ADGRG2 causes male infertility with congenital bilateral absence of the vas deferens. Journal of Assisted Reproduction and Genetics, 2020, 37, 1421-1429.	2.5	11
118	Different Gene Networks Are Disturbed by Zika Virus Infection in A Mouse Microcephaly Model. Genomics, Proteomics and Bioinformatics, 2020, 18, 737-748.	6.9	12
119	Human and mouse studies establish TBX6 in Mendelian CAKUT and as a potential driver of kidney defects associated with the 16p11.2 microdeletion syndrome. Kidney International, 2020, 98, 1020-1030.	5.2	17
120	A genome-wide multiphenotypic association analysis identified candidate genes and gene ontology shared by four common risky behaviors. Aging, 2020, 12, 3287-3297.	3.1	3
121	Proteomic profiling analysis of postmenopausal osteoporosis and osteopenia identifies potential proteins associated with low bone mineral density. PeerJ, 2020, 8, e9009.	2.0	12
122	A fertile male with a single sY86 deletion on the Y chromosome. Asian Journal of Andrology, 2020, 22, 333.	1.6	2
123	Novel compound heterozygous variants in dynein axonemal heavy chain 17 cause asthenoteratospermia with sperm flagellar defects. Journal of Genetics and Genomics, 2020, 47, 713-717.	3.9	6
124	eQTLs Weighted Genetic Correlation Analysis Detected Brain Region Differences in Genetic Correlations for Complex Psychiatric Disorders. Schizophrenia Bulletin, 2019, 45, 709-715.	4.3	6
125	The discovery of Neotropical Lepidosira (Collembola, Entomobryidae) and its systematic position. Zoologica Scripta, 2019, 48, 783-800.	1.7	6
126	Sequence characterization of RET in 117 Chinese Hirschsprung disease families identifies a large burden of de novo and parental mosaic mutations. Orphanet Journal of Rare Diseases, 2019, 14, 237.	2.7	10

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127	Bi-allelic Mutations in TTC29 Cause Male Subfertility with Asthenoteratospermia in Humans and Mice. American Journal of Human Genetics, 2019, 105, 1168-1181.	6.2	62
128	An integrative analysis of transcriptome-wide association study and mRNA expression profile identified candidate genes for attention-deficit/hyperactivity disorder. Psychiatry Research, 2019, 282, 112639.	3.3	16
129	Integrating transcriptome-wide study and mRNA expression profiles yields novel insights into the biological mechanism of chondropathies. Arthritis Research and Therapy, 2019, 21, 194.	3.5	7
130	Rare variants in FANCA induce premature ovarian insufficiency. Human Genetics, 2019, 138, 1227-1236.	3.8	56
131	Screening for Differentially Expressed Circular RNAs in the Cartilage of Osteoarthritis Patients for Their Diagnostic Value. Genetic Testing and Molecular Biomarkers, 2019, 23, 706-716.	0.7	30
132	A High-quality Draft Genome Assembly ofSinella curviseta: A Soil Model Organism (Collembola). Genome Biology and Evolution, 2019, 11, 521-530.	2.5	13
133	Loss-of-function mutations in QRICH2 cause male infertility with multiple morphological abnormalities of the sperm flagella. Nature Communications, 2019, 10, 433.	12.8	108
134	Bi-allelic Mutations in ARMC2 Lead to Severe Astheno-Teratozoospermia Due to Sperm Flagellum Malformations in Humans and Mice. American Journal of Human Genetics, 2019, 104, 331-340.	6.2	113
135	Selenium and Other Elements in Wheat (Triticum aestivum) and Wheat Bread from a Seleniferous Area. Biological Trace Element Research, 2019, 192, 10-17.	3.5	4
136	Integrative Analysis of Genome-Wide Association Studies and DNA Methylation Profile Identified Genetic Control Genes of DNA Methylation for Kashin-Beck Disease. Cartilage, 2019, , 194760351985874.	2.7	4
137	Genome-wide DNA methylation profiling of hip articular cartilage identifies differentially methylated loci associated with osteonecrosis of the femoral head. Bone, 2019, 127, 296-304.	2.9	10
138	Integrative analysis of transcriptome-wide association study data and mRNA expression profiles identified candidate genes and pathways associated with atrial fibrillation. Heart and Vessels, 2019, 34, 1882-1888.	1.2	6
139	Integrative analysis of transcriptomeâ€wide association study data and messenger RNA expression profiles identified candidate genes and pathways for inflammatory bowel disease. Journal of Cellular Biochemistry, 2019, 120, 14831-14837.	2.6	10
140	A de novo mutation in DHD domain of SKI causing spina bifida with no craniofacial malformation or intellectual disability. American Journal of Medical Genetics, Part A, 2019, 179, 936-939.	1.2	3
141	Cytosine, but not adenine, base editors induce genome-wide off-target mutations in rice. Science, 2019, 364, 292-295.	12.6	491
142	BRCA2 in Ovarian Development and Function. New England Journal of Medicine, 2019, 380, 1086-1087.	27.0	38
143	Bi-allelic Mutations in TTC21A Induce Asthenoteratospermia in Humans and Mice. American Journal of Human Genetics, 2019, 104, 738-748.	6.2	103
144	Homozygous loss-of-function mutations in FSIP2 cause male infertility with asthenoteratospermia. Journal of Genetics and Genomics, 2019, 46, 53-56.	3.9	31

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145	PCA-based GRS analysis enhances the effectiveness for genetic correlation detection. Briefings in Bioinformatics, 2019, 20, 2291-2298.	6.5	6
146	Genomeâ€wide association study and identification of chromosomal enhancer maps in multiple brain regions related to autism spectrum disorder. Autism Research, 2019, 12, 26-32.	3.8	15
147	NovelCFAP43 andCFAP44 mutations cause male infertility with multiple morphological abnormalities of the sperm flagella (MMAF). Reproductive BioMedicine Online, 2019, 38, 769-778.	2.4	26
148	Integrative analysis of transcriptomeâ€wide association study and mRNA expression profiles identifies candidate genes associated with autism spectrum disorders. Autism Research, 2019, 12, 33-38.	3.8	10
149	Noncoding rare variants of TBX6 in congenital anomalies of the kidney and urinary tract. Molecular Genetics and Genomics, 2019, 294, 493-500.	2.1	8
150	Whole-exome sequencing reveals SALL4 variants in premature ovarian insufficiency: an update on genotypeâ€“phenotype correlations. Human Genetics, 2019, 138, 83-92.	3.8	27
151	A novel multiplex fluorescent competitive PCR for copy number variation detection. Genomics, 2019, 111, 1745-1751.	2.9	1
152	The copy number variation landscape of congenital anomalies of the kidney and urinary tract. Nature Genetics, 2019, 51, 117-127.	21.4	144
153	Novel homozygousCFAP69mutations in humans and mice cause severe asthenoteratospermia with multiple morphological abnormalities of the sperm flagella. Journal of Medical Genetics, 2019, 56, 96-103.	3.2	70
154	Identification of schizophrenia related biological pathways across eight brain regions. Behavioural Brain Research, 2019, 360, 1-6.	2.2	4
155	Phylogenomics from lowâ€coverage wholeâ€genome sequencing. Methods in Ecology and Evolution, 2019, 10, 507-517.	5.2	59
156	TBX6-associated congenital scoliosis (TACS) as a clinically distinguishable subtype of congenital scoliosis: further evidence supporting the compound inheritance and TBX6 gene dosage model. Genetics in Medicine, 2019, 21, 1548-1558.	2.4	60
157	TBX6 compound inheritance leads to congenital vertebral malformations in humans and mice. Human Molecular Genetics, 2019, 28, 539-547.	2.9	46
158	Assessing the Genetic Correlations Between Blood Plasma Proteins and Osteoporosis: A Polygenic Risk Score Analysis. Calcified Tissue International, 2019, 104, 171-181.	3.1	11
159	Integrative analysis of genome-wide association study and chromosomal enhancer maps identified brain region related pathways associated with ADHD. Comprehensive Psychiatry, 2019, 88, 65-69.	3.1	1
160	Biallelic mutations of CFAP251 cause sperm flagellar defects and human male infertility. Journal of Human Genetics, 2019, 64, 49-54.	2.3	56
161	Molecular phylogeny of Entomobrya (Collembola: Entomobryidae) from China: Color pattern groups and multiple origins. Insect Science, 2019, 26, 587-597.	3.0	15
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