Huan Zhang

List of Publications by Year
in descending order

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39 papers	841 citations	567281 15 h-index	526287 27 g-index
41 all docs	41 docs citations	41 times ranked	1212 citing authors

#	Article	IF	Citations
1	A DNAH17 missense variant causes flagella destabilization and asthenozoospermia. Journal of Experimental Medicine, 2020, 217, .	8.5	88
2	A homozygous FANCM frameshift pathogenic variant causes male infertility. Genetics in Medicine, 2019, 21, 62-70.	2.4	69
3	microRNA 376a regulates follicle assembly by targeting Pcna in fetal and neonatal mouse ovaries. Reproduction, 2014, 148, 43-54.	2.6	55
4	IsomiR Bank: a research resource for tracking IsomiRs. Bioinformatics, 2016, 32, 2069-2071.	4.1	52
5	Specific Deletion of Cdh2 in Sertoli Cells Leads to Altered Meiotic Progression and Subfertility of Mice1. Biology of Reproduction, 2015, 92, 79.	2.7	50
6	Homozygous mutations in C14orf39/SIX6OS1 cause non-obstructive azoospermia and premature ovarian insufficiency in humans. American Journal of Human Genetics, 2021, 108, 324-336.	6.2	50
7	Protective effects of melatonin on sepsis-induced liver injury and dysregulation of gluconeogenesis in rats through activating SIRT1/STAT3 pathway. Biomedicine and Pharmacotherapy, 2019, 117, 109150.	5.6	48
8	DeAnnIso: a tool for online detection and annotation of isomiRs from small RNA sequencing data. Nucleic Acids Research, 2016, 44, W166-W175.	14.5	41
9	Retrospective analysis of clinical features in 134 coronavirus disease 2019 cases. Epidemiology and Infection, 2020, 148, e199.	2.1	37
10	Cardiac injuries in patients with coronavirus disease 2019: Not to be ignored. International Journal of Infectious Diseases, 2020, 96, 294-297.	3.3	37
11	CPSS 2.0: a computational platform update for the analysis of small RNA sequencing data. Bioinformatics, 2017, 33, 3289-3291.	4.1	32
12	DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data. Nucleic Acids Research, 2015, 43, W289-W294.	14.5	29
13	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
14	A TOP6BL mutation abolishes meiotic DNA double-strand break formation and causes human infertility. Science Bulletin, 2020, 65, 2120-2129.	9.0	18
15	A recurrent ZSWIM7 mutation causes male infertility resulting from decreased meiotic recombination. Human Reproduction, 2021, 36, 1436-1445.	0.9	18
16	Whole-exome sequencing of consanguineous families with infertile men and women identifies homologous mutations in SPATA22 and MEIOB. Human Reproduction, 2021, 36, 2793-2804.	0.9	17
17	IsopiRBank: a research resource for tracking piRNA isoforms. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	15
18	CARF promotes spermatogonial self-renewal and proliferation through Wnt signaling pathway. Cell Discovery, 2020, 6, 85.	6.7	13

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19	Novel frameshift mutation in STK33 is associated with asthenozoospermia and multiple morphological abnormalities of the flagella. Human Molecular Genetics, 2021, 30, 1977-1984.	2.9	13
20	Biallelic Variants in CFAP61 Cause Multiple Morphological Abnormalities of the Flagella and Male Infertility. Frontiers in Cell and Developmental Biology, 2021, 9, 803818.	3.7	13
21	RAD51AP2 is required for efficient meiotic recombination between X and Y chromosomes. Science Advances, 2022, 8, eabk1789.	10.3	13
22	ZFP541 maintains the repression of pre-pachytene transcriptional programs and promotes male meiosis progression. Cell Reports, 2022, 38, 110540.	6.4	11
23	Effects of androgen receptor mutation on testicular histopathology of patient having complete androgen insensitivity. Journal of Molecular Histology, 2017, 48, 159-167.	2.2	10
24	Anaconda: AN automated pipeline for somatic COpy Number variation Detection and Annotation from tumor exome sequencing data. BMC Bioinformatics, 2017, 18, 436.	2.6	9
25	A recurrent homozygous missense mutation in CCDC103 causes asthenoteratozoospermia due to disorganized dynein arms. Asian Journal of Andrology, 2022, 24, 255.	1.6	8
26	BiallelicHFM1variants cause non-obstructive azoospermia with meiotic arrest in humans by impairing crossover formation to varying degrees. Human Reproduction, 2022, 37, 1664-1677.	0.9	8
27	Whole exome sequencing identifies a novel dominant missense mutation underlying leukonychia in a Pakistani family. Journal of Human Genetics, 2018, 63, 1071-1076.	2.3	7
28	PedMiner: a tool for linkage analysis-based identification of disease-associated variants using family based whole-exome sequencing data. Briefings in Bioinformatics, 2021, 22, .	6.5	7
29	Novel Loss-of-Function Mutations in DNAH1 Displayed Different Phenotypic Spectrum in Humans and Mice. Frontiers in Endocrinology, 2021, 12, 765639.	3.5	7
30	MeiosisOnline: A Manually Curated Database for Tracking and Predicting Genes Associated With Meiosis. Frontiers in Cell and Developmental Biology, 2021, 9, 673073.	3.7	6
31	Novel biallelic loss-of-function mutations in CFAP43 cause multiple morphological abnormalities of the sperm flagellum in Pakistani families. Asian Journal of Andrology, 2021, 23, 627.	1.6	6
32	A novel stop-gain mutation in ARMC2 is associated with multiple morphological abnormalities of the sperm flagella. Reproductive BioMedicine Online, 2021, 43, 913-919.	2.4	5
33	Identification of pathogenic mutations from nonobstructive azoospermia patients. Biology of Reproduction, 2022, 107, 85-94.	2.7	5
34	Whole Exome Sequencing Revealed a Novel Nonsense Variant in the <i>GNRHR</i> Gene<i></i> Causing Normosmic Hypogonadotropic Hypogonadism in a Pakistani Family. Hormone Research in Paediatrics, 2019, 91, 9-16.	1.8	4
35	FertilityOnline: A Straightforward Pipeline for Functional Gene Annotation and Disease Mutation Discovery. Genomics, Proteomics and Bioinformatics, 2022, 20, 455-465.	6.9	3
36	Meiotic defects and decreased expression of genes located around the chromosomal breakpoint in the testis of a patient with a novel 46,X,t(Y;1)(p11.3;p31) translocation. International Journal of Molecular Medicine, 2017, 40, 367-377.	4.0	2

#	Article	IF	Citations
37	A Novel APTX Variant and Ataxia with Oculomotor Apraxia Type 1. Journal of Clinical Neurology		