

Huan Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5277397/publications.pdf>

Version: 2024-02-01

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	RAD51AP2 is required for efficient meiotic recombination between X and Y chromosomes. <i>Science Advances</i> , 2022, 8, eabk1789.	10.3	13
2	CFTR mutations causing congenital unilateral absence of the vas deferens (CUAVD) and congenital absence of the uterus (CAU) in a consanguineous family. <i>Asian Journal of Andrology</i> , 2022, .	1.6	0
3	A recurrent homozygous missense mutation in CCDC103 causes asthenoteratozoospermia due to disorganized dynein arms. <i>Asian Journal of Andrology</i> , 2022, 24, 255.	1.6	8
4	Computationally predicted pathogenic <i>USP9X</i> mutation identified in infertile men does not affect spermatogenesis in mice. <i>Zoological Research</i> , 2022, 43, 225-228.	2.1	0
5	ZFP541 maintains the repression of pre-pachytene transcriptional programs and promotes male meiosis progression. <i>Cell Reports</i> , 2022, 38, 110540.	6.4	11
6	FertilityOnline: A Straightforward Pipeline for Functional Gene Annotation and Disease Mutation Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 455-465.	6.9	3
7	Biallelic <i>HFM1</i> variants cause non-obstructive azoospermia with meiotic arrest in humans by impairing crossover formation to varying degrees. <i>Human Reproduction</i> , 2022, 37, 1664-1677.	0.9	8
8	Identification of pathogenic mutations from nonobstructive azoospermia patients. <i>Biology of Reproduction</i> , 2022, 107, 85-94.	2.7	5
9	PedMiner: a tool for linkage analysis-based identification of disease-associated variants using family based whole-exome sequencing data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	7
10	Novel loss-of-function variants in <i>DNAH17</i> cause multiple morphological abnormalities of the sperm flagella in humans and mice. <i>Clinical Genetics</i> , 2021, 99, 176-186.	2.0	26
11	Homozygous mutations in <i>C14orf39/SIX6OS1</i> cause non-obstructive azoospermia and premature ovarian insufficiency in humans. <i>American Journal of Human Genetics</i> , 2021, 108, 324-336.	6.2	50
12	A recurrent <i>ZSWIM7</i> mutation causes male infertility resulting from decreased meiotic recombination. <i>Human Reproduction</i> , 2021, 36, 1436-1445.	0.9	18
13	Novel frameshift mutation in <i>STK33</i> is associated with asthenozoospermia and multiple morphological abnormalities of the flagella. <i>Human Molecular Genetics</i> , 2021, 30, 1977-1984.	2.9	13
14	MeiosisOnline: A Manually Curated Database for Tracking and Predicting Genes Associated With Meiosis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 673073.	3.7	6
15	A novel stop-gain mutation in <i>ARMC2</i> is associated with multiple morphological abnormalities of the sperm flagella. <i>Reproductive BioMedicine Online</i> , 2021, 43, 913-919.	2.4	5
16	Whole-exome sequencing of consanguineous families with infertile men and women identifies homologous mutations in <i>SPATA22</i> and <i>MEIOB</i>. <i>Human Reproduction</i> , 2021, 36, 2793-2804.	0.9	17
17	Novel biallelic loss-of-function mutations in <i>CFAP43</i> cause multiple morphological abnormalities of the sperm flagellum in Pakistani families. <i>Asian Journal of Andrology</i> , 2021, 23, 627.	1.6	6
18	Novel Loss-of-Function Mutations in <i>DNAH1</i> Displayed Different Phenotypic Spectrum in Humans and Mice. <i>Frontiers in Endocrinology</i> , 2021, 12, 765639.	3.5	7

#	ARTICLE	IF	CITATIONS
19	Biallelic Variants in CFAP61 Cause Multiple Morphological Abnormalities of the Flagella and Male Infertility. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 803818.	3.7	13
20	A TOP6BL mutation abolishes meiotic DNA double-strand break formation and causes human infertility. <i>Science Bulletin</i> , 2020, 65, 2120-2129.	9.0	18
21	A <i>DNAH17</i> missense variant causes flagella destabilization and asthenozoospermia. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	88
22	Retrospective analysis of clinical features in 134 coronavirus disease 2019 cases. <i>Epidemiology and Infection</i> , 2020, 148, e199.	2.1	37
23	CARF promotes spermatogonial self-renewal and proliferation through Wnt signaling pathway. <i>Cell Discovery</i> , 2020, 6, 85.	6.7	13
24	Cardiac injuries in patients with coronavirus disease 2019: Not to be ignored. <i>International Journal of Infectious Diseases</i> , 2020, 96, 294-297.	3.3	37
25	A homozygous FANCM frameshift pathogenic variant causes male infertility. <i>Genetics in Medicine</i> , 2019, 21, 62-70.	2.4	69
26	Protective effects of melatonin on sepsis-induced liver injury and dysregulation of gluconeogenesis in rats through activating SIRT1/STAT3 pathway. <i>Biomedicine and Pharmacotherapy</i> , 2019, 117, 109150.	5.6	48
27	Whole Exome Sequencing Revealed a Novel Nonsense Variant in the <i>GNRHR</i> Gene Causing Normosmic Hypogonadotropic Hypogonadism in a Pakistani Family. <i>Hormone Research in Paediatrics</i> , 2019, 91, 9-16.	1.8	4
28	IsopiRBank: a research resource for tracking piRNA isoforms. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	15
29	Whole exome sequencing identifies a novel dominant missense mutation underlying leukonychia in a Pakistani family. <i>Journal of Human Genetics</i> , 2018, 63, 1071-1076.	2.3	7
30	CPSS 2.0: a computational platform update for the analysis of small RNA sequencing data. <i>Bioinformatics</i> , 2017, 33, 3289-3291.	4.1	32
31	Effects of androgen receptor mutation on testicular histopathology of patient having complete androgen insensitivity. <i>Journal of Molecular Histology</i> , 2017, 48, 159-167.	2.2	10
32	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. <i>International Journal of Molecular Medicine</i> , 2017, 40, 367-377.	4.0	2
33	A Novel APTX Variant and Ataxia with Oculomotor Apraxia Type 1. <i>Journal of Clinical Neurology</i>		

#	ARTICLE	IF	CITATIONS
37	Specific Deletion of Cdh2 in Sertoli Cells Leads to Altered Meiotic Progression and Subfertility of Mice1. <i>Biology of Reproduction</i> , 2015, 92, 79.	2.7	50
38	DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, W289-W294.	14.5	29
39	microRNA 376a regulates follicle assembly by targeting PcnA in fetal and neonatal mouse ovaries. <i>Reproduction</i> , 2014, 148, 43-54.	2.6	55