Lu Xia

List of Publications by Year
in descending order

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28 papers	951 citations	759233 12 h-index	501196 28 g-index
29 all docs	29 docs citations	29 times ranked	2309 citing authors

#	Article	IF	Citations
1	Performance Comparison of Computational Methods for the Prediction of the Function and Pathogenicity of Non-Coding Variants. Genomics, Proteomics and Bioinformatics, 2023, 21, 649-661.	6.9	7
2	Study on the expression and function of chordinâ€like 1 in oral squamous cell carcinoma. Oral Diseases, 2023, 29, 2034-2051.	3.0	2
3	Cross-Disorder Analysis of De Novo Mutations in Neuropsychiatric Disorders. Journal of Autism and Developmental Disorders, 2022, 52, 1299-1313.	2.7	3
4	Genetic landscape of human mitochondrial genome using whole-genome sequencing. Human Molecular Genetics, 2022, 31, 1747-1761.	2.9	4
5	Biallelic loss-of-function variants in NEMF cause central nervous system impairment and axonal polyneuropathy. Human Genetics, 2021, 140, 579-592.	3.8	14
6	GPCards: An integrated database of genotypeâ€“phenotype correlations in human genetic diseases. Computational and Structural Biotechnology Journal, 2021, 19, 1603-1611.	4.1	5
7	De novo mutations in folate-related genes associated with common developmental disorders. Computational and Structural Biotechnology Journal, 2021, 19, 1414-1422.	4.1	6
8	Genome sequence, transcriptome, and annotation of rodent malaria parasite Plasmodium yoelii nigeriensis N67. BMC Genomics, 2021, 22, 303.	2.8	7
9	SLC39A5 dysfunction impairs extracellular matrix synthesis in high myopia pathogenesis. Journal of Cellular and Molecular Medicine, 2021, 25, 8432-8441.	3.6	9
10	Rare NRXN1 missense variants identified in autism interfered protein degradation and Drosophila sleeping. Journal of Psychiatric Research, 2021, 143, 113-122.	3.1	1
11	Gene4Denovo: an integrated database and analytic platform for de novo mutations in humans. Nucleic Acids Research, 2020, 48, D913-D926.	14.5	41
12	Genomeâ€wide association analysis of autism identified multiple loci that have been reported as strong signals for neuropsychiatric disorders. Autism Research, 2020, 13, 382-396.	3.8	16
13	Functional relationships between recessive inherited genes and genes with de novo variants in autism spectrum disorder. Molecular Autism, 2020, 11, 75.	4.9	5
14	Type I Interferons and Malaria: A Double-Edge Sword Against a Complex Parasitic Disease. Frontiers in Cellular and Infection Microbiology, 2020, 10, 594621.	3.9	29
15	RTP4 inhibits IFN-I response and enhances experimental cerebral malaria and neuropathology. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19465-19474.	7.1	31
16	The E3 ubiquitin ligase MARCH1 regulates antimalaria immunity through interferon signaling and T cell activation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16567-16578.	7.1	26
17	Targeted exome sequencing identifies five novel loci at genome-wide significance for modulating antidepressant response in patients with major depressive disorder. Translational Psychiatry, 2020, 10, 30.	4.8	14
18	Plasmodium Genomics and Genetics: New Insights into Malaria Pathogenesis, Drug Resistance, Epidemiology, and Evolution. Clinical Microbiology Reviews, 2019, 32, .	13.6	65

#	Article	IF	Citations
19	Common genetic variants shared among five major psychiatric disorders: a large-scale genome-wide combined analysis. Global Clinical and Translational Research, 2019, , 21-30.	0.3	10
20	Identification of a VHL gene mutation in a Chinese family with Von Hippelâ€'Lindau syndrome. Molecular Medicine Reports, 2018, 18, 435-440.	2.4	2
21	Inherited and multiple de novo mutations in autism/developmental delay risk genes suggest a multifactorial model. Molecular Autism, 2018, 9, 64.	4.9	114
22	Detection of host pathways universally inhibited after Plasmodium yoelii infection for immune intervention. Scientific Reports, 2018, 8, 15280.	3.3	15
23	Genome-wide copy number variation analysis in a Chinese autism spectrum disorder cohort. Scientific Reports, 2017, 7, 44155.	3.3	50
24	Exome sequencing identifies POU4F3 as the causative gene for a large Chinese family with non-syndromic hearing loss. Journal of Human Genetics, 2017, 62, 317-320.	2.3	25
25	De novo genic mutations among a Chinese autism spectrum disorder cohort. Nature Communications, 2016, 7, 13316.	12.8	293
26	Mutations of P4HA2 encoding prolyl 4-hydroxylase 2 are associated with nonsyndromic high myopia. Genetics in Medicine, 2015, 17, 300-306.	2.4	63
27	SLC39A5mutations interfering with the BMP/TGF-Î² pathway in non-syndromic high myopia. Journal of Medical Genetics, 2014, 51, 518-525.	3.2	83
28	New ZNF644 mutations identified in patients with high myopia. Molecular Vision, 2014, 20, 939-46.	1.1	10