

Qiuju Wang

List of Publications by Year in descending order

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Version: 2024-02-01

11
papers

256
citations

1163117

8
h-index

1281871

11
g-index

11
all docs

11
docs citations

11
times ranked

499
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of a gene corrected human isogenic iPSC line (CPGHi001-A-1) from a hearing loss patient with the TMC1 p.M418K mutation using CRISPR/Cas9. <i>Stem Cell Research</i> , 2022, 60, 102736.	0.7	4
2	Clinical characteristics of patients with unilateral auditory neuropathy. <i>American Journal of Otolaryngology - Head and Neck Medicine and Surgery</i> , 2021, 42, 103143.	1.3	4
3	High Frequency of <i>AIFM1</i> Variants and Phenotype Progression of Auditory Neuropathy in a Chinese Population. <i>Neural Plasticity</i> , 2020, 2020, 1-12.	2.2	10
4	Generation of a human induced pluripotent stem cell line (CPGHi001-A) from a hearing loss patient with the TMC1 p.M418K mutation. <i>Stem Cell Research</i> , 2020, 49, 101982.	0.7	7
5	Recurrent de novo <i>WFS1</i> pathogenic variants in Chinese sporadic patients with nonsyndromic sensorineural hearing loss. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1367.	1.2	9
6	Phenotype prediction of Mohr-Tranebjaerg syndrome (MTS) by genetic analysis and initial auditory neuropathy. <i>BMC Medical Genetics</i> , 2019, 20, 11.	2.1	12
7	Identification of four <i>TMC1</i> variations in different Chinese families with hereditary hearing loss. <i>Molecular Genetics & Genomic Medicine</i> , 2018, 6, 504-513.	1.2	17
8	Novel recessive <i>PDZD7</i> biallelic mutations in two Chinese families with nonsyndromic hearing loss. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 99-106.	1.2	15
9	Mutations in apoptosis-inducing factor cause X-linked recessive auditory neuropathy spectrum disorder. <i>Journal of Medical Genetics</i> , 2015, 52, 523-531.	3.2	92
10	A Novel DFNA36 Mutation in TMC1 Orthologous to the Beethoven (Bth) Mouse Associated with Autosomal Dominant Hearing Loss in a Chinese Family. <i>PLoS ONE</i> , 2014, 9, e97064.	2.5	61
11	Targeted High-Throughput Sequencing Identifies Pathogenic Mutations in KCNQ4 in Two Large Chinese Families with Autosomal Dominant Hearing Loss. <i>PLoS ONE</i> , 2014, 9, e103133.	2.5	25