Shujin Li

List of Publications by Year in descending order

24 papers	352 citations	759233 12 h-index	839539 18 g-index
25 all docs	25 docs citations	25 times ranked	326 citing authors

#	Article	IF	Citations
1	Catenin Î± 1 mutations cause familial exudative vitreoretinopathy by overactivating Norrin/Î²-catenin signaling. Journal of Clinical Investigation, 2021, 131, .	8.2	37
2	Exome sequencing revealed Notch ligand JAG1 as a novel candidate gene for familial exudative vitreoretinopathy. Genetics in Medicine, 2020, 22, 77-84.	2.4	34
3	A splicing mutation in aryl hydrocarbon receptor associated with retinitis pigmentosa. Human Molecular Genetics, 2018, 27, 2563-2572.	2.9	29
4	Whole-exome Sequencing Analysis Identifies Mutations in the EYS Gene in Retinitis Pigmentosa in the Indian Population. Scientific Reports, 2016, 6, 19432.	3.3	27
5	Association of SNPs in miR-146a, miR-196a2, and miR-499 with the risk of endometrial/ovarian cancer. Acta Biochimica Et Biophysica Sinica, 2015, 47, 564-566.	2.0	23
6	Disruption of Tmem30a results in cerebellar ataxia and degeneration of Purkinje cells. Cell Death and Disease, 2018, 9, 899.	6.3	23
7	Loss of Tmem30a leads to photoreceptor degeneration. Scientific Reports, 2017, 7, 9296.	3.3	22
8	Variants in the Wnt co-receptor LRP6 are associated with familial exudative vitreoretinopathy. Journal of Genetics and Genomics, 2022, 49, 590-594.	3.9	18
9	Whole Exome Sequencing Analysis Identifies Mutations in LRP5 in Indian Families with Familial Exudative Vitreoretinopathy. Genetic Testing and Molecular Biomarkers, 2016, 20, 346-351.	0.7	17
10	Whole-Exome Sequencing Identified DLG1 as a Candidate Gene for Familial Exudative Vitreoretinopathy. Genetic Testing and Molecular Biomarkers, 2021, 25, 309-316.	0.7	17
11	CTNND1 variants cause familial exudative vitreoretinopathy through the Wnt/cadherin axis. JCI Insight, 2022, 7, .	5.0	17
12	The ER membrane protein complex subunit Emc3 controls angiogenesis via the FZD4/WNT signaling axis. Science China Life Sciences, 2021, 64, 1868-1883.	4.9	16
13	Tmem30a Deficiency in endothelial cells impairs cell proliferation and angiogenesis. Journal of Cell Science, 2019, 132, .	2.0	12
14	Novel truncating variants inCTNNB1cause familial exudative vitreoretinopathy. Journal of Medical Genetics, 2023, 60, 174-182.	3.2	10
15	Targeted Next-Generation Sequencing Reveals Novel RP1 Mutations in Autosomal Recessive Retinitis Pigmentosa. Genetic Testing and Molecular Biomarkers, 2018, 22, 109-114.	0.7	9
16	Candidate Gene Analysis Identifies Mutations inCYP1B1andLTBP2in Indian Families with Primary Congenital Glaucoma. Genetic Testing and Molecular Biomarkers, 2017, 21, 252-258.	0.7	8
17	Targeted next-generation sequencing reveals that a compound heterozygous mutation in phosphodiesterase 6a gene leads to retinitis pigmentosa in a Chinese family. Ophthalmic Genetics, 2018, 39, 487-491.	1.2	5
18	Targeted Next-Generation Sequencing Reveals a Novel Frameshift Mutation in the MERTK Gene in a Chinese Family with Retinitis Pigmentosa. Genetic Testing and Molecular Biomarkers, 2018, 22, 165-169.	0.7	5

#	Article	IF	Citations
19	Whole-Exome Sequencing Reveals Novel NDP Variants in X-Linked Familial Exudative Vitreoretinopathy. European Journal of Ophthalmology, 2022, 32, 3220-3226.	1.3	5
20	Heterozygote lossâ€ofâ€function variants in the LRP5 gene cause familial exudative vitreoretinopathy. Clinical and Experimental Ophthalmology, 2022, 50, 441-448.	2.6	5
21	LMBR1L regulates the proliferation and migration of endothelial cells through Norrin/Î²-catenin signaling. Journal of Cell Science, 2022, 135, .	2.0	5
22	Whole-Exome Sequencing Reveals Novel TSPAN12 Variants in Autosomal Dominant Familial Exudative Vitreoretinopathy. Genetic Testing and Molecular Biomarkers, 2021, 25, 399-404.	0.7	4
23	A novel frameshift variant in the TSPAN12 gene causes autosomal dominant <scp>FEVR</scp>. Molecular Genetics & Genomic Medicine, 2022, 10, e1949.	1.2	2
24	Identification of Two Novel Variants in the LRP5 Gene that Cause Familial Exudative Vitreoretinopathy. Genetic Testing and Molecular Biomarkers, 2022, 26, 146-151.	0.7	1