Wenmin Sun

List of Publications by Year
in descending order

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50 papers	835 citations	623574 14 h-index	580701 25 g-index
51 all docs	51 docs citations	51 times ranked	1129 citing authors

#	Article	IF	Citations
1	Detection of Mutations in LRPAP1, CTSH, LEPREL1, ZNF644, SLC39A5, and SCO2 in 298 Families With Early-Onset High Myopia by Exome Sequencing. Investigative Ophthalmology and Visual Science, 2015, 56, 339-345.	3.3	96
2	Evaluation of 12 Myopia-Associated Genes in Chinese Patients With High Myopia. Investigative Ophthalmology and Visual Science, 2015, 56, 722-729.	3.3	60
3	Molecular genetics of cone-rod dystrophy in Chinese patients: New data from 61 probands and mutation overview of 163 probands. Experimental Eye Research, 2016, 146, 252-258.	1.2	60
4	Exome Sequencing of 18 Chinese Families with Congenital Cataracts: A New Sight of the NHS Gene. PLoS ONE, 2014, 9, e100455.	1.1	47
5	Molecular Genetic Analysis of Pakistani Families With Autosomal Recessive Congenital Cataracts by Homozygosity Screening. , 2017, 58, 2207.		45
6	Mutation analysis of 12 genes in Chinese families with congenital cataracts. Molecular Vision, 2011, 17, 2197-206.	1.1	45
7	Homozygosity Mapping and Genetic Analysis of Autosomal Recessive Retinal Dystrophies in 144 Consanguineous Pakistani Families. , 2017, 58, 2218.		34
8	Exome sequencing identified null mutations in LOXL3 associated with early-onset high myopia. Molecular Vision, 2016, 22, 161-7.	1.1	31
9	Molecular genetics of Leber congenital amaurosis in Chinese: New data from 66 probands and mutation overview of 159 probands. Experimental Eye Research, 2016, 149, 93-99.	1.2	30
10	Mutational screening of six genes in Chinese patients with congenital cataract and microcornea. Molecular Vision, 2011, 17, 1508-13.	1.1	28
11	CPSF1 mutations are associated with early-onset high myopia and involved in retinal ganglion cell axon projection. Human Molecular Genetics, 2019, 28, 1959-1970.	1.4	27
12	Germline Mutations in CTNNB1 Associated With Syndromic FEVR or Norrie Disease. , 2019, 60, 93.		26
13	Novel truncation mutations in MYRF cause autosomal dominant high hyperopia mapped to 11p12â€“q13.3. Human Genetics, 2019, 138, 1077-1090.	1.8	25
14	<scp>RPE</scp>65 mutation frequency and phenotypic variation according to exome sequencing in a tertiary centre for genetic eye diseases in China. Acta Ophthalmologica, 2020, 98, e181-e190.	0.6	21
15	Pathogenicity discrimination and genetic test reference for CRX variants based on genotype-phenotype analysis. Experimental Eye Research, 2019, 189, 107846.	1.2	18
16	Structural variations in a non-coding region at 1q32.1 are responsible for the NYS7 locus in two large families. Human Genetics, 2020, 139, 1057-1064.	1.8	17
17	Biallelic mutations in USP45, encoding a deubiquitinating enzyme, are associated with Leber congenital amaurosis. Journal of Medical Genetics, 2019, 56, 325-331.	1.5	16
18	Phenotypic characterization of patients with early-onset high myopia due to mutations in or : Why not Stickler syndrome?. Molecular Vision, 2018, 24, 560-573.	1.1	15

#	Article	IF	Citations
19	Clinical manifestation and genetic analysis in Chinese early onset Xâ€linked retinoschisis. Molecular Genetics & Genomic Medicine, 2020, 8, e1421.	0.6	14
20	Spectrum-frequency and genotypeâ€“phenotype analysis of rhodopsin variants. Experimental Eye Research, 2021, 203, 108405.	1.2	14
21	Does the Association BetweenTMEM98and Nanophthalmos Require Further Confirmation?. JAMA Ophthalmology, 2015, 133, 358.	1.4	10
22	Comparative exome sequencing reveals novel candidate genes for retinitis pigmentosa. EBioMedicine, 2020, 56, 102792.	2.7	10
23	Clinical and Genetic Analysis of 63 Families Demonstrating Early and Advanced Characteristic Fundus as the Signature of CRB1 Mutations. American Journal of Ophthalmology, 2021, 223, 160-168.	1.7	10
24	DNAH17 is essential for rat spermatogenesis and fertility. Journal of Genetics, 2021, 100, 1.	0.4	10
25	Genotypeâ€“Phenotype Analysis of RPGR Variations: Reporting of 62 Chinese Families and a Literature Review. Frontiers in Genetics, 2021, 12, 600210.	1.1	10
26	Rare variants in novel and known genes associated with primary angle closure glaucoma based on whole exome sequencing of 549 probands. Journal of Genetics and Genomics, 2019, 46, 353-357.	1.7	9
27	Diseases associated with mutations in CNGA3: Genotypeâ€“phenotype correlation and diagnostic guideline. Progress in Molecular Biology and Translational Science, 2019, 161, 1-27.	0.9	9
28	A novel deep intronic COL2A1 mutation in a family with earlyâ€onset high myopia/ocularâ€only Stickler syndrome. Ophthalmic and Physiological Optics, 2020, 40, 281-288.	1.0	7
29	Pathogenic variants and associated phenotypic spectrum of TSPAN12 based on data from a large cohort. Graefe's Archive for Clinical and Experimental Ophthalmology, 2021, 259, 2929-2939.	1.0	7
30	Novel variants in GUCY2D causing retinopathy and the genotype-phenotype correlation. Experimental Eye Research, 2021, 208, 108637.	1.2	7
31	A novel variant in IDH3A identified in a case with Leber congenital amaurosis accompanied by macular pseudocoloboma. Ophthalmic Genetics, 2018, 39, 662-663.	0.5	6
32	Variants in RCBTB1 are Associated with Autosomal Recessive Retinitis Pigmentosa but Not Autosomal Dominant FEVR. Current Eye Research, 2021, 46, 839-844.	0.7	6
33	Dominant RP in the Middle While Recessive in Both the N- and C-Terminals Due to RP1 Truncations: Confirmation, Refinement, and Questions. Frontiers in Cell and Developmental Biology, 2021, 9, 634478.	1.8	6
34	Pathogenicity evaluation and the genotypeâ€“phenotype analysis of OPA1 variants. Molecular Genetics and Genomics, 2021, 296, 845-862.	1.0	6
35	Characterization of PROM1 p.Arg373Cys Variant in a Cohort of Chinese Patients: Macular Dystrophy Plus Peripheral Bone-Spicule Degeneration. , 2021, 62, 19.		6
36	Biallelic variants inCPAMD8are associated with primary open-angle glaucoma and primary angle-closure glaucoma. British Journal of Ophthalmology, 2022, 106, 1710-1715.	2.1	6

#	Article	IF	Citations
37	Clinical and genetic features of retinoschisis in 120 families withRS1mutations. British Journal of Ophthalmology, 2023, 107, 367-372.	2.1	6
38	Genotypes and phenotypes of genes associated with achromatopsia: A reference for clinical genetic testing. Molecular Vision, 2020, 26, 588-602.	1.1	6
39	Different Phenotypes Represent Advancing Stages of ABCA4-Associated Retinopathy: A Longitudinal Study of 212 Chinese Families From a Tertiary Center. , 2022, 63, 28.		6
40	Genotype-Phenotype of Isolated Foveal Hypoplasia in a Large Cohort: Minor Iris Changes as an Indicator of PAX6 Involvement. , 2021, 62, 23.		5
41	Landscape of pathogenic variants in six preâ€mRNA processing factor genes for retinitis pigmentosa based on large inâ€house data sets and database comparisons. Acta Ophthalmologica, 2022, , .	0.6	4
42	Clinical features and genetic spectrum of NMNAT1-associated retinal degeneration. Eye, 2022, 36, 2279-2285.	1.1	3
43	Correspondence to Rossetti et al.'s review of the phenotypic spectrum associated with haploinsufficiency of MYRF. American Journal of Medical Genetics, Part A, 2019, 179, 2315-2316.	0.7	2
44	Severe exudative vitreoretinopathy as a common feature for CTNNB1, KIF11 and NDP variants plus sector degeneration for KIF11. American Journal of Ophthalmology, 2021, , .	1.7	2
45	Spectrum, frequency, and genotype-phenotype of mutations in. Molecular Vision, 2019, 25, 821-833.	1.1	2
46	Novel BMP4 Truncations Resulted in Opposite Ocular Anomalies: Pathologic Myopia Rather Than Microphthalmia. Frontiers in Cell and Developmental Biology, 2021, 9, 769636.	1.8	2
47	Start and End with Genetics: RCBTB1 and Beyond. Current Eye Research, 2021, 46, 1932-1933.	0.7	1
48	Confirming and expanding the phenotypes of variants: Coloboma, inferior chorioretinal hypoplasia, and high myopia. Molecular Vision, 2021, 27, 50-60.	1.1	1
49	Autosomal Dominant Retinitis Pigmentosaâ€“Associated TOPORS Protein Truncating Variants Are Exclusively Located in the Region of Amino Acid Residues 807 to 867. , 2022, 63, 19.		1
50	Heterozygous variants with ocular phenotype: Missense in domain but truncation out of domain. Molecular Vision, 2021, 27, 309-322.	1.1	0