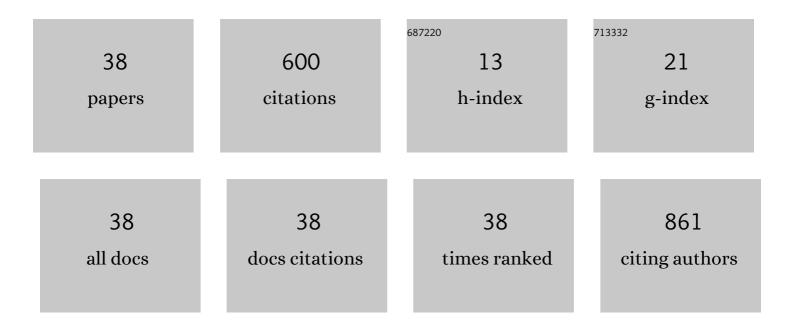
Panfeng Wang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10023240/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	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
2	An Ophthalmic Targeted Exome Sequencing Panel as a Powerful Tool to Identify Causative Mutations in Patients Suspected of Hereditary Eye Diseases. Translational Vision Science and Technology, 2019, 8, 21.	1.1	54
3	High Myopia Is Not Associated with the SNPs in theTGIF, Lumican,TGFB1, andHGFGenes. , 2009, 50, 1546.		43
4	Novel SOX2 Mutation Associated With Ocular Coloboma in a Chinese Family. JAMA Ophthalmology, 2008, 126, 709.	2.6	37
5	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
6	Generation and Characterization of Induced Pluripotent Stem Cells and Retinal Organoids From a Leber's Congenital Amaurosis Patient With Novel RPE65 Mutations. Frontiers in Molecular Neuroscience, 2019, 12, 212.	1.4	30
7	Exome sequencing reveals CHM mutations in six families with atypical choroideremia initially diagnosed as retinitis pigmentosa. International Journal of Molecular Medicine, 2014, 34, 573-577.	1.8	28
8	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
9	Germline Mutations in CTNNB1 Associated With Syndromic FEVR or Norrie Disease. , 2019, 60, 93.		26
10	<i><scp>RPE</scp>65</i> 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
11	Linkage analysis of two families with X-linked recessive congenital motor nystagmus. Journal of Human Genetics, 2006, 51, 76-80.	1.1	20
12	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
13	Biallelic mutations in <i>USP45,</i> encoding a deubiquitinating enzyme, are associated with Leber congenital amaurosis. Journal of Medical Genetics, 2019, 56, 325-331.	1.5	16
14	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
15	<i>PAX6</i> Mutations Identified in 4 of 35 Families with Microcornea. , 2012, 53, 6338.		14
16	Clinical manifestation and genetic analysis in Chinese early onset Xâ€linked retinoschisis. Molecular Genetics & Genomic Medicine, 2020, 8, e1421.	0.6	14
17	Spectrum-frequency and genotype–phenotype analysis of rhodopsin variants. Experimental Eye Research, 2021, 203, 108405.	1.2	14
18	Cone-Rod Dysfunction Is a Sign of Early-Onset High Myopia. Optometry and Vision Science, 2013, 90, 1327-1330.	0.6	13

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#	Article	IF	CITATIONS
19	KIF21A novel deletion and recurrent mutation in patients with congenital fibrosis of the extraocular muscles-1. International Journal of Molecular Medicine, 2011, 28, 973-5.	1.8	12
20	Novel mutations of the PAX6 gene identified in Chinese patients with aniridia. Molecular Vision, 2006, 12, 644-8.	1.1	12
21	Evaluation of MFRP as a candidate gene for high hyperopia. Molecular Vision, 2009, 15, 181-6.	1.1	11
22	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
23	An evaluation of OPTC and EPYC as candidate genes for high myopia. Molecular Vision, 2009, 15, 2045-9.	1.1	8
24	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
25	Novel variants in GUCY2D causing retinopathy and the genotype-phenotype correlation. Experimental Eye Research, 2021, 208, 108637.	1.2	7
26	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
27	Pathogenicity evaluation and the genotype–phenotype analysis of OPA1 variants. Molecular Genetics and Genomics, 2021, 296, 845-862.	1.0	6
28	Characterization of <i>PROM1</i> p.Arg373Cys Variant in a Cohort of Chinese Patients: Macular Dystrophy Plus Peripheral Bone-Spicule Degeneration. , 2021, 62, 19.		6
29	Clinical and genetic features of retinoschisis in 120 families with <i>RS1</i> mutations. British Journal of Ophthalmology, 2023, 107, 367-372.	2.1	6
30	Genotypes and phenotypes of genes associated with achromatopsia: A reference for clinical genetic testing. Molecular Vision, 2020, 26, 588-602.	1.1	6
31	Different Phenotypes Represent Advancing Stages of <i>ABCA4</i> -Associated Retinopathy: A Longitudinal Study of 212 Chinese Families From a Tertiary Center. , 2022, 63, 28.		6
32	Novel ocular findings in oculodentodigital dysplasia (ODDD): a case report and literature review. Ophthalmic Genetics, 2019, 40, 54-59.	0.5	5
33	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
34	Mutation profile of glaucoma candidate genes in Mauritanian families with primary congenital glaucoma. Molecular Vision, 2019, 25, 373-381.	1.1	3
35	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
36	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

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#	Article	IF	CITATIONS
37	An Early Diagnostic Clue for COL18A1- and LAMA1-Associated Diseases: High Myopia With Alopecia Areata in the Cranial Midline. Frontiers in Cell and Developmental Biology, 2021, 9, 644947.	1.8	1

Autosomal Dominant Retinitis Pigmentosa–Associated <i>TOPORS</i> Protein Truncating Variants Are Exclusively Located in the Region of Amino Acid Residues 807 to 867., 2022, 63, 19.

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