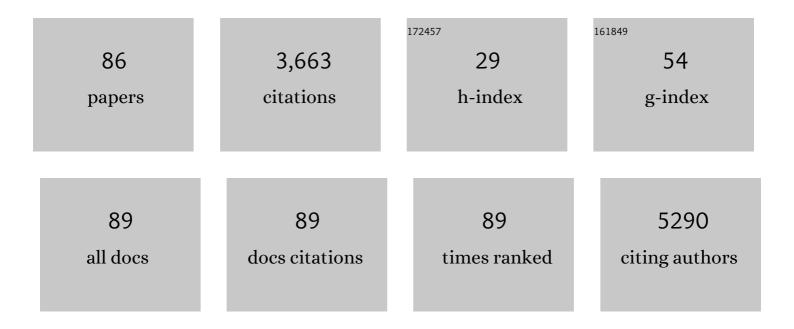
List of Publications by Year in descending order

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ΟΛΥΙΝ ΔΡΝΟ

#	Article	IF	CITATIONS
1	A rare canonical splice-site variant in VPS13B causes attenuated Cohen syndrome. Ophthalmic Genetics, 2022, 43, 110-115.	1.2	2
2	WFS1-Associated Optic Neuropathy: Genotype-Phenotype Correlations and Disease Progression. American Journal of Ophthalmology, 2022, 241, 9-27.	3.3	8
3	Identification of autosomal recessive novel genes and retinal phenotypes in members of the solute carrier (SLC) superfamily. Genetics in Medicine, 2022, 24, 1523-1535.	2.4	5
4	Variability of retinopathy consequent upon novel mutations in LAMA1. Ophthalmic Genetics, 2022, 43, 671-678.	1.2	1
5	A clinical study of patients with novel CDHR1 genotypes associated with late-onset macular dystrophy. Eye, 2021, 35, 1482-1489.	2.1	5
6	Clinical and Genetic Findings in CTNNA1-Associated Macular Pattern Dystrophy. Ophthalmology, 2021, 128, 952-955.	5.2	8
7	Enhanced S-Cone Syndrome. Ophthalmology Retina, 2021, 5, 195-214.	2.4	27
8	Spatial Functional Characteristics of East Asian Patients With Occult Macular Dystrophy (Miyake) Tj ETQq0 0 0 r	gBŢ /Overl	ock 10 Tf 50
	The X-linked retinopathies: Physiological insights, pathogenic mechanisms, phenotypic features and		

9	novel therapies. Progress in Retinal and Eye Research, 2021, 82, 100898.	19.9	00
10	Ceramide synthase TLCD3B is a novel gene associated with human recessive retinal dystrophy. Genetics in Medicine, 2021, 23, 488-497.	2.4	7
11	Genome Analysis for Inherited Retinal Disease: The State of the Art. Essentials in Ophthalmology, 2021, , 153-168.	0.1	1
12	KCNV2-Associated Retinopathy: Detailed Retinal Phenotype and Structural Endpoints—KCNV2 Study Group Report 2. American Journal of Ophthalmology, 2021, 230, 1-11.	3.3	11
13	KCNV2-Associated Retinopathy: Genetics, Electrophysiology, and Clinical Course—KCNV2 Study Group Report 1. American Journal of Ophthalmology, 2021, 225, 95-107.	3.3	17
14	Broadening INPP5E phenotypic spectrum: detection of rare variants in syndromic and non-syndromic IRD. Npj Genomic Medicine, 2021, 6, 53.	3.8	8
15	Comparison of in silico strategies to prioritize rare genomic variants impacting RNA splicing for the diagnosis of genomic disorders. Scientific Reports, 2021, 11, 20607.	3.3	37
16	100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care — Preliminary Report. New England Journal of Medicine, 2021, 385, 1868-1880.	27.0	352
17	Awareness of olfactory impairment in a cohort of patients with CNGB1-associated retinitis pigmentosa. Eye, 2020, 34, 783-784.	2.1	2
18	GUCY2D-Associated Leber Congenital Amaurosis: A Retrospective Natural History Study in Preparation for Trials of Novel Therapies. American Journal of Ophthalmology, 2020, 210, 59-70.	3.3	39

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19	Reanalysis of Association of Pro50Leu Substitution in Guanylate Cyclase Activating Protein-1 With Dominant Retinal Dystrophy. JAMA Ophthalmology, 2020, 138, 200.	2.5	5
20	Practical guide to genetic screening for inherited eye diseases. Therapeutic Advances in Ophthalmology, 2020, 12, 251584142095459.	1.4	17
21	Detailed Phenotyping and Therapeutic Strategies for Intronic ABCA4 Variants in Stargardt Disease. Molecular Therapy - Nucleic Acids, 2020, 21, 412-427.	5.1	55
22	Structural Variants Create New Topological-Associated Domains and Ectopic Retinal Enhancer-Gene Contact in Dominant Retinitis Pigmentosa. American Journal of Human Genetics, 2020, 107, 802-814.	6.2	75
23	DYNC2H1 hypomorphic or retina-predominant variants cause nonsyndromic retinal degeneration. Genetics in Medicine, 2020, 22, 2041-2051.	2.4	38
24	A genetic and clinical study of individuals with nonsyndromic retinopathy consequent upon sequence variants in <scp><i>HGSNAT</i></scp> , the gene associated with Sanfilippo C mucopolysaccharidosis. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 631-643.	1.6	12
25	Clinical and molecular findings in a cohort of 152 Brazilian severe early onset inherited retinal dystrophy patients. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 728-752.	1.6	20
26	Introduction to the special issue on Ophthalmic Genetics: Vision in 2020. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 535-537.	1.6	1
27	Clinical and genetic characteristics of 10 Japanese patients with PROM1 â€associated retinal disorder: A report of the phenotype spectrum and a literature review in the Japanese population. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 656-674.	1.6	21
28	RP2 â€associated retinal disorder in a Japanese cohort: Report of novel variants and a literature review, identifying a genotype–phenotype association. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 675-693.	1.6	5
29	Ocular genetics in the genomics age. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2020, 184, 860-868.	1.6	2
30	Macula-predominant retinopathy associated with biallelic variants in <i>RDH12</i> . Ophthalmic Genetics, 2020, 41, 612-615.	1.2	12
31	Genetic Basis of Inherited Retinal Disease in a Molecularly Characterized Cohort of More Than 3000 Families from the United Kingdom. Ophthalmology, 2020, 127, 1384-1394.	5.2	131
32	Expanding the phenotypic spectrum consequent upon de novo <scp><i>WDR37</i></scp> missense variants. Clinical Genetics, 2020, 98, 191-197.	2.0	8
33	Clinical and Genetic Characteristics of 18 Patients from 13 Japanese Families with CRX-associated retinal disorder: Identification of Genotype-phenotype Association. Scientific Reports, 2020, 10, 9531.	3.3	24
34	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
35	Clinical and Genetic Characteristics of 15 Affected Patients From 12 Japanese Families with <i>GUCY2D</i> -Associated Retinal Disorder. Translational Vision Science and Technology, 2020, 9, 2.	2.2	15
36	The majority of autosomal recessive nanophthalmos and posterior microphthalmia can be attributed to biallelic sequence and structural variants in MERP and PRSS56. Scientific Reports, 2020, 10, 1289	3.3	24

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37	Genetic Spectrum of EYS-associated Retinal Disease in a Large Japanese Cohort: Identification of Disease-associated Variants with Relatively High Allele Frequency. Scientific Reports, 2020, 10, 5497.	3.3	21
38	An Improved Phenotype-Driven Tool for Rare Mendelian Variant Prioritization: Benchmarking Exomiser on Real Patient Whole-Exome Data. Genes, 2020, 11, 460.	2.4	42
39	Phenogenon: Gene to phenotype associations for rare genetic diseases. PLoS ONE, 2020, 15, e0230587.	2.5	6
40	Phenotypical Characteristics of <i>POC1B</i> -Associated Retinopathy in Japanese Cohort: Cone Dystrophy With Normal Funduscopic Appearance. , 2019, 60, 3432.		18
41	<i>SSBP1</i> mutations in dominant optic atrophy with variable retinal degeneration. Annals of Neurology, 2019, 86, 368-383.	5.3	41
42	Clinical and Genetic Characteristics of East Asian Patients with Occult Macular Dystrophy (Miyake) Tj ETQq0 0 0	rg <u>B</u> T/Ove	rlock 10 Tf 5

43	ABCA4-associated disease as a model for missing heritability in autosomal recessive disorders: novel noncoding splice, cis-regulatory, structural, and recurrent hypomorphic variants. Genetics in Medicine, 2019, 21, 1761-1771.	2.4	111
44	Unique noncoding variants upstream of <i>PRDM13</i> are associated with a spectrum of developmental retinal dystrophies including progressive bifocal chorioretinal atrophy. Human Mutation, 2019, 40, 578-587.	2.5	19
45	Delineating the expanding phenotype associated with <i>SCAPER</i> gene mutation. American Journal of Medical Genetics, Part A, 2019, 179, 1665-1671.	1.2	10
46	Isolated rod dysfunction associated with a novel genotype of CNGB1. American Journal of Ophthalmology Case Reports, 2019, 14, 83-86.	0.7	9
47	Clinical and Molecular Characterization of Familial Exudative Vitreoretinopathy Associated With Microcephaly. American Journal of Ophthalmology, 2019, 207, 87-98.	3.3	20
48	Macular maldevelopment in <i>ATF6</i> -mediated retinal dysfunction. Ophthalmic Genetics, 2019, 40, 564-569.	1.2	3
49	The Spectrum of PAX6 Mutations and Genotype-Phenotype Correlations in the Eye. Genes, 2019, 10, 1050.	2.4	111
49 50	The Spectrum of PAX6 Mutations and Genotype-Phenotype Correlations in the Eye. Genes, 2019, 10, 1050. Deep-intronic ABCA4 variants explain missing heritability in Stargardt disease and allow correction of splice defects by antisense oligonucleotides. Genetics in Medicine, 2019, 21, 1751-1760.	2.4 2.4	111
	Deep-intronic ABCA4 variants explain missing heritability in Stargardt disease and allow correction of		
50	Deep-intronic ABCA4 variants explain missing heritability in Stargardt disease and allow correction of splice defects by antisense oligonucleotides. Genetics in Medicine, 2019, 21, 1751-1760. A clinical and molecular characterisation of CRB1-associated maculopathy. European Journal of	2.4	147
50 51	Deep-intronic ABCA4 variants explain missing heritability in Stargardt disease and allow correction of splice defects by antisense oligonucleotides. Genetics in Medicine, 2019, 21, 1751-1760. A clinical and molecular characterisation of CRB1-associated maculopathy. European Journal of Human Genetics, 2018, 26, 687-694.	2.4 2.8	147 51

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55	Missense variants in the X-linked gene <i>PRPS1</i> cause retinal degeneration in females. Human Mutation, 2018, 39, 80-91.	2.5	23
56	Whole genome sequencing reveals novel mutations causing autosomal dominant inherited macular degeneration. Ophthalmic Genetics, 2018, 39, 763-770.	1.2	13
57	Complex structural variants in Mendelian disorders: identification and breakpoint resolution using short- and long-read genome sequencing. Genome Medicine, 2018, 10, 95.	8.2	111
58	Clinical Features of a Retinopathy Associated With a Dominant Allele of the <i>RGR</i> Gene. , 2018, 59, 4812.		9
59	Mutation in the intracellular chloride channel CLCC1 associated with autosomal recessive retinitis pigmentosa. PLoS Genetics, 2018, 14, e1007504.	3.5	25
60	Novel homozygous splicing mutations in cause autosomal recessive retinitis pigmentosa. Molecular Vision, 2018, 24, 603-612.	1.1	6
61	Clinical Characterization of <i>CNGB1</i> -Related Autosomal Recessive Retinitis Pigmentosa. JAMA Ophthalmology, 2017, 135, 137.	2.5	23
62	Biallelic Mutation of ARHGEF18, Involved in the Determination of Epithelial Apicobasal Polarity, Causes Adult-Onset Retinal Degeneration. American Journal of Human Genetics, 2017, 100, 334-342.	6.2	26
63	Mutations in the Spliceosome Component CWC27 Cause Retinal Degeneration with or without Additional Developmental Anomalies. American Journal of Human Genetics, 2017, 100, 592-604.	6.2	61
64	Genome-wide linkage and haplotype sharing analysis implicates the MCDR3 locus as a candidate region for a developmental macular disorder in association with digit abnormalities. Ophthalmic Genetics, 2017, 38, 511-519.	1.2	2
65	Missense mutations in the WD40 domain ofAHI1cause non-syndromic retinitis pigmentosa. Journal of Medical Genetics, 2017, 54, 624-632.	3.2	21
66	Phenopolis: an open platform for harmonization and analysis of genetic and phenotypic data. Bioinformatics, 2017, 33, 2421-2423.	4.1	40
67	Detailed Clinical Phenotype and Molecular Genetic Findings in <i>CLN3</i> -Associated Isolated Retinal Degeneration. JAMA Ophthalmology, 2017, 135, 749.	2.5	61
68	Single-base substitutions in the <i>CHM</i> promoter as a cause of choroideremia. Human Mutation, 2017, 38, 704-715.	2.5	45
69	Association of Steroid 5α-Reductase Type 3 Congenital Disorder of Glycosylation With Early-Onset Retinal Dystrophy. JAMA Ophthalmology, 2017, 135, 339.	2.5	43
70	Benign Yellow Dot Maculopathy. Ophthalmology, 2017, 124, 1004-1013.	5.2	12
71	Comprehensive Rare Variant Analysis via Whole-Genome Sequencing to Determine the Molecular Pathology of Inherited Retinal Disease. American Journal of Human Genetics, 2017, 100, 75-90.	6.2	343
72	Vitamin A deficiency due to bi-allelic mutation of <i>RBP4</i> : There's more to it than meets the eye. Ophthalmic Genetics, 2017, 38, 465-466.	1.2	21

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73	Duplication events downstream of IRX1 cause North Carolina macular dystrophy at the MCDR3 locus. Scientific Reports, 2017, 7, 7512.	3.3	23
74	Reevaluation of the Retinal Dystrophy Due to Recessive Alleles of <i>RGR</i> With the Discovery of a Cis-Acting Mutation in <i>CDHR1</i> . , 2016, 57, 4806.		25
75	Mutations in <i>AGBL5</i> , Encoding α-Tubulin Deglutamylase, Are Associated With Autosomal Recessive Retinitis Pigmentosa. , 2016, 57, 6180.		21
76	Mutations in CACNA2D4 Cause Distinctive Retinal Dysfunction in Humans. Ophthalmology, 2016, 123, 668-671.e2.	5.2	29
77	Mutations in REEP6 Cause Autosomal-Recessive Retinitis Pigmentosa. American Journal of Human Genetics, 2016, 99, 1305-1315.	6.2	121
78	Expanding the Phenotype of <i>TRNT1</i> -Related Immunodeficiency to Include Childhood Cataract and Inner Retinal Dysfunction. JAMA Ophthalmology, 2016, 134, 1049.	2.5	29
79	Exome sequencing revealsADAM9mutations in a child with cone-rod dystrophy. Acta Ophthalmologica, 2015, 93, e392-e393.	1.1	3
80	Somatic mosaicism of a novel <i>IKBKG</i> mutation in a male patient with incontinentia pigmenti. American Journal of Medical Genetics, Part A, 2015, 167, 1601-1604.	1.2	27
81	Lack of Interphotoreceptor Retinoid Binding Protein Caused by Homozygous Mutation of <i>RBP3</i> Is Associated With High Myopia and Retinal Dystrophy. , 2015, 56, 2358.		42
82	Mutations in TUBGCP4 Alter Microtubule Organization via the Î ³ -Tubulin Ring Complex in Autosomal-Recessive Microcephaly with Chorioretinopathy. American Journal of Human Genetics, 2015, 96, 666-674.	6.2	60
83	Neuropathy target esterase impairments cause Oliver–McFarlane and Laurence–Moon syndromes. Journal of Medical Genetics, 2015, 52, 85-94.	3.2	91
84	Clinical and Molecular Characterization of Enhanced S-Cone Syndrome in Children. JAMA Ophthalmology, 2014, 132, 1341.	2.5	39
85	The Phenotypic Variability of Retinal Dystrophies Associated With Mutations in CRX, With Report of a Novel Macular Dystrophy Phenotype. Investigative Ophthalmology and Visual Science, 2014, 55, 6934-6944.	3.3	59
86	Biallelic Variants in TTLL5, Encoding a Tubulin Glutamylase, Cause Retinal Dystrophy. American Journal of Human Genetics, 2014, 94, 760-769.	6.2	67