Eranga N Vithana

List of Publications by Year
in descending order

72 papers	6,195 citations	109321 35 h-index	133252 59 g-index
73 all docs	73 docs citations	73 times ranked	6379 citing authors

#	Article	IF	Citations
1	Comparison of machine learning approaches for structureâ€“function modeling in glaucoma. Annals of the New York Academy of Sciences, 2022, 1515, 237-248.	3.8	3
2	Factors affecting the diagnostic performance of circumpapillary retinal nerve fibre layer measurement in glaucoma. British Journal of Ophthalmology, 2021, 105, 397-402.	3.9	12
3	Evaluation of Primary Angle-Closure Glaucoma Susceptibility Loci for Estimating Angle Closure Disease Severity. Ophthalmology, 2021, 128, 403-409.	5.2	12
4	Characteristics of p.Gln368Ter Myocilin Variant and Influence of Polygenic Risk on Glaucoma Penetrance in the UK Biobank. Ophthalmology, 2021, 128, 1300-1311.	5.2	27
5	Primary angle closure glaucoma genomic associations and disease mechanism. Current Opinion in Ophthalmology, 2020, 31, 101-106.	2.9	9
6	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	4.4	10
7	Integration of Genetic and Biometric Risk Factors for Detection of Primary Angle Closure Glaucoma. American Journal of Ophthalmology, 2019, 208, 160-165.	3.3	10
8	Genome-wide association study identifies seven novel susceptibility loci for primary open-angle glaucoma. Human Molecular Genetics, 2018, 27, 1486-1496.	2.9	111
9	Evaluation of Primary Angle-Closure Glaucoma Susceptibility Loci in Patients with Early Stages of Angle-Closure Disease. Ophthalmology, 2018, 125, 664-670.	5.2	22
10	Social, health and ocular factors associated with primary openâ€angle glaucoma amongst Chinese Singaporeans. Clinical and Experimental Ophthalmology, 2018, 46, 25-34.	2.6	18
11	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
12	Genome-wide association study of Parkinsonâ€™s disease in East Asians. Human Molecular Genetics, 2017, 26, ddw379.	2.9	94
13	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120
14	Genetics of Corneal Endothelial Dystrophies: An Asian Perspective. Essentials in Ophthalmology, 2017, , 353-361.	0.1	0
15	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
16	Primary angle closure glaucoma (PACG) susceptibility gene PLEKHA7 encodes a novel Rac1/Cdc42 GAP that modulates cell migration and blood-aqueous barrier function. Human Molecular Genetics, 2017, 26, 4011-4027.	2.9	21
17	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2016, 48, 556-562.	21.4	147
18	Linking a genomeâ€wide association study signal to a LRRK2 coding variant in Parkinson's disease. Movement Disorders, 2016, 31, 484-487.	3.9	8

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19	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
20	Association of Common SIX6 Polymorphisms With Peripapillary Retinal Nerve Fiber Layer Thickness: The Singapore Chinese Eye Study. Investigative Ophthalmology and Visual Science, 2015, 56, 478-483.	3.3	35
21	Lens Status Influences the Association between CFH Polymorphisms and Age-Related Macular Degeneration: Findings from Two Population-Based Studies in Singapore. PLoS ONE, 2015, 10, e0119570.	2.5	3
22	A common variant near TGFBR3 is associated with primary open angle glaucoma. Human Molecular Genetics, 2015, 24, 3880-3892.	2.9	105
23	Biochemical Properties and Aggregation Propensity of Transforming Growth Factor-Induced Protein (TGFBIp) and the Amyloid Forming Mutants. Ocular Surface, 2015, 13, 9-25.	4.4	10
24	New loci and coding variants confer risk for age-related macular degeneration in East Asians. Nature Communications, 2015, 6, 6063.	12.8	147
25	A common variant mapping to CACNA1A is associated with susceptibility to exfoliation syndrome. Nature Genetics, 2015, 47, 387-392.	21.4	97
26	Aggregate Effects of Intraocular Pressure and Cup-to-Disc Ratio Genetic Variants on Glaucoma in a Multiethnic Asian Population. Ophthalmology, 2015, 122, 1149-1157.	5.2	28
27	Genetic variants and cellular stressors associated with exfoliation syndrome modulate promoter activity of a lncRNA within theLOXL1locus. Human Molecular Genetics, 2015, 24, 6552-6563.	2.9	76
28	Analysis of non-synonymous-coding variants of Parkinson's disease-related pathogenic and susceptibility genes in East Asian populations. Human Molecular Genetics, 2014, 23, 3891-3897.	2.9	28
29	Genotypeâ€“Phenotype Correlation Analysis for Three Primary Angle Closure Glaucoma-Associated Genetic Polymorphisms. , 2014, 55, 1143.		17
30	ABCC5, a Gene That Influences the Anterior Chamber Depth, Is Associated with Primary Angle Closure Glaucoma. PLoS Genetics, 2014, 10, e1004089.	3.5	68
31	Clinical and Genetic Aspects of the TGFBI-associated Corneal Dystrophies. Ocular Surface, 2014, 12, 234-251.	4.4	63
32	Meta-analysis of genome-wide association studies in multiethnic Asians identifies two loci for age-related nuclear cataract. Human Molecular Genetics, 2014, 23, 6119-6128.	2.9	35
33	CMPK1 and RBP3 are associated with corneal curvature in Asian populations. Human Molecular Genetics, 2014, 23, 6129-6136.	2.9	22
34	Expression of the Primary Angle Closure Glaucoma (PACG) Susceptibility GenePLEKHA7in Endothelial and Epithelial Cell Junctions in the Eye. , 2014, 55, 3833.		24
35	Common variants near ABCA1 and in PMM2 are associated with primary open-angle glaucoma. Nature Genetics, 2014, 46, 1115-1119.	21.4	160
36	Transethnic Replication of Association of CTG18.1 Repeat Expansion ofTCF4Gene With Fuchs' Corneal Dystrophy in Chinese Implies Common Causal Variant. , 2014, 55, 7073.		64

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37	Ion Transport Function of SLC4A11 in Corneal Endothelium. , 2013, 54, 4330.		66
38	SLC4A11 is an EIPA-sensitive Na⁺permeable pH_iregulator. American Journal of Physiology - Cell Physiology, 2013, 305, C716-C727.	4.6	51
39	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
40	Transmembrane water-flux through SLC4A11: a route defective in genetic corneal diseases. Human Molecular Genetics, 2013, 22, 4579-4590.	2.9	89
41	Lack of Association Between Primary Angle-Closure Glaucoma Susceptibility Loci and the Ocular Biometric Parameters Anterior Chamber Depth and Axial Length. , 2013, 54, 5824.		23
42	Genome-wide association study identifies ZFHX1B as a susceptibility locus for severe myopia. Human Molecular Genetics, 2013, 22, 5288-5294.	2.9	59
43	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	21.4	269
44	Mice With a Targeted Disruption ofSlc4a11Model the Progressive Corneal Changes of Congenital Hereditary Endothelial Dystrophy. , 2013, 54, 6179.		55
45	Differential expression of the Slc4 bicarbonate transporter family in murine corneal endothelium and cell culture. Molecular Vision, 2013, 19, 1096-106.	1.1	15
46	Association of Genetic Variants on 8p21 and 4q12 with Age-Related Macular Degeneration in Asian Populations. , 2012, 53, 6576.		22
47	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 437-445.	2.9	69
48	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2012, 44, 1142-1146.	21.4	196
49	Depletion ofSLC4A11Causes Cell Death by Apoptosis in an Immortalized Human Corneal Endothelial Cell Line. , 2012, 53, 3270.		41
50	Oligomerization of SLC4A11 protein and the severity of FECD and CHED2 corneal dystrophies caused bySLC4A11mutations. Human Mutation, 2012, 33, 419-428.	2.5	46
51	The Heritability and Sibling Risk of Angle Closure in Asians. Ophthalmology, 2011, 118, 480-485.	5.2	69
52	Relationship of Smoking and Cardiovascular Risk Factors with Polypoidal Choroidal Vasculopathy and Age-related Macular Degeneration in Chinese Persons. Ophthalmology, 2011, 118, 846-852.	5.2	65
53	Association ofTCF4Gene Polymorphisms with Fuchs' Corneal Dystrophy in the Chinese. , 2011, 52, 5573.		51
54	A novel mutation in transforming growth factor-beta induced protein (TGFÂIp) reveals secondary structure perturbation in lattice corneal dystrophy. British Journal of Ophthalmology, 2011, 95, 1457-1462.	3.9	23

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55	Toll-Like Receptor 3 Polymorphism rs3775291 Is Not Associated with Choroidal Neovascularization or Polypoidal Choroidal Vasculopathy in Chinese Subjects. Ophthalmic Research, 2011, 45, 191-196.	1.9	16
56	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Human Molecular Genetics, 2011, 20, 649-658.	2.9	140
57	Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Human Molecular Genetics, 2011, 20, 1864-1872.	2.9	91
58	Absence of Phenotype-Genotype Correlation of Patients Expressing Mutations in the SLC4A11 Gene. Cornea, 2010, 29, 302-306.	1.7	16
59	Missense mutations in the sodium borate cotransporter SLC4A11 cause late-onset Fuchs corneal dystrophya. Human Mutation, 2010, 31, 1261-1268.	2.5	117
60	Polypoidal choroidal vasculopathy and neovascular age-related macular degeneration: Same or different disease?. Progress in Retinal and Eye Research, 2010, 29, 19-29.	15.5	315
61	Association of LOXL1 polymorphisms with pseudoexfoliation in the Chinese. Molecular Vision, 2009, 15, 1120-6.	1.1	46
62	SLC4A11 mutations in Fuchs endothelial corneal dystrophy. Human Molecular Genetics, 2008, 17, 656-666.	2.9	226
63	Analysis of the Posterior Polymorphous Corneal Dystrophy 3 Gene,TCF8, in Late-Onset Fuchs Endothelial Corneal Dystrophy. , 2008, 49, 184.		77
64	Association Analysis ofCFH,C2,BF, andHTRA1Gene Polymorphisms in Chinese Patients with Polypoidal Choroidal Vasculopathy. , 2008, 49, 2613.		105
65	Association ofLOXL1Gene Polymorphisms with Pseudoexfoliation in the Japanese. , 2008, 49, 3976.		95
66	NovelSLC4A11mutations in patients with recessive congenital hereditary endothelial dystrophy (CHED2). Human Mutation, 2007, 28, 522-523.	2.5	80
67	Mutations in sodium-borate cotransporter SLC4A11 cause recessive congenital hereditary endothelial dystrophy (CHED2). Nature Genetics, 2006, 38, 755-757.	21.4	235
68	Expression ofPRPF31mRNA in Patients with Autosomal Dominant Retinitis Pigmentosa: A Molecular Clue for Incomplete Penetrance?. , 2003, 44, 4204.		125
69	Disease mechanism for retinitis pigmentosa (RP11) caused by mutations in the splicing factor gene PRPF31. Human Molecular Genetics, 2002, 11, 3209-3219.	2.9	75
70	Mutations in HPRP3, a third member ofpre-mRNA splicing factor genes, implicated in autosomal dominant retinitis pigmentosa. Human Molecular Genetics, 2002, 11, 87-92.	2.9	217
71	A Human Homolog of Yeast Pre-mRNA Splicing Gene, PRP31, Underlies Autosomal Dominant Retinitis Pigmentosa on Chromosome 19q13.4 (RP11). Molecular Cell, 2001, 8, 375-381.	9.7	305
72	Segregation of a PRKCG Mutation in Two RP11 Families. American Journal of Human Genetics, 1998, 62, 1248-1252.	6.2	21