Michael A Hauser

List of Publications by Year
in descending order

89 papers	7,208 citations	109321 35 h-index	69250 77 g-index
93 all docs	93 docs citations	93 times ranked	10300 citing authors

#	Article	IF	Citations
1	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	1.3	114
2	Enhancing Discovery of Genetic Variants for Posttraumatic Stress Disorder Through Integration of Quantitative Phenotypes and Trauma Exposure Information. Biological Psychiatry, 2022, 91, 626-636.	1.3	21
3	A genome-wide association study of suicide attempts in the million veterans program identifies evidence of pan-ancestry and ancestry-specific risk loci. Molecular Psychiatry, 2022, 27, 2264-2272.	7.9	35
4	Polygenic risk scores for CARDINAL study. Nature Genetics, 2022, 54, 527-530.	21.4	5
5	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	12.8	196
6	Association of Rare CYP39A1 Variants With Exfoliation Syndrome Involving the Anterior Chamber of the Eye. JAMA - Journal of the American Medical Association, 2021, 325, 753.	7.4	16
7	Examining Individual and Synergistic Contributions of PTSD and Genetics to Blood Pressure: A Trans-Ethnic Meta-Analysis. Frontiers in Neuroscience, 2021, 15, 678503.	2.8	10
8	Eyes of Africa: The Genetics of Blindness: Study Design and Methodology. BMC Ophthalmology, 2021, 21, 272.	1.4	2
9	Identification of Estrogen Signaling in a Prioritization Study of Intraocular Pressure-Associated Genes. International Journal of Molecular Sciences, 2021, 22, 10288.	4.1	6
10	Gene Expression Analysis in Three Posttraumatic Stress Disorder Cohorts Implicates Inflammation and Innate Immunity Pathways and Uncovers Shared Genetic Risk With Major Depressive Disorder. Frontiers in Neuroscience, 2021, 15, 678548.	2.8	12
11	Molecular genetic overlap between posttraumatic stress disorder and sleep phenotypes. Sleep, 2020, 43, .	1.1	32
12	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
13	Epigenome-wide meta-analysis of PTSD across 10 military and civilian cohorts identifies methylation changes in AHRR. Nature Communications, 2020, 11, 5965.	12.8	84
14	Integral role for lysyl oxidaseâ€likeâ€1 in conventional outflow tissue function and behavior. FASEB Journal, 2020, 34, 10762-10777.	0.5	20
15	Genetic predictors of hippocampal subfield volume in PTSD cases and trauma-exposed controls. HÃ¶gre Utbildning, 2020, 11, 1785994.	3.0	8
16	An epigenome-wide association study of posttraumatic stress disorder in US veterans implicates several new DNA methylation loci. Clinical Epigenetics, 2020, 12, 46.	4.1	64
17	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
18	Identification and activity of the functional complex between hnRNPL and the pseudoexfoliation syndrome-associated lncRNA, LOXL1-AS1. Human Molecular Genetics, 2020, 29, 1986-1995.	2.9	8

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19	Differential DNA methylation patterns in human Schlemm's canal endothelial cells with glaucoma. Molecular Vision, 2020, 26, 483-493.	1.1	2
20	Association of a Primary Open-Angle Glaucoma Genetic Risk Score With Earlier Age at Diagnosis. JAMA Ophthalmology, 2019, 137, 1190.	2.5	32
21	International meta-analysis of PTSD genome-wide association studies identifies sex- and ancestry-specific genetic risk loci. Nature Communications, 2019, 10, 4558.	12.8	363
22	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 1682.	7.4	50
23	Update on the genetics of primary open-angle glaucoma. Experimental Eye Research, 2019, 188, 107795.	2.6	59
24	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	3.3	12
25	Genomic Approaches to Posttraumatic Stress Disorder: The Psychiatric Genomic Consortium Initiative. Biological Psychiatry, 2018, 83, 831-839.	1.3	47
26	Traumatic stress and accelerated DNA methylation age: A meta-analysis. Psychoneuroendocrinology, 2018, 92, 123-134.	2.7	190
27	Transcriptome analysis of adult and fetal trabecular meshwork, cornea, and ciliary body tissues by RNA sequencing. Experimental Eye Research, 2018, 167, 91-99.	2.6	40
28	Largest GWAS of PTSD (N=20â€‰070) yields genetic overlap with schizophrenia and sex differences in heritability. Molecular Psychiatry, 2018, 23, 666-673.	7.9	374
29	lncRNAs, DNA Methylation, and the Pathobiology of Exfoliation Glaucoma. Journal of Glaucoma, 2018, 27, 202-209.	1.6	13
30	A Common Glaucoma-risk Variant of SIX6 Alters Retinal Nerve Fiber Layer and Optic Disc Measures in a European Population: The EPIC-Norfolk Eye Study. Journal of Glaucoma, 2018, 27, 743-749.	1.6	13
31	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862.	3.8	40
32	Differential Expression of Coding and Long Noncoding RNAs in Keratoconus-Affected Corneas. , 2018, 59, 2717.		45
33	A genome-wide association study of suicide attempts and suicidal ideation in U.S. military veterans. Psychiatry Research, 2018, 269, 64-69.	3.3	41
34	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
35	Genomic locus modulating corneal thickness in the mouse identifies POU6F2 as a potential risk of developing glaucoma. PLoS Genetics, 2018, 14, e1007145.	3.5	31
36	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

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37	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	2.8	18
38	Modeling Glaucoma: Retinal Ganglion Cells Generated from Induced Pluripotent Stem Cells of Patients with SIX6 Risk Allele Show Developmental Abnormalities. Stem Cells, 2017, 35, 2239-2252.	3.2	49
39	Genome-wide association study of subcortical brain volume in PTSD cases and trauma-exposed controls. Translational Psychiatry, 2017, 7, 1265.	4.8	15
40	Major review: Exfoliation syndrome; advances in disease genetics, molecular biology, and epidemiology. Experimental Eye Research, 2017, 154, 88-103.	2.6	97
41	Further evidence for a role of the ADRB2 gene in risk for posttraumatic stress disorder. Journal of Psychiatric Research, 2017, 84, 59-61.	3.1	5
42	miRNA Profile in Three Different Normal Human Ocular Tissues by miRNA-Seq. , 2016, 57, 3731.		46
43	A Common Variant in MIR182 Is Associated With Primary Open-Angle Glaucoma in the NEIGHBORHOOD Consortium. , 2016, 57, 4528.		42
44	Assessing the Association of Mitochondrial Genetic Variation With Primary Open-Angle Glaucoma Using Gene-Set Analyses. , 2016, 57, 5046.		44
45	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2016, 48, 556-562.	21.4	147
46	Addressing ethical challenges in the Genetics Substudy of the National Eye Survey of Trinidad and Tobago (GSNESTT). Applied & Translational Genomics, 2016, 9, 6-14.	2.1	6
47	A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nature Genetics, 2016, 48, 134-143.	21.4	1,167
48	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
49	Epistatic Gene-Based Interaction Analyses for Glaucoma in eMERGE and NEIGHBOR Consortium. PLoS Genetics, 2016, 12, e1006186.	3.5	38
50	Case-control association between CCT-associated variants and keratoconus in a Saudi Arabian population. Journal of Negative Results in BioMedicine, 2015, 14, 10.	1.4	20
51	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
52	Expression Profiling of Human Schlemm's Canal Endothelial Cells From Eyes With and Without Glaucoma. , 2015, 56, 6747.		28
53	Screening of the Seed Region ofMIR184in Keratoconus Patients from Saudi Arabia. BioMed Research International, 2015, 2015, 1-7.	1.9	32
54	A common variant near TGFBR3 is associated with primary open angle glaucoma. Human Molecular Genetics, 2015, 24, 3880-3892.	2.9	105

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55	A common variant mapping to CACNA1A is associated with susceptibility to exfoliation syndrome. Nature Genetics, 2015, 47, 387-392.	21.4	97
56	Effect of genetic variation in the nicotinic receptor genes on risk for posttraumatic stress disorder. Psychiatry Research, 2015, 229, 326-331.	3.3	6
57	EFFECT OF THE APOE Îµ4 ALLELE AND COMBAT EXPOSURE ON PTSD AMONG IRAQ/AFGHANISTAN-ERA VETERANS. Depression and Anxiety, 2015, 32, 307-315.	4.1	21
58	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
59	Genome-wide association study of posttraumatic stress disorder in a cohort of Iraqâ€“Afghanistan era veterans. Journal of Affective Disorders, 2015, 184, 225-234.	4.1	81
60	An Examination of the Association between 5-HTTLPR, Combat Exposure, and PTSD Diagnosis among U.S. Veterans. PLoS ONE, 2015, 10, e0119998.	2.5	29
61	Mitochondrial Polymorphism A10398G and Haplogroup I Are Associated With Fuchs' Endothelial Corneal Dystrophy. , 2014, 55, 4577.		12
62	No association between RORA polymorphisms and PTSD in two independent samples. Molecular Psychiatry, 2014, 19, 1056-1057.	7.9	22
63	Vascular tone pathway polymorphisms in relation to primary open-angle glaucoma. Eye, 2014, 28, 662-671.	2.1	14
64	RNAi-mediated Gene Silencing of Mutant Myotilin Improves Myopathy in LGMD1A Mice. Molecular Therapy - Nucleic Acids, 2014, 3, e160.	5.1	11
65	Discovery and Functional Annotation of SIX6 Variants in Primary Open-Angle Glaucoma. PLoS Genetics, 2014, 10, e1004372.	3.5	78
66	ABCC5, a Gene That Influences the Anterior Chamber Depth, Is Associated with Primary Angle Closure Glaucoma. PLoS Genetics, 2014, 10, e1004089.	3.5	68
67	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	12.8	89
68	DNA Copy Number Variants of Known Glaucoma Genes in Relation to Primary Open-Angle Glaucoma. Investigative Ophthalmology and Visual Science, 2014, 55, 8251-8258.	3.3	27
69	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
70	Common variants near ABCA1, AFAP1 and GMDS confer risk of primary open-angle glaucoma. Nature Genetics, 2014, 46, 1120-1125.	21.4	186
71	Association of CAV1/CAV2 Genomic Variants with Primary Open-Angle Glaucoma Overall and by Gender and Pattern of Visual Field Loss. Ophthalmology, 2014, 121, 508-516.	5.2	91
72	Spink2 Modulates Apoptotic Susceptibility and Is a Candidate Gene in the Rgcs1 QTL That Affects Retinal Ganglion Cell Death after Optic Nerve Damage. PLoS ONE, 2014, 9, e93564.	2.5	13

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73	Lack of association between lysyl oxidase-like 1 polymorphisms and primary open angle glaucoma: a meta-analysis. International Journal of Ophthalmology, 2014, 7, 550-6.	1.1	4
74	Osteogenesis imperfecta and primary open angle glaucoma: genotypic analysis of a new phenotypic association. Molecular Vision, 2014, 20, 1174-81.	1.1	21
75	Association of Variant rs4790904 in Protein Kinase C Alpha with Posttraumatic Stress Disorder in a U.S. Caucasian and African-American Veteran Sample. Journal of Depression & Anxiety, 2013, 02, S4001.	0.1	13
76	Genetic screen of African Americans with Fuchs endothelial corneal dystrophy. Molecular Vision, 2013, 19, 2508-16.	1.1	13
77	Common Variants at 9p21 and 8q22 Are Associated with Increased Susceptibility to Optic Nerve Degeneration in Glaucoma. PLoS Genetics, 2012, 8, e1002654.	3.5	276
78	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2012, 44, 1142-1146.	21.4	196
79	Serotonin transporter gene polymorphisms and brain function during emotional distraction from cognitive processing in posttraumatic stress disorder. BMC Psychiatry, 2011, 11, 76.	2.6	53
80	Serial analysis of gene expression (SAGE) in normal human trabecular meshwork. Molecular Vision, 2011, 17, 885-93.	1.1	19
81	Major LOXL1 risk allele is reversed in exfoliation glaucoma in a black South African population. Molecular Vision, 2010, 16, 705-12.	1.1	86
82	NEIBank: genomics and bioinformatics resources for vision research. Molecular Vision, 2008, 14, 1327-37.	1.1	30
83	Distribution ofWDR36DNA Sequence Variants in Patients with Primary Open-Angle Glaucoma. , 2006, 47, 2542.		114
84	Defining the Human Macula Transcriptome and Candidate Retinal Disease Genes UsingEyeSAGE. , 2006, 47, 2305.		73
85	Expression Profiling of Substantia Nigra in Parkinson Disease, Progressive Supranuclear Palsy, and Frontotemporal Dementia With Parkinsonism. Archives of Neurology, 2005, 62, 917-21.	4.5	146
86	A Novel Mutation in the Gene Encoding Noggin is Not Causative in Human Neural Tube Defects. Journal of Neurogenetics, 2002, 16, 65-71.	1.4	9
87	A Novel Mutation in the Gene Encoding Noggin is Not Causative in Human Neural Tube Defects. Journal of Neurogenetics, 2002, 16, 65-71.	1.4	10
88	Myotilin is mutated in limb girdle muscular dystrophy 1A. Human Molecular Genetics, 2000, 9, 2141-2147.	2.9	255
89	Data Analysis Issues in Expression Profiling. , 0, , 193-217.		0