Todd E Scheetz

List of Publications by Year
in descending order

142	9,732	53794 45	39675 94
papers	citations	h-index	g-index

145	145	145	15164
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16899-16903.	7.1	1,610
2	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). Genome Research, 2004, 14, 2121-2127.	5.5	486
3	Homozygosity mapping with SNP arrays identifiesTRIM32, an E3 ubiquitin ligase, as a Bardetâ€“Biedl syndrome gene (BBS11). Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6287-6292.	7.1	378
4	Clonal selection drives genetic divergence of metastatic medulloblastoma. Nature, 2012, 482, 529-533.	27.8	376
5	Clinically Focused Molecular Investigation of 1000 Consecutive Families with Inherited Retinal Disease. Ophthalmology, 2017, 124, 1314-1331.	5.2	312
6	The air-liquid interface and use of primary cell cultures are important to recapitulate the transcriptional profile of in vivo airway epithelia. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2011, 300, L25-L31.	2.9	297
7	Comprehensive genetic testing for hereditary hearing loss using massively parallel sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21104-21109.	7.1	294
8	A BBSome Subunit Links Ciliogenesis, Microtubule Stability, and Acetylation. Developmental Cell, 2008, 15, 854-865.	7.0	272
9	Single-cell transcriptomics of the human retinal pigment epithelium and choroid in health and macular degeneration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24100-24107.	7.1	234
10	Sleeping Beauty mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5934-5941.	7.1	201
11	Regulation of gene expression in the mammalian eye and its relevance to eye disease. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14429-14434.	7.1	190
12	Copy number variations on chromosome 12q14 in patients with normal tension glaucoma. Human Molecular Genetics, 2011, 20, 2482-2494.	2.9	189
13	Exome sequencing and analysis of induced pluripotent stem cells identify the cilia-related gene male germ cell-associated kinase (MAK) as a cause of retinitis pigmentosa. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E569-76.	7.1	186
14	Migration of the Plastid Genome to the Nucleus in a Peridinin Dinoflagellate. Current Biology, 2004, 14, 213-218.	3.9	172
15	A Modified Sleeping Beauty Transposon System That Can Be Used to Model a Wide Variety of Human Cancers in Mice. Cancer Research, 2009, 69, 8150-8156.	0.9	156
16	Transcriptional patterns in both host and bacterium underlie a daily rhythm of anatomical and metabolic change in a beneficial symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2259-2264.	7.1	149
17	Anopheles gambiae pilot gene discovery project: Identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 6619-6624.	7.1	142
18	Utilizing Ethnic-Specific Differences in Minor Allele Frequency to Recategorize Reported Pathogenic Deafness Variants. American Journal of Human Genetics, 2014, 95, 445-453.	6.2	137

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19	Identifying Components of the NF-Î²B Pathway in the Beneficial Euprymna scolopes - Vibrio fischeri Light Organ Symbiosis. Applied and Environmental Microbiology, 2005, 71, 6934-6946.	3.1	133
20	Insights into a dinoflagellate genome through expressed sequence tag analysis. BMC Genomics, 2005, 6, 80.	2.8	130
21	Carcinoembryonic antigen-related cell adhesion molecule 16 interacts with Î±-tectorin and is mutated in autosomal dominant hearing loss (DFNA4). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4218-4223.	7.1	123
22	Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. Experimental Eye Research, 2014, 129, 93-106.	2.6	122
23	North Carolina Macular Dystrophy Is Caused by Dysregulation of the Retinal Transcription Factor PRDM13. Ophthalmology, 2016, 123, 9-18.	5.2	105
24	Prediction of cochlear implant performance by genetic mutation: The spiral ganglion hypothesis. Hearing Research, 2012, 292, 51-58.	2.0	104
25	Advancing genetic testing for deafness with genomic technology. Journal of Medical Genetics, 2013, 50, 627-634.	3.2	104
26	Molecular characterization of foveal versus peripheral human retina by single-cell RNA sequencing. Experimental Eye Research, 2019, 184, 234-242.	2.6	102
27	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
28	Exon-level expression profiling of ocular tissues. Experimental Eye Research, 2013, 111, 105-111.	2.6	94
29	De Novo and Rare Variants at Multiple Loci Support the Oligogenic Origins of Atrioventricular Septal Heart Defects. PLoS Genetics, 2016, 12, e1005963.	3.5	92
30	Effects of colonization, luminescence, and autoinducer on host transcription during development of the squid-vibrio association. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11323-11328.	7.1	90
31	Genome-wide identification of pseudogenes capable of disease-causing gene conversion. Human Mutation, 2006, 27, 545-552.	2.5	82
32	Novel Molecular and Computational Methods Improve the Accuracy of Insertion Site Analysis in Sleeping Beauty-Induced Tumors. PLoS ONE, 2011, 6, e24668.	2.5	77
33	Identification of Rtl1, a Retrotransposon-Derived Imprinted Gene, as a Novel Driver of Hepatocarcinogenesis. PLoS Genetics, 2013, 9, e1003441.	3.5	76
34	Cell of origin strongly influences genetic selection in a mouse model of T-ALL. Blood, 2011, 118, 4646-4656.	1.4	74
35	Ethnic variation in AMD-associated complement factor H polymorphism p.Tyr402His. Human Mutation, 2006, 27, 921-925.	2.5	66
36	Hypomorphic mutations inTRNT1cause retinitis pigmentosa with erythrocytic microcytosis. Human Molecular Genetics, 2016, 25, 44-56.	2.9	64

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37	Variations in NPHP5 in Patients With Nonsyndromic Leber Congenital Amaurosis and Senior-Loken Syndrome. JAMA Ophthalmology, 2011, 129, 81.	2.4	62
38	Parallelization of local BLAST service on workstation clusters. Future Generation Computer Systems, 2001, 17, 745-754.	7.5	55
39	EST-based gene discovery in pig: virtual expression patterns and comparative mapping to human. Mammalian Genome, 2003, 14, 565-579.	2.2	54
40	Characterization of Cav1.4 Complexes (Î±11.4, Î²2, and Î±2Î´4) in HEK293T Cells and in the Retina. Journal of Biological Chemistry, 2015, 290, 1505-1521.	3.4	52
41	Construction of a medicinal leech transcriptome database and its application to the identification of leech homologs of neural and innate immune genes. BMC Genomics, 2010, 11, 407.	2.8	50
42	Integration Site Choice of a Feline Immunodeficiency Virus Vector. Journal of Virology, 2006, 80, 8820-8823.	3.4	49
43	Eukaryotic operon-like transcription of functionally related genes in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 222-227.	7.1	49
44	Complement Factor H Polymorphism p.Tyr402His and Cuticular Drusen. JAMA Ophthalmology, 2007, 125, 93.	2.4	48
45	Congenital myopathy is caused by mutation of HACD1. Human Molecular Genetics, 2013, 22, 5229-5236.	2.9	48
46	Gene expression profiling of potential PPARÎ³ target genes in mouse aorta. Physiological Genomics, 2004, 18, 33-42.	2.3	47
47	Association of a Novel Mutation in the Retinol Dehydrogenase 12 (RDH12) Gene With Autosomal Dominant Retinitis Pigmentosa. JAMA Ophthalmology, 2008, 126, 1301.	2.4	47
48	Molecular response of chorioretinal endothelial cells to complement injury: implications for macular degeneration. Journal of Pathology, 2016, 238, 446-456.	4.5	47
49	Spectacle: An interactive resource for ocular single-cell RNA sequencing data analysis. Experimental Eye Research, 2020, 200, 108204.	2.6	47
50	Altered gene expression in dry age-related macular degeneration suggests early loss of choroidal endothelial cells. Molecular Vision, 2013, 19, 2274-97.	1.1	47
51	Keeping an Eye on Bardet-Biedl Syndrome: A Comprehensive Review of the Role of Bardet-Biedl Syndrome Genes in the Eye. Medical Research Archives, 2017, 5, .	0.2	45
52	An annotated cDNA library of juvenile Euprymna scolopes with and without colonization by the symbiont Vibrio fischeri. BMC Genomics, 2006, 7, 154.	2.8	43
53	Automated Construction of High-Density Comparative Maps Between Rat, Human, and Mouse. Genome Research, 2001, 11, 1935-1943.	5.5	40
54	A Hyperactive Transposase Promotes Persistent Gene Transfer of a piggyBac DNA Transposon. Molecular Therapy - Nucleic Acids, 2012, 1, e50.	5.1	39

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55	RNA Aptamer-Based Functional Ligands of the Neurotrophin Receptor, TrkB. Molecular Pharmacology, 2012, 82, 623-635.	2.3	39
56	Isolation and characterization of autotrophic, hydrogen-utilizing, perchlorate-reducing bacteria. Applied Microbiology and Biotechnology, 2005, 67, 261-268.	3.6	38
57	CFTR Î”F508 mutation has minimal effect on the gene expression profile of differentiated human airway epithelia. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2005, 289, L545-L553.	2.9	37
58	High-Density Rat Radiation Hybrid Maps Containing Over 24,000 SSLPs, Genes, and ESTs Provide a Direct Link to the Rat Genome Sequence. Genome Research, 2004, 14, 750-757.	5.5	36
59	Genome-wide analysis of copy number variants in age-related macular degeneration. Human Genetics, 2011, 129, 91-100.	3.8	36
60	Genomics-based approaches to gene discovery in innate immunity. Immunological Reviews, 2002, 190, 137-145.	6.0	35
61	Single-Cell RNA Sequencing in Human Retinal Degeneration Reveals Distinct Glial Cell Populations. Cells, 2020, 9, 438.	4.1	35
62	A Genome-Wide Association Study for Primary Open Angle Glaucoma and Macular Degeneration Reveals Novel Loci. PLoS ONE, 2013, 8, e58657.	2.5	35
63	Bulk and single-cell gene expression analyses reveal aging human choriocapillaris has pro-inflammatory phenotype. Microvascular Research, 2020, 131, 104031.	2.5	34
64	Clinical and genetic characterization of a Danish family with North Carolina macular dystrophy. Molecular Vision, 2010, 16, 2659-68.	1.1	33
65	Copy Number Variations and Primary Open-Angle Glaucoma. , 2011, 52, 7122.		31
66	AudioGene: Predicting Hearing Loss Genotypes from Phenotypes to Guide Genetic Screening. Human Mutation, 2013, 34, n/a-n/a.	2.5	31
67	Differential effects of cytokines and corticosteroids on Toll-like receptor 2 expression and activity in human airway epithelia. Respiratory Research, 2009, 10, 96.	3.6	30
68	Automated Axon Counting in Rodent Optic Nerve Sections with AxonJ. Scientific Reports, 2016, 6, 26559.	3.3	30
69	Somatic Mutagenesis with a Sleeping Beauty Transposon System Leads to Solid Tumor Formation in Zebrafish. PLoS ONE, 2011, 6, e18826.	2.5	30
70	Generation of a High-Density Rat EST Map. Genome Research, 2001, 11, 497-502.	5.5	29
71	Differential Gene Expression in Human Conducting Airway Surface Epithelia and Submucosal Glands. American Journal of Respiratory Cell and Molecular Biology, 2009, 40, 189-199.	2.9	29
72	ESTprep: preprocessing cDNA sequence reads. Bioinformatics, 2003, 19, 1318-1324.	4.1	27

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73	Choroidal endothelial and macrophage gene expression in atrophic and neovascular macular degeneration. Human Molecular Genetics, 2022, 31, 2406-2423.	2.9	26
74	Glaucoma Risk Alleles in the Ocular Hypertension Treatment Study. Ophthalmology, 2016, 123, 2527-2536.	5.2	25
75	High-Throughput Gene Discovery in the Rat. Genome Research, 2004, 14, 733-741.	5.5	24
76	A Mutation in LTBP2 Causes Congenital Glaucoma in Domestic Cats (Felis catus). PLoS ONE, 2016, 11, e0154412.	2.5	24
77	RetFM-J, an ImageJ-based module for automated counting andÂquantifying features of nuclei in retinal whole-mounts. Experimental Eye Research, 2016, 146, 386-392.	2.6	24
78	Transplantation of iPSC-TM stimulates division of trabecular meshwork cells in human eyes. Scientific Reports, 2020, 10, 2905.	3.3	24
79	Single-cell RNA sequencing in vision research: Insights into human retinal health and disease. Progress in Retinal and Eye Research, 2021, 83, 100934.	15.5	24
80	Novel TMEM98 mutations in pedigrees with autosomal dominant nanophthalmos. Molecular Vision, 2015, 21, 1017-23.	1.1	24
81	Large-scale gene discovery in human airway epithelia reveals novel transcripts. Physiological Genomics, 2004, 17, 69-77.	2.3	23
82	Quantitative measurement of retinal ganglion cell populations via histology-based random forest classification. Experimental Eye Research, 2016, 146, 370-385.	2.6	23
83	Generation of a High-Density Rat EST Map. Genome Research, 2001, 11, 497-502.	5.5	23
84	Sequencing methods and datasets to improve functional interpretation of sleeping beauty mutagenesis screens. BMC Genomics, 2014, 15, 1150.	2.8	22
85	A HomozygousNme7Mutation Is Associated withSitus Inversus Totalis. Human Mutation, 2016, 37, 727-731.	2.5	22
86	PLET1 (C11orf34), a highly expressed and processed novel gene in pig and mouse placenta, is transcribed but poorly spliced in human. Genomics, 2004, 84, 114-125.	2.9	20
87	Analysis of ASB10 variants in open angle glaucoma. Human Molecular Genetics, 2012, 21, 4543-4548.	2.9	20
88	Microarray Determination of the Expression of Drug Transporters in Humans and Animal Species Used for the Investigation of Nasal Absorption. Molecular Pharmaceutics, 2015, 12, 2742-2754.	4.6	19
89	Transposon mutagenesis identifies candidate genes that cooperate with loss of transforming growth factorâ€beta signaling in mouse intestinal neoplasms. International Journal of Cancer, 2017, 140, 853-863.	5.1	19
90	Parallel creation of non-redundant gene indices from partial mRNA transcripts. Future Generation Computer Systems, 2002, 18, 863-870.	7.5	18

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91	1274 Full-Open Reading Frames of Transcripts Expressed in the Developing Mouse Nervous System. Genome Research, 2004, 14, 2053-2063.	5.5	17
92	Myocilin Mutations in Patients With Normal-Tension Glaucoma. JAMA Ophthalmology, 2019, 137, 559.	2.5	17
93	Human photoreceptor cells from different macular subregions have distinct transcriptional profiles. Human Molecular Genetics, 2021, 30, 1543-1558.	2.9	17
94	Retinal ciliopathies through the lens of Bardet-Biedl Syndrome: Past, present and future. Progress in Retinal and Eye Research, 2022, 89, 101035.	15.5	17
95	VALIDATION OF TABLET-BASED EVALUATION OF COLOR FUNDUS IMAGES. Retina, 2012, 32, 1629-1635.	1.7	16
96	Computational Quantification of Complex Fundus Phenotypes in Age-Related Macular Degeneration and Stargardt Disease. , 2011, 52, 2976.		14
97	Tank-Binding Kinase 1 () Gene and Open-Angle Glaucomas (An American Ophthalmological Society) Tj ETQq1 1 0.784314 rgBT /Overl	1.4	14
98	A targeted sequencing study of glutamatergic candidate genes in suicide attempters with bipolar disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 1080-1087.	1.7	13
99	Analysis of 14-3-3 isoforms expressed in photoreceptors. Experimental Eye Research, 2018, 170, 108-116.	2.6	12
100	Axonopathy precedes cell death in ocular damage mediated by blast exposure. Scientific Reports, 2021, 11, 11774.	3.3	12
101	Correlation between electroretinography, foveal anatomy and visual acuity in albinism. Documenta Ophthalmologica, 2019, 139, 21-32.	2.2	11
102	Microarray mRNA Expression Profiling to Study Cystic Fibrosis. Methods in Molecular Biology, 2011, 742, 193-212.	0.9	11
103	Prioritizing regions of candidate genes for efficient mutation screening. Human Mutation, 2006, 27, 195-200.	2.5	10
104	Heterozygous Triplication of Upstream Regulatory Sequences Leads to Dysregulation of Matrix Metalloproteinase 19 in Patients with Cavitary Optic Disc Anomaly. Human Mutation, 2015, 36, 369-378.	2.5	10
105	Using the Phenome and Genome to Improve Genetic Diagnosis for Deafness. Otolaryngology - Head and Neck Surgery, 2012, 147, 975-977.	1.9	9
106	SQSTM1 Mutations and Glaucoma. PLoS ONE, 2016, 11, e0156001.	2.5	9
107	Exome-based investigation of the genetic basis of human pigmentary glaucoma. BMC Genomics, 2021, 22, 477.	2.8	9
108	Automated Quantification of Inherited Phenotypes from Color Images: A Twin Study of the Variability of Optic Nerve Head Shape. , 2010, 51, 5870.		8

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109	Audioprofile Surfaces. Annals of Otology, Rhinology and Laryngology, 2016, 125, 361-368.	1.1	8
110	A comprehensive nonredundant expressed sequence tag collection for the developing Rattus norvegicus heart. Physiological Genomics, 2004, 17, 245-252.	2.3	7
111	Automated Discovery and Quantification of Image-Based Complex Phenotypes: A Twin Study of Drusen Phenotypes in Age-Related Macular Degeneration. , 2011, 52, 9195.		7
112	Prioritization of Retinal Disease Genes: An Integrative Approach. Human Mutation, 2013, 34, 853-859.	2.5	7
113	Alternative Parallelization Strategies in EST Clustering. Lecture Notes in Computer Science, 2003, , 384-393.	1.3	7
114	Gene transcript clustering: a comparison of parallel approaches. Future Generation Computer Systems, 2005, 21, 731-735.	7.5	6
115	Genomic Organization of TBK1 Copy Number Variations in Glaucoma Patients. Journal of Glaucoma, 2017, 26, 1063-1067.	1.6	6
116	Genetic Association between MMP9 and Choroidal Neovascularization in Age-Related Macular Degeneration. Ophthalmology Science, 2021, 1, 100002.	2.5	6
117	IDOCS: Intelligent Distributed Ontology Consensus Systemâ€”The Use of Machine Learning in Retinal Drusen Phenotyping. , 2007, 48, 2278.		5
118	Automated segmentation of choroidal layers from 3-dimensional macular optical coherence tomography scans. Journal of Neuroscience Methods, 2021, 360, 109267.	2.5	5
119	LADD syndrome with glaucoma is caused by a novel gene. Molecular Vision, 2017, 23, 179-184.	1.1	5
120	Identifying Candidate Disease Genes with High-Performance Computing. Journal of Supercomputing, 2003, 26, 7-24.	3.6	4
121	AUTOIMMUNE RETINOPATHY MIMICKING HERITABLE RETINAL DEGENERATION IN A PATIENT WITH COMMON VARIABLE IMMUNE DEFICIENCY. Retinal Cases and Brief Reports, 2022, 16, 111-117.	0.6	4
122	Clinical albinism score, presence of nystagmus and optic nerves defects are correlated with visual outcome in patients with oculocutaneous albinism. Ophthalmic Genetics, 2021, 42, 539-552.	1.2	4
123	Cordova: Web-based management of genetic variation data. Bioinformatics, 2014, 30, 3438-3439.	4.1	3
124	Stereo Photo Measured ONH Shape Predicts Development of POAG in Subjects With Ocular Hypertension. , 2015, 56, 4470.		3
125	Sensitive quantification of m.3243A>G mutational proportion in non-retinal tissues and its relationship with visual symptoms. Human Molecular Genetics, 2021, , .	2.9	3
126	XenoCluster: A Grid Computing Approach to Finding Ancient Evolutionary Genetic Anomalies. Lecture Notes in Computer Science, 2005, , 355-366.	1.3	3

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127	GenoMap: A distributed system for unifying genotyping and genetic linkage analysis. Parallel Computing, 1998, 24, 1567-1592.	2.1	2
128	A parallel/distributed architecture for hierarchically heterogeneous web-based cooperative applications. Future Generation Computer Systems, 2001, 17, 783-793.	7.5	2
129	A knowledge-based approach to predict intragenic deletions or duplications. Bioinformatics, 2008, 24, 1975-1979.	4.1	2
130	Automated discovery of structural features of the optic nerve head on the basis of image and genetic data. , 2014, , .		2
131	A novel mutation (LEU396ARG) in OPA1 is associated with a severe phenotype in a large dominant optic atrophy pedigree. Eye, 2018, 32, 843-845.	2.1	2
132	Evaluation of sFLT1 protein levels in human eyes with the FLT1 rs9943922 polymorphism. Ophthalmic Genetics, 2018, 39, 68-72.	1.2	2
133	INFORMATICS FOR EFFICIENT EST-BASED GENE DISCOVERY IN NORMALIZED AND SUBTRACTED CDNA LIBRARIES. , 2004, , 435-456.		2
134	TRANSCRIPT ANNOTATION PRIORITIZATION AND SCREENING SYSTEM (TrAPSS) FOR MUTATION SCREENING. Journal of Bioinformatics and Computational Biology, 2007, 05, 1155-1172.	0.8	1
135	Sequencing and disease variation detection tools and techniques. , 2011, , .		1
136	Computational identification of operon-like transcriptional loci in eukaryotes. Computers in Biology and Medicine, 2013, 43, 738-743.	7.0	1
137	Changes in quantitative 3D shape features of the optic nerve head associated with age. Proceedings of SPIE, 2013, , .	0.8	1
138	Selection of Phototransduction Genes inHomo sapiens. , 2013, 54, 5489.		1
139	<title>Mining biological databases for candidate disease genes</title>. , 2001, 4528, 169.		0
140	Multi-granularity Parallel Computing in a Genome-Scale Molecular Evolution Application. Lecture Notes in Computer Science, 2009, 5698, 49-59.	1.3	0
141	AudioGene: Computer-based prediction of genetic factors involved in non-syndromic hearing impairment. , 2011, , .		0
142	Validation of computational prediction of horizontal gene transfer eventsâ€"XenoCluster. Journal of Supercomputing, 2011, 57, 141-150.	3.6	0