

Todd E Scheetz

List of Publications by Year in descending order

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142
papers

9,732
citations

53794

45
h-index

39675

94
g-index

145
all docs

145
docs citations

145
times ranked

15164
citing authors

#	ARTICLE	IF	CITATIONS
1	AUTOIMMUNE RETINOPATHY MIMICKING HERITABLE RETINAL DEGENERATION IN A PATIENT WITH COMMON VARIABLE IMMUNE DEFICIENCY. <i>Retinal Cases and Brief Reports</i> , 2022, 16, 111-117.	0.6	4
2	Choroidal endothelial and macrophage gene expression in atrophic and neovascular macular degeneration. <i>Human Molecular Genetics</i> , 2022, 31, 2406-2423.	2.9	26
3	Retinal ciliopathies through the lens of Bardet-Biedl Syndrome: Past, present and future. <i>Progress in Retinal and Eye Research</i> , 2022, 89, 101035.	15.5	17
4	Genetic Association between MMP9 and Choroidal Neovascularization in Age-Related Macular Degeneration. <i>Ophthalmology Science</i> , 2021, 1, 100002.	2.5	6
5	Human photoreceptor cells from different macular subregions have distinct transcriptional profiles. <i>Human Molecular Genetics</i> , 2021, 30, 1543-1558.	2.9	17
6	Axonopathy precedes cell death in ocular damage mediated by blast exposure. <i>Scientific Reports</i> , 2021, 11, 11774.	3.3	12
7	Exome-based investigation of the genetic basis of human pigmentary glaucoma. <i>BMC Genomics</i> , 2021, 22, 477.	2.8	9
8	Clinical albinism score, presence of nystagmus and optic nerves defects are correlated with visual outcome in patients with oculocutaneous albinism. <i>Ophthalmic Genetics</i> , 2021, 42, 539-552.	1.2	4
9	Single-cell RNA sequencing in vision research: Insights into human retinal health and disease. <i>Progress in Retinal and Eye Research</i> , 2021, 83, 100934.	15.5	24
10	Automated segmentation of choroidal layers from 3-dimensional macular optical coherence tomography scans. <i>Journal of Neuroscience Methods</i> , 2021, 360, 109267.	2.5	5
11	Sensitive quantification of m.3243A>G mutational proportion in non-retinal tissues and its relationship with visual symptoms. <i>Human Molecular Genetics</i> , 2021, , .	2.9	3
12	Spectacle: An interactive resource for ocular single-cell RNA sequencing data analysis. <i>Experimental Eye Research</i> , 2020, 200, 108204.	2.6	47
13	Bulk and single-cell gene expression analyses reveal aging human choriocapillaris has pro-inflammatory phenotype. <i>Microvascular Research</i> , 2020, 131, 104031.	2.5	34
14	Single-Cell RNA Sequencing in Human Retinal Degeneration Reveals Distinct Glial Cell Populations. <i>Cells</i> , 2020, 9, 438.	4.1	35
15	Transplantation of iPSC-TM stimulates division of trabecular meshwork cells in human eyes. <i>Scientific Reports</i> , 2020, 10, 2905.	3.3	24
16	Single-cell transcriptomics of the human retinal pigment epithelium and choroid in health and macular degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24100-24107.	7.1	234
17	Molecular characterization of foveal versus peripheral human retina by single-cell RNA sequencing. <i>Experimental Eye Research</i> , 2019, 184, 234-242.	2.6	102
18	Correlation between electroretinography, foveal anatomy and visual acuity in albinism. <i>Documenta Ophthalmologica</i> , 2019, 139, 21-32.	2.2	11

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19	Myocilin Mutations in Patients With Normal-Tension Glaucoma. <i>JAMA Ophthalmology</i> , 2019, 137, 559.	2.5	17
20	Analysis of 14-3-3 isoforms expressed in photoreceptors. <i>Experimental Eye Research</i> , 2018, 170, 108-116.	2.6	12
21	A novel mutation (LEU396ARG) in OPA1 is associated with a severe phenotype in a large dominant optic atrophy pedigree. <i>Eye</i> , 2018, 32, 843-845.	2.1	2
22	Evaluation of sFLT1 protein levels in human eyes with the FLT1 rs9943922 polymorphism. <i>Ophthalmic Genetics</i> , 2018, 39, 68-72.	1.2	2
23	Clinically Focused Molecular Investigation of 1000 Consecutive Families with Inherited Retinal Disease. <i>Ophthalmology</i> , 2017, 124, 1314-1331.	5.2	312
24	Genomic Organization of TBK1 Copy Number Variations in Glaucoma Patients. <i>Journal of Glaucoma</i> , 2017, 26, 1063-1067.	1.6	6
25	Transposon mutagenesis identifies candidate genes that cooperate with loss of transforming growth factor β signaling in mouse intestinal neoplasms. <i>International Journal of Cancer</i> , 2017, 140, 853-863.	5.1	19
26	Keeping an Eye on Bardet-Biedl Syndrome: A Comprehensive Review of the Role of Bardet-Biedl Syndrome Genes in the Eye. <i>Medical Research Archives</i> , 2017, 5, .	0.2	45
27	LADD syndrome with glaucoma is caused by a novel gene. <i>Molecular Vision</i> , 2017, 23, 179-184.	1.1	5
28	A Mutation in LTBP2 Causes Congenital Glaucoma in Domestic Cats (<i>Felis catus</i>). <i>PLoS ONE</i> , 2016, 11, e0154412.	2.5	24
29	SQSTM1 Mutations and Glaucoma. <i>PLoS ONE</i> , 2016, 11, e0156001.	2.5	9
30	A targeted sequencing study of glutamatergic candidate genes in suicide attempters with bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 1080-1087.	1.7	13
31	Glaucoma Risk Alleles in the Ocular Hypertension Treatment Study. <i>Ophthalmology</i> , 2016, 123, 2527-2536.	5.2	25
32	Automated Axon Counting in Rodent Optic Nerve Sections with AxonJ. <i>Scientific Reports</i> , 2016, 6, 26559.	3.3	30
33	North Carolina Macular Dystrophy Is Caused by Dysregulation of the Retinal Transcription Factor PRDM13. <i>Ophthalmology</i> , 2016, 123, 9-18.	5.2	105
34	Audioprofile Surfaces. <i>Annals of Otology, Rhinology and Laryngology</i> , 2016, 125, 361-368.	1.1	8
35	A Homozygous <i>Nme7</i> Mutation Is Associated with <i>Situs Inversus Totalis</i> . <i>Human Mutation</i> , 2016, 37, 727-731.	2.5	22
36	Molecular response of chorioretinal endothelial cells to complement injury: implications for macular degeneration. <i>Journal of Pathology</i> , 2016, 238, 446-456.	4.5	47

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37	Quantitative measurement of retinal ganglion cell populations via histology-based random forest classification. <i>Experimental Eye Research</i> , 2016, 146, 370-385.	2.6	23
38	RetFM-J, an ImageJ-based module for automated counting and quantifying features of nuclei in retinal whole-mounts. <i>Experimental Eye Research</i> , 2016, 146, 386-392.	2.6	24
39	Hypomorphic mutations in <i>TRNT1</i> cause retinitis pigmentosa with erythrocytic microcytosis. <i>Human Molecular Genetics</i> , 2016, 25, 44-56.	2.9	64
40	De Novo and Rare Variants at Multiple Loci Support the Oligogenic Origins of Atrioventricular Septal Heart Defects. <i>PLoS Genetics</i> , 2016, 12, e1005963.	3.5	92
41	Tank-Binding Kinase 1 () Gene and Open-Angle Glaucomas (An American Ophthalmological Society) Tj ETQq1 1 0.784314 rgBT /Overlo	1.4	14
42	Heterozygous Triplication of Upstream Regulatory Sequences Leads to Dysregulation of Matrix Metalloproteinase 19 in Patients with Cavitory Optic Disc Anomaly. <i>Human Mutation</i> , 2015, 36, 369-378.	2.5	10
43	Stereo Photo Measured ONH Shape Predicts Development of POAG in Subjects With Ocular Hypertension. , 2015, 56, 4470.		3
44	Characterization of Cav1.4 Complexes ($\hat{1}\pm 11.4$, $\hat{1}^22$, and $\hat{1}\pm 2\hat{1}^4$) in HEK293T Cells and in the Retina. <i>Journal of Biological Chemistry</i> , 2015, 290, 1505-1521.	3.4	52
45	Microarray Determination of the Expression of Drug Transporters in Humans and Animal Species Used for the Investigation of Nasal Absorption. <i>Molecular Pharmaceutics</i> , 2015, 12, 2742-2754.	4.6	19
46	Novel TMEM98 mutations in pedigrees with autosomal dominant nanophthalmos. <i>Molecular Vision</i> , 2015, 21, 1017-23.	1.1	24
47	Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. <i>Experimental Eye Research</i> , 2014, 129, 93-106.	2.6	122
48	Automated discovery of structural features of the optic nerve head on the basis of image and genetic data. , 2014, , .		2
49	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53.	9.6	101
50	Sequencing methods and datasets to improve functional interpretation of sleeping beauty mutagenesis screens. <i>BMC Genomics</i> , 2014, 15, 1150.	2.8	22
51	Cordova: Web-based management of genetic variation data. <i>Bioinformatics</i> , 2014, 30, 3438-3439.	4.1	3
52	Utilizing Ethnic-Specific Differences in Minor Allele Frequency to Recategorize Reported Pathogenic Deafness Variants. <i>American Journal of Human Genetics</i> , 2014, 95, 445-453.	6.2	137
53	Prioritization of Retinal Disease Genes: An Integrative Approach. <i>Human Mutation</i> , 2013, 34, 853-859.	2.5	7
54	AudioGene: Predicting Hearing Loss Genotypes from Phenotypes to Guide Genetic Screening. <i>Human Mutation</i> , 2013, 34, n/a-n/a.	2.5	31

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55	Computational identification of operon-like transcriptional loci in eukaryotes. <i>Computers in Biology and Medicine</i> , 2013, 43, 738-743.	7.0	1
56	Exon-level expression profiling of ocular tissues. <i>Experimental Eye Research</i> , 2013, 111, 105-111.	2.6	94
57	Changes in quantitative 3D shape features of the optic nerve head associated with age. <i>Proceedings of SPIE</i> , 2013, , .	0.8	1
58	Identification of Rtl1, a Retrotransposon-Derived Imprinted Gene, as a Novel Driver of Hepatocarcinogenesis. <i>PLoS Genetics</i> , 2013, 9, e1003441.	3.5	76
59	Congenital myopathy is caused by mutation of HACD1. <i>Human Molecular Genetics</i> , 2013, 22, 5229-5236.	2.9	48
60	Advancing genetic testing for deafness with genomic technology. <i>Journal of Medical Genetics</i> , 2013, 50, 627-634.	3.2	104
61	Selection of Phototransduction Genes in <i>Homo sapiens</i> . , 2013, 54, 5489.		1
62	A Genome-Wide Association Study for Primary Open Angle Glaucoma and Macular Degeneration Reveals Novel Loci. <i>PLoS ONE</i> , 2013, 8, e58657.	2.5	35
63	Altered gene expression in dry age-related macular degeneration suggests early loss of choroidal endothelial cells. <i>Molecular Vision</i> , 2013, 19, 2274-97.	1.1	47
64	Using the Phenome and Genome to Improve Genetic Diagnosis for Deafness. <i>Otolaryngology - Head and Neck Surgery</i> , 2012, 147, 975-977.	1.9	9
65	A Hyperactive Transposase Promotes Persistent Gene Transfer of a piggyBac DNA Transposon. <i>Molecular Therapy - Nucleic Acids</i> , 2012, 1, e50.	5.1	39
66	Analysis of ASB10 variants in open angle glaucoma. <i>Human Molecular Genetics</i> , 2012, 21, 4543-4548.	2.9	20
67	<i>Sleeping Beauty</i> mutagenesis reveals cooperating mutations and pathways in pancreatic adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5934-5941.	7.1	201
68	VALIDATION OF TABLET-BASED EVALUATION OF COLOR FUNDUS IMAGES. <i>Retina</i> , 2012, 32, 1629-1635.	1.7	16
69	RNA Aptamer-Based Functional Ligands of the Neurotrophin Receptor, TrkB. <i>Molecular Pharmacology</i> , 2012, 82, 623-635.	2.3	39
70	Prediction of cochlear implant performance by genetic mutation: The spiral ganglion hypothesis. <i>Hearing Research</i> , 2012, 292, 51-58.	2.0	104
71	Clonal selection drives genetic divergence of metastatic medulloblastoma. <i>Nature</i> , 2012, 482, 529-533.	27.8	376
72	AudioGene: Computer-based prediction of genetic factors involved in non-syndromic hearing impairment. , 2011, , .		0

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73	Sequencing and disease variation detection tools and techniques. , 2011, , .		1
74	Computational Quantification of Complex Fundus Phenotypes in Age-Related Macular Degeneration and Stargardt Disease. , 2011, 52, 2976.		14
75	Automated Discovery and Quantification of Image-Based Complex Phenotypes: A Twin Study of Drusen Phenotypes in Age-Related Macular Degeneration. , 2011, 52, 9195.		7
76	Variations in NPHP5 in Patients With Nonsyndromic Leber Congenital Amaurosis and Senior-Loken Syndrome. JAMA Ophthalmology, 2011, 129, 81.	2.4	62
77	Cell of origin strongly influences genetic selection in a mouse model of T-ALL. Blood, 2011, 118, 4646-4656.	1.4	74
78	Validation of computational prediction of horizontal gene transfer eventsâ€”XenoCluster. Journal of Supercomputing, 2011, 57, 141-150.	3.6	0
79	Genome-wide analysis of copy number variants in age-related macular degeneration. Human Genetics, 2011, 129, 91-100.	3.8	36
80	Copy Number Variations and Primary Open-Angle Glaucoma. , 2011, 52, 7122.		31
81	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
82	Copy number variations on chromosome 12q14 in patients with normal tension glaucoma. Human Molecular Genetics, 2011, 20, 2482-2494.	2.9	189
83	Exome sequencing and analysis of induced pluripotent stem cells identify the cilia-related gene <i>male germ cell-associated kinase</i> (<i>MAK</i>) 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
84	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
85	Microarray mRNA Expression Profiling to Study Cystic Fibrosis. Methods in Molecular Biology, 2011, 742, 193-212.	0.9	11
86	Somatic Mutagenesis with a Sleeping Beauty Transposon System Leads to Solid Tumor Formation in Zebrafish. PLoS ONE, 2011, 6, e18826.	2.5	30
87	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
88	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
89	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
90	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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91	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
92	Clinical and genetic characterization of a Danish family with North Carolina macular dystrophy. Molecular Vision, 2010, 16, 2659-68.	1.1	33
93	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
94	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
95	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
96	Multi-granularity Parallel Computing in a Genome-Scale Molecular Evolution Application. Lecture Notes in Computer Science, 2009, 5698, 49-59.	1.3	0
97	A BBSome Subunit Links Ciliogenesis, Microtubule Stability, and Acetylation. Developmental Cell, 2008, 15, 854-865.	7.0	272
98	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
99	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
100	A knowledge-based approach to predict intragenic deletions or duplications. Bioinformatics, 2008, 24, 1975-1979.	4.1	2
101	TRANSCRIPT ANNOTATION PRIORITIZATION AND SCREENING SYSTEM (TrAPSS) FOR MUTATION SCREENING. Journal of Bioinformatics and Computational Biology, 2007, 05, 1155-1172.	0.8	1
102	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
103	IDOCS: Intelligent Distributed Ontology Consensus System—The Use of Machine Learning in Retinal Drusen Phenotyping. , 2007, 48, 2278.		5
104	Complement Factor H Polymorphism p.Tyr402His and Cuticular Drusen. JAMA Ophthalmology, 2007, 125, 93.	2.4	48
105	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
106	Prioritizing regions of candidate genes for efficient mutation screening. Human Mutation, 2006, 27, 195-200.	2.5	10
107	Genome-wide identification of pseudogenes capable of disease-causing gene conversion. Human Mutation, 2006, 27, 545-552.	2.5	82
108	Ethnic variation in AMD-associated complement factor H polymorphism p.Tyr402His. Human Mutation, 2006, 27, 921-925.	2.5	66

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109	Integration Site Choice of a Feline Immunodeficiency Virus Vector. <i>Journal of Virology</i> , 2006, 80, 8820-8823.	3.4	49
110	Regulation of gene expression in the mammalian eye and its relevance to eye disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14429-14434.	7.1	190
111	Homozygosity mapping with SNP arrays identifies <i>TRIM32</i> , an E3 ubiquitin ligase, as a Bardet-Biedl syndrome gene (<i>BBS11</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6287-6292.	7.1	378
112	Gene transcript clustering: a comparison of parallel approaches. <i>Future Generation Computer Systems</i> , 2005, 21, 731-735.	7.5	6
113	Insights into a dinoflagellate genome through expressed sequence tag analysis. <i>BMC Genomics</i> , 2005, 6, 80.	2.8	130
114	CFTR ^{F508} mutation has minimal effect on the gene expression profile of differentiated human airway epithelia. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2005, 289, L545-L553.	2.9	37
115	Identifying Components of the NF- κ B Pathway in the Beneficial <i>Euprymna scolopes</i> - <i>Vibrio fischeri</i> Light Organ Symbiosis. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6934-6946.	3.1	133
116	Isolation and characterization of autotrophic, hydrogen-utilizing, perchlorate-reducing bacteria. <i>Applied Microbiology and Biotechnology</i> , 2005, 67, 261-268.	3.6	38
117	XenoCluster: A Grid Computing Approach to Finding Ancient Evolutionary Genetic Anomalies. <i>Lecture Notes in Computer Science</i> , 2005, , 355-366.	1.3	3
118	Gene expression profiling of potential PPAR γ target genes in mouse aorta. <i>Physiological Genomics</i> , 2004, 18, 33-42.	2.3	47
119	A comprehensive nonredundant expressed sequence tag collection for the developing <i>Rattus norvegicus</i> heart. <i>Physiological Genomics</i> , 2004, 17, 245-252.	2.3	7
120	1274 Full-Open Reading Frames of Transcripts Expressed in the Developing Mouse Nervous System. <i>Genome Research</i> , 2004, 14, 2053-2063.	5.5	17
121	High-Density Rat Radiation Hybrid Maps Containing Over 24,000 SSLPs, Genes, and ESTs Provide a Direct Link to the Rat Genome Sequence. <i>Genome Research</i> , 2004, 14, 750-757.	5.5	36
122	High-Throughput Gene Discovery in the Rat. <i>Genome Research</i> , 2004, 14, 733-741.	5.5	24
123	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	5.5	486
124	Migration of the Plastid Genome to the Nucleus in a Peridinin Dinoflagellate. <i>Current Biology</i> , 2004, 14, 213-218.	3.9	172
125	PLET1 (C11orf34), a highly expressed and processed novel gene in pig and mouse placenta, is transcribed but poorly spliced in human. <i>Genomics</i> , 2004, 84, 114-125.	2.9	20
126	Large-scale gene discovery in human airway epithelia reveals novel transcripts. <i>Physiological Genomics</i> , 2004, 17, 69-77.	2.3	23

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127	INFORMATICS FOR EFFICIENT EST-BASED GENE DISCOVERY IN NORMALIZED AND SUBTRACTED CDNA LIBRARIES. , 2004, , 435-456.		2
128	Identifying Candidate Disease Genes with High-Performance Computing. Journal of Supercomputing, 2003, 26, 7-24.	3.6	4
129	EST-based gene discovery in pig: virtual expression patterns and comparative mapping to human. Mammalian Genome, 2003, 14, 565-579.	2.2	54
130	ESTprep: preprocessing cDNA sequence reads. Bioinformatics, 2003, 19, 1318-1324.	4.1	27
131	Alternative Parallelization Strategies in EST Clustering. Lecture Notes in Computer Science, 2003, , 384-393.	1.3	7
132	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
133	Genomics-based approaches to gene discovery in innate immunity. Immunological Reviews, 2002, 190, 137-145.	6.0	35
134	Parallel creation of non-redundant gene indices from partial mRNA transcripts. Future Generation Computer Systems, 2002, 18, 863-870.	7.5	18
135	Automated Construction of High-Density Comparative Maps Between Rat, Human, and Mouse. Genome Research, 2001, 11, 1935-1943.	5.5	40
136	<title>Mining biological databases for candidate disease genes</title>. , 2001, 4528, 169.		0
137	Parallelization of local BLAST service on workstation clusters. Future Generation Computer Systems, 2001, 17, 745-754.	7.5	55
138	A parallel/distributed architecture for hierarchically heterogeneous web-based cooperative applications. Future Generation Computer Systems, 2001, 17, 783-793.	7.5	2
139	Generation of a High-Density Rat EST Map. Genome Research, 2001, 11, 497-502.	5.5	29
140	Generation of a High-Density Rat EST Map. Genome Research, 2001, 11, 497-502.	5.5	23
141	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
142	GenoMap: A distributed system for unifying genotyping and genetic linkage analysis. Parallel Computing, 1998, 24, 1567-1592.	2.1	2