

Winston A Hide

List of Publications by Year in descending order

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175
papers

25,224
citations

15504

65
h-index

7518

151
g-index

267
all docs

267
docs citations

267
times ranked

44928
citing authors

#	ARTICLE	IF	CITATIONS
1	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
3	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
4	Aberrant lipid metabolism disrupts calcium homeostasis causing liver endoplasmic reticulum stress in obesity. <i>Nature</i> , 2011, 473, 528-531.	27.8	864
5	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
6	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. <i>Nature Biotechnology</i> , 2014, 32, 246-251.	17.5	722
7	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
8	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	28.9	667
9	The future of biocuration. <i>Nature</i> , 2008, 455, 47-50.	27.8	648
10	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , 2012, 44, 67-72.	21.4	545
11	miR-24 Inhibits Cell Proliferation by Targeting E2F2, MYC, and Other Cell-Cycle Genes via Binding to 3' UTR MicroRNA Recognition Elements. <i>Molecular Cell</i> , 2009, 35, 610-625.	9.7	544
12	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	27.8	537
13	Parental origin of sequence variants associated with complex diseases. <i>Nature</i> , 2009, 462, 868-874.	27.8	521
14	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	21.4	501
15	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
16	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
17	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489.	21.4	402
18	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362

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19	Enabling the genomic revolution in Africa. <i>Science</i> , 2014, 344, 1346-1348.	12.6	361
20	Quantitating the Multiplicity of Infection with Human Immunodeficiency Virus Type 1 Subtype C Reveals a Non-Poisson Distribution of Transmitted Variants. <i>Journal of Virology</i> , 2009, 83, 3556-3567.	3.4	354
21	Is the guinea-pig a rodent?. <i>Nature</i> , 1991, 351, 649-652.	27.8	318
22	The ESAT-6 gene cluster of <i>Mycobacterium tuberculosis</i> and other high G+C Gram-positive bacteria. <i>Genome Biology</i> , 2001, 2, research0044.1.	9.6	302
23	Genome-wide analysis of cancer/testis gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20422-20427.	7.1	295
24	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
25	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. <i>Nature Genetics</i> , 2011, 43, 561-564.	21.4	289
26	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
27	ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. <i>Bioinformatics</i> , 2010, 26, 2354-2356.	4.1	247
28	Capture of MicroRNA-Bound mRNAs Identifies the Tumor Suppressor miR-34a as a Regulator of Growth Factor Signaling. <i>PLoS Genetics</i> , 2011, 7, e1002363.	3.5	222
29	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	6.4	199
30	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
31	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. <i>PLoS Genetics</i> , 2014, 10, e1004517.	3.5	191
32	Abdominal Aortic Aneurysm Is Associated with a Variant in Low-Density Lipoprotein Receptor-Related Protein 1. <i>American Journal of Human Genetics</i> , 2011, 89, 619-627.	6.2	185
33	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	3.5	181
34	d2_cluster: A Validated Method for Clustering EST and Full-Length cDNA Sequences. <i>Genome Research</i> , 1999, 9, 1135-1142.	5.5	176
35	A Comprehensive Approach to Clustering of Expressed Human Gene Sequence: The Sequence Tag Alignment and Consensus Knowledge Base. <i>Genome Research</i> , 1999, 9, 1143-1155.	5.5	175
36	Cell-specific translational profiling in acute kidney injury. <i>Journal of Clinical Investigation</i> , 2014, 124, 1242-1254.	8.2	172

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37	Integration of text- and data-mining using ontologies successfully selects disease gene candidates. <i>Nucleic Acids Research</i> , 2005, 33, 1544-1552.	14.5	167
38	A Pathway-Based View of Human Diseases and Disease Relationships. <i>PLoS ONE</i> , 2009, 4, e4346.	2.5	158
39	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. <i>PLoS Biology</i> , 2003, 1, e74.	5.6	156
40	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008, 26, 164-167.	17.5	155
41	Mutations in a novel retina-specific gene cause autosomal dominant retinitis pigmentosa. <i>Nature Genetics</i> , 1999, 22, 255-259.	21.4	154
42	A Genome-wide siRNA Screen Identifies Proteasome Addiction as a Vulnerability of Basal-like Triple-Negative Breast Cancer Cells. <i>Cancer Cell</i> , 2013, 24, 182-196.	16.8	147
43	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. <i>Genome Research</i> , 2003, 13, 1222-1230.	5.5	144
44	Computational disease gene identification: a concert of methods prioritizes type 2 diabetes and obesity candidate genes. <i>Nucleic Acids Research</i> , 2006, 34, 3067-3081.	14.5	134
45	Transmission of HIV-1 CTL Escape Variants Provides HLA-Mismatched Recipients with a Survival Advantage. <i>PLoS Pathogens</i> , 2008, 4, e1000033.	4.7	129
46	Project MinE: study design and pilot analyses of a large-scale whole-genome sequencing study in amyotrophic lateral sclerosis. <i>European Journal of Human Genetics</i> , 2018, 26, 1537-1546.	2.8	129
47	MicroRNA Expression Profile in Human Macrophages in Response to <i>Leishmania major</i> Infection. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2478.	3.0	125
48	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
49	STACK: Sequence Tag Alignment and Consensus Knowledgebase. <i>Nucleic Acids Research</i> , 2001, 29, 234-238.	14.5	112
50	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5289-5294.	7.1	111
51	The generation and utilization of a cancer-oriented representation of the human transcriptome by using expressed sequence tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13418-13423.	7.1	105
52	miR-200 promotes the mesenchymal to epithelial transition by suppressing multiple members of the Zeb2 and Snail1 transcriptional repressor complexes. <i>Oncogene</i> , 2016, 35, 158-172.	5.9	105
53	Transcriptomic Signature of <i>Leishmania</i> Infected Mice Macrophages: A Metabolic Point of View. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1763.	3.0	103
54	Alternative Gene Form Discovery and Candidate Gene Selection from Gene Indexing Projects. <i>Genome Research</i> , 1998, 8, 276-290.	5.5	102

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55	Integrated Genomic Analysis of Diverse Induced Pluripotent Stem Cells from the Progenitor Cell Biology Consortium. <i>Stem Cell Reports</i> , 2016, 7, 110-125.	4.8	101
56	Mining Biological Pathways Using WikiPathways Web Services. <i>PLoS ONE</i> , 2009, 4, e6447.	2.5	100
57	Sex-specific and blood meal-induced proteins of <i>Anopheles gambiae</i> midguts: analysis by two-dimensional gel electrophoresis. <i>Malaria Journal</i> , 2003, 2, 1.	2.3	96
58	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	3.5	95
59	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. <i>Genome Research</i> , 2016, 26, 271-277.	5.5	94
60	Comparison of glioma stem cells to neural stem cells from the adult human brain identifies dysregulated Wnt- signaling and a fingerprint associated with clinical outcome. <i>Experimental Cell Research</i> , 2013, 319, 2230-2243.	2.6	92
61	ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009, 93, 213-220.	2.9	87
62	A network of epigenetic regulators guides developmental haematopoiesis in vivo. <i>Nature Cell Biology</i> , 2013, 15, 1516-1525.	10.3	81
63	Rapid evolution of cancer/testis genes on the X chromosome. <i>BMC Genomics</i> , 2007, 8, 129.	2.8	80
64	Novel Developmental Analyses Identify Longitudinal Patterns of Early Gut Microbiota that Affect Infant Growth. <i>PLoS Computational Biology</i> , 2013, 9, e1003042.	3.2	76
65	Association of TRIM22 with the Type 1 Interferon Response and Viral Control during Primary HIV-1 Infection. <i>Journal of Virology</i> , 2011, 85, 208-216.	3.4	66
66	Biological Evaluation of d^2 , an Algorithm for High-Performance Sequence Comparison. <i>Journal of Computational Biology</i> , 1994, 1, 199-215.	1.6	63
67	A data-driven approach links microglia to pathology and prognosis in amyotrophic lateral sclerosis. <i>Acta Neuropathologica Communications</i> , 2017, 5, 23.	5.2	63
68	The Molecular Taxonomy and Evolution of the Guinea Pig. <i>Journal of Heredity</i> , 1992, 83, 174-181.	2.4	61
69	A functional genomic screen reveals novel host genes that mediate interferon- α 's effects against hepatitis C virus. <i>Journal of Hepatology</i> , 2012, 56, 326-333.	3.7	60
70	Transcriptome-Wide Assessment of Human Brain and Lymphocyte Senescence. <i>PLoS ONE</i> , 2008, 3, e3024.	2.5	60
71	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	14.5	57
72	Prenatal Lead Levels, Plasma Amyloid β Levels, and Gene Expression in Young Adulthood. <i>Environmental Health Perspectives</i> , 2012, 120, 702-707.	6.0	57

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73	Ten Simple Rules for Organizing a Virtual Conference“Anywhere. <i>PLoS Computational Biology</i> , 2010, 6, e1000650.	3.2	54
74	Compound heterozygous variants in <i>NBAS</i> as a cause of atypical osteogenesis imperfecta. <i>Bone</i> , 2017, 94, 65-74.	2.9	54
75	Eukaryotic genes in <i>Mycobacterium tuberculosis</i> could have a role in pathogenesis and immunomodulation. <i>Trends in Genetics</i> , 2002, 18, 5-8.	6.7	53
76	edgeRun: an R package for sensitive, functionally relevant differential expression discovery using an unconditional exact test. <i>Bioinformatics</i> , 2015, 31, 2589-2590.	4.1	53
77	Circadian Gene Variants and Susceptibility to Type 2 Diabetes: A Pilot Study. <i>PLoS ONE</i> , 2012, 7, e32670.	2.5	52
78	Sequencing of Captive Target Transcripts Identifies the Network of Regulated Genes and Functions of Primate-Specific miR-522. <i>Cell Reports</i> , 2014, 8, 1225-1239.	6.4	50
79	Whole-genome sequencing reveals new Alzheimer's disease-associated rare variants in loci related to synaptic function and neuronal development. <i>Alzheimer's and Dementia</i> , 2021, 17, 1509-1527.	0.8	50
80	Assembly, Verification, and Initial Annotation of the NIA Mouse 7.4K cDNA Clone Set. <i>Genome Research</i> , 2002, 12, 1999-2003.	5.5	49
81	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. <i>Scientific Data</i> , 2017, 4, 170030.	5.3	48
82	The Contribution of Exon-Skipping Events on Chromosome 22 to Protein Coding Diversity. <i>Genome Research</i> , 2001, 11, 1848-1853.	5.5	46
83	A direct fate exclusion mechanism by Sonic hedgehog-regulated transcriptional repressors. <i>Development (Cambridge)</i> , 2015, 142, 3286-93.	2.5	42
84	Silencing of the <i>Drosophila</i> ortholog of <i>SOX5</i> leads to abnormal neuronal development and behavioral impairment. <i>Human Molecular Genetics</i> , 2017, 26, 1472-1482.	2.9	42
85	The Pathway Coexpression Network: Revealing pathway relationships. <i>PLoS Computational Biology</i> , 2018, 14, e1006042.	3.2	41
86	Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 201-210.	1.1	40
87	Immunotherapy for breast cancer using EpCAM aptamer tumor-targeted gene knockdown. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	38
88	New methods for finding disease-susceptibility genes: impact and potential. <i>Genome Biology</i> , 2003, 4, 119.	9.6	37
89	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D415-D418.	14.5	36
90	Computational selection and prioritization of candidate genes for Fetal Alcohol Syndrome. <i>BMC Genomics</i> , 2007, 8, 389.	2.8	36

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91	Protein kinase C $\hat{\nu}$ is essential for optimal macrophage-mediated phagosomal containment of <i>Listeria monocytogenes</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16251-16256.	7.1	35
92	Deep phenotyping of peripheral tissue facilitates mechanistic disease stratification in sporadic Parkinson's disease. <i>Progress in Neurobiology</i> , 2020, 187, 101772.	5.7	35
93	An overview of the wcd EST clustering tool. <i>Bioinformatics</i> , 2008, 24, 1542-1546.	4.1	34
94	A Model of Directional Selection Applied to the Evolution of Drug Resistance in HIV-1. <i>Molecular Biology and Evolution</i> , 2007, 24, 1025-1031.	8.9	33
95	The Constrained Maximal Expression Level Owing to Haploidy Shapes Gene Content on the Mammalian X Chromosome. <i>PLoS Biology</i> , 2015, 13, e1002315.	5.6	32
96	A case for a <i>Glossina</i> genome project. <i>Trends in Parasitology</i> , 2005, 21, 107-111.	3.3	31
97	Identification of Novel Alzheimer's Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. <i>Scientific Reports</i> , 2020, 10, 5029.	3.3	31
98	The Stem Cell Discovery Engine: an integrated repository and analysis system for cancer stem cell comparisons. <i>Nucleic Acids Research</i> , 2012, 40, D984-D991.	14.5	29
99	Chronic Endotoxin Exposure Produces Airflow Obstruction and Lung Dendritic Cell Expansion. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2012, 47, 209-217.	2.9	27
100	Comparison of Illumina and 454 Deep Sequencing in Participants Failing Raltegravir-Based Antiretroviral Therapy. <i>PLoS ONE</i> , 2014, 9, e90485.	2.5	27
101	Relatively frequent switching of transcription start sites during cerebellar development. <i>BMC Genomics</i> , 2017, 18, 461.	2.8	27
102	Adaptive changes in HIV-1 subtype C proteins during early infection are driven by changes in HLA-associated immune pressure. <i>Virology</i> , 2010, 396, 213-225.	2.4	26
103	The biochemical phylogeny of guinea-pigs and gundis, and the paraphyly of the order Rodentia. <i>Comparative Biochemistry and Physiology Part B: Comparative Biochemistry</i> , 1992, 101, 495-498.	0.2	25
104	Molecular evolution of <i>Mycobacterium tuberculosis</i> : phylogenetic reconstruction of clonal expansion. <i>Tuberculosis</i> , 2001, 81, 291-302.	1.9	25
105	An in-depth comparison of the male pediatric and adult urinary proteomes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 1044-1050.	2.3	25
106	Origin of rodents and guinea-pigs. <i>Nature</i> , 1992, 359, 277-278.	27.8	24
107	Comparative analysis of resistant and susceptible macrophage gene expression response to <i>Leishmania</i> major parasite. <i>BMC Genomics</i> , 2013, 14, 723.	2.8	22
108	Inferring an Evolutionary Tree of Uveal Melanoma From Genomic Copy Number Aberrations. , 2015, 56, 6801.		22

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109	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. <i>Blood</i> , 2016, 127, 2598-2606.	1.4	22
110	A β -accelerated neurodegeneration caused by Alzheimer's-associated <i>ACE</i> variant R1279Q is rescued by angiotensin system inhibition in mice. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	22
111	Vertical HIV transmission in South Africa: translating research into policy and practice. <i>Lancet</i> , The, 2002, 359, 992-993.	13.7	21
112	Conserved Domains of Subtype C Nef from South African HIV Type 1-Infected Individuals Include Cytotoxic T Lymphocyte Epitope-Rich Regions. <i>AIDS Research and Human Retroviruses</i> , 2001, 17, 1681-1687.	1.1	20
113	Transcript-Specific Expression Profiles Derived from Sequence-Based Analysis of Standard Microarrays. <i>PLoS ONE</i> , 2009, 4, e4702.	2.5	20
114	The S-star trial bioinformatics course: An on-line learning success. <i>Biochemistry and Molecular Biology Education</i> , 2003, 31, 20-23.	1.2	18
115	The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. <i>Nucleic Acids Research</i> , 2004, 33, D567-D572.	14.5	16
116	CLU: A new algorithm for EST clustering. <i>BMC Bioinformatics</i> , 2005, 6, S3.	2.6	16
117	A missense (Asp250→Asn) mutation in the lipoprotein lipase gene in two unrelated families with familial lipoprotein lipase deficiency. <i>Journal of Lipid Research</i> , 1992, 33, 745-54.	4.2	16
118	Assessment of the parallelization approach of <i>fd2_cluster</i> for high-performance sequence clustering. <i>Journal of Computational Chemistry</i> , 2002, 23, 755-757.	3.3	15
119	An Assessment of the Role of DNA Adenine Methyltransferase on Gene Expression Regulation in <i>E. coli</i> . <i>PLoS ONE</i> , 2007, 2, e273.	2.5	15
120	Iterative sorting reveals CD133+ and CD133- melanoma cells as phenotypically distinct populations. <i>BMC Cancer</i> , 2016, 16, 726.	2.6	15
121	Physical and transcriptional map of the critical region for keratolytic winter erythema (KWE) on chromosome 8p22-p23 between D8S550 and D8S1759. <i>European Journal of Human Genetics</i> , 2002, 10, 17-25.	2.8	14
122	The relative resistance of children to sepsis mortality: from pathways to drug candidates. <i>Molecular Systems Biology</i> , 2018, 14, e7998.	7.2	14
123	Pathprinting: An integrative approach to understand the functional basis of disease. <i>Genome Medicine</i> , 2013, 5, 68.	8.2	13
124	<i>Mycoplasma</i> Infection Alters Cancer Stem Cell Properties in Vitro. <i>Stem Cell Reviews and Reports</i> , 2016, 12, 156-161.	5.6	13
125	Most Pathways Can Be Related to the Pathogenesis of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , 0, 14, .	3.4	13
126	Simplified ontologies allowing comparison of developmental mammalian gene expression. <i>Genome Biology</i> , 2007, 8, R229.	9.6	12

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127	Divergent LIN28-mRNA associations result in translational suppression upon the initiation of differentiation. <i>Nucleic Acids Research</i> , 2014, 42, 7997-8007.	14.5	12
128	A prioritization analysis of disease association by data-mining of functional annotation of human genes. <i>Genomics</i> , 2012, 99, 1-9.	2.9	11
129	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
130	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209.	2.3	10
131	GCH1 Deficiency Activates Brain Innate Immune Response and Impairs Tyrosine Hydroxylase Homeostasis. <i>Journal of Neuroscience</i> , 2022, 42, 702-716.	3.6	10
132	Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimer's disease-associated genes: DTNB and DLG2. <i>Molecular Psychiatry</i> , 2022, 27, 1963-1969.	7.9	9
133	Application of eVOC: controlled vocabularies for unifying gene expression data. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1089-1096.	0.2	8
134	Integrative analysis of intraerythrocytic differentially expressed transcripts yields novel insights into the biology of <i>Plasmodium falciparum</i> . <i>Malaria Journal</i> , 2003, 2, 38.	2.3	8
135	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. <i>BMC Genomics</i> , 2008, 9, 481.	2.8	8
136	Computational Analysis of Constraints on Noncoding Regions, Coding Regions and Gene Expression in Relation to <i>Plasmodium</i> Phenotypic Diversity. <i>PLoS ONE</i> , 2008, 3, e3122.	2.5	8
137	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. <i>PLoS ONE</i> , 2012, 7, e34286.	2.5	8
138	Positive Selection Scanning Reveals Decoupling of Enzymatic Activities of Carbamoyl Phosphate Synthetase in <i>Helicobacter pylori</i> . <i>Journal of Molecular Evolution</i> , 2002, 54, 458-464.	1.8	7
139	CAGExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. <i>Bioinformatics</i> , 2014, 30, 1183-1184.	4.1	5
140	A Network Of Epigenetic Regulators Guide Developmental Hematopoiesis In Vivo. <i>Blood</i> , 2013, 122, 1174-1174.	1.4	5
141	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369.	28.9	4
142	FRAGS: estimation of coding sequence substitution rates from fragmentary data. <i>BMC Bioinformatics</i> , 2004, 5, 8.	2.6	3
143	Quantitating the Multiplicity of Infection with Human Immunodeficiency Virus Type 1 Subtype C Reveals a Non-Poisson Distribution of Transmitted Variants. <i>Journal of Virology</i> , 2009, 83, 6974-6974.	3.4	3
144	Message from the ISCB: ISCB Ebola award for important future research on the computational biology of Ebola virus. <i>Bioinformatics</i> , 2015, 31, 616-617.	4.1	3

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145	The Stem Cell Commons: an exemplar for data integration in the biomedical domain driven by the ISA framework. AMIA Summits on Translational Science Proceedings, 2013, 2013, 70.	0.4	3
146	Continuing tsetse and Trypanosoma genome sequencing projects. Trends in Parasitology, 2004, 20, 308-309.	3.3	2
147	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. PLoS Computational Biology, 2015, 11, e1004087.	3.2	2
148	Cell-specific translational profiling in acute kidney injury. Journal of Clinical Investigation, 2014, 124, 2288-2288.	8.2	2
149	Positive Selection Scanning of Parasite DNA Sequences. , 2004, 270, 127-150.		1
150	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. F1000Research, 2015, 4, 12.	1.6	1
151	Clonal-Heterogeneity and Propensity for Bone Metastasis in Multiple Myeloma. Blood, 2014, 124, 3370-3370.	1.4	1
152	Integrating Murine Gene Expression Studies to Understand Obstructive Lung Disease Due to Chronic Inhaled Endotoxin. PLoS ONE, 2013, 8, e62910.	2.5	1
153	The South African EMBnet Node: AGM 2010 report. EMBnet Journal, 2011, 16, 25.	0.6	1
154	Clinical allergy--state of the art. The British Journal of Clinical Practice, 1990, 44, 85-7.	0.2	1
155	A platform for genomics in South Africa. South African Medical Journal, 2001, 91, 1006-7.	0.6	1
156	USE OF A VISUAL COMPARATIVE METHOD TO RESOLVE CONSERVED SEQUENCE MOTIFS IN PROTEINS. , 1993, , .		0
157	ExScript: AN 'EX'-CENTRIC APPROACH TO THE DESCRIPTION OF TRANSCRIPT DIVERSITY. Bioinformatics, 2001, 17, 485-486.	4.1	0
158	Response to Hertz-Fowler and Berriman: Continuing tsetse and Trypanosoma genome sequencing projects. Trends in Parasitology, 2004, 20, 309-310.	3.3	0
159	EST clustering: a short tutorial. , 2005, , .		0
160	IDENTIFICATION OF NOVEL URINARY BIOMARKERS OF RENAL OBSTRUCTION USING TEMPORAL QUANTITATIVE PROTEOMICS. Journal of Urology, 2009, 181, 251-252.	0.4	0
161	Gene-Expression Ontologies and Tag-Based Expression Profiling. , 2009, , 169-178.		0
162	The Data Sharing Challenge. Learning Community From Consortia. Nature Precedings, 2010, , .	0.1	0

#	ARTICLE	IF	CITATIONS
163	Airway Reactivity And Persistent Inflammation Is Associated With Antigen Presenting Cell Population Shifts In A Murine Model Of Chronic Inhalational Endotoxin Exposure. , 2011, , .		0
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