

# Winston A Hide

## List of Publications by Year in descending order

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175  
papers

25,224  
citations

15504

65  
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7518

151  
g-index

267  
all docs

267  
docs citations

267  
times ranked

44928  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reply to Neupane etÂal.: Replication study of ADâ€associated rare variants. Alzheimer's and Dementia, 2022, , .	0.8	0
2	Region-based analysis of rare genomic variants in whole-genome sequencing datasets reveal two novel Alzheimerâ€™s disease-associated genes: DTNB and DLG2. Molecular Psychiatry, 2022, 27, 1963-1969.	7.9	9
3	GCH1 Deficiency Activates Brain Innate Immune Response and Impairs Tyrosine Hydroxylase Homeostasis. Journal of Neuroscience, 2022, 42, 702-716.	3.6	10
4	Immunotherapy for breast cancer using EpCAM aptamer tumor-targeted gene knockdown. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	38
5	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. Nature, 2021, 595, 107-113.	27.8	537
6	Wholeâ€genome sequencing reveals new Alzheimer's diseaseâ€™ associated rare variants in loci related to synaptic function and neuronal development. Alzheimer's and Dementia, 2021, 17, 1509-1527.	0.8	50
7	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
8	Â²-accelerated neurodegeneration caused by Alzheimerâ€™s-associated <i>ACE</i> variant R1279Q is rescued by angiotensin system inhibition in mice. Science Translational Medicine, 2020, 12, .	12.4	22
9	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	6.4	199
10	Identification of Novel Alzheimerâ€™s Disease Loci Using Sex-Specific Family-Based Association Analysis of Whole-Genome Sequence Data. Scientific Reports, 2020, 10, 5029.	3.3	31
11	Deep phenotyping of peripheral tissue facilitates mechanistic disease stratification in sporadic Parkinsonâ€™s disease. Progress in Neurobiology, 2020, 187, 101772.	5.7	35
12	In Vivo Profiling of Leukemic Stem Cell Fitness Identifies Therapeutically Actionable Determinants of Growth. Experimental Hematology, 2018, 64, S86.	0.4	0
13	The relative resistance of children to sepsis mortality: from pathways to drug candidates. Molecular Systems Biology, 2018, 14, e7998.	7.2	14
14	Project MinE: study design and pilot analyses of a large-scale whole-genome sequencing study in amyotrophic lateral sclerosis. European Journal of Human Genetics, 2018, 26, 1537-1546.	2.8	129
15	The Pathway Coexpression Network: Revealing pathway relationships. PLoS Computational Biology, 2018, 14, e1006042.	3.2	41
16	Relatively frequent switching of transcription start sites during cerebellar development. BMC Genomics, 2017, 18, 461.	2.8	27
17	Molecular, phenotypic, and sample-associated data to describe pluripotent stem cell lines and derivatives. Scientific Data, 2017, 4, 170030.	5.3	48
18	A data-driven approach links microglia to pathology and prognosis in amyotrophic lateral sclerosis. Acta Neuropathologica Communications, 2017, 5, 23.	5.2	63

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19	Silencing of the Drosophila ortholog of SOX5 leads to abnormal neuronal development and behavioral impairment. <i>Human Molecular Genetics</i> , 2017, 26, 1472-1482.	2.9	42
20	Compound heterozygous variants in NBAS as a cause of atypical osteogenesis imperfecta. <i>Bone</i> , 2017, 94, 65-74.	2.9	54
21	Iterative sorting reveals CD133+ and CD133- melanoma cells as phenotypically distinct populations. <i>BMC Cancer</i> , 2016, 16, 726.	2.6	15
22	Exome sequencing reveals recurrent germ line variants in patients with familial Waldenström macroglobulinemia. <i>Blood</i> , 2016, 127, 2598-2606.	1.4	22
23	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
24	Mycoplasma Infection Alters Cancer Stem Cell Properties in Vitro. <i>Stem Cell Reviews and Reports</i> , 2016, 12, 156-161.	5.6	13
25	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
26	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
27	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
28	Inferring an Evolutionary Tree of Uveal Melanoma From Genomic Copy Number Aberrations. , 2015, 56, 6801.		22
29	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
30	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	8.8	687
31	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
32	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>PLoS Computational Biology</i> , 2015, 11, e1004087.	3.2	2
33	ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. <i>F1000Research</i> , 2015, 4, 12.	1.6	1
34	A direct fate exclusion mechanism by Sonic hedgehog-regulated transcriptional repressors. <i>Development (Cambridge)</i> , 2015, 142, 3286-93.	2.5	42
35	Comparison of Illumina and 454 Deep Sequencing in Participants Failing Raltegravir-Based Antiretroviral Therapy. <i>PLoS ONE</i> , 2014, 9, e90485.	2.5	27
36	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

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37	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
38	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
39	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
40	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
41	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
42	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
43	Genome Sequence of the Tsetse Fly ( <i>Glossina morsitans</i> ): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
44	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
45	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
46	Enabling the genomic revolution in Africa. <i>Science</i> , 2014, 344, 1346-1348.	12.6	361
47	Cell-specific translational profiling in acute kidney injury. <i>Journal of Clinical Investigation</i> , 2014, 124, 1242-1254.	8.2	172
48	Clonal-Heterogeneity and Propensity for Bone Metastasis in Multiple Myeloma. <i>Blood</i> , 2014, 124, 3370-3370.	1.4	1
49	Cell-specific translational profiling in acute kidney injury. <i>Journal of Clinical Investigation</i> , 2014, 124, 2288-2288.	8.2	2
50	Abstract SY43-03: Screening for triple negative breast cancer vulnerabilities. , 2014, , .		0
51	Identification of a Gene Expression Signature Characterizing Clonal Fitness and Dominance in Vivo in a Murine Model of MLL-AF9 Leukemia. <i>Blood</i> , 2014, 124, 2383-2383.	1.4	0
52	A network of epigenetic regulators guides developmental haematopoiesis in vivo. <i>Nature Cell Biology</i> , 2013, 15, 1516-1525.	10.3	81
53	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
54	Pathprinting: An integrative approach to understand the functional basis of disease. <i>Genome Medicine</i> , 2013, 5, 68.	8.2	13

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55	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
56	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
57	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
58	Comparative analysis of resistant and susceptible macrophage gene expression response to <i>Leishmania major</i> parasite. <i>BMC Genomics</i> , 2013, 14, 723.	2.8	22
59	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
60	Integrating Murine Gene Expression Studies to Understand Obstructive Lung Disease Due to Chronic Inhaled Endotoxin. <i>PLoS ONE</i> , 2013, 8, e62910.	2.5	1
61	A Network Of Epigenetic Regulators Guide Developmental Hematopoiesis In Vivo. <i>Blood</i> , 2013, 122, 1174-1174.	1.4	5
62	The Stem Cell Commons: an exemplar for data integration in the biomedical domain driven by the ISA framework. <i>AMIA Summits on Translational Science Proceedings</i> , 2013, 2013, 70.	0.4	3
63	Title is missing!. , 2013, 9, e1003042.		0
64	Title is missing!. , 2013, 9, e1003042.		0
65	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
66	Prenatal Lead Levels, Plasma Amyloid $\beta^2$ Levels, and Gene Expression in Young Adulthood. <i>Environmental Health Perspectives</i> , 2012, 120, 702-707.	6.0	57
67	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	3.5	181
68	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
69	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
70	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
71	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
72	732 AN IN-DEPTH ANALYSIS OF THE PEDIATRIC URINARY PROTEOME. <i>Journal of Urology</i> , 2012, 187, .	0.4	0

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73	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489.	21.4	402
74	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
75	A functional genomic screen reveals novel host genes that mediate interferon-alpha's effects against hepatitis C virus. <i>Journal of Hepatology</i> , 2012, 56, 326-333.	3.7	60
76	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
77	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
78	Circadian Gene Variants and Susceptibility to Type 2 Diabetes: A Pilot Study. <i>PLoS ONE</i> , 2012, 7, e32670.	2.5	52
79	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. <i>PLoS ONE</i> , 2012, 7, e34286.	2.5	8
80	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glyceimic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
81	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. , 2012, 7, e34286.		0
82	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. , 2012, 7, e34286.		0
83	Population Differences in Transcript-Regulator Expression Quantitative Trait Loci. , 2012, 7, e34286.		0
84	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	21.4	501
85	Airway Reactivity And Persistent Inflammation Is Associated With Antigen Presenting Cell Population Shifts In A Murine Model Of Chronic Inhalational Endotoxin Exposure. , 2011, , .		0
86	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
87	Aberrant lipid metabolism disrupts calcium homeostasis causing liver endoplasmic reticulum stress in obesity. <i>Nature</i> , 2011, 473, 528-531.	27.8	864
88	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
89	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
90	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

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91	The South African EMBnet Node: AGM 2010 report. EMBnet Journal, 2011, 16, 25.	0.6	1
92	Adaptive changes in HIV-1 subtype C proteins during early infection are driven by changes in HLA-associated immune pressure. Virology, 2010, 396, 213-225.	2.4	26
93	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
94	The Data Sharing Challenge. Learning Community From Consortia. Nature Precedings, 2010, , .	0.1	0
95	ISA software suite: supporting standards-compliant experimental annotation and enabling curation at the community level. Bioinformatics, 2010, 26, 2354-2356.	4.1	247
96	Ten Simple Rules for Organizing a Virtual Conference“Anywhere. PLoS Computational Biology, 2010, 6, e1000650.	3.2	54
97	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	28.9	667
98	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	28.9	4
99	Transcript-Specific Expression Profiles Derived from Sequence-Based Analysis of Standard Microarrays. PLoS ONE, 2009, 4, e4702.	2.5	20
100	Quantitating the Multiplicity of Infection with Human Immunodeficiency Virus Type 1 Subtype C Reveals a Non-Poisson Distribution of Transmitted Variants. Journal of Virology, 2009, 83, 3556-3567.	3.4	354
101	A Pathway-Based View of Human Diseases and Disease Relationships. PLoS ONE, 2009, 4, e4346.	2.5	158
102	Quantitating the Multiplicity of Infection with Human Immunodeficiency Virus Type 1 Subtype C Reveals a Non-Poisson Distribution of Transmitted Variants. Journal of Virology, 2009, 83, 6974-6974.	3.4	3
103	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
104	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
105	ASTD: The Alternative Splicing and Transcript Diversity database. Genomics, 2009, 93, 213-220.	2.9	87
106	miR-24 Inhibits Cell Proliferation by Targeting E2F2, MYC, and Other Cell-Cycle Genes via Binding to “Seedless” 3’ UTR MicroRNA Recognition Elements. Molecular Cell, 2009, 35, 610-625.	9.7	544
107	IDENTIFICATION OF NOVEL URINARY BIOMARKERS OF RENAL OBSTRUCTION USING TEMPORAL QUANTITATIVE PROTEOMICS. Journal of Urology, 2009, 181, 251-252.	0.4	0
108	Gene-Expression Ontologies and Tag-Based Expression Profiling. , 2009, , 169-178.		0

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109	Mining Biological Pathways Using WikiPathways Web Services. PLoS ONE, 2009, 4, e6447.	2.5	100
110	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	17.5	155
111	The future of biocuration. Nature, 2008, 455, 47-50.	27.8	648
112	Prioritizing genes of potential relevance to diseases affected by sex hormones: an example of Myasthenia Gravis. BMC Genomics, 2008, 9, 481.	2.8	8
113	Genome-wide analysis of cancer/testis gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20422-20427.	7.1	295
114	Transmission of HIV-1 CTL Escape Variants Provides HLA-Mismatched Recipients with a Survival Advantage. PLoS Pathogens, 2008, 4, e1000033.	4.7	129
115	An overview of the wcd EST clustering tool. Bioinformatics, 2008, 24, 1542-1546.	4.1	34
116	Computational Analysis of Constraints on Noncoding Regions, Coding Regions and Gene Expression in Relation to Plasmodium Phenotypic Diversity. PLoS ONE, 2008, 3, e3122.	2.5	8
117	Transcriptome-Wide Assessment of Human Brain and Lymphocyte Senescence. PLoS ONE, 2008, 3, e3024.	2.5	60
118	Title is missing!. , 2008, 4, e1000033.		0
119	Title is missing!. , 2008, 4, e1000033.		0
120	A Model of Directional Selection Applied to the Evolution of Drug Resistance in HIV-1. Molecular Biology and Evolution, 2007, 24, 1025-1031.	8.9	33
121	Protein kinase C $\hat{\nu}$ is essential for optimal macrophage-mediated phagosomal containment of <i>Listeria monocytogenes</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 16251-16256.	7.1	35
122	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. Nucleic Acids Research, 2007, 36, D793-D799.	14.5	57
123	Simplified ontologies allowing comparison of developmental mammalian gene expression. Genome Biology, 2007, 8, R229.	9.6	12
124	An Assessment of the Role of DNA Adenine Methyltransferase on Gene Expression Regulation in E coli. PLoS ONE, 2007, 2, e273.	2.5	15
125	Computational selection and prioritization of candidate genes for Fetal Alcohol Syndrome. BMC Genomics, 2007, 8, 389.	2.8	36
126	Rapid evolution of cancer/testis genes on the X chromosome. BMC Genomics, 2007, 8, 129.	2.8	80



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127	The LIFEdb database in 2006. <i>Nucleic Acids Research</i> , 2006, 34, D415-D418.	14.5	36
128	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
129	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	3.5	95
130	A case for a <i>Glossina</i> genome project. <i>Trends in Parasitology</i> , 2005, 21, 107-111.	3.3	31
131	CLU: A new algorithm for EST clustering. <i>BMC Bioinformatics</i> , 2005, 6, S3.	2.6	16
132	EST clustering: a short tutorial. , 2005, , .		0
133	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
134	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
135	Positive Selection Scanning of Parasite DNA Sequences. , 2004, 270, 127-150.		1
136	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
137	Continuing tsetse and <i>Trypanosoma</i> genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 308-309.	3.3	2
138	Response to Hertz-Fowler and Berriman: Continuing tsetse and <i>Trypanosoma</i> genome sequencing projects. <i>Trends in Parasitology</i> , 2004, 20, 309-310.	3.3	0
139	FRAGS: estimation of coding sequence substitution rates from fragmentary data. <i>BMC Bioinformatics</i> , 2004, 5, 8.	2.6	3
140	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
141	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
142	Application of eVOC: controlled vocabularies for unifying gene expression data. <i>Comptes Rendus - Biologies</i> , 2003, 326, 1089-1096.	0.2	8
143	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
144	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

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145	New methods for finding disease-susceptibility genes: impact and potential. <i>Genome Biology</i> , 2003, 4, 119.	9.6	37
146	eVOC: A Controlled Vocabulary for Unifying Gene Expression Data. <i>Genome Research</i> , 2003, 13, 1222-1230.	5.5	144
147	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
148	Transcriptome Analysis of Mouse Stem Cells and Early Embryos. <i>PLoS Biology</i> , 2003, 1, e74.	5.6	156
149	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
150	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
151	Vertical HIV transmission in South Africa: translating research into policy and practice. <i>Lancet</i> , The, 2002, 359, 992-993.	13.7	21
152	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
153	Assessment of the parallelization approach of <code>ofd2_cluster</code> for high-performance sequence clustering. <i>Journal of Computational Chemistry</i> , 2002, 23, 755-757.	3.3	15
154	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
155	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
156	The Contribution of Exon-Skipping Events on Chromosome 22 to Protein Coding Diversity. <i>Genome Research</i> , 2001, 11, 1848-1853.	5.5	46
157	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
158	Molecular evolution of <i>Mycobacterium tuberculosis</i> : phylogenetic reconstruction of clonal expansion. <i>Tuberculosis</i> , 2001, 81, 291-302.	1.9	25
159	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
160	STACK: Sequence Tag Alignment and Consensus Knowledgebase. <i>Nucleic Acids Research</i> , 2001, 29, 234-238.	14.5	112
161	ExScript: AN 'EX'-CENTRIC APPROACH TO THE DESCRIPTION OF TRANSCRIPT DIVERSITY. <i>Bioinformatics</i> , 2001, 17, 485-486.	4.1	0
162	A platform for genomics in South Africa. <i>South African Medical Journal</i> , 2001, 91, 1006-7.	0.6	1

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163	d2_cluster: A Validated Method for Clustering EST and Full-Length cDNA Sequences. Genome Research, 1999, 9, 1135-1142.	5.5	176
164	A Comprehensive Approach to Clustering of Expressed Human Gene Sequence: The Sequence Tag Alignment and Consensus Knowledge Base. Genome Research, 1999, 9, 1143-1155.	5.5	175
165	Mutations in a novel retina-specific gene cause autosomal dominant retinitis pigmentosa. Nature Genetics, 1999, 22, 255-259.	21.4	154
166	Alternative Gene Form Discovery and Candidate Gene Selection from Gene Indexing Projects. Genome Research, 1998, 8, 276-290.	5.5	102
167	Biological Evaluation of $d^2$ , an Algorithm for High-Performance Sequence Comparison. Journal of Computational Biology, 1994, 1, 199-215.	1.6	63
168	USE OF A VISUAL COMPARATIVE METHOD TO RESOLVE CONSERVED SEQUENCE MOTIFS IN PROTEINS. , 1993, , .		0
169	The Molecular Taxonomy and Evolution of the Guinea Pig. Journal of Heredity, 1992, 83, 174-181.	2.4	61
170	Origin of rodents and guinea-pigs. Nature, 1992, 359, 277-278.	27.8	24
171	The biochemical phylogeny of guinea-pigs and gundis, and the paraphyly of the order Rodentia. Comparative Biochemistry and Physiology Part B: Comparative Biochemistry, 1992, 101, 495-498.	0.2	25
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