

Terence P Speed

List of Publications by Year in descending order

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235
papers

57,536
citations

9264

74
h-index

1116

231
g-index

262
all docs

262
docs citations

262
times ranked

75354
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. <i>Nature Biotechnology</i> , 2022, 40, 1624-1633.	17.5	31
2	The Ratio of Exhausted to Resident Infiltrating Lymphocytes Is Prognostic for Colorectal Cancer Patient Outcome. <i>Cancer Immunology Research</i> , 2021, 9, 1125-1140.	3.4	18
3	Discrete tissue microenvironments instruct diversity in resident memory T cell function and plasticity. <i>Nature Immunology</i> , 2021, 22, 1140-1151.	14.5	96
4	A hierarchical approach to removal of unwanted variation for large-scale metabolomics data. <i>Nature Communications</i> , 2021, 12, 4992.	12.8	22
5	A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22.	28.9	52
6	Spectral PCA for MANOVA and data over binary trees. <i>Journal of Multivariate Analysis</i> , 2021, , 104905.	1.0	1
7	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793.	12.8	75
8	Controlling technical variation amongst 6693 patient microarrays of the randomized MINDACT trial. <i>Communications Biology</i> , 2020, 3, 397.	4.4	7
9	Serum microRNA is a biomarker for post-operative monitoring in glioma. <i>Journal of Neuro-Oncology</i> , 2020, 149, 391-400.	2.9	27
10	scClassify: sample size estimation and multiscale classification of cells using single and multiple reference. <i>Molecular Systems Biology</i> , 2020, 16, e9389.	7.2	79
11	Multiple sclerosis risk variants regulate gene expression in innate and adaptive immune cells. <i>Life Science Alliance</i> , 2020, 3, e202000650.	2.8	22
12	Removing unwanted variation with CytofRUV to integrate multiple CyTOF datasets. <i>ELife</i> , 2020, 9, .	6.0	31
13	Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. <i>Bioinformatics</i> , 2019, 35, 560-570.	4.1	17
14	Evaluating stably expressed genes in single cells. <i>GigaScience</i> , 2019, 8, .	6.4	44
15	A new normalization for Nanostring nCounter gene expression data. <i>Nucleic Acids Research</i> , 2019, 47, 6073-6083.	14.5	73
16	DECENT: differential expression with capture efficiency adjustment for single-cell RNA-seq data. <i>Bioinformatics</i> , 2019, 35, 5155-5162.	4.1	33
17	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9775-9784.	7.1	130
18	Using long-read sequencing to detect imprinted DNA methylation. <i>Nucleic Acids Research</i> , 2019, 47, e46-e46.	14.5	88

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19	Maps of variability in cell lineage trees. PLoS Computational Biology, 2019, 15, e1006745.	3.2	9
20	Identification of cancer sex-disparity in the functional integrity of p53 and its X chromosome network. Nature Communications, 2019, 10, 5385.	12.8	53
21	Accurate RNA Sequencing From Formalin-Fixed Cancer Tissue to Represent High-Quality Transcriptome From Frozen Tissue. JCO Precision Oncology, 2018, 2018, 1-9.	3.0	35
22	The healthy ageing gene expression signature for Alzheimer's disease diagnosis: a random sampling perspective. Genome Biology, 2018, 19, 97.	8.8	8
23	RLE plots: Visualizing unwanted variation in high dimensional data. PLoS ONE, 2018, 13, e0191629.	2.5	69
24	Single-cell profiling of breast cancer T cells reveals a tissue-resident memory subset associated with improved prognosis. Nature Medicine, 2018, 24, 986-993.	30.7	689
25	Joint Modeling of Mixed Plasmodium Species Infections Using a Bivariate Poisson Lognormal Model. American Journal of Tropical Medicine and Hygiene, 2018, 98, 71-76.	1.4	2
26	Deficiency of microRNA <i>miR-34a</i> expands cell fate potential in pluripotent stem cells. Science, 2017, 355, .	12.6	129
27	GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly. Genome Research, 2017, 27, 2050-2060.	5.5	255
28	Contextual fear conditioning induces differential alternative splicing. Neurobiology of Learning and Memory, 2016, 134, 221-235.	1.9	28
29	Removal of unwanted variation reveals novel patterns of gene expression linked to sleep homeostasis in murine cortex. BMC Genomics, 2016, 17, 727.	2.8	41
30	MicroRNAs in CD4 + T cell subsets are markers of disease risk and T cell dysfunction in individuals at risk for type 1 diabetes. Journal of Autoimmunity, 2016, 68, 52-61.	6.5	42
31	Correcting gene expression data when neither the unwanted variation nor the factor of interest are observed. Biostatistics, 2016, 17, 16-28.	1.5	82
32	The Subclonal Architecture of Metastatic Breast Cancer: Results from a Prospective Community-Based Rapid Autopsy Program "CASCADE". PLoS Medicine, 2016, 13, e1002204.	8.4	119
33	Assessment of DNA methylation profiling and copy number variation as indications of clonal relationship in ipsilateral and contralateral breast cancers to distinguish recurrent breast cancer from a second primary tumour. BMC Cancer, 2015, 15, 669.	2.6	14
34	Systematic noise degrades gene co-expression signals but can be corrected. BMC Bioinformatics, 2015, 16, 309.	2.6	50
35	Removing unwanted variation in a differential methylation analysis of Illumina HumanMethylation450 array data. Nucleic Acids Research, 2015, 43, e106-e106.	14.5	73
36	Statistical Methods for Handling Unwanted Variation in Metabolomics Data. Analytical Chemistry, 2015, 87, 3606-3615.	6.5	152

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37	Signatures of tumour immunity distinguish Asian and non-Asian gastric adenocarcinomas. <i>Cut</i> , 2015, 64, 1721-1731.	12.1	197
38	How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. <i>Nucleic Acids Research</i> , 2015, 43, 7664-7674.	14.5	90
39	Investigating and Correcting Plasma DNA Sequencing Coverage Bias to Enhance Aneuploidy Discovery. <i>PLoS ONE</i> , 2014, 9, e86993.	2.5	24
40	Deciphering clonality in aneuploid breast tumors using SNP array and sequencing data. <i>Genome Biology</i> , 2014, 15, 470.	8.8	11
41	The Role of Spike-In Standards in the Normalization of RNA-seq. , 2014, , 169-190.		8
42	Dating Rare Mutations from Small Samples with Dense Marker Data. <i>Genetics</i> , 2014, 197, 1315-1327.	2.9	61
43	Silencing of Odorant Receptor Genes by G Protein $\beta\gamma$ Signaling Ensures the Expression of One Odorant Receptor per Olfactory Sensory Neuron. <i>Neuron</i> , 2014, 81, 847-859.	8.1	47
44	Normalization of RNA-seq data using factor analysis of control genes or samples. <i>Nature Biotechnology</i> , 2014, 32, 896-902.	17.5	1,570
45	Effect of vascular endothelial growth factor upregulation on retinal gene expression in the Kimba mouse. <i>Clinical and Experimental Ophthalmology</i> , 2013, 41, 251-262.	2.6	9
46	Bayesian Inference of Signaling Network Topology in a Cancer Cell Line. <i>Bioinformatics</i> , 2012, 28, 2804-2810.	4.1	87
47	Tissue-Specific Regulation of Genes by Estrogen Receptors. <i>Seminars in Reproductive Medicine</i> , 2012, 30, 14-22.	1.1	23
48	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496.	5.5	28
49	SRMA: an R package for resequencing array data analysis. <i>Bioinformatics</i> , 2012, 28, 1928-1930.	4.1	1
50	Using control genes to correct for unwanted variation in microarray data. <i>Biostatistics</i> , 2012, 13, 539-552.	1.5	366
51	Normalizing and Integrating Metabolomics Data. <i>Analytical Chemistry</i> , 2012, 84, 10768-10776.	6.5	183
52	Subtype and pathway specific responses to anticancer compounds in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2724-2729.	7.1	417
53	Genome-wide analysis of glucocorticoid receptor-binding sites in myotubes identifies gene networks modulating insulin signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11160-11165.	7.1	127
54	Subcompartmentalisation of Proteins in the Rhoptries Correlates with Ordered Events of Erythrocyte Invasion by the Blood Stage Malaria Parasite. <i>PLoS ONE</i> , 2012, 7, e46160.	2.5	41

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55	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81.	9.6	167
56	Unifying Gene Expression Measures from Multiple Platforms Using Factor Analysis. <i>PLoS ONE</i> , 2011, 6, e17691.	2.5	12
57	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. <i>Nucleic Acids Research</i> , 2011, 39, 44-58.	14.5	37
58	High-quality DNA sequence capture of 524 disease candidate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6549-6554.	7.1	52
59	Statistical Analysis of Single Nucleotide Polymorphism Microarrays in Cancer Studies. , 2011, , 225-255.		4
60	Estrogenic Plant Extracts Reverse Weight Gain and Fat Accumulation without Causing Mammary Gland or Uterine Proliferation. <i>PLoS ONE</i> , 2011, 6, e28333.	2.5	10
61	TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. <i>BMC Bioinformatics</i> , 2010, 11, 245.	2.6	49
62	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	16.8	6,138
63	Poor prognosis in familial acute myeloid leukaemia with combined biallelic <i>CEBPA</i> mutations and downstream events affecting the <i>ATM</i> , <i>FLT3</i> and <i>CDX2</i> genes. <i>British Journal of Haematology</i> , 2010, 150, 382-385.	2.5	17
64	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
65	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. <i>Nature Cell Biology</i> , 2010, 12, 235-246.	10.3	178
66	Identification of Candidate Growth Promoting Genes in Ovarian Cancer through Integrated Copy Number and Expression Analysis. <i>PLoS ONE</i> , 2010, 5, e9983.	2.5	95
67	Genome-Wide Analysis of Glucocorticoid Receptor Binding Regions in Adipocytes Reveal Gene Network Involved in Triglyceride Homeostasis. <i>PLoS ONE</i> , 2010, 5, e15188.	2.5	146
68	Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation. <i>Genome Research</i> , 2010, 20, 1719-1729.	5.5	111
69	A recombination hotspot leads to sequence variability within a novel gene (AK005651) and contributes to type 1 diabetes susceptibility. <i>Genome Research</i> , 2010, 20, 1629-1638.	5.5	14
70	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	3.4	121
71	<i>PIK3CA</i> mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor-positive breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10208-10213.	7.1	324
72	Estrogen Receptor β Binds to and Regulates Three Distinct Classes of Target Genes. <i>Journal of Biological Chemistry</i> , 2010, 285, 22059-22066.	3.4	92

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73	Conserved Role of unc-79 in Ethanol Responses in Lightweight Mutant Mice. <i>PLoS Genetics</i> , 2010, 6, e1001057.	3.5	38
74	Protocol matters: which methylome are you actually studying?. <i>Epigenomics</i> , 2010, 2, 587-598.	2.1	42
75	Unliganded estrogen receptor- β 2 regulation of genes is inhibited by tamoxifen. <i>Molecular and Cellular Endocrinology</i> , 2010, 315, 201-207.	3.2	20
76	Regulation of specific target genes and biological responses by estrogen receptor subtype agonists. <i>Current Opinion in Pharmacology</i> , 2010, 10, 629-636.	3.5	84
77	Background Adjustment for DNA Microarrays Using a Database of Microarray Experiments. <i>Journal of Computational Biology</i> , 2009, 16, 1501-1515.	1.6	11
78	Multiple testing and its applications to microarrays. <i>Statistical Methods in Medical Research</i> , 2009, 18, 543-563.	1.5	22
79	Temporal Global Expression Data Reveal Known and Novel Salicylate-Impacted Processes and Regulators Mediating Powdery Mildew Growth and Reproduction on <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2009, 149, 1435-1451.	4.8	64
80	Time for DNA Disclosure. <i>Science</i> , 2009, 326, 1631-1632.	12.6	15
81	A single-array preprocessing method for estimating full-resolution raw copy numbers from all Affymetrix genotyping arrays including GenomeWideSNP 5 & 6. <i>Bioinformatics</i> , 2009, 25, 2149-2156.	4.1	144
82	Sir2 Paralogues Cooperate to Regulate Virulence Genes and Antigenic Variation in <i>Plasmodium falciparum</i> . <i>PLoS Biology</i> , 2009, 7, e1000084.	5.6	211
83	A single-sample method for normalizing and combining full-resolution copy numbers from multiple platforms, labs and analysis methods. <i>Bioinformatics</i> , 2009, 25, 861-867.	4.1	37
84	Sparse combinatorial inference with an application in cancer biology. <i>Bioinformatics</i> , 2009, 25, 265-271.	4.1	19
85	Differential splicing using whole-transcript microarrays. <i>BMC Bioinformatics</i> , 2009, 10, 156.	2.6	16
86	Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. <i>BMC Medical Genomics</i> , 2009, 2, 37.	1.5	51
87	On Gene Ranking Using Replicated Microarray Time Course Data. <i>Biometrics</i> , 2009, 65, 40-51.	1.4	39
88	Cell type- and estrogen receptor-subtype specific regulation of selective estrogen receptor modulator regulatory elements. <i>Molecular and Cellular Endocrinology</i> , 2009, 299, 204-211.	3.2	27
89	Gene set enrichment analysis made simple. <i>Statistical Methods in Medical Research</i> , 2009, 18, 565-575.	1.5	166
90	Analysis of the platypus genome suggests a transposon origin for mammalian imprinting. <i>Genome Biology</i> , 2009, 10, R1.	9.6	272

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91	Expression profiling of a hemopoietic cell survival transcriptome implicates osteopontin as a functional prognostic factor in AML. <i>Blood</i> , 2009, 114, 4859-4870.	1.4	52
92	Drug and Cell Type-Specific Regulation of Genes with Different Classes of Estrogen Receptor β -Selective Agonists. <i>PLoS ONE</i> , 2009, 4, e6271.	2.5	59
93	SNP mapping and candidate gene sequencing in the class I region of the HLA complex: searching for multiple sclerosis susceptibility genes in Tasmanians. <i>Tissue Antigens</i> , 2008, 71, 42-50.	1.0	48
94	An integrated genetic and functional analysis of the role of type II transmembrane serine proteases (TMPRSSs) in hearing loss. <i>Human Mutation</i> , 2008, 29, 130-141.	2.5	70
95	The power of two-locus affected sib-pair linkage analysis to detect interacting disease loci. <i>Genetic Epidemiology</i> , 2008, 32, 84-88.	1.3	3
96	Replication of KIAA0350, IL2RA, RPL5 and CD58 as multiple sclerosis susceptibility genes in Australians. <i>Genes and Immunity</i> , 2008, 9, 624-630.	4.1	116
97	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	27.8	6,879
98	Integrative analysis of RUNX1 downstream pathways and target genes. <i>BMC Genomics</i> , 2008, 9, 363.	2.8	116
99	Network inference using informative priors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14313-14318.	7.1	158
100	Transcription Factors Bind Thousands of Active and Inactive Regions in the Drosophila Blastoderm. <i>PLoS Biology</i> , 2008, 6, e27.	5.6	428
101	Differential Regulation of Native Estrogen Receptor-Regulatory Elements by Estradiol, Tamoxifen, and Raloxifene. <i>Molecular Endocrinology</i> , 2008, 22, 287-303.	3.7	33
102	Quality Assessment for Short Oligonucleotide Microarray Data. <i>Technometrics</i> , 2008, 50, 241-264.	1.9	104
103	Transcription factor binding site prediction with multivariate gene expression data. <i>Annals of Applied Statistics</i> , 2008, 2, .	1.1	10
104	Multiple Transcription Factor Elements Collaborate with Estrogen Receptor β to Activate an Inducible Estrogen Response Element in the NKG2E Gene. <i>Endocrinology</i> , 2007, 148, 3449-3458.	2.8	20
105	Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. <i>Biostatistics</i> , 2007, 8, 485-499.	1.5	214
106	Evidence for a Common Role for the Serine-Type <i>Plasmodium falciparum</i> Serine Repeat Antigen Proteases: Implications for Vaccine and Drug Design. <i>Infection and Immunity</i> , 2007, 75, 5565-5574.	2.2	82
107	Global analyses of mRNA translational control during early Drosophila embryogenesis. <i>Genome Biology</i> , 2007, 8, R63.	9.6	74
108	SNPs on Chips: The Hidden Genetic Code in Expression Arrays. <i>Biological Psychiatry</i> , 2007, 61, 13-16.	1.3	24

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109	Characterization of the opossum immune genome provides insights into the evolution of the mammalian immune system. <i>Genome Research</i> , 2007, 17, 982-991.	5.5	100
110	A Holm-type procedure controlling the false discovery rate. <i>Statistics and Probability Letters</i> , 2007, 77, 1756-1762.	0.7	3
111	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
112	A dynamic programming approach for the alignment of signal peaks in multiple gas chromatography-mass spectrometry experiments. <i>BMC Bioinformatics</i> , 2007, 8, 419.	2.6	64
113	A comparison of Affymetrix gene expression arrays. <i>BMC Bioinformatics</i> , 2007, 8, 449.	2.6	52
114	Analysis of gene expression during neurite outgrowth and regeneration. <i>BMC Neuroscience</i> , 2007, 8, 100.	1.9	37
115	Analysis of extended HLA haplotypes in multiple sclerosis and narcolepsy families confirms a predisposing effect for the class I region in Tasmanian MS patients. <i>Immunogenetics</i> , 2007, 59, 177-186.	2.4	13
116	Lineage-specific expansion of proteins exported to erythrocytes in malaria parasites. <i>Genome Biology</i> , 2006, 7, R12.	9.6	365
117	Regulation of apicomplexan actin-based motility. <i>Nature Reviews Microbiology</i> , 2006, 4, 621-628.	28.6	151
118	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006, 440, 242-245.	27.8	283
119	Detecting genome wide haplotype sharing using SNP or microsatellite haplotype data. <i>Human Genetics</i> , 2006, 119, 38-50.	3.8	10
120	On the utility of data from the International HapMap Project for Australian association studies. <i>Human Genetics</i> , 2006, 119, 220-222.	3.8	19
121	Mind the gap: analysis of marker-assisted breeding strategies for inbred mouse strains. <i>Mammalian Genome</i> , 2006, 17, 273-287.	2.2	34
122	Proximal genomic localization of STAT1 binding and regulated transcriptional activity. <i>BMC Genomics</i> , 2006, 7, 254.	2.8	18
123	Evolution and comparative analysis of the MHC Class III inflammatory region. <i>BMC Genomics</i> , 2006, 7, 281.	2.8	54
124	A genotype calling algorithm for affymetrix SNP arrays. <i>Bioinformatics</i> , 2006, 22, 7-12.	4.1	327
125	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	5.6	150
126	The Comparative Roles of Suppressor of Cytokine Signaling-1 and -3 in the Inhibition and Desensitization of Cytokine Signaling. <i>Journal of Biological Chemistry</i> , 2006, 281, 11135-11143.	3.4	109

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127	Mapping of the Plasmodium chabaudi Resistance Locus char2. Infection and Immunity, 2006, 74, 5814-5819.	2.2	11
128	A multivariate empirical Bayes statistic for replicated microarray time course data. Annals of Statistics, 2006, 34, 2387.	2.6	173
129	Long-term effect of therapeutic laser photocoagulation on gene expression in the eye. FASEB Journal, 2006, 20, 383-385.	0.5	27
130	Identification and Stoichiometry of Glycosylphosphatidylinositol-anchored Membrane Proteins of the Human Malaria Parasite Plasmodium falciparum. Molecular and Cellular Proteomics, 2006, 5, 1286-1299.	3.8	243
131	Quality Assessment of Affymetrix GeneChip Data. OMICS A Journal of Integrative Biology, 2006, 10, 358-368.	2.0	88
132	Functional Genomic Analysis of Oligodendrocyte Differentiation. Journal of Neuroscience, 2006, 26, 10967-10983.	3.6	284
133	Evolution of the Relaxin-Like Peptide Family: From Neuropeptide to Reproduction. Annals of the New York Academy of Sciences, 2005, 1041, 530-533.	3.8	23
134	Coevolution of the Relaxin-Like Peptides and Their Receptors. Annals of the New York Academy of Sciences, 2005, 1041, 534-539.	3.8	40
135	A statistical approach to the interpretation of molecular dynamics simulations of calmodulin equilibrium dynamics. Protein Science, 2005, 14, 2955-2963.	7.6	58
136	Colon cancer prognosis prediction by gene expression profiling. Oncogene, 2005, 24, 6155-6164.	5.9	92
137	A genetic screen for behavioral mutations that perturb dopaminergic homeostasis in mice. Genes, Brain and Behavior, 2005, 5, 19-28.	2.2	17
138	A comparison of match-only algorithms for the analysis of Plasmodium falciparum oligonucleotide arrays. International Journal for Parasitology, 2005, 35, 523-531.	3.1	2
139	Evolution of the relaxin-like peptide family. BMC Evolutionary Biology, 2005, 5, 14.	3.2	180
140	Rooting a phylogenetic tree with nonreversible substitution models. BMC Evolutionary Biology, 2005, 5, 2.	3.2	33
141	Identifying nineteenth century genealogical links from genotypes. Human Genetics, 2005, 117, 188-199.	3.8	17
142	Evidence for a novel glaucoma locus at chromosome 3p21-22. Human Genetics, 2005, 117, 249-257.	3.8	63
143	Incorporating interference into linkage analysis for experimental crosses. Biostatistics, 2005, 7, 374-386.	1.5	2
144	A systematic approach for comprehensive T-cell epitope discovery using peptide libraries. Bioinformatics, 2005, 21, i29-i37.	4.1	17

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145	Finding Short DNA Motifs Using Permuted Markov Models. <i>Journal of Computational Biology</i> , 2005, 12, 894-906.	1.6	73
146	The wound repair response controls outcome to cutaneous leishmaniasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15551-15556.	7.1	54
147	Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. <i>Nucleic Acids Research</i> , 2005, 33, e175-e175.	14.5	1,654
148	GOstat: find statistically overrepresented Gene Ontologies within a group of genes. <i>Bioinformatics</i> , 2004, 20, 1464-1465.	4.1	1,125
149	Experimental Design and Low-Level Analysis of Microarray Data. <i>International Review of Neurobiology</i> , 2004, 60, 25-58.	2.0	105
150	The Serine Repeat Antigen (SERA) Gene Family Phylogeny in Plasmodium: The Impact of GC Content and Reconciliation of Gene and Species Trees. <i>Molecular Biology and Evolution</i> , 2004, 21, 2161-2171.	8.9	24
151	Neuron-Specific mRNA Complexity Responses during Hippocampal Apoptosis after Traumatic Brain Injury. <i>Journal of Neuroscience</i> , 2004, 24, 2866-2876.	3.6	40
152	Extended haplotype analysis in the HLA complex reveals an increased frequency of the HFE-C282Y mutation in individuals with multiple sclerosis. <i>Human Genetics</i> , 2004, 114, 573-580.	3.8	40
153	Modeling DNA Base Substitution in Large Genomic Regions from Two Organisms. <i>Journal of Molecular Evolution</i> , 2004, 58, 12-18.	1.8	8
154	Deconvolution of Sparse Positive Spikes. <i>Journal of Computational and Graphical Statistics</i> , 2004, 13, 853-870.	1.7	11
155	A benchmark for Affymetrix GeneChip expression measures. <i>Bioinformatics</i> , 2004, 20, 323-331.	4.1	268
156	Spatial patterns of gene expression in the olfactory bulb. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12718-12723.	7.1	26
157	A Proteome Strategy for Fractionating Proteins and Peptides Using Continuous Free-Flow Electrophoresis Coupled Off-Line to Reversed-Phase High-Performance Liquid Chromatography. <i>Analytical Chemistry</i> , 2004, 76, 4811-4824.	6.5	115
158	Power calculations for selective genotyping in QTL mapping in backcross mice. <i>Genetical Research</i> , 2004, 84, 103-108.	0.9	8
159	Resampling-based multiple testing for microarray data analysis. <i>Test</i> , 2003, 12, 1-77.	1.1	416
160	Mining a Tandem Mass Spectrometry Database To Determine the Trends and Global Factors Influencing Peptide Fragmentation. <i>Analytical Chemistry</i> , 2003, 75, 6251-6264.	6.5	247
161	Exploration, normalization, and summaries of high density oligonucleotide array probe level data. <i>Biostatistics</i> , 2003, 4, 249-264.	1.5	9,603
162	Normalization of cDNA microarray data. <i>Methods</i> , 2003, 31, 265-273.	3.8	1,617

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163	Spotted Long Oligonucleotide Arrays for Human Gene Expression Analysis. <i>Genome Research</i> , 2003, 13, 1775-1785.	5.5	153
164	Enzymic, Phylogenetic, and Structural Characterization of the Unusual Papain-like Protease Domain of <i>Plasmodium falciparum</i> SERA5. <i>Journal of Biological Chemistry</i> , 2003, 278, 48169-48177.	3.4	81
165	Summaries of Affymetrix GeneChip probe level data. <i>Nucleic Acids Research</i> , 2003, 31, 15e-15.	14.5	4,372
166	A New Rodent Model to Assess Blood Stage Immunity to the <i>Plasmodium falciparum</i> Antigen Merozoite Surface Protein 119 Reveals a Protective Role for Invasion Inhibitory Antibodies. <i>Journal of Experimental Medicine</i> , 2003, 198, 869-875.	8.5	80
167	Analysis of gene expression in the developing mouse retina. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5491-5496.	7.1	44
168	Deriving statistical models for predicting peptide tandem MS product ion intensities. <i>Biochemical Society Transactions</i> , 2003, 31, 1479-1483.	3.4	43
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