

# 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	Exploration, normalization, and summaries of high density oligonucleotide array probe level data. <i>Biostatistics</i> , 2003, 4, 249-264.	1.5	9,603
2	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	27.8	6,879
3	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
4	Summaries of Affymetrix GeneChip probe level data. <i>Nucleic Acids Research</i> , 2003, 31, 15e-15.	14.5	4,372
5	Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. <i>Nucleic Acids Research</i> , 2002, 30, 15e-15.	14.5	2,946
6	Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. <i>Journal of the American Statistical Association</i> , 2002, 97, 77-87.	3.1	2,177
7	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
8	Evolving gene/transcript definitions significantly alter the interpretation of GeneChip data. <i>Nucleic Acids Research</i> , 2005, 33, e175-e175.	14.5	1,654
9	Normalization of cDNA microarray data. <i>Methods</i> , 2003, 31, 265-273.	3.8	1,617
10	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
11	Gostat: find statistically overrepresented Gene Ontologies within a group of genes. <i>Bioinformatics</i> , 2004, 20, 1464-1465.	4.1	1,125
12	Single-cell profiling of breast cancer T cells reveals a tissue-resident memory subset associated with improved prognosis. <i>Nature Medicine</i> , 2018, 24, 986-993.	30.7	689
13	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	27.8	661
14	Transcription Factors Bind Thousands of Active and Inactive Regions in the <i>Drosophila</i> Blastoderm. <i>PLoS Biology</i> , 2008, 6, e27.	5.6	428
15	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
16	Resampling-based multiple testing for microarray data analysis. <i>Test</i> , 2003, 12, 1-77.	1.1	416
17	Using control genes to correct for unwanted variation in microarray data. <i>Biostatistics</i> , 2012, 13, 539-552.	1.5	366
18	Lineage-specific expansion of proteins exported to erythrocytes in malaria parasites. <i>Genome Biology</i> , 2006, 7, R12.	9.6	365

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19	Comparison of Methods for Image Analysis on cDNA Microarray Data. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 108-136.	1.7	341
20	A genotype calling algorithm for affymetrix SNP arrays. <i>Bioinformatics</i> , 2006, 22, 7-12.	4.1	327
21	<i>PIK3CA</i> mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor <sup>+</sup> 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
22	A model selection approach for the identification of quantitative trait loci in experimental crosses. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2002, 64, 641-656.	2.2	289
23	Functional Genomic Analysis of Oligodendrocyte Differentiation. <i>Journal of Neuroscience</i> , 2006, 26, 10967-10983.	3.6	284
24	Expression profiling in primates reveals a rapid evolution of human transcription factors. <i>Nature</i> , 2006, 440, 242-245.	27.8	283
25	Analysis of the platypus genome suggests a transposon origin for mammalian imprinting. <i>Genome Biology</i> , 2009, 10, R1.	9.6	272
26	A benchmark for Affymetrix GeneChip expression measures. <i>Bioinformatics</i> , 2004, 20, 323-331.	4.1	268
27	GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly. <i>Genome Research</i> , 2017, 27, 2050-2060.	5.5	255
28	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
29	Identification and Stoichiometry of Glycosylphosphatidylinositol-anchored Membrane Proteins of the Human Malaria Parasite <i>Plasmodium falciparum</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1286-1299.	3.8	243
30	Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. <i>Biostatistics</i> , 2007, 8, 485-499.	1.5	214
31	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
32	<i>Normalization for cDNA microarray data</i> . , 2001, 4266, 141.		204
33	Signatures of tumour immunity distinguish Asian and non-Asian gastric adenocarcinomas. <i>Gut</i> , 2015, 64, 1721-1731.	12.1	197
34	Gaussian Markov Distributions over Finite Graphs. <i>Annals of Statistics</i> , 1986, 14, 138.	2.6	185
35	Normalizing and Integrating Metabolomics Data. <i>Analytical Chemistry</i> , 2012, 84, 10768-10776.	6.5	183
36	Evolution of the relaxin-like peptide family. <i>BMC Evolutionary Biology</i> , 2005, 5, 14.	3.2	180

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37	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
38	Analysis of cDNA microarray images. <i>Briefings in Bioinformatics</i> , 2001, 2, 341-349.	6.5	177
39	A multivariate empirical Bayes statistic for replicated microarray time course data. <i>Annals of Statistics</i> , 2006, 34, 2387.	2.6	173
40	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
41	Gene set enrichment analysis made simple. <i>Statistical Methods in Medical Research</i> , 2009, 18, 565-575.	1.5	166
42	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
43	Spotted Long Oligonucleotide Arrays for Human Gene Expression Analysis. <i>Genome Research</i> , 2003, 13, 1775-1785.	5.5	153
44	Statistical Methods for Handling Unwanted Variation in Metabolomics Data. <i>Analytical Chemistry</i> , 2015, 87, 3606-3615.	6.5	152
45	Regulation of apicomplexan actin-based motility. <i>Nature Reviews Microbiology</i> , 2006, 4, 621-628.	28.6	151
46	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	5.6	150
47	A Subset of <i>Plasmodium falciparum</i> SERA Genes Are Expressed and Appear to Play an Important Role in the Erythrocytic Cycle. <i>Journal of Biological Chemistry</i> , 2002, 277, 47524-47532.	3.4	149
48	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
49	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
50	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
51	Deficiency of microRNA <i>miR-34a</i> expands cell fate potential in pluripotent stem cells. <i>Science</i> , 2017, 355, .	12.6	129
52	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
53	Identification of Proteins from <i>Plasmodium falciparum</i> That Are Homologous to Reticulocyte Binding Proteins in <i>Plasmodium vivax</i> . <i>Infection and Immunity</i> , 2001, 69, 1084-1092.	2.2	123
54	Exon-Level Microarray Analyses Identify Alternative Splicing Programs in Breast Cancer. <i>Molecular Cancer Research</i> , 2010, 8, 961-974.	3.4	121

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55	The Subclonal Architecture of Metastatic Breast Cancer: Results from a Prospective Community-Based Rapid Autopsy Program "€œCASCADE" PLoS Medicine, 2016, 13, e1002204.	8.4	119
56	Replication of KIAA0350, IL2RA, RPL5 and CD58 as multiple sclerosis susceptibility genes in Australians. Genes and Immunity, 2008, 9, 624-630.	4.1	116
57	Integrative analysis of RUNX1 downstream pathways and target genes. BMC Genomics, 2008, 9, 363.	2.8	116
58	A Proteome Strategy for Fractionating Proteins and Peptides Using Continuous Free-Flow Electrophoresis Coupled Off-Line to Reversed-Phase High-Performance Liquid Chromatography. Analytical Chemistry, 2004, 76, 4811-4824.	6.5	115
59	Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation. Genome Research, 2010, 20, 1719-1729.	5.5	111
60	The Comparative Roles of Suppressor of Cytokine Signaling-1 and -3 in the Inhibition and Desensitization of Cytokine Signaling. Journal of Biological Chemistry, 2006, 281, 11135-11143.	3.4	109
61	Experimental Design and Low-Level Analysis of Microarray Data. International Review of Neurobiology, 2004, 60, 25-58.	2.0	105
62	Quality Assessment for Short Oligonucleotide Microarray Data. Technometrics, 2008, 50, 241-264.	1.9	104
63	Characterization of the opossum immune genome provides insights into the evolution of the mammalian immune system. Genome Research, 2007, 17, 982-991.	5.5	100
64	Discrete tissue microenvironments instruct diversity in resident memory T cell function and plasticity. Nature Immunology, 2021, 22, 1140-1151.	14.5	96
65	Identification of Candidate Growth Promoting Genes in Ovarian Cancer through Integrated Copy Number and Expression Analysis. PLoS ONE, 2010, 5, e9983.	2.5	95
66	Genetic Dissection of the Human Leukocyte Antigen Region by Use of Haplotypes of Tasmanians with Multiple Sclerosis. American Journal of Human Genetics, 2002, 70, 1125-1137.	6.2	93
67	Colon cancer prognosis prediction by gene expression profiling. Oncogene, 2005, 24, 6155-6164.	5.9	92
68	Estrogen Receptor $\beta$ Binds to and Regulates Three Distinct Classes of Target Genes. Journal of Biological Chemistry, 2010, 285, 22059-22066.	3.4	92
69	How data analysis affects power, reproducibility and biological insight of RNA-seq studies in complex datasets. Nucleic Acids Research, 2015, 43, 7664-7674.	14.5	90
70	Quality Assessment of Affymetrix GeneChip Data. OMICS A Journal of Integrative Biology, 2006, 10, 358-368.	2.0	88
71	Using long-read sequencing to detect imprinted DNA methylation. Nucleic Acids Research, 2019, 47, e46-e46.	14.5	88
72	Bayesian Inference of Signaling Network Topology in a Cancer Cell Line. Bioinformatics, 2012, 28, 2804-2810.	4.1	87

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73	Molecular Analysis of Gene Expression in the Developing Pontocerebellar Projection System. <i>Neuron</i> , 2002, 36, 417-434.	8.1	84
74	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
75	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
76	Correcting gene expression data when neither the unwanted variation nor the factor of interest are observed. <i>Biostatistics</i> , 2016, 17, 16-28.	1.5	82
77	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
78	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
79	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
80	On Genetic Map Functions. <i>Genetics</i> , 1996, 142, 1369-1377.	2.9	78
81	Argon Laser Photocoagulation-Induced Modification of Gene Expression in the Retina. , 2003, 44, 1426.		76
82	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793.	12.8	75
83	Inner cell allocation in the mouse morula: The role of oriented division during fourth cleavage. <i>Developmental Biology</i> , 1990, 137, 13-25.	2.0	74
84	Global analyses of mRNA translational control during early <i>Drosophila</i> embryogenesis. <i>Genome Biology</i> , 2007, 8, R63.	9.6	74
85	Finding Short DNA Motifs Using Permuted Markov Models. <i>Journal of Computational Biology</i> , 2005, 12, 894-906.	1.6	73
86	Removing unwanted variation in a differential methylation analysis of Illumina HumanMethylation450 array data. <i>Nucleic Acids Research</i> , 2015, 43, e106-e106.	14.5	73
87	A new normalization for Nanostring nCounter gene expression data. <i>Nucleic Acids Research</i> , 2019, 47, 6073-6083.	14.5	73
88	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
89	RLE plots: Visualizing unwanted variation in high dimensional data. <i>PLoS ONE</i> , 2018, 13, e0191629.	2.5	69
90	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

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91	Temporal Global Expression Data Reveal Known and Novel Salicylate-Impacted Processes and Regulators Mediating Powdery Mildew Growth and Reproduction on Arabidopsis. <i>Plant Physiology</i> , 2009, 149, 1435-1451.	4.8	64
92	Evidence for a novel glaucoma locus at chromosome 3p21-22. <i>Human Genetics</i> , 2005, 117, 249-257.	3.8	63
93	Over- and Underrepresentation of Short DNA Words in Herpesvirus Genomes. <i>Journal of Computational Biology</i> , 1996, 3, 345-360.	1.6	62
94	Model selection and prediction: Normal regression. <i>Annals of the Institute of Statistical Mathematics</i> , 1993, 45, 35-54.	0.8	61
95	Dating Rare Mutations from Small Samples with Dense Marker Data. <i>Genetics</i> , 2014, 197, 1315-1327.	2.9	61
96	Drug and Cell Type-Specific Regulation of Genes with Different Classes of Estrogen Receptor $\beta$ -Selective Agonists. <i>PLoS ONE</i> , 2009, 4, e6271.	2.5	59
97	Genes for Glycosylphosphatidylinositol Toxin Biosynthesis in <i>Plasmodium falciparum</i> . <i>Infection and Immunity</i> , 2002, 70, 4510-4522.	2.2	58
98	A statistical approach to the interpretation of molecular dynamics simulations of calmodulin equilibrium dynamics. <i>Protein Science</i> , 2005, 14, 2955-2963.	7.6	58
99	A score test for the linkage analysis of qualitative and quantitative traits based on identity by descent data from sib-pairs. <i>Biostatistics</i> , 2000, 1, 1-26.	1.5	54
100	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
101	Evolution and comparative analysis of the MHC Class III inflammatory region. <i>BMC Genomics</i> , 2006, 7, 281.	2.8	54
102	Identification of cancer sex-disparity in the functional integrity of p53 and its X chromosome network. <i>Nature Communications</i> , 2019, 10, 5385.	12.8	53
103	A comparison of Affymetrix gene expression arrays. <i>BMC Bioinformatics</i> , 2007, 8, 449.	2.6	52
104	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
105	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
106	A mouse-specific retrotransposon drives a conserved Cdk2ap1 isoform essential for development. <i>Cell</i> , 2021, 184, 5541-5558.e22.	28.9	52
107	Phatâ€a gene finding program for <i>Plasmodium falciparum</i> . <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 167-174.	1.1	51
108	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

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109	Systematic noise degrades gene co-expression signals but can be corrected. BMC Bioinformatics, 2015, 16, 309.	2.6	50
110	The Effects of Genotyping Errors and Interference on Estimation of Genetic Distance. Human Heredity, 1997, 47, 86-100.	0.8	49
111	TumorBoost: Normalization of allele-specific tumor copy numbers from a single pair of tumor-normal genotyping microarrays. BMC Bioinformatics, 2010, 11, 245.	2.6	49
112	SNP mapping and candidate gene sequencing in the class I region of the HLA complex: searching for multiple sclerosis susceptibility genes in Tasmanians. Tissue Antigens, 2008, 71, 42-50.	1.0	48
113	Silencing of Odorant Receptor Genes by G Protein $\beta\gamma$ Signaling Ensures the Expression of One Odorant Receptor per Olfactory Sensory Neuron. Neuron, 2014, 81, 847-859.	8.1	47
114	Analysis of gene expression in the developing mouse retina. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5491-5496.	7.1	44
115	Evaluating stably expressed genes in single cells. GigaScience, 2019, 8, .	6.4	44
116	Deriving statistical models for predicting peptide tandem MS product ion intensities. Biochemical Society Transactions, 2003, 31, 1479-1483.	3.4	43
117	Protocol matters: which methylome are you actually studying?. Epigenomics, 2010, 2, 587-598.	2.1	42
118	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
119	Estimating the influence of temperature on the survival of chinook salmon smolts ( <i>Oncorhynchus tshawytscha</i> ) in the Columbia River. Journal of Fisheries and Aquatic Sciences, 1995, 52, 855-863.	1.4	41
120	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
121	Subcompartmentalisation of Proteins in the Rhoptries Correlates with Ordered Events of Erythrocyte Invasion by the Blood Stage Malaria Parasite. PLoS ONE, 2012, 7, e46160.	2.5	41
122	Neuron-Specific mRNA Complexity Responses during Hippocampal Apoptosis after Traumatic Brain Injury. Journal of Neuroscience, 2004, 24, 2866-2876.	3.6	40
123	Extended haplotype analysis in the HLA complex reveals an increased frequency of the HFE-C282Y mutation in individuals with multiple sclerosis. Human Genetics, 2004, 114, 573-580.	3.8	40
124	Coevolution of the Relaxin-Like Peptides and Their Receptors. Annals of the New York Academy of Sciences, 2005, 1041, 534-539.	3.8	40
125	On Gene Ranking Using Replicated Microarray Time Course Data. Biometrics, 2009, 65, 40-51.	1.4	39
126	Robustness of the no-interference model for ordering genetic markers.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 3103-3106.	7.1	38



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127	Conserved Role of unc-79 in Ethanol Responses in Lightweight Mutant Mice. <i>PLoS Genetics</i> , 2010, 6, e1001057.	3.5	38
128	Chromosomes X, 9, and the H2 locus interact epistatically to control <i>Leishmania major</i> infection. <i>European Journal of Immunology</i> , 1999, 29, 3047-3050.	2.9	37
129	Analysis of gene expression during neurite outgrowth and regeneration. <i>BMC Neuroscience</i> , 2007, 8, 100.	1.9	37
130	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
131	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
132	Accurate RNA Sequencing From Formalin-Fixed Cancer Tissue to Represent High-Quality Transcriptome From Frozen Tissue. <i>JCO Precision Oncology</i> , 2018, 2018, 1-9.	3.0	35
133	Mind the gap: analysis of marker-assisted breeding strategies for inbred mouse strains. <i>Mammalian Genome</i> , 2006, 17, 273-287.	2.2	34
134	Rooting a phylogenetic tree with nonreversible substitution models. <i>BMC Evolutionary Biology</i> , 2005, 5, 2.	3.2	33
135	Differential Regulation of Native Estrogen Receptor-Regulatory Elements by Estradiol, Tamoxifen, and Raloxifene. <i>Molecular Endocrinology</i> , 2008, 22, 287-303.	3.7	33
136	DECENT: differential expression with capture efficiency adjustment for single-cell RNA-seq data. <i>Bioinformatics</i> , 2019, 35, 5155-5162.	4.1	33
137	Parametric deconvolution of positive spike trains. <i>Annals of Statistics</i> , 2000, 28, .	2.6	32
138	Incorporating Crossover Interference into Pedigree Analysis Using the $\chi^2$ Model. <i>Human Heredity</i> , 1996, 46, 315-322.	0.8	31
139	Removing unwanted variation with CytoFRUV to integrate multiple CyTOF datasets. <i>ELife</i> , 2020, 9, .	6.0	31
140	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
141	Symmetric Wiener-Hopf factorisations in Markov additive processes. <i>Zeitschrift für Wahrscheinlichkeitstheorie Und Verwandte Gebiete</i> , 1973, 26, 105-118.	0.8	30
142	Estimating the fraction of invariable codons with a capture-recapture method. <i>Journal of Molecular Evolution</i> , 1992, 35, 253-60.	1.8	30
143	Multiple genetic loci modify susceptibility to plasmacytoma-related morbidity in <i>E<math>\mu</math>-v-abl</i> transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 11299-11304.	7.1	29
144	Statistical Analysis of Half-Tetrads. <i>Genetics</i> , 1998, 150, 473-485.	2.9	29

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145	An estimate of the crosstalk matrix in four-dye fluorescence-based DNA sequencing. <i>Electrophoresis</i> , 1999, 20, 1433-1442.	2.4	28
146	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496.	5.5	28
147	Contextual fear conditioning induces differential alternative splicing. <i>Neurobiology of Learning and Memory</i> , 2016, 134, 221-235.	1.9	28
148	Long-term effect of therapeutic laser photocoagulation on gene expression in the eye. <i>FASEB Journal</i> , 2006, 20, 383-385.	0.5	27
149	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
150	Serum microRNA is a biomarker for post-operative monitoring in glioma. <i>Journal of Neuro-Oncology</i> , 2020, 149, 391-400.	2.9	27
151	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
152	A note on random walks. <i>Journal of Applied Probability</i> , 1971, 8, 198-201.	0.7	24
153	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
154	SNPs on Chips: The Hidden Genetic Code in Expression Arrays. <i>Biological Psychiatry</i> , 2007, 61, 13-16.	1.3	24
155	Investigating and Correcting Plasma DNA Sequencing Coverage Bias to Enhance Aneuploidy Discovery. <i>PLoS ONE</i> , 2014, 9, e86993.	2.5	24
156	An Algorithm for Haplotype Analysis. <i>Journal of Computational Biology</i> , 1997, 4, 535-546.	1.6	23
157	Evolution of the Relaxin-Like Peptide Family: From Neuropeptide to Reproduction. <i>Annals of the New York Academy of Sciences</i> , 2005, 1041, 530-533.	3.8	23
158	Tissue-Specific Regulation of Genes by Estrogen Receptors. <i>Seminars in Reproductive Medicine</i> , 2012, 30, 14-22.	1.1	23
159	Multiple testing and its applications to microarrays. <i>Statistical Methods in Medical Research</i> , 2009, 18, 543-563.	1.5	22
160	A hierarchical approach to removal of unwanted variation for large-scale metabolomics data. <i>Nature Communications</i> , 2021, 12, 4992.	12.8	22
161	Multiple sclerosis risk variants regulate gene expression in innate and adaptive immune cells. <i>Life Science Alliance</i> , 2020, 3, e202000650.	2.8	22
162	Atypical regions in large genomic DNA sequences.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 7134-7138.	7.1	21

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163	Multiple Transcription Factor Elements Collaborate with Estrogen Receptor $\hat{\pm}$ to Activate an Inducible Estrogen Response Element in the NKG2E Gene. <i>Endocrinology</i> , 2007, 148, 3449-3458.	2.8	20
164	Unliganded estrogen receptor- $\hat{2}$ regulation of genes is inhibited by tamoxifen. <i>Molecular and Cellular Endocrinology</i> , 2010, 315, 201-207.	3.2	20
165	A score test for linkage using identity by descent data from sibships. <i>Annals of Statistics</i> , 1999, 27, .	2.6	20
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