Leming Shi

List of Publications by Year
in descending order

172 papers	16,167 citations	23567 58 h-index	17105 122 g-index
182 all docs	182 docs citations	182 times ranked	21746 citing authors

#	Article	IF	Citations
1	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	17.5	1,927
2	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
3	The Estrogen Receptor Relative Binding Affinities of 188 Natural and Xenochemicals: Structural Diversity of Ligands. Toxicological Sciences, 2000, 54, 138-153.	3.1	689
4	Evaluation of DNA microarray results with quantitative gene expression platforms. Nature Biotechnology, 2006, 24, 1115-1122.	17.5	558
5	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. Nature, 2015, 526, 700-704.	27.8	478
6	Performance comparison of one-color and two-color platforms within the Microarray Quality Control (MAQC) project. Nature Biotechnology, 2006, 24, 1140-1150.	17.5	440
7	Structure–Activity Relationships for a Large Diverse Set of Natural, Synthetic, and Environmental Estrogens. Chemical Research in Toxicology, 2001, 14, 280-294.	3.3	432
8	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
9	Rat toxicogenomic study reveals analytical consistency across microarray platforms. Nature Biotechnology, 2006, 24, 1162-1169.	17.5	389
10	Drug hypersensitivity caused by alteration of the MHC-presented self-peptide repertoire. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9959-9964.	7.1	354
11	The External RNA Controls Consortium: a progress report. Nature Methods, 2005, 2, 731-734.	19.0	328
12	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
13	QSAR Models Using a Large Diverse Set of Estrogens. Journal of Chemical Information and Computer Sciences, 2001, 41, 186-195.	2.8	323
14	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316
15	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. Cancer Cell, 2014, 26, 722-737.	16.8	287
16	Next-generation sequencing in the clinic: Promises and challenges. Cancer Letters, 2013, 340, 284-295.	7.2	272
17	Similarities and Differences in the Expression of Drug-Metabolizing Enzymes between Human Hepatic Cell Lines and Primary Human Hepatocytes. Drug Metabolism and Disposition, 2011, 39, 528-538.	3.3	262
18	A comparison of batch effect removal methods for enhancement of prediction performance using MAQC-II microarray gene expression data. Pharmacogenomics Journal, 2010, 10, 278-291.	2.0	249

#	Article	IF	Citations
19	Mold^2, Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. Journal of Chemical Information and Modeling, 2008, 48, 1337-1344.	5.4	241
20	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. BMC Bioinformatics, 2008, 9, S10.	2.6	215
21	ArrayTrack--supporting toxicogenomic research at the U.S. Food and Drug Administration National Center for Toxicological Research.. Environmental Health Perspectives, 2003, 111, 1819-1826.	6.0	197
22	DRAR-CPI: a server for identifying drug repositioning potential and adverse drug reactions via the chemicalâ€"protein interactome. Nucleic Acids Research, 2011, 39, W492-W498.	14.5	189
23	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	17.5	174
24	Effect of training-sample size and classification difficulty on the accuracy of genomic predictors. Breast Cancer Research, 2010, 12, R5.	5.0	169
25	Using RNA sample titrations to assess microarray platform performance and normalization techniques. Nature Biotechnology, 2006, 24, 1123-1131.	17.5	168
26	Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential. BMC Bioinformatics, 2005, 6, S12.	2.6	164
27	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. Genome Biology, 2014, 15, 523.	8.8	147
28	Next-generation sequencing and its applications in molecular diagnostics. Expert Review of Molecular Diagnostics, 2011, 11, 333-343.	3.1	146
29	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. Scientific Reports, 2017, 7, 4200.	3.3	139
30	Prediction of estrogen receptor binding for 58,000 chemicals using an integrated system of a tree-based model with structural alerts.. Environmental Health Perspectives, 2002, 110, 29-36.	6.0	133
31	Discovery of Molecular Mechanisms of Traditional Chinese Medicinal Formula Si-Wu-Tang Using Gene Expression Microarray and Connectivity Map. PLoS ONE, 2011, 6, e18278.	2.5	127
32	Phytoestrogens and Mycoestrogens Bind to the Rat Uterine Estrogen Receptor. Journal of Nutrition, 2002, 132, 658-664.	2.9	125
33	Reproducible and reliable microarray results through quality control: good laboratory proficiency and appropriate data analysis practices are essential. Current Opinion in Biotechnology, 2008, 19, 10-18.	6.6	125
34	Blood molecular markers associated with COVIDâ€19 immunopathology and multiâ€organ damage. EMBO Journal, 2020, 39, e105896.	7.8	123
35	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
36	k-Nearest neighbor models for microarray gene expression analysis and clinical outcome prediction. Pharmacogenomics Journal, 2010, 10, 292-309.	2.0	102

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37	QA/QC: challenges and pitfalls facing the microarray community and regulatory agencies. Expert Review of Molecular Diagnostics, 2004, 4, 761-777.	3.1	99
38	Development of public toxicogenomics software for microarray data management and analysis. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2004, 549, 241-253.	1.0	98
39	Evaluation of external RNA controls for the assessment of microarray performance. Nature Biotechnology, 2006, 24, 1132-1139.	17.5	97
40	Exploring Off-Targets and Off-Systems for Adverse Drug Reactions via Chemical-Protein Interactome â€" Clozapine-Induced Agranulocytosis as a Case Study. PLoS Computational Biology, 2011, 7, e1002016.	3.2	93
41	Voluntary exploratory data submissions to the US FDA and the EMA: experience and impact. Nature Reviews Drug Discovery, 2010, 9, 435-445.	46.4	92
42	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.9	90
43	Sex Differences in the Expression of Drug-Metabolizing and Transporter Genes in Human Liver. Journal of Drug Metabolism & Toxicology, 2012, 3, 1000119.	0.1	88
44	Assessment of Prediction Confidence and Domain Extrapolation of Two Structure-Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. Environmental Health Perspectives, 2004, 112, 1249-1254.	6.0	87
45	Multi-class cancer classification by total principal component regression (TPCR) using microarray gene expression data. Nucleic Acids Research, 2005, 33, 56-65.	14.5	81
46	Comparing Next-Generation Sequencing and Microarray Technologies in a Toxicological Study of the Effects of Aristolochic Acid on Rat Kidneys. Chemical Research in Toxicology, 2011, 24, 1486-1493.	3.3	80
47	Multi-class tumor classification by discriminant partial least squares using microarray gene expression data and assessment of classification models. Computational Biology and Chemistry, 2004, 28, 235-243.	2.3	79
48	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	1.6	79
49	Assessment of Prediction Confidence and Domain Extrapolation of Two Structureâ€"Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. Environmental Health Perspectives, 2004, 112, 1249-1254.	6.0	78
50	Advances in single-cell RNA sequencing and its applications in cancer research. Oncotarget, 2017, 8, 53763-53779.	1.8	76
51	The EDKB: an established knowledge base for endocrine disrupting chemicals. BMC Bioinformatics, 2010, 11, S5.	2.6	75
52	Microarray scanner calibration curves: characteristics and implications. BMC Bioinformatics, 2005, 6, S11.	2.6	74
53	Differences in hepatotoxicity and gene expression profiles by anti-diabetic PPAR Î³ agonists on rat primary hepatocytes and human HepG2 cells. Molecular Diversity, 2006, 10, 349-360.	3.9	74
54	STRUCTUREâ€"ACTIVITY RELATIONSHIP APPROACHES AND APPLICATIONS. Environmental Toxicology and Chemistry, 2003, 22, 1680.	4.3	71

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55	Molecular Docking to Identify Associations Between Drugs and Class I Human Leukocyte Antigens for Predicting Idiosyncratic Drug Reactions. Combinatorial Chemistry and High Throughput Screening, 2015, 18, 296-304.	1.1	69
56	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	2.0	68
57	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
58	ArrayTrack: An FDA and Public Genomic Tool. Methods in Molecular Biology, 2009, 563, 379-398.	0.9	67
59	DDI-CPI, a server that predicts drug–drug interactions through implementing the chemical–protein interactome. Nucleic Acids Research, 2014, 42, W46-W52.	14.5	63
60	Assessing batch effects of genotype calling algorithm BRLMM for the Affymetrix GeneChip Human Mapping 500 K array set using 270 HapMap samples. BMC Bioinformatics, 2008, 9, S17.	2.6	62
61	An integrated "4-phase" approach for setting endocrine disruption screening priorities--phase I and II predictions of estrogen receptor binding affinity. SAR and QSAR in Environmental Research, 2002, 13, 69-88.	2.2	61
62	Technical Reproducibility of Genotyping SNP Arrays Used in Genome-Wide Association Studies. PLoS ONE, 2012, 7, e44483.	2.5	59
63	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
64	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. Scientific Reports, 2016, 6, 28400.	3.3	57
65	Quality control and quality assessment of data from surface-enhanced laser desorption/ionization (SELDI) time-of flight (TOF) mass spectrometry (MS). BMC Bioinformatics, 2005, 6, S5.	2.6	55
66	Genomic indicators in the blood predict drug-induced liver injury. Pharmacogenomics Journal, 2010, 10, 267-277.	2.0	54
67	A testing strategy to predict risk for drug-induced liver injury in humans using high-content screen assays and the 'rule-of-two' model. Archives of Toxicology, 2014, 88, 1439-1449.	4.2	54
68	Consistency of predictive signature genes and classifiers generated using different microarray platforms. Pharmacogenomics Journal, 2010, 10, 247-257.	2.0	53
69	Assessing QSAR Limitations - A Regulatory Perspective. Current Computer-Aided Drug Design, 2005, 1, 195-205.	1.2	52
70	DNA Microarrays Are Predictive of Cancer Prognosis: A Re-evaluation. Clinical Cancer Research, 2010, 16, 629-636.	7.0	52
71	Reproducibility Probability Score—incorporating measurement variability across laboratories for gene selection. Nature Biotechnology, 2006, 24, 1476-1477.	17.5	51
72	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	1.6	51

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73	Differential gene expression in mouse primary hepatocytes exposed to the peroxisome proliferator-activated receptor Î± agonists. BMC Bioinformatics, 2006, 7, S18.	2.6	47
74	Gene Expression Profiles Distinguish the Carcinogenic Effects of Aristolochic Acid in Target (Kidney) and Non-target (Liver) Tissues in Rats. BMC Bioinformatics, 2006, 7, S20.	2.6	46
75	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. Nucleic Acids Research, 2019, 47, D1090-D1101.	14.5	45
76	Endoplasmic reticulum stress and MAPK signaling pathway activation underlie leflunomide-induced toxicity in HepG2 Cells. Toxicology, 2017, 392, 11-21.	4.2	44
77	Gene Expression Variability in Human Hepatic Drug Metabolizing Enzymes and Transporters. PLoS ONE, 2013, 8, e60368.	2.5	43
78	A multi-omic analysis of human naÃ¯ve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
79	Identifying Unexpected Therapeutic Targets via Chemical-Protein Interactome. PLoS ONE, 2010, 5, e9568.	2.5	42
80	Cytotoxicity and inhibitory effects of low-concentration triclosan on adipogenic differentiation of human mesenchymal stem cells. Toxicology and Applied Pharmacology, 2012, 262, 117-123.	2.8	42
81	Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. Pharmacogenomics Journal, 2010, 10, 310-323.	2.0	41
82	Quantitative Structure-Activity Relationship Study of Histone Deacetylase Inhibitors. Anti-Cancer Agents in Medicinal Chemistry, 2004, 4, 273-299.	7.0	40
83	Multiclass Decision Forestâ€"A Novel Pattern Recognition Method for Multiclass Classification in Microarray Data Analysis. DNA and Cell Biology, 2004, 23, 685-694.	1.9	40
84	A genomic characterization of the influence of silver nanoparticles on bone differentiation in MC3T3â€E1 cells. Journal of Applied Toxicology, 2018, 38, 172-179.	2.8	39
85	Activation of the Nrf2 signaling pathway in usnic acid-induced toxicity in HepG2 cells. Archives of Toxicology, 2017, 91, 1293-1307.	4.2	37
86	Genomic analysis of microRNA time-course expression in liver of mice treated with genotoxic carcinogen N-ethyl-N-nitrosourea. BMC Genomics, 2010, 11, 609.	2.8	36
87	mRNA enrichment protocols determine the quantification characteristics of external RNA spike-in controls in RNA-Seq studies. Science China Life Sciences, 2013, 56, 134-142.	4.9	36
88	Characterizing and annotating the genome using RNA-seq data. Science China Life Sciences, 2017, 60, 116-125.	4.9	35
89	Using Decision Forest to Classify Prostate Cancer Samples on the Basis of SELDI-TOF MS Data: Assessing Chance Correlation and Prediction Confidence. Environmental Health Perspectives, 2004, 112, 1622-1627.	6.0	34
90	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. BMC Genomics, 2011, 12, 590.	2.8	34

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91	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	1.6	34
92	Similarities and differences between variants called with human reference genome HG19 or HG38. BMC Bioinformatics, 2019, 20, 101.	2.6	33
93	Integrating time-course microarray gene expression profiles with cytotoxicity for identification of biomarkers in primary rat hepatocytes exposed to cadmium. Bioinformatics, 2006, 22, 77-87.	4.1	32
94	Improvement in the Reproducibility and Accuracy of DNA Microarray Quantification by Optimizing Hybridization Conditions. BMC Bioinformatics, 2006, 7, S17.	2.6	32
95	Toxicogenomics and Cancer Susceptibility: Advances with Next-Generation Sequencing. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2014, 32, 121-158.	2.9	32
96	Integrated microRNA, mRNA, and protein expression profiling reveals microRNA regulatory networks in rat kidney treated with a carcinogenic dose of aristolochic acid. BMC Genomics, 2015, 16, 365.	2.8	32
97	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	17.5	32
98	Analysis of gene expression changes in relation to toxicity and tumorigenesis in the livers of Big Blue transgenic rats fed comfrey (Symphytum officinale). BMC Bioinformatics, 2006, 7, S16.	2.6	31
99	Critical role of bioinformatics in translating huge amounts of next-generation sequencing data into personalized medicine. Science China Life Sciences, 2013, 56, 110-118.	4.9	31
100	Methysticin and 7,8-Dihydromethysticin are Two Major Kavalactones in Kava Extract to Induce CYP1A1. Toxicological Sciences, 2011, 124, 388-399.	3.1	30
101	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
102	Targeted RNA-Sequencing with Competitive Multiplex-PCR Amplicon Libraries. PLoS ONE, 2013, 8, e79120.	2.5	30
103	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. Rna, 2013, 19, 479-489.	3.5	29
104	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. Genome Biology, 2021, 22, 111.	8.8	29
105	Abnormal gene expression in cerebellum of Npc1â˘ʹ/â˘ʹ mice during postnatal development. Brain Research, 2010, 1325, 128-140.	2.2	27
106	Transcriptional profiling of Chinese medicinal formula Si-Wu-Tang on breast cancer cells reveals phytoestrogenic activity. BMC Complementary and Alternative Medicine, 2013, 13, 11.	3.7	27
107	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. Scientific Reports, 2016, 6, 35996.	3.3	27
108	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. Biology Direct, 2018, 13, 14.	4.6	27

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109	Comparative Analysis of Human Protein-Coding and Noncoding RNAs between Brain and 10 Mixed Cell Lines by RNA-Seq. PLoS ONE, 2011, 6, e28318.	2.5	27
110	Studies on abacavir-induced hypersensitivity reaction: a successful example of translation of pharmacogenetics to personalized medicine. Science China Life Sciences, 2013, 56, 119-124.	4.9	26
111	A Partial Least Squares–Based Consensus Regression Method for the Analysis of Near–Infrared Complex Spectral Data of Plant Samples. Analytical Letters, 2006, 39, 2073-2083.	1.8	24
112	3D QSAR studies on peroxisome proliferator-activated receptor ? agonists using CoMFA and CoMSIA. Journal of Molecular Modeling, 2004, 10, 165-177.	1.8	23
113	Molecular biomarkers: a US FDA effort. Biomarkers in Medicine, 2010, 4, 215-225.	1.4	23
114	Overcoming chemoresistance in prostate cancer with Chinese medicine Tripterygium wilfordii via multiple mechanisms. Oncotarget, 2016, 7, 61246-61261.	1.8	23
115	Microarray platform consistency is revealed by biologically functional analysis of gene expression profiles. BMC Bioinformatics, 2009, 10, S12.	2.6	22
116	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. Scientific Data, 2014, 1, 140013.	5.3	22
117	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. Pharmacogenomics Journal, 2010, 10, 364-374.	2.0	21
118	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
119	Design, synthesis, and evaluation of a new class of noncyclic 1,3-dicarbonyl compounds as PPARα selective activators. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 3507-3511.	2.2	20
120	Evaluation of gene expression data generated from expired Affymetrix GeneChip® microarrays using MAQC reference RNA samples. BMC Bioinformatics, 2010, 11, S10.	2.6	20
121	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
122	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. BMC Bioinformatics, 2015, 16, S9.	2.6	19
123	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	14.5	19
124	A microarray study of MPP+-treated PC12 Cells: Mechanisms of toxicity (MOT) analysis using bioinformatics tools. BMC Bioinformatics, 2005, 6, S8.	2.6	18
125	The Accurate Prediction of Protein Family from Amino Acid Sequence by Measuring Features of Sequence Fragments. Journal of Computational Biology, 2009, 16, 1671-1688.	1.6	16
126	Identifying and annotating human bifunctional RNAs reveals their versatile functions. Science China Life Sciences, 2016, 59, 981-992.	4.9	16

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127	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor Î³ Agonists. Journal of Chemical Information and Computer Sciences, 2004, 44, 230-238.	2.8	15
128	Construction of a virtual combinatorial library using SMILES strings to discover potential structure-diverse PPAR modulators. European Journal of Medicinal Chemistry, 2005, 40, 632-640.	5.5	15
129	Towards the development of an omics data analysis framework. Regulatory Toxicology and Pharmacology, 2020, 112, 104621.	2.7	15
130	An integrated bioinformatics infrastructure essential for advancing pharmacogenomics and personalized medicine in the context of the FDA's Critical Path Initiative. Drug Discovery Today: Technologies, 2007, 4, 3-8.	4.0	13
131	Selecting a single model or combining multiple models for microarray-based classifier development? â€" A comparative analysis based on large and diverse datasets generated from the MAQC-II project. BMC Bioinformatics, 2011, 12, S3.	2.6	13
132	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. Human Genetics, 2013, 132, 899-911.	3.8	13
133	QA/QC issues to aid regulatory acceptance of microarray gene expression data. Environmental and Molecular Mutagenesis, 2007, 48, 349-353.	2.2	12
134	Very Important Pool (VIP) genes â€" an application for microarray-based molecular signatures. BMC Bioinformatics, 2008, 9, S9.	2.6	12
135	ArrayTrack: An FDA and Public Genomic Tool. Methods in Molecular Biology, 2017, 1613, 333-353.	0.9	12
136	Evaluating variations of genotype calling: a potential source of spurious associations in genome-wide association studies. Journal of Genetics, 2010, 89, 55-64.	0.7	11
137	Valence-state speciation of sulfur by x-ray fluorescence spectometry and Kalman filtering. Analytica Chimica Acta, 1991, 248, 257-261.	5.4	9
138	Gaining Confidence on Molecular Classification through Consensus Modeling and Validation. Toxicology Mechanisms and Methods, 2006, 16, 59-68.	2.7	9
139	Investigation of reproducibility of differentially expressed genes in DNA microarrays through statistical simulation. BMC Proceedings, 2009, 3, S4.	1.6	9
140	Standardization efforts enabling next-generation sequencing and microarray based biomarkers for precision medicine. Biomarkers in Medicine, 2015, 9, 1265-1272.	1.4	9
141	Self-self Hybridization As An Alternative Experiment Design to Dye Swap for Two-color Microarrays. OMICS A Journal of Integrative Biology, 2007, 11, 14-24.	2.0	8
142	Estimating relative noise to signal in DNA microarray data. International Journal of Bioinformatics Research and Applications, 2013, 9, 433.	0.2	8
143	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 0, 5, 2333.	1.6	8
144	DNA Microarrays: Applications, Future Trends, and the Need for Standardization. Springer Series on Fluorescence, 2008, , 215-237.	0.8	7

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145	Good practice guidelines for biomarker discovery from array data: a case study for breast cancer prognosis. BMC Systems Biology, 2013, 7, S2.	3.0	7
146	HLADR: a database system for enhancing the discovery of biomarkers for predicting human leukocyte antigen-mediated idiosyncratic adverse drug reactions. Biomarkers in Medicine, 2015, 9, 1079-1093.	1.4	7
147	Maximum predictive power of the microarray-based models for clinical outcomes is limited by correlation between endpoint and gene expression profile. BMC Genomics, 2011, 12, S3.	2.8	6
148	Inhalation Anesthesia-Induced Neuronal Damage and Gene Expression Changes in Developing Rat Brain. Systems Pharmacology, 2012, 1, 1-9.	1.0	6
149	Shifting from Population-wide to Personalized Cancer Prognosis with Microarrays. PLoS ONE, 2012, 7, e29534.	2.5	6
150	The MicroArray Quality Control (MAQC) Project and Cross-Platform Analysis of Microarray Data. , 2011, , 171-192.		6
151	Simultaneous analysis of Co(II), Ni(II), Cu(II), Zn(II) and Cd(II) by spectrophotometry and the Kalman filter. Journal of Chemometrics, 1991, 5, 193-199.	1.3	5
152	Arrays, molecular diagnostics, personalized therapy and informatics. Expert Review of Molecular Diagnostics, 2001, 1, 363-365.	3.1	5
153	Utilization of Gene Expression Signature for Quality Control of Traditional Chinese Medicine Formula Si-Wu-Tang. AAPS Journal, 2013, 15, 884-892.	4.4	5
154	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	4.9	5
155	The Current Status of DNA Microarrays. , 2009, , 3-24.		5
156	Classification of cDNA Array Genes That Have a Highly Significant Discriminative Power Due to Their Unique Distribution in Four Brain Regions. DNA and Cell Biology, 2004, 23, 661-674.	1.9	4
157	Correlation analysis of external RNA controls reveals its utility for assessment of microarray assay. Analytical Biochemistry, 2009, 385, 203-207.	2.4	4
158	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4
159	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	3.3	4
160	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. PLoS ONE, 2013, 8, e66521.	2.5	4
161	Microarray Technology: Unresolved Issues and Future Challenges from aÂRegulatory Perspective. Springer Series on Fluorescence, 2008, , 265-282.	0.8	3
162	The Reproducibility of Lists of Differentially Expressed Genes in Microarray Studies. Nature Precedings, 2007, , .	0.1	2

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163	Potential Sources of Spurious Associations and Batch Effects in Genome-Wide Association Studies. , 0, , 191-201.		2
164	A standardized fold change method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. FEBS Open Bio, 2018, 8, 481-490.	2.3	2
165	Variability of DNA microarray gene expression profiles in cultured rat primary hepatocytes. Gene Regulation and Systems Biology, 2007, 1, 235-49.	2.3	2
166	Comprehensive microRNA-seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. Scientific Data, 2022, 9, 201.	5.3	2
167	Some novel methods based on recursive optimal estimation. Applications to analytical chemistry. Analytica Chimica Acta, 1993, 277, 199-204.	5.4	1
168	An adaptive feature selection method for microarray data analysis. , 2012, , .		1
169	Abstract 2575: DNA microarray and connectivity map analysis reveals estrogen-like activity of Chinese medicinal formula Si-Wu-Tang. , 2012, , .		1
170	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor Î³ Agonists.. ChemInform, 2004, 35, no.	0.0	0
171	Variability of DNA Microarray Gene Expression Profiles in Cultured Rat Primary Hepatocytes. Gene Regulation and Systems Biology, 2007, 1, 117762500700100.	2.3	0
172	Guidelines for terminology for microtechnology in clinical laboratories (IUPAC Technical Report). Pure and Applied Chemistry, 2006, 78, 677-684.	1.9	0