

Leming Shi

List of Publications by Year in descending order

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172
papers

16,167
citations

27035

58
h-index

19470

122
g-index

182
all docs

182
docs citations

182
times ranked

23951
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive microRNA-seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. <i>Scientific Data</i> , 2022, 9, 201.	2.4	2
2	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
3	A verified genomic reference sample for assessing performance of cancer panels detecting small variants of low allele frequency. <i>Genome Biology</i> , 2021, 22, 111.	3.8	29
4	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. <i>Nucleic Acids Research</i> , 2020, 48, 8320-8331.	6.5	19
5	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. <i>EMBO Journal</i> , 2020, 39, e105896.	3.5	123
6	Towards the development of an omics data analysis framework. <i>Regulatory Toxicology and Pharmacology</i> , 2020, 112, 104621.	1.3	15
7	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019, 10, 5026.	5.8	67
8	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. <i>Science China Life Sciences</i> , 2019, 62, 895-904.	2.3	5
9	Similarities and differences between variants called with human reference genome HG19 or HG38. <i>BMC Bioinformatics</i> , 2019, 20, 101.	1.2	33
10	PreMedKB: an integrated precision medicine knowledgebase for interpreting relationships between diseases, genes, variants and drugs. <i>Nucleic Acids Research</i> , 2019, 47, D1090-D1101.	6.5	45
11	A standardized fold change method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. <i>FEBS Open Bio</i> , 2018, 8, 481-490.	1.0	2
12	A genomic characterization of the influence of silver nanoparticles on bone differentiation in MC3T3-E1 cells. <i>Journal of Applied Toxicology</i> , 2018, 38, 172-179.	1.4	39
13	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. <i>Biology Direct</i> , 2018, 13, 14.	1.9	27
14	Characterizing and annotating the genome using RNA-seq data. <i>Science China Life Sciences</i> , 2017, 60, 116-125.	2.3	35
15	Activation of the Nrf2 signaling pathway in usnic acid-induced toxicity in HepG2 cells. <i>Archives of Toxicology</i> , 2017, 91, 1293-1307.	1.9	37
16	Endoplasmic reticulum stress and MAPK signaling pathway activation underlie leflunomide-induced toxicity in HepG2 Cells. <i>Toxicology</i> , 2017, 392, 11-21.	2.0	44
17	ArrayTrack: An FDA and Public Genomic Tool. <i>Methods in Molecular Biology</i> , 2017, 1613, 333-353.	0.4	12
18	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. <i>Nature Biotechnology</i> , 2017, 35, 1127-1128.	9.4	32

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19	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. <i>Scientific Reports</i> , 2017, 7, 4200.	1.6	139
20	Advances in single-cell RNA sequencing and its applications in cancer research. <i>Oncotarget</i> , 2017, 8, 53763-53779.	0.8	76
21	Overcoming chemoresistance in prostate cancer with Chinese medicine <i>Tripterygium wilfordii</i> via multiple mechanisms. <i>Oncotarget</i> , 2016, 7, 61246-61261.	0.8	23
22	Identifying and annotating human bifunctional RNAs reveals their versatile functions. <i>Science China Life Sciences</i> , 2016, 59, 981-992.	2.3	16
23	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <i>Scientific Reports</i> , 2016, 6, 38575.	1.6	4
24	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. <i>Scientific Reports</i> , 2016, 6, 28400.	1.6	57
25	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. <i>Scientific Reports</i> , 2016, 6, 35996.	1.6	27
26	Assessment of pharmacogenomic agreement. <i>F1000Research</i> , 2016, 5, 825.	0.8	34
27	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016, 5, 2333.	0.8	79
28	Revisiting inconsistency in large pharmacogenomic studies. <i>F1000Research</i> , 2016, 5, 2333.	0.8	51
29	A multi-omic analysis of human na ⁺ ve CD4 ⁺ T cells. <i>BMC Systems Biology</i> , 2015, 9, 75.	3.0	43
30	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. <i>Bioinformatics and Biology Insights</i> , 2015, 9s3, BBI.S29466.	1.0	68
31	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. <i>BMC Bioinformatics</i> , 2015, 16, S9.	1.2	19
32	Integrated microRNA, mRNA, and protein expression profiling reveals microRNA regulatory networks in rat kidney treated with a carcinogenic dose of aristolochic acid. <i>BMC Genomics</i> , 2015, 16, 365.	1.2	32
33	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
34	Standardization efforts enabling next-generation sequencing and microarray based biomarkers for precision medicine. <i>Biomarkers in Medicine</i> , 2015, 9, 1265-1272.	0.6	9
35	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. <i>Nature</i> , 2015, 526, 700-704.	13.7	478
36	HLADR: a database system for enhancing the discovery of biomarkers for predicting human leukocyte antigen-mediated idiosyncratic adverse drug reactions. <i>Biomarkers in Medicine</i> , 2015, 9, 1079-1093.	0.6	7

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37	Molecular Docking to Identify Associations Between Drugs and Class I Human Leukocyte Antigens for Predicting Idiosyncratic Drug Reactions. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2015, 18, 296-304.	0.6	69
38	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. <i>Genome Biology</i> , 2014, 15, 523.	3.8	147
39	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140021.	2.4	30
40	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	5.8	316
41	The Risk-Associated Long Noncoding RNA NBAT-1 Controls Neuroblastoma Progression by Regulating Cell Proliferation and Neuronal Differentiation. <i>Cancer Cell</i> , 2014, 26, 722-737.	7.7	287
42	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	5.8	122
43	Detecting and correcting systematic variation in large-scale RNA sequencing data. <i>Nature Biotechnology</i> , 2014, 32, 888-895.	9.4	174
44	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	9.4	420
45	A testing strategy to predict risk for drug-induced liver injury in humans using high-content screen assays and the "rule-of-two" model. <i>Archives of Toxicology</i> , 2014, 88, 1439-1449.	1.9	54
46	Toxicogenomics and Cancer Susceptibility: Advances with Next-Generation Sequencing. <i>Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews</i> , 2014, 32, 121-158.	2.9	32
47	DDI-CPI, a server that predicts drug-drug interactions through implementing the chemical-protein interactome. <i>Nucleic Acids Research</i> , 2014, 42, W46-W52.	6.5	63
48	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. <i>Cancer Research</i> , 2014, 74, 4016-4023.	0.4	90
49	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	2.4	21
50	Comprehensive RNA-Seq transcriptomic profiling across 11 organs, 4 ages, and 2 sexes of Fischer 344 rats. <i>Scientific Data</i> , 2014, 1, 140013.	2.4	22
51	Transcriptional profiling of Chinese medicinal formula Si-Wu-Tang on breast cancer cells reveals phytoestrogenic activity. <i>BMC Complementary and Alternative Medicine</i> , 2013, 13, 11.	3.7	27
52	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. <i>Human Genetics</i> , 2013, 132, 899-911.	1.8	13
53	Utilization of Gene Expression Signature for Quality Control of Traditional Chinese Medicine Formula Si-Wu-Tang. <i>AAPS Journal</i> , 2013, 15, 884-892.	2.2	5
54	Critical role of bioinformatics in translating huge amounts of next-generation sequencing data into personalized medicine. <i>Science China Life Sciences</i> , 2013, 56, 110-118.	2.3	31

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55	mRNA enrichment protocols determine the quantification characteristics of external RNA spike-in controls in RNA-Seq studies. <i>Science China Life Sciences</i> , 2013, 56, 134-142.	2.3	36
56	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4
57	Good practice guidelines for biomarker discovery from array data: a case study for breast cancer prognosis. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	7
58	Next-generation sequencing in the clinic: Promises and challenges. <i>Cancer Letters</i> , 2013, 340, 284-295.	3.2	272
59	Studies on abacavir-induced hypersensitivity reaction: a successful example of translation of pharmacogenetics to personalized medicine. <i>Science China Life Sciences</i> , 2013, 56, 119-124.	2.3	26
60	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. <i>Rna</i> , 2013, 19, 479-489.	1.6	29
61	Estimating relative noise to signal in DNA microarray data. <i>International Journal of Bioinformatics Research and Applications</i> , 2013, 9, 433.	0.1	8
62	Gene Expression Variability in Human Hepatic Drug Metabolizing Enzymes and Transporters. <i>PLoS ONE</i> , 2013, 8, e60368.	1.1	43
63	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. <i>PLoS ONE</i> , 2013, 8, e66521.	1.1	4
64	Targeted RNA-Sequencing with Competitive Multiplex-PCR Amplicon Libraries. <i>PLoS ONE</i> , 2013, 8, e79120.	1.1	30
65	Drug hypersensitivity caused by alteration of the MHC-presented self-peptide repertoire. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9959-9964.	3.3	354
66	An adaptive feature selection method for microarray data analysis. , 2012, , .		1
67	Inhalation Anesthesia-Induced Neuronal Damage and Gene Expression Changes in Developing Rat Brain. <i>Systems Pharmacology</i> , 2012, 1, 1-9.	1.0	6
68	Shifting from Population-wide to Personalized Cancer Prognosis with Microarrays. <i>PLoS ONE</i> , 2012, 7, e29534.	1.1	6
69	Cytotoxicity and inhibitory effects of low-concentration triclosan on adipogenic differentiation of human mesenchymal stem cells. <i>Toxicology and Applied Pharmacology</i> , 2012, 262, 117-123.	1.3	42
70	Abstract 2575: DNA microarray and connectivity map analysis reveals estrogen-like activity of Chinese medicinal formula Si-Wu-Tang. , 2012, , .		1
71	Technical Reproducibility of Genotyping SNP Arrays Used in Genome-Wide Association Studies. <i>PLoS ONE</i> , 2012, 7, e44483.	1.1	59
72	Sex Differences in the Expression of Drug-Metabolizing and Transporter Genes in Human Liver. <i>Journal of Drug Metabolism & Toxicology</i> , 2012, 3, 1000119.	0.1	88

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73	Comparing Next-Generation Sequencing and Microarray Technologies in a Toxicological Study of the Effects of Aristolochic Acid on Rat Kidneys. <i>Chemical Research in Toxicology</i> , 2011, 24, 1486-1493.	1.7	80
74	Similarities and Differences in the Expression of Drug-Metabolizing Enzymes between Human Hepatic Cell Lines and Primary Human Hepatocytes. <i>Drug Metabolism and Disposition</i> , 2011, 39, 528-538.	1.7	262
75	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. <i>BMC Genomics</i> , 2011, 12, 590.	1.2	34
76	Next-generation sequencing and its applications in molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 333-343.	1.5	146
77	Selecting a single model or combining multiple models for microarray-based classifier development? A comparative analysis based on large and diverse datasets generated from the MAQC-II project. <i>BMC Bioinformatics</i> , 2011, 12, S3.	1.2	13
78	Maximum predictive power of the microarray-based models for clinical outcomes is limited by correlation between endpoint and gene expression profile. <i>BMC Genomics</i> , 2011, 12, S3.	1.2	6
79	Methysticin and 7,8-Dihydromethysticin are Two Major Kavalactones in Kava Extract to Induce CYP1A1. <i>Toxicological Sciences</i> , 2011, 124, 388-399.	1.4	30
80	DRAR-CPI: a server for identifying drug repositioning potential and adverse drug reactions via the chemical-protein interactome. <i>Nucleic Acids Research</i> , 2011, 39, W492-W498.	6.5	189
81	Exploring Off-Targets and Off-Systems for Adverse Drug Reactions via Chemical-Protein Interactome Clozapine-Induced Agranulocytosis as a Case Study. <i>PLoS Computational Biology</i> , 2011, 7, e1002016.	1.5	93
82	The MicroArray Quality Control (MAQC) Project and Cross-Platform Analysis of Microarray Data. , 2011, , 171-192.		6
83	Discovery of Molecular Mechanisms of Traditional Chinese Medicinal Formula Si-Wu-Tang Using Gene Expression Microarray and Connectivity Map. <i>PLoS ONE</i> , 2011, 6, e18278.	1.1	127
84	Comparative Analysis of Human Protein-Coding and Noncoding RNAs between Brain and 10 Mixed Cell Lines by RNA-Seq. <i>PLoS ONE</i> , 2011, 6, e28318.	1.1	27
85	Evaluating variations of genotype calling: a potential source of spurious associations in genome-wide association studies. <i>Journal of Genetics</i> , 2010, 89, 55-64.	0.4	11
86	Evaluation of gene expression data generated from expired Affymetrix GeneChip® microarrays using MAQC reference RNA samples. <i>BMC Bioinformatics</i> , 2010, 11, S10.	1.2	20
87	The EDKB: an established knowledge base for endocrine disrupting chemicals. <i>BMC Bioinformatics</i> , 2010, 11, S5.	1.2	75
88	Genomic analysis of microRNA time-course expression in liver of mice treated with genotoxic carcinogen N-ethyl-N-nitrosourea. <i>BMC Genomics</i> , 2010, 11, 609.	1.2	36
89	Abnormal gene expression in cerebellum of <i>Npc1</i> mice during postnatal development. <i>Brain Research</i> , 2010, 1325, 128-140.	1.1	27
90	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	9.4	795

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91	Assessing sources of inconsistencies in genotypes and their effects on genome-wide association studies with HapMap samples. <i>Pharmacogenomics Journal</i> , 2010, 10, 364-374.	0.9	21
92	Consistency of predictive signature genes and classifiers generated using different microarray platforms. <i>Pharmacogenomics Journal</i> , 2010, 10, 247-257.	0.9	53
93	Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. <i>Pharmacogenomics Journal</i> , 2010, 10, 310-323.	0.9	41
94	k-Nearest neighbor models for microarray gene expression analysis and clinical outcome prediction. <i>Pharmacogenomics Journal</i> , 2010, 10, 292-309.	0.9	102
95	A comparison of batch effect removal methods for enhancement of prediction performance using MAQC-II microarray gene expression data. <i>Pharmacogenomics Journal</i> , 2010, 10, 278-291.	0.9	249
96	Voluntary exploratory data submissions to the US FDA and the EMA: experience and impact. <i>Nature Reviews Drug Discovery</i> , 2010, 9, 435-445.	21.5	92
97	Identifying Unexpected Therapeutic Targets via Chemical-Protein Interactome. <i>PLoS ONE</i> , 2010, 5, e9568.	1.1	42
98	DNA Microarrays Are Predictive of Cancer Prognosis: A Re-evaluation. <i>Clinical Cancer Research</i> , 2010, 16, 629-636.	3.2	52
99	Genomic indicators in the blood predict drug-induced liver injury. <i>Pharmacogenomics Journal</i> , 2010, 10, 267-277.	0.9	54
100	Effect of training-sample size and classification difficulty on the accuracy of genomic predictors. <i>Breast Cancer Research</i> , 2010, 12, R5.	2.2	169
101	Molecular biomarkers: a US FDA effort. <i>Biomarkers in Medicine</i> , 2010, 4, 215-225.	0.6	23
102	Microarray platform consistency is revealed by biologically functional analysis of gene expression profiles. <i>BMC Bioinformatics</i> , 2009, 10, S12.	1.2	22
103	Correlation analysis of external RNA controls reveals its utility for assessment of microarray assay. <i>Analytical Biochemistry</i> , 2009, 385, 203-207.	1.1	4
104	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. <i>Neuron</i> , 2009, 63, 585-591.	3.8	58
105	The Accurate Prediction of Protein Family from Amino Acid Sequence by Measuring Features of Sequence Fragments. <i>Journal of Computational Biology</i> , 2009, 16, 1671-1688.	0.8	16
106	Investigation of reproducibility of differentially expressed genes in DNA microarrays through statistical simulation. <i>BMC Proceedings</i> , 2009, 3, S4.	1.8	9
107	The Current Status of DNA Microarrays. , 2009, , 3-24.		5
108	ArrayTrack: An FDA and Public Genomic Tool. <i>Methods in Molecular Biology</i> , 2009, 563, 379-398.	0.4	67

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109	Reproducible and reliable microarray results through quality control: good laboratory proficiency and appropriate data analysis practices are essential. <i>Current Opinion in Biotechnology</i> , 2008, 19, 10-18.	3.3	125
110	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. <i>BMC Bioinformatics</i> , 2008, 9, S10.	1.2	215
111	Assessing batch effects of genotype calling algorithm BRLMM for the Affymetrix GeneChip Human Mapping 500 K array set using 270 HapMap samples. <i>BMC Bioinformatics</i> , 2008, 9, S17.	1.2	62
112	Very Important Pool (VIP) genes – an application for microarray-based molecular signatures. <i>BMC Bioinformatics</i> , 2008, 9, S9.	1.2	12
113	Mold ² , Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1337-1344.	2.5	241
114	DNA Microarrays: Applications, Future Trends, and the Need for Standardization. <i>Springer Series on Fluorescence</i> , 2008, , 215-237.	0.8	7
115	Microarray Technology: Unresolved Issues and Future Challenges from a Regulatory Perspective. <i>Springer Series on Fluorescence</i> , 2008, , 265-282.	0.8	3
116	Self-self Hybridization As An Alternative Experiment Design to Dye Swap for Two-color Microarrays. <i>OMICS A Journal of Integrative Biology</i> , 2007, 11, 14-24.	1.0	8
117	Variability of DNA Microarray Gene Expression Profiles in Cultured Rat Primary Hepatocytes. <i>Gene Regulation and Systems Biology</i> , 2007, 1, 117762500700100.	2.3	0
118	An integrated bioinformatics infrastructure essential for advancing pharmacogenomics and personalized medicine in the context of the FDA's Critical Path Initiative. <i>Drug Discovery Today: Technologies</i> , 2007, 4, 3-8.	4.0	13
119	The Reproducibility of Lists of Differentially Expressed Genes in Microarray Studies. <i>Nature Precedings</i> , 2007, , .	0.1	2
120	QA/QC issues to aid regulatory acceptance of microarray gene expression data. <i>Environmental and Molecular Mutagenesis</i> , 2007, 48, 349-353.	0.9	12
121	Variability of DNA microarray gene expression profiles in cultured rat primary hepatocytes. <i>Gene Regulation and Systems Biology</i> , 2007, 1, 235-49.	2.3	2
122	Gaining Confidence on Molecular Classification through Consensus Modeling and Validation. <i>Toxicology Mechanisms and Methods</i> , 2006, 16, 59-68.	1.3	9
123	Integrating time-course microarray gene expression profiles with cytotoxicity for identification of biomarkers in primary rat hepatocytes exposed to cadmium. <i>Bioinformatics</i> , 2006, 22, 77-87.	1.8	32
124	Reproducibility Probability Score – incorporating measurement variability across laboratories for gene selection. <i>Nature Biotechnology</i> , 2006, 24, 1476-1477.	9.4	51
125	Evaluation of DNA microarray results with quantitative gene expression platforms. <i>Nature Biotechnology</i> , 2006, 24, 1115-1122.	9.4	558
126	Evaluation of external RNA controls for the assessment of microarray performance. <i>Nature Biotechnology</i> , 2006, 24, 1132-1139.	9.4	97

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127	Rat toxicogenomic study reveals analytical consistency across microarray platforms. <i>Nature Biotechnology</i> , 2006, 24, 1162-1169.	9.4	389
128	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 2006, 24, 1151-1161.	9.4	1,927
129	Using RNA sample titrations to assess microarray platform performance and normalization techniques. <i>Nature Biotechnology</i> , 2006, 24, 1123-1131.	9.4	168
130	Performance comparison of one-color and two-color platforms within the Microarray Quality Control (MAQC) project. <i>Nature Biotechnology</i> , 2006, 24, 1140-1150.	9.4	440
131	Differences in hepatotoxicity and gene expression profiles by anti-diabetic PPAR β agonists on rat primary hepatocytes and human HepG2 cells. <i>Molecular Diversity</i> , 2006, 10, 349-360.	2.1	74
132	Analysis of gene expression changes in relation to toxicity and tumorigenesis in the livers of Big Blue transgenic rats fed comfrey (<i>Symphytum officinale</i>). <i>BMC Bioinformatics</i> , 2006, 7, S16.	1.2	31
133	Improvement in the Reproducibility and Accuracy of DNA Microarray Quantification by Optimizing Hybridization Conditions. <i>BMC Bioinformatics</i> , 2006, 7, S17.	1.2	32
134	Differential gene expression in mouse primary hepatocytes exposed to the peroxisome proliferator-activated receptor α agonists. <i>BMC Bioinformatics</i> , 2006, 7, S18.	1.2	47
135	Gene Expression Profiles Distinguish the Carcinogenic Effects of Aristolochic Acid in Target (Kidney) and Non-target (Liver) Tissues in Rats. <i>BMC Bioinformatics</i> , 2006, 7, S20.	1.2	46
136	A Partial Least Squares-Based Consensus Regression Method for the Analysis of Near-Infrared Complex Spectral Data of Plant Samples. <i>Analytical Letters</i> , 2006, 39, 2073-2083.	1.0	24
137	Guidelines for terminology for microtechnology in clinical laboratories (IUPAC Technical Report). <i>Pure and Applied Chemistry</i> , 2006, 78, 677-684.	0.9	0
138	Construction of a virtual combinatorial library using SMILES strings to discover potential structure-diverse PPAR modulators. <i>European Journal of Medicinal Chemistry</i> , 2005, 40, 632-640.	2.6	15
139	The External RNA Controls Consortium: a progress report. <i>Nature Methods</i> , 2005, 2, 731-734.	9.0	328
140	Microarray scanner calibration curves: characteristics and implications. <i>BMC Bioinformatics</i> , 2005, 6, S11.	1.2	74
141	Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential. <i>BMC Bioinformatics</i> , 2005, 6, S12.	1.2	164
142	Quality control and quality assessment of data from surface-enhanced laser desorption/ionization (SELDI) time-of flight (TOF) mass spectrometry (MS). <i>BMC Bioinformatics</i> , 2005, 6, S5.	1.2	55
143	A microarray study of MPP ⁺ -treated PC12 Cells: Mechanisms of toxicity (MOT) analysis using bioinformatics tools. <i>BMC Bioinformatics</i> , 2005, 6, S8.	1.2	18
144	Assessing QSAR Limitations - A Regulatory Perspective. <i>Current Computer-Aided Drug Design</i> , 2005, 1, 195-205.	0.8	52

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145	Multi-class cancer classification by total principal component regression (TPCR) using microarray gene expression data. <i>Nucleic Acids Research</i> , 2005, 33, 56-65.	6.5	81
146	Using Decision Forest to Classify Prostate Cancer Samples on the Basis of SELDI-TOF MS Data: Assessing Chance Correlation and Prediction Confidence. <i>Environmental Health Perspectives</i> , 2004, 112, 1622-1627.	2.8	34
147	Classification of cDNA Array Genes That Have a Highly Significant Discriminative Power Due to Their Unique Distribution in Four Brain Regions. <i>DNA and Cell Biology</i> , 2004, 23, 661-674.	0.9	4
148	Quantitative Structure-Activity Relationship Study of Histone Deacetylase Inhibitors. <i>Anti-Cancer Agents in Medicinal Chemistry</i> , 2004, 4, 273-299.	7.0	40
149	QA/QC: challenges and pitfalls facing the microarray community and regulatory agencies. <i>Expert Review of Molecular Diagnostics</i> , 2004, 4, 761-777.	1.5	99
150	Development of public toxicogenomics software for microarray data management and analysis. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2004, 549, 241-253.	0.4	98
151	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor β Agonists. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 230-238.	2.8	15
152	3D QSAR studies on peroxisome proliferator-activated receptor β agonists using CoMFA and CoMSIA. <i>Journal of Molecular Modeling</i> , 2004, 10, 165-177.	0.8	23
153	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor β Agonists.. <i>ChemInform</i> , 2004, 35, no.	0.1	0
154	Multi-class tumor classification by discriminant partial least squares using microarray gene expression data and assessment of classification models. <i>Computational Biology and Chemistry</i> , 2004, 28, 235-243.	1.1	79
155	Design, synthesis, and evaluation of a new class of noncyclic 1,3-dicarbonyl compounds as PPAR β selective activators. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2004, 14, 3507-3511.	1.0	20
156	Multiclass Decision Forest—A Novel Pattern Recognition Method for Multiclass Classification in Microarray Data Analysis. <i>DNA and Cell Biology</i> , 2004, 23, 685-694.	0.9	40
157	Assessment of Prediction Confidence and Domain Extrapolation of Two Structure-Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. <i>Environmental Health Perspectives</i> , 2004, 112, 1249-1254.	2.8	78
158	Assessment of Prediction Confidence and Domain Extrapolation of Two Structure-Activity Relationship Models for Predicting Estrogen Receptor Binding Activity. <i>Environmental Health Perspectives</i> , 2004, 112, 1249-1254.	2.8	87
159	STRUCTURE-ACTIVITY RELATIONSHIP APPROACHES AND APPLICATIONS. <i>Environmental Toxicology and Chemistry</i> , 2003, 22, 1680.	2.2	71
160	ArrayTrack—supporting toxicogenomic research at the U.S. Food and Drug Administration National Center for Toxicological Research.. <i>Environmental Health Perspectives</i> , 2003, 111, 1819-1826.	2.8	197
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