

Leming Shi

List of Publications by Year in descending order

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Version: 2024-02-01

172
papers

16,167
citations

23500

58
h-index

17055

122
g-index

182
all docs

182
docs citations

182
times ranked

21746
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? â€œA 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 chemicalâ€œprotein 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 â€œClozapine-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 GeneChipÂ® 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 |
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