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	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
2	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
3	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
4	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	14.5	19
5	Blood molecular markers associated with COVID‐19 immunopathology and multi‐organ damage. EMBO Journal, 2020, 39, e105896.	7.8	123
6	Towards the development of an omics data analysis framework. Regulatory Toxicology and Pharmacology, 2020, 112, 104621.	2.7	15
7	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
8	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	4.9	5
9	Similarities and differences between variants called with human reference genome HG19 or HG38. BMC Bioinformatics, 2019, 20, 101.	2.6	33
10	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
11	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
12	A genomic characterization of the influence of silver nanoparticles on bone differentiation in MC3T3‐E1 cells. Journal of Applied Toxicology, 2018, 38, 172-179.	2.8	39
13	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. Biology Direct, 2018, 13, 14.	4.6	27
14	Characterizing and annotating the genome using RNA-seq data. Science China Life Sciences, 2017, 60, 116-125.	4.9	35
15	Activation of the Nrf2 signaling pathway in usnic acid-induced toxicity in HepG2 cells. Archives of Toxicology, 2017, 91, 1293-1307.	4.2	37
16	Endoplasmic reticulum stress and MAPK signaling pathway activation underlie leflunomide-induced toxicity in HepG2 Cells. Toxicology, 2017, 392, 11-21.	4.2	44
17	ArrayTrack: An FDA and Public Genomic Tool. Methods in Molecular Biology, 2017, 1613, 333-353.	0.9	12
18	The international MAQC Society launches to enhance reproducibility of high-throughput technologies. Nature Biotechnology, 2017, 35, 1127-1128.	17.5	32

#	Article	IF	Citations
19	A Comprehensive Mouse Transcriptomic BodyMap across 17 Tissues by RNA-seq. Scientific Reports, 2017, 7, 4200.	3.3	139
20	Advances in single-cell RNA sequencing and its applications in cancer research. Oncotarget, 2017, 8, 53763-53779.	1.8	76
21	Overcoming chemoresistance in prostate cancer with Chinese medicine Tripterygium wilfordii via multiple mechanisms. Oncotarget, 2016, 7, 61246-61261.	1.8	23
22	Identifying and annotating human bifunctional RNAs reveals their versatile functions. Science China Life Sciences, 2016, 59, 981-992.	4.9	16
23	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. Scientific Reports, 2016, 6, 38575.	3.3	4
24	Identification of Tissue-Specific Protein-Coding and Noncoding Transcripts across 14 Human Tissues Using RNA-seq. Scientific Reports, 2016, 6, 28400.	3.3	57
25	DPDR-CPI, a server that predicts Drug Positioning and Drug Repositioning via Chemical-Protein Interactome. Scientific Reports, 2016, 6, 35996.	3.3	27
26	Assessment of pharmacogenomic agreement. F1000Research, 2016, 5, 825.	1.6	34
27	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	1.6	79
28	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 2016, 5, 2333.	1.6	51
29	A multi-omic analysis of human naïve CD4+ T cells. BMC Systems Biology, 2015, 9, 75.	3.0	43
30	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	2.0	68
31	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. BMC Bioinformatics, 2015, 16, S9.	2.6	19
32	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
33	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
34	Standardization efforts enabling next-generation sequencing and microarray based biomarkers for precision medicine. Biomarkers in Medicine, 2015, 9, 1265-1272.	1.4	9
35	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. Nature, 2015, 526, 700-704.	27.8	478
36	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

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37	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
38	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
39	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
40	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316
41	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
42	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
43	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	17.5	174
44	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	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. Archives of Toxicology, 2014, 88, 1439-1449.	4.2	54
46	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
47	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
48	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. Cancer Research, 2014, 74, 4016-4023.	0.9	90
49	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
50	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
51	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
52	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
53	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
54	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

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55	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
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. BMC Systems Biology, 2013, 7, S2.	3.0	7
58	Next-generation sequencing in the clinic: Promises and challenges. Cancer Letters, 2013, 340, 284-295.	7.2	272
59	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
60	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. Rna, 2013, 19, 479-489.	3.5	29
61	Estimating relative noise to signal in DNA microarray data. International Journal of Bioinformatics Research and Applications, 2013, 9, 433.	0.2	8
62	Gene Expression Variability in Human Hepatic Drug Metabolizing Enzymes and Transporters. PLoS ONE, 2013, 8, e60368.	2.5	43
63	Dissecting the Characteristics and Dynamics of Human Protein Complexes at Transcriptome Cascade Using RNA-Seq Data. PLoS ONE, 2013, 8, e66521.	2.5	4
64	Targeted RNA-Sequencing with Competitive Multiplex-PCR Amplicon Libraries. PLoS ONE, 2013, 8, e79120.	2.5	30
65	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
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. Systems Pharmacology, 2012, 1, 1-9.	1.0	6
68	Shifting from Population-wide to Personalized Cancer Prognosis with Microarrays. PLoS ONE, 2012, 7, e29534.	2.5	6
69	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
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. PLoS ONE, 2012, 7, e44483.	2.5	59
72	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

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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. Chemical Research in Toxicology, 2011, 24, 1486-1493.	3.3	80
74	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
75	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. BMC Genomics, 2011, 12, 590.	2.8	34
76	Next-generation sequencing and its applications in molecular diagnostics. Expert Review of Molecular Diagnostics, 2011, 11, 333-343.	3.1	146
77	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
78	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
79	Methysticin and 7,8-Dihydromethysticin are Two Major Kavalactones in Kava Extract to Induce CYP1A1. Toxicological Sciences, 2011, 124, 388-399.	3.1	30
80	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
81	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
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. PLoS ONE, 2011, 6, e18278.	2.5	127
84	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
85	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
86	Evaluation of gene expression data generated from expired Affymetrix GeneChipÂ® microarrays using MAQC reference RNA samples. BMC Bioinformatics, 2010, 11, S10.	2.6	20
87	The EDKB: an established knowledge base for endocrine disrupting chemicals. BMC Bioinformatics, 2010, 11, S5.	2.6	75
88	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
89	Abnormal gene expression in cerebellum of Npc1Ë†/Ë† mice during postnatal development. Brain Research, 2010, 1325, 128-140.	2.2	27
90	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

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91	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
92	Consistency of predictive signature genes and classifiers generated using different microarray platforms. Pharmacogenomics Journal, 2010, 10, 247-257.	2.0	53
93	Functional analysis of multiple genomic signatures demonstrates that classification algorithms choose phenotype-related genes. Pharmacogenomics Journal, 2010, 10, 310-323.	2.0	41
94	k-Nearest neighbor models for microarray gene expression analysis and clinical outcome prediction. Pharmacogenomics Journal, 2010, 10, 292-309.	2.0	102
95	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
96	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
97	Identifying Unexpected Therapeutic Targets via Chemical-Protein Interactome. PLoS ONE, 2010, 5, e9568.	2.5	42
98	DNA Microarrays Are Predictive of Cancer Prognosis: A Re-evaluation. Clinical Cancer Research, 2010, 16, 629-636.	7.0	52
99	Genomic indicators in the blood predict drug-induced liver injury. Pharmacogenomics Journal, 2010, 10, 267-277.	2.0	54
100	Effect of training-sample size and classification difficulty on the accuracy of genomic predictors. Breast Cancer Research, 2010, 12, R5.	5.0	169
101	Molecular biomarkers: a US FDA effort. Biomarkers in Medicine, 2010, 4, 215-225.	1.4	23
102	Microarray platform consistency is revealed by biologically functional analysis of gene expression profiles. BMC Bioinformatics, 2009, 10, S12.	2.6	22
103	Correlation analysis of external RNA controls reveals its utility for assessment of microarray assay. Analytical Biochemistry, 2009, 385, 203-207.	2.4	4
104	CCM2 Mediates Death Signaling by the TrkA Receptor Tyrosine Kinase. Neuron, 2009, 63, 585-591.	8.1	58
105	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
106	Investigation of reproducibility of differentially expressed genes in DNA microarrays through statistical simulation. BMC Proceedings, 2009, 3, S4.	1.6	9
107	The Current Status of DNA Microarrays. , 2009, , 3-24.		5
108	ArrayTrack: An FDA and Public Genomic Tool. Methods in Molecular Biology, 2009, 563, 379-398.	0.9	67

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109	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
110	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. BMC Bioinformatics, 2008, 9, S10.	2.6	215
111	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
112	Very Important Pool (VIP) genes â€" an application for microarray-based molecular signatures. BMC Bioinformatics, 2008, 9, S9.	2.6	12
113	Mold^2, Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. Journal of Chemical Information and Modeling, 2008, 48, 1337-1344.	5.4	241
114	DNA Microarrays: Applications, Future Trends, and the Need for Standardization. Springer Series on Fluorescence, 2008, , 215-237.	0.8	7
115	Microarray Technology: Unresolved Issues and Future Challenges from aÂRegulatory Perspective. Springer Series on Fluorescence, 2008, , 265-282.	0.8	3
116	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
117	Variability of DNA Microarray Gene Expression Profiles in Cultured Rat Primary Hepatocytes. Gene Regulation and Systems Biology, 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. Drug Discovery Today: Technologies, 2007, 4, 3-8.	4.0	13
119	The Reproducibility of Lists of Differentially Expressed Genes in Microarray Studies. Nature Precedings, 2007, , .	0.1	2
120	QA/QC issues to aid regulatory acceptance of microarray gene expression data. Environmental and Molecular Mutagenesis, 2007, 48, 349-353.	2.2	12
121	Variability of DNA microarray gene expression profiles in cultured rat primary hepatocytes. Gene Regulation and Systems Biology, 2007, 1, 235-49.	2.3	2
122	Gaining Confidence on Molecular Classification through Consensus Modeling and Validation. Toxicology Mechanisms and Methods, 2006, 16, 59-68.	2.7	9
123	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
124	Reproducibility Probability Scoreâ€"incorporating measurement variability across laboratories for gene selection. Nature Biotechnology, 2006, 24, 1476-1477.	17.5	51
125	Evaluation of DNA microarray results with quantitative gene expression platforms. Nature Biotechnology, 2006, 24, 1115-1122.	17.5	558
126	Evaluation of external RNA controls for the assessment of microarray performance. Nature Biotechnology, 2006, 24, 1132-1139.	17.5	97

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127	Rat toxicogenomic study reveals analytical consistency across microarray platforms. Nature Biotechnology, 2006, 24, 1162-1169.	17.5	389
128	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
129	Using RNA sample titrations to assess microarray platform performance and normalization techniques. Nature Biotechnology, 2006, 24, 1123-1131.	17.5	168
130	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
131	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
132	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
133	Improvement in the Reproducibility and Accuracy of DNA Microarray Quantification by Optimizing Hybridization Conditions. BMC Bioinformatics, 2006, 7, S17.	2.6	32
134	Differential gene expression in mouse primary hepatocytes exposed to the peroxisome proliferator-activated receptor Î± agonists. BMC Bioinformatics, 2006, 7, S18.	2.6	47
135	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
136	A Partial Least Squaresâ€Based Consensus Regression Method for the Analysis of Nearâ€Infrared Complex Spectral Data of Plant Samples. Analytical Letters, 2006, 39, 2073-2083.	1.8	24
137	Guidelines for terminology for microtechnology in clinical laboratories (IUPAC Technical Report). Pure and Applied Chemistry, 2006, 78, 677-684.	1.9	0
138	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
139	The External RNA Controls Consortium: a progress report. Nature Methods, 2005, 2, 731-734.	19.0	328
140	Microarray scanner calibration curves: characteristics and implications. BMC Bioinformatics, 2005, 6, S11.	2.6	74
141	Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential. BMC Bioinformatics, 2005, 6, S12.	2.6	164
142	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
143	A microarray study of MPP+-treated PC12 Cells: Mechanisms of toxicity (MOT) analysis using bioinformatics tools. BMC Bioinformatics, 2005, 6, S8.	2.6	18
144	Assessing QSAR Limitations - A Regulatory Perspective. Current Computer-Aided Drug Design, 2005, 1, 195-205.	1.2	52

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145	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
146	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
147	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
148	Quantitative Structure-Activity Relationship Study of Histone Deacetylase Inhibitors. Anti-Cancer Agents in Medicinal Chemistry, 2004, 4, 273-299.	7.0	40
149	QA/QC: challenges and pitfalls facing the microarray community and regulatory agencies. Expert Review of Molecular Diagnostics, 2004, 4, 761-777.	3.1	99
150	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
151	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor Î³ Agonists. Journal of Chemical Information and Computer Sciences, 2004, 44, 230-238.	2.8	15
152	3D QSAR studies on peroxisome proliferator-activated receptor ? agonists using CoMFA and CoMSIA. Journal of Molecular Modeling, 2004, 10, 165-177.	1.8	23
153	Eigenvalue Analysis of Peroxisome Proliferator-Activated Receptor Î³ Agonists.. ChemInform, 2004, 35, no.	0.0	0
154	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
155	Design, synthesis, and evaluation of a new class of noncyclic 1,3-dicarbonyl compounds as PPARÎ± selective activators. Bioorganic and Medicinal Chemistry Letters, 2004, 14, 3507-3511.	2.2	20
156	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
157	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
158	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
159	STRUCTUREâ€"ACTIVITY RELATIONSHIP APPROACHES AND APPLICATIONS. Environmental Toxicology and Chemistry, 2003, 22, 1680.	4.3	71
160	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
161	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
162	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

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163	Phytoestrogens and Mycoestrogens Bind to the Rat Uterine Estrogen Receptor. Journal of Nutrition, 2002, 132, 658-664.	2.9	125
164	QSAR Models Using a Large Diverse Set of Estrogens. Journal of Chemical Information and Computer Sciences, 2001, 41, 186-195.	2.8	323
165	Structureâˆ'Activity Relationships for a Large Diverse Set of Natural, Synthetic, and Environmental Estrogens. Chemical Research in Toxicology, 2001, 14, 280-294.	3.3	432
166	Arrays, molecular diagnostics, personalized therapy and informatics. Expert Review of Molecular Diagnostics, 2001, 1, 363-365.	3.1	5
167	The Estrogen Receptor Relative Binding Affinities of 188 Natural and Xenochemicals: Structural Diversity of Ligands. Toxicological Sciences, 2000, 54, 138-153.	3.1	689
168	Some novel methods based on recursive optimal estimation. Applications to analytical chemistry. Analytica Chimica Acta, 1993, 277, 199-204.	5.4	1
169	Valence-state speciation of sulfur by x-ray fluorescence spectometry and Kalman filtering. Analytica Chimica Acta, 1991, 248, 257-261.	5.4	9
170	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
171	Potential Sources of Spurious Associations and Batch Effects in Genome-Wide Association Studies. , 0, , 191-201.		2
172	Revisiting inconsistency in large pharmacogenomic studies. F1000Research, 0, 5, 2333.	1.6	8