Huixiao Hong

List of Publications by Year
in descending order

173 papers	11,780 citations	31976 53 h-index	30922 102 g-index
180 all docs	180 docs citations	180 times ranked	14755 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 concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
4	Study of 202 Natural, Synthetic, and Environmental Chemicals for Binding to the Androgen Receptor. Chemical Research in Toxicology, 2003, 16, 1338-1358.	3.3	356
5	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
6	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	12.8	316
7	Coumarin-Based Inhibitors of HIV Integrase. Journal of Medicinal Chemistry, 1997, 40, 242-249.	6.4	280
8	CERAPP: Collaborative Estrogen Receptor Activity Prediction Project. Environmental Health Perspectives, 2016, 124, 1023-1033.	6.0	264
9	Mold², Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. Journal of Chemical Information and Modeling, 2008, 48, 1337-1344.	5.4	241
10	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. BMC Bioinformatics, 2008, 9, S10.	2.6	215
11	Depsides and Depsidones as Inhibitors of HIV-1 Integrase:â€‰ Discovery of Novel Inhibitors through 3D Database Searching. Journal of Medicinal Chemistry, 1997, 40, 942-951.	6.4	214
12	Persistent Organic Pollutants in Food: Contamination Sources, Health Effects and Detection Methods. International Journal of Environmental Research and Public Health, 2019, 16, 4361.	2.6	214
13	Decision Forest:â€‰ Combining the Predictions of Multiple Independent Decision Tree Models. Journal of Chemical Information and Computer Sciences, 2003, 43, 525-531.	2.8	199
14	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
15	HIV-1 Integrase Pharmacophore:Â Discovery of Inhibitors through Three-Dimensional Database Searchingâ€. Journal of Medicinal Chemistry, 1997, 40, 920-929.	6.4	175
16	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
17	Next-generation sequencing and its applications in molecular diagnostics. Expert Review of Molecular Diagnostics, 2011, 11, 333-343.	3.1	146
18	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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19	Discovery of HIV-1 Integrase Inhibitors by Pharmacophore Searchingâ€. Journal of Medicinal Chemistry, 1997, 40, 930-936.	6.4	126
20	Toward predictive models for drug-induced liver injury in humans: are we there yet?. Biomarkers in Medicine, 2014, 8, 201-213.	1.4	124
21	Predicting Hepatotoxicity Using ToxCast in Vitro Bioactivity and Chemical Structure. Chemical Research in Toxicology, 2015, 28, 738-751.	3.3	124
22	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
23	CoMPARA: Collaborative Modeling Project for Androgen Receptor Activity. Environmental Health Perspectives, 2020, 128, 27002.	6.0	120
24	Deep learning architectures for multi-label classification of intelligent health risk prediction. BMC Bioinformatics, 2017, 18, 523.	2.6	117
25	Hydrazide-Containing Inhibitors of HIV-1 Integraseâ€. Journal of Medicinal Chemistry, 1997, 40, 937-941.	6.4	106
26	Potent Inhibitors of Human Immunodeficiency Virus Type 1 Integrase: Identification of a Novel Four-Point Pharmacophore and Tetracyclines as Novel Inhibitors. Molecular Pharmacology, 1997, 52, 1041-1055.	2.3	104
27	Evaluation of external RNA controls for the assessment of microarray performance. Nature Biotechnology, 2006, 24, 1132-1139.	17.5	97
28	Quantitative Structure-Activity Relationship Models for Predicting Drug-Induced Liver Injury Based on FDA-Approved Drug Labeling Annotation and Using a Large Collection of Drugs. Toxicological Sciences, 2013, 136, 242-249.	3.1	96
29	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
30	A review on machine learning methods forin silicotoxicity prediction. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2018, 36, 169-191.	2.9	91
31	Salicylhydrazine-Containing Inhibitors of HIV-1 Integrase:â€‰ Implication for a Selective Chelation in the Integrase Active Site. Journal of Medicinal Chemistry, 1998, 41, 3202-3209.	6.4	89
32	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
33	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
34	Development of Decision Forest Models for Prediction of Drug-Induced Liver Injury in Humans Using A Large Set of FDA-approved Drugs. Scientific Reports, 2017, 7, 17311.	3.3	84
35	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
36	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

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37	Biomarkers for drug-induced liver injury. Expert Review of Gastroenterology and Hepatology, 2010, 4, 225-234.	3.0	78
38	The EDKB: an established knowledge base for endocrine disrupting chemicals. BMC Bioinformatics, 2010, 11, S5.	2.6	75
39	Experimental Data Extraction and in Silico Prediction of the Estrogenic Activity of Renewable Replacements for Bisphenol A. International Journal of Environmental Research and Public Health, 2016, 13, 705.	2.6	73
40	Human Sex Hormone-Binding Globulin Binding Affinities of 125 Structurally Diverse Chemicals and Comparison with Their Binding to Androgen Receptor, Estrogen Receptor, and Î±-Fetoprotein. Toxicological Sciences, 2015, 143, 333-348.	3.1	69
41	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
42	EADB: An Estrogenic Activity Database for Assessing Potential Endocrine Activity. Toxicological Sciences, 2013, 135, 277-291.	3.1	68
43	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	2.0	68
44	Estrogenic Activity Data Extraction and in Silico Prediction Show the Endocrine Disruption Potential of Bisphenol A Replacement Compounds. Chemical Research in Toxicology, 2015, 28, 1784-1795.	3.3	68
45	Toward best practice in cancer mutation detection with whole-genome and whole-exome sequencing. Nature Biotechnology, 2021, 39, 1141-1150.	17.5	66
46	microRNAs as pharmacogenomic biomarkers for drug efficacy and drug safety assessment. Biomarkers in Medicine, 2015, 9, 1153-1176.	1.4	64
47	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
48	Versatility or Promiscuity: The Estrogen Receptors, Control of Ligand Selectivity and an Update on Subtype Selective Ligands. International Journal of Environmental Research and Public Health, 2014, 11, 8709-8742.	2.6	61
49	Deep learning for predicting toxicity of chemicals: a mini review. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2018, 36, 252-271.	2.9	61
50	Developing QSAR Models with Defined Applicability Domains on PPARÎ³ Binding Affinity Using Large Data Sets and Machine Learning Algorithms. Environmental Science & Technology, 2021, 55, 6857-6866.	10.0	61
51	Homology modeling, molecular docking, and molecular dynamics simulations elucidated Î±-fetoprotein binding modes. BMC Bioinformatics, 2013, 14, S6.	2.6	60
52	Molecular dynamics simulations and applications in computational toxicology and nanotoxicology. Food and Chemical Toxicology, 2018, 112, 495-506.	3.6	59
53	Technical Reproducibility of Genotyping SNP Arrays Used in Genome-Wide Association Studies. PLoS ONE, 2012, 7, e44483.	2.5	59
54	Competitive molecular docking approach for predicting estrogen receptor subtype Î± agonists and antagonists. BMC Bioinformatics, 2014, 15, S4.	2.6	58

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55	Quantitative Structureâ€“Activity Relationship Models for Predicting Inflammatory Potential of Metal Oxide Nanoparticles. Environmental Health Perspectives, 2020, 128, 67010.	6.0	58
56	Individualized network-based drug repositioning infrastructure for precision oncology in the panomics era. Briefings in Bioinformatics, 2016, 18, bbw051.	6.5	57
57	Drug Repositioning Through Network Pharmacology. Current Topics in Medicinal Chemistry, 2016, 16, 3646-3656.	2.1	57
58	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
59	Comprehensive Assessments of RNA-seq by the SEQC Consortium: FDA-Led Efforts Advance Precision Medicine. Pharmaceutics, 2016, 8, 8.	4.5	53
60	Assessing QSAR Limitations - A Regulatory Perspective. Current Computer-Aided Drug Design, 2005, 1, 195-205.	1.2	52
61	Decision Forest Analysis of 61 Single Nucleotide Polymorphisms in a Case-Control Study of Esophageal Cancer; a novel method. BMC Bioinformatics, 2005, 6, S4.	2.6	48
62	Development and Validation of Decision Forest Model for Estrogen Receptor Binding Prediction of Chemicals Using Large Data Sets. Chemical Research in Toxicology, 2015, 28, 2343-2351.	3.3	47
63	Structures of Endocrine-Disrupting Chemicals Determine Binding to and Activation of the Estrogen Receptor Î± and Androgen Receptor. Environmental Science & Technology, 2020, 54, 11424-11433.	10.0	45
64	Next generation sequencing for profiling expression of miRNAs: technical progress and applications in drug development. Journal of Biomedical Science and Engineering, 2011, 04, 666-676.	0.4	45
65	Multiple microRNAs function as self-protective modules in acetaminophen-induced hepatotoxicity in humans. Archives of Toxicology, 2018, 92, 845-858.	4.2	42
66	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
67	Structureâ€“activity relationship-based chemical classification of highly imbalanced Tox21 datasets. Journal of Cheminformatics, 2020, 12, 66.	6.1	39
68	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. Nature Biotechnology, 2021, 39, 1151-1160.	17.5	39
69	In Silico Pharmacoepidemiologic Evaluation of Drug-Induced Cardiovascular Complications Using Combined Classifiers. Journal of Chemical Information and Modeling, 2018, 58, 943-956.	5.4	37
70	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
71	Whole genome sequencing of 35 individuals provides insights into the genetic architecture of Korean population. BMC Bioinformatics, 2014, 15, S6.	2.6	34
72	sNebula, a network-based algorithm to predict binding between human leukocyte antigens and peptides. Scientific Reports, 2016, 6, 32115.	3.3	34

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73	Rat Î±-Fetoprotein Binding Affinities of a Large Set of Structurally Diverse Chemicals Elucidated the Relationships between Structures and Binding Affinities. Chemical Research in Toxicology, 2012, 25, 2553-2566.	3.3	33
74	Similarities and differences between variants called with human reference genome HG19 or HG38. BMC Bioinformatics, 2019, 20, 101.	2.6	33
75	ESSESA: an expert system for elucidation of structures from spectra. 1. Knowledge base of infrared spectra and analysis and interpretation programs. Journal of Chemical Information and Modeling, 1990, 30, 203-210.	5.4	32
76	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
77	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
78	Molecular Docking for Identification of Potential Targets for Drug Repurposing. Current Topics in Medicinal Chemistry, 2016, 16, 3636-3645.	2.1	31
79	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
80	Regulatory application of SAR/QSAR for priority setting of endocrine disruptors: A perspective. Pure and Applied Chemistry, 2003, 75, 2375-2388.	1.9	29
81	Application of genome analysis strategies in the clinical testing for pediatric diseases. Pediatric Investigation, 2018, 2, 72-81.	1.4	29
82	Biomarker-based drug safety assessment in the age of systems pharmacology: from foundational to regulatory science. Biomarkers in Medicine, 2015, 9, 1241-1252.	1.4	28
83	Structural Changes Due to Antagonist Binding in Ligand Binding Pocket of Androgen Receptor Elucidated Through Molecular Dynamics Simulations. Frontiers in Pharmacology, 2018, 9, 492.	3.5	28
84	Alignment of Short Reads: A Crucial Step for Application of Next-Generation Sequencing Data in Precision Medicine. Pharmaceutics, 2015, 7, 523-541.	4.5	27
85	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
86	Structures of androgen receptor bound with ligands: advancing understanding of biological functions and drug discovery. Expert Opinion on Therapeutic Targets, 2016, 20, 1267-1282.	3.4	26
87	Development of estrogen receptor beta binding prediction model using large sets of chemicals. Oncotarget, 2017, 8, 92989-93000.	1.8	24
88	Molecular biomarkers: a US FDA effort. Biomarkers in Medicine, 2010, 4, 215-225.	1.4	23
89	Nanomaterial Databases: Data Sources for Promoting Design and Risk Assessment of Nanomaterials. Nanomaterials, 2021, 11, 1599.	4.1	23
90	Spec2D:Â A Structure Elucidation System Based on1H NMR and Hâ^'H COSY Spectra in Organic Chemistry. Journal of Chemical Information and Modeling, 2006, 46, 775-787.	5.4	22

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91	Modeling Chemical Interaction Profiles: II. Molecular Docking, Spectral Data-Activity Relationship, and Structure-Activity Relationship Models for Potent and Weak Inhibitors of Cytochrome P450 CYP3A4 Isozyme. Molecules, 2012, 17, 3407-3460.	3.8	22
92	Direct comparison of performance of single nucleotide variant calling in human genome with alignment-based and assembly-based approaches. Scientific Reports, 2017, 7, 10963.	3.3	22
93	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
94	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
95	Machine Learning Models for Predicting Cytotoxicity of Nanomaterials. Chemical Research in Toxicology, 2022, 35, 125-139.	3.3	21
96	Comparing genetic variants detected in the 1000 genomes project with SNPs determined by the International HapMap Consortium. Journal of Genetics, 2015, 94, 731-740.	0.7	20
97	Computational prediction models for assessing endocrine disrupting potential of chemicals. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2018, 36, 192-218.	2.9	20
98	Applicability Domains Enhance Application of PPARÎ³ Agonist Classifiers Trained by Drug-like Compounds to Environmental Chemicals. Chemical Research in Toxicology, 2020, 33, 1382-1388.	3.3	20
99	Structures of Endocrine-Disrupting Chemicals Correlate with the Activation of 12 Classic Nuclear Receptors. Environmental Science & Technology, 2021, 55, 16552-16562.	10.0	20
100	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. BMC Bioinformatics, 2015, 16, S9.	2.6	19
101	QSAR Models at the US FDA/NCTR. Methods in Molecular Biology, 2016, 1425, 431-459.	0.9	19
102	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	14.5	19
103	Discriminant models on mitochondrial toxicity improved by consensus modeling and resolving imbalance in training. Chemosphere, 2020, 253, 126768.	8.2	19
104	BPA Replacement Compounds: Current Status and Perspectives. ACS Sustainable Chemistry and Engineering, 2021, 9, 2433-2446.	6.7	19
105	Hidden biases in germline structural variant detection. Genome Biology, 2021, 22, 347.	8.8	19
106	Endocrine Disrupting Chemicals Mediated through Binding Androgen Receptor Are Associated with Diabetes Mellitus. International Journal of Environmental Research and Public Health, 2018, 15, 25.	2.6	18
107	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	8.8	18
108	ESSESA: An expert system for structure elucidation from spectra. 6. Substructure constraints from analysis of 13C-NMR spectra. Journal of Chemical Information and Computer Sciences, 1995, 35, 979-1000.	2.8	17

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109	Ionotropic GABA receptor antagonism-induced adverse outcome pathways for potential neurotoxicity biomarkers. Biomarkers in Medicine, 2015, 9, 1225-1239.	1.4	17
110	Consensus Modeling for Prediction of Estrogenic Activity of Ingredients Commonly Used in Sunscreen Products. International Journal of Environmental Research and Public Health, 2016, 13, 958.	2.6	17
111	ESSESA, an expert system for structure elucidation from spectral analysis. Analytica Chimica Acta, 1992, 262, 179-191.	5.4	16
112	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
113	Quantitative Structureâ€“Activity Relationship Models for Predicting Risk of Drug-Induced Liver Injury in Humans. Methods in Pharmacology and Toxicology, 2018, , 77-100.	0.2	16
114	ESSESA: An Expert System for Structure Elucidation from Spectra. 4. Canonical Representation of Structures. Journal of Chemical Information and Computer Sciences, 1994, 34, 730-734.	2.8	15
115	Consensus analysis of multiple classifiers using non-repetitive variables: Diagnostic application to microarray gene expression data. Computational Biology and Chemistry, 2007, 31, 48-56.	2.3	15
116	Emerging efforts for discovering new biomarkers of liver disease and hepatotoxicity. Biomarkers in Medicine, 2014, 8, 143-146.	1.4	15
117	A Rat Î±-Fetoprotein Binding Activity Prediction Model to Facilitate Assessment of the Endocrine Disruption Potential of Environmental Chemicals. International Journal of Environmental Research and Public Health, 2016, 13, 372.	2.6	15
118	Whole genome and exome sequencing reference datasets from a multi-center and cross-platform benchmark study. Scientific Data, 2021, 8, 296.	5.3	15
119	Mechanistic roles of microRNAs in hepatocarcinogenesis: A study of thioacetamide with multiple doses and time-points of rats. Scientific Reports, 2017, 7, 3054.	3.3	14
120	A Review of Feature Reduction Methods for QSAR-Based Toxicity Prediction. Challenges and Advances in Computational Chemistry and Physics, 2019, , 119-139.	0.6	14
121	Development of a Nicotinic Acetylcholine Receptor nAChR Î±7 Binding Activity Prediction Model. Journal of Chemical Information and Modeling, 2020, 60, 2396-2404.	5.4	14
122	Predictive Models to Identify Small Molecule Activators and Inhibitors of Opioid Receptors. Journal of Chemical Information and Modeling, 2021, 61, 2675-2685.	5.4	14
123	Modeling Chemical Interaction Profiles: I. Spectral Data-Activity Relationship and Structure-Activity Relationship Models for Inhibitors and Non-inhibitors of Cytochrome P450 CYP3A4 and CYP2D6 Isozymes. Molecules, 2012, 17, 3383-3406.	3.8	13
124	Genomic Discoveries and Personalized Medicine in Neurological Diseases. Pharmaceutics, 2015, 7, 542-553.	4.5	13
125	Challenges, Solutions, and Quality Metrics of Personal Genome Assembly in Advancing Precision Medicine. Pharmaceutics, 2016, 8, 15.	4.5	13
126	Very Important Pool (VIP) genes â€“ an application for microarray-based molecular signatures. BMC Bioinformatics, 2008, 9, S9.	2.6	12

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127	Molecular regulation of miRNAs and potential biomarkers in the progression of hepatic steatosis to NASH. Biomarkers in Medicine, 2015, 9, 1189-1200.	1.4	12
128	Development of classification models for predicting inhibition of mitochondrial fusion and fission using machine learning methods. Chemosphere, 2021, 273, 128567.	8.2	12
129	ESSESA: An Expert System for Structure Elucidation from Spectra. 5. Substructure Constraints from Analysis of First-Order 1H-NMR Spectra. Journal of Chemical Information and Computer Sciences, 1994, 34, 1259-1266.	2.8	11
130	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
131	Achieving robust somatic mutation detection with deep learning models derived from reference data sets of a cancer sample. Genome Biology, 2022, 23, 12.	8.8	11
132	ESSESA: An expert system for structure elucidation from spectra. 3. LNSCS for chemical knowledge representation. Journal of Chemical Information and Computer Sciences, 1992, 32, 116-120.	2.8	9
133	Gaining Confidence on Molecular Classification through Consensus Modeling and Validation. Toxicology Mechanisms and Methods, 2006, 16, 59-68.	2.7	9
134	Quality control metrics improve repeatability and reproducibility of single-nucleotide variants derived from whole-genome sequencing. Pharmacogenomics Journal, 2015, 15, 298-309.	2.0	9
135	Pathway Analysis Revealed Potential Diverse Health Impacts of Flavonoids that Bind Estrogen Receptors. International Journal of Environmental Research and Public Health, 2016, 13, 373.	2.6	9
136	Elucidation of Agonist and Antagonist Dynamic Binding Patterns in ER-Î± by Integration of Molecular Docking, Molecular Dynamics Simulations and Quantum Mechanical Calculations. International Journal of Molecular Sciences, 2021, 22, 9371.	4.1	9
137	Estimating relative noise to signal in DNA microarray data. International Journal of Bioinformatics Research and Applications, 2013, 9, 433.	0.2	8
138	Applications of Molecular Dynamics Simulations in Computational Toxicology. Challenges and Advances in Computational Chemistry and Physics, 2019, , 181-212.	0.6	8
139	Pitfall of genome-wide association studies: Sources of inconsistency in genotypes and their effects. Journal of Biomedical Science and Engineering, 2012, 05, 557-573.	0.4	8
140	Machine learning models on chemical inhibitors of mitochondrial electron transport chain. Journal of Hazardous Materials, 2022, 426, 128067.	12.4	8
141	Comparative toxicogenomics of three insensitive munitions constituents 2,4-dinitroanisole, nitroguanidine and nitrotriazolone in the soil nematode Caenorhabditis elegans. BMC Systems Biology, 2018, 12, 92.	3.0	7
142	Human transthyretin binding affinity of halogenated thiophenols and halogenated phenols: An in vitro and in silico study. Chemosphere, 2021, 280, 130627.	8.2	7
143	Competitive docking model for prediction of the human nicotinic acetylcholine receptor Î±7 binding of tobacco constituents. Oncotarget, 2018, 9, 16899-16916.	1.8	7
144	Machine Learning Models for Predicting Liver Toxicity. Methods in Molecular Biology, 2022, 2425, 393-415.	0.9	7

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145	Applying network analysis and Nebula (neighbor-edges based and unbiased leverage algorithm) to ToxCast data. Environment International, 2016, 89-90, 81-92.	10.0	6
146	Target-specific toxicity knowledgebase (TsTKb): a novel toolkit for in silico predictive toxicology. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2018, 36, 219-236.	2.9	6
147	In silico identification of genetic mutations conferring resistance to acetohydroxyacid synthase inhibitors: A case study of Kochia scoparia. PLoS ONE, 2019, 14, e0216116.	2.5	6
148	Machine Learning for Predicting Risk of Drug-Induced Autoimmune Diseases by Structural Alerts and Daily Dose. International Journal of Environmental Research and Public Health, 2021, 18, 7139.	2.6	6
149	QUICK: Quality and Usability Investigation and Control Kit for Mass Spectrometric Data from Detection of Persistent Organic Pollutants. International Journal of Environmental Research and Public Health, 2019, 16, 4203.	2.6	5
150	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	4.9	5
151	Identification of Epidemiological Traits by Analysis of SARSâˆ’CoVâˆ’2 Sequences. Viruses, 2021, 13, 764.	3.3	5
152	Informing selection of drugs for COVID-19 treatment through adverse events analysis. Scientific Reports, 2021, 11, 14022.	3.3	5
153	Homology Model and Ligand Binding Interactions of the Extracellular Domain of the Human <i>Î±</i>4<i>Î²</i>2 Nicotinic Acetylcholine Receptor. Journal of Biomedical Science and Engineering, 2016, 09, 41-100.	0.4	5
154	Correlation analysis of external RNA controls reveals its utility for assessment of microarray assay. Analytical Biochemistry, 2009, 385, 203-207.	2.4	4
155	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. , 2013, , 39-61.		4
156	Advancing translation of biomarkers into regulatory science. Biomarkers in Medicine, 2015, 9, 1043-1046.	1.4	3
157	Reproducibility challenges for biomarker detection with uncertain but informative experimental data. Biomarkers in Medicine, 2020, 14, 1255-1263.	1.4	3
158	Assessing Consistency Between Versions of Genotype-Calling Algorithm Birdseed for the Genome-Wide Human SNP Array 6.0 Using HapMap Samples. Advances in Experimental Medicine and Biology, 2010, 680, 355-360.	1.6	3
159	Sustainable Management of Synthetic Chemicals. ACS Sustainable Chemistry and Engineering, 2021, 9, 13703-13704.	6.7	3
160	Potential Sources of Spurious Associations and Batch Effects in Genome-Wide Association Studies. , 0, , 191-201.		2
161	Quantum chemical simulations revealed the toxicokinetic mechanisms of organic phosphorus flame retardants catalyzed by P450 enzymes. Journal of Environmental Science and Health, Part C: Environmental Carcinogenesis and Ecotoxicology Reviews, 2018, 36, 272-291.	2.9	2
162	dnAQET: a framework to compute a consolidated metric for benchmarking quality of de novo assemblies. BMC Genomics, 2019, 20, 706.	2.8	2

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163	Mode-of-Action-Guided, Molecular Modeling-Based Toxicity Prediction: A Novel Approach for In Silico Predictive Toxicology. Challenges and Advances in Computational Chemistry and Physics, 2019, , 99-118.	0.6	2
164	Software-Assisted Pattern Recognition of Persistent Organic Pollutants in Contaminated Human and Animal Food. Molecules, 2021, 26, 685.	3.8	2
165	Next-Generation Sequencing and Its Impact on Pharmacogenetics. Journal of Pharmacogenomics & Pharmacoproteomics, 2012, 03, .	0.2	2
166	Research Highlights: Highlights from the latest research in cytochromes pharmacogenomics. Pharmacogenomics, 2013, 14, 459-463.	1.3	1
167	Computational Toxicology Promotes Regulatory Science. Challenges and Advances in Computational Chemistry and Physics, 2019, , 1-11.	0.6	1
168	SELDI Based Proteomic Determination of Hepatic Biomarkers in Mouse Serum Following Acetaminophen Administration. Journal of Proteomics and Bioinformatics, 2008, 01, 424-436.	0.4	1
169	CYP2A6, CYP2B6 and CYP2E1 copy number variation in five ethnic groups. Pharmacogenomics, 2013, 14, 461-2.	1.3	1
170	Factorial analysis of error correction performance using simulated next-generation sequencing data. , 2016, , .		0
171	Predicting the Risks of Drug-Induced Liver Injury in Humans Utilizing Computational Modeling. Challenges and Advances in Computational Chemistry and Physics, 2019, , 259-278.	0.6	0
172	Linkage disequilibrium characterization of CYP2C and CYP2D genomic regions in European populations. Pharmacogenomics, 2013, 14, 460-1.	1.3	0
173	CYP2D6 genotype predicts tamoxifen side effects but not cancer-free or survival benefits in postmenopausal ER+ and/or PgR+ breast cancers. Pharmacogenomics, 2013, 14, 462-3.	1.3	0