Joshua Xu

List of Publications by Year in descending order

36 papers	2,490 citations	471509 17 h-index	395702 33 g-index
39 all docs	39 docs citations	39 times ranked	4676 citing authors

#	Article	IF	Citations
1	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
2	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	17.5	420
3	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
4	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
5	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. Nature Biotechnology, 2021, 39, 1115-1128.	17.5	126
6	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
7	Comparing SVM and ANN based Machine Learning Methods for Species Identification of Food Contaminating Beetles. Scientific Reports, 2018, 8, 6532.	3.3	72
8	An FDA bioinformatics tool for microbial genomics research on molecular characterization of bacterial foodborne pathogens using microarrays. BMC Bioinformatics, 2010, 11, S4.	2.6	53
9	Comprehensive Assessments of RNA-seq by the SEQC Consortium: FDA-Led Efforts Advance Precision Medicine. Pharmaceutics, 2016, 8, 8.	4.5	53
10	FDA drug labeling: rich resources to facilitate precision medicine, drug safety, and regulatory science. Drug Discovery Today, 2016, 21, 1566-1570.	6.4	38
11	Towards accurate and reliable resolution of structural variants for clinical diagnosis. Genome Biology, 2022, 23, 68.	8.8	34
12	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	5.3	30
13	Study of pharmacogenomic information in FDA-approved drug labeling to facilitate application of precision medicine. Drug Discovery Today, 2020, 25, 813-820.	6.4	29
14	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
15	A deep learning model to recognize food contaminating beetle species based on elytra fragments. Computers and Electronics in Agriculture, 2019, 166, 105002.	7.7	28
16	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	5.3	21
17	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	8.8	20
18	ArrayTrack: a free FDA bioinformatics tool to support emerging biomedical research -- an update. Human Genomics, 2010, 4, 428-34.	2.9	19

#	Article	IF	Citations
19	ATP-Binding Cassette Genes Genotype and Expression: A Potential Association with Pancreatic Cancer Development and Chemoresistance?. Gastroenterology Research and Practice, 2014, 2014, 1-9.	1.5	15
20	Two new ArrayTrack libraries for personalized biomedical research. BMC Bioinformatics, 2010, 11, S6.	2.6	12
21	Technical advance in targeted NGS analysis enables identification of lung cancer risk-associated low frequency TP53, PIK3CA, and BRAF mutations in airway epithelial cells. BMC Cancer, 2019, 19, 1081.	2.6	12
22	Species Identification of Food Contaminating Beetles by Recognizing Patterns in Microscopic Images of Elytra Fragments. PLoS ONE, 2016, 11, e0157940.	2.5	11
23	DLI-IT: a deep learning approach to drug label identification through image and text embedding. BMC Medical Informatics and Decision Making, 2020, 20, 68.	3.0	10
24	NETBAGs: a network-based clustering approach with gene signatures for cancer subtyping analysis. Biomarkers in Medicine, 2015, 9, 1053-1065.	1.4	9
25	Advancing NGS quality control to enable measurement of actionable mutations in circulating tumor DNA. Cell Reports Methods, 2021, 1, 100106.	2.9	9
26	FDALabel for drug repurposing studies and beyond. Nature Biotechnology, 2020, 38, 1378-1379.	17.5	8
27	Deep oncopanel sequencing reveals within block position-dependent quality degradation in FFPE processed samples. Genome Biology, 2022, 23, .	8.8	8
28	Estimating Bacterial Concentrations in Fibrous Substrates Through a Combination of Scanning Electron Microscopy and ImageJ. Analytical Chemistry, 2019, 91, 4405-4412.	6.5	7
29	The Sequencing Quality Control 2 study: establishing community standards for sequencing in precision medicine. Genome Biology, 2021, 22, 306.	8.8	7
30	HetEnc: a deep learning predictive model for multi-type biological dataset. BMC Genomics, 2019, 20, 638.	2.8	4
31	FDA-led consortium studies advance quality control of targeted next generation sequencing assays for precision oncology. Precision Cancer Medicine, 2021, 4, 32-32.	1.8	4
32	Ultra-deep sequencing data from a liquid biopsy proficiency study demonstrating analytic validity. Scientific Data, 2022, 9, 170.	5.3	4
33	SNPTrackTM: an integrated bioinformatics system for genetic association studies. Human Genomics, 2012, 6, 5.	2.9	2
34	Optimized imaging methods for species-level identification of food-contaminating beetles. Scientific Reports, 2021, 11, 7957.	3.3	1
35	Advancing Genomics for Drug Development and Safety Evaluation. International Journal of Genomics, 2018, 2018, 1-2.	1.6	0
36	Ultra-deep multi-oncopanel sequencing of benchmarking samples with a wide range of variant allele frequencies. Scientific Data, 2022, 9, .	5.3	0