

# Zhenqiang Su

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10650980/publications.pdf>

Version: 2024-02-01

25  
papers

5,412  
citations

361413

20  
h-index

610901

24  
g-index

30  
all docs

30  
docs citations

30  
times ranked

8800  
citing authors

#	ARTICLE	IF	CITATIONS
1	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. <i>Nature Biotechnology</i> , 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. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
3	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. <i>Nature Biotechnology</i> , 2014, 32, 926-932.	17.5	420
4	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	8.8	325
5	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. <i>Nature Communications</i> , 2014, 5, 3230.	12.8	316
6	Mold<sup>2</sup>, Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. <i>Journal of Chemical Information and Modeling</i> , 2008, 48, 1337-1344.	5.4	241
7	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. <i>BMC Bioinformatics</i> , 2008, 9, S10.	2.6	215
8	Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential. <i>BMC Bioinformatics</i> , 2005, 6, S12.	2.6	164
9	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. <i>Genome Biology</i> , 2014, 15, 523.	8.8	147
10	Next-generation sequencing and its applications in molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011, 11, 333-343.	3.1	146
11	Blood molecular markers associated with COVID-19 immunopathology and multi-organ damage. <i>EMBO Journal</i> , 2020, 39, e105896.	7.8	123
12	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
13	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.	3.3	80
14	Microarray scanner calibration curves: characteristics and implications. <i>BMC Bioinformatics</i> , 2005, 6, S11.	2.6	74
15	EADB: An Estrogenic Activity Database for Assessing Potential Endocrine Activity. <i>Toxicological Sciences</i> , 2013, 135, 277-291.	3.1	68
16	The Liver Toxicity Biomarker Study: Phase I Design and Preliminary Results. <i>Toxicologic Pathology</i> , 2009, 37, 52-64.	1.8	53
17	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
18	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140021.	5.3	30

#	ARTICLE	IF	CITATIONS
19	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.	4.9	26
20	Microarray platform consistency is revealed by biologically functional analysis of gene expression profiles. <i>BMC Bioinformatics</i> , 2009, 10, S12.	2.6	22
21	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. <i>Scientific Data</i> , 2014, 1, 140020.	5.3	21
22	Evaluation of gene expression data generated from expired Affymetrix GeneChip® microarrays using MAQC reference RNA samples. <i>BMC Bioinformatics</i> , 2010, 11, S10.	2.6	20
23	The Liver Toxicity Biomarker Study Phase I: Markers for the Effects of Tolcapone or Entacapone. <i>Toxicologic Pathology</i> , 2012, 40, 951-964.	1.8	20
24	Very Important Pool (VIP) genes – an application for microarray-based molecular signatures. <i>BMC Bioinformatics</i> , 2008, 9, S9.	2.6	12
25	The MicroArray Quality Control (MAQC) Project and Cross-Platform Analysis of Microarray Data. , 2011, , 171-192.		6