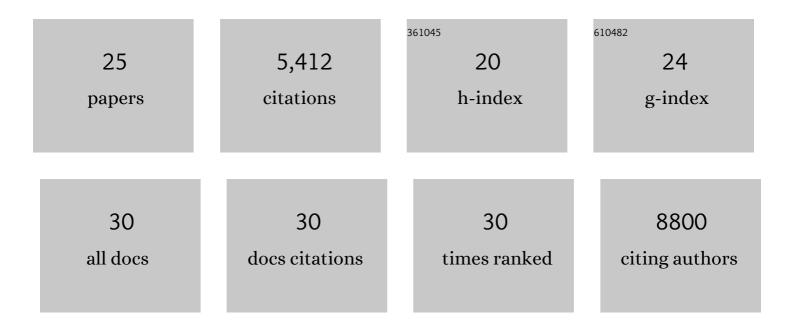
Zhenqiang Su

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10650980/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Blood molecular markers associated with COVIDâ€19 immunopathology and multiâ€organ damage. EMBO Journal, 2020, 39, e105896.	3.5	123
2	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	3.8	325
3	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. Genome Biology, 2014, 15, 523.	3.8	147
4	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. Scientific Data, 2014, 1, 140021.	2.4	30
5	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. Nature Communications, 2014, 5, 3230.	5.8	316
6	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	5.8	122
7	The concordance between RNA-seq and microarray data depends on chemical treatment and transcript abundance. Nature Biotechnology, 2014, 32, 926-932.	9.4	420
8	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
9	Cross-platform ultradeep transcriptomic profiling of human reference RNA samples by RNA-Seq. Scientific Data, 2014, 1, 140020.	2.4	21
10	EADB: An Estrogenic Activity Database for Assessing Potential Endocrine Activity. Toxicological Sciences, 2013, 135, 277-291.	1.4	68
11	Studies on abacavir-induced hypersensitivity reaction: a successful example of translation of pharmacogenetics to personalized medicine. Science China Life Sciences, 2013, 56, 119-124.	2.3	26
12	The Liver Toxicity Biomarker Study Phase I: Markers for the Effects of Tolcapone or Entacapone. Toxicologic Pathology, 2012, 40, 951-964.	0.9	20
13	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.	1.7	80
14	Next-generation sequencing and its applications in molecular diagnostics. Expert Review of Molecular Diagnostics, 2011, 11, 333-343.	1.5	146
15	The MicroArray Quality Control (MAQC) Project and Cross-Platform Analysis of Microarray Data. , 2011, , 171-192.		6
16	Evaluation of gene expression data generated from expired Affymetrix GeneChip® microarrays using MAQC reference RNA samples. BMC Bioinformatics, 2010, 11, S10.	1.2	20
17	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.	9.4	795
18	The Liver Toxicity Biomarker Study: Phase I Design and Preliminary Results. Toxicologic Pathology, 2009. 37. 52-64.	0.9	53

ZHENQIANG SU

#	Article	IF	CITATIONS
19	Microarray platform consistency is revealed by biologically functional analysis of gene expression profiles. BMC Bioinformatics, 2009, 10, S12.	1.2	22
20	The balance of reproducibility, sensitivity, and specificity of lists of differentially expressed genes in microarray studies. BMC Bioinformatics, 2008, 9, S10.	1.2	215
21	Very Important Pool (VIP) genes – an application for microarray-based molecular signatures. BMC Bioinformatics, 2008, 9, S9.	1.2	12
22	Mold ² , Molecular Descriptors from 2D Structures for Chemoinformatics and Toxicoinformatics. Journal of Chemical Information and Modeling, 2008, 48, 1337-1344.	2.5	241
23	The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. Nature Biotechnology, 2006, 24, 1151-1161.	9.4	1,927
24	Microarray scanner calibration curves: characteristics and implications. BMC Bioinformatics, 2005, 6, S11.	1.2	74
25	Cross-platform comparability of microarray technology: Intra-platform consistency and appropriate data analysis procedures are essential BMC Bioinformatics 2005 6 S12	1.2	164