Haiyan Huang

List of Publications by Year
in descending order

56 papers	8,646 citations	236925 25 h-index	161849 54 g-index
58 all docs	58 docs citations	58 times ranked	15877 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
2	Measuring reproducibility of high-throughput experiments. Annals of Applied Statistics, 2011, 5, .	1.1	868
3	The Genomes of Oryza sativa: A History of Duplications. PLoS Biology, 2005, 3, e38.	5.6	808
4	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
5	Profiling protein expression in circulating tumour cells using microfluidic western blotting. Nature Communications, 2017, 8, 14622.	12.8	201
6	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	27.8	184
7	Review on statistical methods for gene network reconstruction using expression data. Journal of Theoretical Biology, 2014, 362, 53-61.	1.7	160
8	Functional annotation and network reconstruction through cross-platform integration of microarray data. Nature Biotechnology, 2005, 23, 238-243.	17.5	137
9	Comparison of *D. melanogaster* and *C. elegans* developmental stages, tissues, and cells by modENCODE RNA-seq data. Genome Research, 2014, 24, 1086-1101.	5.5	88
10	Clustering analysis of SAGE data using a Poisson approach. Genome Biology, 2004, 5, R51.	9.6	76
11	Single cell clustering based on cell-pair differentiability correlation and variance analysis. Bioinformatics, 2018, 34, 3684-3694.	4.1	74
12	Finding Short DNA Motifs Using Permuted Markov Models. Journal of Computational Biology, 2005, 12, 894-906.	1.6	73
13	Systematic discovery of functional modules and context-specific functional annotation of human genome. Bioinformatics, 2007, 23, i222-i229.	4.1	73
14	Single-chain heteropolymers transport protons selectively and rapidly. Nature, 2020, 577, 216-220.	27.8	64
15	Transcription Profile Analyses Identify Genes and Pathways Central to Root Cap Functions in Maize. Plant Molecular Biology, 2006, 60, 343-363.	3.9	58
16	Subsampling methods for genomic inference. Annals of Applied Statistics, 2010, 4, .	1.1	58
17	Bayesian approach to transforming public gene expression repositories into disease diagnosis databases. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6823-6828.	7.1	49
18	The maize root stem cell niche: a partnership between two sister cell populations. Planta, 2010, 231, 411-424.	3.2	46

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19	Characterization of the Zebrafish *Ugt* Repertoire Reveals a New Class of Drug-Metabolizing UDP Glucuronosyltransferases. Molecular Pharmacology, 2014, 86, 62-75.	2.3	39
20	Determination of Local Statistical Significance of Patterns in Markov Sequences with Application to Promoter Element Identification. Journal of Computational Biology, 2004, 11, 1-14.	1.6	38
21	Cell characterization using a protein-functionalized pore. Lab on A Chip, 2008, 8, 1478.	6.0	36
22	Cloning and Comparative Analyses of the Zebrafish Ugt Repertoire Reveal Its Evolutionary Diversity. PLoS ONE, 2010, 5, e9144.	2.5	35
23	A Genetic Variant Ameliorates Î²-Thalassemia Severity by Epigenetic-Mediated Elevation of Human Fetal Hemoglobin Expression. American Journal of Human Genetics, 2017, 101, 130-138.	6.2	31
24	Spontaneous low-frequency fluctuations in the neural system for emotional perception in major psychiatric disorders: amplitude similarities and differences across frequency bands. Journal of Psychiatry and Neuroscience, 2019, 44, 132-141.	2.4	30
25	Gene coexpression measures in large heterogeneous samples using count statistics. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16371-16376.	7.1	29
26	Cas9 has no exonuclease activity resulting in staggered cleavage with overhangs and predictable di- and tri-nucleotide CRISPR insertions without template donor. Cell Discovery, 2019, 5, 53.	6.7	29
27	An overview of recent developments in genomics and associated statistical methods. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2009, 367, 4313-4337.	3.4	27
28	Measuring similarities between gene expression profiles through new data transformations. BMC Bioinformatics, 2007, 8, 29.	2.6	25
29	Sorting single satellite cells from individual myofibers reveals heterogeneity in cell-surface markers and myogenic capacity. Integrative Biology (United Kingdom), 2013, 5, 692-702.	1.3	25
30	Inferring geneâ€"gene interactions and functional modules using sparse canonical correlation analysis. Annals of Applied Statistics, 2015, 9, .	1.1	25
31	Linking invasive motility to protein expression in single tumor cells. Lab on A Chip, 2018, 18, 371-384.	6.0	23
32	Integrative disease classification based on cross-platform microarray data. BMC Bioinformatics, 2009, 10, S25.	2.6	20
33	Genetic Variations and Haplotype Diversity of the UGT1 Gene Cluster in the Chinese Population. PLoS ONE, 2012, 7, e33988.	2.5	19
34	A Statistical Framework to Infer Functional Gene Relationships From Biologically Interrelated Microarray Experiments. Journal of the American Statistical Association, 2009, 104, 465-473.	3.1	18
35	CRISPR Double Cutting through the Labyrinthine Architecture of 3D Genomes. Journal of Genetics and Genomics, 2016, 43, 273-288.	3.9	17
36	SIDEseq: A Cell Similarity Measure Defined by Shared Identified Differentially Expressed Genes for Single-Cell RNA sequencing Data. Statistics in Biosciences, 2017, 9, 200-216.	1.2	17

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37	Improvement of Vero cell growth in glutamate-based culture by supplementing ammoniagenic compounds. Process Biochemistry, 2006, 41, 2386-2392.	3.7	14
38	Patterns of nucleotide diversity in wild and cultivated rice. Plant Systematics and Evolution, 2009, 281, 97-106.	0.9	13
39	Klf5 establishes bi-potential cell fate by dual regulation of ICM and TE specification genes. Cell Reports, 2021, 37, 109982.	6.4	13
40	Using biologically interrelated experiments to identify pathway genes in *Arabidopsis*. Bioinformatics, 2012, 28, 815-822.	4.1	11
41	Electrophoretic cytopathology resolves ERBB2 forms with single-cell resolution. Npj Precision Oncology, 2018, 2, 10.	5.4	11
42	Identifying Cell Subpopulations and Their Genetic Drivers from Single-Cell RNA-Seq Data Using a Biclustering Approach. Journal of Computational Biology, 2017, 24, 663-674.	1.6	10
43	Clustering Analysis of SAGE Transcription Profiles Using a Poisson Approach. Methods in Molecular Biology, 2008, 387, 185-198.	0.9	10
44	Nitrogen metabolism of asparagine and glutamate in Vero cells studied by 1H/15N NMR spectroscopy. Applied Microbiology and Biotechnology, 2007, 77, 427-436.	3.6	9
45	Bi*c*lustering of *Li*near *P*atterns In Gene Expression Data. Journal of Computational Biology, 2012, 19, 619-631.	1.6	9
46	Generalized correlation measure using count statistics for gene expression data with ordered samples. Bioinformatics, 2018, 34, 617-624.	4.1	9
47	GeneFishing to reconstruct context specific portraits of biological processes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18943-18950.	7.1	6
48	Probe-target hybridization depends on spatial uniformity of initial concentration condition across large-format chips. Scientific Reports, 2020, 10, 8768.	3.3	6
49	Network Modeling in Biology: Statistical Methods for Gene and Brain Networks. Statistical Science, 2021, 36, 89-108.	2.8	6
50	Bipartite graph-based approach for clustering of cell lines by gene expression–drug response associations. Bioinformatics, 2021, 37, 2617-2626.	4.1	6
51	Measuring expression heterogeneity of single-cell cytoskeletal protein complexes. Nature Communications, 2021, 12, 4969.	12.8	6
52	Arcsine laws for random walks generated from random permutations with applications to genomics. Journal of Applied Probability, 2021, 58, 851-867.	0.7	4
53	Biclustering by sparse canonical correlation analysis. Quantitative Biology, 2018, 6, 56-67.	0.5	3
54	TRANSCRIPTOME ANALYSIS USING NEXT-GENERATION SEQUENCING. , 2015, , 915-936.		1

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55	Data Wisdom in Computational Genomics Research. Statistics in Biosciences, 2017, 9, 646-661.	1.2	0
56	Multiregion Sequence Analysis to Predict Intratumor Heterogeneity and Clonal Evolution. Methods in Molecular Biology, 2021, 2243, 283-296.	0.9	0