

Joshua Ho

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

115 papers	3,109 citations	30 h-index	53 g-index
139 ext. papers	4,322 ext. citations	7.5 avg, IF	5.33 L-index

#	Paper	IF	Citations
115	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014 , 512, 449-52	50.4	265
114	CIDR: Ultrafast and accurate clustering through imputation for single-cell RNA-seq data. <i>Genome Biology</i> , 2017 , 18, 59	18.3	253
113	Single-cell expression profiling reveals dynamic flux of cardiac stromal, vascular and immune cells in health and injury. <i>ELife</i> , 2019 , 8,	8.9	191
112	Testing and Validating Machine Learning Classifiers by Metamorphic Testing. <i>Journal of Systems and Software</i> , 2011 , 84, 544-558	3.3	153
111	NAD Deficiency, Congenital Malformations, and Niacin Supplementation. <i>New England Journal of Medicine</i> , 2017 , 377, 544-552	59.2	114
110	Male-lineage transmission of an acquired metabolic phenotype induced by grand-paternal obesity. <i>Molecular Metabolism</i> , 2016 , 5, 699-708	8.8	104
109	ChIP-chip versus ChIP-seq: lessons for experimental design and data analysis. <i>BMC Genomics</i> , 2011 , 12, 134	4.5	103
108	Lung stem cell self-renewal relies on BMI1-dependent control of expression at imprinted loci. <i>Cell Stem Cell</i> , 2011 , 9, 272-81	18	101
107	Heart failure-associated changes in RNA splicing of sarcomere genes. <i>Circulation: Cardiovascular Genetics</i> , 2010 , 3, 138-46		91
106	Differential variability analysis of gene expression and its application to human diseases. <i>Bioinformatics</i> , 2008 , 24, i390-8	7.2	88
105	An innovative approach for testing bioinformatics programs using metamorphic testing. <i>BMC Bioinformatics</i> , 2009 , 10, 24	3.6	85
104	A Wnt-bmp feedback circuit controls intertissue signaling dynamics in tooth organogenesis. <i>Science Signaling</i> , 2012 , 5, ra4	8.8	81
103	iSyTE: integrated Systems Tool for Eye gene discovery 2012 , 53, 1617-27		76
102	A dynamic H3K27ac signature identifies VEGFA-stimulated endothelial enhancers and requires EP300 activity. <i>Genome Research</i> , 2013 , 23, 917-27	9.7	64
101	Targeted next-generation sequencing identifies pathogenic variants in familial congenital heart disease. <i>Journal of the American College of Cardiology</i> , 2014 , 64, 2498-506	15.1	60
100	Impact of sequencing depth in ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2014 , 42, e74	20.1	49
99	SeqVis: visualization of compositional heterogeneity in large alignments of nucleotides. <i>Bioinformatics</i> , 2006 , 22, 2162-3	7.2	47

98	Impact of sequencing depth and read length on single cell RNA sequencing data of T cells. <i>Scientific Reports</i> , 2017 , 7, 12781	4.9	45
97	iSyTE 2.0: a database for expression-based gene discovery in the eye. <i>Nucleic Acids Research</i> , 2018 , 46, D875-D885	20.1	45
96	Host and microbiome multi-omics integration: applications and methodologies. <i>Biophysical Reviews</i> , 2019 , 11, 55-65	3.7	42
95	Verification and validation of bioinformatics software without a gold standard: a case study of BWA and Bowtie. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 16, S15	3.6	40
94	Sequence-specific targeting of dosage compensation in Drosophila favors an active chromatin context. <i>PLoS Genetics</i> , 2012 , 8, e1002646	6	40
93	Application of Metamorphic Testing to Supervised Classifiers. <i>Proceedings International Conference on Quality Software</i> , 2010 , 2009, 135-144		39
92	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001978	5.2	37
91	Intercalated discs: multiple proteins perform multiple functions in non-failing and failing human hearts. <i>Biophysical Reviews</i> , 2009 , 1, 43	3.7	36
90	hiHMM: Bayesian non-parametric joint inference of chromatin state maps. <i>Bioinformatics</i> , 2015 , 31, 2066-74	7.4	35
89	The short isoform of the CEACAM1 receptor in intestinal T cells regulates mucosal immunity and homeostasis via Tfh cell induction. <i>Immunity</i> , 2012 , 37, 930-46	32.3	35
88	Gene-gene interaction filtering with ensemble of filters. <i>BMC Bioinformatics</i> , 2011 , 12 Suppl 1, S10	3.6	32
87	Light-focusing human micro-lenses generated from pluripotent stem cells model lens development and drug-induced cataract. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	30
86	Binding of transcription factor GabR to DNA requires recognition of DNA shape at a location distinct from its cognate binding site. <i>Nucleic Acids Research</i> , 2016 , 44, 1411-20	20.1	27
85	Effect of machine learning re-sampling techniques for imbalanced datasets in F-FDG PET-based radiomics model on prognostication performance in cohorts of head and neck cancer patients. <i>European Journal of Nuclear Medicine and Molecular Imaging</i> , 2020 , 47, 2826-2835	8.8	25
84	Identification of clinically actionable variants from genome sequencing of families with congenital heart disease. <i>Genetics in Medicine</i> , 2019 , 21, 1111-1120	8.1	25
83	GEOMI: GEOMetry for Maximum Insight. <i>Lecture Notes in Computer Science</i> , 2006 , 468-479	0.9	25
82	Scalability and Validation of Big Data Bioinformatics Software. <i>Computational and Structural Biotechnology Journal</i> , 2017 , 15, 379-386	6.8	23
81	Crim1 regulates integrin signaling in murine lens development. <i>Development (Cambridge)</i> , 2016 , 143, 356-66	6.6	23

80	Computed tomography-based deep-learning prediction of neoadjuvant chemoradiotherapy treatment response in esophageal squamous cell carcinoma. <i>Radiotherapy and Oncology</i> , 2021 , 154, 6-13 ^{5.3}	22
79	Sierra: discovery of differential transcript usage from polyA-captured single-cell RNA-seq data. <i>Genome Biology</i> , 2020 , 21, 167	18.3 21
78	PARC: ultrafast and accurate clustering of phenotypic data of millions of single cells. <i>Bioinformatics</i> , 2020 , 36, 2778-2786	7.2 20
77	Assessment of Intratumoral and Peritumoral Computed Tomography Radiomics for Predicting Pathological Complete Response to Neoadjuvant Chemoradiation in Patients With Esophageal Squamous Cell Carcinoma. <i>JAMA Network Open</i> , 2020 , 3, e2015927	10.4 18
76	An evolutionarily conserved enhancer regulates Bmp4 expression in developing incisor and limb bud. <i>PLoS ONE</i> , 2012 , 7, e38568	3.7 18
75	How difficult is inference of mammalian causal gene regulatory networks?. <i>PLoS ONE</i> , 2014 , 9, e111661	3.7 18
74	A genetic ensemble approach for gene-gene interaction identification. <i>BMC Bioinformatics</i> , 2010 , 11, 524	3.6 17
73	Ularcirc: visualization and enhanced analysis of circular RNAs via back and canonical forward splicing. <i>Nucleic Acids Research</i> , 2019 , 47, e123	20.1 14
72	Efficient differentiation of steroidogenic and germ-like cells from epigenetically-related iPSCs derived from ovarian granulosa cells. <i>PLoS ONE</i> , 2015 , 10, e0119275	3.7 14
71	Identification of active signaling pathways by integrating gene expression and protein interaction data. <i>BMC Systems Biology</i> , 2018 , 12, 120	3.5 14
70	Ultrafast clustering of single-cell flow cytometry data using FlowGrid. <i>BMC Systems Biology</i> , 2019 , 13, 35	3.5 13
69	Biologically active constituents of the secretome of human W8B2 cardiac stem cells. <i>Scientific Reports</i> , 2018 , 8, 1579	4.9 13
68	A computer algorithm for the identification of protein interactions from the spectra of masses (PRISM). <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 563-6	3.5 13
67	Discovery of cell-type specific DNA motif grammar in cis-regulatory elements using random Forest. <i>BMC Genomics</i> , 2018 , 19, 929	4.5 12
66	How to test bioinformatics software?. <i>Biophysical Reviews</i> , 2015 , 7, 343-352	3.7 12
65	XGSA: A statistical method for cross-species gene set analysis. <i>Bioinformatics</i> , 2016 , 32, i620-i628	7.2 12
64	Falco: a quick and flexible single-cell RNA-seq processing framework on the cloud. <i>Bioinformatics</i> , 2017 , 33, 767-769	7.2 11
63	Multi-omic profiling reveals associations between the gut mucosal microbiome, the metabolome, and host DNA methylation associated gene expression in patients with colorectal cancer. <i>BMC Microbiology</i> , 2020 , 20, 83	4.5 11

62	Dam mutants provide improved sensitivity and spatial resolution for profiling transcription factor binding. <i>Epigenetics and Chromatin</i> , 2019 , 12, 36	5.8	10
61	An Embryonic and Induced Pluripotent Stem Cell Model for Ovarian Granulosa Cell Development and Steroidogenesis. <i>Reproductive Sciences</i> , 2018 , 25, 712-726	3	10
60	Verification of phylogenetic inference programs using metamorphic testing. <i>Journal of Bioinformatics and Computational Biology</i> , 2011 , 9, 729-47	1	10
59	Author response: Single-cell expression profiling reveals dynamic flux of cardiac stromal, vascular and immune cells in health and injury 2019 ,		10
58	Cisplatin prevents breast cancer metastasis through blocking early EMT and retards cancer growth together with paclitaxel. <i>Theranostics</i> , 2021 , 11, 2442-2459	12.1	10
57	Identification of satellite cells from anole lizard skeletal muscle and demonstration of expanded musculoskeletal potential. <i>Developmental Biology</i> , 2018 , 433, 344-356	3.1	9
56	Enhanced cardiac repair by telomerase reverse transcriptase over-expression in human cardiac mesenchymal stromal cells. <i>Scientific Reports</i> , 2019 , 9, 10579	4.9	9
55	Integrative analysis identifies co-dependent gene expression regulation of BRG1 and CHD7 at distal regulatory sites in embryonic stem cells. <i>Bioinformatics</i> , 2017 , 33, 1916-1920	7.2	9
54	Drawing Clustered Graphs in Three Dimensions. <i>Lecture Notes in Computer Science</i> , 2006 , 492-502	0.9	9
53	Cellular diversity and lineage trajectory: insights from mouse single cell transcriptomes. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	9
52	SeqVis: a tool for detecting compositional heterogeneity among aligned nucleotide sequences. <i>Methods in Molecular Biology</i> , 2009 , 537, 65-91	1.4	8
51	An antibody-based leukocyte-capture microarray for the diagnosis of systemic lupus erythematosus. <i>PLoS ONE</i> , 2013 , 8, e58199	3.7	8
50	A model selection approach to discover age-dependent gene expression patterns using quantile regression models. <i>BMC Genomics</i> , 2009 , 10 Suppl 3, S16	4.5	6
49	Machine learning application for the prediction of SARS-CoV-2 infection using blood tests and chest radiograph. <i>Scientific Reports</i> , 2021 , 11, 14250	4.9	6
48	Non-self mutation: double-stranded RNA elicits antiviral pathogenic response in a Drosophila model of expanded CAG repeat neurodegenerative diseases. <i>Human Molecular Genetics</i> , 2019 , 28, 3000-3012	5.6	5
47	Challenges and emerging systems biology approaches to discover how the human gut microbiome impact host physiology. <i>Biophysical Reviews</i> , 2020 , 12, 851-863	3.7	5
46	A voting approach to identify a small number of highly predictive genes using multiple classifiers. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S19	3.6	5
45	Crim1 regulates integrin signaling in murine lens development. <i>Journal of Cell Science</i> , 2016 , 129, e1.2-e1.3	1.3	5

44	Maternal obesity heritably perturbs offspring metabolism for three generations without serial programming. <i>International Journal of Obesity</i> , 2018 , 42, 911-914	5.5	5
43	Aberrant Expression of Circulating MicroRNA Leads to the Dysregulation of Alpha-Synuclein and Other Pathogenic Genes in Parkinson's Disease. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 695007	5.7	5
42	Deep Learning for Clinical Image Analyses in Oral Squamous Cell Carcinoma: A Review. <i>JAMA Otolaryngology - Head and Neck Surgery</i> , 2021 , 147, 893-900	3.9	5
41	Discovery of perturbation gene targets via free text metadata mining in Gene Expression Omnibus. <i>Computational Biology and Chemistry</i> , 2019 , 80, 152-158	3.6	4
40	dv-trio: a family-based variant calling pipeline using DeepVariant. <i>Bioinformatics</i> , 2020 , 36, 3549-3551	7.2	4
39	Network modelling of gene regulation. <i>Biophysical Reviews</i> , 2011 , 3, 1-13	3.7	4
38	Customising an antibody leukocyte capture microarray for systemic lupus erythematosus: beyond biomarker discovery. <i>Proteomics - Clinical Applications</i> , 2010 , 4, 179-89	3.1	4
37	starmap: Immersive visualisation of single cell data using smartphone-enabled virtual reality		4
36	A cloud-based framework for applying metamorphic testing to a bioinformatics pipeline 2016 ,		3
35	CIDR: Ultrafast and accurate clustering through imputation for single-cell RNA-Seq data		3
34	Sierra: discovery of differential transcript usage from polyA-captured single-cell RNA-seq data		3
33	Comparison of somatic variant detection algorithms using Ion Torrent targeted deep sequencing data. <i>BMC Medical Genomics</i> , 2019 , 12, 181	3.7	3
32	Genetic screening reveals phospholipid metabolism as a key regulator of the biosynthesis of the redox-active lipid coenzyme Q. <i>Redox Biology</i> , 2021 , 46, 102127	11.3	3
31	CardiacProfileR: an R package for extraction and visualisation of heart rate profiles from wearable fitness trackers. <i>Biophysical Reviews</i> , 2019 , 11, 119-121	3.7	2
30	Adjuvant radiotherapy and chemotherapy in early-stage diffuse large B cell lymphoma of head and neck with extranodal involvement. <i>Hematology</i> , 2019 , 24, 268-275	2.2	2
29	Systems Biology of Early Tooth Development 2013 , 179-202		2
28	Using Genomics Feature Selection Method in Radiomics Pipeline Improves Prognostication Performance in Locally Advanced Esophageal Squamous Cell Carcinoma-A Pilot Study. <i>Cancers</i> , 2021 , 13,	6.6	2
27	Automatic flow delay through passive wax valves for paper-based analytical devices. <i>Lab on A Chip</i> , 2021 , 21, 4166-4176	7.2	2

26	Lineage tracing and single-cell analysis reveal proliferative Prom1+ tumour-propagating cells and their dynamic cellular transition during liver cancer progression. <i>Gut</i> , 2021 ,	19.2	2
25	Inferring differential leukocyte activity from antibody microarrays using a latent variable model. <i>Genome Informatics</i> , 2008 , 21, 126-37		2
24	Evaluation of experimental protocols for shotgun whole-genome metagenomic discovery of antibiotic resistance genes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	1
23	Harnessing Multiple Source Test Cases in Metamorphic Testing: A Case Study in Bioinformatics 2017 ,		1
22	PBrowse: a web-based platform for real-time collaborative exploration of genomic data. <i>Nucleic Acids Research</i> , 2017 , 45, e67	20.1	1
21	Genome-Wide Mapping of ProteinDNA Interactions by ChIP-Seq 2012 , 139-151		1
20	Application of a systems approach to study developmental gene regulation. <i>Biophysical Reviews</i> , 2012 , 4, 245-253	3.7	1
19	Scavenger: A pipeline for recovery of unaligned reads utilising similarity with aligned reads. <i>F1000Research</i> , 2019 , 8, 1587	3.6	1
18	Falco: A quick and flexible single-cell RNA-seq processing framework on the cloud		1
17	Discovery of perturbation gene targets via free text metadata mining in Gene Expression Omnibus		1
16	Impact of sequencing depth and read length on single cell RNA sequencing data: lessons from T cells		1
15	Hactive: a smartphone application for heart rate profiling. <i>Biophysical Reviews</i> , 2020 , 12, 777-779	3.7	1
14	Cloud accelerated alignment and assembly of full-length single-cell RNA-seq data using Falco. <i>BMC Genomics</i> , 2019 , 20, 927	4.5	1
13	C3: An R package for cross-species compendium-based cell-type identification. <i>Computational Biology and Chemistry</i> , 2018 , 77, 187-192	3.6	1
12	Generalized and scalable trajectory inference in single-cell omics data with VIA. <i>Nature Communications</i> , 2021 , 12, 5528	17.4	1
11	The method to quantify cell elasticity based on the precise measurement of pressure inducing cell deformation in microfluidic channels. <i>MethodsX</i> , 2021 , 8, 101247	1.9	1
10	The method to dynamically screen and print single cells using microfluidics with pneumatic microvalves. <i>MethodsX</i> , 2021 , 8, 101190	1.9	1
9	MQuad enables clonal substructure discovery using single cell mitochondrial variants.. <i>Nature Communications</i> , 2022 , 13, 1205	17.4	1

8	Expression Clustering 2019 , 388-395		o
7	Modelling, inference and big data in biophysics. <i>Biophysical Reviews</i> , 2017 , 9, 297-298	3.7	o
6	A High-Throughput Genome-Integrated Assay Reveals Spatial Dependencies Governing Tcf7l2 Binding. <i>Cell Systems</i> , 2020 , 11, 315-327.e5	10.6	o
5	Announcing the call for the Special Issue on "The Australian Society for Biophysics (ASB) - 2021 Meeting". <i>Biophysical Reviews</i> , 2021 , 13, 1-2	3.7	o
4	Dynamic changes in antibiotic resistance genes and gut microbiota after <i>Helicobacter pylori</i> eradication therapies.. <i>Helicobacter</i> , 2021 , e12871	4.9	o
3	Machine learning-coupled combinatorial mutagenesis enables resource-efficient engineering of CRISPR-Cas9 genome editor activities.. <i>Nature Communications</i> , 2022 , 13, 2219	17.4	o
2	Decoding the complex genetic causes of heart diseases using systems biology. <i>Biophysical Reviews</i> , 2015 , 7, 141-159	3.7	
1	Congenital Heart Disease Gene: a Curated Database for Congenital Heart Disease Genes.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , 101161CIRCGEN121003539	5.2	