

Jean Y H Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4919374/publications.pdf>

Version: 2024-02-01

197
papers

29,048
citations

43973

48
h-index

5806

161
g-index

221
all docs

221
docs citations

221
times ranked

55136
citing authors

#	ARTICLE	IF	CITATIONS
1	Bioconductor: open software development for computational biology and bioinformatics. <i>Genome Biology</i> , 2004, 5, R80.	13.9	10,796
2	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
3	Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. <i>Nucleic Acids Research</i> , 2002, 30, 15e-15.	6.5	2,946
4	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	13.7	1,068
5	Genome-wide profiling identifies epithelial cell genes associated with asthma and with treatment response to corticosteroids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15858-15863.	3.3	743
6	Design issues for cDNA microarray experiments. <i>Nature Reviews Genetics</i> , 2002, 3, 579-588.	7.7	671
7	A Review of Ensemble Methods in Bioinformatics. <i>Current Bioinformatics</i> , 2010, 5, 296-308.	0.7	399
8	Dynamic Adipocyte Phosphoproteome Reveals that Akt Directly Regulates mTORC2. <i>Cell Metabolism</i> , 2013, 17, 1009-1020.	7.2	352
9	Statistical Issues in cDNA Microarray Data Analysis. , 2003, 224, 111-136.		344
10	Comparison of Methods for Image Analysis on cDNA Microarray Data. <i>Journal of Computational and Graphical Statistics</i> , 2002, 11, 108-136.	0.9	341
11	Circulating Cytokines Predict Immune-Related Toxicity in Melanoma Patients Receiving Anti-PD-1-Based Immunotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 1557-1563.	3.2	249
12	Dissecting asthma using focused transgenic modeling and functional genomics. <i>Journal of Allergy and Clinical Immunology</i> , 2005, 116, 305-311.	1.5	215
13	Gene Expression Profiling Reveals Renin mRNA Overexpression in Human Hypertensive Kidneys and a Role for MicroRNAs. <i>Hypertension</i> , 2011, 58, 1093-1098.	1.3	208
14	A Distinctive Alveolar Macrophage Activation State Induced by Cigarette Smoking. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2005, 172, 1383-1392.	2.5	194
15	Analysis of cDNA microarray images. <i>Briefings in Bioinformatics</i> , 2001, 2, 341-349.	3.2	177
16	Transcriptional downregulation of MHC class I and melanoma de-differentiation in resistance to PD-1 inhibition. <i>Nature Communications</i> , 2020, 11, 1897.	5.8	165
17	Gene Expression Profiling of the Human Maternal-Fetal Interface Reveals Dramatic Changes between Midgestation and Term. <i>Endocrinology</i> , 2007, 148, 1059-1079.	1.4	162
18	Ensemble deep learning in bioinformatics. <i>Nature Machine Intelligence</i> , 2020, 2, 500-508.	8.3	162

#	ARTICLE	IF	CITATIONS
19	BRAF Mutation, NRAS Mutation, and the Absence of an Immune-Related Expressed Gene Profile Predict Poor Outcome in Patients with Stage III Melanoma. <i>Journal of Investigative Dermatology</i> , 2013, 133, 509-517.	0.3	156
20	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9775-9784.	3.3	130
21	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10.	2.9	111
22	Impact of similarity metrics on single-cell RNA-seq data clustering. <i>Briefings in Bioinformatics</i> , 2019, 20, 2316-2326.	3.2	107
23	Disease-Specific Gene Expression Profiling in Multiple Models of Lung Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2008, 177, 376-387.	2.5	96
24	Comparison study of microarray meta-analysis methods. <i>BMC Bioinformatics</i> , 2010, 11, 408.	1.2	95
25	Phyllodes tumours of the breast: A clinicopathological analysis of 65 cases from a single institution. <i>Breast</i> , 2009, 18, 165-170.	0.9	92
26	PD-L1 Negative Status is Associated with Lower Mutation Burden, Differential Expression of Immune-Related Genes, and Worse Survival in Stage III Melanoma. <i>Clinical Cancer Research</i> , 2016, 22, 3915-3923.	3.2	91
27	Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. <i>ELife</i> , 2018, 7, .	2.8	91
28	Freshly isolated rat alveolar type I cells, type II cells, and cultured type II cells have distinct molecular phenotypes. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2005, 288, L179-L189.	1.3	89
29	c-Myc and Her2 cooperate to drive a stem-like phenotype with poor prognosis in breast cancer. <i>Oncogene</i> , 2014, 33, 3992-4002.	2.6	88
30	Identifying differentially expressed genes from microarray experiments via statistic synthesis. <i>Bioinformatics</i> , 2005, 21, 1084-1093.	1.8	86
31	Molecular Analysis of Gene Expression in the Developing Pontocerebellar Projection System. <i>Neuron</i> , 2002, 36, 417-434.	3.8	84
32	Targeting activating mutations of EZH2 leads to potent cell growth inhibition in human melanoma by derepression of tumor suppressor genes. <i>Oncotarget</i> , 2015, 6, 27023-27036.	0.8	83
33	Identification, Review, and Systematic Cross-Validation of microRNA Prognostic Signatures in Metastatic Melanoma. <i>Journal of Investigative Dermatology</i> , 2016, 136, 245-254.	0.3	82
34	Impaired Akt phosphorylation in insulin-resistant human muscle is accompanied by selective and heterogeneous downstream defects. <i>Diabetologia</i> , 2013, 56, 875-885.	2.9	81
35	scClassify: sample size estimation and multiscale classification of cells using single and multiple reference. <i>Molecular Systems Biology</i> , 2020, 16, e9389.	3.2	79
36	PD-L1 Expression and Immune Escape in Melanoma Resistance to MAPK Inhibitors. <i>Clinical Cancer Research</i> , 2017, 23, 6054-6061.	3.2	75

#	ARTICLE	IF	CITATIONS
37	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793.	5.8	75
38	Combining BET and HDAC inhibitors synergistically induces apoptosis of melanoma and suppresses AKT and YAP signaling. <i>Oncotarget</i> , 2015, 6, 21507-21521.	0.8	72
39	Single-cell RNA-Seq analysis reveals dynamic trajectories during mouse liver development. <i>BMC Genomics</i> , 2017, 18, 946.	1.2	70
40	scJoint integrates atlas-scale single-cell RNA-seq and ATAC-seq data with transfer learning. <i>Nature Biotechnology</i> , 2022, 40, 703-710.	9.4	70
41	Shark bites and public attitudes: Policy implications from the first before and after shark bite survey. <i>Marine Policy</i> , 2013, 38, 545-547.	1.5	68
42	Determination of prognosis in metastatic melanoma through integration of clinicopathologic, mutation, mRNA, microRNA, and protein information. <i>International Journal of Cancer</i> , 2015, 136, 863-874.	2.3	67
43	miR-10a is aberrantly overexpressed in Nucleophosmin1 mutated acute myeloid leukaemia and its suppression induces cell death. <i>Molecular Cancer</i> , 2012, 11, 8.	7.9	63
44	CiteFuse enables multi-modal analysis of CITE-seq data. <i>Bioinformatics</i> , 2020, 36, 4137-4143.	1.8	63
45	Genome-wide analysis of primary CD4+ and CD8+ T cell transcriptomes shows evidence for a network of enriched pathways associated with HIV disease. <i>Retrovirology</i> , 2011, 8, 18.	0.9	59
46	MicroRNA and mRNA expression profiling in metastatic melanoma reveal associations with BRAF mutation and patient prognosis. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 254-266.	1.5	59
47	Plasma levels of trimethylamine-N-oxide can be increased with "healthy" and "unhealthy" diets and do not correlate with the extent of atherosclerosis but with plaque instability. <i>Cardiovascular Research</i> , 2021, 117, 435-449.	1.8	58
48	Identification of microRNA-mRNA modules using microarray data. <i>BMC Genomics</i> , 2011, 12, 138.	1.2	57
49	Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K BRAF-Mutant Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 1272-1279.	3.2	57
50	Meta-Analysis of Genome-Wide Gene Expression Differences in Onset and Maintenance Phases of Genetic Hypertension. <i>Hypertension</i> , 2010, 56, 319-324.	1.3	56
51	Review and Cross-Validation of Gene Expression Signatures and Melanoma Prognosis. <i>Journal of Investigative Dermatology</i> , 2012, 132, 274-283.	0.3	52
52	Investigating higher-order interactions in single-cell data with scHOT. <i>Nature Methods</i> , 2020, 17, 799-806.	9.0	51
53	Utilizing state-of-the-art omics technology and bioinformatics to identify new biological mechanisms and biomarkers for coronary artery disease. <i>Microcirculation</i> , 2019, 26, e12488.	1.0	49
54	Benchmarking clustering algorithms on estimating the number of cell types from single-cell RNA-sequencing data. <i>Genome Biology</i> , 2022, 23, 49.	3.8	48

#	ARTICLE	IF	CITATIONS
55	Gene-gene interaction filtering with ensemble of filters. BMC Bioinformatics, 2011, 12, S10.	1.2	47
56	Fluid intake and all-cause mortality, cardiovascular mortality and kidney function: a population-based longitudinal cohort study. Nephrology Dialysis Transplantation, 2014, 29, 1377-1384.	0.4	47
57	Analysis of the prototypical Staphylococcus aureus multiresistance plasmid pSK1. Plasmid, 2010, 64, 135-142.	0.4	45
58	Analysis of gene expression in the developing mouse retina. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5491-5496.	3.3	44
59	Evaluating stably expressed genes in single cells. GigaScience, 2019, 8, .	3.3	44
60	PD-L1 expression in tonsillar cancer is associated with human papillomavirus positivity and improved survival: implications for anti-PD1 clinical trials. Oncotarget, 2016, 7, 77010-77020.	0.8	44
61	Expression profiling of cytogenetically normal acute myeloid leukemia identifies MicroRNAs that target genes involved in monocytic differentiation. American Journal of Hematology, 2011, 86, 2-11.	2.0	43
62	Significant association of PD-L1 expression with human papillomavirus positivity and its prognostic impact in oropharyngeal cancer. Oral Oncology, 2019, 92, 33-39.	0.8	43
63	A multi-array multi-SNP genotyping algorithm for Affymetrix SNP microarrays. Bioinformatics, 2007, 23, 1459-1467.	1.8	40
64	Reduced p16 and Increased Cyclin D1 and pRb Expression Are Correlated With Progression in Cutaneous Melanocytic Tumors. International Journal of Surgical Pathology, 2009, 17, 361-367.	0.4	40
65	Autoencoder-based cluster ensembles for single-cell RNA-seq data analysis. BMC Bioinformatics, 2019, 20, 660.	1.2	39
66	Core functional nodes and sex-specific pathways in human ischaemic and dilated cardiomyopathy. Nature Communications, 2020, 11, 2843.	5.8	39
67	Regularised shortest-path extraction. Pattern Recognition Letters, 1997, 18, 621-629.	2.6	37
68	Transcriptional profiles in CD8+ T cells from HIV+ progressors on HAART are characterized by coordinated up-regulation of oxidative phosphorylation enzymes and interferon responses. Virology, 2008, 380, 124-135.	1.1	37
69	Gene expression profiles of human inner cell mass cells and embryonic stem cells. Differentiation, 2009, 78, 18-23.	1.0	37
70	AdaSampling for Positive-Unlabeled and Label Noise Learning With Bioinformatics Applications. IEEE Transactions on Cybernetics, 2019, 49, 1932-1943.	6.2	37
71	Increased DNA microarray hybridization specificity using sscDNA targets. BMC Genomics, 2005, 6, 57.	1.2	36
72	The Yeast Homolog of Heme Oxygenase-1 Affords Cellular Antioxidant Protection via the Transcriptional Regulation of Known Antioxidant Genes. Journal of Biological Chemistry, 2011, 286, 2205-2214.	1.6	36

#	ARTICLE	IF	CITATIONS
73	Biobanking for discovery of novel cardiovascular biomarkers using imaging-quantified disease burden: protocol for the longitudinal, prospective, BioHEART-CT cohort study. <i>BMJ Open</i> , 2019, 9, e028649.	0.8	36
74	Positive-unlabeled ensemble learning for kinase substrate prediction from dynamic phosphoproteomics data. <i>Bioinformatics</i> , 2016, 32, 252-259.	1.8	34
75	Identification of microRNAs with regulatory potential using a matched microRNA-mRNA time-course data. <i>Nucleic Acids Research</i> , 2009, 37, e60-e60.	6.5	33
76	ZRANB2 localizes to supraspliceosomes and influences the alternative splicing of multiple genes in the transcriptome. <i>Molecular Biology Reports</i> , 2013, 40, 5381-5395.	1.0	33
77	Proteins from the Wnt pathway are involved in the pathogenesis and progression of mammary phyllodes tumours. <i>Journal of Clinical Pathology</i> , 2009, 62, 1016-1020.	1.0	32
78	Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004403.	1.5	32
79	Effect of chronic exercise in healthy young male adults: a metabolomic analysis. <i>Cardiovascular Research</i> , 2021, 117, 613-622.	1.8	32
80	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.	1.8	31
81	p16 and pRb immunohistochemical expression increases with increasing tumour grade in mammary phyllodes tumours. <i>Histopathology</i> , 2010, 56, 868-875.	1.6	30
82	Transcriptomic Analysis of the Highly Derived Radial Body Plan of a Sea Urchin. <i>Genome Biology and Evolution</i> , 2014, 6, 964-973.	1.1	29
83	Direction pathway analysis of large-scale proteomics data reveals novel features of the insulin action pathway. <i>Bioinformatics</i> , 2014, 30, 808-814.	1.8	29
84	scDC: single cell differential composition analysis. <i>BMC Bioinformatics</i> , 2019, 20, 721.	1.2	29
85	A benchmark study of simulation methods for single-cell RNA sequencing data. <i>Nature Communications</i> , 2021, 12, 6911.	5.8	29
86	Global identification of the genes and pathways differentially expressed in hypothalamus in early and established neurogenic hypertension. <i>Physiological Genomics</i> , 2011, 43, 766-771.	1.0	28
87	KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. <i>Proteomics</i> , 2016, 16, 1868-1871.	1.3	27
88	Differential gene expression by integrin beta 7+ and beta 7- memory T helper cells. <i>BMC Immunology</i> , 2004, 5, 13.	0.9	26
89	Spatial patterns of gene expression in the olfactory bulb. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12718-12723.	3.3	26
90	CD103+ tumor-resident CD8+ T cell numbers underlie improved patient survival in oropharyngeal squamous cell carcinoma. , 2020, 8, e000452.		26

#	ARTICLE	IF	CITATIONS
91	Systematic functional identification of cancer multi-drug resistance genes. <i>Genome Biology</i> , 2020, 21, 27.	3.8	26
92	Genes Influencing Circadian Differences in Blood Pressure in Hypertensive Mice. <i>PLoS ONE</i> , 2011, 6, e19203.	1.1	26
93	Combining serum microRNA and CA-125 as prognostic indicators of preoperative surgical outcome in women with high-grade serous ovarian cancer. <i>Gynecologic Oncology</i> , 2018, 148, 181-188.	0.6	25
94	Health-Related Quality of Life in People Across the Spectrum of CKD. <i>Kidney International Reports</i> , 2020, 5, 2264-2274.	0.4	25
95	Clonal evolution in liver cancer at single-cell and single-variant resolution. <i>Journal of Hematology and Oncology</i> , 2021, 14, 22.	6.9	25
96	Nodal and BMP expression during the transition to pentamery in the sea urchin <i>Heliocidaris erythrogramma</i> : insights into patterning the enigmatic echinoderm body plan. <i>BMC Developmental Biology</i> , 2017, 17, 4.	2.1	24
97	Downregulation of cAMP-dependent protein kinase inhibitor \hat{I}^3 is required for BMP-2-induced osteoblastic differentiation. <i>International Journal of Biochemistry and Cell Biology</i> , 2006, 38, 2064-2073.	1.2	23
98	Discriminating lymphomas and reactive lymphadenopathy in lymph node biopsies by gene expression profiling. <i>BMC Medical Genomics</i> , 2011, 4, 27.	0.7	23
99	Characterizing mutation-expression network relationships in multiple cancers. <i>Computational Biology and Chemistry</i> , 2016, 63, 73-82.	1.1	22
100	A hierarchical approach to removal of unwanted variation for large-scale metabolomics data. <i>Nature Communications</i> , 2021, 12, 4992.	5.8	22
101	Network-based biomarkers enhance classical approaches to prognostic gene expression signatures. <i>BMC Systems Biology</i> , 2014, 8, S5.	3.0	21
102	Integrated single cell data analysis reveals cell specific networks and novel coactivation markers. <i>BMC Systems Biology</i> , 2016, 10, 127.	3.0	21
103	PhosphOrtholog: a web-based tool for cross-species mapping of orthologous protein post-translational modifications. <i>BMC Genomics</i> , 2015, 16, 617.	1.2	20
104	Positive unlabeled learning via wrapper-based adaptive sampling. , 2017, , .		20
105	Tuning of delta-protocadherin adhesion through combinatorial diversity. <i>ELife</i> , 2018, 7, .	2.8	20
106	Hepatic metallothionein expression in chronic hepatitis C virus infection is IFNL3 genotype-dependent. <i>Genes and Immunity</i> , 2014, 15, 88-94.	2.2	19
107	Transcriptome-wide targets of alternative splicing by RBM4 and possible role in cancer. <i>Genomics</i> , 2016, 107, 138-144.	1.3	19
108	One-Time Fecal Immunochemical Screening for Advanced Colorectal Neoplasia in Patients with CKD (DETECT Study). <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 1061-1072.	3.0	19

#	ARTICLE	IF	CITATIONS
109	The impact of device-assisted therapies on the gut microbiome in Parkinson's disease. <i>Journal of Neurology</i> , 2022, 269, 780-795.	1.8	19
110	Analysis of a Splice Array Experiment Elucidates Roles of Chromatin Elongation Factor Spt4 in Splicing. <i>PLoS Computational Biology</i> , 2005, 1, e39.	1.5	18
111	A prediction model for viability at the end of the first trimester after a single early pregnancy evaluation. <i>Australian and New Zealand Journal of Obstetrics and Gynaecology</i> , 2013, 53, 51-57.	0.4	18
112	scReClassify: post hoc cell type classification of single-cell rRNA-seq data. <i>BMC Genomics</i> , 2019, 20, 913.	1.2	18
113	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. <i>Proteomics</i> , 2013, 13, 3393-3405.	1.3	17
114	ClassifyR: an R package for performance assessment of classification with applications to transcriptomics. <i>Bioinformatics</i> , 2015, 31, 1851-1853.	1.8	17
115	Improving X!Tandem on Peptide Identification from Mass Spectrometry by Self-Boosted Percolator. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1273-1280.	1.9	16
116	Protein signatures correspond to survival outcomes of AJCC stage III melanoma patients. <i>Pigment Cell and Melanoma Research</i> , 2014, 27, 1106-1116.	1.5	16
117	Differential distribution improves gene selection stability and has competitive classification performance for patient survival. <i>Nucleic Acids Research</i> , 2016, 44, e119-e119.	6.5	16
118	Metabolic Signatures in Coronary Artery Disease: Results from the BioHEART-CT Study. <i>Cells</i> , 2021, 10, 980.	1.8	16
119	Immunoglobulin E Sensitization to Mammalian Oligosaccharide Galactose-1,3 (α -Gal) Is Associated With Noncalcified Plaque, Obstructive Coronary Artery Disease, and ST-Segment Elevation Myocardial Infarction. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 352-361.	1.1	16
120	Uncovering cell identity through differential stability with Cepo. <i>Nature Computational Science</i> , 2021, 1, 784-790.	3.8	16
121	Hyperactivation of the Insulin Signaling Pathway Improves Intracellular Proteostasis by Coordinately Up-regulating the Proteostatic Machinery in Adipocytes. <i>Journal of Biological Chemistry</i> , 2016, 291, 25629-25640.	1.6	15
122	The Gut Microbiome in Parkinson's Disease: A Longitudinal Study of the Impacts on Disease Progression and the Use of Device-Assisted Therapies. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, .	1.7	15
123	Quantifying the effect of body mass index, age, and depression severity on 24-h activity patterns in persons with a lifetime history of affective disorders. <i>BMC Psychiatry</i> , 2016, 16, 317.	1.1	14
124	Analysis of the Whole-Exome Sequencing of Tumor and Circulating Tumor DNA in Metastatic Melanoma. <i>Cancers</i> , 2019, 11, 1905.	1.7	14
125	A dynamic wavelet-based algorithm for pre-processing tandem mass spectrometry data. <i>Bioinformatics</i> , 2010, 26, 2242-2249.	1.8	13
126	Differential Gene Expression Profiling after Conditional Müller-Cell Ablation in a Novel Transgenic Model. , 2013, 54, 2142.		13

#	ARTICLE	IF	CITATIONS
127	Disturbed protein-protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 708-722.	1.5	12
128	Mutational and transcriptomic landscapes of a rare human prostate basal cell carcinoma. <i>Prostate</i> , 2020, 80, 508-517.	1.2	12
129	Novel subdomains of the mouse olfactory bulb defined by molecular heterogeneity in the nascent external plexiform and glomerular layers. <i>BMC Developmental Biology</i> , 2007, 7, 48.	2.1	11
130	Cross-species gene expression analysis identifies a novel set of genes implicated in human insulin sensitivity. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15010.	1.4	11
131	Transcriptomic analysis of Nodal- and BMP-associated genes during juvenile development of the sea urchin <i>Heliocidaris erythrogramma</i> . <i>Marine Genomics</i> , 2015, 24, 41-45.	0.4	11
132	Transcriptomic analysis of sea star development through metamorphosis to the highly derived pentamerous body plan with a focus on neural transcription factors. <i>DNA Research</i> , 2020, 27, .	1.5	11
133	ISL1 Regulates Peroxisome Proliferator-Activated Receptor α Activation and Early Adipogenesis via Bone Morphogenetic Protein 4-Dependent and -Independent Mechanisms. <i>Molecular and Cellular Biology</i> , 2014, 34, 3607-3617.	1.1	10
134	Treatment usage patterns of oral appliances for obstructive sleep apnea over the first 60 days: a cluster analysis. <i>Journal of Clinical Sleep Medicine</i> , 2021, 17, 1785-1792.	1.4	10
135	A multi-step classifier addressing cohort heterogeneity improves performance of prognostic biomarkers in three cancer types. <i>Oncotarget</i> , 2017, 8, 2807-2815.	0.8	10
136	Nutritional Intake and Gut Microbiome Composition Predict Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, .	1.7	10
137	Prediction of alternatively skipped exons and splicing enhancers from exon junction arrays. <i>BMC Genomics</i> , 2008, 9, 551.	1.2	9
138	Two-Step Cross-Entropy Feature Selection for Microarrays' Power Through Complementarity. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 1148-1151.	1.9	9
139	OCAP: an open comprehensive analysis pipeline for iTRAQ. <i>Bioinformatics</i> , 2012, 28, 1404-1405.	1.8	9
140	VAN: an R package for identifying biologically perturbed networks via differential variability analysis. <i>BMC Research Notes</i> , 2013, 6, 430.	0.6	9
141	The transcriptional response to oxidative stress is part of, but not sufficient for, insulin resistance in adipocytes. <i>Scientific Reports</i> , 2018, 8, 1774.	1.6	9
142	scREMOTE: Using multimodal single cell data to predict regulatory gene relationships and to build a computational cell reprogramming model. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac023.	1.5	9
143	Genetic variation of macronutrient tolerance in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2022, 13, 1637.	5.8	9
144	Survival and Quality of Life Impact of a Risk-based Allocation Algorithm for Deceased Donor Kidney Transplantation. <i>Transplantation</i> , 2018, 102, 1530-1537.	0.5	8

#	ARTICLE	IF	CITATIONS
145	Factors Associated With Advanced Colorectal Neoplasia in Patients With CKD. American Journal of Kidney Diseases, 2022, 79, 549-560.	2.1	8
146	Gene expression allelic imbalance in ovine brown adipose tissue impacts energy homeostasis. PLoS ONE, 2017, 12, e0180378.	1.1	8
147	Detection and classification of peaks in 5' cap RNA sequencing data. BMC Genomics, 2013, 14, S9.	1.2	7
148	Analysis of Post-Liver Transplant Hepatitis C Virus Recurrence Using Serial Cluster of Differentiation Antibody Microarrays. Transplantation, 2015, 99, e120-e126.	0.5	7
149	DCARS: differential correlation across ranked samples. Bioinformatics, 2019, 35, 823-829.	1.8	7
150	Prediction modelingâ€™ part 2: using machine learning strategies to improve transplantation outcomes. Kidney International, 2021, 99, 817-823.	2.6	7
151	Construction of a Human Cell Landscape of COVID-19 Infection at Single-cell Level. , 2021, 12, 705.		7
152	Integrative Analysis of Prognostic Biomarkers for Acute Rejection in Kidney Transplant Recipients. Transplantation, 2021, 105, 1225-1237.	0.5	7
153	Asthma investigators begin to reap the fruits of genomics. Genome Biology, 2003, 4, 232.	13.9	6
154	Re-Fraction: A Machine Learning Approach for Deterministic Identification of Protein Homologues and Splice Variants in Large-scale MS-based Proteomics. Journal of Proteome Research, 2012, 11, 3035-3045.	1.8	6
155	Estimation of data-specific constitutive exons with RNA-Seq data. BMC Bioinformatics, 2013, 14, 31.	1.2	6
156	Challenges for Brain Data Analysis in VR Environments. , 2019, , .		6
157	Psychosocial stratification of antenatal indicators to guide population-based programs in perinatal depression. BMC Pregnancy and Childbirth, 2021, 21, 277.	0.9	6
158	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	2.6	6
159	Oral Squamous Cell Carcinoma in Young Patients Show Higher Rates of EGFR Amplification: Implications for Novel Personalized Therapy. Frontiers in Oncology, 2021, 11, 750852.	1.3	6
160	3D reconstruction of spatial expression. Nature Methods, 2022, 19, 526-527.	9.0	6
161	QCMAP: An Interactive Webâ€™Tool for Performance Diagnosis and Prediction of LCâ€™MS Systems. Proteomics, 2019, 19, 1900068.	1.3	5
162	Melanoma Explorer: a web application to allow easy reanalysis of publicly available and clinically annotated melanoma omics data sets. Melanoma Research, 2019, 29, 342-344.	0.6	5

#	ARTICLE	IF	CITATIONS
163	Quantitative Performance Evaluator for Proteomics (QPEP): Web-based Application for Reproducible Evaluation of Proteomics Preprocessing Methods. <i>Journal of Proteome Research</i> , 2017, 16, 2359-2369.	1.8	5
164	Measures of Association for Identifying MicroRNA-mRNA Pairs of Biological Interest. <i>PLoS ONE</i> , 2012, 7, e29612.	1.1	5
165	Inferring data-specific micro-RNA function through the joint ranking of micro-RNA and pathways from matched micro-RNA and gene expression data. <i>Bioinformatics</i> , 2015, 31, 2822-2828.	1.8	4
166	Taking Kidneys for Granted? Time to Reflect on the Choices We Make. <i>Transplantation</i> , 2017, 101, 2812-2813.	0.5	4
167	Metabolite signatures of heart failure, sleep apnoea, their interaction, and outcomes in the community. <i>ESC Heart Failure</i> , 2021, , .	1.4	4
168	Computational approaches for direct cell reprogramming: from the bulk omics era to the single cell era. <i>Briefings in Functional Genomics</i> , 2022, 21, 270-279.	1.3	4
169	78Gy with Fiducial Marker Image-Guided Radiotherapy in Prostate Cancer: Single Center Analysis of 301 Patients. <i>Asia-Pacific Journal of Clinical Oncology</i> , 2017, 13, e356-e363.	0.7	3
170	An Uncertainty Visual Analytics Framework for fMRI Functional Connectivity. <i>Neuroinformatics</i> , 2019, 17, 211-223.	1.5	3
171	Fast and approximate exhaustive variable selection for generalised linear models with APES. <i>Australian and New Zealand Journal of Statistics</i> , 2019, 61, 445-465.	0.4	3
172	Jurisdictional inequalities in deceased donor kidney allocation in Australia. <i>Kidney International</i> , 2021, 100, 49-54.	2.6	3
173	Association of Global Coagulation Profiles With Cardiovascular Risk Factors and Atherosclerosis: A Sex Disaggregated Analysis From the BioHEART-CT Study. <i>Journal of the American Heart Association</i> , 2021, 10, e020604.	1.6	3
174	treekoR: identifying cellular-to-phenotype associations by elucidating hierarchical relationships in high-dimensional cytometry data. <i>Genome Biology</i> , 2021, 22, 324.	3.8	3
175	Cross-Platform Omics Prediction procedure: a statistical machine learning framework for wider implementation of precision medicine. <i>Npj Digital Medicine</i> , 2022, 5, .	5.7	3
176	Stepwise Normalization of Two-Channel Spotted Microarrays. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2005, 4, Article4.	0.2	2
177	Microarrays-Planning Your Experiment. <i>Methods in Molecular Medicine</i> , 2008, , 71-85.	0.8	2
178	Improved moderation for gene-wise variance estimation in RNA-Seq via the exploitation of external information. <i>BMC Genomics</i> , 2013, 14, S9.	1.2	2
179	Authors' Reply. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2276-2277.	3.0	2
180	Diagonal Discriminant Analysis With Feature Selection for High-Dimensional Data. <i>Journal of Computational and Graphical Statistics</i> , 2020, 29, 114-127.	0.9	2

#	ARTICLE	IF	CITATIONS
181	LC-N2G: a local consistency approach for nutrigenomics data analysis. BMC Bioinformatics, 2020, 21, 530.	1.2	2
182	Transcriptomic analysis of Nodal and BMP- associated genes during development to the juvenile seastar in Parvulastra exigua (Asterinidae). Marine Genomics, 2021, 59, 100857.	0.4	2
183	Cross-Species PTM Mapping from Phosphoproteomic Data. Methods in Molecular Biology, 2017, 1558, 459-469.	0.4	2
184	SU-EJ-156: A Feasibility Study for Real-Time Tumor Tracking Using Positron Emission Tomography (PET). Medical Physics, 2011, 38, 3479-3479.	1.6	2
185	Distinct gene expression, mutational profile and clinical outcomes of V600E and V600K/R BRAF-mutant metastatic melanoma (MM).. Journal of Clinical Oncology, 2017, 35, 9541-9541.	0.8	2
186	Whole genome duplication in oral squamous cell carcinoma in patients younger than 50 years: implications for prognosis and adverse clinicopathological factors. Genes Chromosomes and Cancer, 2022, 61, 561-571.	1.5	2
187	bcGST an interactive bias-correction method to identify over-represented gene-sets in boutique arrays. Bioinformatics, 2019, 35, 1350-1357.	1.8	1
188	Modelling maternal and perinatal risk factors to predict poorly controlled childhood asthma. PLoS ONE, 2021, 16, e0252215.	1.1	1
189	OP06.05: Development of a new model to predict viability at the end of the 1 st trimester after a single visit to an early pregnancy unit-preliminary results. Ultrasound in Obstetrics and Gynecology, 2009, 34, 80-80.	0.9	0
190	Latin square dataset for evaluating the accuracy of mass spectrometry-based protein identification and quantification. , 2013, , .		0
191	A 14-Protein Signature for Rapid Identification of Poor Prognosis Stage III Metastatic Melanoma. Proteomics - Clinical Applications, 2018, 12, 1700094.	0.8	0
192	Metabolites downstream of predicted loss-of-function variants inform relationship to disease. Molecular Genetics and Metabolism, 2019, 128, 476-482.	0.5	0
193	O37...The gut microbiome in Parkinson's disease: longitudinal insights into disease progression and the use of device-assisted therapies. , 2021, , .		0
194	Trash or Treasure: Rescuing Discard Kidneys. Transplantation, 2021, 105, 1914-1915.	0.5	0
195	O91...The impact of device-assisted therapy initiation on the gut microbiome in Parkinson's disease. , 2021, , .		0
196	O15...Gut microbiota and nutritional profiles of Parkinson's disease patients. , 2021, , .		0
197	Microarrays-planning your experiment. Methods in Molecular Medicine, 2008, 141, 71-85.	0.8	0