

Jean Y H Yang

List of Publications by Year in descending order

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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 | 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 |
| 2 | Factors Associated With Advanced Colorectal Neoplasia in Patients With CKD. <i>American Journal of Kidney Diseases</i> , 2022, 79, 549-560. | 2.1 | 8 |
| 3 | 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 |
| 4 | Immunoglobulin E Sensitization to Mammalian Oligosaccharide Galactose-1,3 (α -Gal) Is Associated With Noncalcified Plaque, Obstructive Coronary Artery Disease, and ST-Segment-Elevated Myocardial Infarction. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022, 42, 352-361. | 1.1 | 16 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | Genetic variation of macronutrient tolerance in <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2022, 13, 1637. | 5.8 | 9 |
| 9 | Nutritional Intake and Gut Microbiome Composition Predict Parkinson's Disease. <i>Frontiers in Aging Neuroscience</i> , 2022, 14, . | 1.7 | 10 |
| 10 | 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 |
| 11 | 3D reconstruction of spatial expression. <i>Nature Methods</i> , 2022, 19, 526-527. | 9.0 | 6 |
| 12 | Whole genome duplication in oral squamous cell carcinoma in patients younger than 50 years: implications for prognosis and adverse clinicopathological factors. <i>Genes Chromosomes and Cancer</i> , 2022, 61, 561-571. | 1.5 | 2 |
| 13 | 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 |
| 14 | Effect of chronic exercise in healthy young male adults: a metabolomic analysis. <i>Cardiovascular Research</i> , 2021, 117, 613-622. | 1.8 | 32 |
| 15 | 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 |
| 16 | Prediction modeling" part 2: using machine learning strategies to improve transplantation outcomes. <i>Kidney International</i> , 2021, 99, 817-823. | 2.6 | 7 |
| 17 | Construction of a Human Cell Landscape of COVID-19 Infection at Single-cell Level. , 2021, 12, 705. | | 7 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | Psychosocial stratification of antenatal indicators to guide population-based programs in perinatal depression. <i>BMC Pregnancy and Childbirth</i> , 2021, 21, 277. | 0.9 | 6 |
| 20 | Metabolic Signatures in Coronary Artery Disease: Results from the BioHEART-CT Study. <i>Cells</i> , 2021, 10, 980. | 1.8 | 16 |
| 21 | Modelling maternal and perinatal risk factors to predict poorly controlled childhood asthma. <i>PLoS ONE</i> , 2021, 16, e0252215. | 1.1 | 1 |
| 22 | Jurisdictional inequalities in deceased donor kidney allocation in Australia. <i>Kidney International</i> , 2021, 100, 49-54. | 2.6 | 3 |
| 23 | 037â€¦The gut microbiome in Parkinsonâ€™s disease: longitudinal insights into disease progression and the use of device-assisted therapies. , 2021, , . | | 0 |
| 24 | Trash or Treasure: Rescuing Discard Kidneys. <i>Transplantation</i> , 2021, 105, 1914-1915. | 0.5 | 0 |
| 25 | A hierarchical approach to removal of unwanted variation for large-scale metabolomics data. <i>Nature Communications</i> , 2021, 12, 4992. | 5.8 | 22 |
| 26 | 091â€¦The impact of device-assisted therapy initiation on the gut microbiome in Parkinsonâ€™s disease. , 2021, , . | | 0 |
| 27 | 015â€¦Gut microbiota and nutritional profiles of Parkinsonâ€™s disease patients. , 2021, , . | | 0 |
| 28 | 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 |
| 29 | Transcriptomic analysis of Nodal â€œ and BMP- associated genes during development to the juvenile seastar in <i>Parvulastra exigua</i> (Asterinidae). <i>Marine Genomics</i> , 2021, 59, 100857. | 0.4 | 2 |
| 30 | Integrative Analysis of Prognostic Biomarkers for Acute Rejection in Kidney Transplant Recipients. <i>Transplantation</i> , 2021, 105, 1225-1237. | 0.5 | 7 |
| 31 | A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419. | 2.6 | 6 |
| 32 | Association of Global Coagulation Profiles With Cardiovascular Risk Factors and Atherosclerosis: A Sex Disaggregated Analysis From the BioHEARTâ€™CT Study. <i>Journal of the American Heart Association</i> , 2021, 10, e020604. | 1.6 | 3 |
| 33 | Metabolite signatures of heart failure, sleep apnoea, their interaction, and outcomes in the community. <i>ESC Heart Failure</i> , 2021, , . | 1.4 | 4 |
| 34 | A benchmark study of simulation methods for single-cell RNA sequencing data. <i>Nature Communications</i> , 2021, 12, 6911. | 5.8 | 29 |
| 35 | Oral Squamous Cell Carcinoma in Young Patients Show Higher Rates of EGFR Amplification: Implications for Novel Personalized Therapy. <i>Frontiers in Oncology</i> , 2021, 11, 750852. | 1.3 | 6 |
| 36 | treeoR: identifying cellular-to-phenotype associations by elucidating hierarchical relationships in high-dimensional cytometry data. <i>Genome Biology</i> , 2021, 22, 324. | 3.8 | 3 |

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|----|---|-----|-----------|
| 37 | Uncovering cell identity through differential stability with Cepo. Nature Computational Science, 2021, 1, 784-790. | 3.8 | 16 |
| 38 | Diagonal Discriminant Analysis With Feature Selection for High-Dimensional Data. Journal of Computational and Graphical Statistics, 2020, 29, 114-127. | 0.9 | 2 |
| 39 | Investigating higher-order interactions in single-cell data with scHOT. Nature Methods, 2020, 17, 799-806. | 9.0 | 51 |
| 40 | LC-N2G: a local consistency approach for nutrigenomics data analysis. BMC Bioinformatics, 2020, 21, 530. | 1.2 | 2 |
| 41 | Strategies to enable large-scale proteomics for reproducible research. Nature Communications, 2020, 11, 3793. | 5.8 | 75 |
| 42 | Ensemble deep learning in bioinformatics. Nature Machine Intelligence, 2020, 2, 500-508. | 8.3 | 162 |
| 43 | Health-Related Quality of Life in People Across the Spectrum of CKD. Kidney International Reports, 2020, 5, 2264-2274. | 0.4 | 25 |
| 44 | CiteFuse enables multi-modal analysis of CITE-seq data. Bioinformatics, 2020, 36, 4137-4143. | 1.8 | 63 |
| 45 | Transcriptomic analysis of sea star development through metamorphosis to the highly derived pentamer body plan with a focus on neural transcription factors. DNA Research, 2020, 27, . | 1.5 | 11 |
| 46 | CD103+ tumor-resident CD8+ T cell numbers underlie improved patient survival in oropharyngeal squamous cell carcinoma. , 2020, 8, e000452. | | 26 |
| 47 | Core functional nodes and sex-specific pathways in human ischaemic and dilated cardiomyopathy. Nature Communications, 2020, 11, 2843. | 5.8 | 39 |
| 48 | Systematic functional identification of cancer multi-drug resistance genes. Genome Biology, 2020, 21, 27. | 3.8 | 26 |
| 49 | Mutational and transcriptomic landscapes of a rare human prostate basal cell carcinoma. Prostate, 2020, 80, 508-517. | 1.2 | 12 |
| 50 | Transcriptional downregulation of MHC class I and melanoma de-differentiation in resistance to PD-1 inhibition. Nature Communications, 2020, 11, 1897. | 5.8 | 165 |
| 51 | scClassify: sample size estimation and multiscale classification of cells using single and multiple reference. Molecular Systems Biology, 2020, 16, e9389. | 3.2 | 79 |
| 52 | Utilizing <i>state-of-the-art</i> omics technology and bioinformatics to identify new biological mechanisms and biomarkers for coronary artery disease. Microcirculation, 2019, 26, e12488. | 1.0 | 49 |
| 53 | Impact of similarity metrics on single-cell RNA-seq data clustering. Briefings in Bioinformatics, 2019, 20, 2316-2326. | 3.2 | 107 |
| 54 | DCARS: differential correlation across ranked samples. Bioinformatics, 2019, 35, 823-829. | 1.8 | 7 |

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|----|--|-----|-----------|
| 55 | An Uncertainty Visual Analytics Framework for fMRI Functional Connectivity. <i>Neuroinformatics</i> , 2019, 17, 211-223. | 1.5 | 3 |
| 56 | AdaSampling for Positive-Unlabeled and Label Noise Learning With Bioinformatics Applications. <i>IEEE Transactions on Cybernetics</i> , 2019, 49, 1932-1943. | 6.2 | 37 |
| 57 | Challenges for Brain Data Analysis in VR Environments. , 2019, , . | | 6 |
| 58 | Metabolites downstream of predicted loss-of-function variants inform relationship to disease. <i>Molecular Genetics and Metabolism</i> , 2019, 128, 476-482. | 0.5 | 0 |
| 59 | Evaluating stably expressed genes in single cells. <i>GigaScience</i> , 2019, 8, . | 3.3 | 44 |
| 60 | 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 |
| 61 | 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 |
| 62 | Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10. | 2.9 | 111 |
| 63 | QCMAP: An Interactive Web Tool for Performance Diagnosis and Prediction of LC-MS Systems. <i>Proteomics</i> , 2019, 19, 1900068. | 1.3 | 5 |
| 64 | 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 |
| 65 | Significant association of PD-L1 expression with human papillomavirus positivity and its prognostic impact in oropharyngeal cancer. <i>Oral Oncology</i> , 2019, 92, 33-39. | 0.8 | 43 |
| 66 | Authors' Reply. <i>Journal of the American Society of Nephrology: JASN</i> , 2019, 30, 2276-2277. | 3.0 | 2 |
| 67 | Analysis of the Whole-Exome Sequencing of Tumor and Circulating Tumor DNA in Metastatic Melanoma. <i>Cancers</i> , 2019, 11, 1905. | 1.7 | 14 |
| 68 | Autoencoder-based cluster ensembles for single-cell RNA-seq data analysis. <i>BMC Bioinformatics</i> , 2019, 20, 660. | 1.2 | 39 |
| 69 | scDC: single cell differential composition analysis. <i>BMC Bioinformatics</i> , 2019, 20, 721. | 1.2 | 29 |
| 70 | scReClassify: post hoc cell type classification of single-cell rNA-seq data. <i>BMC Genomics</i> , 2019, 20, 913. | 1.2 | 18 |
| 71 | 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 |
| 72 | Melanoma Explorer: a web application to allow easy reanalysis of publicly available and clinically annotated melanoma omics data sets. <i>Melanoma Research</i> , 2019, 29, 342-344. | 0.6 | 5 |

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|----|--|------|-----------|
| 73 | bcGSTâ€”an interactive bias-correction method to identify over-represented gene-sets in boutique arrays. <i>Bioinformatics</i> , 2019, 35, 1350-1357. | 1.8 | 1 |
| 74 | Circulating Cytokines Predict Immune-Related Toxicity in Melanoma Patients Receiving Anti-PD-1â€”Based Immunotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 1557-1563. | 3.2 | 249 |
| 75 | Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K <i>BRAF</i> -Mutant Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 1272-1279. | 3.2 | 57 |
| 76 | 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 |
| 77 | 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 |
| 78 | A 14â€”Protein Signature for Rapid Identification of Poor Prognosis Stage III Metastatic Melanoma. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1700094. | 0.8 | 0 |
| 79 | 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 |
| 80 | Mitochondrial CoQ deficiency is a common driver of mitochondrial oxidants and insulin resistance. <i>ELife</i> , 2018, 7, . | 2.8 | 91 |
| 81 | Tuning of delta-protocadherin adhesion through combinatorial diversity. <i>ELife</i> , 2018, 7, . | 2.8 | 20 |
| 82 | 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 |
| 83 | Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180. | 13.7 | 1,068 |
| 84 | Taking Kidneys for Granted? Time to Reflect on the Choices We Make. <i>Transplantation</i> , 2017, 101, 2812-2813. | 0.5 | 4 |
| 85 | PD-L1 Expression and Immune Escape in Melanoma Resistance to MAPK Inhibitors. <i>Clinical Cancer Research</i> , 2017, 23, 6054-6061. | 3.2 | 75 |
| 86 | 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 |
| 87 | 78Gy with Fiducial Marker Imageâ€”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 |
| 88 | Single-cell RNA-Seq analysis reveals dynamic trajectories during mouse liver development. <i>BMC Genomics</i> , 2017, 18, 946. | 1.2 | 70 |
| 89 | Cross-Species PTM Mapping from Phosphoproteomic Data. <i>Methods in Molecular Biology</i> , 2017, 1558, 459-469. | 0.4 | 2 |
| 90 | 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 |

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| 91 | 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 |
| 92 | Gene expression allelic imbalance in ovine brown adipose tissue impacts energy homeostasis. PLoS ONE, 2017, 12, e0180378. | 1.1 | 8 |
| 93 | A multi-step classifier addressing cohort heterogeneity improves performance of prognostic biomarkers in three cancer types. Oncotarget, 2017, 8, 2807-2815. | 0.8 | 10 |
| 94 | Positive unlabeled learning via wrapper-based adaptive sampling., 2017, , . | | 20 |
| 95 | Positive-unlabeled ensemble learning for kinase substrate prediction from dynamic phosphoproteomics data. Bioinformatics, 2016, 32, 252-259. | 1.8 | 34 |
| 96 | 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. BMC Psychiatry, 2016, 16, 317. | 1.1 | 14 |
| 97 | KinasePA: Phosphoproteomics data annotation using hypothesis driven kinase perturbation analysis. Proteomics, 2016, 16, 1868-1871. | 1.3 | 27 |
| 98 | Characterizing mutationâ€“expression network relationships in multiple cancers. Computational Biology and Chemistry, 2016, 63, 73-82. | 1.1 | 22 |
| 99 | Hyperactivation of the Insulin Signaling Pathway Improves Intracellular Proteostasis by Coordinately Up-regulating the Proteostatic Machinery in Adipocytes. Journal of Biological Chemistry, 2016, 291, 25629-25640. | 1.6 | 15 |
| 100 | Integrated single cell data analysis reveals cell specific networks and novel coactivation markers. BMC Systems Biology, 2016, 10, 127. | 3.0 | 21 |
| 101 | Differential distribution improves gene selection stability and has competitive classification performance for patient survival. Nucleic Acids Research, 2016, 44, e119-e119. | 6.5 | 16 |
| 102 | PD-L1 Negative Status is Associated with Lower Mutation Burden, Differential Expression of Immune-Related Genes, and Worse Survival in Stage III Melanoma. Clinical Cancer Research, 2016, 22, 3915-3923. | 3.2 | 91 |
| 103 | Transcriptome-wide targets of alternative splicing by RBM4 and possible role in cancer. Genomics, 2016, 107, 138-144. | 1.3 | 19 |
| 104 | Identification, Review, and Systematic Cross-Validation of microRNA Prognostic Signatures in Metastatic Melanoma. Journal of Investigative Dermatology, 2016, 136, 245-254. | 0.3 | 82 |
| 105 | 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 |
| 106 | Cross-species gene expression analysis identifies a novel set of genes implicated in human insulin sensitivity. Npj Systems Biology and Applications, 2015, 1, 15010. | 1.4 | 11 |
| 107 | Analysis of Post-Liver Transplant Hepatitis C Virus Recurrence Using Serial Cluster of Differentiation Antibody Microarrays. Transplantation, 2015, 99, e120-e126. | 0.5 | 7 |
| 108 | Targeting activating mutations of EZH2 leads to potent cell growth inhibition in human melanoma by derepression of tumor suppressor genes. Oncotarget, 2015, 6, 27023-27036. | 0.8 | 83 |

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|-----|---|-----|-----------|
| 109 | Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004403. | 1.5 | 32 |
| 110 | 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 |
| 111 | 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 |
| 112 | Determination of prognosis in metastatic melanoma through integration of clinico-pathologic, mutation, mRNA, microRNA, and protein information. <i>International Journal of Cancer</i> , 2015, 136, 863-874. | 2.3 | 67 |
| 113 | ClassifyR: an R package for performance assessment of classification with applications to transcriptomics. <i>Bioinformatics</i> , 2015, 31, 1851-1853. | 1.8 | 17 |
| 114 | The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660. | 6.0 | 4,659 |
| 115 | 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 |
| 116 | MicroRNA and mRNA expression profiling in metastatic melanoma reveal associations with <i>BRAF</i> mutation and patient prognosis. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 254-266. | 1.5 | 59 |
| 117 | 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 |
| 118 | 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 |
| 119 | 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 |
| 120 | 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 |
| 121 | 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 |
| 122 | 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 |
| 123 | Fluid intake and all-cause mortality, cardiovascular mortality and kidney function: a population-based longitudinal cohort study. <i>Nephrology Dialysis Transplantation</i> , 2014, 29, 1377-1384. | 0.4 | 47 |
| 124 | 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 |
| 125 | Network-based biomarkers enhance classical approaches to prognostic gene expression signatures. <i>BMC Systems Biology</i> , 2014, 8, S5. | 3.0 | 21 |
| 126 | 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 |

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|-----|---|-----|-----------|
| 127 | Estimation of data-specific constitutive exons with RNA-Seq data. BMC Bioinformatics, 2013, 14, 31. | 1.2 | 6 |
| 128 | Improved moderation for gene-wise variance estimation in RNA-Seq via the exploitation of external information. BMC Genomics, 2013, 14, S9. | 1.2 | 2 |
| 129 | Impaired Akt phosphorylation in insulin-resistant human muscle is accompanied by selective and heterogeneous downstream defects. Diabetologia, 2013, 56, 875-885. | 2.9 | 81 |
| 130 | Detection and classification of peaks in 5' cap RNA sequencing data. BMC Genomics, 2013, 14, S9. | 1.2 | 7 |
| 131 | Latin square dataset for evaluating the accuracy of mass spectrometry-based protein identification and quantification. , 2013, , . | | 0 |
| 132 | Dynamic Adipocyte Phosphoproteome Reveals that Akt Directly Regulates mTORC2. Cell Metabolism, 2013, 17, 1009-1020. | 7.2 | 352 |
| 133 | Shark bites and public attitudes: Policy implications from the first before and after shark bite survey. Marine Policy, 2013, 38, 545-547. | 1.5 | 68 |
| 134 | VAN: an R package for identifying biologically perturbed networks via differential variability analysis. BMC Research Notes, 2013, 6, 430. | 0.6 | 9 |
| 135 | Differential Gene Expression Profiling after Conditional MÃ¼ller-Cell Ablation in a Novel Transgenic Model. , 2013, 54, 2142. | | 13 |
| 136 | Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. Proteomics, 2013, 13, 3393-3405. | 1.3 | 17 |
| 137 | A prediction model for viability at the end of the first trimester after a single early pregnancy evaluation. Australian and New Zealand Journal of Obstetrics and Gynaecology, 2013, 53, 51-57. | 0.4 | 18 |
| 138 | Disturbed proteinâ€“protein interaction networks in metastatic melanoma are associated with worse prognosis and increased functional mutation burden. Pigment Cell and Melanoma Research, 2013, 26, 708-722. | 1.5 | 12 |
| 139 | BRAF Mutation, NRAS Mutation, and the Absence of an Immune-Related Expressed Gene Profile Predict Poor Outcome in Patients with Stage III Melanoma. Journal of Investigative Dermatology, 2013, 133, 509-517. | 0.3 | 156 |
| 140 | Review and Cross-Validation of Gene Expression Signatures and Melanoma Prognosis. Journal of Investigative Dermatology, 2012, 132, 274-283. | 0.3 | 52 |
| 141 | Improving X!Tandem on Peptide Identification from Mass Spectrometry by Self-Boosted Percolator. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1273-1280. | 1.9 | 16 |
| 142 | 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 |
| 143 | OCAP: an open comprehensive analysis pipeline for iTRAQ. Bioinformatics, 2012, 28, 1404-1405. | 1.8 | 9 |
| 144 | miR-10a is aberrantly overexpressed in Nucleophosmin1 mutated acute myeloid leukaemia and its suppression induces cell death. Molecular Cancer, 2012, 11, 8. | 7.9 | 63 |

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|-----|---|-----|-----------|
| 145 | Measures of Association for Identifying MicroRNA-mRNA Pairs of Biological Interest. PLoS ONE, 2012, 7, e29612. | 1.1 | 5 |
| 146 | Two-Step Cross-Entropy Feature Selection for Microarraysâ€™Power Through Complementarity. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1148-1151. | 1.9 | 9 |
| 147 | Discriminating lymphomas and reactive lymphadenopathy in lymph node biopsies by gene expression profiling. BMC Medical Genomics, 2011, 4, 27. | 0.7 | 23 |
| 148 | Genome-wide analysis of primary CD4+ and CD8+ T cell transcriptomes shows evidence for a network of enriched pathways associated with HIV disease. Retrovirology, 2011, 8, 18. | 0.9 | 59 |
| 149 | Gene-gene interaction filtering with ensemble of filters. BMC Bioinformatics, 2011, 12, S10. | 1.2 | 47 |
| 150 | Identification of microRNA-mRNA modules using microarray data. BMC Genomics, 2011, 12, 138. | 1.2 | 57 |
| 151 | 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 |
| 152 | Gene Expression Profiling Reveals Renin mRNA Overexpression in Human Hypertensive Kidneys and a Role for MicroRNAs. Hypertension, 2011, 58, 1093-1098. | 1.3 | 208 |
| 153 | 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 |
| 154 | Global identification of the genes and pathways differentially expressed in hypothalamus in early and established neurogenic hypertension. Physiological Genomics, 2011, 43, 766-771. | 1.0 | 28 |
| 155 | SU-E-J-156: A Feasibility Study for Real-Time Tumor Tracking Using Positron Emission Tomography (PET). Medical Physics, 2011, 38, 3479-3479. | 1.6 | 2 |
| 156 | Genes Influencing Circadian Differences in Blood Pressure in Hypertensive Mice. PLoS ONE, 2011, 6, e19203. | 1.1 | 26 |
| 157 | Analysis of the prototypical Staphylococcus aureus multiresistance plasmid pSK1. Plasmid, 2010, 64, 135-142. | 0.4 | 45 |
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