

Tianwei Yu

List of Publications by Year in descending order

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Version: 2024-02-01

109
papers

5,235
citations

109321

35
h-index

95266

68
g-index

110
all docs

110
docs citations

110
times ranked

8452
citing authors

#	ARTICLE	IF	CITATIONS
1	Salivary proteomic and genomic biomarkers for primary Sjögren's syndrome. <i>Arthritis and Rheumatism</i> , 2007, 56, 3588-3600.	6.7	333
2	The safety, immunogenicity, and acceptability of inactivated influenza vaccine delivered by microneedle patch (TIV-MNP 2015): a randomised, partly blinded, placebo-controlled, phase 1 trial. <i>Lancet, The</i> , 2017, 390, 649-658.	13.7	309
3	apLCMS-adaptive processing of high-resolution LC/MS data. <i>Bioinformatics</i> , 2009, 25, 1930-1936.	4.1	303
4	xMSanalyzer: automated pipeline for improved feature detection and downstream analysis of large-scale, non-targeted metabolomics data. <i>BMC Bioinformatics</i> , 2013, 14, 15.	2.6	301
5	Transcriptomic dissection of tongue squamous cell carcinoma. <i>BMC Genomics</i> , 2008, 9, 69.	2.8	276
6	Metabolic Phenotypes of Response to Vaccination in Humans. <i>Cell</i> , 2017, 169, 862-877.e17.	28.9	234
7	Characterization of RNA in Saliva. <i>Clinical Chemistry</i> , 2006, 52, 988-994.	3.2	182
8	Longitudinal Analysis of the Human B Cell Response to Ebola Virus Infection. <i>Cell</i> , 2019, 177, 1566-1582.e17.	28.9	153
9	An expectation-maximization algorithm for probabilistic reconstructions of full-length isoforms from splice graphs. <i>Nucleic Acids Research</i> , 2006, 34, 3150-3160.	14.5	136
10	Use of high-resolution metabolomics for the identification of metabolic signals associated with traffic-related air pollution. <i>Environment International</i> , 2018, 120, 145-154.	10.0	113
11	A graph-embedded deep feedforward network for disease outcome classification and feature selection using gene expression data. <i>Bioinformatics</i> , 2018, 34, 3727-3737.	4.1	105
12	A Deep Neural Network Model using Random Forest to Extract Feature Representation for Gene Expression Data Classification. <i>Scientific Reports</i> , 2018, 8, 16477.	3.3	102
13	Integrated study of copy number states and genotype calls using high-density SNP arrays. <i>Nucleic Acids Research</i> , 2009, 37, 5365-5377.	14.5	99
14	A practical approach to detect unique metabolic patterns for personalized medicine. <i>Analyst, The</i> , 2010, 135, 2864.	3.5	90
15	Replicative fitness of transmitted HIV-1 drives acute immune activation, proviral load in memory CD4 ⁺ T cells, and disease progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1480-9.	7.1	87
16	Role of Transmitted Gag CTL Polymorphisms in Defining Replicative Capacity and Early HIV-1 Pathogenesis. <i>PLoS Pathogens</i> , 2012, 8, e1003041.	4.7	86
17	Optical protein sensor for detecting cancer markers in saliva. <i>Biosensors and Bioelectronics</i> , 2008, 24, 266-271.	10.1	83
18	Hybrid Feature Detection and Information Accumulation Using High-Resolution LC-MS Metabolomics Data. <i>Journal of Proteome Research</i> , 2013, 12, 1419-1427.	3.7	81

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19	Perturbations of the arginine metabolome following exposures to traffic-related air pollution in a panel of commuters with and without asthma. <i>Environment International</i> , 2019, 127, 503-513.	10.0	78
20	Characterization of salivary RNA by cDNA library analysis. <i>Archives of Oral Biology</i> , 2007, 52, 30-35.	1.8	75
21	GM-CSF DNA: An adjuvant for higher avidity IgG, rectal IgA, and increased protection against the acute phase of a SHIV-89.6P challenge by a DNA/MVA immunodeficiency virus vaccine. <i>Virology</i> , 2007, 369, 153-167.	2.4	75
22	Distinct Effector Memory CD4+ T Cell Signatures in Latent Mycobacterium tuberculosis Infection, BCG Vaccination and Clinically Resolved Tuberculosis. <i>PLoS ONE</i> , 2012, 7, e36046.	2.5	75
23	Dietary sulfur amino acid effects on fasting plasma cysteine/cystine redox potential in humans. <i>Nutrition</i> , 2011, 27, 199-205.	2.4	65
24	A system for enhancing genome-wide coexpression dynamics study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 15561-15566.	7.1	64
25	Inference of transcriptional regulatory network by two-stage constrained space factor analysis. <i>Bioinformatics</i> , 2005, 21, 4033-4038.	4.1	62
26	Novel Metabolic Markers for the Risk of Diabetes Development in American Indians. <i>Diabetes Care</i> , 2015, 38, 220-227.	8.6	62
27	Deregulation of Snai2 is associated with metastasis and poor prognosis in tongue squamous cell carcinoma. <i>International Journal of Cancer</i> , 2012, 130, 2249-2258.	5.1	57
28	Location analysis for the estrogen receptor- β reveals binding to diverse ERE sequences and widespread binding within repetitive DNA elements. <i>Nucleic Acids Research</i> , 2010, 38, 2355-2368.	14.5	54
29	CD40L-Adjuvanted DNA/Modified Vaccinia Virus Ankara Simian Immunodeficiency Virus SIV239 Vaccine Enhances SIV-Specific Humoral and Cellular Immunity and Improves Protection against a Heterologous SIVE660 Mucosal Challenge. <i>Journal of Virology</i> , 2014, 88, 9579-9589.	3.4	53
30	Downregulation of tumor suppressor MTUS1/ATIP is associated with enhanced proliferation, poor differentiation and poor prognosis in oral tongue squamous cell carcinoma. <i>Molecular Oncology</i> , 2012, 6, 73-80.	4.6	50
31	RNAprotect Saliva: An Optimal Room- Temperature Stabilization Reagent for the Salivary Transcriptome. <i>Clinical Chemistry</i> , 2006, 52, 2303-2304.	3.2	49
32	Metabolomics profile comparisons of irradiated and nonirradiated stored donor red blood cells. <i>Transfusion</i> , 2015, 55, 544-552.	1.6	49
33	microRNA-21 and microRNA-375 from oral cytology as biomarkers for oral tongue cancer detection. <i>Oral Oncology</i> , 2016, 57, 15-20.	1.5	48
34	Improving peak detection in high-resolution LC/MS metabolomics data using preexisting knowledge and machine learning approach. <i>Bioinformatics</i> , 2014, 30, 2941-2948.	4.1	47
35	miR-486-3p, miR-139-5p, and miR-21 as Biomarkers for the Detection of Oral Tongue Squamous Cell Carcinoma. <i>Biomarkers in Cancer</i> , 2017, 9, 1-8.	3.6	38
36	Particulate metal exposures induce plasma metabolome changes in a commuter panel study. <i>PLoS ONE</i> , 2018, 13, e0203468.	2.5	37

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37	Metabolomic profiles of plasma, exhaled breath condensate, and saliva are correlated with potential for air toxics detection. <i>Journal of Breath Research</i> , 2018, 12, 016008.	3.0	36
38	Detection of eQTL modules mediated by activity levels of transcription factors. <i>Bioinformatics</i> , 2007, 23, 2290-2297.	4.1	35
39	Quantification and deconvolution of asymmetric LC-MS peaks using the bi-Gaussian mixture model and statistical model selection. <i>BMC Bioinformatics</i> , 2010, 11, 559.	2.6	34
40	Deletion of Specific Immune-Modulatory Genes from Modified Vaccinia Virus Ankara-Based HIV Vaccines Engenders Improved Immunogenicity in Rhesus Macaques. <i>Journal of Virology</i> , 2012, 86, 12605-12615.	3.4	34
41	miR-486-3p, miR-139-5p, and miR-21 as Biomarkers for the Detection of Oral Tongue Squamous Cell Carcinoma. <i>Biomarkers in Cancer</i> , 2017, 9, 1179299X1700900.	3.6	33
42	Plasma High-Resolution Metabolomics Differentiates Adults with Normal Weight Obesity from Lean Individuals. <i>Obesity</i> , 2019, 27, 1729-1737.	3.0	32
43	Deregulation of manganese superoxide dismutase (SOD2) expression and lymph node metastasis in tongue squamous cell carcinoma. <i>BMC Cancer</i> , 2010, 10, 365.	2.6	31
44	HIV-1 subtype C superinfected individuals mount low autologous neutralizing antibody responses prior to intrasubtype superinfection. <i>Retrovirology</i> , 2012, 9, 76.	2.0	31
45	Accurate feature selection improves single-cell RNA-seq cell clustering. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	31
46	Identification and Classification of Acute Cardiac Rejection by Intragraft Transcriptional Profiling. <i>Circulation</i> , 2011, 123, 2236-2243.	1.6	30
47	Balance between transmitted HLA preadapted and nonassociated polymorphisms is a major determinant of HIV-1 disease progression. <i>Journal of Experimental Medicine</i> , 2016, 213, 2049-2063.	8.5	30
48	Decreased humoral immunity to mumps in young adults immunized with MMR vaccine in childhood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19071-19076.	7.1	30
49	Immunogenicity in Macaques of the Clinical Product for a Clade B DNA/MVA HIV Vaccine: Elicitation of IFN- γ , IL-2, and TNF- α Coproducing CD4 and CD8 T Cells. <i>AIDS Research and Human Retroviruses</i> , 2007, 23, 1555-1562.	1.1	29
50	A new dynamic correlation algorithm reveals novel functional aspects in single cell and bulk RNA-seq data. <i>PLoS Computational Biology</i> , 2018, 14, e1006391.	3.2	29
51	Postprandial Cysteine/Cystine Redox Potential in Human Plasma Varies with Meal Content of Sulfur Amino Acids. <i>Journal of Nutrition</i> , 2010, 140, 760-765.	2.9	28
52	Addressing the batch effect issue for LC/MS metabolomics data in data preprocessing. <i>Scientific Reports</i> , 2020, 10, 13856.	3.3	28
53	Mitigating the adverse impact of batch effects in sample pattern detection. <i>Bioinformatics</i> , 2018, 34, 2634-2641.	4.1	25
54	A forward-backward fragment assembling algorithm for the identification of genomic amplification and deletion breakpoints using high-density single nucleotide polymorphism (SNP) array. <i>BMC Bioinformatics</i> , 2007, 8, 145.	2.6	24

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55	Incorporating Nonlinear Relationships in Microarray Missing Value Imputation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 723-731.	3.0	24
56	Global Gene Expression Profiling of Endothelium Exposed to Heme Reveals an Organ-Specific Induction of Cytoprotective Enzymes in Sickle Cell Disease. <i>PLoS ONE</i> , 2011, 6, e18399.	2.5	24
57	Metabolic effects of albumin therapy in acute lung injury measured by proton nuclear magnetic resonance spectroscopy of plasma: A pilot study*. <i>Critical Care Medicine</i> , 2011, 39, 2308-2313.	0.9	24
58	EgoNet: identification of human disease ego-network modules. <i>BMC Genomics</i> , 2014, 15, 314.	2.8	24
59	Local false discovery rate estimation using feature reliability in LC/MS metabolomics data. <i>Scientific Reports</i> , 2015, 5, 17221.	3.3	24
60	Comparative studies on in vitro expression and in vivo immunogenicity of supercoiled and open circular forms of plasmid DNA vaccines. <i>Vaccine</i> , 2008, 26, 1136-1141.	3.8	23
61	Metabolic profiles of biological aging in American Indians: The strong heart family study. <i>Aging</i> , 2014, 6, 176-186.	3.1	22
62	forgeNet: a graph deep neural network model using tree-based ensemble classifiers for feature graph construction. <i>Bioinformatics</i> , 2020, 36, 3507-3515.	4.1	22
63	scBatch: batch-effect correction of RNA-seq data through sample distance matrix adjustment. <i>Bioinformatics</i> , 2020, 36, 3115-3123.	4.1	22
64	ROCS: Receiver Operating Characteristic Surface for Class-Skewed High-Throughput Data. <i>PLoS ONE</i> , 2012, 7, e40598.	2.5	21
65	The exposome in practice: an exploratory panel study of biomarkers of air pollutant exposure in Chinese people aged 60–69 years (China BAPE Study). <i>Environment International</i> , 2021, 157, 106866.	10.0	21
66	A single-cell analysis of the molecular lineage of chordate embryogenesis. <i>Science Advances</i> , 2020, 6, .	10.3	18
67	Missing value imputation for LC-MS metabolomics data by incorporating metabolic network and adduct ion relations. <i>Bioinformatics</i> , 2018, 34, 1555-1561.	4.1	17
68	Hepatic fat is a stronger correlate of key clinical and molecular abnormalities than visceral and abdominal subcutaneous fat in youth. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001126.	2.8	15
69	Immunologic mechanisms of seasonal influenza vaccination administered by microneedle patch from a randomized phase I trial. <i>Npj Vaccines</i> , 2021, 6, 89.	6.0	15
70	Hierarchical Clustering of High- Throughput Expression Data Based on General Dependences. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1080-1085.	3.0	14
71	Elevation of Alanine Aminotransferase Activity Occurs after Activation of the Cell-Death Signaling Initiated by Pattern-Recognition Receptors –but before Activation of Cytolytic Effectors in NK or CD8+ T Cells in the Liver During Acute HCV Infection. <i>PLoS ONE</i> , 2016, 11, e0165533.	2.5	14
72	Strong T _H 1-biased CD4 T cell responses are associated with diminished SIV vaccine efficacy. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	14

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73	The Oxidative Potential of Fine Particulate Matter and Biological Perturbations in Human Plasma and Saliva Metabolome. <i>Environmental Science & Technology</i> , 2022, 56, 7350-7361.	10.0	14
74	ROC Curve Analysis in the Presence of Imperfect Reference Standards. <i>Statistics in Biosciences</i> , 2017, 9, 91-104.	1.2	13
75	Study of coordinative gene expression at the biological process level. <i>Bioinformatics</i> , 2005, 21, 3651-3657.	4.1	11
76	Capturing changes in gene expression dynamics by gene set differential coordination analysis. <i>Genomics</i> , 2011, 98, 469-477.	2.9	11
77	Nonlinear Network Reconstruction from Gene Expression Data Using Marginal Dependencies Measured by DCOL. <i>PLoS ONE</i> , 2016, 11, e0158247.	2.5	11
78	Bayesian network feature finder (BANFF): an R package for gene network feature selection. <i>Bioinformatics</i> , 2016, 32, 3685-3687.	4.1	11
79	Network Marker Selection for Untargeted LC-MS Metabolomics Data. <i>Journal of Proteome Research</i> , 2017, 16, 1261-1269.	3.7	11
80	AIME: Autoencoder-based integrative multi-omics data embedding that allows for confounder adjustments. <i>PLoS Computational Biology</i> , 2022, 18, e1009826.	3.2	11
81	An exploratory data analysis method to reveal modular latent structures in high-throughput data. <i>BMC Bioinformatics</i> , 2010, 11, 440.	2.6	10
82	A Sulfur Amino Acid-Free Meal Increases Plasma Lipids in Humans. <i>Journal of Nutrition</i> , 2011, 141, 1424-1431.	2.9	10
83	A Bayesian nonparametric mixture model for selecting genes and gene subnetworks. <i>Annals of Applied Statistics</i> , 2014, 8, 999-1021.	1.1	10
84	$\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" id="M1"} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mi} \rangle K \langle \text{mml:mi} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:math} \rangle$ -Profiles: A Nonlinear Clustering Method for Pattern Detection in High Dimensional Data. <i>BioMed Research International</i> , 2015, 2015, 1-10.	1.9	10
85	Dimension reduction and mixed-effects model for microarray meta-analysis of cancer. <i>Frontiers in Bioscience - Landmark</i> , 2008, 13, 2714.	3.0	10
86	Analyzing LC/MS Metabolic Profiling Data in the Context of Existing Metabolic Networks. <i>Current Metabolomics</i> , 2012, 1, 84-91.	0.5	7
87	Differential gene network analysis from single cell RNA-seq. <i>Journal of Genetics and Genomics</i> , 2017, 44, 331-334.	3.9	7
88	Detecting subnetwork-level dynamic correlations. <i>Bioinformatics</i> , 2017, 33, 256-265.	4.1	7
89	Bayesian Network Marker Selection via the Thresholded Graph Laplacian Gaussian Prior. <i>Bayesian Analysis</i> , 2020, 15, 79-102.	3.0	7
90	Advancement in characterization of genomic alterations for improved diagnosis, treatment and prognostics in cancer. <i>Expert Review of Molecular Diagnostics</i> , 2006, 6, 39-50.	3.1	6

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91	A hypergraph-based method for large-scale dynamic correlation study at the transcriptomic scale. BMC Genomics, 2019, 20, 397.	2.8	6
92	The Regulation of Subtilisin-cleaved Actin by Tropomyosin/Troponin. Journal of Biological Chemistry, 2003, 278, 5517-5522.	3.4	5
93	Metabolomic Profiling After a Meal Shows Greater Changes and Lower Metabolic Flexibility in Cardiometabolic Diseases. Journal of the Endocrine Society, 2020, 4, bvaa127.	0.2	5
94	Improving gene expression data interpretation by finding latent factors that co-regulate gene modules with clinical factors. BMC Genomics, 2011, 12, 563.	2.8	3
95	Fc-gamma receptor IIA and IIIA variants in two African cohorts: Lack of consistent impact on heterosexual HIV acquisition, viral control, and disease progression. Virology, 2018, 525, 132-142.	2.4	3
96	Macronutrient, Energy, and Bile Acid Metabolism Pathways Altered Following a Physiological Meal Challenge, Relative to Fasting, among Guatemalan Adults. Journal of Nutrition, 2020, 150, 2031-2040.	2.9	3
97	Elevated levels of inflammatory plasma biomarkers are associated with risk of HIV infection. Retrovirology, 2021, 18, 8.	2.0	3
98	Comparative plasma high-resolution metabolomic profiling in patients with drug-susceptible and multi-drug resistant pulmonary tuberculosis. FASEB Journal, 2015, 29, .	0.5	3
99	Network-based modular latent structure analysis. BMC Bioinformatics, 2014, 15, S6.	2.6	2
100	Clustering based on periodicity in high-throughput time course data. Statistical Analysis and Data Mining, 2011, 4, 579-589.	2.8	1
101	AAPL: assessing association between p -value lists. Statistical Analysis and Data Mining, 2013, 6, 144-155.	2.8	1
102	DNLC: differential network local consistency analysis. BMC Bioinformatics, 2019, 20, 489.	2.6	1
103	Feature selection and classification over the network with missing node observations. Statistics in Medicine, 2022, 41, 1242-1262.	1.6	1
104	Sphinganine is associated with 24-h MAP in the non-sleepy with OSA. Metabolomics, 2022, 18, 23.	3.0	1
105	Incorporating feature reliability in false discovery rate estimation improves statistical power to detect differentially expressed features. , 2014, , .		0
106	MeDiA: Mean Distance Association and Its Applications in Nonlinear Gene Set Analysis. PLoS ONE, 2015, 10, e0124620.	2.5	0
107	Nonlinear variable selection with continuous outcome: A fully nonparametric incremental forward stagewise approach. Statistical Analysis and Data Mining, 2018, 11, 188-197.	2.8	0
108	Metabolomic Profile Responses to a Standardized Meal Challenge Differ by Cardiometabolic Disease Status. Current Developments in Nutrition, 2020, 4, nzaa049_068.	0.3	0

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109	An Untargeted Metabolomic Study of the Effects of Vitamin D and/or Calcium Supplementation Among Individuals at High Risk for Colorectal Neoplasms. <i>Current Developments in Nutrition</i> , 2020, 4, nzaa044_042.	0.3	0