

# Yufei Huang

## List of Publications by Year in descending order

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Version: 2024-02-01

113  
papers

3,417  
citations

186265

28  
h-index

175258

52  
g-index

121  
all docs

121  
docs citations

121  
times ranked

3825  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global profiling reveals common and distinct N6-methyladenosine (m6A) regulation of innate immune responses during bacterial and viral infections. <i>Cell Death and Disease</i> , 2022, 13, 234.	6.3	16
2	mAexpress-Reader: Prediction of m6A regulated expression genes by integrating m6A sites and reader binding information in specific- context. <i>Methods</i> , 2022, , .	3.8	2
3	Deep learning tackles single-cell analysisâ€”a survey of deep learning for scRNA-seq analysis. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	19
4	SSVEP-assisted RSVP brainâ€”computer interface paradigm for multi-target classification. <i>Journal of Neural Engineering</i> , 2021, 18, 016021.	3.5	10
5	ES-ARCNN: Predicting enhancer strength by using data augmentation and residual convolutional neural network. <i>Analytical Biochemistry</i> , 2021, 618, 114120.	2.4	14
6	Prediction of Elastic Behavior of Human Trabecular Bone Using A DXA Image-Based Deep Learning Model. <i>Jom</i> , 2021, 73, 2366-2376.	1.9	3
7	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training. <i>BMC Bioinformatics</i> , 2021, 22, 244.	2.6	8
8	Prediction and interpretation of cancer survival using graph convolution neural networks. <i>Methods</i> , 2021, 192, 120-130.	3.8	29
9	Predicting and characterizing a cancer dependency map of tumors with deep learning. <i>Science Advances</i> , 2021, 7, .	10.3	29
10	NucHMM: a method for quantitative modeling of nucleosome organization identifying functional nucleosome states distinctly associated with splicing potentiality. <i>Genome Biology</i> , 2021, 22, 250.	8.8	4
11	<i>m6A-express</i>: uncovering complex and condition-specific m6A regulation of gene expression. <i>Nucleic Acids Research</i> , 2021, 49, e116-e116.	14.5	24
12	Can DXA image-based deep learning model predict the anisotropic elastic behavior of trabecular bone?. <i>Journal of the Mechanical Behavior of Biomedical Materials</i> , 2021, 124, 104834.	3.1	6
13	GRWD1-WDR5-MLL2 Epigenetic Complex Mediates H3K4me3 Mark and Is Essential for Kaposiâ€™s Sarcoma-Associated Herpesvirus-Induced Cellular Transformation. <i>MBio</i> , 2021, 12, e0343121.	4.1	2
14	Deep learning of pharmacogenomics resources: moving towards precision oncology. <i>Briefings in Bioinformatics</i> , 2020, 21, 2066-2083.	6.5	43
15	Prediction of trabecular bone architectural features by deep learning models using simulated DXA images. <i>Bone Reports</i> , 2020, 13, 100295.	0.4	13
16	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1587-1604.	4.1	38
17	Modeling EEG Data Distribution With a Wasserstein Generative Adversarial Network to Predict RSVP Events. <i>IEEE Transactions on Neural Systems and Rehabilitation Engineering</i> , 2020, 28, 1720-1730.	4.9	30
18	Classification of Cancer Types Using Graph Convolutional Neural Networks. <i>Frontiers in Physics</i> , 2020, 8, .	2.1	64

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19	Predicting Sites of Epitranscriptome Modifications Using Unsupervised Representation Learning Based on Generative Adversarial Networks. <i>Frontiers in Physics</i> , 2020, 8, .	2.1	9
20	Signatures of oral microbiome in HIV-infected individuals with oral Kaposi's sarcoma and cell-associated KSHV DNA. <i>PLoS Pathogens</i> , 2020, 16, e1008114.	4.7	31
21	Convolutional neural network models for cancer type prediction based on gene expression. <i>BMC Medical Genomics</i> , 2020, 13, 44.	1.5	103
22	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019, 35, i90-i98.	4.1	34
23	Predicting drug response of tumors from integrated genomic profiles by deep neural networks. <i>BMC Medical Genomics</i> , 2019, 12, 18.	1.5	123
24	Feature Selection of Deep Learning Models for EEG-Based RSVP Target Detection. <i>IEICE Transactions on Information and Systems</i> , 2019, E102.D, 836-844.	0.7	8
25	CRISPR-Cas9 Screening of Kaposi's Sarcoma-Associated Herpesvirus-Transformed Cells Identifies XPO1 as a Vulnerable Target of Cancer Cells. <i>MBio</i> , 2019, 10, .	4.1	20
26	DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. <i>Frontiers in Genetics</i> , 2019, 10, 266.	2.3	32
27	Predicting Auditory Spatial Attention from EEG using Single- and Multi-task Convolutional Neural Networks. , 2019, , .		0
28	Generating EEG signals of an RSVP Experiment by a Class Conditioned Wasserstein Generative Adversarial Network. , 2019, , .		13
29	A Semi-Supervised Wasserstein Generative Adversarial Network for Classifying Driving Fatigue from EEG signals. , 2019, , .		9
30	Target Classification in a Novel SSVEP-RSVP Based BCI Gaming System. , 2019, , .		5
31	Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. <i>PLoS Computational Biology</i> , 2019, 15, e1006663.	3.2	41
32	MeTDiff: A Novel Differential RNA Methylation Analysis for MeRIP-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 526-534.	3.0	79
33	Deep EEG super-resolution: Upsampling EEG spatial resolution with Generative Adversarial Networks. , 2018, , .		43
34	Generating target/non-target images of an RSVP experiment from brain signals in by conditional generative adversarial network. , 2018, , .		8
35	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. <i>Nucleic Acids Research</i> , 2018, 46, D281-D287.	14.5	115
36	Viral and cellular N6-methyladenosine and N6,2â€²-O-dimethyladenosine epitranscriptomes in the KSHV life cycle. <i>Nature Microbiology</i> , 2018, 3, 108-120.	13.3	137

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37	CLIPSeed: Achieving High Precision miRNA Binding Sites Prediction using PAR-CLIP Data. , 2018, , .		0
38	GSAE: an autoencoder with embedded gene-set nodes for genomics functional characterization. BMC Systems Biology, 2018, 12, 142.	3.0	52
39	Deep-2'-O-Me: Predicting 2'-O-methylation sites by Convolutional Neural Networks. , 2018, 2018, 2394-2397.		16
40	Malware Detection in Cloud Infrastructures Using Convolutional Neural Networks. , 2018, , .		43
41	Cross-talk among writers, readers, and erasers of m <sup>6</sup> A regulates cancer growth and progression. Science Advances, 2018, 4, eaar8263.	10.3	245
42	Prediction of Human Performance Using Electroencephalography under Different Indoor Room Temperatures. Brain Sciences, 2018, 8, 74.	2.3	15
43	Topological Characterization of Human and Mouse m <sup>5</sup> C Epi-transcriptome Revealed by Bisulfite Sequencing. International Journal of Genomics, 2018, 2018, 1-19.	1.6	17
44	Base-pair resolution detection of transcription factor binding site by deep deconvolutional network. Bioinformatics, 2018, 34, 3446-3453.	4.1	18
45	Clustering Count-based RNA Methylation Data Using a Nonparametric Generative Model. Current Bioinformatics, 2018, 14, 11-23.	1.5	13
46	Asynchronous control of unmanned aerial vehicles using a steady-state visual evoked potential-based brain computer interface. Brain-Computer Interfaces, 2017, 4, 122-135.	1.8	15
47	Driver's fatigue prediction by deep covariance learning from EEG. , 2017, , .		14
48	QNB: differential RNA methylation analysis for count-based small-sample sequencing data with a quad-negative binomial model. BMC Bioinformatics, 2017, 18, 387.	2.6	40
49	Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. BioMed Research International, 2016, 2016, 1-8.	1.9	95
50	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. PLoS Computational Biology, 2016, 12, e1005287.	3.2	38
51	A hierarchical model for clustering m6A methylation peaks in MeRIP-seq data. BMC Genomics, 2016, 17, 520.	2.8	17
52	Detection of high variability in gene expression from single-cell RNA-seq profiling. BMC Genomics, 2016, 17, 508.	2.8	39
53	Guest Editorial IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2015 Special Issue. IEEE Transactions on Nanobioscience, 2016, 15, 306-308.	3.3	0
54	CrossLink: a novel method for cross-condition classification of cancer subtypes. BMC Genomics, 2016, 17, 549.	2.8	2

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55	A novel algorithm for calling mRNA m 6 A peaks by modeling biological variances in MeRIP-seq data. <i>Bioinformatics</i> , 2016, 32, i378-i385.	4.1	81
56	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016, 499, 15-23.	2.4	18
57	Effects of Physical Practice and Imagery Practice on Bilateral Transfer in Learning a Sequential Tapping Task. <i>PLoS ONE</i> , 2016, 11, e0152228.	2.5	28
58	Quantitative Proteomic Approach for MicroRNA Target Prediction Based on 18O/16O Labeling. <i>Cancer Informatics</i> , 2015, 14s5, CIN.S30563.	1.9	1
59	HEPeak: an HMM-based exome peak-finding package for RNA epigenome sequencing data. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	15
60	Frontiers in Integrative Genomics and Translational Bioinformatics. <i>BioMed Research International</i> , 2015, 2015, 1-3.	1.9	2
61	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. <i>BioMed Research International</i> , 2015, 2015, 1-12.	1.9	11
62	Feature extraction with deep belief networks for driver's cognitive states prediction from EEG data. , 2015, , .		27
63	Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , .		0
64	Prediction of driver's drowsy and alert states from EEG signals with deep learning. , 2015, , .		38
65	MeT-DB: a database of transcriptome methylation in mammalian cells. <i>Nucleic Acids Research</i> , 2015, 43, D197-D203.	14.5	63
66	Modeling of replicates variances for detecting RNA methylation site in MERIP-SEQ data. , 2015, , .		0
67	Integrative Genomics and Computational Systems Medicine. <i>BioMed Research International</i> , 2014, 2014, 1-3.	1.9	1
68	Genomewide Mapping and Screening of Kaposi's Sarcoma-Associated Herpesvirus (KSHV) 3' Untranslated Regions Identify Bicistronic and Polycistronic Viral Transcripts as Frequent Targets of KSHV MicroRNAs. <i>Journal of Virology</i> , 2014, 88, 377-392.	3.4	43
69	TraceRNA: A Web Application for Competing Endogenous RNA Exploration. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 548-557.	5.1	2
70	Prediction of Signal Peptide Cleavage Sites with Subsite-Coupled and Template Matching Fusion Algorithm. <i>Molecular Informatics</i> , 2014, 33, 230-239.	2.5	7
71	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , .		2
72	Viral miRNA targeting of bicistronic and polycistronic transcripts. <i>Current Opinion in Virology</i> , 2014, 7, 66-72.	5.4	12

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73	A protocol for RNA methylation differential analysis with MeRIP-Seq data and exomePeak R/Bioconductor package. <i>Methods</i> , 2014, 69, 274-281.	3.8	253
74	Computational methods for omics data. <i>International Journal of Computational Biology and Drug Design</i> , 2014, 7, 97-101.	0.3	0
75	A system based approach to construct a Kaposi sarcoma-associated herpesvirus (KSHV) specific pathway crosstalk network. , 2013, , .		0
76	NetceRNA: An algorithm for construction of phenotype-specific regulation networks via competing endogenous RNAs. , 2013, , .		1
77	KSHV MicroRNAs Mediate Cellular Transformation and Tumorigenesis by Redundantly Targeting Cell Growth and Survival Pathways. <i>PLoS Pathogens</i> , 2013, 9, e1003857.	4.7	90
78	Unveiling the dynamics in RNA epigenetic regulations. , 2013, , .		6
79	Exome-based analysis for RNA epigenome sequencing data. <i>Bioinformatics</i> , 2013, 29, 1565-1567.	4.1	139
80	A bag-of-words model for task-load prediction from EEG in complex environments. , 2013, , .		8
81	Gene Regulation, Modulation, and Their Applications in Gene Expression Data Analysis. <i>Advances in Bioinformatics</i> , 2013, 2013, 1-11.	5.7	25
82	Prediction of microRNAs Associated with Human Diseases Based on Weighted k Most Similar Neighbors. <i>PLoS ONE</i> , 2013, 8, e70204.	2.5	266
83	Gene Regulation. , 2013, , 797-801.		0
84	A new algorithm for predicting competing endogenous rnas. , 2012, , .		3
85	Basis-expansion factor models for uncovering transcription factor regulatory network. , 2012, , .		0
86	Exploiting correlated discriminant features in time frequency and space for characterization and robust classification of image RSVP events with EEG data. , 2012, , .		1
87	An investigation of clinical outcome prediction from integrative genomic profiles in ovarian cancer. , 2012, , .		4
88	Classification of EEG recordings without perfectly time-locked events. , 2012, , .		1
89	Characterization and Robust Classification of EEG Signal from Image RSVP Events with Independent Time-Frequency Features. <i>PLoS ONE</i> , 2012, 7, e44464.	2.5	17
90	A Bayesian decision fusion approach for microRNA target prediction. <i>BMC Genomics</i> , 2012, 13, S13.	2.8	17

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91	Advances in systems biology: computational algorithms and applications. BMC Systems Biology, 2012, 6, S1.	3.0	6
92	Iterative decoding in Factor Graph representation using Particle Filtering. , 2012, 22, 212-218.		2
93	Direct and efficient cellular transformation of primary rat mesenchymal precursor cells by KSHV. Journal of Clinical Investigation, 2012, 122, 1076-1081.	8.2	98
94	Computational prediction of microRNA regulatory pathways. , 2011, , .		1
95	Gene sets enrichment analysis of miRNA expression profile. , 2011, , .		0
96	Bayesian non-negative factor analysis for reconstructing transcriptional regulatory network. , 2011, , .		0
97	Clustering DNA methylation expressions using nonparametric beta mixture model. , 2011, , .		2
98	Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. Proteome Science, 2011, 9, S9.	1.7	7
99	Beyond seed match: Improving miRNA target prediction using PAR-CLIP data. , 2011, , .		0
100	MaturePred: Efficient Identification of MicroRNAs within Novel Plant Pre-miRNAs. PLoS ONE, 2011, 6, e27422.	2.5	61
101	Improving performance of mammalian microRNA target prediction. BMC Bioinformatics, 2010, 11, 476.	2.6	99
102	An Iterated Conditional Modes solution for sparse Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
103	Computational prediction of MicroRNA regulatory pathways. , 2010, , .		0
104	An iterated conditional mode solution for Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
105	Mapping miRNA Regulation to Functional Gene Sets. , 2009, , .		1
106	Reverse engineering gene regulatory networks. IEEE Signal Processing Magazine, 2009, 26, 76-97.	5.6	50
107	A Bayesian Approach for Uncovering Gene Network Motifs. , 2007, , .		0
108	Inferring the skeleton cell cycle regulatory network of malaria parasite using comparative genomic and variational Bayesian approaches. Genetica, 2007, 132, 131-142.	1.1	10

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109	Turbo Data Integration for Uncovering Gene Networks. , 2006, , .		1
110	Uncovering gene regulatory networks using variational Bayes variable selection. , 2006, , .		1
111	Adaptive Blind Multiuser Detection over Flat Fast Fading Channels Using Particle Filtering. Eurasip Journal on Wireless Communications and Networking, 2005, 2005, 1.	2.4	9
112	Sensor scheduling and target tracking using expectation propagation. , 2005, , .		2
113	Iterative decoding in factor graph representation using particle filtering. , 0, , .		3