Yufei Huang

List of Publications by Year
in descending order

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	Prediction of microRNAs Associated with Human Diseases Based on Weighted k Most Similar Neighbors. PLoS ONE, 2013, 8, e70204.	2.5	266
2	A protocol for RNA methylation differential analysis with MeRIP-Seq data and exomePeak R/Bioconductor package. Methods, 2014, 69, 274-281.	3.8	253
3	Cross-talk among writers, readers, and erasers of m^{6}A regulates cancer growth and progression. Science Advances, 2018, 4, eaar8263.	10.3	245
4	Exome-based analysis for RNA epigenome sequencing data. Bioinformatics, 2013, 29, 1565-1567.	4.1	139
5	Viral and cellular N6-methyladenosine and N6,2′-O-dimethyladenosine epitranscriptomes in the KSHV life cycle. Nature Microbiology, 2018, 3, 108-120.	13.3	137
6	Predicting drug response of tumors from integrated genomic profiles by deep neural networks. BMC Medical Genomics, 2019, 12, 18.	1.5	123
7	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287.	14.5	115
8	Convolutional neural network models for cancer type prediction based on gene expression. BMC Medical Genomics, 2020, 13, 44.	1.5	103
9	Improving performance of mammalian microRNA target prediction. BMC Bioinformatics, 2010, 11, 476.	2.6	99
10	Direct and efficient cellular transformation of primary rat mesenchymal precursor cells by KSHV. Journal of Clinical Investigation, 2012, 122, 1076-1081.	8.2	98
11	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
12	KSHV MicroRNAs Mediate Cellular Transformation and Tumorigenesis by Redundantly Targeting Cell Growth and Survival Pathways. PLoS Pathogens, 2013, 9, e1003857.	4.7	90
13	A novel algorithm for calling mRNA m^{6}A peaks by modeling biological variances in MeRIP-seq data. Bioinformatics, 2016, 32, i378-i385.	4.1	81
14	MeTDiff: A Novel Differential RNA Methylation Analysis for MeRIP-Seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 526-534.	3.0	79
15	Classification of Cancer Types Using Graph Convolutional Neural Networks. Frontiers in Physics, 2020, 8, .	2.1	64
16	MeT-DB: a database of transcriptome methylation in mammalian cells. Nucleic Acids Research, 2015, 43, D197-D203.	14.5	63
17	MaturePred: Efficient Identification of MicroRNAs within Novel Plant Pre-miRNAs. PLoS ONE, 2011, 6, e27422.	2.5	61
18	GSAE: an autoencoder with embedded gene-set nodes for genomics functional characterization. BMC Systems Biology, 2018, 12, 142.	3.0	52

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19	Reverse engineering gene regulatory networks. IEEE Signal Processing Magazine, 2009, 26, 76-97.	5.6	50
20	Genomewide Mapping and Screening of Kaposi's Sarcoma-Associated Herpesvirus (KSHV) 3â€² Untranslated Regions Identify Bicistronic and Polycistronic Viral Transcripts as Frequent Targets of KSHV MicroRNAs. Journal of Virology, 2014, 88, 377-392.	3.4	43
21	Deep EEG super-resolution: Upsampling EEG spatial resolution with Generative Adversarial Networks. , 2018, , .		43
22	Malware Detection in Cloud Infrastructures Using Convolutional Neural Networks. , 2018, , .		43
23	Deep learning of pharmacogenomics resources: moving towards precision oncology. Briefings in Bioinformatics, 2020, 21, 2066-2083.	6.5	43
24	Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. PLoS Computational Biology, 2019, 15, e1006663.	3.2	41
25	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
26	Detection of high variability in gene expression from single-cell RNA-seq profiling. BMC Genomics, 2016, 17, 508.	2.8	39
27	Prediction of driver's drowsy and alert states from EEG signals with deep learning. , 2015, , .		38
28	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. PLoS Computational Biology, 2016, 12, e1005287.	3.2	38
29	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. Computational and Structural Biotechnology Journal, 2020, 18, 1587-1604.	4.1	38
30	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. Bioinformatics, 2019, 35, i90-i98.	4.1	34
31	DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. Frontiers in Genetics, 2019, 10, 266.	2.3	32
32	Signatures of oral microbiome in HIV-infected individuals with oral Kaposi's sarcoma and cell-associated KSHV DNA. PLoS Pathogens, 2020, 16, e1008114.	4.7	31
33	Modeling EEG Data Distribution With a Wasserstein Generative Adversarial Network to Predict RSVP Events. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2020, 28, 1720-1730.	4.9	30
34	Prediction and interpretation of cancer survival using graph convolution neural networks. Methods, 2021, 192, 120-130.	3.8	29
35	Predicting and characterizing a cancer dependency map of tumors with deep learning. Science Advances, 2021, 7, .	10.3	29
36	Effects of Physical Practice and Imagery Practice on Bilateral Transfer in Learning a Sequential Tapping Task. PLoS ONE, 2016, 11, e0152228.	2.5	28

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37	Feature extraction with deep belief networks for driver's cognitive states prediction from EEG data. , 2015, , .		27
38	Gene Regulation, Modulation, and Their Applications in Gene Expression Data Analysis. Advances in Bioinformatics, 2013, 2013, 1-11.	5.7	25
39	*m6A-express*: uncovering complex and condition-specific m6A regulation of gene expression. Nucleic Acids Research, 2021, 49, e116-e116.	14.5	24
40	CRISPR-Cas9 Screening of Kaposi's Sarcoma-Associated Herpesvirus-Transformed Cells Identifies XPO1 as a Vulnerable Target of Cancer Cells. MBio, 2019, 10, .	4.1	20
41	Deep learning tackles single-cell analysis—a survey of deep learning for scRNA-seq analysis. Briefings in Bioinformatics, 2022, 23, .	6.5	19
42	DRME: Count-based differential RNA methylation analysis at small sample size scenario. Analytical Biochemistry, 2016, 499, 15-23.	2.4	18
43	Base-pair resolution detection of transcription factor binding site by deep deconvolutional network. Bioinformatics, 2018, 34, 3446-3453.	4.1	18
44	Characterization and Robust Classification of EEG Signal from Image RSVP Events with Independent Time-Frequency Features. PLoS ONE, 2012, 7, e44464.	2.5	17
45	A Bayesian decision fusion approach for microRNA target prediction. BMC Genomics, 2012, 13, S13.	2.8	17
46	A hierarchical model for clustering m6A methylation peaks in MeRIP-seq data. BMC Genomics, 2016, 17, 520.	2.8	17
47	Topological Characterization of Human and Mouse m^{5}C Epitranscriptome Revealed by Bisulfite Sequencing. International Journal of Genomics, 2018, 2018, 1-19.	1.6	17
48	Deep-2'-O-Me: Predicting 2'-O-methylation sites by Convolutional Neural Networks. , 2018, 2018, 2394-2397.		16
49	Global profiling reveals common and distinct N6-methyladenosine (m6A) regulation of innate immune responses during bacterial and viral infections. Cell Death and Disease, 2022, 13, 234.	6.3	16
50	HEPeak: an HMM-based exome peak-finding package for RNA epigenome sequencing data. BMC Genomics, 2015, 16, S2.	2.8	15
51	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
52	Prediction of Human Performance Using Electroencephalography under Different Indoor Room Temperatures. Brain Sciences, 2018, 8, 74.	2.3	15
53	Driver's fatigue prediction by deep covariance learning from EEG. , 2017, , .		14
54	ES-ARCNN: Predicting enhancer strength by using data augmentation and residual convolutional neural network. Analytical Biochemistry, 2021, 618, 114120.	2.4	14

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55	Generating EEG signals of an RSVP Experiment by a Class Conditioned Wasserstein Generative Adversarial Network. , 2019, , .		13
56	Prediction of trabecular bone architectural features by deep learning models using simulated DXA images. Bone Reports, 2020, 13, 100295.	0.4	13
57	Clustering Count-based RNA Methylation Data Using a Nonparametric Generative Model. Current Bioinformatics, 2018, 14, 11-23.	1.5	13
58	Viral miRNA targeting of bicistronic and polycistronic transcripts. Current Opinion in Virology, 2014, 7, 66-72.	5.4	12
59	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. BioMed Research International, 2015, 2015, 1-12.	1.9	11
60	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
61	SSVEP-assisted RSVP brain–computer interface paradigm for multi-target classification. Journal of Neural Engineering, 2021, 18, 016021.	3.5	10
62	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
63	A Semi-Supervised Wasserstein Generative Adversarial Network for Classifying Driving Fatigue from EEG signals. , 2019, , .		9
64	Predicting Sites of Epitranscriptome Modifications Using Unsupervised Representation Learning Based on Generative Adversarial Networks. Frontiers in Physics, 2020, 8, .	2.1	9
65	A bag-of-words model for task-load prediction from EEG in complex environments. , 2013, , .		8
66	Generating target/non-target images of an RSVP experiment from brain signals in by conditional generative adversarial network. , 2018, , .		8
67	Feature Selection of Deep Learning Models for EEG-Based RSVP Target Detection. IEICE Transactions on Information and Systems, 2019, E102.D, 836-844.	0.7	8
68	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training. BMC Bioinformatics, 2021, 22, 244.	2.6	8
69	Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. Proteome Science, 2011, 9, S9.	1.7	7
70	Prediction of Signal Peptide Cleavage Sites with Subsite–Coupled and Template Matching Fusion Algorithm. Molecular Informatics, 2014, 33, 230-239.	2.5	7
71	Advances in systems biology: computational algorithms and applications. BMC Systems Biology, 2012, 6, S1.	3.0	6
72	Unveiling the dynamics in RNA epigenetic regulations. , 2013, , .		6

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73	Can DXA image-based deep learning model predict the anisotropic elastic behavior of trabecular bone?. Journal of the Mechanical Behavior of Biomedical Materials, 2021, 124, 104834.	3.1	6
74	Target Classification in a Novel SSVEP-RSVP Based BCI Gaming System. , 2019, , .		5
75	An investigation of clinical outcome prediction from integrative genomic profiles in ovarian cancer. , 2012, , .		4
76	NucHMM: a method for quantitative modeling of nucleosome organization identifying functional nucleosome states distinctly associated with splicing potentiality. Genome Biology, 2021, 22, 250.	8.8	4
77	Iterative decoding in factor graph representation using particle filtering. , 0, , .		3
78	A new algorithm for predicting competing endogenous rnas. , 2012, , .		3
79	Prediction of Elastic Behavior of Human Trabecular Bone Using A DXA Image-Based Deep Learning Model. Jom, 2021, 73, 2366-2376.	1.9	3
80	Sensor scheduling and target tracking using expectation propagation. , 2005, , .		2
81	Clustering DNA methylation expressions using nonparametric beta mixture model. , 2011, , .		2
82	Iterative decoding in Factor Graph representation using Particle Filtering. , 2012, 22, 212-218.		2
83	TraceRNA: A Web Application for Competing Endogenous RNA Exploration. Circulation: Cardiovascular Genetics, 2014, 7, 548-557.	5.1	2
84	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , .		2
85	Frontiers in Integrative Genomics and Translational Bioinformatics. BioMed Research International, 2015, 2015, 1-3.	1.9	2
86	CrossLink: a novel method for cross-condition classification of cancer subtypes. BMC Genomics, 2016, 17, 549.	2.8	2
87	mAexpress-Reader: Prediction of m6A regulated expression genes by integrating m6A sites and reader binding information in specific- context. Methods, 2022, , .	3.8	2
88	GRWD1-WDR5-MLL2 Epigenetic Complex Mediates H3K4me3 Mark and Is Essential for Kaposiâ€™s Sarcoma-Associated Herpesvirus-Induced Cellular Transformation. MBio, 2021, 12, e0343121.	4.1	2
89	Turbo Data Integration for Uncovering Gene Networks. , 2006, , .		1
90	Uncovering gene regulatory networks using variational Bayes variable selection. , 2006, , .		1

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91	Mapping miRNA Regulation to Functional Gene Sets. , 2009, , .		1
92	Computational prediction of microRNA regulatory pathways. , 2011, , .		1
93	Exploiting correlated discriminant features in time frequency and space for characterization and robust classification of image RSVP events with EEG data. , 2012, , .		1
94	Classification of EEG recordings without perfectly time-locked events. , 2012, , .		1
95	NetceRNA: An algorithm for construction of phenotype-specific regulation networks via competing endogenous RNAs. , 2013, , .		1
96	Integrative Genomics and Computational Systems Medicine. BioMed Research International, 2014, 2014, 1-3.	1.9	1
97	Quantitative Proteomic Approach for MicroRNA Target Prediction Based on 18O/16O Labeling. Cancer Informatics, 2015, 14s5, CIN.S30563.	1.9	1
98	A Bayesian Approach for Uncovering Gene Network Motifs. , 2007, , .		0
99	An Iterated Conditional Modes solution for sparse Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
100	Computational prediction of MicroRNA regulatory pathways. , 2010, , .		0
101	An iterated conditional mode solution for Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
102	Gene sets enrichment analysis of miRNA expression profile. , 2011, , .		0
103	Bayesian non-negative factor analysis for reconstructing transcriptional regulatory network. , 2011, , .		0
104	Beyond seed match: Improving miRNA target prediction using PAR-CLIP data. , 2011, , .		0
105	Basis-expansion factor models for uncovering transcription factor regulatory network. , 2012, , .		0
106	A system based approach to construct a Kaposi sarcoma-associated herpesvirus (KSHV) specific pathway crosstalk network. , 2013, , .		0
107	Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , .		0
108	Modeling of replicates variances for detecting RNA methylation site in MERIP-SEQ data. , 2015, , .		0

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109	Guest Editorial IEEE International Conference on Bioinformatics and Biomedicine (BIBM) 2015 Special Issue. IEEE Transactions on Nanobioscience, 2016, 15, 306-308.	3.3	0
110	CLIPSeed: Achieving High Precision miRNA Binding Sites Prediction using PAR-CLIP Data. , 2018, , .		0
111	Predicting Auditory Spatial Attention from EEG using Single- and Multi-task Convolutional Neural Networks. , 2019, , .		0
112	Gene Regulation. , 2013, , 797-801.		0
113	Computational methods for omics data. International Journal of Computational Biology and Drug Design, 2014, 7, 97-101.	0.3	0