

Yang Dai

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

2,178
citations

279798

23
h-index

243625

44
g-index

73
all docs

73
docs citations

73
times ranked

3798
citing authors

#	ARTICLE	IF	CITATIONS
1	Endothelial heterogeneity across distinct vascular beds during homeostasis and inflammation. <i>ELife</i> , 2020, 9, .	6.0	209
2	MicroRNA-7 targets IGF1R (insulin-like growth factor 1 receptor) in tongue squamous cell carcinoma cells. <i>Biochemical Journal</i> , 2010, 432, 199-207.	3.7	202
3	MicroRNA-138 suppresses epithelialâ€mesenchymal transition in squamous cell carcinoma cell lines. <i>Biochemical Journal</i> , 2011, 440, 23-31.	3.7	173
4	Genome-Wide DNA Methylation Analysis Predicts an Epigenetic Switch for GATA Factor Expression in Endometriosis. <i>PLoS Genetics</i> , 2014, 10, e1004158.	3.5	154
5	MicroRNA-99 Family Targets AKT/mTOR Signaling Pathway in Dermal Wound Healing. <i>PLoS ONE</i> , 2013, 8, e64434.	2.5	142
6	Positive Cross-Talk between Estrogen Receptor and NF- κ B in Breast Cancer. <i>Cancer Research</i> , 2009, 69, 8918-8925.	0.9	131
7	Metabolome of human gut microbiome is predictive of host dysbiosis. <i>GigaScience</i> , 2015, 4, 42.	6.4	95
8	Intrinsic Differences between Oral and Skin Keratinocytes. <i>PLoS ONE</i> , 2014, 9, e101480.	2.5	95
9	Prediction of MHC class II binders using the ant colony search strategy. <i>Artificial Intelligence in Medicine</i> , 2005, 35, 147-156.	6.5	59
10	PopPhy-CNN: A Phylogenetic Tree Embedded Architecture for Convolutional Neural Networks to Predict Host Phenotype From Metagenomic Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020, 24, 2993-3001.	6.3	55
11	Prediction of MHC class II binding peptides based on an iterative learning model. <i>Immunome Research</i> , 2005, 1, 6.	0.1	49
12	Vitamin D receptor promotes healthy microbial metabolites and microbiome. <i>Scientific Reports</i> , 2020, 10, 7340.	3.3	47
13	MetaLonDA: a flexible R package for identifying time intervals of differentially abundant features in metagenomic longitudinal studies. <i>Microbiome</i> , 2018, 6, 32.	11.1	45
14	MiMeNet: Exploring microbiome-metabolome relationships using neural networks. <i>PLoS Computational Biology</i> , 2021, 17, e1009021.	3.2	42
15	Multi-Omics Approach Identifies Molecular Mechanisms of Plant-Fungus Mycorrhizal Interaction. <i>Frontiers in Plant Science</i> , 2015, 6, 1061.	3.6	39
16	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
17	Regulation of Microbiota by Vitamin D Receptor: A Nuclear Weapon in Metabolic Diseases. <i>Nuclear Receptor Research</i> , 2018, 5, .	2.5	37
18	MicroRNA-99 Family Members Suppress Homeobox A1 Expression in Epithelial Cells. <i>PLoS ONE</i> , 2013, 8, e80625.	2.5	34

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19	An Integrated Bioinformatics Approach Identifies Elevated Cyclin E2 Expression and E2F Activity as Distinct Features of Tamoxifen Resistant Breast Tumors. PLoS ONE, 2011, 6, e22274.	2.5	33
20	miR-486-3p, miR-139-5p, and miR-21 as Biomarkers for the Detection of Oral Tongue Squamous Cell Carcinoma. Biomarkers in Cancer, 2017, 9, 1179299X1700900.	3.6	33
21	Differential microRNA profile underlies the divergent healing responses in skin and oral mucosal wounds. Scientific Reports, 2019, 9, 7160.	3.3	30
22	Using convolutional neural networks to explore the microbiome. , 2017, 2017, 4269-4272.		29
23	Computational methods for the identification of microRNA targets. Open Access Bioinformatics, 2010, 2, 29.	0.9	26
24	Utilizing longitudinal microbiome taxonomic profiles to predict food allergy via Long Short-Term Memory networks. PLoS Computational Biology, 2019, 15, e1006693.	3.2	26
25	WEVOTE: Weighted Voting Taxonomic Identification Method of Microbial Sequences. PLoS ONE, 2016, 11, e0163527.	2.5	25
26	A probabilistic meta-predictor for the MHC class II binding peptides. Immunogenetics, 2008, 60, 25-36.	2.4	24
27	Computing all nonsingular solutions of cyclic-n polynomial using polyhedral homotopy continuation methods. Journal of Computational and Applied Mathematics, 2003, 152, 83-97.	2.0	22
28	MicroRNA-21 regulates prostaglandin E2 signaling pathway by targeting 15-hydroxyprostaglandin dehydrogenase in tongue squamous cell carcinoma. BMC Cancer, 2016, 16, 685.	2.6	21
29	Single-cell transcriptomic profiling of lung endothelial cells identifies dynamic inflammatory and regenerative subpopulations. JCI Insight, 2022, 7, .	5.0	21
30	Efficient Algorithms and Implementations for Optimizing the Sum of Linear Fractional Functions, with Applications. Journal of Combinatorial Optimization, 2005, 9, 69-90.	1.3	19
31	Conical Partition Algorithm for Maximizing the Sum of dc Ratios. Journal of Global Optimization, 2005, 31, 253-270.	1.8	19
32	Overexpression of the Oral Mucosa-Specific microRNA-31 Promotes Skin Wound Closure. International Journal of Molecular Sciences, 2019, 20, 3679.	4.1	17
33	Predicting Ecological Roles in the Rhizosphere Using Metabolome and Transportome Modeling. PLoS ONE, 2015, 10, e0132837.	2.5	17
34	A SUPPORT VECTOR MACHINE APPROACH FOR PREDICTION OF T CELL EPITOPES. , 2005, , .		16
35	Correlative Analysis of miRNA Expression and Oncotype Dx Recurrence Score in Estrogen Receptor Positive Breast Carcinomas. PLoS ONE, 2015, 10, e0145346.	2.5	16
36	Targeting DNA Methylation Depletes Uterine Leiomyoma Stem Cellâ€enriched Population by Stimulating Their Differentiation. Endocrinology, 2020, 161, .	2.8	15

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37	Progesterone receptor-DNA methylation crosstalk regulates depletion of uterine leiomyoma stem cells: A potential therapeutic target. <i>Stem Cell Reports</i> , 2021, 16, 2099-2106.	4.8	11
38	A computational approach to identify cellular heterogeneity and tissue-specific gene regulatory networks. <i>BMC Bioinformatics</i> , 2018, 19, 217.	2.6	10
39	Identifying transcription factors and microRNAs as key regulators of pathways using Bayesian inference on known pathway structures. <i>Proteome Science</i> , 2012, 10, S15.	1.7	9
40	MeDEStrand: an improved method to infer genome-wide absolute methylation levels from DNA enrichment data. <i>BMC Bioinformatics</i> , 2018, 19, 540.	2.6	7
41	A Bayesian inference transcription factor activity model for the analysis of single-cell transcriptomes. <i>Genome Research</i> , 2021, 31, 1296-1311.	5.5	7
42	Temporal transcriptomic analysis using TrendCatcher identifies early and persistent neutrophil activation in severe COVID-19. <i>JCI Insight</i> , 2022, 7, .	5.0	7
43	Modeling the <i>Pseudomonas</i> Sulfur Regulome by Quantifying the Storage and Communication of Information. <i>MSystems</i> , 2018, 3, .	3.8	6
44	Predicting Host Phenotype Based on Gut Microbiome Using a Convolutional Neural Network Approach. <i>Methods in Molecular Biology</i> , 2021, 2190, 249-266.	0.9	6
45	GLOBAL OPTIMIZATION PROBLEM WITH MULTIPLE REVERSE CONVEX CONSTRAINTS AND ITS APPLICATION TO OUT-OF-ROUNDNESS PROBLEM. <i>Journal of the Operations Research Society of Japan</i> , 1996, 39, 356-371.	0.2	5
46	A Meta-predictor for MHC Class II Binding Peptides Based on Naive Bayesian Approach. , 2006, 2006, 5322-5.		4
47	A block-based evolutionary optimization strategy to investigate gene-gene interactions in genetic association studies. , 2010, , .		4
48	LMethyR-SVM: Predict Human Enhancers Using Low Methylated Regions based on Weighted Support Vector Machines. <i>PLoS ONE</i> , 2016, 11, e0163491.	2.5	4
49	Meta-Signer: Metagenomic Signature Identifier based on rank aggregation of features. <i>F1000Research</i> , 0, 10, 194.	1.6	4
50	BindSDB: A binding-information spatial database. , 2010, , .		3
51	Relational database index choices for genome annotation data. , 2010, , .		3
52	Site-Specific Expression Pattern of PIWI-Interacting RNA in Skin and Oral Mucosal Wound Healing. <i>International Journal of Molecular Sciences</i> , 2020, 21, 521.	4.1	3
53	Observation of a Curve Crossing Mechanism in the Field Ionization of Inner-Shell Excited Single <math display="block">\text{Xe}^{33+} \{ (2s) \text{Tj} \} <math display="block">\text{Xe}^{34+} \{ (2s) \text{p} \} Vacancy States. <i>IEEE Journal of Quantum Electronics</i> , 2012, 48, 806-813.	1.9	2
54	On Simplified Global Nonlinear Function for Fitness Landscape: A Case Study of Inverse Protein Folding. <i>PLoS ONE</i> , 2014, 9, e104403.	2.5	2

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55	Regulatory Elements in Low-Methylated Regions Predict Directional Change of Gene Expression. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1293-1300.	6.3	2
56	Building a Meta-Predictor for MHC Class II-Binding Peptides. Methods in Molecular Biology, 2007, 409, 355-364.	0.9	2
57	Using machine learning to predict rapid decline of kidney function in sickle cell anemia. EJHaem, 2021, 2, 257-260.	1.0	1
58	Integrating microbiome and metabolome data for host disease prediction via deep neural networks. , 2021, , .		1
59	Using Conditional Generative Adversarial Networks to Boost the Performance of Machine Learning in Microbiome Datasets. , 2020, , .		1
60	Demonstration of ultrahigh brightness X-ray amplification from xenon hollow atom states at 2.71 - 2.93 angstroms. , 0, , .		0
61	Identifying Transcription Factors and microRNAs as Key Regulators of Pathways Using Bayesian Inference on Known Pathway Structures. , 2011, , .		0
62	PARALLEL IMPLEMENTATION OF POLYHEDRAL CONTINUATION METHODS FOR SYSTEMS OF POLYNOMIAL EQUATIONS. , 2002, , .		0
63	Sample Scale-Free Gene Regulatory Network Using Gene Ontology. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0
64	Correlated Discretized Expression Score: A Method for Identifying Gene Interaction Networks from Time Course Microarray Expression Data. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0