Yang Dai

List of Publications by Year
in descending order

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	Temporal transcriptomic analysis using TrendCatcher identifies early and persistent neutrophil activation in severe COVID-19. JCI Insight, 2022, 7, .	5.0	7
2	Single-cell transcriptomic profiling of lung endothelial cells identifies dynamic inflammatory and regenerative subpopulations. JCI Insight, 2022, 7, .	5.0	21
3	Using machine learning to predict rapid decline of kidney function in sickle cell anemia. EJHaem, 2021, 2, 257-260.	1.0	1
4	MiMeNet: Exploring microbiome-metabolome relationships using neural networks. PLoS Computational Biology, 2021, 17, e1009021.	3.2	42
5	A Bayesian inference transcription factor activity model for the analysis of single-cell transcriptomes. Genome Research, 2021, 31, 1296-1311.	5.5	7
6	Integrating microbiome and metabolome data for host disease prediction via deep neural networks. , 2021, , .		1
7	Progesterone receptor-DNA methylation crosstalk regulates depletion of uterine leiomyoma stem cells: A potential therapeutic target. Stem Cell Reports, 2021, 16, 2099-2106.	4.8	11
8	Predicting Host Phenotype Based on Gut Microbiome Using a Convolutional Neural Network Approach. Methods in Molecular Biology, 2021, 2190, 249-266.	0.9	6
9	Targeting DNA Methylation Depletes Uterine Leiomyoma Stem Cellâ€"enriched Population by Stimulating Their Differentiation. Endocrinology, 2020, 161, .	2.8	15
10	Site-Specific Expression Pattern of PIWI-Interacting RNA in Skin and Oral Mucosal Wound Healing. International Journal of Molecular Sciences, 2020, 21, 521.	4.1	3
11	Vitamin D receptor promotes healthy microbial metabolites and microbiome. Scientific Reports, 2020, 10, 7340.	3.3	47
12	PopPhy-CNN: A Phylogenetic Tree Embedded Architecture for Convolutional Neural Networks to Predict Host Phenotype From Metagenomic Data. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 2993-3001.	6.3	55
13	Endothelial heterogeneity across distinct vascular beds during homeostasis and inflammation. ELife, 2020, 9, .	6.0	209
14	Using Conditional Generative Adversarial Networks to Boost the Performance of Machine Learning in Microbiome Datasets. , 2020, , .		1
15	Overexpression of the Oral Mucosa-Specific microRNA-31 Promotes Skin Wound Closure. International Journal of Molecular Sciences, 2019, 20, 3679.	4.1	17
16	Utilizing longitudinal microbiome taxonomic profiles to predict food allergy via Long Short-Term Memory networks. PLoS Computational Biology, 2019, 15, e1006693.	3.2	26
17	Differential microRNA profile underlies the divergent healing responses in skin and oral mucosal wounds. Scientific Reports, 2019, 9, 7160.	3.3	30
18	MetaLonDA: a flexible R package for identifying time intervals of differentially abundant features in metagenomic longitudinal studies. Microbiome, 2018, 6, 32.	11.1	45

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19	Regulation of Microbiota by Vitamin D Receptor: A Nuclear Weapon in Metabolic Diseases. Nuclear Receptor Research, 2018, 5, .	2.5	37
20	MeDEStrand: an improved method to infer genome-wide absolute methylation levels from DNA enrichment data. BMC Bioinformatics, 2018, 19, 540.	2.6	7
21	Modeling the <i>Pseudomonas</i> Sulfur Regulome by Quantifying the Storage and Communication of Information. MSystems, 2018, 3, .	3.8	6
22	A computational approach to identifyÂcellular heterogeneity andÂtissue-specific gene regulatory networks. BMC Bioinformatics, 2018, 19, 217.	2.6	10
23	Using convolutional neural networks to explore the microbiome. , 2017, 2017, 4269-4272.		29
24	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
25	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, 1-8.	3.6	38
26	LMethyR-SVM: Predict Human Enhancers Using Low Methylated Regions based on Weighted Support Vector Machines. PLoS ONE, 2016, 11, e0163491.	2.5	4
27	WEVOTE: Weighted Voting Taxonomic Identification Method of Microbial Sequences. PLoS ONE, 2016, 11, e0163527.	2.5	25
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	Metabolome of human gut microbiome is predictive of host dysbiosis. GigaScience, 2015, 4, 42.	6.4	95
30	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
31	Multi-Omics Approach Identifies Molecular Mechanisms of Plant-Fungus Mycorrhizal Interaction. Frontiers in Plant Science, 2015, 6, 1061.	3.6	39
32	Predicting Ecological Roles in the Rhizosphere Using Metabolome and Transportome Modeling. PLoS ONE, 2015, 10, e0132837.	2.5	17
33	Correlative Analysis of miRNA Expression and Oncotype Dx Recurrence Score in Estrogen Receptor Positive Breast Carcinomas. PLoS ONE, 2015, 10, e0145346.	2.5	16
34	On Simplified Global Nonlinear Function for Fitness Landscape: A Case Study of Inverse Protein Folding. PLoS ONE, 2014, 9, e104403.	2.5	2
35	Genome-Wide DNA Methylation Analysis Predicts an Epigenetic Switch for GATA Factor Expression in Endometriosis. PLoS Genetics, 2014, 10, e1004158.	3.5	154
36	Intrinsic Differences between Oral and Skin Keratinocytes. PLoS ONE, 2014, 9, e101480.	2.5	95

#	ARTICLE	IF	CITATIONS
37	MicroRNA-99 Family Targets AKT/mTOR Signaling Pathway in Dermal Wound Healing. PLoS ONE, 2013, 8, e64434.	2.5	142
38	MicroRNA-99 Family Members Suppress Homeobox A1 Expression in Epithelial Cells. PLoS ONE, 2013, 8, e80625.	2.5	34
39	Observation of a Curve Crossing Mechanism in the Field Ionization of Inner-Shell Excited Single <formula formulatype="inline"><tex Notation="TeX">${\rm Xe}^{33+}({2ar{m}}$ Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Notation="TeX">${\rm Xe}^{34+}({2ar{m s}2ar{m p}})$</tex></formula> Vacancy States. IEEE Journal of Quantum Electronics, 2012, 48, 806-813.	1.9	2
40	Identifying transcription factors and microRNAs as key regulators of pathways using Bayesian inference on known pathway structures. Proteome Science, 2012, 10, S15.	1.7	9
41	Identifying Transcription Factors and microRNAs as Key Regulators of Pathways Using Bayesian Inference on Known Pathway Structures. , 2011, , .		0
42	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
43	MicroRNA-138 suppresses epithelialâ€"mesenchymal transition in squamous cell carcinoma cell lines. Biochemical Journal, 2011, 440, 23-31.	3.7	173
44	MicroRNA-7 targets IGF1R (insulin-like growth factor 1 receptor) in tongue squamous cell carcinoma cells. Biochemical Journal, 2010, 432, 199-207.	3.7	202
45	Computational methods for the identification of microRNA targets. Open Access Bioinformatics, 2010, 2, 29.	0.9	26
46	BindSDb: A binding-information spatial database. , 2010, , .		3
47	A block-based evolutionary optimization strategy to investigate gene-gene interactions in genetic association studies. , 2010, , .		4
48	Relational database index choices for genome annotation data. , 2010, , .		3
49	Positive Cross-Talk between Estrogen Receptor and NF-ΊºB in Breast Cancer. Cancer Research, 2009, 69, 8918-8925.	0.9	131
50	A probabilistic meta-predictor for the MHC class II binding peptides. Immunogenetics, 2008, 60, 25-36.	2.4	24
51	Building a Meta-Predictor for MHC Class II-Binding Peptides. Methods in Molecular Biology, 2007, 409, 355-364.	0.9	2
52	A Meta-predictor for MHC Class II Binding Peptides Based on Naive Bayesian Approach. , 2006, 2006, 5322-5.		4
53	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
54	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

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55	Prediction of MHC class II binders using the ant colony search strategy. Artificial Intelligence in Medicine, 2005, 35, 147-156.	6.5	59
56	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
57	Conical Partition Algorithm for Maximizing the Sum of dc Ratios. Journal of Global Optimization, 2005, 31, 253-270.	1.8	19
58	Prediction of MHC class II binding peptides based on an iterative learning model. Immunome Research, 2005, 1, 6.	0.1	49
59	A SUPPORT VECTOR MACHINE APPROACH FOR PREDICTION OF T CELL EPITOPES. , 2005, , .		16
60	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
61	PARALLEL IMPLEMENTATION OF POLYHEDRAL CONTINUATION METHODS FOR SYSTEMS OF POLYNOMIAL EQUATIONS. , 2002, , .		0
62	GLOBAL OPTIMIZATION PROBLEM WITH MULTIPLE REVERSE CONVEX CONSTRAINTS AND ITS APPLICATION TO OUT-OF-ROUNDNESS PROBLEM. Journal of the Operations Research Society of Japan, 1996, 39, 356-371.	0.2	5
63	Demonstration of ultrahigh brightness X-ray amplification from xenon hollow atom states at 2.71 - 2.93 angstroms. , 0, , .		0
64	Meta-Signer: Metagenomic Signature Identifier based onrank aggregation of features. F1000Research, 0, 10, 194.	1.6	4