Minghua Deng

List of Publications by Year
in descending order

98 papers	**3,651** citations	186265 **28** h-index	144013 **57** g-index
101 all docs	**101** docs citations	**101** times ranked	**4645** citing authors

#	Article	IF	Citations
1	Inferring Domain-Domain Interactions From Protein-Protein Interactions. Genome Research, 2002, 12, 1540-1548.	5.5	376
2	A dynamic programming algorithm for haplotype block partitioning. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7335-7339.	7.1	312
3	Prediction of Protein Function Using Protein–Protein Interaction Data. Journal of Computational Biology, 2003, 10, 947-960.	1.6	274
4	A critical assessment of Mus musculus gene function prediction using integrated genomic evidence. Genome Biology, 2008, 9, S2.	9.6	214
5	Mapping gene ontology to proteins based on protein-protein interaction data. Bioinformatics, 2004, 20, 895-902.	4.1	149
6	An Integrated Probabilistic Model for Functional Prediction of Proteins. Journal of Computational Biology, 2004, 11, 463-475.	1.6	134
7	CCLasso: correlation inference for compositional data through Lasso. Bioinformatics, 2015, 31, 3172-3180.	4.1	133
8	New developments of alignment-free sequence comparison: measures, statistics and next-generation sequencing. Briefings in Bioinformatics, 2014, 15, 343-353.	6.5	126
9	A Lasso regression model for the construction of microRNA-target regulatory networks. Bioinformatics, 2011, 27, 2406-2413.	4.1	110
10	Cell Culture System for Analysis of Genetic Heterogeneity Within Hepatocellular Carcinomas and Response to Pharmacologic Agents. Gastroenterology, 2017, 152, 232-242.e4.	1.3	107
11	An integrated approach to the prediction of domain-domain interactions. BMC Bioinformatics, 2006, 7, 269.	2.6	102
12	Diffusion Kernel-Based Logistic Regression Models for Protein Function Prediction. OMICS A Journal of Integrative Biology, 2006, 10, 40-55.	2.0	90
13	Alignment-Free Sequence Comparison Based on Next-Generation Sequencing Reads. Journal of Computational Biology, 2013, 20, 64-79.	1.6	76
14	Comparison of metagenomic samples using sequence signatures. BMC Genomics, 2012, 13, 730.	2.8	74
15	RNA Editome in Rhesus Macaque Shaped by Purifying Selection. PLoS Genetics, 2014, 10, e1004274.	3.5	71
16	Stochastic model of yeast cell-cycle network. Physica D: Nonlinear Phenomena, 2006, 219, 35-39.	2.8	67
17	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. Environmental Microbiology, 2018, 20, 734-754.	3.8	53
18	Differential network analysis via lasso penalized D-trace loss. Biometrika, 2017, 104, 755-770.	2.4	49

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19	Deep soft K-means clustering with self-training for single-cell RNA sequence data. NAR Genomics and Bioinformatics, 2020, 2, lqaa039.	3.2	48
20	Transcription and splicing regulation in human umbilical vein endothelial cells under hypoxic stress conditions by exon array. BMC Genomics, 2009, 10, 126.	2.8	47
21	Searching for bidirectional promoters in Arabidopsis thaliana. BMC Bioinformatics, 2009, 10, S29.	2.6	45
22	CD4 T-cell transcriptome analysis reveals aberrant regulation of STAT3 and Wnt signaling pathways in rheumatoid arthritis: evidence from a case–control study. Arthritis Research and Therapy, 2015, 17, 76.	3.5	45
23	RaptorX-Angle: real-value prediction of protein backbone dihedral angles through a hybrid method of clustering and deep learning. BMC Bioinformatics, 2018, 19, 100.	2.6	44
24	scRMD: imputation for single cell RNA-seq data via robust matrix decomposition. Bioinformatics, 2020, 36, 3156-3161.	4.1	42
25	gCoda: Conditional Dependence Network Inference for Compositional Data. Journal of Computational Biology, 2017, 24, 699-708.	1.6	40
26	Assessment of the reliability of protein-protein interactions and protein function prediction. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2003, , 140-51.	0.7	39
27	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. Oncotarget, 2016, 7, 2867-2877.	1.8	38
28	Combinatorial regulation of transcription factors and microRNAs. BMC Systems Biology, 2010, 4, 150.	3.0	37
29	A microscopic landscape of the invasive breast cancer genome. Scientific Reports, 2016, 6, 27545.	3.3	33
30	Prediction of protein function using protein-protein interaction data. , 0, , .		31
31	Detecting differentially expressed genes by relative entropy. Journal of Theoretical Biology, 2005, 234, 395-402.	1.7	31
32	Systematic identification of conserved motif modules in the human genome. BMC Genomics, 2010, 11, 567.	2.8	28
33	Single-cell RNA-seq data semi-supervised clustering and annotation via structural regularized domain adaptation. Bioinformatics, 2021, 37, 775-784.	4.1	28
34	Detecting virus integration sites based on multiple related sequencing data by VirTect. BMC Medical Genomics, 2019, 12, 19.	1.5	27
35	A Survey on Deep Hashing Methods. ACM Transactions on Knowledge Discovery From Data, 2023, 17, 1-50.	3.5	27
36	Inference of Markovian properties of molecular sequences from NGS data and applications to comparative genomics. Bioinformatics, 2016, 32, 993-1000.	4.1	25

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37	Etiologic Diagnosis of Lower Respiratory Tract Bacterial Infections Using Sputum Samples and Quantitative Loop-Mediated Isothermal Amplification. PLoS ONE, 2012, 7, e38743.	2.5	24
38	Binding Energy Landscape Analysis Helps to Discriminate True Hits from High-Scoring Decoys in Virtual Screening. Journal of Chemical Information and Modeling, 2010, 50, 1855-1864.	5.4	23
39	Integrating Deep Supervised, Self-Supervised and Unsupervised Learning for Single-Cell RNA-seq Clustering and Annotation. Genes, 2020, 11, 792.	2.4	23
40	GHNN: Graph Harmonic Neural Networks for semi-supervised graph-level classification. Neural Networks, 2022, 151, 70-79.	5.9	23
41	Pysim-sv: a package for simulating structural variation data with GC-biases. BMC Bioinformatics, 2017, 18, 53.	2.6	22
42	Expectation pooling: an effective and interpretable pooling method for predicting DNA–protein binding. Bioinformatics, 2020, 36, 1405-1412.	4.1	22
43	Improving residue–residue contact prediction via low-rank and sparse decomposition of residue correlation matrix. Biochemical and Biophysical Research Communications, 2016, 472, 217-222.	2.1	19
44	scNAME: neighborhood contrastive clustering with ancillary mask estimation for scRNA-seq data. Bioinformatics, 2022, 38, 1575-1583.	4.1	18
45	Statistical Analysis Reveals Co-Expression Patterns of Many Pairs of Genes in Yeast Are Jointly Regulated by Interacting Loci. PLoS Genetics, 2013, 9, e1003414.	3.5	17
46	scMRA: a robust deep learning method to annotate scRNA-seq data with multiple reference datasets. Bioinformatics, 2022, 38, 738-745.	4.1	17
47	Integrative Approaches for microRNA Target Prediction: Combining Sequence Information and the Paired mRNA and miRNA Expression Profiles. Current Bioinformatics, 2013, 8, 37-45.	1.5	16
48	Insights into the transmission of respiratory infectious diseases through empirical human contact networks. Scientific Reports, 2016, 6, 31484.	3.3	16
49	Single-Cell Transcriptome Data Clustering via Multinomial Modeling and Adaptive Fuzzy K-Means Algorithm. Frontiers in Genetics, 2020, 11, 295.	2.3	15
50	Uncovering the Dominant Motion Modes of Allosteric Regulation Improves Allosteric Site Prediction. Journal of Chemical Information and Modeling, 2022, 62, 187-195.	5.4	14
51	Deepprune: Learning Efficient and Interpretable Convolutional Networks Through Weight Pruning for Predicting DNA-Protein Binding. Frontiers in Genetics, 2019, 10, 1145.	2.3	13
52	Yeast cell fate control by temporal redundancy modulation of transcription factor paralogs. Nature Communications, 2021, 12, 3145.	12.8	12
53	Multiple alignment-free sequence comparison. Bioinformatics, 2013, 29, 2690-2698.	4.1	11
54	Compositional data network analysis via lasso penalized D-trace loss. Bioinformatics, 2019, 35, 3404-3411.	4.1	11

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55	Prediction of protein function using protein-protein interaction data. Proceedings, 2002, 1, 197-206.	0.1	11
56	CLEAR: Cluster-Enhanced Contrast for Self-Supervised Graph Representation Learning. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 899-912.	11.3	11
57	Modular analysis of the probabilistic genetic interaction network. Bioinformatics, 2011, 27, 853-859.	4.1	10
58	VCNet: vector-based gene co-expression network construction and its application to RNA-seq data. Bioinformatics, 2017, 33, 2173-2181.	4.1	9
59	Inferring Gene-Disease Association by an Integrative Analysis of eQTL Genome-Wide Association Study and Protein-Protein Interaction Data. Human Heredity, 2018, 83, 117-129.	0.8	9
60	Sparsity-Penalized Stacked Denoising Autoencoders for Imputing Single-Cell RNA-seq Data. Genes, 2020, 11, 532.	2.4	8
61	Conservation and implications of eukaryote transcriptional regulatory regions across multiple species. BMC Genomics, 2008, 9, 623.	2.8	7
62	Adjustment method for microarray data generated using two-cycle RNA labeling protocol. BMC Genomics, 2013, 14, 31.	2.8	6
63	SVmine improves structural variation detection by integrative mining of predictions from multiple algorithms. Bioinformatics, 2017, 33, 3348-3354.	4.1	6
64	Direct interaction network and differential network inference from compositional data via lasso penalized D-trace loss. PLoS ONE, 2019, 14, e0207731.	2.5	6
65	Predicting protein inter-residue contacts using composite likelihood maximization and deep learning. BMC Bioinformatics, 2019, 20, 537.	2.6	6
66	Nonlinear cooperation of p53-ING1-induced bax expression and protein S-nitrosylation in GSNO-induced thymocyte apoptosis: a quantitative approach with cross-platform validation. Apoptosis: an International Journal on Programmed Cell Death, 2009, 14, 236-245.	4.9	5
67	Integrating multiple types of data to predict novel cell cycle-related genes. BMC Systems Biology, 2011, 5, S9.	3.0	5
68	Imputing missing values for genetic interaction data. Methods, 2014, 67, 269-277.	3.8	5
69	A Novel Noninvasive Program for Staging Liver Fibrosis in Untreated Patients With Chronic Hepatitis B. Clinical and Translational Gastroenterology, 2019, 10, e00033.	2.5	5
70	Profiling transcription factor activity dynamics using intronic reads in time-series transcriptome data. PLoS Computational Biology, 2022, 18, e1009762.	3.2	5
71	Statistical Methods for Microbiome Compositional Data Network Inference: A Survey. Journal of Computational Biology, 2022, , .	1.6	5
72	REMAS: a new regression model to identify alternative splicing events from exon array data. BMC Bioinformatics, 2009, 10, S18.	2.6	4

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73	Predicting MicroRNA targets by integrating sequence and expression data in cancer. , 2011, , .		4
74	Hybridization and amplification rate correction for affymetrix SNP arrays. BMC Medical Genomics, 2012, 5, 24.	1.5	4
75	Estimation of isoform expression in RNA-seq data using a hierarchical Bayesian model. Journal of Bioinformatics and Computational Biology, 2015, 13, 1542001.	0.8	4
76	DNA-GCN: Graph Convolutional Networks for Predicting DNA-Protein Binding. Lecture Notes in Computer Science, 2021, , 458-466.	1.3	4
77	Improve Deep Unsupervised Hashing via Structural and Intrinsic Similarity Learning. IEEE Signal Processing Letters, 2022, 29, 602-606.	3.6	4
78	Using graphical adaptive lasso approach to construct transcription factor and microRNA's combinatorial regulatory network in breast cancer. IET Systems Biology, 2014, 8, 87-95.	1.5	3
79	Low-Rank and Sparse Matrix Decomposition for Genetic Interaction Data. BioMed Research International, 2015, 2015, 1-11.	1.9	3
80	A study of biases of DNA copy number estimation based on PICR model. Frontiers of Mathematics in China, 2011, 6, 1203-1216.	0.7	2
81	Comparison and evaluation of network clustering algorithms applied to genetic interaction networks. Frontiers in Bioscience - Elite, 2012, E4, 2150.	1.8	2
82	Using a Stochastic AdaBoost Algorithm to Discover Interactome Motif Pairs from Sequences. Lecture Notes in Computer Science, 2006, , 622-630.	1.3	2
83	Alignment-Free Sequence Comparison Based on Next Generation Sequencing Reads: Extended Abstract. Lecture Notes in Computer Science, 2012, , 272-285.	1.3	2
84	Rare variant association tests for ancestry-matched case-control data based on conditional logistic regression. Briefings in Bioinformatics, 2022, , .	6.5	2
85	A network based covariance test for detecting multivariate eQTL in saccharomyces cerevisiae. BMC Systems Biology, 2016, 10, 8.	3.0	1
86	DHWP: Learning High-Quality Short Hash Codes Via Weight Pruning. , 2022, , .		1
87	On Design of Oligonucleotide SNP Arrays and Methods for Genotype Calling. , 2008, , .		0
88	Pathway Detection Based on Hierarchical LASSO Regression Model. , 2009, , .		0
89	Feature-Based Causal Structure Discovery in Protein and Gene Expression Data with Bayesian Network. , 2009, , .		0
90	A Robust Empirical Bayesian Method for Detecting Differentially Expressed Genes. , 2009, , .		0

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91	Prediction of Protein Functions from Protein-Protein Interaction Data Based on a New Measure of Network Betweenness. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
92	A hybridization model for tiling array analysis. , 2010, , .		0
93	Integrative Approaches for microRNA Target Prediction: Combining Sequence Information and the Paired mRNA and miRNA Expression Profiles. Current Bioinformatics, 2013, 8, 37-45.	1.5	0
94	Estimation of isoform expression using hierarchical Bayesian model by RNA-seq. , 2015, , .		0
95	International Workshop on Applications of Probability and Statistics to Biology, July 11â€â€13, 2019 â€"â€"In Honor of Professor Minping Qianâ€™s 80th Birthday. Quantitative Biology, 2020, 8, 177-186.	0.5	0
96	Direct interaction network inference for compositional data via codaloss. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050037.	0.8	0
97	Predicting kinase functional sites using hierarchical stochastic language modelling. Statistics and Its Interface, 2010, 3, 523-531.	0.3	0
98	An Interpretation of Convolutional Neural Networks for Motif Finding from the View of Probability. , 2021, , .		0