

Jianyang Zeng

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

2,862
citations

279798

23
h-index

276875

41
g-index

54
all docs

54
docs citations

54
times ranked

3333
citing authors

#	ARTICLE	IF	CITATIONS
1	A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. <i>Nature Communications</i> , 2017, 8, 573.	12.8	543
2	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drug-target interactions. <i>Bioinformatics</i> , 2019, 35, 104-111.	4.1	218
3	A deep learning framework for modeling structural features of RNA-binding protein targets. <i>Nucleic Acids Research</i> , 2016, 44, e32-e32.	14.5	213
4	Integrative Data Analysis of Multi-Platform Cancer Data with a Multimodal Deep Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 928-937.	3.0	204
5	Predicting drug-target interactions using restricted Boltzmann machines. <i>Bioinformatics</i> , 2013, 29, i126-i134.	4.1	172
6	DeepPicker: A deep learning approach for fully automated particle picking in cryo-EM. <i>Journal of Structural Biology</i> , 2016, 195, 325-336.	2.8	158
7	MONN: A Multi-objective Neural Network for Predicting Compound-Protein Interactions and Affinities. <i>Cell Systems</i> , 2020, 10, 308-322.e11.	6.2	132
8	An integrative drug repositioning framework discovered a potential therapeutic agent targeting COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 165.	17.1	89
9	A deep-learning framework for multi-level peptide-protein interaction prediction. <i>Nature Communications</i> , 2021, 12, 5465.	12.8	87
10	TITER: predicting translation initiation sites by deep learning. <i>Bioinformatics</i> , 2017, 33, i234-i242.	4.1	83
11	ACME: pan-specific peptide-MHC class I binding prediction through attention-based deep neural networks. <i>Bioinformatics</i> , 2019, 35, 4946-4954.	4.1	79
12	Inferential modeling of 3D chromatin structure. <i>Nucleic Acids Research</i> , 2015, 43, e54-e54.	14.5	77
13	Modeling gene regulatory networks using neural network architectures. <i>Nature Computational Science</i> , 2021, 1, 491-501.	8.0	59
14	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. <i>Cell Systems</i> , 2017, 5, 212-220.e6.	6.2	58
15	DeepCPI: A Deep Learning-based Framework for Large-scale in silico Drug Screening. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 478-495.	6.9	53
16	Reconstructing spatial organizations of chromosomes through manifold learning. <i>Nucleic Acids Research</i> , 2018, 46, e50-e50.	14.5	50
17	Integrating Hi-C and FISH data for modeling of the 3D organization of chromosomes. <i>Nature Communications</i> , 2019, 10, 2049.	12.8	45
18	DeepHINT: understanding HIV-1 integration via deep learning with attention. <i>Bioinformatics</i> , 2019, 35, 1660-1667.	4.1	41

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19	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	12.8	41
20	A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. <i>Nature Machine Intelligence</i> , 2020, 2, 347-355.	16.0	37
21	High-resolution protein structure determination starting with a global fold calculated from exact solutions to the RDC equations. <i>Journal of Biomolecular NMR</i> , 2009, 45, 265-281.	2.8	33
22	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	6.5	33
23	Understanding the phase separation characteristics of nucleocapsid protein provides a new therapeutic opportunity against SARS-CoV-2. <i>Protein and Cell</i> , 2021, 12, 734-740.	11.0	31
24	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. <i>Bioinformatics</i> , 2019, 35, i284-i294.	4.1	28
25	Modeling multi-species RNA modification through multi-task curriculum learning. <i>Nucleic Acids Research</i> , 2021, 49, 3719-3734.	14.5	23
26	Secure multiparty computation for privacy-preserving drug discovery. <i>Bioinformatics</i> , 2020, 36, 2872-2880.	4.1	21
27	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. <i>Nucleic Acids Research</i> , 2017, 45, e129-e129.	14.5	19
28	An efficient parallel algorithm for accelerating computational protein design. <i>Bioinformatics</i> , 2014, 30, i255-i263.	4.1	17
29	Protein side-chain resonance assignment and NOE assignment using RDC-defined backbones without TOCSY data. <i>Journal of Biomolecular NMR</i> , 2011, 50, 371-395.	2.8	13
30	A machine learning-based framework for modeling transcription elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	9
31	A HAUSDORFF-BASED NOE ASSIGNMENT ALGORITHM USING PROTEIN BACKBONE DETERMINED FROM RESIDUAL DIPOLAR COUPLINGS AND ROTAMER PATTERNS. , 2008, , .		8
32	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. <i>BMC Bioinformatics</i> , 2019, 20, 678.	2.6	6
33	A Bayesian Approach for Determining Protein Side-Chain Rotamer Conformations Using Unassigned NOE Data. <i>Journal of Computational Biology</i> , 2011, 18, 1661-1679.	1.6	5
34	Computational Protein Design Using AND/OR Branch-and-Bound Search. <i>Journal of Computational Biology</i> , 2016, 23, 439-451.	1.6	5
35	Characterizing RNA Pseudouridylation by Convolutional Neural Networks. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 815-833.	6.9	5
36	Parallel Computational Protein Design. <i>Methods in Molecular Biology</i> , 2017, 1529, 265-277.	0.9	4

#	ARTICLE	IF	CITATIONS
37	Elastic restricted Boltzmann machines for cancer data analysis. <i>Quantitative Biology</i> , 2017, 5, 159-172.	0.5	4
38	Full-length ribosome density prediction by a multi-input and multi-output model. <i>PLoS Computational Biology</i> , 2021, 17, e1008842.	3.2	4
39	A Hausdorff-based NOE assignment algorithm using protein backbone determined from residual dipolar couplings and rotamer patterns. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2008, 7, 169-81.	0.4	4
40	Hash: a program to accurately predict protein H δ shifts from neighboring backbone shifts. <i>Journal of Biomolecular NMR</i> , 2013, 55, 105-118.	2.8	3
41	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	2
42	MONN: A Multi-objective Neural Network for Predicting Pairwise Non-covalent Interactions and Binding Affinities Between Compounds and Proteins. <i>Lecture Notes in Computer Science</i> , 2020, , 259-260.	1.3	2
43	DRUG-TARGET INTERACTION PREDICTION BY INTEGRATING CHEMICAL, GENOMIC, FUNCTIONAL AND PHARMACOLOGICAL DATA. , 2013, , .		1