Jianyang Zeng

List of Publications by Year
in descending order

43 papers	2,862 citations	279487 23 h-index	276539 41 g-index
54 all docs	54 docs citations	54 times ranked	3333 citing authors

#	Article	IF	Citations
1	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	3.3	33
2	A machine learning-based framework for modeling transcription elongation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
3	Characterizing RNA Pseudouridylation by Convolutional Neural Networks. Genomics, Proteomics and Bioinformatics, 2021, 19, 815-833.	3.0	5
4	Modeling multi-species RNA modification through multi-task curriculum learning. Nucleic Acids Research, 2021, 49, 3719-3734.	6.5	23
5	Full-length ribosome density prediction by a multi-input and multi-output model. PLoS Computational Biology, 2021, 17, e1008842.	1.5	4
6	Understanding the phase separation characteristics of nucleocapsid protein provides a new therapeutic opportunity against SARS-CoV-2. Protein and Cell, 2021, 12, 734-740.	4.8	31
7	An integrative drug repositioning framework discovered a potential therapeutic agent targeting COVID-19. Signal Transduction and Targeted Therapy, 2021, 6, 165.	7.1	89
8	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	5.8	41
9	Modeling gene regulatory networks using neural network architectures. Nature Computational Science, 2021, 1, 491-501.	3.8	59
10	A deep-learning framework for multi-level peptideâ€“protein interaction prediction. Nature Communications, 2021, 12, 5465.	5.8	87
11	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. Briefings in Bioinformatics, 2021, 22, .	3.2	2
12	A novel machine learning framework for automated biomedical relation extraction from large-scale literature repositories. Nature Machine Intelligence, 2020, 2, 347-355.	8.3	37
13	Secure multiparty computation for privacy-preserving drug discovery. Bioinformatics, 2020, 36, 2872-2880.	1.8	21
14	MONN: A Multi-objective Neural Network for Predicting Compound-Protein Interactions and Affinities. Cell Systems, 2020, 10, 308-322.e11.	2.9	132
15	MONN: A Multi-objective Neural Network for Predicting Pairwise Non-covalent Interactions and Binding Affinities Between Compounds and Proteins. Lecture Notes in Computer Science, 2020, , 259-260.	1.0	2
16	NeoDTI: neural integration of neighbor information from a heterogeneous network for discovering new drugâ€“target interactions. Bioinformatics, 2019, 35, 104-111.	1.8	218
17	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. Bioinformatics, 2019, 35, i284-i294.	1.8	28
18	ACME: pan-specific peptideâ€“MHC class I binding prediction through attention-based deep neural networks. Bioinformatics, 2019, 35, 4946-4954.	1.8	79

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19	Integrating Hi-C and FISH data for modeling of the 3D organization of chromosomes. Nature Communications, 2019, 10, 2049.	5.8	45
20	DeepCPI: A Deep Learning-based Framework for Large-scale in silico Drug Screening. Genomics, Proteomics and Bioinformatics, 2019, 17, 478-495.	3.0	53
21	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. BMC Bioinformatics, 2019, 20, 678.	1.2	6
22	DeepHINT: understanding HIV-1 integration via deep learning with attention. Bioinformatics, 2019, 35, 1660-1667.	1.8	41
23	Reconstructing spatial organizations of chromosomes through manifold learning. Nucleic Acids Research, 2018, 46, e50-e50.	6.5	50
24	A deep boosting based approach for capturing the sequence binding preferences of RNA-binding proteins from high-throughput CLIP-seq data. Nucleic Acids Research, 2017, 45, e129-e129.	6.5	19
25	Parallel Computational Protein Design. Methods in Molecular Biology, 2017, 1529, 265-277.	0.4	4
26	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. Cell Systems, 2017, 5, 212-220.e6.	2.9	58
27	A network integration approach for drug-target interaction prediction and computational drug repositioning from heterogeneous information. Nature Communications, 2017, 8, 573.	5.8	543
28	TITER: predicting translation initiation sites by deep learning. Bioinformatics, 2017, 33, i234-i242.	1.8	83
29	Elastic restricted Boltzmann machines for cancer data analysis. Quantitative Biology, 2017, 5, 159-172.	0.3	4
30	Computational Protein Design Using AND/OR Branch-and-Bound Search. Journal of Computational Biology, 2016, 23, 439-451.	0.8	5
31	DeepPicker: A deep learning approach for fully automated particle picking in cryo-EM. Journal of Structural Biology, 2016, 195, 325-336.	1.3	158
32	A deep learning framework for modeling structural features of RNA-binding protein targets. Nucleic Acids Research, 2016, 44, e32-e32.	6.5	213
33	Integrative Data Analysis of Multi-Platform Cancer Data with a Multimodal Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 928-937.	1.9	204
34	Inferential modeling of 3D chromatin structure. Nucleic Acids Research, 2015, 43, e54-e54.	6.5	77
35	An efficient parallel algorithm for accelerating computational protein design. Bioinformatics, 2014, 30, i255-i263.	1.8	17
36	Hash: a program to accurately predict protein HÎ± shifts from neighboring backbone shifts. Journal of Biomolecular NMR, 2013, 55, 105-118.	1.6	3

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37	Predicting drug-target interactions using restricted Boltzmann machines. Bioinformatics, 2013, 29, i126-i134.	1.8	172
38	DRUG-TARGET INTERACTION PREDICTION BY INTEGRATING CHEMICAL, GENOMIC, FUNCTIONAL AND PHARMACOLOGICAL DATA. , 2013, , .		1
39	Protein side-chain resonance assignment and NOE assignment using RDC-defined backbones without TOCSY data. Journal of Biomolecular NMR, 2011, 50, 371-395.	1.6	13
40	A Bayesian Approach for Determining Protein Side-Chain Rotamer Conformations Using Unassigned NOE Data. Journal of Computational Biology, 2011, 18, 1661-1679.	0.8	5
41	High-resolution protein structure determination starting with a global fold calculated from exact solutions to the RDC equations. Journal of Biomolecular NMR, 2009, 45, 265-281.	1.6	33
42	A HAUSDORFF-BASED NOE ASSIGNMENT ALGORITHM USING PROTEIN BACKBONE DETERMINED FROM RESIDUAL DIPOLAR COUPLINGS AND ROTAMER PATTERNS. , 2008, , .		8
43	A Hausdorff-based NOE assignment algorithm using protein backbone determined from residual dipolar couplings and rotamer patterns. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2008, 7, 169-81.	0.4	4