

# Hailin Hu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5156853/publications.pdf>

Version: 2024-02-01

17  
papers

790  
citations

840776

11  
h-index

940533

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19  
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19  
docs citations

19  
times ranked

1209  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	TITER: predicting translation initiation sites by deep learning. <i>Bioinformatics</i> , 2017, 33, i234-i242.	4.1	83
3	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
4	Analysis of Ribosome Stalling and Translation Elongation Dynamics by Deep Learning. <i>Cell Systems</i> , 2017, 5, 212-220.e6.	6.2	58
5	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
6	Reconstructing spatial organizations of chromosomes through manifold learning. <i>Nucleic Acids Research</i> , 2018, 46, e50-e50.	14.5	50
7	Inhibitor Discovery for the Human GLUT1 from Homology Modeling and Virtual Screening. <i>ACS Chemical Biology</i> , 2016, 11, 1908-1916.	3.4	49
8	DeepHINT: understanding HIV-1 integration via deep learning with attention. <i>Bioinformatics</i> , 2019, 35, 1660-1667.	4.1	41
9	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	12.8	41
10	SNAC-tag for sequence-specific chemical protein cleavage. <i>Nature Methods</i> , 2019, 16, 319-322.	19.0	36
11	Secure multiparty computation for privacy-preserving drug discovery. <i>Bioinformatics</i> , 2020, 36, 2872-2880.	4.1	21
12	DATSING., 2020, , .		16
13	De novo designed transmembrane peptides activating the $\alpha 5 \beta 1$ integrin. <i>Protein Engineering, Design and Selection</i> , 2018, 31, 181-190.	2.1	14
14	Evaluation of work resumption strategies after COVID-19 reopening in the Chinese city of Shenzhen: a mathematical modeling study. <i>Public Health</i> , 2021, 193, 17-22.	2.9	12
15	Dense: An enhanced non-commutative representation for knowledge graph embedding with adaptive semantic hierarchy. <i>Neurocomputing</i> , 2022, 476, 115-125.	5.9	9
16	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. <i>BMC Bioinformatics</i> , 2019, 20, 678.	2.6	6
17	Riboexp: an interpretable reinforcement learning framework for ribosome density modeling. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	2